Color Atlas of Biochemistry
Second edition, revised and enlarged

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215 color plates by Juergen Wirth

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About the Authors

Jan Koolman (left) was born in Lübeck, Germany, and grew up with the sea wind blowing off the Baltic. The high school he attended in the Hanseatic city of Lübeck was one that focused on providing a classical education, which left its mark on him. From 1963 to 1969, he studied biochemistry at the University of Tübingen. He then took his doctorate (in the discipline of chemistry) at the University of Marburg, under the supervision of biochemist Peter Karlson. In Marburg, he began to study the biochemistry of insects and other invertebrates. He took his postdoctoral degree in 1977 in the field of human medicine, and was appointed Honorary Professor in 1984. His field of study today is biochemical endocrinology. His other interests include educational methods in biochemistry. He is currently Dean of Studies in the Department of Medicine in Marburg; he is married to an art teacher.

Klaus-Heinrich Rühm (right) comes from Stuttgart, Germany. After graduating from the School of Protestant Theology in Urach—another institution specializing in classical studies—and following a period working in the field of physics, he took a diploma in biochemistry at the University of Tübingen, where the two authors first met. Since 1970, he has also worked in the Department of Medicine at the University of Marburg. He took his doctorate under the supervision of Friedhelm Schneider, and his postdoctoral degree in 1980 was in the Department of Chemistry. He has been an Honorary Professor since 1986. His research group is concerned with the structure and function of enzymes involved in amino acid metabolism. He is married to a biologist and has two children. Jürgen Wirth (center) studied in Berlin and at the College of Design in Offenbach, Germany. His studies focused on free graphics and illustration, and his diploma topic was “The development and function of scientific illustration.” From 1963 to 1977, Jürgen Wirth was involved in designing the exhibition space in the Senckenberg Museum of Natural History in Frankfurt am Main, while at the same time working as a freelance associate with several publishing companies, providing illustrations for schoolbooks, non-fiction titles, and scientific publications. He has received several awards for book illustration and design. In 1978, he was appointed to a professorship at the College of Design in Schwäbisch Gmünd, Germany, and in 1986 he became Professor of Design at the Academy of Design in Darmstadt, Germany. His specialist fields include scientific graphics/information graphics and illustration methods. He is married and has three children.
Preface

Biochemistry is a dynamic, rapidly growing field, and the goal of this color atlas is to illustrate this fact visually. The precise boundaries between biochemistry and related fields, such as cell biology, anatomy, physiology, genetics, and pharmacology, are difficult to define and, in many cases, arbitrary. This overlap is not coincidental. The object being studied is often the same—a nerve cell or a mitochondrion, for example—and only the point of view differs.

For a considerable period of its history, biochemistry was strongly influenced by chemistry and concentrated on investigating metabolic conversions and energy transfers. Explaining the composition, structure, and metabolism of biologically important molecules has always been in the foreground. However, new aspects inherited from biochemistry’s other parent, the biological sciences, are now increasingly being added: the relationship between chemical structure and biological function, the pathways of information transfer, observance of the ways in which biomolecules are spatially and temporally distributed in cells and organisms, and an awareness of evolution as a biochemical process.

These new aspects of biochemistry are bound to become more and more important. Owing to space limitations, we have concentrated here on the biochemistry of humans and mammals, although the biochemistry of other animals, plants, and microorganisms is no less interesting. In selecting the material for this book, we have put the emphasis on subjects relevant to students of human medicine. The main purpose of the atlas is to serve as an overview and to provide visual information quickly and efficiently. Referring to textbooks can easily fill any gaps. For readers encountering biochemistry for the first time, some of the plates may look rather complex. It must be emphasized, therefore, that the atlas is not intended as a substitute for a comprehensive textbook of biochemistry. As the subject matter is often difficult to visualize, symbols, models, and other graphic elements had to be found that make complicated phenomena appear tangible. The graphics were designed conservatively, the aim being to avoid illustrations that might look too spectacular or exaggerated. Our goal was to achieve a visual and aesthetic way of representing scientific facts that would be simple and at the same time effective for teaching purposes. Use of graphics software helped to maintain consistency in the use of shapes, colors, dimensions, and labels, in particular. Formulae and other repetitive elements and structures could be handled easily and precisely with the assistance of the computer.

Color-coding has been used throughout to aid the reader, and the key to this is given in two special color plates on the front and rear inside covers. For example, in molecular models each of the more important atoms has a particular color: gray for carbon, white for hydrogen, blue for nitrogen, red for oxygen, and so on. The different classes of biomolecules are also distinguished by color: proteins are always shown in brown tones, carbohydrates in violet, lipids in yellow, DNA in blue, and RNA in green. In addition, specific symbols are used for the important coenzymes, such as ATP and NAD⁺. The compartments in which biochemical processes take place are color-coded as well. For example, the cytoplasm is shown in yellow, while the extracellular space is shaded in blue. Arrows indicating a chemical reaction are always black and those representing a transport process are gray.

In terms of the visual clarity of its presentation, biochemistry has still to catch up with anatomy and physiology. In this book, we sometimes use simplified ball-and-stick models instead of the classical chemical formulae. In addition, a number of compounds are represented by space-filling models. In these cases, we have tried to be as realistic as possible. The models of small molecules are based on conformations calculated by computer-based molecular modeling. In illustrating macromolecules, we used structural infor-
formation obtained by X-ray crystallography that is stored in the Protein Data Bank. In naming enzymes, we have followed the official nomenclature recommended by the IUBMB. For quick identification, EC numbers (in italics) are included with enzyme names. To help students assess the relevance of the material (while preparing for an examination, for example), we have included symbols on the text pages next to the section headings to indicate how important each topic is. A filled circle stands for “basic knowledge,” a half-filled circle indicates “standard knowledge,” and an empty circle stands for “in-depth knowledge.” Of course, this classification only reflects our subjective views. This second edition was carefully revised and a significant number of new plates were added to cover new developments.

We are grateful to many readers for their comments and valuable criticisms during the preparation of this book. Of course, we would also welcome further comments and suggestions from our readers.

August 2004

Jan Koolman,
Klaus-Heinrich Rohm
Marburg

Jürgen Wirth
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## Contents

<table>
<thead>
<tr>
<th>Section</th>
</tr>
</thead>
<tbody>
<tr>
<td>Introduction</td>
</tr>
<tr>
<td><strong>Basics</strong></td>
</tr>
<tr>
<td>Chemistry</td>
</tr>
<tr>
<td>Periodic table</td>
</tr>
<tr>
<td>Bonds</td>
</tr>
<tr>
<td>Molecular structure</td>
</tr>
<tr>
<td>Isomerism</td>
</tr>
<tr>
<td>Biomolecules I</td>
</tr>
<tr>
<td>Biomolecules II</td>
</tr>
<tr>
<td>Chemical reactions</td>
</tr>
<tr>
<td>Physical Chemistry</td>
</tr>
<tr>
<td>Energetics</td>
</tr>
<tr>
<td>Equilibria</td>
</tr>
<tr>
<td>Enthalpy and entropy</td>
</tr>
<tr>
<td>Reaction kinetics</td>
</tr>
<tr>
<td>Catalysis</td>
</tr>
<tr>
<td>Water as a solvent</td>
</tr>
<tr>
<td>Hydrophobic interactions</td>
</tr>
<tr>
<td>Acids and bases</td>
</tr>
<tr>
<td>Redox processes</td>
</tr>
<tr>
<td>Biomolecules</td>
</tr>
<tr>
<td>Carbohydrates</td>
</tr>
<tr>
<td>Overview</td>
</tr>
<tr>
<td>Chemistry of sugars</td>
</tr>
<tr>
<td>Mono saccharides and disaccharides</td>
</tr>
<tr>
<td>Poly saccharides: overview</td>
</tr>
<tr>
<td>Plant poly saccharides</td>
</tr>
<tr>
<td>Glycosaminoglycans and glycoproteins</td>
</tr>
<tr>
<td>Lipids</td>
</tr>
<tr>
<td>Overview</td>
</tr>
<tr>
<td>Fatty acids and fats</td>
</tr>
<tr>
<td>Phospholipids and glycolipids</td>
</tr>
<tr>
<td>Isoprenoids</td>
</tr>
<tr>
<td>Steroid structure</td>
</tr>
<tr>
<td>Steroids: overview</td>
</tr>
<tr>
<td>Amino Acids</td>
</tr>
<tr>
<td>Chemistry and properties</td>
</tr>
<tr>
<td>Non-proteinogenic amino acids</td>
</tr>
<tr>
<td>Peptides and Proteins</td>
</tr>
<tr>
<td>Overview</td>
</tr>
<tr>
<td>Peptide bonds</td>
</tr>
<tr>
<td>Secondary structures</td>
</tr>
<tr>
<td>Structural proteins</td>
</tr>
<tr>
<td>Globular proteins</td>
</tr>
<tr>
<td>Protein folding</td>
</tr>
<tr>
<td>Molecular models: insulin</td>
</tr>
<tr>
<td>Isolation and analysis of proteins</td>
</tr>
<tr>
<td>Nucleotides and Nucleic Acids</td>
</tr>
<tr>
<td>Bases and nucleotides</td>
</tr>
<tr>
<td>RNA</td>
</tr>
<tr>
<td>DNA</td>
</tr>
<tr>
<td>Molecular models: DNA and RNA</td>
</tr>
<tr>
<td>Metabolism</td>
</tr>
<tr>
<td>Enzymes</td>
</tr>
<tr>
<td>Basics</td>
</tr>
<tr>
<td>Enzyme catalysis</td>
</tr>
<tr>
<td>Enzyme kinetics I</td>
</tr>
<tr>
<td>Enzyme kinetics II</td>
</tr>
<tr>
<td>Inhibitors</td>
</tr>
<tr>
<td>Lactate dehydrogenase: structure</td>
</tr>
<tr>
<td>Lactate dehydrogenase: mechanism</td>
</tr>
<tr>
<td>Enzymatic analysis</td>
</tr>
<tr>
<td>Coenzymes 1</td>
</tr>
<tr>
<td>Coenzymes 2</td>
</tr>
<tr>
<td>Coenzymes 3</td>
</tr>
<tr>
<td>Activated metabolites</td>
</tr>
<tr>
<td>Metabolic Regulation</td>
</tr>
<tr>
<td>Intermediary metabolism</td>
</tr>
<tr>
<td>Regulatory mechanisms</td>
</tr>
<tr>
<td>Allosteric regulation</td>
</tr>
<tr>
<td>Transcription control</td>
</tr>
<tr>
<td>Hormonal control</td>
</tr>
<tr>
<td>Energy Metabolism</td>
</tr>
<tr>
<td>ATP</td>
</tr>
<tr>
<td>Energetic coupling</td>
</tr>
<tr>
<td>Energy conservation at membranes</td>
</tr>
<tr>
<td>Photosynthesis: light reactions</td>
</tr>
<tr>
<td>Photosynthesis: dark reactions</td>
</tr>
<tr>
<td>Molecular models: membrane proteins</td>
</tr>
<tr>
<td>Oxo acid dehydrogenases</td>
</tr>
<tr>
<td>Tricarboxylic acid cycle: reactions</td>
</tr>
<tr>
<td>Tricarboxylic acid cycle: functions</td>
</tr>
<tr>
<td>Respiratory chain</td>
</tr>
<tr>
<td>ATP synthesis</td>
</tr>
<tr>
<td>Regulation</td>
</tr>
<tr>
<td>Respiration and fermentation</td>
</tr>
<tr>
<td>Fermentations</td>
</tr>
<tr>
<td>Carbohydrate Metabolism</td>
</tr>
<tr>
<td>---------------------------------</td>
</tr>
<tr>
<td>Glycolysis</td>
</tr>
<tr>
<td>Pentose phosphate pathway</td>
</tr>
<tr>
<td>Gluconeogenesis</td>
</tr>
<tr>
<td>Glycogen metabolism</td>
</tr>
<tr>
<td>Regulation</td>
</tr>
<tr>
<td>Diabetes mellitus</td>
</tr>
<tr>
<td>Lipid Metabolism</td>
</tr>
<tr>
<td>Overview</td>
</tr>
<tr>
<td>Fatty acid degradation</td>
</tr>
<tr>
<td>Minor pathways of fatty acid</td>
</tr>
<tr>
<td>degradation</td>
</tr>
<tr>
<td>Fatty acid synthesis</td>
</tr>
<tr>
<td>Biosynthesis of complex lipids</td>
</tr>
<tr>
<td>Biosynthesis of cholesterol</td>
</tr>
<tr>
<td>Protein Metabolism</td>
</tr>
<tr>
<td>Protein metabolism: overview</td>
</tr>
<tr>
<td>Proteolysis</td>
</tr>
<tr>
<td>Transamination and deamination</td>
</tr>
<tr>
<td>Amino acid degradation</td>
</tr>
<tr>
<td>Urea cycle</td>
</tr>
<tr>
<td>Amino acid biosynthesis</td>
</tr>
<tr>
<td>Nucleotide Metabolism</td>
</tr>
<tr>
<td>Nucleotide degradation</td>
</tr>
<tr>
<td>Purine and pyrimidine biosynthesis</td>
</tr>
<tr>
<td>Nucleotide biosynthesis</td>
</tr>
<tr>
<td>Porphyrin Metabolism</td>
</tr>
<tr>
<td>Heme biosynthesis</td>
</tr>
<tr>
<td>Heme degradation</td>
</tr>
<tr>
<td>Organelles</td>
</tr>
<tr>
<td>Basics</td>
</tr>
<tr>
<td>Structure of cells</td>
</tr>
<tr>
<td>Centrifugation</td>
</tr>
<tr>
<td>Cell components and cytoplasm</td>
</tr>
<tr>
<td>Cytoskeleton</td>
</tr>
<tr>
<td>Components</td>
</tr>
<tr>
<td>Structure and functions</td>
</tr>
<tr>
<td>Nucleus</td>
</tr>
<tr>
<td>Mitochondria</td>
</tr>
<tr>
<td>Structure and functions</td>
</tr>
<tr>
<td>Transport systems</td>
</tr>
<tr>
<td>Biological Membranes</td>
</tr>
<tr>
<td>Structure and components</td>
</tr>
<tr>
<td>Functions and composition</td>
</tr>
<tr>
<td>Transport processes</td>
</tr>
<tr>
<td>Transport proteins</td>
</tr>
<tr>
<td>Ion channels</td>
</tr>
<tr>
<td>Membrane receptors</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Endoplasmic Reticulum and Golgi Apparatus</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>ER: structure and function</td>
<td>226</td>
</tr>
<tr>
<td>Protein sorting</td>
<td>228</td>
</tr>
<tr>
<td>Protein synthesis and maturation</td>
<td>230</td>
</tr>
<tr>
<td>Protein maturation</td>
<td>232</td>
</tr>
<tr>
<td>Lysosomes</td>
<td>234</td>
</tr>
<tr>
<td>Molecular Genetics</td>
<td></td>
</tr>
<tr>
<td>Overview</td>
<td>236</td>
</tr>
<tr>
<td>Genome</td>
<td>238</td>
</tr>
<tr>
<td>Replication</td>
<td>240</td>
</tr>
<tr>
<td>Transcription</td>
<td>242</td>
</tr>
<tr>
<td>Transcriptional control</td>
<td>244</td>
</tr>
<tr>
<td>RNA maturation</td>
<td>246</td>
</tr>
<tr>
<td>Amino acid activation</td>
<td>248</td>
</tr>
<tr>
<td>Translation I: initiation</td>
<td>250</td>
</tr>
<tr>
<td>Translation II: elongation and termination</td>
<td>252</td>
</tr>
<tr>
<td>Antibiotics</td>
<td>254</td>
</tr>
<tr>
<td>Mutation and repair</td>
<td>256</td>
</tr>
<tr>
<td>Genetic engineering</td>
<td></td>
</tr>
<tr>
<td>DNA cloning</td>
<td>258</td>
</tr>
<tr>
<td>DNA sequencing</td>
<td>260</td>
</tr>
<tr>
<td>PCR and protein expression</td>
<td>262</td>
</tr>
<tr>
<td>Genetic engineering in medicine</td>
<td>264</td>
</tr>
<tr>
<td>Tissues and organs</td>
<td></td>
</tr>
<tr>
<td>Digestion</td>
<td></td>
</tr>
<tr>
<td>Overview</td>
<td>266</td>
</tr>
<tr>
<td>Digestive secretions</td>
<td>268</td>
</tr>
<tr>
<td>Digestive processes</td>
<td>270</td>
</tr>
<tr>
<td>Resorption</td>
<td>272</td>
</tr>
<tr>
<td>Blood</td>
<td></td>
</tr>
<tr>
<td>Composition and functions</td>
<td>274</td>
</tr>
<tr>
<td>Plasma proteins</td>
<td>276</td>
</tr>
<tr>
<td>Lipoproteins</td>
<td>278</td>
</tr>
<tr>
<td>Hemoglobin</td>
<td>280</td>
</tr>
<tr>
<td>Gas transport</td>
<td>282</td>
</tr>
<tr>
<td>Erythrocyte metabolism</td>
<td>284</td>
</tr>
<tr>
<td>Iron metabolism</td>
<td>286</td>
</tr>
<tr>
<td>Acid–base balance</td>
<td>288</td>
</tr>
<tr>
<td>Blood clotting</td>
<td>290</td>
</tr>
<tr>
<td>Fibrinolysis, blood groups</td>
<td>292</td>
</tr>
<tr>
<td>Immune system</td>
<td></td>
</tr>
<tr>
<td>Immune response</td>
<td>294</td>
</tr>
<tr>
<td>T-cell activation</td>
<td>296</td>
</tr>
<tr>
<td>Complement system</td>
<td>298</td>
</tr>
<tr>
<td>Antibodies</td>
<td>300</td>
</tr>
<tr>
<td>Antibody biosynthesis</td>
<td>302</td>
</tr>
<tr>
<td>Monoclonal antibodies, immunoassay</td>
<td>304</td>
</tr>
<tr>
<td>Topic</td>
<td>Page</td>
</tr>
<tr>
<td>-------------------------------</td>
<td>------</td>
</tr>
<tr>
<td>Liver</td>
<td>306</td>
</tr>
<tr>
<td>Buffer function in organ metabolism</td>
<td>308</td>
</tr>
<tr>
<td>Carbohydrate metabolism</td>
<td>310</td>
</tr>
<tr>
<td>Lipid metabolism</td>
<td>312</td>
</tr>
<tr>
<td>Bile acids</td>
<td>314</td>
</tr>
<tr>
<td>Biotransformations</td>
<td>316</td>
</tr>
<tr>
<td>Cytochrome P450 systems</td>
<td>318</td>
</tr>
<tr>
<td>Ethanol metabolism</td>
<td>320</td>
</tr>
<tr>
<td>Kidney</td>
<td>322</td>
</tr>
<tr>
<td>Functions</td>
<td>324</td>
</tr>
<tr>
<td>Urine</td>
<td>326</td>
</tr>
<tr>
<td>Functions in the acid–base balance</td>
<td>326</td>
</tr>
<tr>
<td>Electrolyte and water recycling</td>
<td>328</td>
</tr>
<tr>
<td>Renal hormones</td>
<td>330</td>
</tr>
<tr>
<td>Muscle</td>
<td>332</td>
</tr>
<tr>
<td>Muscle contraction</td>
<td>334</td>
</tr>
<tr>
<td>Control of muscle contraction</td>
<td>334</td>
</tr>
<tr>
<td>Muscle metabolism I</td>
<td>336</td>
</tr>
<tr>
<td>Muscle metabolism II</td>
<td>338</td>
</tr>
<tr>
<td>Connective tissue</td>
<td>340</td>
</tr>
<tr>
<td>Bone and teeth</td>
<td>342</td>
</tr>
<tr>
<td>Calcium metabolism</td>
<td>344</td>
</tr>
<tr>
<td>Collagens</td>
<td>346</td>
</tr>
<tr>
<td>Extracellular matrix</td>
<td>346</td>
</tr>
<tr>
<td>Brain and Sensory Organs</td>
<td>348</td>
</tr>
<tr>
<td>Signal transmission in the CNS</td>
<td>350</td>
</tr>
<tr>
<td>Resting potential and action potential</td>
<td>352</td>
</tr>
<tr>
<td>Neurotransmitters</td>
<td>354</td>
</tr>
<tr>
<td>Receptors for neurotransmitters</td>
<td>356</td>
</tr>
<tr>
<td>Metabolism</td>
<td>356</td>
</tr>
<tr>
<td>Sight</td>
<td>338</td>
</tr>
<tr>
<td>Nutrition</td>
<td>360</td>
</tr>
<tr>
<td>Nutrients</td>
<td>362</td>
</tr>
<tr>
<td>Organic substances</td>
<td>364</td>
</tr>
<tr>
<td>Minerals and trace elements</td>
<td>366</td>
</tr>
<tr>
<td>Vitamins</td>
<td>368</td>
</tr>
<tr>
<td>Lipid-soluble vitamins</td>
<td>370</td>
</tr>
<tr>
<td>Water-soluble vitamins I</td>
<td>372</td>
</tr>
<tr>
<td>Water-soluble vitamins II</td>
<td>374</td>
</tr>
<tr>
<td>Hormones</td>
<td>376</td>
</tr>
<tr>
<td>Hormonal system</td>
<td>378</td>
</tr>
<tr>
<td>Basics</td>
<td>380</td>
</tr>
<tr>
<td>Plasma levels and hormone hierarchy</td>
<td>382</td>
</tr>
<tr>
<td>Lipophilic hormones</td>
<td>384</td>
</tr>
<tr>
<td>Metabolism of action</td>
<td>386</td>
</tr>
<tr>
<td>Hydrophilic hormones</td>
<td>388</td>
</tr>
<tr>
<td>Metabolism of peptide hormones</td>
<td>390</td>
</tr>
<tr>
<td>Mechanisms of action</td>
<td>392</td>
</tr>
<tr>
<td>Second messengers</td>
<td>394</td>
</tr>
<tr>
<td>Signal cascades</td>
<td>396</td>
</tr>
<tr>
<td>Other signaling substances</td>
<td>398</td>
</tr>
<tr>
<td>Eicosanoids</td>
<td>400</td>
</tr>
<tr>
<td>Cytokines</td>
<td>402</td>
</tr>
<tr>
<td>Growth and development</td>
<td>404</td>
</tr>
<tr>
<td>Cell proliferation</td>
<td>406</td>
</tr>
<tr>
<td>Cell cycle</td>
<td>407</td>
</tr>
<tr>
<td>Apoptosis</td>
<td>408</td>
</tr>
<tr>
<td>Oncogenes</td>
<td>409</td>
</tr>
<tr>
<td>Tumors</td>
<td>410</td>
</tr>
<tr>
<td>Cytostatic drugs</td>
<td>411</td>
</tr>
<tr>
<td>Viruses</td>
<td>412</td>
</tr>
<tr>
<td>Metabolic charts</td>
<td>413</td>
</tr>
<tr>
<td>Calvin cycle</td>
<td>414</td>
</tr>
<tr>
<td>Carbohydrate metabolism</td>
<td>415</td>
</tr>
<tr>
<td>Biosynthesis of fats and membrane liquids</td>
<td>416</td>
</tr>
<tr>
<td>Biosynthesis of ketone bodies and steroids</td>
<td>417</td>
</tr>
<tr>
<td>Degradation of fats and phospholipids</td>
<td>418</td>
</tr>
<tr>
<td>Biosynthesis of the essential amino acids</td>
<td>419</td>
</tr>
<tr>
<td>Biosynthesis of the non-essential amino acids</td>
<td>420</td>
</tr>
<tr>
<td>Amino acid degradation I</td>
<td>421</td>
</tr>
<tr>
<td>Amino acid degradation II</td>
<td>422</td>
</tr>
<tr>
<td>Ammonia metabolism</td>
<td>423</td>
</tr>
<tr>
<td>Biosynthesis of purine nucleotides</td>
<td>424</td>
</tr>
<tr>
<td>Biosynthesis of the pyrimidine nucleotides and C, metabolism</td>
<td>425</td>
</tr>
<tr>
<td>Nucleotide degradation</td>
<td>426</td>
</tr>
<tr>
<td>Annotated enzyme list</td>
<td>427</td>
</tr>
<tr>
<td>Abbreviations</td>
<td>428</td>
</tr>
<tr>
<td>Quantities and units</td>
<td>429</td>
</tr>
<tr>
<td>Further reading</td>
<td>430</td>
</tr>
<tr>
<td>Source credits</td>
<td>431</td>
</tr>
<tr>
<td>Index</td>
<td>432</td>
</tr>
</tbody>
</table>

Key to color-coding:
see front and rear inside covers

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Introduction

This paperback atlas is intended for students of medicine and the biological sciences. It provides an introduction to biochemistry, but with its modular structure it can also be used as a reference book for more detailed information. The 216 color plates provide knowledge in the field of biochemistry, accompanied by detailed information in the text on the facing page. The degree of difficulty of the subject-matter is indicated by symbols in the text:

● stands for “basic biochemical knowledge”
● indicates “standard biochemical knowledge”
○ means “specialist biochemical knowledge.”

Some general rules used in the structure of the illustrations are summed up in two explanatory plates inside the front and back covers. Keywords, definitions, explanations of unfamiliar concepts and chemical formulas can be found using the index. The book starts with a few basics in biochemistry (pp. 2–33). There is a brief explanation of the concepts and principles of chemistry (pp. 2–15). These include the periodic table of the elements, chemical bonds, the general rules governing molecular structure, and the structures of important classes of compounds. Several basic concepts of physical chemistry are also essential for an understanding of biochemical processes. Pages 16–33 therefore discuss the various forms of energy and their interconversion, reaction kinetics and catalysis, the properties of water, acids and bases, and redox processes.

These basic concepts are followed by a section on the structure of the important biomolecules (pp. 34–87). This part of the book is arranged according to the different classes of metabolites. It discusses carbohydrates, lipids, amino acids, peptides and proteins, nucleotides, and nucleic acids.

The next part presents the reactions involved in the interconversion of these compounds—the part of biochemistry that is commonly referred to as metabolism (pp. 88–195). The section starts with a discussion of the enzymes and coenzymes, and discusses the mechanisms of metabolic regulation and the so-called energy metabolism. After this, the central metabolic pathways are presented, once again arranged according to the class of metabolite (pp. 150–195).

The second half of the book begins with a discussion of the functional compartments within the cell, the cellular organelles (pp. 196–235). This is followed on pp. 236–265 by the current field of molecular genetics (molecular biology). A further extensive section is devoted to the biochemistry of individual tissues and organs (pp. 266–359). Here, it has only been possible to focus on the most important organs and organ systems—the digestive system, blood, liver, kidneys, muscles, connective and supportive tissues, and the brain.

Other topics include the biochemistry of nutrition (pp. 360–369), the structure and function of important hormones (pp. 370–393), and growth and development (pp. 394–405).

The paperback atlas concludes with a series of schematic metabolic “charts” (pp. 407–419). These plates, which are not accompanied by explanatory text apart from a brief introduction on p. 406, show simplified versions of the most important synthetic and degradative pathways. The charts are mainly intended for reference, but they can also be used to review previously learned material. The enzymes catalyzing the various reactions are only indicated by their EC numbers. Their names can be found in the systematically arranged and annotated enzyme list (pp. 420–430).
Periodic table

A. Biologically important elements

There are 81 stable elements in nature. Fifteen of these are present in all living things, and a further 8–10 are only found in particular organisms. The illustration shows the first half of the periodic table, containing all of the biologically important elements. In addition to physical and chemical data, it also provides information about the distribution of the elements in the living world and their abundance in the human body. The laws of atomic structure underlying the periodic table are discussed in chemistry textbooks.

More than 99% of the atoms in animals’ bodies are accounted for by just four elements—hydrogen (H), oxygen (O), carbon (C) and nitrogen (N). Hydrogen and oxygen are the constituents of water, which alone makes up 60–70% of cell mass (see p. 196). Together with carbon and nitrogen, hydrogen and oxygen are also the major constituents of the organic compounds on which most living processes depend. Many biomolecules also contain sulfur (S) or phosphorus (P). The above macroelements are essential for all organisms.

A second biologically important group of elements, which together represent only about 0.5% of the body mass, are present almost exclusively in the form of inorganic ions. This group includes the alkali metals sodium (Na) and potassium (K), and the alkaline earth metals magnesium (Mg) and calcium (Ca). The halogen chlorine (Cl) is also almost ionized in the cell. All other elements important for life are present in such small quantities that they are referred to as trace elements. These include transition metals such as iron (Fe), zinc (Zn), copper (Cu), cobalt (Co) and manganese (Mn). A few nonmetals, such as iodine (I) and selenium (Se), can also be classed as essential trace elements.

B. Electron configurations: examples

The chemical properties of atoms and the types of bond they form with each other are determined by their electron shells. The electron configurations of the elements are therefore also shown in Fig. A. Fig. B explains the symbols and abbreviations used. More detailed discussions of the subject are available in chemistry textbooks.

The possible states of electrons are called orbitals. These are indicated by what is known as the principal quantum number and by a letter—s, p, or d. The orbitals are filled one by one as the number of electrons increases. Each orbital can hold a maximum of two electrons, which must have oppositely directed “spins.” Fig. A shows the distribution of the electrons among the orbitals for each of the elements. For example, the six electrons of carbon (B1) occupy the 1s orbital, the 2s orbital, and two 2p orbitals. A filled 1s orbital has the same electron configuration as the noble gas helium (He). This region of the electron shell of carbon is therefore abbreviated as “He” in Fig. A. Below this, the numbers of electrons in each of the other filled orbitals (2s and 2p in the case of carbon) are shown on the right margin. For example, the electron shell of chlorine (B2) consists of that of neon (Ne) and seven additional electrons in 3s and 3p orbitals. In iron (B3), a transition metal of the first series, electrons occupy the 4s orbital even though the 3d orbitals are still partly empty. Many reactions of the transition metals involve empty d orbitals—e.g., redox reactions or the formation of complexes with bases.

Particularly stable electron arrangements arise when the outermost shell is fully occupied with eight electrons (the “octet rule”). This applies, for example, to the noble gases, as well as to ions such as Cl\(^+\) (3s\(^2\)3p\(^6\)) and Na\(^+\) (2s\(^2\)2p\(^6\)). It is only in the cases of hydrogen and helium that two electrons are already sufficient to fill the outermost 1s orbital.
Bonds

A. Orbital hybridization and chemical bonding

Stable, covalent bonds between nonmetal atoms are produced when orbitals (see p. 2) of the two atoms form molecular orbitals that are occupied by one electron from each of the atoms. Thus, the four bonding electrons of the carbon atom occupy 2s and 2p atomic orbitals (1a). The 2s orbital is spherical in shape, while the three 2p orbitals are shaped like dumbbells arranged along the x, y, and z axes. It might therefore be assumed that carbon atoms should form at least two different types of molecular orbital. However, this is not normally the case. The reason is an effect known as orbital hybridization. Combination of the s orbital and the three p orbitals of carbon gives rise to four equivalent, tetrahedrally arranged sp³ atomic orbitals (sp³ hybridization). When these overlap with the 1s orbitals of H atoms, four equivalent σ-molecular orbitals (1b) are formed. For this reason, carbon is capable of forming four bonds—i.e., it has a valency of four. Single bonds between nonmetal atoms arise in the same way as the four σ or single bonds in methane (CH₄). For example, the hydrogen phosphate ion (HPO₄²⁻) and the ammonium ion (NH₄⁺) are also tetrahedral in structure (1c).

A second common type of orbital hybridization involves the 2s orbital and only two of the three 2p orbitals (2a). This process is therefore referred to as sp² hybridization. The result is three equivalent sp² hybrid orbitals lying in one plane at an angle of 120° to one another. The remaining 2p orbital is oriented perpendicular to this plane. In contrast to their sp³ counterparts, sp²-hybridized atoms form two different types of bond when they combine into molecular orbitals (2b). The three sp² orbitals enter into σ bonds, as described above. In addition, the electrons in the two 2p, orbitals, known as π electrons, combine to give an additional, elongated π molecular orbital, which is located above and below the plane of the σ bonds. Bonds of this type are called double bonds. They consist of a σ bond and a π bond, and arise only when both of the atoms involved are capable of sp² hybridization. In contrast to single bonds, double bonds are not freely rotatable, since rotation would distort the π-molecular orbital. This is why all of the atoms lie in one plane (2c); in addition, cis–trans isomerism arises in such cases (see p. 8). Double bonds that are common in biomolecules are C=C and C=O. C=N double bonds are found in amines (Schiff bases; see p. 178).

B. Resonance

Many molecules that have several double bonds are much less reactive than might be expected. The reason for this is that the double bonds in these structures cannot be localized unequivocally. Their π orbitals are not confined to the space between the double-bonded atoms, but form a shared, extended π-molecular orbital. Structures with this property are referred to as resonance hybrids, because it is impossible to describe their actual bonding structure using standard formulas. One can either use what are known as resonance structures—i.e., idealized configurations in which π electrons are assigned to specific atoms (cf. pp. 32 and 66, for example)—or one can use dashed lines as in Fig. B to suggest the extent of the delocalized orbitals. (Details are discussed in chemistry textbooks.)

Resonance-stabilized systems include carboxylate groups, as in formate; allylic hydrocarbons with conjugated double bonds, such as 1,3-butadiene; and the systems known as aromatic ring systems. The best-known aromatic compound is benzene, which has six delocalized π electrons in its ring. Extended resonance systems with 10 or more π electrons absorb light within the visible spectrum and are therefore colored. This group includes the aliphatic carotenoids (see p. 132), for example, as well as the heme group, in which 18 π electrons occupy an extended molecular orbital (see p. 106).
A. Orbital hybridization and chemical bonding

1a

$sp^3$ Hybridization

4 Equivalent $sp^3$ atomic orbitals (tetrahedral)

1b

$1s$ Orbital of hydrogen atom

$sp^3$ Atomic orbitals of carbon atom

$4$ Bonding $\sigma$-molecular orbitals

1c

Methane

Hydrogen phosphate

Ammonium ion

$H\equiv H$

$H\equiv H$

$H\equiv H$

$H\equiv H$

$O\equiv O$

$O\equiv O$

$H\equiv H$

$H\equiv H$

$H\equiv H$

$H\equiv H$

B. Resonance

<table>
<thead>
<tr>
<th></th>
<th>Formate</th>
<th>1,3-Butadiene</th>
<th>Benzene</th>
</tr>
</thead>
<tbody>
<tr>
<td>s Molecular orbitals</td>
<td><img src="image" alt="Formate" /></td>
<td><img src="image" alt="1,3-Butadiene" /></td>
<td><img src="image" alt="Benzene" /></td>
</tr>
<tr>
<td>Formula</td>
<td>$H-C\equiv O$</td>
<td>$H-C\equiv C\equiv C$</td>
<td>$H-C\equiv C\equiv C\equiv C$</td>
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</tbody>
</table>
Molecular structure

The physical and chemical behavior of molecules is largely determined by their constitution (the type and number of the atoms they contain and their bonding). Structural formulas can therefore be used to predict not only the chemical reactivity of a molecule, but also its size and shape, and to some extent its conformation (the spatial arrangement of the atoms). Some data providing the basis for such predictions are summarized here and on the facing page. In addition, L-dihydroxyphenylalanine (L-tyrosine; see p. 352), is used as an example to show the way in which molecules are illustrated in this book.

A. Molecule illustrations

In traditional two-dimensional structural formulas (A1), atoms are represented as letter symbols and electron pairs are shown as lines. Lines between two atomic symbols symbolize two bonding electrons (see p. 4), and all of the other lines represent free electron pairs, such as those that occur in O and N atoms. Free electrons are usually not represented explicitly (and this is the convention used in this book as well). Dashed or continuous circles or arcs are used to emphasize delocalized electrons.

Ball-and-stick models (A2) are used to illustrate the spatial structure of molecules. Atoms are represented as colored balls (for the color coding, see the inside front cover) and bonds (including multiple bonds) as gray cylinders. Although the relative bond lengths and angles correspond to actual conditions, the size at which the atoms are represented is too small to make the model more comprehensible.

Space-filling van der Waals models (A3) are useful for illustrating the actual shape and size of molecules. These models represent atoms as truncated balls. Their effective extent is determined by what is known as the van der Waals radius. This is calculated from the energetically most favorable distance between atoms that are not chemically bonded to one another.

B. Bond lengths and angles

Atomic radii and distances are now usually expressed in picometers (pm; 1 pm = \(10^{-12}\) m). The old angstrom unit (Å, \(\AA = 10^{-10}\) pm) is now obsolete. The length of single bonds approximately corresponds to the sum of what are known as the covalent radii of the atoms involved (see inside front cover). Double bonds are around 10–20% shorter than single bonds. In sp\(^2\)-hybridized atoms, the angle between the individual bonds is approx. 110°; in sp\(^3\)-hybridized atoms it is approx. 120°.

C. Bond polarity

Depending on the position of the element in the periodic table (see p. 2), atoms have different electronegativity—i.e., a different tendency to take up extra electrons. The values given in \(r_2\) are on a scale between 2 and 4. The higher the value, the more electronegative the atom. When two atoms with very different electronegativities are bound to one another, the bonding electrons are drawn toward the more electronegative atom, and the bond is polarized. The atoms involved then carry positive or negative partial charges. In Cl, the van der Waals surface is colored according to the different charge conditions (red = negative, blue = positive). Oxygen is the most strongly electronegative of the biochemically important elements, with C–O double bonds being especially highly polar.

D. Hydrogen bonds

The hydrogen bond, a special type of noncovalent bond, is extremely important in biochemistry. In this type of bond, hydrogen atoms of OH, NH, or SH groups (known as hydrogen bond donors) interact with free electrons of acceptor atoms (for example, O, N, or S). The bonding energies of hydrogen bonds (10–40 kJ mol\(^{-1}\)) are much lower than those of covalent bonds (approx. 400 kJ mol\(^{-1}\)). However, as hydrogen bonds can be very numerous in proteins and DNA, they play a key role in the stabilization of these molecules (see pp. 68, 84). The importance of hydrogen bonds for the properties of water is discussed on p. 26.
A. Molecule illustrations

1. Formula illustration

2. Ball-and-stick model

3. Van der Waals model

B. Bond lengths and angles

C. Bond polarity

1. Partial charges in L-dopa

2. Electronegativities

D. Hydrogen bonds

<table>
<thead>
<tr>
<th>Acid</th>
<th>Base</th>
<th>Initial state</th>
<th>Hydrogen bond</th>
<th>Complete reaction</th>
</tr>
</thead>
<tbody>
<tr>
<td>A—H</td>
<td>B—H</td>
<td>Hydrogen bond</td>
<td>Complete reaction</td>
<td></td>
</tr>
</tbody>
</table>

1. Principle

2. Examples

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Isomerism

Isomers are molecules with the same composition (i.e. the same molecular formula), but with different chemical and physical properties. If isomers differ in the way in which their atoms are bonded in the molecule, they are described as structural isomers (cf. citric acid and isocitric acid, D). Other forms of isomerism are based on different arrangements of the substituents of bonds (A, B) or on the presence of chiral centers in the molecule (C).

A. cis–trans isomers

Double bonds are not freely rotatable (see p. 4). If double-bonded atoms have different substituents, there are two possible orientations for these groups. In fumaric acid, an intermediate of the tricarboxylic acid cycle (see p. 136), the carboxy groups lie on different sides of the double bond (trans or E position). In its isomer maleic acid, which is not produced in metabolic processes, the carboxy groups lie on the same side of the bond (cis or Z position). cis–trans isomers (geometric isomers) have different chemical and physical properties—e.g., their melting points (Tm) and pK values. They can only be interconverted by chemical reactions.

In lipid metabolism, cis–trans isomerism is particularly important. For example, double bonds in natural fatty acids (see p. 48) usually have a cis configuration. By contrast, unsaturated intermediates of β oxidation have a trans configuration. This makes the breakdown of unsaturated fatty acids more complicated (see p. 166). Light-induced cis–trans isomerization of retinal is of central importance in the visual cycle (see p. 358).

B. Conformation

Molecular forms that arise as a result of rotation around freely rotatable bonds are known as conformers. Even small molecules can have different conformations in solution. In the two conformations of succinic acid illustrated opposite, the atoms are arranged in a similar way to fumaric acid and maleic acid. Both forms are possible, although conformation 1 is more favorable due to the greater distance between the COOH groups and therefore occurs more frequently. Biologically active macromolecules such as proteins or nucleic acids usually have well-defined (“native”) conformations, which are stabilized by interactions in the molecule (see p. 74).

C. Optical isomers

Another type of isomerism arises when a molecule contains a chiral center or is chiral as a whole. Chirality (from the Greek cheir, hand) leads to the appearance of structures that behave like image and mirror-image and that cannot be superimposed (“mirror” isomers). The most frequent cause of chiral behavior is the presence of an asymmetric C atom—i.e., an atom with four different substituents. Then there are two forms (enantiomers) with different configurations. Usually, the two enantiomers of a molecule are designated as L and D forms. Clear classification of the configuration is made possible by the R/S system (see chemistry textbooks).

Enantiomers have very similar chemical properties, but they rotate polarized light in opposite directions (optical activity, see pp. 36, 58). The same applies to the enantiomers of lactic acid. The dextrorotatory L-lactic acid occurs in animal muscle and blood, while the D form produced by microorganisms is found in milk products, for example (see p. 148). The Fischer projection is often used to represent the formulas for chiral centers (cf. p. 58).

D. The aconitase reaction

Enzymes usually function stereospecifically. In chiral substrates, they only accept one of the enantiomers, and the reaction products are usually also sterically uniform. Aconitase hydratase (aconitase) catalyzes the conversion of citric acid into the constitution isomer isocitric acid (see p. 136). Although citric acid is not chiral, aconitase only forms one of the four possible isomeric forms of isocitric acid (2R,3S-isocitric acid). The intermediate of the reaction, the unsaturated tricarboxylic acid aconitate, only occurs in the cis form in the reaction. The trans form of aconitate is found as a constituent of certain plants.
A. cis–trans isomers

Fumaric acid
Fp. 287 °C
pK_a 3.0, 4.5
Maleic acid
Fp. 130 °C
pK_a 1.9, 6.5

B. Conformers

Succinic acid
Conformation 1
Freely rotatable
Succinic acid
Conformation 2
Not rotatable

C. Optical isomers

\( \text{L(S)} \)
\( \text{D(R)} \)
Fischer projections

D. The aconitase reaction

Citrate (prochiral) → cis-Aconitate (intermediate product) → (2R,3S)-Isocitrate

trans-Aconitate occurs in plants

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Biomolecules I

A. Important classes of compounds

Most biomolecules are derivatives of simple compounds of the non-metals oxygen (O), hydrogen (H), nitrogen (N), sulfur (S), and phosphorus (P). The biochemically important oxygen, nitrogen, and sulfur compounds can be formally derived from their compounds with hydrogen (i.e., H₂O, NH₃, and H₂S). In biological systems, phosphorus is found almost exclusively in derivatives of phosphoric acid, H₃PO₄.

If one or more of the hydrogen atoms of a non-metal hydride are replaced formally with another group, R—e.g., alkyl residues—then derived compounds of the type R-XHᵢ₋₁, R-XHᵢ₋₂-R, etc., are obtained. In this way, alcohols (R-OH) and ethers (R-O-R) are derived from water (H₂O); primary amines (R-NH₂), secondary amines (R-NH-R) and tertiary amines (R-N-R'R'R'″) amines are obtained from ammonia (NH₃); and thiols (R-SH) and thioethers (R-S-R') arise from hydrogen sulfide (H₂S). Polar groups such as -OH and -NH₂ are found as substituents in many organic compounds. As such groups are much more reactive than the hydrocarbon structures to which they are attached, they are referred to as functional groups.

New functional groups can arise as a result of oxidation of the compounds mentioned above. For example, the oxidation of a thiol yields a disulfide (R-S-S-R). Double oxidation of a primary alcohol (R-CH₂-OH) gives rise initially to an aldehyde (R-C=O-H), and then to a carboxylic acid (R-C(=O)-OH). In contrast, the oxidation of a secondary alcohol yields a ketone (R-C=O-R). The carbonyl group (C=O) is characteristic of aldehydes and ketones.

The addition of an amine to the carbonyl group of an aldehyde yields an aldime (not shown; see p. 178). Amino acids are intermediates in amino acid metabolism (see p. 178) and serve to bond aldhydes to amino groups in proteins (see p. 62, for example). The addition of an alcohol to the carbonyl group of an aldehyde yields a hemiacetel (R-O-C(H)OH-R). The cyclic forms of sugars are well-known examples of hemiacetals (see p. 36). The oxidation of hemiacetals produces carboxylic acid esters.

Very important compounds are the carboxylic acids and their derivatives, which can be formally obtained by exchanging the OH group for another group. In fact, derivatives of this type are formed by nucleophilic substitution of activated intermediate compounds and the release of water (see p. 14). Carboxylic acid esters (R-O-CO-R') arise from carboxylic acids and alcohols. This group includes the fats, for example (see p. 48). Similarly, a carboxylic acid and a thiol yield a thioester (R-S-CO-R'). Thioesters play an extremely important role in carboxylic acid metabolism. The best-known compound of this type is acetyl-coenzyme A (see p. 12).

Carboxylic acids and primary amines react to form carboxylic acid amides (R-NH-CO-R'). The amino acid constituents of peptides and proteins are linked by carboxylic acid amide bonds, which are therefore also known as peptide bonds (see p. 66).

Phosphoric acid, H₃PO₄, is a tribasic (three-protonic) acid—i.e., it contains three hydroxyl groups able to donate H⁺ ions. At least one of these three groups is fully dissociated under normal physiological conditions, while the other two can react with alcohols. The resulting products are phosphoric acid monoesters (R-O-P(O)(OH) and diesters (R-O-P(O)(O-R'). Phosphoric acid monoesters are found in carbohydrate metabolism, for example (see p. 36), whereas phosphoric acid diester bonds occur in phospholipids (see p. 50) and nucleic acids (see p. 82).}

Compounds of one acid with another are referred to as acid anhydrides. A particularly large amount of energy is required for the formation of an acid—anhydride bond. Phosphoric acid anhydride bonds therefore play a central role in the storage and release of chemical energy in the cell (see p. 122). Mixed anhydrides between carboxylic acids and phosphoric acid are also very important "energy-rich metabolites" in cellular metabolism.
A. Important classes of compounds

**Oxygen (O)**
- Water
- Secondary alcohol
- Primary alcohol
- Ether
- Phosphoric acid ester
- Carboxylic acid ester
- Carbonyl group
- Oxidation

**Nitrogen (N)**
- Primary amine
- Secondary amine
- Tertiary amine
- Amino group
- Keto
- Aldehyde

**Sulfur (S)**
- Hydrogen sulfide
- Thiol
- Sulfhydryl group
- Disulfide

**Phosphorus (P)**
- Dihydrogen phosphate
- Phosphoric acid ester
- Mixed anhydride

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Biomolecules II

Many biomolecules are made up of smaller units in a modular fashion, and they can be broken down into these units again. The construction of these molecules usually takes place through condensation reactions involving the removal of water. Conversely, their breakdown functions in a hydrolytic fashion—i.e., as a result of water uptake. The page opposite illustrates this modular principle using the example of an important coenzyme.

A. Acetyl CoA ⚫

Coenzyme A (see also p.106) is a nucleotide with a complex structure (see p.80). It serves to activate residues of carboxylic acids (acyl residues). Bonding of the carboxy group of the carboxylic acid with the thiol group of the coenzyme creates a thioester bond (-S-CO-R; see p.10) in which the acyl residue has a high chemical potential. It can therefore be transferred to other molecules in exergonic reactions. This fact plays an important role in lipid metabolism in particular (see pp.162ff.), as well as in two reactions of the tricarboxylic acid cycle (see p.136).

As discussed on p.16, the group transfer potential can be expressed quantitatively as the change in free enthalpy (ΔG) during hydrolysis of the compound concerned. This is an arbitrary determination, but it provides important indications of the chemical energy stored in such a group. In the case of acetyl-CoA, the reaction to be considered is:

Acetyl CoA + H₂O → acetate + CoA

In standard conditions and at pH 7, the change in the chemical potential G(ΔG°, see p.18) in this reaction amounts to 32 kJ mol⁻¹ and it is therefore as high as the ΔG° of ATP hydrolysis (see p.18). In addition to the “energy-rich” thioester bond, acetyl-CoA also has seven other hydrolyzable bonds with different degrees of stability. These bonds, and the fragments that arise when they are hydrolyzed, will be discussed here in sequence.

(1) The reactive thiol group of coenzyme A is located in the part of the molecule that is derived from cysteamine. Cysteamine is a biogenic amine (see p.62) formed by decarboxylation of the amino acid cysteine.

(2) The amino group of cysteamine is bound to the carboxy group of another biogenic amine via an acid amide bond (-CO-NH-). β-Alanine arises through decarboxylation of the amino acid aspartate, but it can also be formed by breakdown of pyrimidine bases (see p.186).

(3) Another acid amide bond (-CO-NH-) creates the compound for the next constituent, pantoinate. This compound contains a chiral center and can therefore appear in two enantiomeric forms (see p.8). In natural coenzyme A, only one of the two forms is found, the (R)-pantoinate. Human metabolism is not capable of producing pantoinate itself, and it therefore has to take up a compound of β-alanine and pantoinate—pantothenate (“pantothenic acid”)—in the form of a vitamin in food (see p.366).

(4) The hydroxy group at C-4 of pantoinate is bound to a phosphate residue by an ester bond.

The section of the molecule discussed so far represents a functional unit. In the cell, it is produced from pantothenate. The molecule also occurs in a protein-bound form as 4' phosphopantetheine in the enzyme fatty acid synthase (see p.168). In coenzyme A, however, it is bound to 3',5'-adenosine diphosphate.

(5) When two phosphate residues bond, they do not form an ester, but an “energy-rich” phosphoric acid anhydride bond, as also occurs in other nucleoside phosphates. By contrast, (6) and (7) are ester bonds again.

(8) The base adenine is bound to C-1 of ribose by an N-glycosidic bond (see p.36). In addition to C-2 to C-4, C-1 of ribose also represents a chiral center. The β-configuration is usually found in nucleotides.

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A. Acetyl CoA

- **Acetate**
  - Thioester bond

- **Cysteamine**
  - Acid–amide bond

- **β-Alanine**
  - Acid–amide bond

- **Pantoinate**
  - Phosphoric acid ester bond

- **Phosphate**
  - Phosphoric acid anhydride bond

- **Ribose**
  - Phosphoric acid ester bond

- **Phosphate**
  - Phosphoric acid ester bond

Van der Waals model

Adenine

N-glycosidic bond

Energy-rich bond

Chiral centers
Chemical reactions

Chemical reactions are processes in which electrons or groups of atoms are taken up into molecules, exchanged between molecules, or shifted within molecules. Illustrated here are the most important types of reaction in organic chemistry, using simple examples. Electron shifts are indicated by red arrows.

A. Redox reactions

In redox reactions (see also p. 19), electrons are transferred from one molecule (the reducing agent) to another (the oxidizing agent). One or two protons are often also transferred in the process, but the decisive criterion for the presence of a redox reaction is the electron transfer. The reducing agent is oxidized during the reaction, and the oxidizing agent is reduced.

Fig. A shows the oxidation of an alcohol into an aldehyde (1) and the reduction of the aldehyde to alcohol (2). In the process, one hydride ion is transferred (two electrons and one proton; see p. 19), which moves to the oxidizing agent A in reaction 1. The superfluous proton is bound by the catalytic effect of a base B. In the reduction of the aldehyde (2), A-H serves as the reducing agent and the acid H-B is involved as the catalyst.

B. Acid–base reactions

In contrast to redox reactions, only proton transfer takes place in acid–base reactions (see also p. 19). When an acid dissociates (1), water serves as a proton acceptor (i.e., as a base). Conversely, water has the function of an acid in the protonation of a carboxylate anion (2).

C. Additions/eliminations

A reaction in which atoms or molecules are taken up by a multiple bond is described as addition. The converse of addition—i.e., the removal of groups with the formation of a double bond, is termed elimination. When water is added to an alkene (1a), a proton is first transferred to the alkene. The unstable carbenium cation that occurs as an intermediate initially takes up water (not shown), before the separation of a proton produces alcohol (1b). The elimination of water from the alcohol (2, dehydration) is also catalyzed by an acid and passes via the same intermediate as the addition reaction.

D. Nucleophilic substitutions

A reaction in which one functional group (see p. 19) is replaced by another is termed substitution. Depending on the process involved, a distinction is made between nucleophilic and electrophilic substitution reactions (see chemistry textbooks). Nucleophilic substitutions start with the addition of one molecule to another, followed by elimination of the so-called leaving group.

The hydrolysis of an ester to alcohol and acid (1) and the esterification of a carboxylic acid with an alcohol (2) are shown here as an example of the S_N2 mechanism. Both reactions are made easier by the marked polarity of the C=O double bond. In the form of ester hydrolysis shown here, a proton is removed from a water molecule by the catalytic effect of the base B. The resulting strongly nucleophilic OH\(^-\) ion attacks the positively charged carbonyl C of the ester (1a), and an unstable sp\(^3\)-hybridized transition state is produced. From this, either water is eliminated (2b) and the ester re-forms, or the alcohol ROH is eliminated (1b) and the free acid results. In esterification (2), the same steps take place in reverse.

Further information

In rearrangements (isomerizations, not shown), groups are shifted within one and the same molecule. Examples of this in biochemistry include the isomerization of sugar phosphates (see p. 36) and of methylmalonyl-CoA to succinyl CoA (see p. 166).
Energetics

To obtain a better understanding of the processes involved in energy storage and conversion in living cells, it may be useful first to recall the physical basis for these processes.

A. Forms of work ●

There is essentially no difference between work and energy. Both are measured in joule (J = 1 N m). An outdated unit is the calorie (1 cal = 4.187 J). Energy is defined as the ability of a system to perform work. There are many different forms of energy—e.g., mechanical, chemical, and radiation energy.

A system is capable of performing work when matter is moving along a potential gradient. This abstract definition is best understood by an example involving mechanical work (A1). Due to the earth’s gravitational pull, the mechanical potential energy of an object is the greater the further the object is away from the center of the earth. A potential difference (ΔP) therefore exists between a higher location and a lower one. In a waterfall, the water spontaneously follows this potential gradient and, in doing so, is able to perform work—e.g., turning a mill.

Work and energy consist of two quantities: an intensity factor, which is a measure of the potential difference—i.e., the “driving force” of the process—(here it is the height difference) and a capacity factor, which is a measure of the quantity of the substance being transported (here it is the weight of the water). In the case of electrical work (A2), the intensity factor is the voltage—i.e., the electrical potential difference between the source of the electrical current and the “ground,” while the capacity factor is the amount of charge that is flowing.

Chemical work and chemical energy are defined in an analogous way. The intensity factor here is the chemical potential of a molecule or combination of molecules. This is stated as free enthalpy G (also known as “Gibbs free energy”). When molecules spontaneously react with one another, the result is products at lower potential. The difference in the chemical potentials of the educts and products (the change in free enthalpy, ΔG) is a measure of the “driving force” of the reaction. The capacity factor in chemical work is the amount of matter reacting (in mol). Although absolute values for free enthalpy G cannot be determined, ΔG can be calculated from the equilibrium constant of the reaction (see p. 18).

B. Energetics and the course of processes ●

Everyday experience shows that water never flows uphill spontaneously. Whether a particular process can occur spontaneously or not depends on whether the potential difference between the final and the initial state, ΔP = P₂ − P₁, is positive or negative. If P₂ is smaller than P₁, then ΔP will be negative, and the process will take place and perform work. Processes of this type are called exergonic (B1). If there is no potential difference, then the system is in equilibrium (B2). In the case of endergonic processes, ΔP is positive (B3). Processes of this type do not proceed spontaneously.

Forcing endergonic processes to take place requires the use of the principle of energetic coupling. This effect can be illustrated by a mechanical analogy (B4). When two masses M₁ and M₂ are connected by a rope, M₁ will move upward even though this part of the process is endergonic. The sum of the two potential differences (ΔP₁ + ΔP₂) is the determining factor in coupled processes. When ΔP₁ is negative, the entire process can proceed.

Energetic coupling makes it possible to convert different forms of work and energy into one another. For example, in a flashlight, an exergonic chemical reaction provides an electrical voltage that can then be used for the endergonic generation of light energy. In the luminous organs of various animals, it is a chemical reaction that produces the light. In the musculature (see p. 336), chemical energy is converted into mechanical work and heat energy. A form of storage for chemical energy that is used in all forms of life is adenine triphosphate (ATP; see p. 122). Endergonic processes are usually driven by coupling to the strongly exergonic breakdown of ATP (see p. 122).
### A. Forms of work

1. **Mechanical work**
   - Height
   - Weight

2. **Electrical work**
   - Voltage
   - Charge

3. **Chemical work**
   - Free-energy change
     - $\Delta G$

### B. Energetics and the course of processes

<table>
<thead>
<tr>
<th>$\Delta P$</th>
<th>$\Delta P = 0$</th>
<th>$\Delta P &gt; 0$</th>
<th>$\Delta P_{eff} &lt; 0$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Process occurs spontaneously</td>
<td>Process cannot occur</td>
<td>Coupled processes can occur spontaneously</td>
<td></td>
</tr>
</tbody>
</table>

1. **Exergonic**
2. **Equilibrium**
3. **Endergonic**
4. **Energetically coupled**

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Equilibria

A. Group transfer reactions

Every chemical reaction reaches after a time a state of equilibrium in which the forward and back reactions proceed at the same speed. The law of mass action describes the concentrations of the educts (A, B) and products (C, D) in equilibrium. The equilibrium constant K is directly related to ΔG°, the change in free enthalpy G involved in the reaction (see p. 16) under standard conditions (ΔG° = −RT ln K). For any given concentrations, the lower equation applies. At ΔG < 0, the reaction proceeds spontaneously for as long as it takes for equilibrium to be reached (i.e., until ΔG = 0). At ΔG > 0, a spontaneous reaction is no longer possible (endergonic case; see p. 16). In biochemistry, ΔG is usually related to pH 7, and this is indicated by the "prime" symbol (ΔG°' or ΔG').

As examples, we can look at two group transfer reactions (on the right). In ATP (see p. 122), the terminal phosphate residue is at a high chemical potential. Its transfer to water (reaction a, below) is therefore strongly exergonic. The equilibrium of the reaction (ΔG = 0; see p. 122) is only reached when more than 99.9% of the originally available ATP has been hydrolyzed. ATP and similar compounds have a high group transfer potential for phosphate residues. Quantitatively, this is expressed as the ΔG of hydrolysis (ΔG°H₂O = −32 kJ mol⁻¹; see p. 122).

In contrast, the endergonic transfer of ammonia (NH₃) to glutamate (Glu, reaction b, ΔG° = +14 kJ mol⁻¹) reaches equilibrium so quickly that only minimal amounts of the product glutamine (Gln) can be formed in this way. The synthesis of glutamine from these preliminary stages is only possible through energetic coupling (see pp. 16, 124).

B. Redox reactions

The course of electron transfer reactions (redox reactions, see p. 14) also follows the law of mass action. For a single redox system (see p. 32), the Nernst equation applies (top). The electron transfer potential of a redox system (i.e., its tendency to give off or take up electrons) is given by its redox potential E (in standard conditions, E° or E°'). The lower the redox potential of a system is, the higher the chemical potential of the transferred electrons. To describe reactions between two redox systems, ΔE—the difference between the two systems' redox potentials—is usually used instead of ΔG. ΔG and ΔE have a simple relationship, but opposite signs (below). A redox reaction proceeds spontaneously when ΔE > 0, i.e. ΔG < 0.

The right side of the illustration shows the way in which the redox potential E is dependent on the composition (the proportion of the reduced form as a %) in two biochemically important redox systems (pyruvate/lactate and NAD⁺/NADH⁺⁺; see pp. 98, 104). In the standard state (both systems reduced to 50%), electron transfer from lactate to NAD⁺ is not possible, because ΔE is negative (ΔE = −0.13 V, red arrow). By contrast, transfer can proceed successfully if the pyruvate/lactate system is reduced to 98% and NAD⁺/NADH is 98% oxidized (green arrow, ΔE = +0.08 V).

C. Acid–base reactions

Pairs of conjugated acids and bases are always involved in proton exchange reactions (see p. 30). The dissociation state of an acid–base pair depends on the H⁺ concentration. Usually, it is not this concentration itself that is expressed, but its negative decadic logarithm, the pH value. The connection between the pH value and the dissociation state is described by the Henderson–Hasselbalch equation (below). As a measure of the proton transfer potential of an acid–base pair, its pKₐ value is used—the negative logarithm of the acid constant Kₐ (where "a" stands for acid).

The stronger an acid is, the lower its pKₐ value. The acid of the pair with the lower pKₐ value (the stronger acid—in this case acetic acid, CH₃COOH) can protonate (green arrow) the base of the pair with the higher pKₐ (in this case NH₃), while ammonium acetate (NH₄⁺ and CH₃COO⁻) only forms very little CH₃COOH and NH₃.

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A. Group transfer reactions

Reaction: A + B ↔ C + D

Law of mass action: $K = \frac{[C][D]}{[A][B]}$

Equilibrium constant

Relationship between $\Delta G^0$ and $K$

$\Delta G^0 = -RT \ln K$

In any conditions

$\Delta G = \Delta G^0 + RT \ln \frac{[C][D]}{[A][B]}$

Measure of group transfer potential

B. Redox reactions

For a redox system

$E = E^0 + \frac{R \cdot T}{n \cdot F} \ln \frac{[A_{\text{red}}]}{[A_{\text{ox}}]}$

Measure of electron transfer potential

For any redox reaction

$\Delta E = \Delta E^0 + \frac{R \cdot T}{n \cdot F} \ln \frac{[A_{\text{red}}]}{[A_{\text{ox}}]}$

Definition and sizes

$\Delta E = E_{\text{acceptor}} - E_{\text{donor}}$

$\Delta G = -n \cdot F \cdot \Delta E$

$n =$ No. of electrons transferred

$F =$ Faraday constant

C. Acid–base reactions

Standard reaction: HA + H2O ↔ A0 + H3O0

Law of mass action: $K = \frac{[A_0][H_3O^0]}{[HA][H_2O]}$

Simplified: $K_a = \frac{[A_0][H_3O^0]}{[HA]}$

Henderson–Hasselbalch equation

$pH = pK_a + \log \frac{[A_0]}{[HA]}$

Measure of proton transfer potential

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Enthalpy and entropy

The change in the free enthalpy of a chemical reaction (i.e., its ΔG) depends on a number of factors—e.g., the concentrations of the reactants and the temperature (see p.18). Two further factors associated with molecular changes occurring during the reaction are discussed here.

A. Heat of reaction and calorimetry

All chemical reactions involve heat exchange. Reactions that release heat are called exothermic, and those that consume heat are called endothermic. Heat exchange is measured as the enthalpy change ΔH (the heat of reaction). This corresponds to the heat exchange at constant pressure. In exothermic reactions, the system loses heat, and ΔH is negative. When the reaction is endothermic, the system gains heat, and ΔH becomes positive.

In many reactions, ΔH and ΔG are similar in magnitude (see B1, for example). This fact is used to estimate the caloric content of foods. In living organisms, nutrients are usually oxidized by oxygen to CO₂ and H₂O (see p.112). The maximum amount of chemical work supplied by a particular foodstuff (i.e., the ΔG for the oxidation of the utilizable constituents) can be estimated by burning a weighed amount in a calorimeter in an oxygen atmosphere. The heat of the reaction increases the water temperature in the calorimeter. The reaction heat can then be calculated from the temperature difference Δt.

B. Enthalpy and entropy

The reaction enthalpy ΔH and the change in free enthalpy ΔG are not always of the same magnitude. There are even reactions that occur spontaneously (ΔG < 0) even though they are endothermic (ΔH > 0). The reason for this is that changes in the degree of order of the system also strongly affect the progress of a reaction. This change is measured as the entropy change ΔS.

Entropy is a physical value that describes the degree of order of a system. The lower the degree of order, the larger the entropy. Thus, when a process leads to increase in disorder—and everyday experience shows that this is the normal state of affairs—ΔS is positive for this process. An increase in the order in a system (ΔS < 0) always requires an input of energy. Both of these statements are consequences of an important natural law, the Second Law of Thermodynamics. The connection between changes in enthalpy and entropy is described quantitatively by the Gibbs-Helmholtz equation (ΔG = ΔH - TΔS). The following examples will help explain these relationships.

In the knall-gas (oxyhydrogen) reaction (1), gaseous oxygen and gaseous hydrogen react to form liquid water. Like many redox reactions, this reaction is strongly exothermic (i.e., ΔH < 0). However, during the reaction, the degree of order increases. The total number of molecules is reduced by one-third, and a more highly ordered liquid is formed from freely moving gas molecules. As a result of the increase in the degree of order (ΔS < 0), the term -TΔS becomes positive. However, this is more than compensated for by the decrease in enthalpy, and the reaction is still strongly exergonic (ΔG < 0).

The dissolution of salt in water (2) is endothermic (ΔH > 0) — i.e., the liquid cools. Nevertheless, the process still occurs spontaneously, since the degree of order in the system decreases. The Na⁺ and Cl⁻ ions are initially rigidly fixed in a crystal lattice. In solution, they move about independently and in random directions through the fluid. The decrease in order (ΔS > 0) leads to a negative -TΔS term, which compensates for the positive ΔH term and results in a negative ΔG term overall. Processes of this type are described as being entropy-driven.

The folding of proteins (see p.74) and the formation of ordered lipid structures in water (see p.28) are also mainly entropy-driven.
A. Heat of reaction and calorimetry

- Thermometer
- Ignition wire to start the reaction
- Water
- Temperature insulation
- Pressurized metal container
- Sample
- Stirrer

Combustion

B. Enthalpy and entropy

ΔH: change of enthalpy, heat exchange

Gibbs-Helmholtz equation

ΔG = ΔH - T · ΔS

ΔS: change of entropy, i.e. degree of order

ΔH = -287 kJ · mol⁻¹
ΔG = -238 kJ · mol⁻¹
-T · ΔS = +49 kJ · mol⁻¹

1 mol H₂
1/2 mol O₂

Low degree of order

System releases heat, ΔH < 0 (exothermic)

1 mol H₂O (liquid)

Higher degree of order, ΔS < 0

ΔH = -287 kJ · mol⁻¹
ΔG = -238 kJ · mol⁻¹
-T · ΔS = +49 kJ · mol⁻¹

1 mol NaCl (crystalline)

High degree of order

System absorbs heat, ΔH > 0 (endothermic)

1 mol Na⁺
1 mol Cl⁻

Lower degree of order, ΔS > 0

ΔH = +3.8 kJ · mol⁻¹
ΔG = -9.0 kJ · mol⁻¹
-T · ΔS = -2.8 kJ · mol⁻¹

1. “Knall-gas” reaction
2. Dissolution of NaCl in water

1 mol H₂
1/2 mol O₂

Low degree of order

System releases heat, ΔH < 0 (exothermic)

1 mol H₂O (liquid)

Higher degree of order, ΔS < 0

ΔH = -287 kJ · mol⁻¹
ΔG = -238 kJ · mol⁻¹
-T · ΔS = +49 kJ · mol⁻¹

1 mol NaCl (crystalline)

High degree of order

System absorbs heat, ΔH > 0 (endothermic)

1 mol Na⁺
1 mol Cl⁻

Lower degree of order, ΔS > 0

ΔH = +3.8 kJ · mol⁻¹
ΔG = -9.0 kJ · mol⁻¹
-T · ΔS = -2.8 kJ · mol⁻¹

1. “Knall-gas” reaction
2. Dissolution of NaCl in water

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Reaction kinetics

The change in free enthalpy, $\Delta G$, in a reaction indicates whether or not the reaction can take place spontaneously in given conditions and how much work it can perform (see p. 18). However, it does not tell us anything about the rate of the reaction—i.e., its kinetics.

A. Activation energy

Most organic chemical reactions (with the exception of acid–base reactions) proceed only very slowly, regardless of the value of $\Delta G$. The reason for the slow reaction rate is that the molecules that react—the educts—have to have a certain minimum energy before they can enter the reaction. This is best understood with the help of an energy diagram (1) of the simplest possible reaction $A \rightarrow B$. The educt A and the product B are each at a specific chemical potential ($G_m$ and $G_p$, respectively). The change in the free enthalpy of the reaction, $\Delta G$, corresponds to the difference between these two potentials. To be converted into B, A first has to overcome a potential energy barrier, the peak of which, $G_1$, lies well above $G_m$. The potential difference $G_1 - G_m$ is the activation energy $E_a$ of the reaction (in kJ mol$^{-1}$).

The fact that A can be converted into B at all is because the potential $G_1$ only represents the average potential of all the molecules. Individual molecules may occasionally reach much higher potentials—e.g., due to collisions with other molecules. When the increase in energy thus gained is greater than $E_a$, these molecules can overcome the barrier and be converted into B. The energy distribution for a group of molecules of this type, as calculated from a simple model, is shown in (2) and (3). $\alpha/n$ is the fraction of molecules that have reached or exceeded energy $E$ (in kJ per mol).

At 27 °C, for example, approximately 10% of the molecules have energies $> 6$ kJ mol$^{-1}$. The typical activation energies of chemical reactions are much higher. The course of the energy function at energies of around 50 kJ mol$^{-1}$ is shown in (3). Statistically, at 27 °C only two out of 10$^6$ molecules reach this energy. At 37 °C, the figure is already four. This is the basis for the long-familiar “$Q_10$ law”—a rule of thumb that states that the speed of biological processes approximately doubles with an increase in temperature of 10 °C.

B. Reaction rate

The velocity $v$ of a chemical reaction is determined experimentally by observing the change in the concentration of an educt or product over time. In the example shown (again a reaction of the $A \rightarrow B$ type), 3 mmol of the educt A is converted per second and 3 mmol of the product B is formed per second in one liter of the solution. This corresponds to a rate of

$$v = 3 \text{ mM s}^{-1} = 3 \times 10^{-3} \text{ mol L}^{-1} \text{ s}^{-1}$$

C. Reaction order

Reaction rates are influenced not only by the activation energy and the temperature, but also by the concentrations of the reactants. When there is only one educt, A (1), $v$ is proportional to the concentration [A] of this substance, and a first-order reaction is involved. When two educts, A and B, react with one another (2), it is a second order reaction (shown on the right). In this case, the rate $v$ is proportional to the product of the educt concentrations (12 mM$^2$ at the top, 24 mM$^2$ in the middle, and 36 mM$^2$ at the bottom). The proportionality factors $k$ and $k'$ are the rate constants of the reaction. They are not dependent on the reaction concentrations, but depend on the external conditions for the reaction, such as temperature.

In 2, only the kinetics of simple irreversible reactions is shown. More complicated cases, such as reaction with three or more reversible steps, can usually be broken down into first-order or second-order partial reactions and described using the corresponding equations (for an example, see the Michaelis–Menten reaction, p. 92).
A. Activation energy

[Diagram of chemical potential and activation energy]

B. Reaction rate

[Diagram with reaction rates and substrate concentrations]

C. Reaction order

[Diagram with reaction order and rate constants]

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Catalysis

Catalysts are substances that accelerate chemical reactions without themselves being consumed in the process. Since catalysts emerge from the catalyzed reaction without being changed, even small amounts are usually sufficient to cause a powerful acceleration of the reaction. In the cell, enzymes (see p. 88) generally serve as catalysts. A few chemical changes are catalyzed by special RNA molecules, known as ribozymes (see p. 246).

A. Catalysis: principle ●

The reason for the slow rates of most reactions involving organic substances is the high activation energy (see p. 22) that the reacting molecules have to reach before they can react. In aqueous solution, a large proportion of the activation energy is required to remove the hydration shells surrounding the educts. During the course of a reaction, resonance-stabilized structures (see p. 4) are often temporarily suspended; this also requires energy. The highest point on the reaction coordinates corresponds to an energetically unfavorable transition state of this type (1).

A catalyst creates a new pathway for the reaction (2). When all of the transition states arising have a lower activation energy than that of the uncatalyzed reaction, the reaction will proceed more rapidly along the alternative pathway, even when the number of intermediates is greater. Since the starting points and end points are the same in both routes, the change in the enthalpy ΔH of the reaction is not influenced by the catalyst. Catalysts—including enzymes—are in principle not capable of altering the equilibrium state of the catalyzed reaction.

The often-heard statement that “a catalyst reduces the activation energy of a reaction” is not strictly correct, since a completely different reaction takes place in the presence of a catalyst than in uncatalyzed conditions. However, its activation energy is lower than in the uncatalyzed reaction.

B. Catalysis of H₂O₂ – breakdown by iodide ○

As a simple example of a catalyzed reaction, we can look at the disproportionation of hydrogen peroxide (H₂O₂) into oxygen and water. In the uncatalyzed reaction (at the top), an H₂O₂ molecule initially decays into H₂O and atomic oxygen (O), which then reacts with a second H₂O₂ molecule to form water and molecular oxygen (O₂). The activation energy Eₐ required for this reaction is relatively high, at 75 kJ mol⁻¹. In the presence of iodide (I⁻) as a catalyst, the reaction takes a different course (bottom). The intermediate arising in this case is hypiodide (OI⁻), which also forms H₂O and O₂ with another H₂O₂ molecule. In this step, the I⁻ ion is released and can once again take part in the reaction. The lower activation energy of the reaction catalyzed by iodide (Eₐ = 56 kJ mol⁻¹) causes acceleration of the reaction by a factor of 2000, as the reaction rate depends exponentially on Eₐ (v = e⁻Eₐ/kT).

Free metal ions such as iron (Fe) and platinum (Pt) are also effective catalysts for the breakdown of H₂O₂. Catalase (see p. 284), an enzyme that protects cells against the toxic effects of hydrogen peroxide (see p. 284), is much more catalytically effective still. In the enzyme-catalyzed disproportionation, H₂O₂ is bound to the enzyme’s heme group, where it is quickly converted to atomic oxygen and water, supported by amino acid residues of the enzyme protein. The oxygen atom is temporarily bound to the central iron atom of the heme group, and then transferred from there to the second H₂O₂ molecule. The activation energy of the enzyme-catalyzed reaction is only 23 kJ mol⁻¹, which in comparison with the uncatalyzed reaction leads to acceleration by a factor of 1.3 x 10⁷.

Catalase is one of the most efficient enzymes there are. A single molecule can convert up to 10⁹ (a hundred million) H₂O₂ molecules per second.
A. Catalysis: principle

1. Energy profile without catalyst

2. Energy profile with catalyst

B. Catalysis of $\text{H}_2\text{O}_2$ – breakdown by iodide

1. Breakdown of hydrogen peroxide

$\text{H}_2\text{O}_2 + \text{H}_2\text{O}_2 \rightarrow \text{O}_2 + \text{H}_2\text{O} + \text{H}_2\text{O}$

2. Catalyzed reaction

3. Activation energies

$\Delta G, E_a$
Water as a solvent

Life as we know it evolved in water and is still absolutely dependent on it. The properties of water are therefore of fundamental importance to all living things.

A. Water and methane

The special properties of water (H$_2$O) become apparent when it is compared with methane (CH$_4$). The two molecules have a similar mass and size. Nevertheless, the boiling point of water is more than 250 °C above that of methane. At temperatures on the earth’s surface, water is liquid, whereas methane is gaseous. The high boiling point of water results from its high vaporization enthalpy, which in turn is due to the fact that the density of the electrons within the molecule is unevenly distributed. Two corners of the tetrahedrally-shaped water molecule are occupied by unshared electrons (green), and the other two by hydrogen atoms. As a result, the H–O–H bond has an angled shape. In addition, the O–H bonds are polarized due to the high electronegativity of oxygen (see p. 6). One side of the molecule carries a partial charge (δ) of about –0.6 units, whereas the other is correspondingly positively charged. The spatial separation of the positive and negative charges gives the molecule the properties of an electrical dipole. Water molecules are therefore attracted to one another like tiny magnets, and are also connected by hydrogen bonds (B) (see p. 6). When liquid water vaporizes, a large amount of energy has to be expended to disrupt these interactions. By contrast, methane molecules are not dipolar, and therefore interact with one another only weakly. This is why liquid methane vaporizes at very low temperatures.

B. Structure of water and ice

The dipolar nature of water molecules favors the formation of hydrogen bonds (see p. 6). Each molecule can act either as a donor or an acceptor of H bonds, and many molecules in liquid water are therefore connected by H bonds (1). The bonds are in a state of constant fluctuation. Tetrahedral networks of molecules, known as water “clusters,” often arise. As the temperature decreases, the proportion of water clusters increases until the water begins to crystallize. Under normal atmospheric pressure, this occurs at 0 °C. In ice, most of the water molecules are fixed in a hexagonal lattice (3). Since the distance between the individual molecules in the frozen state is on average greater than in the liquid state, the density of ice is lower than that of liquid water. This fact is of immense biological importance—it means, for example, that in winter, ice forms on the surface of open stretches of water first, and the water rarely freezes to the bottom.

C. Hydration

In contrast to most other liquids, water is an excellent solvent for ions. In the electrical field of cations and anions, the dipolar water molecules arrange themselves in a regular fashion corresponding to the charge of the ion. They form hydration shells and shield the central ion from oppositely charged ions. Metal ions are therefore often present as hexahydrates ([Me(H$_2$O)$_6$]$^n^+$, on the right). In the inner hydration sphere of this type of ion, the water molecules are practically immobilized and follow the central ion. Water has a high dielectric constant of 78—i.e., the electrostatic attraction force between ions is reduced to 1/78 by the solvent. Electrically charged groups in organic molecules (e.g., carboxylate, phosphate, and ammonium groups) are also well hydrated and contribute to water solubility. Neutral molecules with several hydroxy groups, such as glycerol (on the left) or sugars, are also easily soluble, because they can form H bonds with water molecules. The higher the proportion of polar functional groups there is in a molecule, the more water-soluble (hydrophilic) it is. By contrast, molecules that consist exclusively or mainly of hydrocarbons are poorly soluble or insoluble in water. These compounds are called hydrophobic (see p. 28).
A. Water and methane

<table>
<thead>
<tr>
<th></th>
<th>( \delta = +0.3 )</th>
<th>( \delta = -0.6 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Water</td>
<td>(H(_2)O)</td>
<td></td>
</tr>
<tr>
<td>Methane</td>
<td>(CH(_4))</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>H(_2)O</th>
<th>CH(_4)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Molecular mass</td>
<td>18 Da</td>
<td>16 Da</td>
</tr>
<tr>
<td>Boiling point</td>
<td>+100 °C</td>
<td>-162 °C</td>
</tr>
<tr>
<td>Heat of vaporization</td>
<td>41</td>
<td>8</td>
</tr>
<tr>
<td>Dipole moment</td>
<td>6.2 D</td>
<td>0 D</td>
</tr>
</tbody>
</table>

B. Structure of water and ice

- Liquid water density 1.00 g · cm\(^{-3}\)
- Short-lived clusters
- Ethanol
- Ice density 0.92 g · cm\(^{-3}\)
- Hexagonal lattice, stabilized by hydrogen bonds

C. Hydration

- Glycerol
- Water
- [Me(H\(_2\)O)]\(^{2+}\)
Hydrophobic interactions

Water is an excellent solvent for ions and for substances that contain polarized bonds (see p. 20). Substances of this type are referred to as polar or hydrophilic (“water-loving”). In contrast, substances that consist mainly of hydrocarbon structures dissolve only poorly in water. Such substances are said to be apolar or hydrophobic.

A. Solubility of methane

To understand the reasons for the poor water solubility of hydrocarbons, it is useful first to examine the energetics (see p. 16) of the processes involved. In (1), the individual terms of the Gibbs–Helmholtz equation (see p. 20) for the simplest compound of this type, methane, are shown (see p. 4). As can be seen, the transition from gaseous methane to water is actually exothermic (ΔH° < 0). Nevertheless, the change in the free enthalpy ΔG° is positive (the process is endergonic), because the entropy term T ΔS° has a strongly positive value. The entropy change in the process (ΔS°) is evidently negative—i.e., a solution of methane in water has a higher degree of order than either water or gaseous methane. One reason for this is that the methane molecules are less mobile when surrounded by water. More importantly, however, the water around the apolar molecules forms cage-like “clathrate” structures, which—as in ice—are stabilized by H bonds. This strongly increases the degree of order in the water—and the more so the larger the area of surface contact between the water and the apolar phase.

B. The “oil drop effect”

The spontaneous separation of oil and water, a familiar observation in everyday life, is due to the energetically unfavorable formation of clathrate structures. When a mixture of water and oil is firmly shaken, lots of tiny oil drops form to begin with, but these quickly coalesce spontaneously to form larger drops—the two phases separate. A larger drop has a smaller surface area than several small drops with the same volume. Separation therefore reduces the area of surface contact between the water and the oil, and consequently also the extent of clathrate formation. The ΔS for this process is therefore positive (the disorder in the water increases), and the negative term −T ΔS makes the separation process exergonic (ΔG < 0), so that it proceeds spontaneously.

C. Arrangements of amphipathic substances in water

Molecules that contain both polar and apolar groups are called amphiphatic or amphipilic. This group includes soaps (see p. 48), phospholipids (see p. 50), and bile acids (see p. 56).

As a result of the “oil drop effect” amphipathic substances in water tend to arrange themselves in such a way as to minimize the area of surface contact between the apolar regions of the molecule and water. On water surfaces, they usually form single-layer films (top) in which the polar “head groups” face toward the water. Soap bubbles (right) consist of double films, with a thin layer of water enclosed between them. In water, depending on their concentration, amphipathic compounds form micelles—i.e., spherical aggregates with their head groups facing toward the outside, or extended bilayered double membranes. Most biological membranes are assembled according to this principle (see p. 214). Closed hollow membrane sacs are known as vesicles. This type of structure serves to transport substances within cells and in the blood (see p. 278).

The separation of oil and water (8) can be prevented by adding a strongly amphipathic substance. During shaking, a more or less stable emulsion then forms, in which the surface of the oil drops is occupied by amphipathic molecules that provide it with polar properties externally. The emulsification of fats in food by bile acids and phospholipids is a vital precondition for the digestion of fats (see p. 314).
C. Arrangements of amphipathic substances in water

A. Solubility of methane

\[ T \cdot \Delta S^0 = -39.6 \text{ kJ mol}^{-1} \]
\[ -13.2 \text{ kJ mol}^{-1} \]

10 x 1 mL
Total surface area: 48 cm²

B. The “oil drop effect”

1 x 10 mL
Surface area: 22 cm²

C. Arrangements of amphipathic substances in water

Air
Surface film
Micelle
Vesicle
Soap bubble

Water
Clathrate structure
Double membrane

Air

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Acids and bases

A. Acids and bases

In general, acids are defined as substances that can donate hydrogen ions (protons), while bases are compounds that accept protons.

Water enhances the acidic or basic properties of dissolved substances, as water itself can act as either an acid or a base. For example, when hydrogen chloride (HCl) is in aqueous solution, it donates protons to the solvent (1). This results in the formation of chloride ions (Cl\(^-\)) and protonated water molecules (hydronium ions, H\(_3\)O\(^+\), usually simply referred to as H\(^+\)). The proton exchange between HCl and water is virtually quantitative: in water, HCl behaves as a very strong acid with a negative pK\(_a\) value (see p.18).

Bases such as ammonia (NH\(_3\)) take over protons from water molecules. As a result of this, hydroxyl ions (OH\(^-\)) and positively charged ammonium ions (NH\(_4^+\), 3) form. Hydronium and hydroxyl ions, like other ions, exist in water in hydrated rather than free form (see p.26).

Acid–base reactions always involve pairs of acids and the associated conjugated bases (see p.18). The stronger the acid or base, the weaker the conjugate base or acid, respectively. For example, the very strongly acidic hydrogen chloride belongs to the very weakly basic chloride ion (1). The weakly acidic ammonium ion is conjugated with the moderately strong base ammonia (3).

The equilibrium constant \(K\) for the acid–base reaction between H\(_2\)O molecules (2) is very small. At 25 °C,

\[
K = \frac{[H^+][OH^-]}{[H_2O]} = 2 \times 10^{-16} \text{ mol L}^{-1}
\]

In pure water, the concentration [H\(_2\)O] is practically constant at 55 mol L\(^{-1}\). Substituting this value into the equation, it gives:

\[
K_w = [H^+][OH^-] = 1 \times 10^{-14} \text{ mol L}^{-1}
\]

The product [H\(^+\)][OH\(^-\)]—the ion product of water—is constant even when additional acid–base pairs are dissolved in the water. At 25 °C, pure water contains H\(^+\) and OH\(^-\) at concentrations of 1 × 10\(^{-7}\) mol L\(^{-1}\) each; it is neutral and has a pH value of exactly 7.

B. pH values in the organism

pH values in the cell and in the extracellular fluid are kept constant within narrow limits. In the blood, the pH value normally ranges only between 7.35 and 7.45 (see p.288). This corresponds to a maximum change in the H\(^+\) concentration of ca. 30%. The pH value of cytoplasm is slightly lower than that of blood, at 7.0–7.3. In lysosomes (see p.234; pH 4.5–5.5), the H\(^+\) concentration is several hundred times higher than in the cytoplasm. In the lumen of the gastrointestinal tract, which forms part of the outside world relative to the organism, and in the body’s excretion products, the pH values are more variable. Extreme values are found in the stomach (ca. 2) and in the small bowel (> 8). Since the kidney can excrete either acids or bases, depending on the state of the metabolism, the pH of urine has a particularly wide range of variation (4.8–7.5).

C. Buffers

Short-term pH changes in the organism are cushioned by buffer systems. These are mixtures of a weak acid, HB, with its conjugate base, B\(^-\), or of a weak base with its conjugate acid. This type of system can neutralize both hydronium ions and hydroxyl ions.

In the first case (left), the base (B\(^-\)) binds a large proportion of the added protons (H\(^+\)) and HB and water are formed. If hydroxyl ions (OH\(^-\)) are added, they react with HB to give B\(^-\) and water (right). In both cases, it is primarily the [HB]/[B\(^-\)] ratio that shifts, while the pH value only changes slightly. The titration curve (top) shows that buffer systems are most effective at the pH values that correspond to the pK\(_a\) value of the acid. This is where the curve is at its steepest, so that the pH change, ΔpH, is at its smallest with a given increase in [H\(^+\)] or [OH\(^-\)]. In other words, the buffer capacity ΔpH/pK\(_a\) is highest at the pK\(_a\) value.

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A. Acids and bases

<table>
<thead>
<tr>
<th>Hydrogen chloride</th>
<th>Water</th>
<th>Ammonia</th>
</tr>
</thead>
<tbody>
<tr>
<td>Very strong acid</td>
<td>Very weak base</td>
<td>Strong base</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cl</th>
<th>H</th>
<th>O</th>
<th>H</th>
<th>H</th>
<th>O</th>
<th>H</th>
<th>H</th>
<th>N</th>
<th>H</th>
<th>H</th>
</tr>
</thead>
</table>

**Chloride ion**
- **Very weak base**
- \( pK_a = -7 \)
- \( K_{eq} = 9 \cdot 10^6 \text{ mol} \cdot \text{L}^{-1} \)

**Hydronium ion**
- **Very strong acid**
- \( pK_a = 1 \)
- \( K_{eq} = 2 \cdot 10^{-14} \text{ mol} \cdot \text{L}^{-1} \)

**Hydroxyl ion**
- **Very strong base**
- \( pK_a = -9.2 \)
- \( K_{eq} = 6 \cdot 10^{-10} \text{ mol} \cdot \text{L}^{-1} \)

**Ammonium ion**
- **Weak acid**

B. pH values in the body

<table>
<thead>
<tr>
<th>pH</th>
<th>Buffer solution</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Gastro juice</td>
</tr>
<tr>
<td>3</td>
<td>Lysosomes</td>
</tr>
<tr>
<td>4</td>
<td>Sweat</td>
</tr>
<tr>
<td>5</td>
<td>Urine</td>
</tr>
<tr>
<td>6</td>
<td>Cytosolam</td>
</tr>
<tr>
<td>7</td>
<td>Blood plasma</td>
</tr>
<tr>
<td>8</td>
<td>Small intestine</td>
</tr>
</tbody>
</table>

C. Buffers

*Buffer solution: mixture of a weak acid with the conjugate base*
Redox processes

A. Redox reactions

Redox reactions are chemical changes in which electrons are transferred from one reductant partner to another (1; see also p. 18). Like acid–base reactions (see p. 30), redox reactions always involve pairs of compounds. A pair of this type is referred to as a redox system (2). The essential difference between the two components of a redox system is the number of electrons they contain. The more electron-rich component is called the reduced form of the compound concerned, while the other one is referred to as the oxidized form. The reduced form of one system (the reducing agent) donates electrons to the oxidized form of another one (the oxidizing agent). In the process, the reducing agent becomes oxidized and the oxidizing agent is reduced (3). Any given reducing agent can reduce only certain other redox systems. On the basis of this type of observation, redox systems can be arranged to form what are known as redox series (4).

The position of a system within one of these series is established by its redox potential E (see p. 18). The redox potential has a sign; it can be more negative or more positive than a reference potential arbitrarily set at zero (the normal potential of the system [2 H⁺/H₂]). In addition, E depends on the concentrations of the reactants and on the reaction conditions (see p. 18). In redox series (4), the systems are arranged according to their increasing redox potentials. Spontaneous electron transfers are only possible if the redox potential of the donor is more negative than that of the acceptor (see p. 18).

B. Reduction equivalents

In redox reactions, protons (H⁺) are often transferred along with electrons (e⁻), or protons may be released. The combinations of electrons and protons that occur in redox processes are summed up in the term reduction equivalents. For example, the combination 1 e⁻/1 H⁺ corresponds to a hydrogen atom, while 2 e⁻ and 2 H⁺ together produce a hydrogen molecule. However, this does not mean that atomic or molecular hydrogen is actually transferred from one molecule to the other (see below). Only the combination 2 e⁻/1 H⁺, the hydride ion, is transferred as a unit.

C. Biological redox systems

In the cell, redox reactions are catalyzed by enzymes, which work together with soluble or bound redox cofactors.

Some of these factors contain metal ions as redox-active components. In these cases, it is usually single electrons that are transferred, with the metal ion changing its valency. Unpaired electrons often occur in this process, but these are located in d orbitals (see p. 2) and are therefore less dangerous than single electrons in non-metal atoms (“free radicals”; see below).

We can only show here a few examples from the many organic redox systems that are found. In the complete reduction of the flavin coenzymes FMN and FAD (see p. 104), 2 e⁻ and 2 H⁺ are transferred. This occurs in two separate steps, with a semiquinone radical appearing as an intermediate. Since organic radicals of this type can cause damage to biomolecules, flavin coenzymes never occur freely in solution, but remain firmly bound in the interior of proteins.

In the reduction or oxidation of quinone/quinol systems, free radicals also appear as intermediate steps, but these are less reactive than flavin radicals. Vitamin E, another quinone-type redox system (see p. 104), even functions as a radical scavenger, by delocalizing unpaired electrons so effectively that they can no longer react with other molecules.

The pyridine nucleotides NAD⁺ and NADH always function in unbound form. The oxidized forms contain an aromatic nicotinamide ring in which the positive charge is delocalized. The right-hand example of the two resonance structures shown contains an electron-poor, positively charged C atom at the para position to nitrogen. If a hydride ion is added at this point (see above), the reduced forms NADH or NADPH arise. No radical intermediate steps occur. Because a proton is released at the same time, the reduced pyridine nucleotide coenzymes are correctly expressed as NAD(P)H+H⁺.
A. Redox reactions

1. Principle

2. Redox systems

3. Possible electron transfers

4. Redox series

B. Reducing equivalents

<table>
<thead>
<tr>
<th>Transferred components</th>
<th>1e(^{-})</th>
<th>1e(^{-})</th>
<th>1H(^{+})</th>
<th>2e(^{-})</th>
<th>2e(^{-})</th>
<th>2H(^{+})</th>
</tr>
</thead>
<tbody>
<tr>
<td>Equivalent</td>
<td>Electron</td>
<td>Hydrogen atom</td>
<td>Hydride ion</td>
<td>Hydrogen molecule</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

C. Biological redox systems

Metal complexes

Flavin

Quinone/hydroquinone

Oxidized oxygen species (ROS)

NAD (P)
Overview

The carbohydrates are a group of naturally occurring carbonyl compounds (aldehydes or ketones) that also contain several hydroxyl groups. The carbohydrates include single sugars (monosaccharides) and their polymers, the oligosaccharides and polysaccharides.

A. Carbohydrates: overview

Polymeric carbohydrates—above all starch, as well as some disaccharides—are important (but not essential) components of food (see p. 360). In the gut, they are broken down into monosaccharides and resorbed in this form (see p. 272). The form in which carbohydrates are distributed by the blood of vertebrates is glucose (“blood sugar”). This is taken up by the cells and either broken down to obtain energy (glycolysis) or converted into other metabolites (see pp. 150–159). Several organs (particularly the liver and muscles) store glycogen as a polymeric reserve carbohydrate (right; see p. 156). The glycogen molecules are covalently bound to a protein, glycogenin. Polysaccharides are used by many organisms as building materials. For example, the cell walls of bacteria contain murein as a stabilizing component (see p. 40), while in plants cellulose and other polysaccharides fulfill this role (see p. 42). Oligomeric or polymeric carbohydrates are often covalently bound to lipids or proteins. The glycolipids and glycoproteins formed in this way are found, for example, in cell membranes (center). Glycoproteins also occur in the blood in solute form (plasma proteins; see p. 276) and, as components of proteoglycans, form important constituents of the intercellular substance (see p. 346).

B. Monosaccharides: structure

The most important natural monosaccharide, D-glucose, is an aliphatic aldehyde with six C atoms, five of which carry a hydroxyl group (1). Since C atoms 2 to 5 represent chiral centers (see p. 8), there are 15 further isomeric aldohexoses in addition to D-glucose, although only a few of these are important in nature (see p. 38). Most natural monosaccharides have the same configuration at C-5 as D-glyceraldehyde—they belong to the D series.

The open-chained form of glucose shown in (1) is found in neutral solution in less than 0.1% of the molecules. The reason for this is an intramolecular reaction in which one of the OH groups of the sugar is added to the aldehyde group of the same molecule (2). This gives rise to a cyclic hemiacetal (see p. 16). In aldohexoses, the hydroxy group at C-5 reacts preferentially, and a six-membered pyran ring is formed. Sugars that contain this ring are called pyranoses. By contrast, if the OH group at C-4 reacts, a five-part furan ring is formed. In solution, pyranose forms and furanose forms are present in equilibrium with each other and with the open-chained form, while in glucose polymers only the pyranose form occurs.

The Haworth projection (2) is usually used to depict sugars in the cyclic form, with the ring being shown in perspective as viewed from above. Depending on the configuration, the substituents of the chiral C atoms are then found above or below the ring. OH groups that lie on the right in the Fischer projection (1) appear under the ring level in the Haworth projection, while those on the left appear above it.

As a result of hemiacetal formation, an additional chiral center arises at C-1, which can be present in both possible configurations (anomers) (see p. 8). To emphasize this, the corresponding bonds are shown here using wavy lines.

The Haworth formula does not take account of the fact that the pyran ring is not plain, but usually has a chair conformation. In B3, two frequent conformations of D-glucopyranose are shown as ball-and-stick models. In the 1C4 conformation (bottom), most of the OH groups appear vertical to the ring level, as in the Haworth projection (axial or z position). In the slightly more stable 3C1 conformation (top), the OH groups take the equatorial or e position. At room temperature, each form can change into the other, as well as into other conformations.
A. Carbohydrates: overview

B. Monosaccharides: structure

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Chemistry of sugars

A. Reactions of the monosaccharides

The sugars (monosaccharides) occur in the metabolism in many forms (derivatives). Only a few important conversion reactions are discussed here, using D-glucose as an example.

1. Mutarotation. In the cyclic form, as opposed to the open-chain form, aldoses have a chiral center at C-1 (see p. 34). The corresponding isomeric forms are called anomers. In the β-anomer (center left), the OH group at C-1 (the anemic OH group) and the CH₂OH group lie on the same side of the ring. In the α-anomer (right), they are on different sides. The reaction that interconverts anomers into each other is known as mutarotation (B).

2. Glycoside formation. When the anemic OH group of a sugar reacts with an alcohol, with elimination of water, it yields an O-glycoside (in the case shown, α –methylglucoside). The glycosidic bond is not a normal ether bond, because the OH group at C-1 has a hemiacetal quality. Oligosaccharides and polysaccharides also contain O-glycosidic bonds. Reaction of the anemic OH group with an NH₃ or NH₂ group yields an N-glycoside (not shown). N-glycosidic bonds occur in nucleotides (see p.80) and in glycoproteins (see p.44).

3. Reduction and oxidation. Reduction of the anemic center at C-1 of glucose (2) produces the sugar alcohol sorbitol. Oxidation of the aldehyde group at C-1 gives the intramolecular ester (lactone) of gluconic acid (a gluconic acid). Phosphorylated glucuronolactone is an intermediate of the pentose phosphate pathway (see p.152). When glucose is oxidized at C-6, glucuronic acid (a glucuronic acid) is formed. The strongly polar glucuronic acid plays an important role in biotransformations in the liver (see pp.194, 316).

4. Epimerization. In weakly alkaline solutions, glucose is in equilibrium with the ketohexose D-fructose and the aldohexose D-mannose, via an enediol intermediate (not shown). The only difference between glucose and mannose is the configuration at C-2. Pairs of sugars of this type are referred to as epimers, and their interconversion is called epimerization.

5. Esterification. The hydroxyl groups of monosaccharides can form esters with acids. In metabolism, phosphoric acid esters such as glucose 6-phosphate and glucose 1-phosphate (6) are particularly important.

B. Polarimetry, mutarotation

Sugar solutions can be analyzed by polarimetry, a method based on the interaction between chiral centers and linearly polarized light—i.e., light that oscillates in only one plane. It can be produced by passing normal light through a special filter (a polarizer). A second polarizing filter of the same type (the analyzer), placed behind the first, only lets the polarized light pass through when the polarizer and the analyzer are in alignment. In this case, the field of view appears bright when one looks through the analyzer (1). Solutions of chiral substances rotate the plane of polarized light by an angle α either to the left or to the right. When a solution of this type is placed between the polarizer and the analyzer, the field of view appears darker (2). The angle of rotation, α, is determined by turning the analyzer until the field of view becomes bright again (3). A solution’s optical rotation depends on the type of chiral compound, its concentration, and the thickness of the layer of the solution. This method makes it possible to determine the sugar content of wines, for example.

Certain procedures make it possible to obtain the α and β anomers of glucose in pure form. A 1-molar solution of α-D-glucose has a rotation value δ₁₀₀₀ of +112°, while a corresponding solution of β-D-glucose has a value of +19°. These values change spontaneously, however, and after a certain time reach the same end point of +52°. The reason for this is that, in solution, mutarotation leads to an equilibrium between the α and β forms in which, independently of the starting conditions, 62% of the molecules are present in the β form and 38% in the α form.
A. Reactions of the monosaccharides

1. Esterification
2. Epimerization
3. Glycoside formation

B. Polarimetry, mutarotation
Monosaccharides and disaccharides

A. Important monosaccharides

Only the most important of the large number of naturally occurring monosaccharides are mentioned here. They are classified according to the number of C atoms (into pentoses, hexoses, etc.) and according to the chemical nature of the carbonyl function into aldoses and ketoses.

The best-known aldotetrose (1) is D-glucose. It is a component of RNA and of nucleotide coenzymes and is widely distributed. In these compounds, ribose always exists in the furanose form (see p. 34). Like ribose, D-xylose and L-arabinose are rarely found in free form. However, large amounts of both sugars are found as constituents of polysaccharides in the walls of plant cells (see p. 42).

The most important of the aldohexoses (1) is D-glucose. A substantial proportion of the biomass is accounted for by glucose polymers, above all cellulose and starch. Free D-glucose is found in plant juices (“grape sugar”) and as “blood sugar” in the blood of higher animals. As a constituent of lactose (milk sugar), D-galactose is part of the human diet. Together with D-mannose, galactose is also found in glycolipids and glycoproteins (see p. 44).

Phosphoric acid esters of the ketopentose D-ribose (2) are intermediates in the pentose phosphate pathway (see p. 152) and in photosynthesis (see p. 128). The most widely distributed of the ketohexoses is D-fructose. In free form, it is present in fruit juices and in honey. Bound fructose is found in sucrose (8) and plant polysaccharides (e.g., inulin).

In the deoxyaloses (3), an OH group is replaced by a hydrogen atom. In addition to 2-deoxy-D-ribose, a component of DNA (see p. 84) that is reduced at C-2, L-fucose is shown as another example of these. Fucose, a sugar in the β series (see p. 34) is reduced at C-6.

The acetylated amino sugars N-acetyl-D-glucosamine and N-acetyl-D-galactosamine (4) are often encountered as components of glycoproteins.

N-acetylneuraminic acid (sialic acid, 5), is a characteristic component of glycoproteins. Other acidic monosaccharides such as D-glucuronic acid, D-galacturonic acid, and iduronic acid, are typical constituents of the glycosaminoglycans found in connective tissue.

Sugar alcohols (6) such as sorbitol and mannitol do not play an important role in animal metabolism.

B. Disaccharides

When the anomeric hydroxyl group of one monosaccharide is bound glycosidically with one of the OH groups of another, a disaccharide is formed. As in all glycosides, the glycosidic bond does not allow mutarotation. Since this type of bond is formed stereospecifically by enzymes in natural disaccharides, they are only found in one of the possible configurations (α or β).

Maltose (1) occurs as a breakdown product of the starches contained in malt (“malt sugar”; see p. 148) and as an intermediate in intestinal digestion. In maltose, the anomeric OH group of one glucose molecule has an α-glycosidic bond with C-4 in a second glucose residue.

Lactose (“milk sugar,” 2) is the most important carbohydrate in the milk of mammals. Cow’s milk contains 4.5% lactose, while human milk contains up to 7.5%. In lactose, the anomeric OH group of galactose forms a β-glycosidic bond with C-4 of a glucose. The lactose molecule is consequently elongated, and both of its pyran rings lie in the same plane.

Sucrose (3) serves in plants as the form in which carbohydrates are transported, and as a soluble carbohydrate reserve. Humans value it because of its intensely sweet taste. Sources used for sucrose are plants that contain particularly high amounts of it, such as sugar cane and sugar beet (cane sugar, beet sugar). Enzymatic hydrolysis of sucrose-containing flower nectar in the digestive tract of bees—catalyzed by the enzyme invertase—produces honey, a mixture of glucose and fructose. In sucrose, the two anomeric OH groups of glucose and fructose have a glycosidic bond; sucrose is therefore one of the non-reducing sugars.

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A. Important monosaccharides

1. Aldoses
   - D-Ribose (Rib)
   - D-Xylose (Xyl)
   - L-Arabinose (Ara)

2. Ketoses
   - D-Ribulose (Rub)
   - D-Fructose (Fru)

3. Deoxyaldoses
   - 2-Deoxy-D-ribose (dRib)
   - L-Fucose (Fuc)

4. Acetylated amino sugars
   - N-Acetyl-D-glucosamine (GlcNAc)
   - N-Acetyl-[D-galactosamine (GalNAc)

5. Acidic monosaccharides
   - D-Glucuronic acid (GlcUA)
   - L-Muramic acid (MurA)

6. Sugar alcohols (alditols)
   - D-Sorbitol
   - D-Manitol

B. Disaccharides

1. Maltose
   - α-D-Glucopyranosyl-\(\beta\)-D-glucopyranose

2. Lactose
   - β-D-Galactopyranosyl-\(\beta\)-D-glucopyranoside

3. Sucrose
   - α-D-Glucopyranosyl-\(\beta\)-D-fructofuranoside
Polysaccharides: overview

Polysaccharides are ubiquitous in nature. They can be classified into three separate groups, based on their different functions. Structural polysaccharides provide mechanical stability to cells, organs, and organisms. Waterbinding polysaccharides are strongly hydrated and prevent cells and tissues from drying out. Finally, reserve polysaccharides serve as carbohydrate stores that release monosaccharides as required. Due to their polymeric nature, reserve carbohydrates are osmotically less active, and they can therefore be stored in large quantities within the cell.

A. Polysaccharides: structure

Polysaccharides that are formed from only one type of monosaccharide are called homoglycans, while those formed from different sugar constituents are called heteroglycans. Both forms can exist as either linear or branched chains.

A section of a glycoprotein molecule is shown here as an example of a branched homoglycan. Amylopectin, the branched component of vegetable starch (see p. 42), has a very similar structure. Both molecules mainly consist of α1→4-linked glucose residues. In glycogen, on average every 8th to 10th residue carries −via an α1→6 bond−another 1,4-linked chain of glucose residues. This gives rise to branched, tree-like structures, which in animal glycogen are covalently bound to a protein, glycogenin (see p. 156).

The linear heteroglycan murein, a structural polysaccharide that stabilizes the cell walls of bacteria, has a more complex structure. Only a short segment of this thread-like molecule is shown here. In murein, two different components, both β1→4-linked, alternate: N-acetylglicosamine (GlcNAc) and N-acetylmuraminic acid (MurNAc), a lacto acid ether of N-acetylglicosamine. Peptides are bound to the carbonyl group of the lactyl groups, and attach the individual strands of murein to each other to form a three-dimensional network (not shown). Synthesis of the network-forming peptides in murein is inhibited by penicillin (see p. 254).

B. Important polysaccharides

The table gives an overview of the composition and make-up both of the glyans mentioned above and of several more.

In addition to murein, bacterial polysaccharides include dextran—glucose polymers that are mostly α1→6-linked and α1→3-branched. In water, dextran forms viscous slime or gels that are used for chromatographic separation of macromolecules after chemical treatment (see p. 78). Dextran are also used as components of blood plasma substitutes (plasma expanders) and food-stuffs.

Carbohydrates from algae (e.g., agarose and carrageenan) can also be used to produce gels. Agarose has been used in microbiology for more than 100 years to reinforce culture media (“agar-agar”). Algal polysaccharides are also added to cosmetics and ready-made foods to modify the consistency of these products.

The starches, the most important vegetable reserve carbohydrate and polysaccharides from plant cell walls, are discussed in greater detail on the following page. Inulin, a fructose polymer, is used as a starch substitute in diabetic’s dietary products (see p. 160). In addition, it serves as a test substance for measuring renal clearance (see p. 322).

Chitin, a homopolymer from β1→4-linked N-acetylglicosamine, is the most important structural substance in insect and crustacean shells, and is thus the most common animal polysaccharide. It also occurs in the cell wall of fungi.

Glycogen, the reserve carbohydrate of higher animals, is stored in the liver and muscle in particular (A, see pp. 156, 336). The formation and breakdown of glycogen are subject to complex regulation by hormones and other factors (see p. 120).
## A. Polysaccharides: structure

![Polysaccharides structure diagram](image)

A. Polysaccharides: structure

- **Glycogen**
  - Branched homopolymer
  - Reducing end

- **Murein**
  - Linear heteropolymer
  - Peptide

## B. Important polysaccharides

<table>
<thead>
<tr>
<th>Polysaccharide</th>
<th>Monosaccharide 1</th>
<th>Monosaccharide 2</th>
<th>Linkage</th>
<th>Branching</th>
<th>Occurrence</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Bacteria</strong></td>
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<td></td>
<td></td>
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<tr>
<td>Murein</td>
<td>D-GlcNAc</td>
<td>D-MurNAc(^1)</td>
<td>β1→4</td>
<td>α1→6</td>
<td>Cell wall</td>
<td>SC</td>
</tr>
<tr>
<td>Dextran</td>
<td>D-Glc</td>
<td>D-Glc</td>
<td>β1→4</td>
<td>α1→6</td>
<td>slime</td>
<td>WB</td>
</tr>
<tr>
<td><strong>Plants</strong></td>
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<tr>
<td>Agarose</td>
<td>D-Gal</td>
<td>L-αGal(^2)</td>
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<td>β1→3</td>
<td>Red algae</td>
<td>WB</td>
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<td>Carrageenan</td>
<td>D-Gal</td>
<td>D-βGlc</td>
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<td>Red algae</td>
<td>WB</td>
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<td>D-Glc</td>
<td>D-Xyl (D-Gal, L-Fuc)</td>
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<td>β1→6</td>
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<td>SC</td>
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<td>Xyloglucan</td>
<td>D-Glc</td>
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<td>β1→3</td>
<td>β1→6</td>
<td>Cell wall (Hemicellulose)</td>
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<td>Arabinan</td>
<td>L-Ara</td>
<td>D-Glc</td>
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<td>α1→4</td>
<td>Cell wall (Pectin)</td>
<td>RC</td>
</tr>
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<td>Amylose</td>
<td>D-Glc</td>
<td>D-Glc</td>
<td>α1→4</td>
<td>α1→4</td>
<td>Amyloplasts</td>
<td>RC</td>
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<td>Amylopectin</td>
<td>D-Glc</td>
<td></td>
<td>β2→1</td>
<td>α1→6</td>
<td>Amyloplasts</td>
<td>RC</td>
</tr>
<tr>
<td>Inulin</td>
<td>D-Fru</td>
<td></td>
<td></td>
<td></td>
<td>Storage cells</td>
<td>RC</td>
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<td><strong>Animals</strong></td>
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<td></td>
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</tr>
<tr>
<td>Chitin</td>
<td>D-GlcNAc</td>
<td></td>
<td>β1→4</td>
<td>α1→4</td>
<td>Insects, crabs, liver, muscle</td>
<td>SK, RK</td>
</tr>
<tr>
<td>Glycogen</td>
<td>D-Glc</td>
<td>D-GlcNAc</td>
<td>β1→4</td>
<td>α1→6</td>
<td>Liver, muscle, connective tissue</td>
<td>SK, WB</td>
</tr>
<tr>
<td>Hyaluronic acid</td>
<td>D-Glc</td>
<td>D-GlcNAc</td>
<td>β1→4</td>
<td>α1→4</td>
<td></td>
<td></td>
</tr>
<tr>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

SC = structural carbohydrate, RC = reserve carbohydrate, WB = water-binding carbohydrate; \(^1\)N-acetylmuramic acid, \(^2\)3,6-anhydrogalactose
Plant polysaccharides

Two glucose polymers of plant origin are of special importance among the polysaccharides: $\beta_1 \rightarrow 4$-linked polymer cellulose and starch, which is mostly $\alpha_1 \rightarrow 4$-linked.

A. Cellulose

Cellulose, a linear homoglycan of $\beta_1 \rightarrow 4$-linked glucose residues, is the most abundant organic substance in nature. Almost half of the total biomass consists of cellulose. Some 40–50% of plant cell walls are formed by cellulose. The proportion of cellulose in cotton fibers, an important raw material, is 98%. Cellulose molecules can contain more than $10^4$ glucose residues (mass 1–2 $\times 10^6$ Da) and can reach lengths of 6–8 $\mu$m.

Naturally occurring cellulose is extremely mechanically stable and is highly resistant to chemical and enzymatic hydrolysis. These properties are due to the conformation of the molecules and their supramolecular organization. The unbranched $\beta_1 \rightarrow 4$ linkage results in linear chains that are stabilized by hydrogen bonds within the chain and between neighboring chains (1). Already during biosynthesis, 50–100 cellulose molecules associate to form an elementary fibril with a diameter of 4 nm. About 20 such elementary fibrils then form a microfibril (2), which is readily visible with the electron microscope.

Cellulose microfibrils make up the basic framework of the primary wall of young plant cells (3), where they form a complex network with other polysaccharides. The linking polysaccharides include hemicellulose, which is a mixture of predominantly neutral heteroglycans (xylans, xyloglucans, arabinoxylans, etc.). Hemicellulose associates with the cellulose fibrils via noncovalent interactions. These complexes are connected by neutral and acidic pectins, which typically contain galacturonic acid. Finally, a collagen-related protein, extensin, is also involved in the formation of primary walls.

In the higher animals, including humans, cellulose is indigestible, but important as roughage (see p. 273). Many herbivores (e.g., the ruminants) have symbiotic unicellular organisms in their digestive tracts that break down cellulose and make it digestible by the host.

B. Starch

Starch, a reserve polysaccharide widely distributed in plants, is the most important carbohydrate in the human diet. In plants, starch is present in the chloroplasts in leaves, as well as in fruits, seeds, and tubers. The starch content is especially high in cereal grains (up to 75% of the dry weight), potato tubers (approximately 65%), and in other plant storage organs.

In these plant organs, starch is present in the form of macroscopically small granules in special organelles known as amyleplasts. Starch granules are virtually insoluble in cold water, but swell dramatically when the water is heated. Some 15–25% of the starch goes into solution in colloidal form when the mixture is subjected to prolonged boiling. This proportion is called amylose (“soluble starch”).

Amylose consists of unbranched $\alpha_1 \rightarrow 4$-linked chains of 200–300 glucose residues. Due the $\alpha$ configuration at $\gamma-1$, these chains form a helix with 6–8 residues per turn (1). The blue coloring that soluble starch takes on when iodine is added (the “iodine–starch reaction”) is caused by the presence of these helices—the iodine atoms form chains inside the amylose helix, and in this largely non-aqueous environment take on a deep blue color. Highly branched polysaccharides turn brown or reddish-brown in the presence of iodine.

Unlike amylose, amylpectin, which is practically insoluble, is branched. On average, one in 20–25 glucose residues is linked to another chain via an $\alpha_1 \rightarrow 6$ bond. This leads to an extended tree-like structure, which—like amylose—contains only one anemic OH group (a “reducing end”). Amylopectin molecules can contain hundreds of thousands of glucose residues; their mass can be more than $10^6$ Da.
A. Cellulose

B. Starch
Glycosaminoglycans and glycoproteins

A. Hyaluronic acid

As constituents of proteoglycans (see p. 346), the glycosaminoglycans—a group of acidic heteropolysaccharides—are important structural elements of the extracellular matrix.

Glycosaminoglycans contain amino sugars as well as glucuronic acid and iduronic acid as characteristic components (see p. 38). In addition, most polysaccharides in this group are esterified to varying extents by sulfuric acid, increasing their acidic quality. Glycosaminoglycans can be found in free form, or as components of proteoglycans throughout the organism.

Hyaluronic acid, an unesterified glycosaminoglycan with a relatively simple structure, consists of disaccharide units in which N-acetylglucosamine and glucuronic acid are alternately β1→4-linked and β1→3-linked. Due to the unusual β1→3 linkage, hyaluronic acid molecules—which may contain several thousand monosaccharide residues—are coiled like a helix. Three disaccharide units form each turn of the helix. The outward-facing hydrophilic carboxylate groups of the glucuronic acid residues are able to bind Ca²⁺ ions. The strong hydration of these groups enables hyaluronic acid and other glycosaminoglycans to bind water up to 10 000 times their own volume in gel form. This is the function which hyaluronic acid has in the vitreous body of the eye, which contains approximately 1% hyaluronic acid and 98% water.

B. Oligosaccharide in immunoglobulin G (IgG)

Many proteins on the surface of the plasma membrane, and the majority of secreted proteins, contain oligosaccharide residues that are post-translationally added to the endoplasmic reticulum and in the Golgi apparatus (see p. 230). By contrast, cytoplasmic proteins are rarely glycosylated. Glycoproteins can contain more than 50% carbohydrate; however, the proportion of protein is generally much greater.

As an example of the carbohydrate component of a glycoprotein, the structure of one of the oligosaccharide chains of immunoglobulin G (IgG; see p. 300) is shown here. The oligosaccharide has an N-glycosidic link to the amide group of an asparagine residue in the F₃ part of the protein. Its function is not known.

Like all N-linked carbohydrates, the oligosaccharide in IgG contains a T-shaped core structure consisting of two N-acetylgalactosamines and three mannose residues (shown in violet). In addition, in this case the structure contains two further N-acetylglucosamine residues, as well as a fucose residue and a galactose residue. Glycoproteins show many different types of branching. In this case, we not only have β1→4 linkage, but also β1→2, α1→3, and α1→6 bonds.

C. Glycoproteins: forms

On the cell surface of certain glycoproteins, O-glycosidic links are found between the carbohydrate part and a serine or threonine residue, instead of N-glycosidic links to asparagine residues. This type of link is less common than the N-glycosidic one.

There are two types of oligosaccharide structure with N-glycosidic links, which arise through two different biosynthetic pathways. During glycosylation in the ER, the protein is initially linked to an oligosaccharide, which in addition to the core structure contains six further mannose residues and three terminal glucose residues (see p. 230). The simpler from of oligosaccharide (the mannose-rich type) is produced when only the glucose residues are cleaved from the primary product, and no additional residues are added. In other cases, the mannose residues that are located outside the core structure are also removed and replaced by other sugars. This produces oligosaccharides such as those shown on the right (the complex type). At the external end of the structure, glycoproteins of the complex type often contain N-acetyleneuraminic acid residues, which give the oligosaccharide components negative charges.
A. Hyaluronic acid

Disaccharide unit

B. Oligosaccharide in immunoglobulin G (IgG)

C. Glycoproteins: forms
Overview

A. Classification

The lipids are a large and heterogeneous group of substances of biological origin that are easily dissolved in organic solvents such as methanol, acetone, chloroform, and benzene. By contrast, they are either insoluble or only poorly soluble in water. Their low water solubility is due to a lack of polarizing atoms such as O, N, S, and P (see p. 6).

Lipids can be classified into substances that are either hydrolyzable—i.e., able to undergo hydrolytic cleavage—or nonhydrolyzable. Only a few examples of the many lipids known can be mentioned here. The individual classes of lipids are discussed in more detail in the following pages.

Hydrolyzable lipids (components shown in brackets). The simple esters include the fats (triaclylglycerol; one glycerol + three acyl residues); the waxes (one fatty alcohol + one acyl residue); and the sterol esters (one sterol + one acyl residue). The phospholipids are esters with more complex structures. Their characteristic component is a phosphate residue. The phospholipids include the phosphatic acids (one glycerol + two acyl residues + one phosphate) and the phosphatides (one glycerol + two acyl residues + one phosphate + one amino alcohol). In the sphingolipids, glycerol and one acyl residue are replaced by sphingosine. Particularly important in this group are the sugar-containing glycolipids (one sphingosine + one fatty acid + sugar). The cerebroside (one sphingosine + one fatty acid + one sugar) and ganglioside (one sphingosine + one fatty acid + several different sugars, including neuraminic acid) are representatives of this group.

The components of the hydrolyzable lipids are linked to one another by ester bonds. They are easily broken down either enzymatically or chemically.

Non-hydrolyzable lipids. The hydrocarbons include the alkanes and carotenoids. The lipid alcohols are also not hydrolyzable. They include long-chained alkanols and cyclic sterols such as cholesterol, and steroids such as estradiol and testosterone. The most important acids among the lipids are fatty acids. The eicosanoids also belong to this group; these are derivatives of the polyunsaturated fatty acid arachidonic acid (see p. 290).

B. Biological roles

1. Fuel. Lipids are an important source of energy in the diet. In quantitative terms, they represent the principal energy reserve in animals. Neutral fats in particular are stored in specialized cells, known as adipocytes. Fatty acids are released from these again as needed, and these are then oxidized in the mitochondria to form water and carbon dioxide, with oxygen being consumed. This process also gives rise to reduced coenzymes, which are used for ATP production in the respiratory chain (see p. 140).

2. Nutrients. Amphipathic lipids are used by cells to build membranes (see p. 214). Typical membrane lipids include phospholipids, glycolipids, and cholesterol. Fats are only weakly amphipathic and are therefore not suitable as membrane components.

3. Insulation. Lipids are excellent insulators. In the higher animals, neutral fats are found in the subcutaneous tissue and around various organs, where they serve as mechanical and thermal insulators. As the principal constituent of cell membranes, lipids also insulate cells from their environment mechanically and electrically. The impermeability of lipid membranes to ions allows the formation of the membrane potential (see p. 126).

4. Special tasks. Some lipids have adopted special roles in the body. Steroids, eicosanoids, and some metabolites of phospholipids have signaling functions. They serve as hormones, mediators, and second messengers (see p. 370). Other lipids form anchors to attach proteins to membranes (see p. 214). The lipids also produce cofactors for enzymatic reactions—e.g., vitamin K (see p. 52) and ubiquinone (see p. 104). The carotenoid retinol, a light-sensitive lipid, is of central importance in the process of vision (see p. 358).

Several lipids are not formed independently in the human body. These substances, as essential fatty acids and fat-soluble vitamins, are indispensable components of nutrition (see pp. 364ff.).
**A. Classification**

- **Hydrolyzable lipids**
  - Esters
  - Fats
  - Waxes
  - Sterol esters

- **Non-hydrolyzable lipids**
  - Hydrocarbons
    - Alkanes
    - Carotenoids
  - Alcohols
    - Long-chain alkanols
    - Sterols
  - Acids
    - Fatty acids
    - Eicosanoids

- **Glycolipids**
  - Cerebrosides
  - Gangliosides

**B. Biological roles**

1. **Fuel**
   - Glycerol
   - Fatty acid
   - ADP + P
   - O2
   - ATP
   - Mitochondrion

2. **Building block**
   - Membrane
   - Cytoplasm
   - Phospholipid
   - Lipid bilayer

3. **Thermal insulator**
   - Cell
   - 37°C
   - 0°C

4. **Special tasks**
   - CoQ
   - Cofactor
   - Signaling
   - Anchor
   - Visual pigment

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Fatty acids and fats

A. Carboxylic acids

The naturally occurring fatty acids are carboxylic acids with unbranched hydrocarbon chains of 4–24 carbon atoms. They are present in all organisms as components of fats and membrane lipids. In these compounds, they are esterified with alcohols (glycerol, sphingosine, or cholesterol). However, fatty acids are also found in small amounts in unesterified form. In this case, they are known as free fatty acids (FFAs). As free fatty acids have strongly amphipathic properties (see p. 28), they are usually present in protein-bound forms.

The table lists the full series of aliphatic carboxylic acids that are found in plants and animals. In higher plants and animals, unbranched, longchain fatty acids with either 16 or 18 carbon atoms are the most common—e.g., palmitic and stearic acid. The number of carbon atoms in the longer, natural fatty acids is always even. This is because they are biosynthesized from C2 building blocks (see p. 168).

Some fatty acids contain one or more isolated double bonds, and are therefore “unsaturated.” Common unsaturated fatty acids include oleic acid and linoleic acid. Of the two possible cis–trans isomers (see p.8), usually only the cis forms are found in natural lipids. Branched fatty acids only occur in bacteria. A shorthand notation with several numbers is used for precise characterization of the structure of fatty acids—e.g., 18:2(n-6) for linoleic acid. The first figure stands for the number of C atoms, while the second gives the number of double bonds. The positions of the double bonds follow after the semicolon. As usual, numbering starts at the carbon with the highest oxidation state (i.e., the carboxyl group corresponds to C-1). Greek letters are also commonly used (α = C-2; β = C-3; ω = the last carbon, ω-3 = the third last carbon).

Essential fatty acids are fatty acids that have to be supplied in the diet. Without exception, these are all polyunsaturated fatty acids: the C18 fatty acid arachidonic acid (20:4; 5,8,11,14) and the two C20 acids linoleic acid (18:2;9,12) and linolenic acid (18:3;9,12,15). The animal organism requires arachidonic acid to synthesize eicosanoids (see p. 390). As the organism is capable of elongating fatty acids by adding C2 units, but is not able to introduce double bonds into the end sections of fatty acids (after C-9), arachidonic acid has to be supplied with the diet. Linoleic and linolenic acid can be converted into arachidonic acid by elongation, and they can therefore replace arachidonic acid in the diet.

B. Structure of fats

Fats are esters of the trivalent alcohol glycerol with three fatty acids. When a single fatty acid is esterified with glycerol, the product is referred to as a monoaicylglycerol (fatty acid residue = acyl residue).

Formally, esterification with additional fatty acids leads to diacylglycerol and ultimately to triacylglycerol, the actual fat (formerly termed “triglyceride”). As triacylglycerols are uncharged, they are also referred to as neutral fats. The carbon atoms of glycerol are not usually equivalent in fats. They are distinguished by their “sn” number, where sn stands for “stereospecific numbering.”

The three acyl residues of a fat molecule may differ in terms of their chain length and the number of double bonds they contain. This results in a large number of possible combinations of individual fat molecules. When extracted from biological materials, fats always represent mixtures of very similar compounds, which differ in their fatty acid residues. A chiral center can arise at the middle C atom (sn-2) of a triacylglycerol if the two external fatty acids are different. The monoaicylglycerols and diacylglycerols shown here are also chiral compounds. Nutritional fats contain palmitic, stearic, oleic acid, and linoleic acid particularly often. Unsaturated fatty acids are usually found at the central C atom of glycerol.

The length of the fatty acid residues and the number of their double bonds affect the melting point of the fats. The shorter the fatty acid residues and the more double bonds they contain, the lower their melting points.
A. Carboxylic acids

<table>
<thead>
<tr>
<th>Name</th>
<th>Number of carbons</th>
<th>Number of double bonds</th>
<th>Position of double bonds</th>
</tr>
</thead>
<tbody>
<tr>
<td>Formic acid</td>
<td>1:0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Acetic acid</td>
<td>2:0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionic acid</td>
<td>3:0</td>
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</tr>
<tr>
<td>Butyric acid</td>
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<td>Valeric acid</td>
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<td>Caproic acid</td>
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<td>Lauric acid</td>
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<td>Myristic acid</td>
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<td>Palmitic acid</td>
<td>16:0</td>
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<td>Stearic acid</td>
<td>18:0</td>
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<td>Oleic acid</td>
<td>18:1; 9</td>
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<td>Linoleic acid</td>
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<td>Linolenic acid</td>
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<td>Behenic acid</td>
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<td>Erucic acid</td>
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<td>Lignoceric acid</td>
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<tr>
<td>Nervonic acid</td>
<td>24:1; 15</td>
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</table>

- Not contained in lipids

B. Structure of fats

- Ester bonding
- Chiral center
- sn number
- Fatty acids
- Glycerol
- Van der Waals model of tristearglycerol

Rotatable around C-C bond
Phospholipids and glycolipids

A. Structure of phospholipids and glycolipids

Fats (triacylglycerol, 1) are esters of glycerol with three fatty acids (see p. 48). Within the cell, they mainly occur as fat droplets. In the blood, they are transported in the hydrophobic interior of lipoproteins (see p. 278).

Phospholipids (2) are the main constituents of biological membranes (see pp. 214–217). Their common feature is a phosphate residue that is esterified with the hydroxyl group at C-3 of glycerol. Due to this residue, phospholipids have at least one negative charge at a neutral pH.

Phosphatidates (anions of the phosphatidic acids), the simplest phospholipids, are phosphate esters of diacylglycerol. They are important intermediates in the biosynthesis of fats and phospholipids (see p. 170). Phosphatidates can also be released from phospholipids by phospholipases.

The other phospholipids can be derived from phosphatidates (residue = phosphatidyl). Their phosphate residues are esterified with the hydroxyl group of an amino alcohol (choline, ethanolamine, or serine) or with the cyclohexane derivative myo-inositol. Phosphatidylcholine is shown here as an example of this type of compound. When two phosphatidyl residues are linked with one glycerol, the result is cardiolipin (not shown), a phospholipid that is characteristic of the inner mitochondrial membrane. Lysophospholipids arise from phospholipids by enzymatic cleavage of an acyl residue. The hemolytic effect of bee and snake venoms is due in part to this reaction.

Phosphatidylcholine (lecithin) is the most abundant phospholipid in membranes. Phosphatidylethanolamine (cephalin) has an ethanolamine residue instead of choline, and phosphatidylserine has a serine residue. In phosphatidylinositol, phosphatidate is esterified with the sugarlike cyclic polyalcohol myo-inositol. A doubly phosphorylated derivative of this phospholipid, phosphatidylinositol 4,5-bisphosphate, is a special component of membranes, which, by enzymatic cleavage, can give rise to two second messengers, diacylglycerol (DAG) and inositol 1,4,5trisphosphate (InsP3; see p. 386).

Some phospholipids carry additional charges, in addition to the negative charge at the phosphate residue. In phosphatidyethanolamine and phosphatidylethanolamine, the N-atom of the amino alcohol is positively charged. As a whole, these two phosphatides therefore appear to be neutral. In contrast, phosphatidylserine—with one additional positive charge and one additional negative charge in the serine residue—and phosphatidylinositol (with no additional charge) have a negative net charge, due to the phosphate residue.

Sphingolipids (3), which are found in large quantities in the membranes of nerve cells in the brain and in neural tissues, have a slightly different structure from the other membrane lipids discussed so far. In sphingolipids, sphingosine, an amino alcohol with an unsaturated alkyl side chain, replaces glycerol and one of the acyl residues. When sphingosine forms an amide bond to a fatty acid, the compound is called ceramide (3). This is the precursor of the sphingolipids. Sphingomyelin (2)—the most important sphingolipid—has an additional phosphate residue with a choline group attached to it on the sphingosine, in addition to the fatty acid.

Glycolipids (3) are present in all tissues on the outer surface of the plasma membrane. They consist of sphingosine, a fatty acid, and an oligosaccharide residue, which can sometimes be quite large. The phosphate residue typical of phospholipids is absent. Galactosylceramide and glucosylceramide (known as cerebrosides) are simple representatives of this group. Cerebrosides in which the sugar is esterified with sulfuric acid are known as sulfatides. Gangliosides are the most complex glycolipids. They constitute a large family of membrane lipids with receptor functions that are as yet largely unknown. A characteristic component of many gangliosides is N-acetyleneuraminic acid (sialic acid; see p. 38).

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A. Structure of fats, phospholipids, and glycolipids

1. Fats

2. Phospholipids

3. Sphingolipids

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Isoprenoids

A. Activated acetic acid as a component of lipids

Although the lipids found in plant and animal organisms occur in many different forms, they are all closely related biogenetically; they are all derived from acetyl-CoA, the “activated acetic acid” (see pp. 12, 110).

1. One major pathway leads from acetyl-CoA to the activated fatty acids (acyl-CoA; for details, see p. 168). Fats, phospholipids, and glycolipids are synthesized from these, and fatty acid derivatives in particular are formed. Quantitatively, this is the most important pathway in animals and most plants.

2. The second pathway leads from acetyl-CoA to isopentenyl diphosphate (“active isoprene”), the basic component for the isoprenoids. Its biosynthesis is discussed in connection with biosynthesis of the isoprenoid, cholesterol (see p. 172).

B. Isoprenoids

Formally, isoprenoids are derived from a single common building block, isoprene (2-methyl-1,3-butadiene), a methyl-branched compound with five C atoms. Activated isoprene, isopentenyl diphosphate, is used by plants and animals to biosynthesize linear and cyclic oligomers and polymers. For the isoprenoids listed here—which only represent a small selection—the number of isoprene units (1) is shown.

From activated isoprene, the metabolic pathway leads via dimerization to activated geraniol (1 + 2) and then to activated farnesol (1 + 3). At this point, the pathway divides into two. Further extension of farnesol leads to chains with increasing numbers of isoprene units—e.g., phytol (1 + 4), dolichol (1 + 14–24), and rubber (1 + 700–5000). The other pathway involves a “head-to-head” linkage between two farnesol residues, giving rise to squalene (1 + 6), which, in turn, is converted to cholesterol (1 + 6) and the other steroids.

The ability to synthesize particular isoprenoids is limited to a few species of plants and animals. For example, rubber is only formed by a few plant species, including the rubber tree (Hevea brasiliensis). Several isoprenoids that are required by animals for metabolism, but cannot be produced by them independently, are vitamins; this group includes vitamins A, D, E, and K. Due to its structure and function, vitamin D is now usually classified as a steroid hormone (see pp. 56, 330). Isoprene metabolism in plants is very complex. Plants can synthesize many types of aromatic substances and volatile oils from isoprenoids. Examples include menthol (1 + 2), camphor (1 + 2), and citronellol (1 + 2). These C_{10} compounds are also called monoterpenes. Similarly, compounds consisting of three isoprene units (1 + 3) are termed sesquiterpenes, and the steroids (1 + 6) are called triterpenes.

Isoprenoids that have hormonal and signaling functions form an important group. These include steroid hormones (1 + 6) and retinoic (the anion of retinoic acid; 1 + 3) in vertebrates, and juvenile hormone (1 + 3) in arthropods. Some plant hormones also belong to the isoprenoids—e.g., the cytokinins, abscisic acid, and brassinosteroids.

Isoprene chains are sometimes used as lipid anchors to fix molecules to membranes (see p. 214). Chlorophyll has a phytyl residue (1 + 4) as a lipid anchor. Coenzymes with isoprenoid anchors of various lengths include ubiquinone (coenzyme Q; 1 + 6–10), plastoquinone (1 + 9), and menaquinone (vitamin K; 1 + 4–6). Proteins can also be anchored to membranes by isoprenylation.

In some cases, an isoprene residue is used as an element to modify molecules chemically. One example of this is N-isopentenyl-AMP, which occurs as a modified component in tRNA.
A. Activated acetic acid as a component of lipids

1. Activated acetic acid
2. Active isoprene

B. Isoprenoids

Metabolite

Building block of all isoprenoids

Biosynthesis only in plants and micro-organisms

Isoprenoids
Steroid structure

A. Steroid building blocks

Common to all of the steroids is a molecular core structure consisting of four saturated rings, known as guanne. At the end of the steroid core, many steroids also carry a side chain, as seen in cholestane, the basic component of the steroids (steroid alcohols).

B. Spatial structure

The four rings of the steroids are distinguished using the letters A, B, C, and D. Due to the tetrahedral arrangement of the single carbon bonds, the rings are not flat, but puckered. Various ring conformations are known by the terms "chair," "boat," and "twisted" (not shown). The chair and boat conformations are common. Fivemembered rings frequently adopt a conformation referred to as an "envelope". Some rings can be converted from one conformation to another at room temperature, but with steroids this is difficult.

Substituents of the steroid core lie either approximately in the same plane as the ring (e = equatorial) or nearly perpendicular to it (a = axial). In three-dimensional representations, substituents pointing toward the observer are indicated by an unbroken line (β position), while bonds pointing into the plane of the page are indicated by a dashed line (α position). The so-called angular methyl groups at C-10 and C-13 of the steroids always adopt the β position.

Neighboring rings can lie in the same plane (trans; 2) or at an angle to one another (cis; 1). This depends on the positions of the substituents of the shared ring carbons, which can be arranged either cis or trans to the angular methyl group at C-10. The substituents of steroid that lie at the points of intersection of the individual rings are usually in trans position. As a whole, the core of most steroids is more or less planar, and looks like a flat disk. The only exceptions to this are the ecdysteroids, bile acids (in which A:B is cis), cardiac glycosides, and toad toxins.

A more realistic impression of the threedimensional structure of steroids is provided by the space-filling model of cholesterol (3). The four rings form a fairly rigid scaffolding, onto which the much more mobile side chain is attached.

Steroids are relatively apolar (hydrophobic). Some polar groups—e.g., hydroxyl and oxo groups—give them amphipathic properties. This characteristic is especially pronounced with the bile acids (see p. 314).

C. Thin-layer chromatography

Thin-layer chromatography (TLC) is a powerful, mainly analytic, technique for rapidly separating lipids and other small molecules such as amino acids, nucleotides, vitamins, and drugs. The sample being analyzed is applied to a plate made of glass, aluminum, or plastic, which is covered with a thin layer of silica gel or other material (1). The plate is then placed in a chromatography chamber that contains some solvent. Driven by capillary forces, the solvent moves up the plate (2). The substances in the sample move with the solvent. The speed at which they move is determined by their distribution between the stationary phase (the hydrophilic silica), and the mobile phase (the hydrophobic solvent). When the solvent reaches the top edge of the plate, the chromatography is stopped. After evaporation of the solvent, the separated substances can be made visible using appropriate staining methods or with physical processes (e.g., ultraviolet light) (3). The movement of a substance in a given TLC system is expressed as its R<sub>f</sub> value. In this way, compounds that are not known can be identified by comparison with reference substances.

A process in which the polarity of the stationary and mobile phases is reversed—i.e., the stationary phase is apolar and the solvent is polar—is known as "reversed-phase thin-layer chromatography" (RP-TLC).
A. Steroid building blocks

B. 3D structure

C. Thin-layer chromatography
Steroids: overview

The three most important groups of steroids are the steroids, bile acids, and steroid hormones. Particularly in plants, compounds with steroid structures are also found that are notable for their pharmacological effects—steroid alkaloids, digitalis glycosides, and saponins.

A. Sterols

Sterols are steroid alcohols. They have a β-positioned hydroxyl group at C-3 and one or more double bonds in ring B and in the side chain. There are no further oxygen functions, as in the carbonyl and carboxyl groups.

The most important sterol in animals is cholesterol. Plants and microorganisms have a wide variety of closely related sterols instead of cholesterol—e.g., ergosterol, β-sitosterol, and stigmasterol.

Cholesterol is present in all animal tissues, and particularly in neural tissue. It is a major constituent of cellular membranes, in which it regulates fluidity (see p. 216). The storage and transport forms of cholesterol are its esters with fatty acids. In lipoproteins, cholesterol and its fatty acid esters are associated with other lipids (see p. 278). Cholesterol is a constituent of the bile and is therefore found in many gallstones. Its biosynthesis, metabolism, and transport are discussed elsewhere (see pp. 172, 312).

Cholesterol-rich lipoproteins of the LDL type are particularly important in the development of arteriosclerosis, in which the arterial walls are altered in connection with an excess plasma cholesterol level. In terms of dietary physiology, it is important that plant foods are low in cholesterol. By contrast, animal foods can contain large amounts of cholesterol—particularly butter, egg yolk, meat, liver, and brain.

B. Bile acids

Bile acids are synthesized from cholesterol in the liver (see p. 314). Their structures can therefore be derived from that of cholesterol. Characteristic for the bile acids is a side chain shortened by three C atoms in which the last carbon atom is oxidized to a carboxyl group. The double bond in ring B is reduced and rings A and B are in cis position relative to each other (see p. 54). One to three hydroxyl groups (in α position) are found in the steroid core at positions 3, 7, and 12. Bile acids keep bile cholesterol in a soluble state as micelles and promote the digestion of lipids in the intestine (see p. 270). Cholic acid and chenodeoxycholic acid are primary bile acids that are formed by the liver. Their dehydroxylation at C-7 by microorganisms from the intestinal flora gives rise to the secondary bile acids lithocholic acid and deoxycholic acid.

C. Steroid hormones

The conversion of cholesterol to steroid hormones (see p. 376) is of minor importance quantitatively, but of major importance in terms of physiology. The steroid hormones are a group of lipophilic signal substances that regulate metabolism, growth, and reproduction (see p. 374).

Humans have six steroid hormones: progesterone, cortisol, aldosterone, testosterone, estradiol, and calcitriol. With the exception of calcitriol, these steroids have either no side chain or only a short side one consisting of two carbons. Characteristic for most of them is an oxo group at C-3, conjugated with a double bond between C-4 and C-5 of ring A. Differences occur in rings C and D. Estradiol is aromatic in ring A, and its hydroxyl group at C-3 is therefore phenolic. Calcitriol differs from other vertebrate steroid hormones; it still contains the complete carbon framework of cholesterol, but light-dependent opening of ring B turns it into what is termed a “secosteroid” (a steroid with an open ring).

Ec dysone is the steroid hormone of the arthropods. It can be regarded as an early form of the steroid hormones. Steroid hormones with signaling functions also occur in plants.
### A. Sterols

- **Animal sterol**
- **Cholesterol**
- **Ergosterol**
- **Plant sterols**
- **Stigmasterol**
- **β-Sitosterol**

### B. Bile acids

- **Lithocholic acid**
- **Cholic acid**
- **Chenodeoxycholic acid**
- **Deoxycholic acid**

### C. Steroid hormones

- **Cortisol**
- **Aldosterone**
- **Testosterone**
- **Estradiol**
- **Progesterone**
- **Calcitriol**
- **Ecdysone**

**Molting hormone of insects, spiders, and crabs**

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Amino acids: chemistry and properties

A. Amino acids: functions

The amino acids (2-amino carboxylic acids) fulfill various functions in the organism. Above all, they serve as the components of peptides and proteins. Only the 20 proteinogenic amino acids (see p. 60) are included in the genetic code and therefore regularly found in proteins. Some of these amino acids undergo further (post-translational) change following their incorporation into proteins (see p. 62). Amino acids or their derivatives are also components of lipids—e.g., serine in phospholipids and glycine in bile salts. Several amino acids function as neurotransmitters (see p. 352), while others are precursors of neurotransmitters, mediators, or hormones (see p. 380). Amino acids are important (and sometimes essential) components of food (see p. 360). Specific amino acids form precursors for other metabolites—e.g., for glucose in gluconeogenesis, for purine and pyrimidine bases, for heme, and for other molecules. Several non-proteinogenic amino acids function as intermediates in the synthesis and breakdown of proteinogenic amino acids (see p. 412) and in the urea cycle (see p. 182).

B. Optical activity

The natural amino acids are mainly α-amino acids, in contrast to β-amino acids such as β-alanine and taurine. Most α-amino acids have four different substituents at C-2 (Ca). The α atom therefore represents a chiral center—i.e., there are two different enantiomers (L- and D-amino acids; see p. 8). Among the proteinogenic amino acids, only glycine is not chiral (R = H). In nature, it is almost exclusively L-amino acids that are found. D-Amino acids occur in bacteria—e.g., in murein (see p. 40)—and in peptide antibiotics. In animal metabolism, D-Amino acids would disturb the enzymatic reactions of L-amino acids and they are therefore broken down in the liver by the enzyme D-amino acid oxidase.

The Fischer projection (center) is used to present the formulas for chiral centers in biomolecules. It is derived from their three-di-
mensional structure as follows: firstly, the tetrahedron is rotated in such a way that the most oxidized group (the carboxylate group) is at the top. Rotation is then continued until the line connecting line COO⁻ and R (red) is level with the page. In L-amino acids, the NH₃⁺ group is then on the left, while in D-amino acids it is on the right.

C. Dissociation curve of histidine

All amino acids have at least two ionizable groups, and their net charge therefore depends on the pH value. The COOH groups at the α-C atom have pKₐ values of between 1.8 and 2.8 and are therefore more acidic than simple monocarboxylic acids. The basicity of the α-amino function also varies, with pKₐ values of between 8.8 and 10.6, depending on the amino acid. Acidic and basic amino acids have additional ionizable groups in their side chain. The pKₐ values of these side chains are listed on p. 60. The electrical charges of peptides and proteins are mainly determined by groups in the side chains, as most α-carboxyl and α-amino functions are linked to peptide bonds (see p. 66).

Histidine can be used here as an example of the pH-dependence of the net charge of an amino acid. In addition to the carboxyl group and the amino group at the α-C atom with pKₐ values of 1.8 and 9.2, respectively, histidine also has an imidazole residue in its side chain with a pKₐ value of 6.0. As the pH increases, the net charge (the sum of the positive and negative charges) therefore changes from +2 to −1. At pH 7.6, the net charge is zero, even though the molecule contains two almost completely ionized groups in these conditions. This pH value is called the isoelectric point.

At its isoelectric point, histidine is said to be zwitterionic, as it has both anionic and cationic properties. Most other amino acids are also zwitterionic at neutral pH. Peptides and proteins also have isoelectric points, which can vary widely depending on the composition of the amino acids.
A. Amino acids: functions

Components of:
- Peptides
- Proteins
- Phospholipids

Precursors of:
- Keto acids
- Biogenic amines
- Glucose
- Nucleotides
- Heme, creatine

Transport molecule for:
- NH₃ groups

Neurotransmitters:
- Glutamate
- Aspartate
- Glycine

B. Optical activity

Fischer projections:
- L-Amino acid
- D-Amino acid (mirror image)

C. Dissociation curve of histidine

(pH 0.5)

(Two values)

(pH 5)

(pH 11)
Proteinogenic amino acids

A. The proteinogenic amino acids

The amino acids that are included in the genetic code (see p. 248) are described as “proteinogenic.” With a few exceptions (see p. 58), only these amino acids can be incorporated into proteins through translation. Only the side chains of the 20 proteinogenic amino acids are shown here. Their classification is based on the chemical structure of the side chains, on the one hand, and on their polarity on the other (see p. 6). The literature includes several slightly different systems for classifying amino acids, and details may differ from those in the system used here.

For each amino acid, the illustration names:
- Membership of structural classes I–VII (see below; e.g., III and VI for histidine)
- Name and abbreviation, formed from the first three letters of the name (e.g., histidine, His)
- The one-letter symbol introduced to save space in the electronic processing of sequence data (H for histidine)
- A quantitative value for the polarity of the side chain (bottom left; 10.3 for histidine). The more positive this value is, the more polar the amino acid is.

In addition, the polarity of the side chains is indicated by color. It increases from yellow, through light and dark green, to bluish green.

For ionizing side chains, the corresponding pKₐ values are also given (red numbers).

The aliphatic amino acids (class I) include glycine, alanine, valine, leucine, and isoleucine. These amino acids do not contain heteroatoms (N, O, or S) in their side chains and do not contain a ring system. Their side chains are markedly apolar. Together with threonine (see below), valine, leucine, and isoleucine form the group of branched-chain amino acids. The sulfur-containing amino acids cysteine and methionine (class II), are also apolar. However, in the case of cysteine, this only applies to the undissociated state. Due to its ability to form disulfide bonds, cysteine plays an important role in the stabilization of proteins (see p. 72). Two cysteine residues linked by a disulfide bridge are referred to as cystine (not shown).

The aromatic amino acids (class III) contain resonance-stabilized rings. In this group, only phenylalanine has strongly apolar properties. Tyrosine and tryptophan are moderately polar, and histidine is even strongly polar. The imidazole ring of histidine is already protonated at weakly acidic pH values. Histidine, which is only aromatic in protonated form (see p. 58), can therefore also be classified as a basic amino acid. Tyrosine and tryptophan show strong light absorption at wavelengths of 250–300 nm.

The neutral amino acids (class IV) have hydroxyl groups (serine, threonine) or amide groups (asparagine, glutamine). Despite their nonionic nature, the amide groups of asparagine and glutamine are markedly polar.

The carboxyl groups in the side chains of the acidic amino acids aspartic acid and glutamic acid (class V) are almost completely ionized at physiological pH values. The side chains of the basic amino acids lysine and arginine are also fully ionized—i.e., positively charged—at neutral pH. Arginine, with its positively charge guanidinium group, is particularly strongly basic, and therefore extremely polar.

Proline (VII) is a special case. Together with the α-C atom and the α-NH₂ group, its side chain forms a five-membered ring. Its nitrogen atom is only weakly basic and is not protonated at physiological pH. Due to its ring structure, proline causes bending of the peptide chain in proteins (this is important in collagen, for example; see p. 70).

Several proteinogenic amino acids cannot be synthesized by the human organism, and therefore have to be supplied from the diet. These essential amino acids (see p. 360) are marked with a star in the illustration. Histidine and possibly also arginine are essential for infants and small children.
Non-proteinogenic amino acids

In addition to the 20 proteinogenic amino acids (see p.60), there are also many more compounds of the same type in nature. These arise during metabolic reactions (A) or as a result of enzymatic modifications of amino acid residues in peptides or proteins (B). The “biogenic amines” (C) are synthesized from α-amino acids by decarboxylation.

A. Rare amino acids 

Only a few important representatives of the non-proteinogenic amino acids are mentioned here. The basic amino acid ornithine is an analogue of lysine with a shortened side chain. Transfer of a carboxamyl residue to ornithine yields citrulline. Both of these amino acids are intermediates in the urea cycle (see p.182). Dopaa (an acronym of 3,4-dihydroxyphenylalanine) is synthesized by hydroxylation of tyrosine. It is an intermediate in the biosynthesis of catecholamines (see p.352) and of melanin. It is in clinical use in the treatment of Parkinson’s disease. Selenocysteine, a cysteine analogue, occurs as a component of a few proteins—e.g., in the enzyme glutathione peroxidase (see p.284).

B. Post-translational protein modification

Subsequent alteration of amino acid residues in finished peptides and proteins is referred to as post-translational modification. These reactions usually only involve polar amino acid residues, and they serve various purposes.

The free α-amino group at the N-terminus is blocked in many proteins by an acetyl residue or a longer acyl residue (acylation). N-terminal glutamate can cyclize into a pyroglutamate residue, while the C-terminal carboxylate group can be present in an amidated form (see TSH, p.380). The side chains of serine and asparagine residues are often linked to oligosaccharides (glycosylation, see p.239).

Phosphorylation of proteins mainly affects serine and tyrosine residues. These reactions have mainly regulatory functions (see p.114). Aspartate and histidine residues of enzymes are sometimes phosphorylated, too. A special modification of glutamate residues, γ-carboxylation, is found in coagulation factors. It is essential for blood coagulation (see p.290).

The ε-amino group of lysine residues is subject to a particularly large number of modifications. Its acetylation (or deacetylation) is an important mechanism for controlling genetic activity (see p.244). Many coenzymes and cofactors are covalently linked to lysine residues. These include biotin (see p.108), lipop acid (see p.106), and pyridoxal phosphate (see p.108), as well as retinal (see p.358). Covalent modification with ubiquitin marks proteins for breakdown (see p.176). In collagen, lysine and proline residues are modified by hydroxylation to prepare for the formation of stable fibrils (see p.70). Cysteine residues form disulfide bonds with one another (see p.72). Cysteine prenylation serves to anchor proteins in membranes (see p.214). Covalent bonding of a cysteine residue with heme occurs in cytochrome c. Flavins are sometimes covalently bound to cysteine or histidine residues of enzymes. Among the modifications of tyrosine residues, conversion into iodinated thyroxine (see p.374) is particularly interesting.

C. Biogenic amines

Several amino acids are broken down by decarboxylation. This reaction gives rise to what are known as biogenic amines, which have various functions. Some of them are components of biomolecules, such as ethanolamine in phospholipids (see p.50). Cysteamine and γ-alanine are components of coenzyme A (see p.12) and of pantetheine (see pp.108, 168). Other amines function as signaling substances. An important neurotransmitter derived from glutamate is γ-aminobutyrate (GABA, see p.356). The transmitter dopamine is also a precursor for the catecholamines epinephrine and norepinephrine (see p.352). The biogenic amine serotonin, a substance that has many effects, is synthesized from tryptophan via the intermediate 5-hydroxytryptophan.

Monamines are inactivated into aldehydes by amine oxidase (monoamine oxidase, “MAO”) with deamination and simultaneous oxidation. MAO inhibitors therefore play an important role in pharmacological interventions in neurotransmitter metabolism.

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A. Rare amino acids

- Ornithine
- Citrulline
- L-Dopa
- Selenocysteine

B. Post-translational protein modification

- Pyroglutamyl-Acetyl-Formyl-Myristoyl
- Oligosaccharide (O-glycosylation)
- Oligosaccharide (N-glycosylation)
- Acetyl-Methyl-Hydroxy
- Pyrido-Liponat

C. Biogenic amines

<table>
<thead>
<tr>
<th>Amino acid</th>
<th>Amine</th>
<th>Function</th>
<th>Amino acid</th>
<th>Amine</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Serine</td>
<td>Ethanolamine</td>
<td>Glutamate</td>
<td>Glutamate</td>
<td>γ-Aminobutyrate</td>
<td>Neurotransmitter (GABA)</td>
</tr>
<tr>
<td>Cysteine</td>
<td>Cysteamine</td>
<td>Component of coenzyme A</td>
<td>Histidine</td>
<td>Histamine</td>
<td>Mediator, neurotransmitter</td>
</tr>
<tr>
<td>Threonine</td>
<td>Amino-propanol</td>
<td>Component of vitamin B12</td>
<td>Dopa</td>
<td>Dopamine</td>
<td>Neurotransmitter</td>
</tr>
<tr>
<td>Aspartate</td>
<td>β-Alanine</td>
<td>Component of coenzyme A</td>
<td>5-Hydroxytryptophan</td>
<td>Serotonin</td>
<td>Mediator, neurotransmitter</td>
</tr>
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</table>

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Peptides and proteins: overview

A. Proteins

When amino acids are linked together by acid–amide bonds, linear macromolecules (polypeptides) are produced. Those containing more than ca. 100 amino acid residues are described as proteins. Every organism contains thousands of different proteins, which have a variety of functions. At a magnification of ca. 1.5 million, the semi-schematic illustration shows the structures of a few intra and extracellular proteins, giving an impression of their variety. The functions of proteins can be classified as follows.

Establishment and maintenance of structure. Structural proteins are responsible for the shape and stability of cells and tissues. A small part of a collagen molecule is shown as an example (right; see p.70). The complete molecule is 1.5 300 nm in size, and at the magnification used here it would be as long as three pages of the book. Histones are also structural proteins. They organize the arrangement of DNA in chromatin. The basic components of chromatin, the nucleosomes (top right; see p.218) consist of an octameric complex of histones, around which the DNA is coiled.

Transport. A well-known transport protein is hemoglobin in the erythrocytes (bottom left). It is responsible for the transport of oxygen and carbon dioxide between the lungs and tissues (see p.282). The blood plasma also contains many other proteins with transport functions. Prealbumin (transferrin; middle), for example, transports the thyroid hormones thyroxin and triiodothyronine. Ion channels and other integral membrane proteins (see p.220) facilitate the transport of ions and metabolites across biological membranes.

Protection and defense. The immune system protects the body from pathogens and foreign substances. An important component of this system is immunoglobulin G (bottom left; see p.300). The molecule shown here is bound to an erythrocyte by complex formation with surface glycolipids (see p.292).

Control and regulation. In biochemical signal chains, proteins function as signaling substances (hormones) and as hormone receptors. The complex between the growth hormone somatotropin and its receptor is shown here as an example (middle). Here, the extracellular domains of two receptor molecules here bind one molecule of the hormone. This binding activates the cytoplasmic domains of the complex, leading to further conduction of the signal to the interior of the cell (see p.384). The small peptide hormone insulin is discussed in detail elsewhere (see pp.76, 160). DNA-binding proteins (transcription factors; see p.118) are decisively involved in regulating the metabolism and in differentiation processes. The structure and function of the catabolite activator protein (top left) and similar bacterial transcription factors have been particularly well investigated.

Catalysis. Enzymes, with more than 2000 known representatives, are the largest group of proteins in terms of numbers (see p.88). The smallest enzymes have molecular masses of 10–15 kDa. Intermediate-sized enzymes, such as alcohol dehydrogenase (top left) are around 100–200 kDa, and the largest—including glutamine synthetase with its 12 monomers (top right)—can reach more than 500 kDa.

Movement. The interaction between actin and myosin is responsible for muscle contraction and cell movement (see p.332). Myosin (right), with a length of over 150 nm, is among the largest proteins there are. Actin filaments (F-actin) arise due to the polymerization of relatively small protein subunits (G-actin). Along with other proteins, tropomyosin, which is associated with F-actin, controls contraction.

Storage. Plants contain special storage proteins, which are also important for human nutrition (not shown). In animals, muscle proteins constitute a nutrient reserve that can be mobilized in emergencies.
Peptide bonds

A. Peptide bond 

The amino acid components of peptides and proteins are linked together by amide bonds (see p. 60) between α-carboxyl and α-amino groups. This type of bonding is therefore also known as peptide bonding. In the dipeptide shown here, the serine residue has a free ammonium group, while the carboxylate group in alanine is free. Since the amino acid with the free NH$_2$ group is named first, the peptide is known as seryl alanine, or in abbreviated form Ser-Ala or SA.

B. Resonance 

Like all acid–amide bonds, the peptide bond is stabilized by resonance (see p. 4). In the conventional notation (top right) it is represented as a combination of a C=O double bond with a C–N single bond. However, a C=N double bond with charges at O and N could also be written (middle). Both of these are only extreme cases of electron distribution, known as resonance structures. In reality, the π electrons are delocalized throughout all the atoms (bottom). As a mesomeric system, the peptide bond is planar. Rotation around the C–N bond would only be possible at the expense of large amounts of energy, and the bond is therefore not freely rotatable. Rotations are only possible around the single bonds marked with arrows. The state of these is expressed using the angles ϕ and ψ (see D). The plane in which the atoms of the peptide bond lie is highlighted in light blue here and on the following pages.

C. Peptide nomenclature 

Peptide chains have a direction and therefore two different ends. The amino terminus (N terminus) of a peptide has a free ammonium group, while the carboxyl terminus (C terminus) is formed by the carboxylate group of the last amino acid. In peptides and proteins, the amino acid components are usually linked in linear fashion. To express the sequence of a peptide, it is therefore sufficient to combine the three-letter or single-letter abbreviations for the amino acid residues (see p. 60). This sequence always starts at the N terminus. For example, the peptide hormone angiotensin II (see p. 330) has the sequence Asp-Arg-Val-Tyr-Ile-His-Pro-Phe, or DRVYIHFP.

D. Conformational space of the peptide chain 

With the exception of the terminal residues, every amino acid in a peptide is involved in two peptide bonds (one with the preceding residue and one with the following one). Due to the restricted rotation around the C–N bond, rotations are only possible around the N–C$_N$ and C$_N$–C bonds (2). As mentioned above, these rotations are described by the dihedral angles ϕ (phi) and ψ (psi). The angle describes rotation around the N–C$_N$ bond; ψ describes rotation around C$_N$–C–i.e., the position of the subsequent bond.

For steric reasons, only specific combinations of the dihedral angles are possible. These relationships can be illustrated clearly by a so-called ϕ ψ diagram (1). Most combinations of ϕ and ψ are sterically “forbidden” (red areas). For example, the combination ϕ = 0° and ψ = 180° (4) would place the two carbonyl oxygen atoms less than 115 pm apart—i.e., at a distance much smaller than the sum of their van der Waals radii (see p. 6). Similarly, in the case of ϕ = 180° and ψ = 0° (5), the two NH hydrogen atoms would collide. The combinations located within the green areas are the only ones that are sterically feasible (e.g., 2 and 3). The important secondary structures that are discussed in the following pages are also located in these areas. The conformations located in the yellow areas are energetically less favorable, but still possible.

The ϕ ψ diagram (also known as a Ramachandran plot) was developed from modeling studies of small peptides. However, the conformations of most of the amino acids in proteins are also located in the permitted areas. The corresponding data for the small protein, insulin (see p. 76), are represented by black dots in 1.
A. Peptide bonds

Seryl alanine (Ser-Ala, H$_3$N-Ser-Ala-COOH, SA)

B. Resonance

C. Peptide nomenclature

D. Conformation space of the peptide chain
Secondary structures

In proteins, specific combinations of the dihedral angles \( \phi \) and \( \psi \) (see p. 66) are much more common than others. When several successive residues adopt one of these conformations, defined secondary structures arise, which are stabilized by hydrogen bonds either within the peptide chain or between neighboring chains. When a large part of a protein takes on a defined secondary structure, the protein often forms mechanically stable filaments or fibers. Structural proteins of this type (see p. 70) usually have characteristic amino acid compositions.

The most important secondary structural elements of proteins are discussed here first. The illustrations only show the course of the peptide chain; the side chains are omitted. To make the course of the chains clearer, the levels of the peptide bonds are shown as blue planes. The dihedral angles of the structures shown here are also marked in diagram D1 on p. 67.

A. \( \alpha \)-Helix

The right-handed \( \alpha \)-helix (\( \alpha_h \)) is one of the most common secondary structures. In this conformation, the peptide chain is wound like a screw. Each turn of the screw (the screw axis in shown in orange) covers approximately 3.6 amino acid residues. The pitch of the screw (i.e., the smallest distance between two equivalent points) is 0.54 nm. \( \alpha \)-Helices are stabilized by almost linear hydrogen bonds between the NH and CO groups of residues, which are four positions apart from each another in the sequence (indicated by red dots; see p. 6). In longer helices, most amino acid residues thus enter into two H bonds. Apolar or amphipathic \( \alpha \)-helices with five to seven turns often serve to anchor proteins in biological membranes (transmembrane helices; see p. 214).

The mirror image of the \( \alpha_h \) helix, the left-handed \( \alpha \)-helix (\( \alpha_l \)), is rarely found in nature, although it would be energetically "permissible."

B. Collagen helix

Another type of helix occurs in the collagens, which are important constituents of the connective tissue matrix (see pp. 70, 344). The collagen helix is left-handed, and with a pitch of 0.96 nm and 3.3 residues per turn, it is steeper than the \( \alpha \)-helix. In contrast to the \( \alpha \)-helix, H bonds are not possible within the collagen helix. However, the conformation is stabilized by the association of three helices to form a righthanded collagen triple helix (see p. 70).

C. Pleated-sheet structures

Two additional, almost stretched, conformations of the peptide chain are known as \( \beta \) pleated sheets, as the peptide planes are arranged like a regularly folded sheet of paper. Again, H bonds can only form between neighboring chains ("strands") in pleated sheets. When the two strands run in opposite directions (1), the structure is referred to as an antiparallel pleated sheet (\( \beta_{\alpha} \)). When they run in the same direction (2), it is a parallel pleated sheet (\( \beta_{\parallel} \)). In both cases, the \( \alpha-C \) atoms occupy the highest and lowest points in the structure, and the side chains point alternately straight up or straight down (see p. 71 C). The \( \beta_{\parallel} \) structure, with its almost linear H bonds, is energetically more favorable. In extended pleated sheets, the individual strands of the sheet are usually not parallel, but twisted relative to one another (see p. 74).

D. \( \beta \) Turns

\( \beta \) Turns are often found at sites where the peptide chain changes direction. These are sections in which four amino acid residues are arranged in such a way that the course of the chain reverses by about 180° into the opposite direction. The two turns shown (types I and II) are particularly frequent. Both are stabilized by hydrogen bonds between residues 1 and 4. \( \beta \) Turns are often located between the individual strands of antiparallel pleated sheets, or between strands of pleated sheets and \( \alpha \) helices.
A. α Helix

B. Collagen helix

1. Type I
2. Type II

ϕ = –139˚
ψ = +135˚

ϕ = –57˚
ψ = –47˚

ϕ = –191˚
ψ = +135˚

C. Pleated-sheet structures

1. Antiparallel
ϕ = –139˚
ψ = +135˚

2. Parallel
ϕ = –119˚
ψ = +113˚

D. β Turns

1. Type I

2. Type II
Structural proteins

The structural proteins give extracellular structures mechanical stability, and are involved in the structure of the cytoskeleton (see p. 204). Most of these proteins contain a high percentage of specific secondary structures (see p. 68). For this reason, the amino acid composition of many structural proteins is also characteristic (see below).

A. α Keratin

α-Keratin is a structural protein that predominantly consists of α helices. Hair (wool), feathers, nails, claws and the hooves of animals consist largely of keratin. It is also an important component of the cytoskeleton (cytokeratin), where it appears in intermediate filaments (see p. 204).

In the keratins, large parts of the peptide chain show right-handed α-helical coiling. Two chains each form a left-handed superhelix, as is also seen in myosin (see p. 65). The superhelical keratin dimers join to form tetramers, and these aggregate further to form protofilaments, with a diameter of 3 nm. Finally, eight protofilaments then form an intermediate filament, with a diameter of 10 nm (see p. 204).

Similar keratin filaments are found in hair. In a single wool fiber with a diameter of about 20 μm, millions of filaments are bundled together within dead cells. The individual keratin helices are cross-linked and stabilized by numerous disulfide bonds (see p. 72). This fact is exploited in the perming of hair. Initially, the disulfide bonds of hair keratin are disrupted by reduction with thiol compounds (see p. 8). The hair is then styled in the desired shape and heat-dried. In the process, new disulfide bonds are formed by oxidation, which maintain the hairstyle for some time.

two latter amino acids are only formed during collagen biosynthesis as a result of posttranslational modification (see p. 344).

The triplet Gly-X-Y (2) is constantly repeated in the sequence of collagen, with the X position often being occupied by Pro and the Y position by Hyp. The reason for this is that collagen is largely present as a triple helix made up of three individual collagen helices (1). In triple helices, every third residue lies on the inside of the molecule, where for steric reasons there is only room for glycine residues (3: the glycine residues are shown in yellow). Only a small section of a triple helix is illustrated here. The complete collagen molecule is approximately 300 nm long.

C. Silk fibroin

Silk is produced from the spun threads from silkworms (the larvae of the moth Bombyx mori and related species). The main protein in silk, fibroin, consists of antiparallel pleated sheet structures arranged one on top of the other in numerous layers (1). Since the amino acid side chains in pleated sheets point either straight up or straight down (see p. 68), only compact side chains fit between the layers. In fact, more than 80% of fibroin consists of glycine, alanine, and serine, the three amino acids with the shortest side chains. A typical repetitive amino acid sequence is (Gly-Ala-Gly-Ala-Gly-Ser). The individual pleated sheet layers in fibroin are found to lie alternately 0.35 nm and 0.57 nm apart. In the first case, only glycine residues (R = H) are opposed to one another. The slightly greater distance of 0.57 nm results from repulsion forces between the side chains of alanine and serine residues (2).
A. α-Keratin

B. Collagen

C. Silk fibroin

1. Spatial illustration

2. Front view

3. Triple helix (view from above)

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Globular proteins

Soluble proteins have a more complex structure than the fibrous, completely insoluble structural proteins. The shape of soluble proteins is more or less spherical (globular). In their biologically active form, globular proteins have a defined spatial structure (the native conformation). If this structure is destroyed (denaturation; see p. 74), not only does the biological effect disappear, but the protein also usually precipitates in insoluble form. This happens, for example, when eggs are boiled; the proteins dissolved in the egg white are denatured by the heat and produce the solid egg white.

To illustrate protein conformations in a clear (but extremely simplified) way, Richardson diagrams are often used. In these diagrams, α-helices are symbolized by red cylinders or spirals and strands of pleated sheets by green arrows. Less structured areas of the chain, including the β-turns, are shown as sections of gray tubing.

A. Conformation-stabilizing interactions

The native conformation of proteins is stabilized by a number of different interactions. Among these, only the disulfide bonds (B) represent covalent bonds. Hydrogen bonds, which can form inside secondary structures, as well as between more distant residues, are involved in all proteins (see p. 6). Many proteins are also stabilized by complex formation with metal ions (see pp. 76, 342, and 378, for example). The hydrophobic effect is particularly important for protein stability. In globular proteins, most hydrophobic amino acid residues are arranged in the interior of the structure in the native conformation, while the polar amino acids are mainly found on the surface (see pp. 28, 76).

B. Disulfide bonds

Disulfide bonds arise when the SH groups of two cysteine residues are covalently linked as a dithiol by oxidization. Bonds of this type are only found (with a few exceptions) in extracellular proteins, because in the interior of the cell glutathione (see p. 284) and other reducing compounds are present in such high concentrations that disulfides would be reduc-tively cleaved again. The small plant protein crambin (46 amino acids) contains three disulfide bonds and is therefore very stable. The high degree of stability of insulin (see p. 76) has a similar reason.

C. Protein dynamics

The conformations of globular proteins are not rigid, but can change dramatically on binding of ligands or in contact with other proteins. For example, the enzyme adenylate kinase (see p. 336) has a mobile domain (domain = independently folded partial structure), which folds shut after binding of the substrate (yellow). The larger domain (bottom) also markedly alters its conformation. There are large numbers of allosteric proteins of this type. This group includes, for example, hemoglobin (see p. 280), calmodulin (see p. 386), and many allosteric enzymes such as aspartate carbamoyltransferase (see p. 116).

D. Folding patterns

The globular proteins show a high degree of variability in folding of their peptide chains. Only a few examples are shown here. Purely helically folded proteins such as myoglobin (1; see p. 74, heme yellow) are rare. In general, pleated sheet and helical elements exist alongside each other. In the hormone-binding domain of the estrogen receptor (2; see p. 378), a small, two-stranded pleated sheet functions as a “cover” for the hormone binding site (estradiol yellow). In flavodoxin, a small flavoprotein with a redox function (3; FMN yellow), a fan-shaped, pleated sheet made up of five parallel strands forms the core of the molecule. The conformation of the β subunit of the G-protein transducin (4; see pp. 224, 358) is very unusual. Seven pleated sheets form a large, symmetrical “β propeller.” The N-terminal section of the protein contains one long and one short helix.
1. Myoglobin
2. Estrogen receptor (domain)
3. Flavodoxin
4. Transducin (β subunit)
Protein folding

Information about the biologically active (native) conformation of proteins is already encoded in their amino acid sequences. The native forms of many proteins arise spontaneously in the test tube and within a few minutes. Nevertheless, there are special auxiliary proteins (chaperonines) that support the folding of other proteins in the conditions present within the cell (see p. 232). An important goal of biochemistry is to understand the laws governing protein folding. This would make it possible to predict the conformation of a protein from the easily accessible DNA sequence (see p. 260).

A. Folding and denaturation of ribonuclease A

The folding of proteins to the native form is favored under physiological conditions. The native conformation is lost, as the result of denaturation, at extreme pH values, at high temperatures, and in the presence of organic solvents, detergents, and other denaturing substances, such as urea.

The fact that a denatured protein can spontaneously return to its native conformation was demonstrated for the first time with ribonuclease, a digestive enzyme (see p. 266) consisting of 124 amino acids. In the native form (top right), there are extensive pleated sheet structures and three α helices. The eight cysteine residues of the protein are forming four disulfide bonds. Residues His-12, lys-41 and His-119 (pink) are particularly important for catalysis. Together with additional amino acids, they form the enzyme’s active center.

The disulfide bonds can be reductively cleaved by thiols (e.g., mercaptoethanol, HO-CH₂-CH₂-SH). If urea at a high concentration is also added, the protein unfolds completely. In this form (left), it is up to 35 nm long. Polar (green) and apolar (yellow) side chains are distributed randomly. The denatured enzyme is completely inactive, because the catalytically important amino acids (pink) are too far away from each other to be able to interact with each other and with the substrate.

When the urea and thiol are removed by dialysis (see p. 78), secondary and tertiary structures develop again spontaneously. The cysteine residues thus return to a sufficiently close spatial vicinity that disulfide bonds can once again form under the oxidative effect of atmospheric oxygen. The active center also reestablishes itself. In comparison with the denatured protein, the native form is astonishingly compact, at 4.5–2.5 nm. In this state, the apolar side chains (yellow) predominate in the interior of the protein, while the polar residues are mainly found on the surface. This distribution is due to the “hydrophobic effect” (see p. 28), and it makes a vital contribution to the stability of the native conformation (B).

B. Energetics of protein folding

The energetics of protein folding are not at present satisfactorily understood. Only a simplified model is discussed here. The conformation of a molecule is stable in any given conditions if the change in its free enthalpy during folding (ΔHfolding) is negative (see p. 16). The magnitude of the folding enthalpy is affected by several factors. The main factor working against folding is the strong increase in the ordering of the molecule involved. As discussed on p. 20, this leads to a negative change in entropy of ΔSfolding and therefore to a strongly positive entropy term TΔS (violet arrow). By contrast, the covalent and noncovalent bonds in the interior of the protein have a stabilizing influence. For this reason, the change in folding enthalpy ΔHfolding is negative (red arrow). A third factor is the change in the system’s entropy due to the hydrophobic effect. During folding, the degree of order in the surrounding water decreases—i.e., ΔShydration is positive and therefore TΔS is negative (blue arrow). When the sum of these effects is negative (green arrow), the protein folds spontaneously into its native conformation.
A. Folding and denaturation of ribonuclease A

B. Energetics of protein folding

\[ \Delta G_{\text{fold}} = \Delta H_{\text{fold}} - T \Delta S_{\text{water}} - T \Delta S_{\text{conf}} \]
Molecular models: insulin

The opposite page presents models of insulin, a small protein. The biosynthesis and function of this important hormone are discussed elsewhere in this book (pp. 386, 388). Monomeric insulin consists of 51 amino acids, and with a molecular mass of 5.5 kDa it is only half the size of the smallest enzymes. Nevertheless, it has the typical properties of a globular protein.

Large quantities of pure insulin are required for the treatment of diabetes mellitus (see p. 160). The annual requirement for insulin is over 500 kg in a country the size of Germany. Formerly, the hormone had to be obtained from the pancreas of slaughtered animals in a complicated and expensive procedure. Human insulin, which is produced by overexpression in genetically engineered bacteria, is now mainly used (see p. 262).

A. Structure of insulin

There are various different structural levels in proteins, and these can be briefly discussed again here using the example of insulin.

The primary structure of a protein is its amino acid sequence. During the biosynthesis of insulin in the pancreas, a continuous peptide chain with 84 residues is first synthesized—proinsulin (see p. 160). After folding of the molecule, the three disulfide bonds are first formed, and residues 31 to 63 are then proteolytically cleaved releasing the so-called C peptide. The molecule that is left over (1) now consists of two peptide chains, the A chain (21 residues, shown in yellow) and the B chain (30 residues, orange). One of the disulfide bonds is located inside the A chain, and the two others link the two chains together.

Secondary structures are regions of the peptide chain with a defined conformation (see p. 148) that are stabilized by H-bonds. In insulin (2), the α-helical areas are predominant, making up 57% of the molecule; 6% consists of β-pleated-sheet structures, and 10% of β-turns, while the remainder (27%) cannot be assigned to any of the secondary structures.

The three-dimensional conformation of a protein, made up of secondary structural elements and unordered sections, is referred to as the tertiary structure. In insulin, it is compact and wedge-shaped (B). The tip of the wedge is formed by the B chain, which changes its direction at this point.

Quaternary structure. Due to non-covalent interactions, many proteins assemble to form symmetrical complexes (oligomers). The individual components of oligomeric proteins (usually 2–12) are termed subunits or monomers. Insulin also forms quaternary structures. In the blood, it is partly present as a dimer. In addition, there are also hexamers stabilized by Zn²⁺ ions (light blue) (3), which represent the form in which insulin is stored in the pancreas (see p. 160).

B. Insulin (monomer)

The van der Waals model of monomeric insulin (1) once again shows the wedge-shaped tertiary structure formed by the two chains together. In the second model (3, bottom), the side chains of polar amino acids are shown in blue, while apolar residues are yellow or pink. This model emphasizes the importance of the “hydrophobic effect” for protein folding (see p. 144). In insulin as well, most hydrophobic side chains are located on the inside of the molecule, while the hydrophilic residues are located on the surface. Apparently in contradiction to this rule, several apolar side chains (pink) are found on the surface. However, all of these residues are involved in hydrophobic interactions that stabilize the dimeric and hexameric forms of insulin.

In the third model (2, right), the colored residues are those that are located on the surface and occur invariably (red) or almost invariably (orange) in all known insulins. It is assumed that amino acid residues that are not replaced by other residues during the course of evolution are essential for the protein’s function. In the case of insulin, almost all of these residues are located on one side of the molecule. They are probably involved in the binding of the hormone to its receptor (see p. 224).
A. Structure of insulin

1. Primary structure

2. Secondary and tertiary structure

3. Quaternary structure

B. Insulin (monomeric)

1.  

2.  

3.  


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Isolation and analysis of proteins

Purified proteins are nowadays required for a wide variety of applications in research, medicine, and biotechnology. Since the globular proteins in particular are very unstable (see p. 72), purification is carried out at low temperatures (0–5 °C) and particularly gentle separation processes are used. A few of the methods of purifying and characterizing proteins are discussed on this page.

A. Salt precipitation

The solubility of proteins is strongly dependent on the salt concentration (ionic strength) of the medium. Proteins are usually poorly soluble in pure water. Their solubility increases as the ionic strength increases, because more and more of the well-hydrated anorganic ions (blue circles) are bound to the protein’s surface, preventing aggregation of the molecules (salting in). At very high ionic strengths, the salt withdraws the hydration water from the proteins and thus leads to aggregation and precipitation of the molecules (salting out). For this reason, adding salts such as ammonium sulfate (NH₄)₂SO₄ makes it possible to separate proteins from a mixture according to their degree of solubility (fractionation).

B. Dialysis

Dialysis is used to remove lower-molecular components from protein solutions, or to exchange the medium. Dialysis is based on the fact that due to their size, protein molecules are unable to pass through the pores of a semipermeable membrane, while lower-molecular substances distribute themselves evenly between the inner and outer spaces over time. After repeated exchanging of the external solution, the conditions inside the dialysis tube (salt concentration, pH, etc.) will be the same as in the surrounding solution.

C. Gel filtration

Gel permeation chromatography (”gel filtration”) separates proteins according to their size and shape. This is done using a chromatography column, which is filled with spherical gel particles (diameter 10–500 μm) of polymeric material (shown schematically in 1a). The insides of the particles are traversed by channels that have defined diameters. A protein mixture is then introduced at the upper end of the column (1b) and elution is carried out by passing a buffer solution through the column. Large protein molecules (red) are unable to penetrate the particles, and therefore pass through the column quickly. Medium-sized (green) and small particles (blue) are delayed for longer or shorter periods (1c). The proteins can be collected separately from the eluent (eluate) (2). Their elution volume Vₑ depends mainly on their molecular mass (3).

D. SDS gel electrophoresis

The most commonly used procedure for checking the purity of proteins is sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). In electrophoresis, molecules move in an electrical field (see p. 276). Normally, the speed of their movement depends on three factors—their size, their shape, and their electrical charge.

In SDS-PAGE, the protein mixture is treated in such a way that only the molecules’ mass affects their movement. This is achieved by adding sodium dodecyl sulfate (C₁₂H₂₅–SO₄Na), the sulfuric acid ester of lauryl alcohol (dodecyl alcohol). SDS is a detergent with strongly amphipathic properties (see p. 28). It separates oligomeric proteins into their subunits and denatures them. SDS molecules bind to the unfolded peptide chains (ca. 0.4 g SDS / g protein) and give them a strongly negative charge. To achieve complete denaturation, thiods are also added in order to cleave the disulfide bonds (1).

Following electrophoresis, which is carried out in a vertically arranged gel of polymeric acrylamide (2), the separated proteins are made visible by staining. In example (3), the following were separated: a) a cell extract with hundreds of different proteins, b) a protein purified from this, and c) a mixture of proteins with known masses.

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A. Salt precipitation

B. Dialysis

C. Gel filtration

D. SDS gel electrophoresis

1. Principle
2. Apparatus
3. Analysis
4. Analysis

Exclusion volume

Distance

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Bases and nucleotides

The nucleic acids play a central role in the storage and expression of genetic information (see p. 236). They are divided into two major classes: deoxyribonucleic acid (DNA) functions solely in information storage, while ribonucleic acids (RNAs) are involved in most steps of gene expression and protein biosynthesis. All nucleic acids are made up from nucleotide components, which in turn consist of a base, a sugar, and a phosphate residue. DNA and RNA differ from one another in the type of the sugar and in one of the bases that they contain.

A. Nucleic acid bases

The bases that occur in nucleic acids are aromatic heterocyclic compounds derived from either pyrimidine or purine. Five of these bases are the main components of nucleic acids in all living creatures. The purine bases adenosine (abbreviation Ade, not “A”) and guanine (Gua) and the pyrimidine base cytosine (Cyt) are present in both RNA and DNA. In contrast, uracil (Ura) is only found in RNA. In DNA, uracil is replaced by thymine (Thy), the 5-methyl derivative of uracil. 5-methylcytosine also occurs in small amounts in the DNA of the higher animals. A large number of other modified bases occur in RNA (see p. 82) and in other types of RNA.

B. Nucleosides, nucleotides

When a nucleic acid base is N-glycosidically linked to ribose or 2-deoxyribose (see p. 38), it yields a nucleoside. The nucleoside adenosine (abbreviation: A) is formed in this way from adenine and ribose, for example. The corresponding derivatives of the other bases are called guanosine (G), uridine (U), thymidine (T) and cytidine (C). When the sugar component is 2-deoxyribose, the product is a deoxyribonucleoside—e.g., 2’-deoxadenosine (dA, not shown). In the cell, the 5’OH group of the sugar component of the nucleoside is usually esterified with phosphoric acid. 2’-Deoxythymidine (dT) therefore gives rise to 2’-deoxythymidine-5’-monophosphate (dTMP), one of the components of DNA (2). If the 5’ phosphate residue is linked via an acid-anhydride bond to additional phosphate residues, it yields nucleoside diphosphates and triphosphates—e.g., ADP and ATP, which are important coenzymes in energy metabolism (see p. 106). All of these nucleoside phosphates are classified as nucleotides.

In nucleosides and nucleotides, the pentose residues are present in the furanose form (see p. 34). The sugars and bases are linked by an N-glycosidic bond between the C-1 of the sugar and either the N-9 of the purine ring or N-1 of the pyrimidine ring. This bond always adopts the β-configuration.

C. Oligonucleotides, polynucleotides

Phosphoric acid molecules can form acid–anhydride bonds with each other. It is therefore possible for two nucleotides to be linked via the phosphate residues. This gives rise to dinucleotides with a phosphoric acid–anhydride structure. This group includes the coenzymes NAD(P)⁺ and CoA, as well as the flavin derivative FAD (1; see p. 104).

If the phosphate residue of a nucleotide reacts with the 3’-OH group of a second nucleotide, the result is a dinucleotide with a phosphoric acid diester structure. Dinucleotides of this type have a free phosphate residue at the 5’ end and a free OH group at the 3’ end. They can therefore be extended with additional mononucleotides by adding further phosphoric acid diester bonds. This is the way in which oligonucleotides, and ultimately polynucleotides, are synthesized.

Polynucleotides consisting of ribonucleotide components are called ribonucleic acid (RNA), while those consisting of deoxyribonucleotide monomers are called deoxyribonucleic acid (DNA; see p. 84). To describe the structure of polynucleotides, the abbreviations for the nucleoside components are written from left to right in the 5’→3’ direction. The position of the phosphate residue is also sometimes indicated by a “p”. In this way, the structure of the RNA segment shown Fig. 2 can be abbreviated as ...5’–3’...
A. Nucleic acid bases

Pyrimidine bases
- Uracil (Ura)
- Thymine (Thy)
- Cytosine (Cyt)

Purine bases
- Adenine (Ade)
- Guanine (Gua)

B. Nucleosides, nucleotides

1. Adenosine (Ado)
2. 2'-Deoxythymidine 5'-monophosphate (dtMP)

C. Oligonucleotides, polynucleotides

1. Flavin adenine dinucleotide (FAD)
2. RNA (section)
RNA

Ribonucleic acids (RNAs) are polymers consisting of nucleotide phosphate components that are linked by phosphoric acid diester bonds (see p. 86). The bases the contain are mainly uracil, cytosine, adenine, and guanine, but many unusual and modified bases are also found in RNAs (B).

A. Ribonucleic acids (RNAs)

RNAs are involved in all the individual steps of gene expression and protein biosynthesis (see pp. 242–253). The properties of the most important forms of RNA are summarized in the table. The schematic diagram also gives an idea of the secondary structure of these molecules.

In contrast to DNA, RNAs do not form extended double helices. In RNAs, the base pairs (see p.84) usually only extend over a few residues. For this reason, substructures often arise that have a finger shape or clover-leaf shape in two-dimensional representations. In these, the paired stem regions are linked by loops. Large RNAs such as ribosomal 16S-rRNA (center) contain numerous “stem and loop” regions of this type. These sections are again folded three-dimensionally—i.e., like proteins, RNAs have a tertiary structure (see p. 86). However, tertiary structures are only known of small RNAs, mainly tRNAs. The diagrams in Fig. 4 and on p. 86 show that the “clover-leaf” structure is not recognizable in a three-dimensional representation.

Cellular RNAs vary widely in their size, structure, and lifespan. The great majority of them are ribosomal RNA (rRNA), which in several forms is a structural and functional component of ribosomes (see p. 250). Ribosomal RNA is produced from DNA by transcription in the nucleolus, and it is processed there and assembled with proteins to form ribosome subunits (see pp. 208, 242). The bacterial 16S-rRNA shown in Fig. 4, with 1542 nucleotides (nt), is a component of the small ribosomal subunit, while the much smaller SS-rRNA (118 nt) is located in the large subunit.

Messenger RNAs (mRNAs) transfer genetic information from the cell nucleus to the cytoplasm. The primary transcripts are substantially modified while still in the nucleus (mRNA maturation; see p. 246). Since mRNAs have to be read codon by codon in the ribosome, they must not form a stable tertiary structure. This is ensured in part by the attachment of RNA-binding proteins, which prevent base pairing. Due to the varying amounts of information that they carry, the lengths of mRNAs also vary widely. Their lifespan is usually short, as they are quickly broken down after translation.

Small nuclear RNAs (snRNAs) are involved in the splicing of mRNA precursors (see p. 246). They associate with numerous proteins to form “spliceosomes.”

B. Transfer RNA (tRNA™)

The transfer RNAs (tRNAs) function during translation (see p.250) as links between the nucleic acids and proteins. They are small RNA molecules consisting of 70–90 nucleotides, which “recognize” specific mRNA codons with their anticodons through base pairing. At the same time, at their 3' end (sequence ... -CCA-3') they carry the amino acid that is assigned to the relevant mRNA codon according to the genetic code (see p. 248).

The base sequence and the tertiary structure of the yeast tRNA specific for phenylalanine (tRNA^Phe) is typical of all tRNAs. The molecule (see also p.86) contains a high proportion of unusual and modified components (shaded in dark green in Fig. 1). These include pseudouridine (°P), dihydrouridine (D), thymidine (T), which otherwise only occurs in DNA, and many methylated nucleotides such as 7-methylguanidine (m^7G) and—in the anticodon—2'-O-methylguanidine (m^2G). Numerous base pairs, sometimes deviating from the usual pattern, stabilize the molecule's conformation (2).
A. Ribonucleic acids (RNAs)

<table>
<thead>
<tr>
<th>Type</th>
<th>mRNA</th>
<th>snRNA</th>
</tr>
</thead>
<tbody>
<tr>
<td>&gt;50</td>
<td>&gt;1000</td>
<td>~10</td>
</tr>
<tr>
<td>74-95</td>
<td>120-500</td>
<td>400-6000</td>
</tr>
<tr>
<td>10-20%</td>
<td>80%</td>
<td>5%</td>
</tr>
<tr>
<td>Long</td>
<td>Long</td>
<td>Short</td>
</tr>
<tr>
<td>Translation</td>
<td>Translation</td>
<td>Function</td>
</tr>
</tbody>
</table>

B. Transfer RNA (tRNA)

1. Structure

- Dihydrouridine (D)
- Pseudouridine (Ψ)
- 2'-O-methylguanidine (m2G)
- 7-methylguanidine (m7G)

2. Conformation

- Normal base pairing
- Unusual base pairing

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DNA

A. DNA: structure

Like RNAs (see p. 82), deoxyribonucleic acids (DNAs) are polymeric molecules consisting of nucleotide building blocks. Instead of ribose, however, DNA contains 2’-deoxyribose, and the uracil base in RNA is replaced by thymine. The spatial structure of the two molecules also differs (see p. 86).

The first evidence of the special structure of DNA was the observation that the amounts of adenine and thymine are almost equal in every type of DNA. The same applies to guanine and cytosine. The model of DNA structure formulated in 1953 explains these constant base ratios: intact DNA consists of two polynucleotide molecules (“strands”). Each base in one strand is linked to a complementary base in the other strand by H-bonds. Adenine is complementary to thymine, and guanine is complementary to cytosine. One purine base and one pyrimidine base are thus involved in each base pair.

The complementarity of A with T and of G with C can be understood by considering the H-bonds that are possible between the different bases. Potential donors (see p. 6) are amino groups (Ade, Cyt, Gua) and ring NH groups. Possible acceptors are carbonyl oxygen atoms (Thy, Cyt, Gua) and ring nitrogen atoms. Two linear and therefore highly stable bonds can thus be formed in A–T pairs, and three in G–C pairs.

Base pairings of this type are only possible, however, when the polarity of the two strands differs—i.e., when they run in opposite directions (see p. 80). In addition, the two strands have to be intertwined to form a double helix. Due to steric hindrance by the 2’-OH groups of the ribose residues, RNA is unable to form a double helix. The structure of RNA is therefore less regular than that of DNA (see p. 82).

The conformation of DNA that predominates within the cell (known as B-DNA) is shown schematically in Fig. A2 and as a van der Waals model in Fig. B1. In the schematic diagram (A2), the deoxyribose–phosphate “backbone” is shown as a ribbon. The bases (indicated by lines) are located on the inside of the double helix. This area of DNA is therefore apolar. By contrast, the molecule’s surface is polar and negatively charged, due to the sugar and phosphate residues in the backbone. Along the whole length of the DNA molecule, there are two depressions—referred to as the “minor groove” and the “major groove”—that lie between the strands.

B. Coding of genetic information

In all living cells, DNA serves to store genetic information. Specific segments of DNA (“genes”) are transcribed as needed into RNAs, which either carry out structural or catalytic tasks themselves or provide the basis for synthesizing proteins (see p. 82). In the latter case, the DNA codes for the primary structure of proteins. The “language” used in this process has four letters (A, G, C, and T). All of the words (“codons”) contain three letters (“triplets”), and each triplet stands for one of the 20 proteinogenic amino acids.

The two strands of DNA are not functionally equivalent. The template strand (the (−) strand or “codogenic strand,” shown in light gray in Fig. 1) is the one that is read during the synthesis of RNA (transcription; see p. 242). Its sequence is complementary to the RNA formed. The sense strand (the (+) strand or “coding strand,” shown in color in Figs. 1 and 2) has the same sequence as the RNA, except that T is exchanged for U. By convention, it is agreed that gene sequences are expressed by reading the sequence of the sense strand in the 5’ → 3’ direction. Using the genetic code (see p. 248), in this case the protein sequence (3) is obtained directly in the reading direction usual for proteins—i.e., from the N terminus to the C terminus.

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A. DNA: structure

1. Formula

2. Double strand

B. Coding of genetic information

1. Sense strand (+) strand, "coding strand"

2. Template strand (−) strand, "codogenic strand"

Codon (triplet)

C: Phe
T: Tyr
A: Ala
T: Thr
C: Glu
A: Glu
T: Met
N: Met
Molecular models: DNA and RNA

The illustration opposite shows selected nucleic acid molecules. Fig. A shows various conformations of DNA, and Fig. B shows the spatial structures of two small RNA molecules. In both, the van der Waals models (see p. 6) are accompanied by ribbon diagrams that make the course of the chains clear. In all of the models, the polynucleotide “backbone” of the molecule is shown in a darker color, while the bases are lighter.

A. DNA: conformation □

Investigations of synthetic DNA molecules have shown that DNA can adopt several different conformations. All of the DNA segments shown consist of 21 base pairs (bp) and have the same sequence.

By far the most common form is B-DNA (2). As discussed on p. 84, this consists of two antiparallel polydeoxynucleotide strands intertwined with one another to form a right-handed double helix. The “backbone” of these strands is formed by deoxyribose and phosphate residues linked by phosphoric acid diester bonds.

In the B conformation, the aromatic rings of the nucleobases are stacked at a distance of 0.34 nm almost at right angles to the axis of the helix. Each base is rotated relative to the preceding one by an angle of 35°. A complete turn of the double helix (360°) therefore contains about 10 base pairs (abbreviation: bp), i.e., the pitch of the helix is 3.4 nm. Between the backbones of the two individual strands there are two grooves with different widths. The major groove is visible at the top and bottom, while the narrower minor groove is seen in the middle. DNA-binding proteins and transcription factors (see pp. 118, 244) usually enter into interactions in the area of the major groove, with its more easily accessible bases.

In certain conditions, DNA can adopt the A conformation (1). In this arrangement, the double helix is still right-handed, but the bases are no longer arranged at right angles to the axis of the helix, as in the B form. As can be seen, the A conformation is more compact than the other two conformations. The minor groove almost completely disappears, and the major groove is narrower than in the B form.

A-DNA arises when B-DNA is dehydrated. It probably does not occur in the cell.

In the Z-conformation (3), which can occur within GC-rich regions of B-DNA, the organization of the nucleotides is completely different. In this case, the helix is left-handed, and the backbone adopts a characteristic zig-zag conformation (hence “Z-DNA”). The Z double helix has a smaller pitch than B-DNA. DNA segments in the Z conformation probably have physiological significance, but details are not yet known.

B. RNA □

RNA molecules are unable to form extended double helices, and are therefore less highly ordered than DNA molecules. Nevertheless, they have defined secondary and tertiary structures, and a large proportion of the nucleotide components enter into base pairings with other nucleotides. The examples shown here are 5S-rRNA (see p. 242), which occurs as a structural component in ribosomes, and a tRNA molecule from yeast (see p. 82) that is specific for phenylalanine.

Both molecules are folded in such a way that the 3′ end and the 5′ end are close together. As in DNA, most of the bases are located in the inside of the structures, while the much more polar “backbone” is turned outward. An exception to this is seen in the three bases of the anticodon of the tRNA (pink), which have to interact with mRNA and therefore lie on the surface of the molecule. The bases of the conserved CCA triplet at the 3′ end (red) also jut outward. During amino acid activation (see p. 248), they are recognized and bound by the ligases.
A. DNA: conformation

1. A-DNA
2. B-DNA
3. Z-DNA

B. RNA

1. 5S-rRNA (118 nucleotides)
2. Phe-tRNA^tyt (77 nucleotides)
Enzymes: basics

Enzymes are biological catalysts—i.e., substances of biological origin that accelerate chemical reactions (see p. 24). The orderly course of metabolic processes is only possible because each cell is equipped with its own genetically determined set of enzymes. It is only this that allows coordinated sequences of reactions (metabolic pathways; see p. 112). Enzymes are also involved in many regulatory mechanisms that allow the metabolism to adapt to changing conditions (see p. 114). Almost all enzymes are proteins. However, there are also catalytically active ribonucleic acids, the "ribozymes" (see pp. 246, 252).

A. Enzymatic activity

The catalytic action of an enzyme, its activity, is measured by determining the increase in the reaction rate under precisely defined conditions—i.e., the difference between the turnover (violet) of the catalyzed reaction (orange) and uncatalyzed reaction (yellow) in a specific time interval. Normally, reaction rates are expressed as the change in concentration per unit of time (mol · L⁻¹ · s⁻¹; see p. 22). Since the catalytic activity of an enzyme is independent of the volume, the unit used for enzymes is usually turnover per unit time, expressed in katal (kat, mol s⁻¹). However, the international unit U is still more commonly used (µmol turnover min⁻¹; 1 U = 16.7 nkat).

B. Reaction and substrate specificity

The action of enzymes is usually very specific. This applies not only to the type of reaction being catalyzed (reaction specificity), but also to the nature of the reactants ("substrates") that are involved (substrate specificity; see p. 94). In Fig. B, this is illustrated schematically using a bond-breaking enzyme as an example. Highly specific enzymes (type A, top) catalyze the cleavage of only one type of bond, and only when the structure of the substrate is the correct one. Other enzymes (type B, middle) have narrow reaction specificity, but broad substrate specificity. Type C enzymes (with low reaction specificity and low substrate specificity, bottom) are very rare.

C. Enzyme classes

More than 2000 different enzymes are currently known. A system of classification has been developed that takes into account both their reaction specificity and their substrate specificity. Each enzyme is entered in the Enzyme Catalogue with a four-digit Enzyme Commission number (EC number). The first digit indicates membership of one of the six major classes. The next two indicate subclasses and sub-subclasses. The last digit indicates where the enzyme belongs in the subclass. For example, lactate dehydrogenase (see pp. 98–101) has the EC number 1.1.1.27 (class 1, oxidoreductases; subclass 1.1, CH–OH group as electron donor; sub-subclass 1.1.1, NAD(P)⁺ as electron acceptor).

Enzymes with similar reaction specificities are grouped into each of the six major classes:

The oxidoreductases (class 1) catalyze the transfer of reducing equivalents from one reduct system to another.

The transferases (class 2) catalyze the transfer of other groups from one molecule to another. Oxidoreductases and transferases generally require coenzymes (see pp. 104ff).

The hydrolases (class 3) are also involved in group transfer, but the acceptor is always a water molecule.

The lyases (class 4, often also referred to as "synthetases") catalyze reactions involving either the cleavage or formation of chemical bonds, with double bonds either arising or disappearing.

The isomerases (class 5) move groups within a molecule, without changing the gross composition of the substrate.

The ligation reactions catalyzed by ligases ("synthetases, class 6) are energy-dependent and are therefore always coupled to the hydrolysis of nucleoside triphosphates.

In addition to the enzyme name, we also usually give its EC number. The annotated enzyme list (pp. 420ff) includes all of the enzymes mentioned in this book, classified according to the Enzyme Catalog system.
A. Enzymatic activity

- Turnover (mol product s\(^{-1}\))
  - without enzyme
  - with enzyme
- Enzyme activity (mol s\(^{-1}\) = kat)

1 Katal (kat): Amount of enzyme which increases turnover by 1 mol s\(^{-1}\)

B. Reaction and substrate specificity

<table>
<thead>
<tr>
<th>Reaction specificity</th>
<th>Substrate specificity</th>
</tr>
</thead>
<tbody>
<tr>
<td>High</td>
<td>High</td>
</tr>
<tr>
<td>High</td>
<td>Low</td>
</tr>
<tr>
<td>Low</td>
<td>Low</td>
</tr>
</tbody>
</table>

C. The enzyme classes

<table>
<thead>
<tr>
<th>Class</th>
<th>Reaction type</th>
<th>Important subclasses</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Oxidoreductases</td>
<td>(\text{Red}) (\rightarrow) (\text{Red}^+)</td>
<td>Dehydrogenases, Oxidases, Peroxidases, Reductases, Monooxygenases, Dioxygenases</td>
</tr>
<tr>
<td>2 Transferases</td>
<td>(\text{A-B}) (\rightarrow) (\text{C})</td>
<td>C(_1)-Transferases, Glycosyltransferases, Aminotransferases, Phosphotransferases</td>
</tr>
<tr>
<td>3 Hydrolases</td>
<td>(\text{A-B}) (\rightarrow) (\text{H}_2\text{O})</td>
<td>Esterases, Glycosidases, Peptidases, Amidases</td>
</tr>
<tr>
<td>4 Lyases (&quot;synthases&quot;)</td>
<td>(\text{A}) (\rightarrow) (\text{B})</td>
<td>C-C-Lyases, C-O-Lyases, C-N-Lyases, C-S-Lyases</td>
</tr>
<tr>
<td>5 Isomerases</td>
<td>(\text{A} \rightarrow \text{iso-A})</td>
<td>Epimerases, cis-trans Isomerases, Intramolecular transferases</td>
</tr>
<tr>
<td>6 Ligases (&quot;synthetases&quot;)</td>
<td>(\text{A} + \text{XTP} \rightarrow \text{A} + \text{XDP})</td>
<td>C-C-Ligases, C-O-Ligases, C-N-Ligases, C-S-Ligases</td>
</tr>
</tbody>
</table>
Enzyme catalysis

Enzymes are extremely effective catalysts. They can increase the rate of a catalyzed reaction by a factor of $10^{9}$ or more. To grasp the mechanisms involved in enzyme catalysis, we can start by looking at the course of an uncatalyzed reaction more closely.

A. Uncatalyzed reaction

The reaction $A + B \rightarrow C + D$ is used as an example. In solution, reactants A and B are surrounded by a shell of water molecules (the hydration shell), and they move in random directions due to thermal agitation. They can only react with each other if they collide in a favorable orientation. This is not very probable, and therefore only occurs rarely. Before conversion into the products C + D, the collision complex A-B has to pass through a transition state, the formation of which usually requires a large amount of activation energy, $E_a$ (see p.22). Since only a few A-B complexes can produce this amount of energy, a productive transition state arises even less often than a collision complex. In solution, a large proportion of the activation energy is required for the removal of the hydration shells between A and B. However, charge displacements and other chemical processes within the reactants also play a role. As a result of these limitations, conversion only happens occasionally in the absence of a catalyst, and the reaction rate $v$ is low, even when the reaction is thermodynamically possible—i.e., when $\Delta G < 0$ (see p.18).

B. Enzyme-catalyzed reaction

Shown here is a sequential mechanism in which substrates A and B are bound and products C and D are released, in that order. Another possible reaction sequence, known as the "ping-pong mechanism," is discussed on p.54.

Enzymes are able to bind the reactants (their substrates) specifically at the active center. In the process, the substrates are oriented in relation to each other in such a way that they take on the optimal orientation for the formation of the transition state (1-3). The proximity and orientation of the substrates therefore strongly increase the likelihood that productive A-B complexes will arise. In addition, binding of the substrates results in removal of their hydration shells. As a result of the exclusion of water, very different conditions apply in the active center of the enzyme during catalysis than in solution (3-5).

A third important factor is the stabilization of the transition state as a result of interactions between the amino acid residues of the protein and the substrate (4). This further reduces the activation energy needed to create the transition state. Many enzymes also take up groups from the substrates or transfer them to the substrates during catalysis.

Proton transfers are particularly common. This acid-base catalysis by enzymes is much more effective than the exchange of protons between acids and bases in solution. In many cases, chemical groups are temporarily bound covalently to the amino acid residues of the enzyme or to coenzymes during the catalytic cycle. This effect is referred to as covalent catalysis (see the transaminases, for example: p.178). The principles of enzyme catalysis sketched out here are discussed in greater detail on p.100 using the example of lactate dehydrogenase.

C. Principles of enzyme catalysis

Although it is difficult to provide quantitative estimates of the contributions made by individual catalytic effects, it is now thought that the enzyme's stabilization of the transition state is the most important factor. It is not tight binding of the substrate that is important, therefore—this would increase the activation energy required by the reaction, rather than reducing it—but rather the binding of the transition state. This conclusion is supported by the very high affinity of many enzymes for analogues of the transition state (see p.96). A simple mechanical analogy may help clarify this (right). To transfer the metal balls (the reactants) from location EA (the substrate state) via the higher-energy transition state to EP (the product state), the magnet (the catalyst) has to be orientated in such a way that its attractive force acts on the transition state (bottom) rather than on EA (top).
A. Uncatalyzed reaction

B. Enzyme-catalyzed reaction

C. Principles of enzyme catalysis

- a. Approximation and orientation of the substrates
- b. Exclusion of water
- c. Stabilization of the transition state
- d. Group transfer

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Enzyme kinetics

The kinetics of enzyme-catalyzed reactions (i.e., the dependence of the reaction rate on the reaction conditions) is mainly determined by the properties of the catalyst. It is therefore more complex than the kinetics of an uncatalyzed reaction (see p.22). Here we discuss these issues using the example of a simple first-order reaction (see p.22).

A. Michaelis–Menten kinetics

In the absence of an enzyme, the reaction rate v is proportional to the concentration of substrate A (top). The constant k is the rate constant of the uncatalyzed reaction. Like all catalysts, the enzyme E (total concentration [E]t) creates a new reaction pathway. Initially, A is bound to E (partial reaction 1, left). If this reaction is in chemical equilibrium, then with the help of the law of mass action—and taking into account the fact that [E]t = [E] + [EA]one can express the concentration [EA] of the enzyme-substrate complex as a function of [A] (left). The Michaelis constant K_m thus describes the state of equilibrium of the reaction. In addition, we know that k_cat > k—in other words, enzyme-bound substrate reacts to B much faster than A alone (partial reaction 2, right). k_cat, the enzyme’s turnover number, corresponds to the number of substrate molecules converted by one enzyme molecule per second. Like the conversion A → B, the formation of B from EA is a first-order reaction—i.e., v = k [EA] applies. When this equation is combined with the expression already derived for EA, the result is the Michaelis–Menten equation.

In addition to the variables v and [A], the equation also contains two parameters that do not depend on the substrate concentration [A], but describe properties of the enzyme itself: the product k_cat [E]t is the limiting value for the reaction rate at a very high [A], the maximum velocity V_max of the reaction (recommended abbreviation: V). The Michaelis constant K_m characterizes the affinity of the enzyme for a substrate. It corresponds to the substrate concentration at which v reaches half of V_max (if v = V_max/2, then [A]/(K_m + [A]) = 1/2, i.e. [A] is then = K_m). A high affinity of the enzyme for a substrate therefore leads to a low K_m value, and vice versa. Of the two enzymes whose substrate saturation curves are shown in diagram 1, enzyme 2 has the higher affinity for A (K_m = 1 mmol L⁻¹); V_max by contrast, is much lower than with enzyme 1.

Since v approaches V asymptotically with increasing values of [A], it is difficult to obtain reliable values for V_max—and thus for K_m as well—from diagrams plotting v against [A]. To get around this, the Michaelis–Menten equation can be arranged in such a way that the measured points lie on a straight line. In the Lineweaver–Burk plot (2), 1/v is plotted against 1/[A]. The intersections of the line of best fit with the axes then produce 1/V_max and −1/K_m. This type of diagram is very clear, but for practical purposes it is less suitable for determining V_max and K_m. Calculation methods using personal computers are faster and more objective.

B. Isoteric and allosteric enzymes

Many enzymes can occur in various conformations (see p.72), which have different catalytic properties and whose proportion of the total number of enzyme molecules is influenced by substrates and other ligands (see pp.116 and 280, for example). Allosteric enzymes of this type, which are usually present in oligomeric form, can be recognized by their S-shaped (sigmoidal) saturation curves, which cannot be described using the Michaelis model. In the case of isometric enzymes (with only one enzyme conformation, 1), the efficiency of substrate binding (dashed curve) declines constantly with increasing [A], because the number of free binding sites is constantly decreasing. In most allosteric enzymes (2), the binding efficiency initially rises with increasing [A], because the free enzyme is present in a low-affinity conformation (square symbols), which is gradually converted into a higher-affinity form (round symbols) as a result of binding with A. It is only at high [A] values that a lack of free binding sites becomes noticeable and the binding strength decreases again. In other words, the affinity of allosteric enzymes is not constant, but depends on the type and concentration of the ligand.
A. Michaelis Menten kinetics

Partial reaction 1: formation and decay of enzyme–substrate complex EA

\[ E + A \rightleftharpoons K_m \] [EA] = [E]g \frac{[A]}{K_m + [A]} \]

Michaelis constant
\( K_m \) (mol \( \cdot \) l\(^{-1} \))

Uncatalyzed reaction

Partial reaction 2: formation of the product of EA

\[ [EA] \xrightarrow{k_{cat}} E + B \]

Maximum velocity
\( v_{max} = k_{cat} \cdot [E]_g \) (mol \( \cdot \) l\(^{-1} \) \( \cdot \) s\(^{-1} \))

Maximum velocity
\( v = k_{cat} \cdot [EA] \)

B. Isosteric and allosteric enzymes

Isosteric (\( n = 1 \))

Allosteric (\( n = 3 \))

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Enzyme kinetics

The catalytic properties of enzymes, and consequently their activity (see p. 90), are influenced by numerous factors, which all have to be optimized and controlled if activity measurements are to be carried out in a useful and reproducible fashion. These factors include physical quantities (temperature, pressure), the chemical properties of the solution (pH value, ionic strength), and the concentrations of the relevant substrates, cofactors, and inhibitors.

A. pH and temperature dependency of enzyme activity

The effect of enzymes is strongly dependent on the pH value (see p. 30). When the activity is plotted against pH, a bell-shaped curve is usually obtained (1). With animal enzymes, the pH optimum—i.e., the pH value at which enzyme activity is at its maximum—is often close to the pH value of the cells (i.e., pH 7). However, there are also exceptions to this. For example, the proteinase pepsin (see p. 270), which is active in the acidic gastric lumen, has a pH optimum of 2, while other enzymes (at least in the test tube) are at their most active at pH values higher than 9. The bell shape of the activity–pH profile results from the fact that amino acid residues with ionizable groups in the side chain are essential for catalysis. In example (1), these are a basic group B (pK_a > 8), which has to be protonated in order to become active, and a second acidic group A (pK_a > 6), which is only active in a dissociated state. At the optimum pH of 7, around 90% of both groups are present in the active form; at higher and lower values, one or the other of the groups increasingly passes into the inactive state.

The temperature dependency of enzymatic activity is usually asymmetric. With increasing temperature, the increased thermal movement of the molecules initially leads to a rate acceleration (see p. 22). At a certain temperature, the enzyme then becomes unstable, and its activity is lost within a narrow temperature difference as a result of denaturation (see p. 74). The optimal temperatures of the enzymes in higher organisms rarely exceed 50 °C, while enzymes from thermophilic bacteria found in hot springs, for instance, may still be active at 100 °C.

B. Substrate specificity

Enzymes “recognize” their substrates in a highly specific way (see p. 88). It is only the marked substrate specificity of the enzymes that makes a regulated metabolism possible. This principle can be illustrated using the example of the two closely related proteinases trypsin and chymotrypsin. Both belong to the group of serine proteinases and contain the same “triad” of catalytically active residues (Asp–His–Ser, shown here in green; see p. 176). Trypsin selectively cleaves peptide bonds on the C-terminal side of basic amino acids (lysine and arginine), while chymotrypsin is specific for hydrophobic residues. The substrate binding “pockets” of both enzymes have a similar structure, but their amino acid sequences differ slightly. In trypsin, a negatively charged aspartate residue (Asp-189, red) is arranged in such a way that it can bind and fix the basic group in the side chain of the substrate. In chymotrypsin, the “binding pocket” is slightly narrower, and it is lined with neutral and hydrophobic residues that stabilize the side chains of apolar substrate amino acids through hydrophobic interactions (see p. 28).

C. Bisubstrate kinetics

Almost all enzymes—in contrast to the simplified description given on p. 92—have more than one substrate or product. On the other hand, it is rare for more than two substrates to be bound simultaneously. In bisubstrate reactions of the type A + B → C + D, a number of reaction sequences are possible. In addition to the sequential mechanisms (see p. 90), in which all substrates are bound in a specific sequence before the product is released, there are also mechanisms in which the first substrate A is bound and immediately cleaved. A part of this substrate remains bound to the enzyme, and is then transferred to the second substrate B after the first product C has been released. This is known as the ping-pong mechanism, and it is used by transaminases, for example (see p. 178). In the Lineweaver—Burk plot (right; see p. 92), it can be recognized in the parallel shifting of the lines when [B] is varied.
1. pH and temperature dependency of enzyme activity

- **Activity**
- **pH**
- **Temperature (°C)**

<table>
<thead>
<tr>
<th>Enzyme active</th>
<th>Enzyme denatured</th>
</tr>
</thead>
<tbody>
<tr>
<td>Increased activity due to temperature increase</td>
<td></td>
</tr>
<tr>
<td>Denaturation</td>
<td></td>
</tr>
</tbody>
</table>

**Proportion BH**

**Proportion A**

**Denaturation**

**Enzyme active**

**Enzyme denatured**

2. Substrate specificity

- **Asp-189** Substrate (-X-Arg-Y-)
- **Ser-189** Substrate (-X-Phe-Y-)

3. Bisubstrate kinetics

- **1. Free enzyme E**
- **2. EA complex**
- **3. Covalent intermediate product E'**
- **4. EB complex**
- **5. EP2 complex**

**Active center**

**Velocity**

**1/velocity**

1/[A](mM⁻¹)

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Inhibitors

Many substances can affect metabolic processes by influencing the activity of enzymes. Enzyme inhibitors are particularly important here. A large proportion of medicines act as enzyme inhibitors. Enzyme-kinetic experiments are therefore an important aspect of drug development and testing procedures. Natural metabolites are also involved in regulatory processes as inhibitors (see p.114).

A. Types of inhibitor

Most enzyme inhibitors act reversibly—i.e., they do not cause any permanent changes in the enzyme. However, there are also irreversible inhibitors that permanently modify the target enzyme. The mechanism of action of an inhibitor—its inhibition type—can be determined by comparing the kinetics (see p.92) of the inhibited and uninhibited reactions (8). This makes it possible to distinguish competitive inhibitors (left) from noncompetitive inhibitors (right), for example. Allosteric inhibition is particularly important for metabolic regulation (see below).

Substrate analogs (2) have properties similar to those of one of the substrates of the target enzyme. They are bound by the enzyme, but cannot be converted further and therefore reversibly block some of the enzyme molecules present. A higher substrate concentration is therefore needed to achieve a half-maximum rate; the Michaelis constant $K_m$ increases (8). High concentrations of the substrate displace the inhibitor again. The maximum rate $V_{max}$ is therefore not influenced by this type of inhibition. Because the substrate and the inhibitor compete with one another for the same binding site on the enzyme, this type of inhibition is referred to as competitive. Analogs of the transition state (3) usually also act competitively.

When an inhibitor interacts with a group that is important for enzyme activity, but does not affect binding of the substrate, the inhibition is non-competitive (right). In this case, $K_m$ remains unchanged, but the concentration of functional enzyme $[E]$, and thus $V_{max}$ decrease. Non-competitive inhibitors generally act irreversibly, by modifying functional groups of the target enzyme (4).

“Suicide substrates” (5) are substrate analogs that also contain a reactive group. Initially, they bind reversibly, and then they form a covalent bond with the active center of the enzyme. Their effect is therefore also non-competitive. A well-known example of this is the antibiotic penicillin (see p.254).

Allosteric inhibitors bind to a separate binding site outside the active center (6). This results in a conformational change in the enzyme protein that indirectly reduces its activity (see p.116). Allosteric effects practically only occur in oligomeric enzymes. The kinetics of this type of system can no longer be described using the simple Michaelis–Menten model.

B. Inhibition kinetics

In addition to the Lineweaver–Burk plot (see p.92), the Eadie–Hofstee plot is also commonly used. In this case, the velocity $v$ is plotted against $v /[A]$. In this type of plot, $V_{max}$ corresponds to the intersection of the approximation lines with the $v$ axis, while $K_m$ is derived from the gradient of the lines. Competitive and non-competitive inhibitors are also easily distinguishable in the Eadie–Hofstee plot. As mentioned earlier, competitive inhibitors only influence $K_m$ and not $V_{max}$. The lines obtained in the absence and presence of an inhibitor therefore intersect on the ordinate. Non-competitive inhibitors produce lines that have the same slope ($K_m$ unchanged) but intersect with the ordinate at a lower level. Another type of inhibitor, not shown here, in which $V_{max}$ and $K_m$ are reduced by the same factor, is referred to as uncompetitive. Inhibitors with purely uncompetitive effects are rare. A possible explanation for this type of inhibition is selective binding of the inhibitor to the E$A$ complex.

Allosteric enzymes shift the target enzyme’s saturation curve to the left (see p.92). In Eadie–Hofstee and Lineweaver–Burk plots (see p.92), allosteric enzymes are recognizable because they produce curved lines (not shown).
A. Types of inhibitor

1. Uninhibited

2. Substrate analogs

3. Transition state analog

4. Modifying reagent

5. “Suicide substrate”

B. Kinetics of inhibition

1. Hyperbolic plot

2. Eadie-Hofstee plot
**Lactate dehydrogenase: structure**

**Lactate dehydrogenase (LDH, EC 1.1.1.27)** is discussed in some detail here and on the next page as an example of the structure and function of an enzyme.

### A. Lactate dehydrogenase: structure

The active form of lactate dehydrogenase (mass 144 kDa) is a tetramer consisting of four subunits (1). Each monomer is formed by a peptide chain of 334 amino acids (36 kDa). In the tetramer, the subunits occupy equivalent positions (1); each monomer has an active center. Depending on metabolic conditions, LDH catalyzes NADH-dependent reduction of pyruvate to lactate, or NAD\(^+\)-dependent oxidation of lactate to pyruvate (see p. 18).

The active center of an LDH subunit is shown schematically in Fig. 2. The peptide backbone is shown as a light blue tube. Also shown are the substrate lactate (red), the coenzyme NAD\(^+\) (yellow), and three amino acid side chains (Arg-109, Arg-171, and His-195; green), which are directly involved in the catalysis. A peptide loop (pink) formed by amino acid residues 98–111 is also shown. In the absence of substrate and coenzyme, this partial structure is open and allows access to the substrate binding site (not shown). In the enzyme lactate NAD\(^+\) complex shown, the peptide loop closes the active center. The catalytic cycle of lactate dehydrogenase is discussed on the next page.

### B. Isoenzymes

There are two different LDH subunits in the organism—M and H—which have a slightly different amino acid sequence and consequently different catalytic properties. As these two subunits can associate to form tetramers randomly, a total of five different isoenzymes of LDH are found in the body.

Fig. 1 shows sections from the amino acid sequences of the two subunits, using the single-letter notation (see p. 60). A common precursor gene was probably duplicated at some point in evolution. The two genes then continued to develop further independently of each other through mutation and selection.

The differences in sequence between the M and H subunits are mainly conservative—i.e., both residues are of the same type, e.g. glycine (G) and alanine (A), or arginine (R) and lysine (K). Non-conservative exchanges are less frequent—e.g., lysine (K) for glutamine (Q), or threonine (T) for glutamic acid (E). Overall, the H subunit contains more acidic and fewer basic residues than the M form, and it therefore has a more strongly negative charge. This fact is exploited to separate the isoenzymes using electrophoresis (2; see pp. 78, 276). The isoenzyme LDH-1, consisting of four H subunits, migrates fastest, and the M\(_{4}\) isoenzyme is slowest.

The separation and analysis of isoenzymes in blood samples is important in the diagnosis of certain diseases. Normally, only small amounts of enzyme activity are found in serum. When an organ is damaged, intracellular enzymes enter the blood and can be demonstrated in it (serum enzyme diagnosis). The total activity of an enzyme reflects the severity of the damage, while the type of isoenzyme found in the blood provides evidence of the site of cellular injury, since each of the genes is expressed in the various organs at different levels. For example, the liver and skeletal muscles mainly produce M subunits of lactate dehydrogenase (M for muscle), while the brain and cardiac muscle mainly express H subunits (H for heart). In consequence, each organ has a characteristic isoenzyme pattern (3). Following cardiac infarction, for example, there is a strong increase in the amount of LDH-1 in the blood, while the concentration of LDH-5 hardly changes. The isoenzymes of creatine kinase (see p. 336) are also of diagnostic importance.
A. Lactate dehydrogenase: structure

1. Tetramer 144 kDa

2. Active center
- Essential amino acids: Arg-109, His-195, Arg-171
- Substrate (lactate)
- Mobile loop
- Coenzyme (NAD\(^+\))
- Enzyme protein

B. Isoenzymes

<table>
<thead>
<tr>
<th>Lactate dehydrogenase M</th>
<th>Lactate dehydrogenase H</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gene</td>
<td>RYLMGERLVHPSCHGW/LGEHGDSSVPVWSG/MTVAGCS/LTLPDLGTD..</td>
</tr>
<tr>
<td>LDH1 (H(_4))</td>
<td>RYLMERLGVHPSCHGW/LGEHGDSSVPVWSG/MTVAGCS/LTLPDLGTD..</td>
</tr>
<tr>
<td>LDH2 (M(_2)H(_2))</td>
<td></td>
</tr>
<tr>
<td>LDH3 (M(_3)H(_1))</td>
<td></td>
</tr>
<tr>
<td>LDH4 (M(_1)H(_3))</td>
<td></td>
</tr>
<tr>
<td>LDH5 (M(_4))</td>
<td></td>
</tr>
</tbody>
</table>

- Skeletal muscle
- Liver
- Brain
- Cardiac muscle

2. Forms
3. Separation by gel electrophoresis
Lactate dehydrogenase: mechanism

The principles of enzyme catalysis discussed on p. 90 can be illustrated using the reaction mechanism of lactate dehydrogenase (LDH) as an example.

A. Lactate dehydrogenase: catalytic cycle

LDH catalyzes the transfer of hydride ions (see p. 32) from lactate to NAD⁺ or from NADH to pyruvate.

L-lactate + NAD⁺ → pyruvate + NADH + H⁺

The equilibrium of the reaction strongly favors lactate formation. At high concentrations of lactate and NAD⁺, however, oxidation of lactate to pyruvate is also possible (see p. 18). LDH catalyzes the reaction in both directions, but—like all enzymes—it has no effect on chemical equilibrium.

As the reaction is reversible, the catalytic process can be represented as a closed loop. The catalytic cycle of LDH is reduced to six “snapshots” here. Intermediate steps in catalysis such as those shown here are extremely short-lived and therefore difficult to detect.

Their existence was deduced indirectly from a large number of experimental findings—e.g., kinetic and binding measurements.

Many amino acid residues play a role in the active center of LDH. They can mediate the binding of the substrate and coenzyme, or take part in one of the steps in the catalytic cycle directly. Only the side chains of three particularly important residues are shown here. The positively charged guanidinium group of arginine-171 binds the carboxylate group of the substrate by electrostatic interaction. The imidazole group of histidine-195 is involved in acid–base catalysis, and the side chain of arginine-109 is important for the stabilization of the transition state. In contrast to His-195, which changes its charge during catalysis, the two essential arginine residues are constantly protonated. In addition to these three residues, the peptide loop 98–111 mentioned on p. 98 is also shown here schematically (red). Its function consists of closing the active center after binding of the substrate and coenzyme, so that water molecules are largely excluded during the electron transfer.

We can now look at the partial reactions involved in LDH-catalyzed pyruvate reduction.

In the free enzyme, His195 is protonated (1). This form of the enzyme is therefore described as E·H⁺. The coenzyme NADH is bound first (2), followed by pyruvate (3). It is important that the carbonyl group of the pyruvate in the enzyme and the active site in the nicotinamide ring of the coenzyme should have a fairly optimal position in relation to each other, and that this orientation should become fixed (proximity and orientation of the substrates). The 98–111 loop now closes over the active center. This produces a marked decrease in polarity, which makes it easier to achieve the transition state (4; water exclusion). In the transition state, a hydride ion, H⁺ (see p. 32), is transferred from the coenzyme to the carbonyl carbon (group transfer). The transient—and energetically unfavorable—negative charge on the oxygen that occurs here is stabilized by electrostatic interaction with Arg-109 (stabilization of the transition state). At the same time, a proton from His-195 is transferred to this oxygen atom (group transfer), giving rise to the enzyme-bound products lactate and NAD⁺ (5). After the loop opens, lactate dissociates from the enzyme, and the temporarily uncharged imidazole group in His-195 again binds a proton from the surrounding water (6). Finally, the oxidized coenzyme NAD⁺ is released, and the initial state (1) is restored. As the diagram shows, the proton that appears in the reaction equation (NADH + H⁺) is not bound together with NADH, but after release of the lactate—i.e., between steps (5) and (6) of the previous cycle. Exactly the same steps occur during the oxidation of lactate to pyruvate, but in the opposite direction. As mentioned earlier, the direction which the reaction takes depends not on the enzyme, but on the equilibrium state—i.e., on the concentrations of all the reactants and the pH value (see p. 18).
A. Lactate dehydrogenase: catalytic cycle

1. Free enzyme
2. NADH bound
3. Pyruvate bound
4. Redox reaction
5. Lactate bound
6. NAD⁺ bound

E • H₆
E • H₆NADH
E • H₆NADH • Pyruvate
E • H₆NADH • Lactate
E • NAD⁺Lactate
Transition state

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Enzymatic analysis

Enzymes play an important role in biochemical analysis. In biological material—e.g., in body fluids—even tiny quantities of an enzyme can be detected by measuring its catalytic activity. However, enzymes are also used as reagents to determine the concentrations of metabolites—e.g., the blood glucose level. Most enzymatic analysis procedures use the method of spectrophotometry.

A. Principle of spectrophotometry

Many substances absorb light in the visible or ultraviolet region of the spectrum. This property can be used to determine the concentration of such a substance. The extent of light absorption depends on the type and concentration of the substance and on the wavelength of the light used. Monochromatic light—i.e., light with a defined wavelength isolated from white light using a monochromator—is therefore used. Monochromatic light with an intensity of $I_0$ is passed through a rectangular vessel made of glass or quartz (a cuvet), which contains a solution of the absorbing substance. The absorption $A$ of the solution (often also referred to as its extinction) is defined as the negative decadic logarithm of the quotient $I/I_0$. The Beer–Lambert law states that $A$ is proportional to the concentration $c$ of the absorbing substance and the thickness $d$ of the solution it passes through. As mentioned earlier, the absorption coefficient $e$ depends on the type of substance and the wavelength.

B. Measurement of lactate dehydrogenase activity

Measurement of lactate dehydrogenase (LDH) activity takes advantage of the fact that while the reduced coenzyme $\text{NAD}^+ + \text{H}^+$ absorbs light at 340 nm, oxidized NAD$^+$ does not. Absorption spectra (i.e., plots of $A$ against the wavelength) for the substrates and the coenzymes of the LDH reaction are shown in Fig. 1. Differences in absorption behavior between NAD$^+$ and NADH between 300 and 400 nm result from changes in the nicotinamide ring during oxidation or reduction (see p. 32). To measure the activity, a solution containing lactate and NAD$^+$ is placed in a cuvet, and absorption is recorded at a constant wavelength of 340 nm. The uncatalyzed LDH reaction is very slow. It is only after addition of the enzyme that measurable quantities of NADH are formed and absorption increases. Since according to the Beer–Lambert law the rate of the increase in absorption $\Delta A/\Delta t$ is proportional to the reaction rate $\Delta c/\Delta t$. The absorption coefficient $e$ at 340 nm or comparison with a standard solution can be used to calculate LDH activity.

C. Enzymatic determination of glucose

Most biomolecules do not show any absorption in the visible or ultraviolet spectrum. In addition, they are usually present in the form of mixtures with other—similar—compounds that would also react to a chemical test procedure. These two problems can be avoided by using an appropriate enzyme to produce a colored dye selectively from the metabolite that is being analyzed. The absorption of the dye can then be measured.

A procedure (1) that is often used to measure glucose when monitoring blood glucose levels (see p. 160) involves two successive reactions. The glucose-specific enzyme glucose oxidase (obtained from fungi) first produces hydrogen peroxide, $\text{H}_2\text{O}_2$, which in the second step—catalyzed by a peroxidase—oxidizes a colorless precursor into a green dye (2). When all of the glucose in the sample has been used up, the amount of dye formed—which can be measured on the basis of its light absorption—is equivalent to the quantity of glucose originally present.
A. Principle of spectrophotometry

\[
A = -\log \frac{I_b}{I} = \varepsilon \cdot c \cdot d \quad \text{Beer-Lambert law}
\]

B. Assay of lactate dehydrogenase activity

\[
\frac{\Delta A}{\Delta t} = \frac{\Delta c}{\varepsilon} = \frac{\Delta c}{\varepsilon} \cdot \varepsilon = v \quad \text{Activity}
\]

C. Enzymatic determination of glucose

1. Reaction

2. Procedure

1. Monochromatic light, intensity \( I_b \), Monochromatic light, intensity \( I \)
2. Sample solution, concentration \( c \)
3. Instrument

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Coenzymes 1

A. Coenzymes: definitions

In many enzyme-catalyzed reactions, electrons or groups of atoms are transferred from one substrate to another. This type of reaction always also involves additional molecules, which temporarily accept the group being transferred. Helper molecules of this type are called coenzymes. As they are not catalytically active themselves, the less frequently used term “cosubstrate” would be more appropriate. In contrast to substrates for which a given enzyme is usually specific (see p. 88), coenzymes cooperate with many enzymes of varying substrate specificity. We have rather arbitrarily divided the coenzymes here into group-transferring and redox coenzymes. Strictly speaking, redox coenzymes also transfer groups—namely, reducing equivalents (see p. 32).

Depending on the type of interaction with the enzyme, a distinction is made between soluble coenzymes and prosthetic groups. Soluble coenzymes (1) are bound like substrates during a reaction, undergo a chemical change, and are then released again. The original form of the coenzyme is regenerated by a second, independent reaction. Prosthetic groups (2), on the other hand, are coenzymes that are tightly bound to the enzyme and remain associated with it during the reaction. The part of the substrate bound by the coenzyme is later transferred to another substrate or coenzyme of the same enzyme (not shown in Fig. 2).

B. Redox coenzymes 1

All oxidoreductases (see p. 88) require coenzymes. The most important of these redox coenzymes are shown here. They can act in soluble form (5) or prosthetically (P). Their normal potentials (5) are shown in addition to the type of reducing equivalent that they transfer (see p. 18).

The pyridine nucleotides NAD+ and NADP+ (1) are widely distributed as coenzymes of dehydrogenases. They transport hydride ions (2e− and 1 H+; see p. 32) and always act in soluble form. NAD+ transfers reducing equivalents from catabolic pathways to the respiratory chain and thus contributes to energy metabolism. In contrast, reduced NADP+ is the most important reductant involved in biosynthesis (see p. 112).

The flavin coenzymes FMN and FAD (2, 3) contain flavin (isoalloxazine) as a redox-active group. This is a three-membered, N-containing ring system that can accept a maximum of two electrons and two protons during reduction. FMN carries the phosphorylated sugar alcohol ribitol at the flavin ring. FAD arises from FMN through bonding with AMP. The two coenzymes are functionally similar. They are found in dehydrogenases, oxidases, and monoxygenases. In contrast to the pyridine nucleotides, flavin reactions give rise to radical intermediates (see p. 32). To prevent damage to cell components, the flavins always remain bound as prosthetic groups in the enzyme protein.

The role of ubiquinone (coenzyme Q, 4) in transferring reducing equivalents in the respiratory chain is discussed on p. 140. During reduction, the quinone is converted into the hydroquinone (ubiquinol). The isoprenoid side chain of ubiquinone can have various lengths. It holds the molecule in the membrane, where it is freely mobile. Similar coenzymes are also found in photosynthesis (plastoquinone; see p. 132). Vitamins E and K (see p. 52) also belong to the quinone/hydroquinone systems.

L-Ascorbic acid (vitamin C, 5) is a powerful reducing agent. As an antioxidant, it provides nonspecific protection against oxidative damage (see p. 284), but it is also an essential cofactor for various monooxygenases and dioxygenases. Ascorbic acid is involved in the hydroxylation of proline and lysine residues during the biosynthesis of collagen (see p. 344), in the synthesis of catecholamines (see p. 352) and bile acids (see p. 314), as well as in the breakdown of tyrosine (see p. 415). The reduced form of the coenzyme is a relatively strong acid and forms salts, the ascorbates. The oxidized form is known as dehydroascorbic acid. The stimulation of the immune system caused by ascorbic acid has not yet been fully explained.
### A. Coenzymes: definitions

![Diagram of coenzyme interactions]

1. **Coenzyme**
   - **oxidized form**
   - **reduced form**
   - **type**
   - **transferred**
   - **E° (V)**

<table>
<thead>
<tr>
<th>Coenzyme</th>
<th>Oxidized form</th>
<th>Reduced form</th>
<th>Type</th>
<th>Transferred</th>
<th>E° (V)</th>
</tr>
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<tbody>
<tr>
<td>NAD(P)H</td>
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<td></td>
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<tr>
<td>Flavin adenine dinucleotide (FAD)</td>
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<td></td>
<td></td>
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<td>-0.3</td>
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<tr>
<td>Ubiquinone (coenzym Q)</td>
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<td></td>
<td></td>
<td></td>
<td>0</td>
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<tr>
<td>Ascorbic acid</td>
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<td></td>
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<td>0.1</td>
</tr>
</tbody>
</table>

### B. Redox coenzymes

![Diagram of redox coenzymes]

1. **NAD(P)H**
2. **Flavin mononucleotide (FMN)**
3. **Flavin adenine dinucleotide (FAD)**
4. **Ubiquinone (coenzym Q)**
5. **Ascorbic acid**

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Coenzymes 2

A. Redox coenzymes 2

In lipic acid (6), an intramolecular disulfide bond functions as a redox-active structure. As a result of reduction, it is converted into the corresponding dithiol. As a prosthetic group, lipic acid is usually covalently bound to a lysine residue (R) of the enzyme, and it is then referred to as lipamide. Lipamide is mainly involved in oxidative decarboxylation of 2-oxo acids (see p. 134). The peptide coenzyme glutathione is a similar disulfide/dithiol system (not shown; see p. 284).

Iron–sulfur clusters (7) occur as prosthetic groups in oxidoreductases, but they are also found in lyses—e.g., aconitase (see p. 136) and other enzymes. Iron–sulfur clusters consist of 2–4 iron ions that are coordinated with cysteine residues of the protein (~SR) and with anorganic sulfide ions (~S). Structures of this type are only stable in the interior of proteins. Depending on the number of iron and sulfide ions, distinctions are made between [Fe₂S₂], [Fe₃S₄], and [Fe₄S₄] clusters. These structures are particularly numerous in the respiratory chain (see p. 140), and they are found in all complexes except complex IV.

Heme coenzymes (8) with redox functions exist in the respiratory chain (see p. 140), in photosynthesis (see p. 128), and in monooxygenases and peroxidases (see p. 24). Heme-containing proteins with redox functions are also referred to as cytochromes. In cytochromes, in contrast to hemoglobin and myoglobin, the iron changes its valence (usually between +2 and +3). There are several classes of heme (a, b, and c), which have different types of substituent — Rₐ to — Rₐ. Hemoglobin, myoglobin, and the heme enzymes contain heme b. Two types of heme a are found in cytochrome c oxidase (see p. 132), while heme c mainly occurs in cytochrome c, where it is covalently bound with cysteine residues of the protein part via thioester bonds.

B. Group-transferring coenzymes 1

The nucleoside phosphates (1) are not only precursors for nucleic acid biosynthesis; many of them also have coenzyme functions. They serve for energy conservation, and as a result of energetic coupling (see p. 124) also allow endergonic processes to proceed. Metabolites are often made more reactive (“activated”) as a result of the transfer of phosphate residues (phosphorylation). Bonding with nucleoside diphosphate residues (mainly UDP and CDP) provides activated precursors for polysaccharides and lipids (see p. 110). Endergonic formation of bonds by ligases (enzyme class 6) also depends on nucleoside triphosphates.

Acyl residues are usually activated by transfer to coenzyme A (2). In coenzyme A (see p. 12), pantetheine is linked to 3’-phospho-ADP by a phosphoric anhydride bond. Pantetheine consists of three components connected by amide bonds—pantoic acid, β-alanine, and cysteamine. The latter two components are biogenic amines formed by the decarboxylation of aspartate and cysteine, respectively. The compound formed from pantoic acid and β-alanine (pantothenic acid) has vitamin-like characteristics for humans (see p. 368). Reactions between the thiol group of the cysteamine residue and carboxylic acids give rise to thioesters, such as acetyl CoA. This reaction is strongly endergonic, and it is therefore coupled to exergonic processes. Thioesters represent the activated form of carboxylic acids, because acyl residues of this type have a high chemical potential and are easily transferred to other molecules. This property is often exploited in metabolism.

Thiamine diphosphate (TPP, 3), in cooperation with enzymes, is able to activate aldehydes or ketones as hydroxalkyl groups and then to pass them on to other molecules. This type of transfer is important in the transketolase reaction, for example (see p. 152). Hydroxalkyl residues also arise in the decarboxylation of α-ketoc acids. In this case, they are released as aldehydes or transferred to lipoamide residues of 2-oxoacid dehydrogenases (see p. 134). The functional component of TPP is the sulfur- and nitrogen-containing thiazole ring.

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### A. Redox coenzymes 2

<table>
<thead>
<tr>
<th>Coenzyme</th>
<th>Oxidized form</th>
<th>Reduced form</th>
<th>Type</th>
<th>Transferred</th>
<th>$E^0$</th>
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<tbody>
<tr>
<td>6. Lipoamide</td>
<td><img src="image1" alt="Lipoamide Oxidized" /></td>
<td><img src="image2" alt="Lipoamide Reduced" /></td>
<td>P</td>
<td>2[H]</td>
<td>−0.29</td>
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<tr>
<td>7. Iron–sulfur cluster</td>
<td><img src="image3" alt="Iron-Sulfur Cluster Oxidized" /></td>
<td><img src="image4" alt="Iron-Sulfur Cluster Reduced" /></td>
<td>P</td>
<td>1e0</td>
<td>−0.6 to +0.5</td>
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<tr>
<td>8. Heme</td>
<td><img src="image5" alt="Heme" /></td>
<td><img src="image6" alt="Heme" /></td>
<td>P</td>
<td>1e0</td>
<td>0 to +0.5</td>
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### B. Group-transferring coenzymes 1

<table>
<thead>
<tr>
<th>Coenzyme (symbol)</th>
<th>Free form</th>
<th>Charged form</th>
<th>Group(s) transferred</th>
<th>Important enzymes</th>
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<tbody>
<tr>
<td>1. Nucleoside phosphates</td>
<td><img src="image7" alt="Nucleoside Phosphates" /></td>
<td><img src="image8" alt="Nucleoside Phosphates" /></td>
<td>B-Rib</td>
<td>Phospho-transferases, Nucleotidyl-transferases (2.7.n.n) Ligases (6.n.n.n)</td>
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<td>2. Coenzyme A</td>
<td><img src="image9" alt="Coenzyme A" /></td>
<td><img src="image10" alt="Coenzyme A" /></td>
<td>Acyl residues</td>
<td>Acyltransferases (2.3.n.n), CoA transferases (2.8.3.n)</td>
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<tr>
<td>3. Thiamine diphosphate</td>
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<td><img src="image12" alt="Thiamine Diphosphate" /></td>
<td>Hydroxy-alkyl residues</td>
<td>Decarboxylases (4.1.1.n), Oxaacid dehydrogenases (1.2.x.x), Transketolase (2.2.1.1)</td>
</tr>
</tbody>
</table>
Coenzymes 3

A. Group-transferring coenzymes

Pyridoxal phosphate (4) is the most important coenzyme in amino acid metabolism. Its role in transamination reactions is discussed in detail on p. 178. Pyridoxal phosphate is also involved in other reactions involving amino acids, such as decarboxylations and dehydrations. The aldehyde form of pyridoxal phosphate shown here (left) is not generally found in free form. In the absence of substrates, the aldehyde group is covalently bound to the ε-amino group of a lysine residue as aldmine (“Schiff’s base”). Pyridoxamine phosphate (right) is an intermediate of transamination reactions. It reverts to the aldehyde form by reacting with 2-oxoacids (see p. 178).

Biotin (5) is the coenzyme of the carboxy- lases. Like pyridoxal phosphate, it has an amide-type bond via the carboxyl group with a lysine residue of the carboxylase. This bond is catalyzed by a specific enzyme. Using ATP, biotin reacts with hydrogen carbonate (HCO₃⁻) to form N-carboxybiotin. From this activated form, carbon dioxide (CO₂) is then transferred to other molecules, into which a carboxyl group is introduced in this way. Examples of biotin-dependent reactions of this type include the formation of oxaloacetic acid from pyruvate (see p. 154) and the synthesis of malonyl-CoA from acetyl-CoA (see p. 162).

Tetrahydrofolate (THF, 6) is a coenzyme that can transfer C₅ residues in different oxidation states. THF arises from the vitamin folic acid (see p. 366) by double hydrogenation of the heterocyclic pterin ring. The C₅ units being transferred are bound to N-5, N-10, or both nitrogen atoms. The most important derivatives are:

a) N⁵-formyl-THF and N⁵⁰-formyl-THF, in which the formyl residue has the oxidation state of a carboxylic acid;

b) N⁵-methylene-THF, with a C₅ residue in the oxidation state of an aldehyde; and

c) N⁵-methyl-THF, in which the methyl group has the oxidation state of an alcohol. C₅ units transferred by THF play a role in the synthesis of methionine (see p. 412), purine nucleotides (see p. 188), and dTMP (see p. 190), for example. Due to the central role of THF derivatives in the biosynthesis of DNA precursors, the enzymes involved in THF metabolism are primary targets for cytostatic drugs (see p. 402).

The cobalamin (7) are the chemically most complex form of coenzyme. They also represent the only natural substances that contain the transition metal cobalt (Co) as an essential component. Higher organisms are unable to synthesize cobalamin themselves, and are therefore dependent on a supply of vitamin B₁₂ synthesized by bacteria (see p. 368).

The central component of the cobalamin is the corrin ring, a member of the tetrapyrroles, at the center of which the cobalt ion is located. The end of one of the side chains of the ring carries a nucleotide with the unusual base dimethylbenzimidazole. The ligands for the metal ion are the four N atoms of the pyrrole ring, a nitrogen from dimethylbenzimidazole, and a group X, which is organo-metallically bound—i.e., mainly covalently.

In methylcobalamin, X is a methyl group. This compound functions as a coenzyme for several methyltransferases, and among other things is involved in the synthesis of methionine from homocysteine (see p. 418). However, in human metabolism, in which methionine is an essential amino acid, this reaction does not occur.

Adenosylcobalamin (coenzyme B₁₂) carries a covalently bound adenosyl residue at the metal atom. This is a coenzyme of various isomerases, which catalyze rearrangements following a radical mechanism. The radical arises here through homolytic cleavage of the bond between the metal and the adenosyl group. The most important reaction of this type in animal metabolism is the rearrangement of methylmalonyl-CoA to form succinyl-CoA, which completes the breakdown of odd-numbered fatty acids and of the branched amino acids valine and isoleucine (see pp. 166 and 414).
### A. Group-transferring coenzymes 2

<table>
<thead>
<tr>
<th>Coenzyme</th>
<th>Free form</th>
<th>Charged form</th>
<th>Group(s) transferred</th>
<th>Important enzymes</th>
</tr>
</thead>
<tbody>
<tr>
<td>4. Pyridoxal phosphate</td>
<td><img src="image1" alt="Pyridoxal phosphate" /></td>
<td><img src="image2" alt="Pyridoxal phosphate" /></td>
<td>Amino group</td>
<td>Transaminases (2.6.1.n)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Amino acid residues</td>
<td>Many kinases (4.6.1.n)</td>
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<tr>
<td>5. Biotin</td>
<td><img src="image3" alt="Biotin" /></td>
<td><img src="image4" alt="Biotin" /></td>
<td>[CO₂]</td>
<td>Carboxylases (6.4.1.n)</td>
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<td>4. Pyridoxal phosphate</td>
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<td><img src="image6" alt="Pyridoxal phosphate" /></td>
<td>C₄ groups</td>
<td>C₄ transfers (2.1.n)</td>
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<tr>
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<td></td>
<td></td>
<td>a) α-C formyl</td>
<td></td>
</tr>
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<td></td>
<td>b) α-C formyl</td>
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<td>c) α-C formyl</td>
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<td>d) α-C formyl</td>
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<td></td>
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<td></td>
<td>e) α-C formyl</td>
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<tr>
<td>7. Cobalamin coenzymes</td>
<td><img src="image7" alt="Cobalamin coenzymes" /></td>
<td><img src="image8" alt="Cobalamin coenzymes" /></td>
<td>X = Adenosyl</td>
<td>Mutasas (5.4.n)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>X = Methyl</td>
<td>Methyltransferases (2.1.1.n)</td>
</tr>
</tbody>
</table>

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Activated metabolites

Many coenzymes (see pp. 104ff.) serve to activate molecules or groups that are poorly reactive. Activation consists of the formation of reactive intermediate compounds in which the group concerned is located at a higher chemical potential and can therefore be transferred to other molecules in an exergonic reaction (see p. 124). Acetyl-CoA is an example of this type of compound (see p. 12). ATP and the other nucleoside triphosphate coenzymes not only transfer phosphate residues, but also provide the nucleotide components for this type of activation reaction. On this page, we discuss metabolites or groups that are activated in the metabolism by bonding with nucleosides or nucleotides. Intermediates of this type are mainly found in the metabolism of complex carbohydrates and lipids.

A. Activated metabolites

1. Uridine diphosphate glucose (UDPGlucose)
The inclusion of glucose residues into polymers such as glycogen or starches is an endergonic process. The activation of the glucose building blocks that is required for this takes place in several steps, in which two ATPs are used per glucose. After the phosphorylation of free glucose, glucose 6-phosphate is isomerized to glucose 1-phosphate (a), reaction with UTP (b) then gives rise to UDPGlucose, in which the anemic OH group at C-1 of the sugar is bound with phosphate. This “energy-rich” compound (an acetal phosphate) allows exergonic transfer of glucose residues to glycogen (c; see pp. 156, 408) or other acceptors.

2. Cytidine diphosphate choline (CDPcholine)
The amino alcohol choline is activated for inclusion in phospholipids following a similar principle (see p. 170). Choline is first phosphorylated by ATP to form choline phosphate (a), which by reaction with CTP and cleavage of diphosphate, then becomes CDPcholine. In contrast to (1), it is not choline that is transferred from CDPcholine, but rather choline phosphate, which with diacylglycerol yields phosphatidylcholine (lecithin).

3. Phosphoadenosine phosphosulfate (PAPS)
Sulfate residues occur as strongly polar groups in various biomolecules—e.g., in glycosaminoglycans (see p. 346) and conjugates of steroid hormones and xenobiotics (see p. 316). In the synthesis of the “activated sulfate” PAPS, ATP first reacts with anorganic sulfate to form adenosine phosphosulfate (APS, a). This intermediate already contains the “energy-rich” mixed anhydride bond between phosphoric acid and sulfuric acid. In the second step, the 3’-OH group of APS is phosphorylated, with ATP being used again. After transfer of the sulfate residue to OH groups (c), adenosine-3’,5’-bisphosphate remains.

4. S-adenosyl methionine (SAM)
The coenzyme tetrahydrofolate (THF) is the main agent by which C1 fragments are transferred in the metabolism. THF can bind this type of group in various oxidation states and pass it on (see p. 108). In addition, there is “activated methyl,” in the form of S-adenosyl methionine (SAM). SAM is involved in many methylation reactions—e.g., in creatine synthesis (see p. 336), the conversion of norepinephrine into epinephrine (see p. 352), the inactivation of norepinephrine by methylation of a phenolic OH group (see p. 316), and in the formation of the active form of the cytostatic drug 6-mercaptopurine (see p. 402).

SAM is derived from degradation of the proteinogenic amino acid methionine, to which the adenosyl residue of an ATP molecule is transferred. After release of the activated methyl group, S-adenosyl homocysteine (SAH) is left over. This can be converted back into methionine in two further steps. Firstly, cleavage of the adenosine residue gives rise to the non-proteinogenic amino acid homocysteine, to which a methyl group is transferred once again with the help of N5-methyl-THF (see p. 418). Alternatively, homocysteine can also be broken down into propionyl-CoA.
A. Activated metabolites

1. Uridine diphosphate glucose (UDP-glucose)

2. Cytidine diphosphate choline (CDP-choline)

3. Phosphoadenosine phosphosulfate (PAPS)

4. S-adenosyl methionine (SAM)
Intermediary metabolism

Hundreds of chemical reactions are constantly taking place in every cell, and taken together these are referred to as the metabolism. The chemical compounds involved in this are known as metabolites. Outside of the cell, almost all of the chemical changes in metabolites would only take place very slowly and without any specific direction. By contrast, organized sequences of chemical reactions with a high rate of throughput, known as metabolic pathways, become possible through the existence of specific enzymes (see p. 88).

A. Intermediary metabolism: overview

A number of central metabolic pathways are common to most cells and organisms. These pathways, which serve for synthesis, degradation, and interconversion of important metabolites, and also for energy conservation, are referred to as the intermediary metabolism.

In order to survive, all cells constantly require organic and inorganic nutrients, as well as chemical energy, which is mainly derived from ATP (see below). Depending on the way in which these needs are satisfied, organisms can be classified into autotrophic and heterotrophic groups. The autotrophs, which include plants and many microorganisms, can synthesize organic molecules from inorganic precursors (CO₂). An autotrophic lifestyle is possible through photosynthesis, for example (see p. 128). The heterotrophs—e.g., animals and fungi—depend on organic substances supplied in their diet. The schema shown on this page provides an overview of animal metabolism.

The polymeric substances contained in the diet (proteins, carbohydrates, and nucleic acids—top) cannot be used by the organism directly. Digestive processes first have to degrade them to monomers (amino acids, sugars, nucleotides). These are then mostly broken down by catabolic pathways (pink arrows) into smaller fragments. The metabolites produced in this way (generally referred to as the “metabolite pool”) are then either used to obtain energy through further catabolic conversion, or are built up again into more complex molecules by anabolic pathways (blue arrows). Of the numerous metabolites in the pool, only three particularly important representatives—pyruvate, acetyl-CoA, and glycerol—are shown here. These molecules represent connecting links between the metabolism of proteins, carbohydrates, and lipids. The metabolite pool also includes the intermediates of the tricarboxylic acid cycle (6). This cyclic pathway has both catabolic and anabolic functions—i.e., it is amphipathic (violet; see p. 138).

Waste products from the degradation of organic substances in animal metabolism include carbon dioxide (CO₂), water (H₂O), and ammonia (NH₃). In mammals, the toxic substance ammonia is incorporated into urea and excreted in this form (see p. 182).

The most important form of storage for chemical energy in all cells is adenosine triphosphate (ATP; see p. 122). ATP synthesis requires energy—i.e., the reaction is endergonic. Conversely, cleavage of ATP into ADP and phosphate releases energy. Exergonic hydrolysis of ATP, as a result of energetic coupling (see p. 16), makes energy-dependent (endergonic) processes possible. For example, most anabolic pathways, as well as movement and transport processes, are energy-dependent.

The most important pathway for the synthesis of ATP is oxidative phosphorylation (see p. 122). In this process, catabolic pathways first form reduced cofactors (NADH+H⁺, QH₂, ETFH₂). Electrons are then transferred from these compounds to oxygen. This strongly exergonic process is catalyzed by the respiratory chain and used indirectly for the ATP synthesis (see p. 140). In anaerobic conditions—i.e., in the absence of oxygen—most organisms can fall back on ATP that arises in glycolysis (3). This less of cien type of ATP synthesis is referred to as fermentation (see p. 146).

While NADH exclusively supplies oxidative phosphorylation, NADPH+H⁺—a very similar coenzyme—is the reducing agent for anabolic pathways. NADPH + H⁺ is mainly formed in the pentose phosphate pathway (PPP; 1; see p. 152).
A. Intermediary metabolism: overview

- **Proteins**
- **Poly saccharides**
- **Nucleic acids**
- **Fats**
- **Iso-prenoids**
- **Amino acids**
- **Pentoses**
- **Fatty acids**
- **Bases**
- **Glycerol**
- **Pyruvate**
- **Acetyl CoA**
- **Glucose**
- **NADPH**
- **ATP**
- **NADH**
- **QH2**
- **NH3**
- **O2**
- **Urea**
- **H2O**
- **CO2**

**Metabolic Pathways**:
- **Catabolic pathway**
- **Anabolic pathway**
- **Amphibolic pathway**
- **Storage compound**
  - 1. Pentose phosphate pathway
  - 2. Gluconeogenesis
  - 3. Glycolysis
  - 4. β-Oxidation
  - 5. Fatty acid biosynthesis
  - 6. Tricarboxylic acid cycle
  - 7. Urea cycle

**Waste products**

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Regulatory mechanisms

A. Fundamental mechanisms of metabolic regulation

The activities of all metabolic pathways are subject to precise regulation in order to adjust the synthesis and degradation of metabolites to physiological requirements. An overview of the regulatory mechanisms is presented here. Further details are shown on pp. 116ff.

Metabolite flow along a metabolic pathway is mainly determined by the activities of the enzymes involved (see p. 88). To regulate the pathway, it is sufficient to change the activity of the enzyme that catalyzes the slowest step in the reaction chain. Most metabolic pathways have key enzymes of this type on which the regulatory mechanisms operate. The activity of key enzymes is regulated at three independent levels:

Transcriptional control. Here, Biosynthesis of the enzyme protein is influenced at the genetic level (1). Interventions in enzyme synthesis mainly affect synthesis of the corresponding mRNA—i.e., transcription of the gene coding for the enzyme. The term “transcriptional control” is therefore used (see pp. 118, 244). This mechanism is mediated by regulatory proteins (transcription factors) that act directly on DNA. The genes have a special regulatory segment for this purpose, known as the promoter region, which contains binding sites (control elements) for regulatory proteins. The activity of these proteins is, in turn, affected by metabolites or hormones. When synthesis of a protein is increased by transcriptional control, the process is referred to as induction; when it is reduced or suppressed, it is referred to as repression. Induction and repression processes take some time and are therefore not immediately effective.

Interconversion of key enzymes (2) takes effect considerably faster than transcriptional control. In this case, the enzyme is already present at its site of effect, but it is initially still inactive. It is only when needed that it is converted into the catalytically active form, after signaling and mediation from second messengers (see p. 120) through an activating enzyme (E1). If the metabolic pathway is no longer required, an inactivating enzyme (E2) returns the key enzyme to its inactive resting state.

Interconversion processes in most cases involve ATP-dependent phosphorylation of the enzyme protein by a protein kinase or dephosphorylation of it by a protein phosphatase (see p. 120). The phosphorylated form of the key enzyme is usually the more active one, but the reverse may also occur.

Modulation by ligands. An important variable that regulates flow through a metabolic pathway is precursor availability (metabolite A in the case shown here). The availability of precursor A increases along with the activity of the metabolic pathways that form A (3) and it decreases with increasing activity of other pathways that also consume A (4). Transport from one cell compartment to another can also restrict the availability of A.

Coenzyme availability can also often have a limiting effect (5). If the coenzyme is regenerated by a second, independent metabolic pathway, the speed of the second pathway can limit that of the first one. For example, glycolysis and the tricarboxylic acid cycle are mainly regulated by the availability of NAD+ (see p. 146). Since NAD+ is regenerated by the respiratory chain, the latter indirectly controls the breakdown of glucose and fatty acids (respiratory control, see p. 144).

Finally, the activity of key enzymes can be regulated by ligands (substrates, products, coenzymes, or other effectors), which as allosteric effectors do not bind at the active center itself, but at another site in the enzyme, thereby modulating enzyme activity (6; see p. 116). Key enzymes are often inhibited by immediate reaction products, by end products of the reaction chain concerned ("feed-back inhibition"), or by metabolites from completely different metabolic pathways. The precursors for a reaction chain can stimulate their own utilization through enzyme activation.
A. Fundamental mechanisms of metabolic regulation

**Transcriptional control**
- Induction
- Repression

**Interconversion**
- Hormone
- Key enzyme (inactive)
- Second messenger
- Activated enzyme

**Modulation by ligands**
- Key enzyme (active)
- End product
- Feedback inhibition
- Availability precursors, compartmentation
- Competition for substrates or coenzymes
- Regeneration of the coenzyme

Key concepts include: gene repression, induction, transcriptional control, translational control, metabolic regulation, second messengers, coenzyme regeneration.
Allosteric regulation

The regulation of aspartate carbamoyltransferase (ACTase), a key enzyme of pyrimidine biosynthesis (see p. 188) is discussed here as an example of allosteric regulation of enzyme activity. Allosteric effects are mediated by the substrate itself or by inhibitors and activators (allosteric effectors, see p. 114). The latter bind at special sites outside the active center, producing a conformational change in the enzyme protein and thus indirectly lead to an alteration in its activity.

A. Aspartate carbamoyltransferase: reaction

ACTase catalyzes the transfer of a carbamoyl residue from carbamoyl phosphate to the amino group of L-aspartate. The N-carbamoyl L-aspartate formed in this way already contains all of the atoms of the later pyrimidine ring (see p. 188). The ACTase of the bacterium Escherichia coli is inhibited by cytidine triphosphate (CTP), an end product of the anaerobic metabolism of pyrimidines, and is activated by the precursor ATP.

B. Kinetics

In contrast to the kinetics of isosteric (normal) enzymes, allosteric enzymes such as ACTase have sigmoidal (S-shaped) substrate saturation curves (see p. 92). In allosteric systems, the enzyme’s affinity to the substrate is not constant, but depends on the substrate concentration \( [S] \). Instead of the Michaelis constant \( K_M \) (see p. 92), the substrate concentration at half-maximal rate \( [A]_{0.5} \) is given. The sigmoidal character of the curve is described by the Hill coefficient \( h \). In isosteric systems, \( h = 1 \), and \( h \) increases with increasing sigmoidicity.

Depending on the enzyme, allosteric effectors can influence the maximum rate \( V_{max} \), the semi-saturation concentration \( [A]_{0.5} \), and the Hill coefficient \( h \). If it is mainly \( V_{max} \) that is changed, the term “\( V \) system” is used. Much more common are “\( K \) systems”, in which allosteric effects only influence \( [A]_{0.5} \) and \( h \).

The \( K \) type also includes ACTase. The inhibitor CTP in this case leads to right-shifting of the curve, with an increase in \( [A]_{0.5} \) and \( h \) (curve II). By contrast, the activator ATP causes a left shift; it reduces both \( [A]_{0.5} \) and \( h \) (curve III). This type of allosteric effect was first observed in hemoglobin (see p. 280), which can be regarded as an “honorary” enzyme.

C. R and T states

Allosteric enzymes are almost always oligomers with 2–12 subunits. ACTase consists of six catalytic subunits (blue) and six regulatory subunits (yellow). The latter bind the allosteric effectors CTP and ATP. Like hemoglobin, ACTase can also be present in two conformations—the less active T state (for “tense”) and the more active R state (for “relaxed”). Substrates and effectors influence the equilibrium between the two states, and thereby give rise to sigmoidal saturation behavior. With increasing aspartate concentration, the equilibrium is shifted more and more toward the R form. ATP also stabilizes the R conformation by binding to the regulatory subunits. By contrast, binding of CTP to the same sites promotes a transition to the T state. In the case of ACTase, the structural differences between the R and T conformations are particularly dramatic. In T → R conversion, the catalytic subunits separate from one another by 1.2 nm, and the subunits also rotate around the axis of symmetry. The conformations of the subunits themselves change only slightly, however.

D. Structure of a dimer

The subunits of ACTase each consist of two domains—i.e., independently folded partial structures. The N-terminal domain of the regulatory subunit (right) mediates interaction with CTP or ATP (green). A second, Zn\(^{2+}\)-containing domain (Zn\(^{2+}\) shown in light blue) establishes contact with the neighboring catalytic subunit. Between the two domains of the catalytic subunit lies the active center, which is occupied here by two substrate analogs (red).
A. Aspartate carbamoyltransferase: reaction

B. Kinetics

C. R and T conformation

D. Structure of a dimer
Transcription control

A. Functioning of regulatory proteins

Regulatory proteins (transcription factors) are involved in controlling gene expression in all cells. These regulatory proteins bind to specific DNA sequences and thereby activate or inhibit the transcription of genes (Transcription control). The effects of transcription factors are usually reversible and are often controlled by ligands or by interconversion.

The nomenclature for transcription factors is confusing. Depending on their mode of action, various terms are in use both for the proteins themselves and for the DNA sequences to which they bind. If a factor blocks transcription, it is referred to as a repressor; otherwise, it is called an inducer. DNA sequences to which regulatory proteins bind are referred to as control elements. In prokaryotes, control elements that serve as binding sites for RNA polymerases are called promoters, whereas repressor-binding sequences are usually called operators. Control elements that bind activating factors are termed enhancers, whereas elements that bind inhibiting factors are known as silencers.

The numerous regulatory proteins that are known can be classified into four different groups (1–4), based on their mechanisms of action. Negative gene regulation—i.e., switching off of the gene concerned—is carried out by repressors. Some repressors only bind to DNA (1a) in the absence of specific ligands (1). In this case, the complex between the repressor and the ligand loses its ability to bind to the DNA, and the promoter region becomes accessible for binding of RNA polymerase (1b). It is often the free repressor that does not bind to the DNA, so that transcription is only blocked in the presence of the ligand (2a, 2b). A distinction between two different types of positive gene regulation can be made in the same way. If it is only the free inducer that binds, then transcription is inhibited by the appropriate ligand (3). Conversely, many inducers only become active when they have bound a ligand (4). This group includes the receptors for steroid hormones, for example (see p. 378).

B. Lactose operon

The well-investigated lactose operon of the bacterium Escherichia coli can be used here as an example of transcriptional control. The lac operon is a DNA sequence that is simultaneously subject to negative and positive control. The operon contains the structural genes for three proteins that are required for the utilization of lactose (one transporter and two enzymes), as well as control elements that serve to regulate the operon.

Since lactose is converted to glucose in the cell, there is no point in expressing the genes if glucose is already available. And indeed, the genes are in fact only transcribed when glucose is absent and lactose is present (3). This is achieved by interaction between two regulatory proteins. In the absence of lactose, the lac repressor blocks the promoter region (2). When lactose is available, it is converted into allolactose, which binds to the repressor and thereby detaches it from the operator (3). However, this is still not sufficient for the transcription of the structural genes. For binding of the RNA polymerase to take place, an inducer—the catabolite activator protein (CAP)—is required, which only binds to the DNA when it is present as a complex with 3',5'-cyclo-AMP (cAMP; see p. 386). cAMP, a signal for nutrient deficiency, is only formed by E. coli in the absence of glucose.

The interaction between the CAP–cAMP complex and DNA is shown in Fig. 4. Each subunit of the dimeric inducer (yellow or orange) binds one molecule of cAMP (red). Contact with the DNA (blue) is mediated by two “recognition helices” that interact with the major groove of the DNA. The bending of the DNA strand caused by CAP has functional significance.

Transcription control is much more complex in eukaryotes (see p. 244). The number of transcription factors involved is larger, and in addition the gene activity is influenced by the state of the chromatin (see p. 238).
A. Functions of regulatory proteins

<table>
<thead>
<tr>
<th>Negative regulation</th>
<th>Positive regulation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Without ligand</td>
<td>With ligand</td>
</tr>
<tr>
<td>RNA polymerase DNA</td>
<td>mRNA</td>
</tr>
<tr>
<td>Gen</td>
<td>Ligand</td>
</tr>
<tr>
<td>1a</td>
<td>2b</td>
</tr>
<tr>
<td>3a</td>
<td>4a</td>
</tr>
</tbody>
</table>

B. Lactose operon

1. Catabolite activator protein (CAP) only binds in the presence of CAP · cAMP

2. RNA polymerase (lac Repressor) lac Repressor

3. CAMP bound to DNA

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Hormonal control
In higher organisms, metabolic and other processes (growth, differentiation, control of the internal environment) are controlled by hormones (see pp. 370ff.)

A. Principles of hormone action

Depending on the type of hormone, hormone signals are transmitted to the target cells in different ways. Apolar (lipophilic) hormones penetrate the cell and act in the cell nucleus, while polar (hydrophilic) hormones act on the external cell membrane.

Lipophilic hormones, which include the steroid hormones, thyroxine, and retinoic acid, bind to a specific receptor protein inside their target cells. The complex formed by the hormone and the receptor then influences transcription of specific genes in the cell nucleus (see pp. 118, 244). The group of hydrophilic hormones (see p. 380) consists of hormones derived from amino acids, as well as peptide hormones and proteohormones. Their receptors are located in the plasma membrane. Binding of the hormone to this type of receptor triggers a signal that is transmitted to the interior of the cell, where it controls the processes that allow the hormone signal to take effect (signal transduction; see pp. 384ff.)

B. Hormonal regulation of glucose metabolism in the liver

The liver plays a major role in glucose homeostasis in the organism (see p. 310). If glucose deficiency arises, the liver releases glucose into the blood, and when blood sugar levels are high, it takes glucose up from the blood and converts it into different metabolites. Several hormones from both groups are involved in controlling these processes. A very simplified version of the way in which they work is presented here. Glycogen is the form in which glucose is stored in the liver and muscles. The rate of glycogen synthesis is determined by glycogen synthase (bottom right), while its breakdown is catalyzed by glycogen phosphorylase (bottom left).

Regulation by interconversion (bottom). If the blood glucose level falls, the peptide hormone glucagon is released. This activates glycogen breakdown, releasing glucose, and at the same time inhibits glycogen synthesis. Glucagon binds to receptors in the plasma membrane (bottom left) and, with mediation by a G-protein (see p. 386), activates the enzyme adenylate cyclase, which forms the second messenger 3,5'-cyclo-AMP (cAMP) from ATP. cAMP binds to another enzyme, protein kinase A (PK-A), and activates it. PK-A has several points of attack. Through phosphorylation, it converts the active form of glycogen synthase into the inactive form, thereby terminating the synthesis of glycogen. Secondly, it activates another protein kinase (not shown), which ultimately converts the inactive form of glycogen phosphorylase into the active form through phosphorylation. The active phosphorylase releases glucose 1-phosphate from glycogen, which, after conversion into glucose 6-phosphate supplies free glucose. In addition, via an inhibitor (1) of protein phosphatase (PP), active PK-A inhibits inactivation of glycogen phosphorylase. When the cAMP level falls again, phosphoprotein phosphatases become active, which dephosphorylate the various phosphoproteins in the cascade described, and thereby arrest glycogen breakdown and re-start glycogen synthesis. Activation and inactivation of proteins through phosphorylation or dephosphorylation is referred to as interconversion.

In contrast to glucagon, the peptide hormone insulin (see p. 76) increases glycogen synthesis and inhibits glycogen breakdown. Via several intermediates, it inhibits protein kinase GSK-3 (bottom right; for details, see p. 388) and thereby prevents inactivation of glycogen synthase. In addition, insulin reduces the cAMP level by activating cAMP phosphodiesterase (PDE).

Regulation by transcriptional control (top). If the liver’s glycogen reserves have been exhausted, the steroid hormone cortisol maintains glucose release by initiating the conversion of amino acids into glucose (gluconeogenesis; see p. 154). In the cell nucleus, the complex of cortisol and its receptor (see p. 378) binds to the promoter regions of various key enzymes of gluconeogenesis and leads to their transcription. The active enzymes are produced through translation of the mRNA formed. Control of the transcription of the gluconeogenesis enzyme PEP carboxykinase is discussed on p. 244.
A. Principles of hormone action

- **Lipophilic hormones**
  - DNA → mRNA → Translation → Protein → Cell response

- **Hydrophilic hormones**
  - Receptor → Second messenger → Cell response

B. Hormonal regulation of glucose metabolism in the liver

- Cortisol and glucocorticoid receptor
- Glucagon receptor
- Insulin receptor

- Glucose metabolism:
  - Glucose → Glc-6-P → Gluconeogenesis
  - ATP → cAMP → PKA → GSK-3 → Glycogen phosphorylase
  - PDE → cAMP → PKA → GSK-3 → Glycogen synthase

- Amino acids → Gluconeogenesis

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ATP

The nucleotide coenzyme adenosine triphosphate (ATP) is the most important form of chemical energy in all cells. Cleavage of ATP is strongly exergonic. The energy this provides ($\Delta G^\circ$; see p. 16) is used to drive endergonic processes (such as biosynthesis and movement and transport processes) through energetic coupling (see p. 124). The other nucleoside triphosphate coenzymes (GTP, CTP, and UTP) have similar chemical properties to ATP, but they are used for different tasks in metabolism (see p. 110).

A. ATP: structure

In ATP, a chain of three phosphate residues is linked to the 3'-OH group of the nucleoside adenosine (see p. 80). These phosphate residues are termed $\alpha$, $\beta$, and $\gamma$. The $\alpha$ phosphate is bound to ribose by a phosphoric acid ester bond. The linkages between the three phosphate residues, on the other hand, involve much more unstable phosphoric acid anhydride bonds. The active coenzyme is in fact generally a complex of ATP with an Mg$^{2+}$ ion, which is coordinatively bound to the $\alpha$ and $\beta$ phosphates (Mg$^{2+}$ ATP$^\circ$). However, the term “ATP” is usually used for the sake of simplicity.

B. Hydrolysis of ATP

The formula for ATP has been shown in Fig. A, with single and double bonds, is not an accurate representation of the actual charge distribution. In ATP, the oxygen atoms of all three phosphate residues have similarly strong negative charges (orange), while the phosphorus atoms represent centers of positive charge. One of the reasons for the instability of phosphoric anhydride bonds is the repulsion between these negatively charged oxygen atoms, which is partly relieved by cleavage of a phosphate residue. In addition, the free phosphate anion formed by hydrolysis of ATP is better hydrated and more strongly resonance-stabilized than the corresponding residue in ATP. This also contributes to the strongly exergonic character of ATP hydrolysis.

In standard conditions, the change in free enthalpy $\Delta H^\circ$ (see p. 18) that occurs in the hydrolysis of phosphoric acid anhydride bonds amounts to $-30$ to $-35$ kJ mol$^{-1}$ at pH 7. The particular anhydride bond of ATP that is cleaved only has a minor influence on $\Delta G^\circ$ (1–2). Even the hydrolysis of diphosphate (also known as pyrophosphate; 4) still yields more than $-30$ kJ mol$^{-1}$. By contrast, cleavage of the ester bond between ribose and phosphate only provides $-9$ kJ mol$^{-1}$ (3).

In the cell, the $\Delta G$ of ATP hydrolysis is substantially larger, because the concentrations of ATP, ADP, and $\Pi$, are much lower than in standard conditions and there is an excess of ATP over ADP (see p. 18). The pH value and Mg$^{2+}$ concentration also affect the value of $\Delta G$. The physiological energy yield of ATP hydrolysis to ADP and anorganic phosphate ($\Pi_n$) is probably around $-50$ kJ mol$^{-1}$.

C. Types of ATP formation

Only a few compounds contain phosphate residues with a group transfer potential (see p. 18) that is high enough to transfer them to ADP and thus allow ATP synthesis. Processes that raise anorganic phosphate to this type of high potential are called substrate level phosphorylations (see p. 124). Reactions of this type take place in glycolysis (see p. 150) and in the tricarboxylic acid cycle (see p. 136). Another “energy-rich” phosphate compound is creatine phosphate, which is formed from ATP in muscle and can regenerate ATP as needed (see p. 336).

Most cellular ATP does not arise in the way described above (i.e., by transfer of phosphate residues from organic molecules to ADP), but rather by oxidative phosphorylation. This process takes place in mitochondria (or as light-driven phosphorylation in chloroplasts) and is energetically coupled to a proton gradient over a membrane. These H$^+$ gradients are established by electron transport chains and are used by the enzyme ATP synthase as a source of energy for direct linking of anorganic phosphate to ADP. In contrast to substrate level phosphorylation, oxidative phosphorylation requires the presence of oxygen (i.e., aerobic conditions).
A. ATP: structure

1. Formula

\[ \begin{align*}
\text{Phosphoric acid anhydride bonds} & : \text{Phosphoric acid ester bond} \\
\text{1. Formula} & : \text{Mg}^{2+} \text{-Complex}
\end{align*} \]

2. Mg \textsuperscript{2+} Complex

B. Hydrolysis energies

1. Hydrolysis energies

2. ATP: charge density

C. Types of ATP formation

1. Phosphate transfer

2. Oxidative phosphorylation

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Energetic coupling

The cell stores chemical energy in the form of “energy-rich” metabolites. The most important metabolite of this type is adenosine triphosphate (ATP), which drives a large number of energy-dependent reactions via energetic coupling (see p. 16).

A. Energetic coupling

The change in free enthalpy $\Delta G^\circ$ during hydrolysis (see p. 18) has been arbitrarily selected as a measure of the group transfer potential of “energy-rich” compounds. However, this does not mean that ATP is in fact hydrolyzed in energetically coupled reactions. If ATP hydrolysis and an endergonic process were simply allowed to run alongside each other, the hydrolysis would only produce heat, without influencing the endergonic process. For coupling, the two reactions have to be linked in such a way that a common intermediate arises. This connection is illustrated here using the example of the glutamine synthetase reaction.

Direct transfer of NH$_3$ to glutamate is endergonic ($\Delta G^\circ = +14$ kJ mol$^{-1}$; see p. 18), and can therefore not take place. In the cell, the reaction is divided into two exergonic steps. First, the $\gamma$-phosphate residue is transferred from ATP to glutamate. This gives rise to an “energy-rich” mixed acid anhydride. In the second step, the phosphate residue from the intermediate is substituted by NH$_3$, and glutamine and free phosphate are produced. The energy balance of the reaction as a whole ($\Delta G^\circ = -17$ kJ mol$^{-1}$) is the sum of the changes in free enthalpy of direct glutamine synthesis ($\Delta G^\circ = -14$ kJ mol$^{-1}$) plus ATP hydrolysis ($\Delta G^\circ = -31$ kJ mol$^{-1}$), although ATP has not been hydrolyzed at all.

B. Substrate-level phosphorylation

As mentioned earlier (see p. 122), there are a few metabolites that transfer phosphate to ADP in an exergonic reaction and can therefore form ATP. In ATP synthesis, anorganic phosphate or phosphate bound in an ester-like fashion is transferred to bonds with a high phosphate transfer potential. Reactions of this type are termed “substrate-level phos-

phorylations,” as they represent individual steps within metabolic pathways.

In the glyceraldehyde 3-phosphate dehydrogenation reaction, a step involved in glycolysis (1; see also C), the aldehyde group in glyceraldehyde 3-phosphate is oxidized into a carboxyl group. During the reaction, an anorganic phosphate is also introduced into the product, producing a mixed acid anhydride—1,3-bisphosphoglycerate. Phosphopyruvate hydratase (“enolase,” 2) catalyzes the elimination of water from 2-phosphoglycerate. In the enol phosphate formed (phosphoenolpyruvate), the phosphate residue—in contrast to 2-phosphoglycerate—is at an extremely high potential ($\Delta G^\circ$ of hydrolysis: $-62$ kJ mol$^{-1}$). A third reaction of this type is the formation of succinyl phosphate, which occurs in the tricarboxylic acid cycle as an individual step in the succinyl CoA ligase reaction. Here again, anorganic phosphate is introduced into a mixed acid anhydride bond to be transferred from there to GDP. Succinyl phosphate is only an intermediate here, and is not released by the enzyme.

In the literature, the term “substrate level phosphorylation” is used inconsistently. Some authors use it to refer to reactions in which anorganic phosphate is raised to a high potential, while others use it for the subsequent reactions, in which ATP or GTP is formed from the energy-rich intermediates.

C. Glyceraldehyde 3-phosphate dehydrogenase

The reaction catalyzed during glycolysis by glyceraldehyde-3-phosphate dehydrogenase (GAPDH) is shown here in detail. Initially, the SH group of a cysteine residue of the enzyme is added to the carbonyl group of glyceraldehyde 3-phosphate (a). This intermediate is oxidized by NAD$^+$ into an “energy-rich” thioester (b). In the third step (c), anorganic phosphate displaces the thiol, and the mixed anhydride 1,3-bisphosphoglycerate arises. In this bond, the phosphate residue is at a high enough potential for it to be transferred to ADP in the next step (not shown; see p. 150).
1. Glutamine synthetase reaction

Reaction 1: Glutamate + NH$_3$ → $\Delta G^{\circ} = -14$ kJ/mol

Reaction 2: ATP + H$_2$O → $\Delta G^{\circ} = -31$ kJ/mol

Total: Glutamate + NH$_3$ + ATP → $\Delta G^{\circ} = -17$ kJ/mol

2. Energy balance

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Energy conservation at membranes

Metabolic energy can be stored not only in the form of “energy-rich” bonds (see p. 122), but also by separating electric charges from each other using an insulating layer to prevent them from redistributing. In the field of technology, this type of system would be called a condenser. Using the same principle, energy is also stored (“conserved”) at cell membranes. The membrane functions as an insulator; electrically charged atoms and molecules (ions) function as charges.

A. Electrochemical gradient

Although artificial lipid membranes are almost impermeable to ions, biological membranes contain ion channels that selectively allow individual ion types to pass through (see p. 222). Whether an ion can cross this type of membrane, and if so in which direction, depends on the electrochemical gradient—i.e., on the concentrations of the ion on each side of the membrane (the concentration gradient) and on the difference in the electrical potential between the interior and exterior, the membrane potential.

The membrane potential of resting cells (resting potential; see p. 350) is ~0.05 to ~0.09 V; i.e., there is an excess negative charge on the inner side of the plasma membrane. The main contributors to the resting potential are the two cations Na⁺ and K⁺, as well as Cl⁻ and organic anions (1). Data on the concentrations of these ions outside and inside animal cells, and permeability coefficients, are shown in the table (2).

The behavior of an ion type is described quantitatively by the Nernst equation (3): ΔΨ is the membrane potential (in volts, V) at which there is no net transport of the ion concerned across the membrane (equilibrium potential). The factor RT/F.n has a value of 0.026 V for monovalent ions at 25 °C. Thus, for K⁺, the table (2) gives an equilibrium potential of ca. ~0.09 V; i.e., a value more or less the same as that of the resting potential. By contrast, for Na⁺ ions, ΔΨ is much higher than the resting potential, at +0.07 V. Na⁺ ions therefore immediately flow into the cell when Na⁺ channels open (see p. 350). The disequilibrium between Na⁺ and K⁺ ions is constantly maintained by the enzyme Na⁺/K⁺-ATPase, which consumes ATP.

B. Proton motive force

Hydrogen ions (“H⁺ ions”) can also develop electrochemical gradients. Such a proton gradient plays a decisive part in cellular ATP synthesis (see p. 142). As usual, the energy content of the gradient depends on the concentration gradients—i.e., on the pH difference (1) between the two sides of the membrane. In addition, the membrane potential ΔΨ also makes a contribution. Together, these two values give the proton motive force ΔpH, a measure for the work that the H⁺ gradient can do. The proton gradient across the inner mitochondrial membrane thus delivers approximately 24 kJ per mol H⁺.

C. Energy conservation in proton gradients

Proton gradients can be built up in various ways. A very unusual type is represented by bacteriorhodopsin (1), a light-driven proton pump that various bacteria use to produce energy. As with rhodopsin in the eye, the light-sensitive component used here is covalently bound retinal (see p. 358). In photosynthesis (see p. 130), reduced plastoquinone (QH₂) transports protons, as well as electrons, through the membrane (Q cycle, 2). The formation of the proton gradient by the respiratory chain is also coupled to redox processes (see p. 140). In complex III, a Q cycle is responsible for proton translocation (not shown). In cytochrome c oxidase (complex IV, 3), H⁺ transport is coupled to electron flow from cytochrome c to O₂.

In each of these cases, the H⁺ gradient is utilized by an ATP synthase (4) to form ATP: ATP synthases consist of two components—a proton channel (Fₒ) and an inwardly directed protein complex (F₁), which conserves the energy of back-flowing protons through ATP synthesis (see p. 142).
A. Electrochemical gradient

B. Proton motive force

Proton motive force \( \approx 0.06 \text{ V} \)

\[ \Delta \psi = \Delta p \cdot \frac{Z \cdot T}{F} \cdot \ln \left( \frac{C_{\text{outside}}}{C_{\text{inside}}} \right) \]

\( R = \text{gas constant} \)

\( T = \text{temperature (K)} \)

\( F = \text{Faraday constant} \)

C. Energy conservation in proton gradients

1. Light-driven proton pump (bacteriorhodopsin)

2. Q cycle (plastoquinone cycle in plants)

3. Electron-driven proton pump (cytochrome C oxidase)

4. Proton-driven ATP synthesis
Photosynthesis: light reactions

Sunlight is the most important source of energy for nearly all living organisms. With the help of photosynthesis, light energy is used to produce organic substances from CO₂ and water. This property of phototrophic organisms (plants, algae, and some bacteria) is exploited by heterotrophic organisms (e.g., animals), which are dependent on a supply of organic substances in their diet (see p. 112).

The atmospheric oxygen that is vital to higher organisms is also derived from photosynthesis.

A. Photosynthesis: overview

The chemical balance of photosynthesis is simple. Six molecules of CO₂ are used to form one hexose molecule (right). The hydrogen required for this reduction process is taken from water, and molecular oxygen is formed as a by-product (left). Light energy is required, since water is a very poor reducing agent and is therefore not capable of reducing CO₂.

In the light-dependent part of photosynthesis—the “light reactions”—H₂O molecules are split into protons, electrons, and oxygen atoms. The electrons undergo excitation by light energy and are raised to an energy level that is high enough to reduce NADP⁺. The NADPH⁺ formed in this way, in contrast to H₂O, is capable of “fixing” CO₂ reducebly—i.e., of incorporating it into organic bonds.

Another product of the light reactions is ATP, which is also required for CO₂ fixation. If NADPH⁺ is formed, ATP, and the appropriate enzymes are available, CO₂ fixation can also take place in darkness. This process is therefore known as the “dark reaction.”

The excitation of electrons to form NADPH is a complex photochemical process that involves chlorophyll, a tetrapyrrole dye containing Mg²⁺ that bears an extra phytol residue (see p. 132).

B. Light reactions

In green algae and higher plants, photosynthesis occurs in chloroplasts. These are organelles, which—like mitochondria—are surrounded by two membranes and contain their own DNA. In their interior, the stroma, thylakoids or flattened membrane sacs are stacked on top of each other to form grana. The inside of the thylakoid is referred to as the lumen. The light reactions are catalyzed by enzymes located in the thylakoid membrane, whereas the dark reactions take place in the stroma.

As in the respiratory chain (see p. 140), the light reactions cause electrons to pass from one redox system to the next in an electron transport chain. However, the direction of transport is opposite to that found in the respiratory chain. In the respiratory chain, electrons flow from NADH⁺⁺ to O₂, with the production of water and energy.

In photosynthesis, electrons are taken up from water and transferred to NADP⁺, with an expenditure of energy. Photosynthetic electron transport is therefore energetically “uphill work.” To make this possible, the transport is stimulated at two points by the absorption of light energy. This occurs through two photosystems—protein complexes that contain large numbers of chlorophyll molecules and other pigments (see p. 132). Another component of the transport chain is the cytochrome b/f complex, an aggregate of integral membrane proteins that includes two cytochromes (b and f). Plastoquinone, which is comparable to ubiquinone, and two soluble proteins, the copper-containing plastocyanin and ferredoxin, function as mobile electron carriers. At the end of the chain, there is an enzyme that transfers the electrons to NADP⁺.

Because photosystem II and the cytochrome b/f complex release protons from reduced plastoquinone into the lumen (via a Q cycle), photosynthetic electron transport establishes an electrochemical gradient across the thylakoid membrane (see p. 126), which is used for ATP synthesis by an ATP synthase. ATP and NADPH⁺⁺, which are both needed for the dark reactions, are formed in the stroma.
A. Photosynthesis: overview

- Electron flow
- Proton flow

6 \( \text{H}_2\text{O} \rightarrow 3 \text{O}_2 + 12 \text{H}^+ + 18 \text{ATP} + 12 \text{NADPH} + 6 \text{CO}_2 

B. Light reactions

- Light
- Water splitting
- ATP synthesis

Ferredoxin (Fd)

- Ferredoxin-NADP
- Cytochrome b/f complex

Plastoquinone

Photosystem I

Photosystem II

1. ATP synthase

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Photosynthesis: dark reactions

The “light reactions” in photosynthesis bring about two strongly endergonic reactions—the reduction of NADP⁺ to NADPH+H⁺ and ATP synthesis (see p. 122). The chemical energy needed for this is produced from radiant energy by two photosystems.

A. Photosystem II

The photosynthetic electron transport chain in plants starts in photosystem II (PS II; see p. 128). PS II consists of numerous protein subunits (brown) that contain bound pigments—i.e., dye molecules that are involved in the absorption and transfer of light energy.

The schematic overview of PS II presented here (1) only shows the important pigments. These include a special chlorophyll molecule, the reaction center \( P_{680} \); a neighboring \( \text{Mg}^{2+} \)-free chlorophyll (pheophytin); and two bound plastoquinones \( \text{Q}_a \) and \( \text{Q}_b \). A third quinone \( \text{Q}_c \) is not linked to PS II, but belongs to the plastoquinone pool. The white arrows indicate the direction of electron flow from water to \( \text{Q}_a \). Only about 1% of the chlorophyll molecules in PS II are directly involved in photochemical excitation (see p. 128). Most of them are found, along with other pigments, in what are known as light-harvesting or antenna complexes (green). The energy of light quanta striking these can be passed on to the reaction center, where it can be utilized.

In Fig. 2, photosynthetic electron transport in PS II is separated into the individual steps involved. Light energy from the light-harvesting complexes (a) raises an electron of the chlorophyll in the reaction center to an excited “singlet state.” The excited electron is immediately passed on to the neighboring pheophytin. This leaves behind an “electron gap” in the reaction center—i.e., a positively charged \( P_{680} \) radical (b). This gap is now filled by an electron removed from an \( \text{H}_2\text{O} \) molecule by the water-splitting enzyme (b). The excited electron passes on to the pheophytin via \( \text{Q}_a \) to \( \text{Q}_b \), converting the latter into a semiquinone radical (c). \( \text{Q}_b \) is then reduced to hydroquinone by a second excited electron, and is then exchanged for an oxidized quinone \( \text{Q}_c \) from the plastoquinone pool. Further transport of electrons from the plastoquinone pool takes place as described on the preceding page and shown in B.

B. Redox series

It can be seen from the normal potentials \( E^0 \) (see p. 18) of the most important redox systems involved in the light reactions why two excitation processes are needed in order to transfer electrons from \( \text{H}_2\text{O} \) to NADP⁺. After excitation in PS II, \( E^0 \) rises from around −1 V back to positive values in plastocyanin (PC)—i.e., the energy of the electrons has to be increased again in PS I. If there is no NADP⁺ available, photosynthetic electron transport can still be used for ATP synthesis. During cyclic photophosphorylation, electrons return from ferredoxin (Fd) via the plastoquinone pool to the b/f complex. This type of electron transport does not produce any NADPH, but does lead to the formation of an \( \text{H}^+ \) gradient and thus to ATP synthesis.

C. Calvin cycle

The synthesis of hexoses from \( \text{CO}_2 \) is only shown in a very simplified form here; a complete reaction scheme is given on p. 407. The actual \( \text{CO}_2 \) fixation—i.e., the incorporation of \( \text{CO}_2 \) into an organic compound—is catalyzed by ribulose bisphosphate carboxylase/oxygenase (“rubisco”). Rubisco, the most abundant enzyme on Earth, converts ribulose 1.5-bisphosphate, \( \text{CO}_2 \) and water into two molecules of 3-phosphoglycerate. These are then converted, via 1.3-bisphosphoglycerate and 3-phosphoglycerate, into glyceraldehyde 3-phosphate (glyceral 3-phosphate). In this way, 12 glyceraldehyde 3-phosphates are synthesized from six \( \text{CO}_2 \). Two molecules of this intermediate are used by gluconeogenesis reactions to synthesize glucone 6-phosphate (bottom right). From the remaining 10 molecules, six molecules of ribulose 1.5-bisphosphate are regenerated, and the cycle then starts over again. In the Calvin cycle, ATP is required for phosphorylation of 3-phosphoglycerate and ribulose 5-phosphate. NADPH+H⁺, the second product of the light reaction, is consumed in the reduction of 1.3-bisphosphoglycerate to glyceraldehyde 3-phosphate.
A. Photosystem II

B. Redox series

C. Calvin cycle

Ribulose-bisphosphate carboxylase 4.1.1.39
Phosphoglycerate kinase 2.7.2.3
Glyceraldehyde 3-phosphate dehydrogenase (NADP) 1.2.1.13
Phosphoribulokinase 2.7.1.19

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Molecular models: membrane proteins

The plates show, in simplified form, the structures of cytochrome c oxidase (A; complex IV of the respiratory chain) and of photosystem I of a cyanobacterium (B). These two molecules are among the few integral membrane proteins for which the structure is known in detail. Both structures were determined by X-ray crystallography.

A. Cytochrome c oxidase O

The enzyme cytochrome c oxidase ("COX," EC 1.9.3.1) catalyzes the final step of the respiratory chain. It receives electrons from the small heme protein cytochrome c and transfers them to molecular oxygen, which is thereby reduced to water (see p. 140). At the same time, 2–4 protons per water molecule formed are pumped from the matrix into the intermembrane space.

Mammalian COX (the illustration shows the enzyme from bovine heart) is a dimer that has two identical subunits with masses of 204 kDa each. Only one subunit is shown in detail here; the other is indicated by gray lines. Each subunit consists of 13 different polypeptides, which all span the inner mitochondrial membrane. Only polypeptides I (light blue) and II (dark blue) and the linked cofactors are involved in electron transport. The other chains, which are differently expressed in the different organs, probably have regulatory functions. The two heme groups, heme a (orange) and heme a₁ (red) are bound in polypeptide I. The copper center Cu₅₈ consists of two copper ions (green), which are coordinated by amino acid residues in polypeptide II. The second copper (Cu₅₃) is located in polypeptide I near heme a₇.

To reduce an O₂ molecule to two molecules of H₂O, a total of four electrons are needed, which are supplied by cytochrome c (pink, top left) and initially given off to Cu₅₈. From there, they are passed on via heme a and heme a₇ to the enzyme’s reaction center, which is located between heme a₈ and Cu₅₈. The reduction of the oxygen takes place in several steps, without any intermediate being released. The four protons needed to produce water and the H⁺ ions pumped into the intermembrane space are taken up by two channels (D and K, not shown). The mechanism that links proton transport to electron transfer is still being investigated.

B. Reaction center of Synechococcus elongatus O

Photosystem I (PS I) in the cyanobacterium Synechococcus elongatus is the first system of this type for which the structure has been solved in atomic detail. Although the bacterial photosystem differs slightly from the systems in higher plants, the structure provides valuable hints about the course of the light reactions in photosynthesis (see p. 128). The functioning of the photosystem is discussed in greater detail on p. 130.

The functional form of PS I in S. elongatus consists of a trimer with a mass of more than 10⁶ Da that is integrated into the membrane. Only one of the three subunits is shown here. This consists of 12 different polypeptides (gray-blue), 96 chlorophyll molecules (green), 22 carotenoids (orange), several phylloquinones (yellow), and other components. Most of the chlorophyll molecules are so-called antenna pigments. These collect light energy and conduct it to the reaction center, which is located in the center of the structure and therefore not visible. In the reaction center, an electron is excited and transferred via various intermediate steps to a ferredoxin molecule (see p. 128). The chlorophylls (see formula) are heme-like pigments with a highly modified tetrapyrrole ring, a central Mg²⁺ ion, and an apolar phytol side chain. Shown here is chlorophyll a, which is also found in the reaction center of the S. elongatus photosystem.

The yellow and orange–colored carotenoids—e.g., β-carotene (see formula)—are auxiliary pigments that serve to protect the chloroplasts from oxidative damage. Dangerous radicals can be produced during the light reaction—particularly singlet oxygen. Carotenoids prevent compounds of this type from arising, or render them inactive. Carotenoids are also responsible for the coloring of leaves seen during fall. They are left behind when plants break down chlorophyll in order to recover the nitrogen it contains.

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A. Cytochrome C oxidase

B. Photosystem I
Oxooacid dehydrogenases

The intermediary metabolism has multi-enzyme complexes which, in a complex reaction, catalyze the oxidative decarboxylation of 2-oxoacids and the transfer to coenzyme A of the acyl residue produced. NAD$^+$ acts as the electron acceptor. In addition, thiamine diphosphate, lipoamide, and FAD are also involved in the reaction. The oxooacid dehydrogenase include: a) the pyruvate dehydrogenase complex (PDH, pyruvate → acetyl CoA), b) the 2-oxoglutarate dehydrogenase complex of the tricarboxylic acid cycle (ODH, 2-oxoglutarate → succinyl CoA), and c) the branched chain dehydrogenase complex, which is involved in the catabolism of valine, leucine, and isoleucine (see p. 414).

A. Pyruvate dehydrogenase: reactions

The pyruvate dehydrogenase reaction takes place in the mitochondrial matrix (see p. 210). Three different enzymes [E1–E3] form the PDH multi-enzyme complex (see B).

1. Initially, pyruvate dehydrogenase [E1] catalyzes the decarboxylation of pyruvate and the transfer of the resulting hydroxyethyl residue to thiamine diphosphate (TPP, 1a). The same enzyme then catalyzes oxidation of the TPP-bound hydroxyethyl group to yield an acetyl residue. This residue and the reducing equivalents obtained are then transferred to lipoamide (1b).

2. The second enzyme, dihydrolipoamide acetyltransferase [E2], shifts the acetyl residue from lipoamide to coenzyme A (2), with dihydrolipoamide being left over.

3. The third enzyme, dihydrolipoamide dehydrogenase [E3], reoxidizes dihydrolipoamide, with NADH+H$^+$ being formed. The electrons are first taken over by enzyme-bound FAD (3a) and then transferred via a catalytically active disulfide bond in the E3 subunit (not shown) to soluble NAD$^+$ (3b).

The five different enzymes involved are associated with the enzyme components in different ways. Thiamine diphosphate is non-covalently bound to E1, whereas lipoamide is covalently bound to a lysine residue of E2 and FAD is bound as a prosthetic group to E3. NAD$^+$ and coenzyme A, being soluble coenzymes, are only temporarily associated with the complex.

An important aspect of PDH catalysis is the spatial relationship between the components of the complex. The covalently bound lipoamide coenzyme is part of a mobile domain of E2, and is therefore highly mobile. This structure is known as the lipoamide arm, and swings back and forth between E1 and E3 during catalysis. In this way, lipoamide can interact with the TPP bound at E1, with solute coenzyme A, and also with the FAD that serves as the electron acceptor in E3.

B. PDH complex of Escherichia coli

The PDH complex of the bacterium Escherichia coli has been particularly well studied. It has a molecular mass of $5.3 \times 10^6$, and with a diameter of more than 30 nm it is larger than a ribosome. The complex consists of a total of 60 polypeptides (1, 2): 24 molecules of E2 (eight trimers) form the almost cube-shaped core of the complex. Each of the six surfaces of the cube is occupied by a dimer of E3 components, while each of the twelve edges of the cube is occupied by dimers of E1 molecules. Animal oxooacid dehydrogenases have similar structures, but differ in the numbers of subunits and their molecular masses.

Further information

The PDH reaction, which is practically irreversible, occupies a strategic position at the interface between carbohydrate and fatty acid metabolism, and also supplies acetyl residues to the tricarboxylic acid cycle. PDH activity is therefore strictly regulated (see p. 144). Interconversion is particularly important in animal cells (see p. 120). Several PDH-specific protein kinases inactivate the E1 components through phosphorylation, while equally specific protein phosphatases reactivate it again. The binding of the kinases and phosphatases to the complex is in turn regulated by metabolites. For example, high concentrations of acetyl CoA promote binding of kinases and thereby inhibit the reaction, while Ca$^{2+}$ increases the activity of the phosphatase. Insulin activates PDH via inhibition of phosphorylation.
A. Pyruvate dehydrogenase: reactions

1. \[ E_1 + E_2 + E_3 = 60 \]
   \[ E_1 \cdot 12 = 24 \]
   \[ E_2 \cdot 8 = 24 \]
   \[ E_3 \cdot 6 = 12 \]

2. CO₂

B. PDH complex of Escherichia coli

1. E₁ 12 · 2 = 24
   E₂ 8 · 3 = 24
   E₃ 6 · 2 = 12
   E₁ + E₂ + E₃ = 60

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Tricarboxylic acid cycle: reactions

The tricarboxylic acid cycle (TCA cycle, also known as the citric acid cycle or Krebs cycle) is a cyclic metabolic pathway in the mitochondrial matrix (see p. 210). In eight steps, it oxidizes acetyl residues (CH₃CO·) to carbon dioxide (CO₂). The reducing equivalents obtained in this process are transferred to NAD⁺ or ubiquinone, and from there to the respiratory chain (see p. 140). Additional metabolic functions of the cycle are discussed on p. 138.

A. Tricarboxylic acid cycle

The acetyl-CoA that supplies the cycle with acetyl residues is mainly derived from β-oxidation of fatty acids (see p. 164) and from the pyruvate dehydrogenase reaction. Both of these processes take place in the mitochondrial matrix.

[1] In the first step of the cycle, citrate synthase catalyzes the transfer of an acetyl residue from acetyl CoA to a carrier molecule, oxaloacetic acid. The product of this reaction, tricarboxylic acid, gives the cycle its name.

[2] In the next step, tricarboxylic acid undergoes isomerization to yield isocitrate. In the process, only the hydroxyl group is shifted within the molecule. The corresponding enzyme is called aconitate hydratase (“aconitase”), because unsaturated aconitate arises as an enzyme-bound intermediate during the reaction (not shown; see p. 8). Due to the properties of aconitate, the isomerization is absolutely stereospecific. Although citrate is not chiral, isocitrate has two chiral centers, so that it could potentially appear in four isomeric forms. However, in the tricarboxylic acid cycle, only one of these stereoisomers, (2R,3S)-isocitrate, is produced.

[3] The first oxidative step now follows. Isocitrate dehydrogenase oxidizes the hydroxyl group of isocitrate into an oxo group. At the same time, a carboxyl group is released as CO₂, and 2-oxoglutarate (also known as α-ketoglutarate) and NADH⁺H⁺ are formed.

[4] The next step, the formation of succinyl CoA, also involves one oxidation and one dehydroxylation. It is catalyzed by 2-oxoglutarate dehydrogenase, a multienzyme complex closely resembling the PDH complex (see p. 134). NADH⁺H⁺ is once again formed in this reaction.

[5] The subsequent cleavage of the thioester succinylCoA into succinate and coenzyme A by succinic acid-CoA ligase (succinyl CoA synthetase, succinic thiokinase) is strongly exergonic and is used to synthesize a phosphoric acid anhydride bond (“substrate level phosphorylation”, see p. 124). However, it is not ATP that is produced here as is otherwise usually the case, but instead guanosine triphosphate (GTP). However, GTP can be converted into ATP by a nucleoside diphosphate kinase (not shown).

[6] Via the reactions described so far, the acetyl residue has been completely oxidized to CO₂. At the same time, however, the carrier molecule oxaloacetate has been reduced to succinate. Three further reactions in the cycle now regenerate oxaloacetate from succinate. Initially, succinate dehydrogenase oxidizes succinate to fumarate. In contrast to the other enzymes in the cycle, succinate dehydrogenase is an integral protein of the inner mitochondrial membrane. It is therefore also assigned to the respiratory chain as complex II. Although succinate dehydrogenase contains FAD as a prosthetic group, ubiquinone is the real electron acceptor of the reaction.

[7] Water is now added to the double bond of fumarate by fumarate hydratase (“fumase”), and chiral (2S)-malate is produced.

[8] In the last step of the cycle, malate is again oxidized by malate dehydrogenase into oxaloacetate, with NADH⁺H⁺ again being produced. With this reaction, the cycle is complete and can start again from the beginning. As the equilibrium of the reaction lies well on the side of malate, the formation of oxaloacetic acid by reaction [8] depends on the strongly exergonic reaction [1], which immediately removes it from the equilibrium.

The net outcome is that each rotation of the tricarboxylic acid cycle converts one acetyl residue and two molecules of H₂O into two molecules of CO₂. At the same time, one GTP, three NADH⁺H⁺ and one reduced ubiquinone (QH₂) are produced. By oxidative phosphorylation (see p. 122), the cell obtains around nine molecules of ATP from these reduced coenzymes (see p. 146). Together with the directly formed GTP, this yields a total of 10 ATP per acetyl group.
A. Tricarboxylic acid cycle

1. Citrate synthase 4.1.3.7
2. Aconitase 4.2.1.3 [Fe₄S₄]
3. Isocitrate DH 1.1.1.41
4. 2-Oxoglutarate DH complex 1.2.4.2, 1.8.1.4, 2.3.1.61
5. Succinate-CoA ligase 6.2.1.4
6. Succinate DH 1.3.5.1 [FAD, Fe₂S₂, Fe₄S₄]
7. Fumarate hydratase 4.2.1.2
8. Malate DH 1.1.1.37

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Tricarboxylic acid cycle: functions

A. Tricarboxylic acid cycle: functions

The tricarboxylic acid cycle (see p. 136) is often described as the "hub of intermediary metabolism." It has both catabolic and anabolic functions—it is **amphibolic**.

As a **catabolic pathway**, it initiates the **terminal oxidation** of energy substrates. Many catabolic pathways lead to intermediates of the tricarboxylic acid cycle, or supply metabolites such as pyruvate and acetyl-CoA that can enter the cycle, where their C atoms are oxidized to CO₂. The reducing equivalents (see p. 14) obtained in this way are then used for **oxidative phosphorylation**—i.e., to aerobically synthesize ATP (see p. 122).

The tricarboxylic acid cycle also supplies important **precursors for anabolic pathways**. Intermediates in the cycle are converted into:

- Glucose (gluconeogenesis; precursors: oxaloacetate and malate—see p. 154)
- Porphyrins (precursor: succinyl-CoA—see p. 192)
- Amino acids (precursors: 2-oxoglutarate, oxaloacetate—see p. 184)
- Fatty acids and isoprenoids (precursor: citrate—see below)

The intermediates of the tricarboxylic acid cycle are present in the mitochondria only in very small quantities. After the oxidation of acetyl-CoA to CO₂, they are constantly regenerated, and their concentrations therefore remain constant, averaged over time. Anabolic pathways, which remove intermediates of the cycle (e.g., gluconeogenesis) would quickly use up the small quantities present in the mitochondria if metabolites did not reenter the cycle at other sites to replace the compounds consumed. Processes that replenish the cycle in this way are called **anaplerotic reactions**.

The degradation of most amino acids is anaplerotic, because it produces either intermediates of the cycle or pyruvate (gluconeogenic amino acids; see p. 180). Gluconeogenesis is in fact largely sustained by the degradation of amino acids. A particularly important anaplerotic step in animal metabolism leads from pyruvate to oxaloacetic acid. This ATP-dependent reaction is catalyzed by pyruvate carboxylase [1]. It allows pyruvate yielding amino acids and lactate to be used for gluconeogenesis.

By contrast, acetyl CoA does not have **anaplerotic effects** in animal metabolism. Its carbon skeleton is completely oxidized to CO₂ and is therefore no longer available for biosynthesis. Since fatty acid degradation only supplies acetyl CoA, animals are unable to convert fatty acids into glucose. During periods of hunger, it is therefore not the fat reserves that are initially drawn on, but proteins. In contrast to fatty acids, the amino acids released are able to maintain the blood glucose level (see p. 308).

The tricarboxylic acid cycle not only takes up acetyl CoA from fatty acid degradation, but also supplies the material for the **biosynthesis of fatty acids and isoprenoids**. Acetyl CoA, which is formed in the matrix space of mitochondria by pyruvate dehydrogenase (see p. 134), is not capable of passing through the inner mitochondrial membrane. The acetyl residue is therefore condensed with oxaloacetate by mitochondrial citrate synthase to form citrate. This then leaves the mitochondria by antiport with malate (right; see p. 212). In the cytoplasm, it is cleaved again by ATP-dependent citrate lyase [4] into acetyl-CoA and oxaloacetate. The oxaloacetate formed is reduced by a cytoplasmic malate dehydrogenase to malate [2], which then returns to the mitochondrion via the antiport already mentioned. Alternatively, the malate can be oxidized by "malic enzyme" [5], with decarboxylation to pyruvate. The NADPH+H⁺ formed in this process is also used for fatty acid biosynthesis.

Additional information

Using the so-called **glyoxyllic acid cycle**, plants and bacteria are able to convert acetyl-CoA into succinate, which then enters the tricarboxylic acid cycle. For these organisms, fat degradation therefore functions as an anaplerotic process. In plants, this pathway is located in special organelles, the glyoxysomes.
Respiratory chain

The respiratory chain is one of the pathways involved in oxidative phosphorylation (see p. 122). It catalyzes the steps by which electrons are transported from NADH+H+ or reduced ubiquinone (QH2) to molecular oxygen. Due to the wide difference between the redox potentials of the donor (NADH+H+ or QH2) and the acceptor (O2), this reaction is strongly exergonic (see p. 18). Most of the energy released is used to establish a proton gradient across the inner mitochondrial membrane (see p. 126), which is then ultimately used to synthesize ATP with the help of ATP synthase.

A. Components of the respiratory chain

The electron transport chain consists of three protein complexes (complexes I, III, and IV), which are integrated into the inner mitochondrial membrane, and two mobile carrier molecules—ubiquinone (coenzyme Q) and cytochrome c. Succinate dehydrogenase, which actually belongs to the tricarboxylic acid cycle, is also assigned to the respiratory chain as complex II. ATP synthase (see p. 142) is sometimes referred to as complex V, although it is not involved in electron transport. With the exception of complex I, detailed structural information is now available for every complex of the respiratory chain.

All of the complexes in the respiratory chain are made up of numerous polypeptides and contain a series of different protein bound redox coenzymes (see pp. 104, 106). These include flavins (FMN or FAD in complexes I and II), iron–sulfur clusters (in I, II, and III), and heme groups (in II, III, and IV). Of the more than 80 polypeptides in the respiratory chain, only 13 are coded by the mitochondrial genome (see p. 210). The remainder are encoded by nuclear genes, and have to be imported into the mitochondria after being synthesized in the cytoplasm (see p. 228).

Electrons enter the respiratory chain in various different ways. In the oxidation of NADH+H+ by complex I, electrons pass via FMN and Fe/S clusters to ubiquinone (Q). Electrons arising during the oxidation of succinate, acyl CoA, and other substrates are passed to ubiquinone by succinate dehydrogenase or other mitochondrial dehydrogenases via enyzme-bound FADH2 and the electron-transporting flavoprotein (ETF; see p. 164). Ubiquinol passes electrons on to complex III, which transfers them via two b-type heme groups, one Fe/S cluster, and heme c1 to the small heme protein cytochrome c. Cytochrome c then transports the electrons to complex IV—cytochrome c oxidase. Cytochrome c oxidase contains redox-active components in the form of two copper centers (CuA and CuB) and hemes a and a3, through which the electrons finally reach oxygen (see p. 132). As the result of the two-electron reduction of O2, the strongly basic O2− anion is produced (at least formally), and this is converted into water by binding of two protons. The electron transfer is coupled to the formation of a proton gradient by complexes I, III, and IV (see p. 126).

B. Organization

Proton transport via complexes I, III, and IV takes place vectorially from the matrix into the intermembrane space. When electrons are being transported through the respiratory chain, the H+ concentration in this space increases—i.e., the pH value there is reduced by about one pH unit. For each H2O molecule formed, around 10 H+ ions are pumped into the intermembrane space. If the inner membrane is intact, then generally only ATP synthase (see p. 142) can allow protons to flow back into the matrix. This is the basis for the coupling of electron transport to ATP synthesis, which is important for regulation purposes (see p. 144).

As mentioned, although complexes I through V are all integrated into the inner membrane of the mitochondrion, they are not usually in contact with one another, since the electrons are transferred by ubiquinone and cytochrome c. With its long apolar side chain, ubiquinone is freely mobile within the membrane. Cytochrome c is water-soluble and is located on the outside of the inner membrane. NADH oxidation via complex I takes place on the inside of the membrane—i.e., in the matrix space, where the tricarboxylic acid cycle and β-oxidation (the most important sources of NADH) are also located. O2 reduction and ATP formation also take place in the matrix.
A. Components of the respiratory chain

- Pyruvate
- NADH
- 2-Oxoglutarate
- Malate
- Isocitrate
- α-Ketoglutarate
- Lipoamide-H_2
- Acyl CoA
- 3-Hydroxyacyl CoA
- Dihydropyruvate
- ETF
- Fumarate
- Succinate
- Cytochrome c
- Ubiquinol-cytochrome c reductase
- Cytochrome c oxidase
- H⁺-transporting ATP synthase

B. Organization

- Electron flow
- Proton flow
- NADH dehydrogenase (ubiquinone)
- Succinate dehydrogenase
- Ubiquinol-cytochrome c reductase
- Cytochrome c oxidase
- H⁺-transporting ATP synthase
ATP synthesis

In the respiratory chain (see p. 140), electrons are transferred from NADH or ubiquinol (QH$_2$) to O$_2$. The energy obtained in this process is used to establish a proton gradient across the inner mitochondrial membrane. ATP synthesis is ultimately coupled to the return of protons from the intermembrane space into the matrix.

A. Redox systems of the respiratory chain

The electrons provided by NADH do not reach oxygen directly, but instead are transferred to it in various steps. They pass through at least 10 intermediate redox systems, most of which are bound as prosthetic groups in complexes I, III, and IV. The large number of coenzymes involved in electron transport may initially appear surprising. However, as discussed on p. 18, in redox reactions, the change in free enthalpy $\Delta G$, i.e., the chemical work that is done—depends only on the difference in redox potentials $\Delta E^\circ$ between the donor and the acceptor. Introducing additional redox systems does not alter the reaction’s overall energy yield. In the case of the respiratory chain, the difference between the normal potential of the donor (NAD$^+$/NADH$^+$, $E^\circ = -0.32$ V) and that of the acceptor (O$_2$/H$_2$O, $E^\circ = +0.82$ V) corresponds to an energy difference $\Delta E^\circ$ of more than 200 kJ mol$^{-1}$. This large amount is divided into smaller, more manageable“packages,” the size of which is determined by the difference in redox potentials between the respective intermediates. It is assumed that this division is responsible for the astonishingly high energy yield (about 60%) achieved by the respiratory chain.

The illustration shows the important redox systems involved in mitochondrial electron transport and their approximate redox potentials. These potentials determine the path followed by the electrons, as the members of a redox series have to be arranged in order of increasing redox potential if transport is to occur spontaneously (see p. 32).

In complex I, the electrons are passed from NADH$+H^+$ first to FMN (see p. 104) and then on to several iron–sulfur (Fe$S$) clusters. These redox systems are only stable in the interior of proteins. Depending on the type, Fe$S$ clusters may contain two to six iron ions, which form complexes with inorganic sulfide and the SH groups of cysteine residues (see p. 286). Ubiquinone (coenzyme Q; see p. 104) is a mobile carrier that takes up electrons from complexes I and II and from reduced ETF and passes them on to complex III. Heme groups are also involved in electron transport in a variety of ways. Type b hemes correspond to that found in hemoglobin (see p. 280). Heme c in cytochrome c is covalently bound to the protein, while the tetapyrrole ring of heme a is isoprenylated and carries a formyl group. In complex IV, a copper ion (Cu$_{IV}$) and heme a$_3$ react directly with oxygen.

B. ATP synthase

The ATP synthase (EC 3.6.1.34, complex V) that transports $H^+$ is a complex molecular machine. The enzyme consists of two parts—a proton channel ($F_0$, for “oligomycin-sensitive”) that is integrated into the membrane; and a catalytic unit ($F_1$) that protrudes into the matrix. The $F_0$ part consists of 12 membrane-spanning c-peptides and one a-subunit. The “head” of the $F_1$ part is composed of three $\alpha$ and three $\beta$ subunits, between which there are three active centers. The “stem” between $F_0$ and $F_1$ consists of one $\gamma$ and one $\epsilon$ subunit. Two more polypeptides, b and $\delta$, form a kind of “stator,” fixing the $\alpha$ and $\beta$ subunits relative to the $F_0$ part.

The catalytic cycle can be divided into three phases, through each of which the three active sites pass in sequence. First, ADP and P$_i$ are bound (1), then the anhydride bond forms (2), and finally the product is released (3). Each time protons pass through the $F_0$ channel protein into the matrix, all three active sites change from their current state to the next. It has been shown that the energy for proton transport is initially converted into a rotation of the $\gamma$ subunit, which in turn cyclically alters the conformation of the $\alpha$ and $\beta$ subunits, which are stationary relative to the $F_0$ part, and thereby drives ATP synthesis.
A. Redox systems of the respiratory chain

\[
AG = -n \cdot F \cdot \Delta E
\]

B. ATP synthase

1. Structure and location
2. Catalytic cycle
Regulation

The amount of nutrient degradation and ATP synthesis have to be continually adjusted to the body's changing energy requirements. The need to coordinate the production and consumption of ATP is already evident from the fact that the total amounts of coenzymes in the organism are low. The human body forms about 65 kg ATP per day, but only contains 3–4 g of adenine nucleotides (AMP, ADP, and ATP). Each ADP molecule therefore has to be phosphorylated to ATP and dephosphorylated again many thousand times a day.

A. Respiratory control

The simple regulatory mechanism which ensures that ATP synthesis is “automatically” coordinated with ATP consumption is known as respiratory control. It is based on the fact that the different parts of the oxidative phosphorylation process are coupled via shared coenzymes and other factors (left).

If a cell is not using any ATP, hardly any ADP will be available in the mitochondria. Without ADP, ATP synthase (3) is unable to break down the proton gradient across the inner mitochondrial membrane. This in turn inhibits electron transport in the respiratory chain (2), which means that NADH can no longer be reoxidized to NAD⁺. Finally, the resulting high NADH/NAD⁺ ratio inhibits the tricarboxylic acid cycle (C), and thus slows down the degradation of the substrate SH₂ (1). Conversely, high rates of ATP utilization stimulate nutrient degradation and the respiratory chain via the same mechanism.

If the formation of a proton gradient is prevented (right), substrate oxidation (1) and electron transport (2) proceed much more rapidly. However, instead of ATP, only heat is produced.

B. Uncouplers

Substances that functionally separate oxidation and phosphorylation from one another are referred to as uncouplers. They break down the proton gradient by allowing H⁺ ions to pass from the intermembrane space back into the mitochondrial matrix without the involvement of ATP synthase. Uncoupling effects are produced by mechanical damage to the inner membrane (1) or by lipid-soluble substances that can transport protons through the membrane, such as 2,4-dinitrophenol (DNP, 2), Thermogenin (uncoupling protein-1, UCP-1, 3)—an ion channel (see p. 222) in mitochondria of brown fat tissue—is a naturally occurring uncoupler. Brown fat is found, for example, in newborns and in hibernating animals, and serves exclusively to generate heat. In cold periods, nor- epinephrine activates the hormone-sensitive lipase (see p. 162). Increased lipolysis leads to the production of large quantities of free fatty acids. Like DNP, these bind H⁺ ions in the intermembrane space, pass the UCP in this form, and then release the protons in the matrix again. This makes fatty acid degradation independent of ADP availability—i.e., it takes place at maximum velocity and only produces heat (A). It is becoming increasingly clear that there are also UCPs in other cells, which are controlled by hormones such as thyroxine (see p. 374). This regulates the ATP yield and what is known as the basal metabolic rate.

C. Regulation of the tricarboxylic acid cycle

The most important factor in the regulation of the cycle is the NADH/NAD⁺ ratio. In addition to pyruvate dehydrogenase (PDH) and oxoglutarate dehydrogenase (ODH, see p. 134), citrate synthase and isocitrate dehydrogenase are also inhibited by NAD⁺ deficiency or an excess of NADH⁺. With the exception of isocitrate dehydrogenase, these enzymes are also subject to product inhibition by acetyl-CoA, succinyl-CoA, or citrate.

Interconversion processes (see p. 120) also play an important role. They are shown here in detail using the example of the PDH complex (see p. 134). The inactivating protein kinase (1a) is inhibited by the substrate pyruvate and is activated by the products acetyl-CoA and NAD⁺H⁺. The protein phosphatase (1b)—like isocitrate dehydrogenase (3)—is activated by Ca²⁺. This is particularly important during muscle contraction, when large amounts of ATP are needed. Insulin also activates the PDH complex (through inhibition of phosphorylation) and thereby promotes the breakdown of glucose and its conversion into fatty acids.
A. Respiratory control

1. Coupled
   - Dehydrogenases
   - Respiratory chain
   - ATP synthase
   - Endergonic processes

2. Uncoupled
   - ATP synthesis uncoupled from proton transport
   - Heat
   - Endergonic processes

B. Uncouplers

1. Membrane damage
2. Mobile carriers
3. Gated proton channels

B.1. 2,4-Dinitrophenol

C. Regulation of the tricarboxylic acid cycle

1. Insulin
2. Pyruvate
3. Acetyl CoA
4. Oxaloacetate
5. Citrate
6. Isocitrate
7. 2-Oxoglutarate
8. Succinyl CoA

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Respiration and fermentation

A. Aerobic and anaerobic oxidation of glucose

In the presence of oxygen (i.e., in aerobic conditions), most animal cells are capable of "respiring" various types of nutrient (lipids, amino acids, and carbohydrates)—i.e., using oxidative processes to break them down completely. If oxygen is lacking (i.e., in anaerobic conditions), only glucose can be used for ATP synthesis. Although in these conditions glucose breakdown in animals already ends in lactate and only produces small quantities of ATP, it is decisively important for the survival of cells at times of oxygen deficiency.

In aerobic conditions (left), ATP is derived almost exclusively from oxidative phosphorylation (see p. 140). Fatty acids enter the mitochondria with the help of carnitine (see p. 164), and are broken down there into CoA-bound acetyl residues. Glucose is converted into pyruvate by glycolysis (see p. 150) in the cytoplasm. Pyruvate is then also transported into the mitochondrial matrix, where it is oxidatively decarboxylated by the pyruvate dehydrogenase complex (see p. 134) to yield acetyl-CoA. The reducing equivalents (2 NADH+H+ per glucose) that arise in glycolysis enter the mitochondrial matrix via the malate shuttle (see p. 212). The acetyl residues that are formed are oxidized to CO2 in the tricarboxylic acid cycle (see p. 136). Breakdown of amino acids also produces acetyl residues or products that can directly enter the tricarboxylic acid cycle (see p. 180). The reducing equivalents that are obtained are transferred to oxygen via the respiratory chain as required. In the process, chemical energy is released, which is used (via a proton gradient) to synthesize ATP (see p. 140).

In the absence of oxygen—i.e., in anaerobic conditions—the picture changes completely. Since O2 is missing as the electron acceptor for the respiratory chain, NADH+H+ and QH2 can no longer be reoxidized. Consequently, not only is mitochondrial ATP synthesis halted, but also almost the whole metabolism in the mitochondrial matrix. The main reason for this is the high NADH+H+ concentration and lack of NAD+, which inhibit the tricarboxylic acid cycle and the pyruvate dehydrogenase reaction (see p. 144). β-Oxidation and the malate shuttle, which are dependent on free NAD+, also come to a standstill. Since amino acid degradation is also no longer able to contribute to energy production, the cell becomes totally dependent on ATP synthesized via the degradation of glucose by glycolysis. For this process to proceed continuously, the NADH+H+ formed in the cytoplasm has to be constantly reoxidized. Since this can no longer occur in the mitochondria, in anaerobic conditions animal cells reduce pyruvate to lactate and pass it into the blood. This type of process is called fermentation (see p. 148). The ATP yield is low, with only two ATPs per glucose arising during lactate synthesis.

To estimate the number of ATP molecules formed in an aerobic state, it is necessary to know the P/O quotient—i.e., the molar ratio between synthesized ATP ("P") and the water formed ("O"). During transport of two electrons from NADH+H+ to oxygen, about 10 protons are transported into the intermembrane space, while from ubiquinol (QH2), the number is only six. ATP synthase (see p. 142) probably requires three H+ to synthesize one ATP, so that maximum P/O quotients of around 3 or 2 are possible. This implies a yield of up to 38 ATP per mol of glucose. However, the actual value is much lower. It needs to be taken into account that the transport of specific metabolites into the mitochondrial matrix and the exchange of ATP for ADP are also driven by the proton gradient (see p. 212). The P/O quotients for the oxidation of NADH+H+ and QH2 are therefore more in the range of 2.5 and 1.5. If the energy balance of aerobic glycolysis is calculated on this basis, the result is a yield of around 32 ATP per glucose. However, this value is also not constant, and can be adjusted as required by the cell’s own uncouplers (UCPs; see p. 144) and other mechanisms.
A. Aerobic and anaerobic oxidation of glucose

1. Aerobic

2. Anaerobic

<table>
<thead>
<tr>
<th>ATP</th>
<th>Coenzymes</th>
<th>Enzymes</th>
<th>Coenzymes</th>
<th>ATP</th>
</tr>
</thead>
<tbody>
<tr>
<td>–1</td>
<td>–1 ATP</td>
<td>Hexokinase</td>
<td>–1 ATP</td>
<td>–1</td>
</tr>
<tr>
<td>–2</td>
<td>–1 ATP</td>
<td>6-Phosphofructokinase</td>
<td>–1 ATP</td>
<td>–2</td>
</tr>
<tr>
<td>+3</td>
<td>+5 ATP</td>
<td>Glyceraldehyde-3-PDH</td>
<td>+2 NADH</td>
<td>–2</td>
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<td>+5</td>
<td>+2 ATP</td>
<td>Phosphoglycerate kinase</td>
<td>+2 ATP</td>
<td>0</td>
</tr>
<tr>
<td>+7</td>
<td>+2 ATP</td>
<td>Pyruvate kinase</td>
<td>+2 ATP recycled</td>
<td>+2</td>
</tr>
<tr>
<td>+12</td>
<td>+5 ATP</td>
<td>Lactate dehydrogenase</td>
<td>–2 NADH</td>
<td></td>
</tr>
<tr>
<td>+17</td>
<td>+5 ATP</td>
<td>Pyruvate dehydrogenase</td>
<td>+2 NADH</td>
<td></td>
</tr>
<tr>
<td>+22</td>
<td>+5 ATP</td>
<td>Isocitrate dehydrogenase</td>
<td>+2 NADH</td>
<td></td>
</tr>
<tr>
<td>+27</td>
<td>+5 ATP</td>
<td>Oxoglutarate dehydrogenase</td>
<td>+2 NADH</td>
<td></td>
</tr>
<tr>
<td>+30</td>
<td>+3 ATP</td>
<td>Malate dehydrogenase</td>
<td>+2 NADH</td>
<td></td>
</tr>
<tr>
<td>+32</td>
<td>+2 ATP</td>
<td>Succinate dehydrogenase</td>
<td>+2 NADH</td>
<td></td>
</tr>
</tbody>
</table>

Sum: 32 ATP/glucose

DH = dehydrogenase

Sum: 2 ATP/glucose

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Fermentations

As discussed on p. 146, degradation of glucose to pyruvate is the only way for most organisms to synthesize ATP in the absence of oxygen. The NADH+H⁺ that is also formed in this process has to be constantly reoxidized to NAD⁺ in order to maintain glycolysis and thus ATP synthesis. In the animal organism, this is achieved by the reduction of pyruvate to lactate. In microorganisms, there are many other forms of NAD⁺ regeneration. Processes of this type are referred to as fermentations. Microbial fermentation processes are often used to produce foodstuffs and alcoholic beverages, or to preserve food. Features common to all fermentation processes are that they start with pyruvate and only occur under anaerobic conditions.

A. Lactic acid and propionic acid fermentation

Many milk products, such as sour milk, yogurt, and cheese are made by bacterial lactic acid fermentation (1). The reaction is the same as in animals. Pyruvate, which is mainly derived from degradation of the disaccharide lactose (see p. 38), is reduced to lactate by lactate dehydrogenase (1). Lactic acid fermentation also plays an important role in the production of sauerkraut and silage. These products usually keep for a long time, because the pH reduction that occurs during fermentation inhibits the growth of putrefying bacteria.

Bacteria from the genera Lactobacillus and Streptococcus are involved in the first steps of dairy production (3). The raw materials produced by their effects usually only acquire their final properties after additional fermentation processes. For example, the characteristic taste of Swiss cheese develops during a subsequent propionic acid fermentation. In this process, bacteria from the genus Propionibacterium convert pyruvate to propionate in a complex series of reactions (2).

B. Alcoholic fermentation

Alcoholic beverages are produced by the fermentation of plant products that have a high carbohydrate content. Pyruvate, which is formed from glucose, is initially decarboxylated by pyruvate decarboxylase (2), which does not occur in animal metabolism, to produce acetaldehyde (ethanol). When this is reduced by alcohol dehydrogenase (3), with NADH being consumed, ethanol (3) is formed.

Yeast, unicellular fungi that belong to the eukaryotes (3), rather than bacteria, are responsible for this type of fermentation. Yeasts are also often used in baking. They produce CO₂ and ethanol, which raise the dough. Brewers’ and bakers’ yeasts (Saccharomyces cerevisiae) are usually haploid and reproduce asexually by budding (3). They can live both aerobically and anaerobically. Wine is produced by other types of yeast, some of which already live on the grapes. To promote the formation of ethanol, efforts are made to generally exclude oxygen during alcoholic fermentation—for example, by covering dough with a cloth when it is rising and by fermenting liquids in barrels that exclude air.

C. Beer brewing

Barley is the traditional starting material for the brewing of beer. Although cereal grains contain starch, they hardly have any free sugars. The barley grains are therefore first allowed to germinate so that starch- cleaving amylases are formed. Careful warming of the sprouting grain produces malt. This is then ground, soaked in water, and kept warm for a certain time. In the process, a substantial proportion of the starch is broken down into the disaccharide maltose (see p. 38). The product (the wort) is then boiled. Yeast and hops are added, and the mixture is allowed to ferment for several days. The addition of hops makes the beer less perishable and gives it its slightly bitter taste. Other substances contained in hops act as sedatives and diuretics.
A. Lactic acid and propionic acid fermentation

1. **Propionate**
   - Lactate → Propionate
   - **Lactate dehydrogenase** 1.1.1.27
   - Pyruvate dehydrogenase [TPP] 4.1.1.1
   - Alcohol dehydrogenase [Zn²⁺] 1.1.1.1

2. **Lactobacillus**
   - Propionibacterium
   - **DNA**
   - **Cell wall**
   - **78 µm**

**Propionate**

3. **Propionate**
   - **Propionate**
   - **Streptococcus**
   - Propionate

B. Alcoholic fermentation

1. **Pyruvate**
   - **Pyruvate decarboxylase**
   - **CO₂**
   - **Ethanol (Acetaldehyde)**
   - **[TPP]** 4.1.1.1
   - **[Zn²⁺]** 1.1.1.1

2. **Vacuole**
   - **Septum**
   - **Daughter cell**
   - **Nucleus**
   - **Mitochondrion**
   - **Tonoplast**
   - **Cell wall**
   - **40 µm**

C. Beer brewing

1. **Grain**
   - **Germinate, dry**
   - **Malt**
   - **Grind, incubate in water**
   - **Wort**
   - **Hops**
   - **Yeast**
   - **Amylases**
   - **Maltose**
   - **Glucose**
   - **Ethanol + CO₂**

2. **Maltoose**
   - **Yeast**
   - **Glucose**
   - **Ethanol + CO₂**

3. **Ethanol**
   - **Yeast**
   - **S. cerevisiae**
   - **Propionibacterium**
   - **Streptococcus**
   - **Propionate**

**Barley**

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Glycolysis

A. Balance

Glycolysis is a catabolic pathway in the cytoplasm that is found in almost all organisms—irrespective of whether they live aerobically or anaerobically. The balance of glycolysis is simple: glucose is broken down into two molecules of pyruvate, and in addition two molecules of ATP and two of NADH+H⁺ are formed.

In the presence of oxygen, pyruvate and NADH+H⁺ reach the mitochondria, where they undergo further transformation (aerobic glycolysis; see p. 146). In anaerobic conditions, fermentation products such as lactate or ethanol have to be formed in the cytoplasm from pyruvate and NADH+H⁺, in order to regenerate NAD⁺ so that glycolysis can continue (anaerobic glycolysis; see p. 146). In the anaerobic state, glycolysis is the only means of obtaining ATP that animal cells have.

B. Reactions

Glycolysis involves ten individual steps, including three isomerizations and four phosphorylations. The only redox reaction takes place in step [6].

[1] Glucose, which is taken up by animal cells from the blood and other sources, is first phosphorylated to glucose 6-phosphate, with ATP being consumed. The glucose 6-phosphate is not capable of leaving the cell.

[2] In the next step, glucose 6-phosphate is isomerized into fructose 1,6-bisphosphate. Phosphofructokinase is the most important key enzyme in glycolysis (see p. 144).

[3] Using ATP again, another phosphorylation takes place, giving rise to fructose 1,6-bisphosphatase. Phosphofructokinase is the most important key enzyme in glycolysis (see p. 144).

[4] Fructose 1,6-bisphosphate is broken down by aldolase into the C₃ compounds glyceraldehyde 3-phosphate (also known as glycerol 3-phosphate) and dihydroyacetone 3-phosphate.

[5] The latter two products are placed in fast equilibrium by triosephosphate isomerase.

[6] Glyceraldehyde 3-phosphate is now oxidized by glyceraldehyde-3-phosphate dehydrogenase, with NADH+H⁺ being formed. In this reaction, inorganic phosphate is taken up into the molecule (substrate-level phosphorylation; see p. 124), and 1,3-bisphosphoglycerate is produced. This intermediate contains a mixed acid–anhydride bond, the phosphate part of which is at a high chemical potential.

[7] Catalyzed by phosphoglycerate kinase, this phosphate residue is transferred to ADP, producing 3-phosphoglycerate and ATP. The ATP balance is thus once again in equilibrium.

[8] As a result of shifting of the remaining phosphate residue within the molecule, the isomer 2-phosphoglycerate is formed.

[9] Elimination of water from 2-phosphoglycerate produces the phosphate ester of the enol form of pyruvate—phosphoenolpyruvate (PEP). This reaction also raises the second phosphate residue to a high potential.

[10] In the last step, pyruvate kinase transfers this residue to ADP. The remaining enol pyruvate is immediately rearranged into pyruvate, which is much more stable. Along with step [7] and the thio kinase reaction in the tricarboxylic acid cycle (see p. 136), the pyruvate kinase reaction is one of the three reactions in animal metabolism that are able to produce ATP independently of the respiratory chain.

In glycolysis, two molecules of ATP are initially used for activation ([1], [3]). Later, two ATPs are formed per C₃ fragment. Overall, therefore, there is a small net gain of 2 mol ATP per mol of glucose.

C. Energy profile

The energy balance of metabolic pathways depends not only on the standard changes in enthalpy ΔH°, but also on the concentrations of the metabolites (see p. 18). Fig. C shows the actual enthalpy changes ΔH for the individual steps of glycolysis in erythrocytes.

As can be seen, only three reactions ([1], [3], and [10]), are associated with large changes in free enthalpy. In these cases, the equilibrium lies well on the side of the products (see p. 18). All of the other steps are freely reversible. The same steps are also followed—in the reverse direction—in gluconeogenesis (see p. 154), with the same enzymes being activated as in glucose degradation. The non-reversible steps [1], [3], and [10] are bypassed in glucose biosynthesis (see p. 154).
A. Glycolysis: balance

\[ \Delta G' (kJ \cdot mol^{-1}) \]

B. Reactions

C. Energy profile

Steps 1, 3 and 10 are bypassed in gluconeogenesis

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Pentose phosphate pathway

The pentose phosphate pathway (PPP, also known as the hexose monophosphate pathway) is an oxidative metabolic pathway located in the cytoplasm, which, like glycolysis, starts from glucose 6-phosphate. It supplies two important precursors for anabolic pathways: NADPH+H+, which is required for the biosynthesis of fatty acids and isoprenoids, for example (see p. 168), and ribose 5-phosphate, a precursor in nucleotide biosynthesis (see p. 188).

A. Pentose phosphate pathway:

oxidative part

The oxidative segment of the PPP converts glucose 6-phosphate to ribulose 5-phosphate. One CO₂ and two NADPH+H⁺ are formed in the process. Depending on the metabolic state, the much more complex regenerative part of the pathway (see B) can convert some of the pentose phosphates back to hexose phosphates, or it can pass them on to glycolysis for breakdown. In most cells, less than 10% of glucose 6-phosphate is degraded via the pentose phosphate pathway.

B. Reactions

[1] The oxidative part starts with the oxidation of glucose 6-phosphate by glucose-6-phosphate dehydrogenase. This forms NADPH+H⁺ for the first time. The second product, 6-phosphogluconolactone, is an intramolecular ester (lactone) of 6-phosphogluconate.

[2] A specific hydrolase then cleaves the lactone, exposing the carbonyl group of 6-phosphogluconate.

[3] The last enzyme in the oxidative part is phosphogluconate dehydrogenase [3], which releases the carboxylate group of 6-phosphogluconate as CO₂ and at the same time oxidizes the hydroxyl group at C₅ to an oxo group. In addition to a second NADPH+H⁺, this also produces the ketopentose ribulose 5-phosphate. This is converted by an isomerase to ribulose 5-phosphate, the initial compound for nucleotide synthesis (top).

The regenerative part of the PPP is only shown here schematically. A complete reaction scheme is given on p. 408. The function of the regenerative branch is to adjust the net production of NADPH+H⁺ and pentose phosphates to the cell’s current requirements. Normally, the demand for NADPH+H⁺ is much higher than that for pentose phosphates. In these conditions, the reaction steps shown first convert six ribulose 5-phosphates to five molecules of fructose 6-phosphate and then, by isomerization, regenerate five glucose 6-phosphates. These can once again supply NADPH+H⁺ to the oxidative part of the PPP. Repeating these reactions finally results in the oxidation of one glucose 6-phosphate into six CO₂. Twelve NADPH+H⁺ arise in the same process. In sum, no pentose phosphates are produced via this pathway.

In the recombination of sugar phosphates in the regenerative part of the PPP, there are two enzymes that are particularly important:

[5] Transaldolase transfers C₂ units from sedoheptulose 7-phosphate, a ketone with seven C atoms, to the aldehyde group of glyceraldehyde 3-phosphate.

[4] Transketolase, which contains thiamine diphosphate, transfers C₂ fragments from one sugar phosphate to another.

The reactions in the regenerative segment of the PPP are freely reversible. It is therefore easily possible to use the regenerative part of the pathway to convert hexose phosphates into pentose phosphates. This can occur when there is a high demand for pentose phosphates—e.g., during DNA replication in the S phase of the cell cycle (see p. 394).

Additional information

When energy in the form of ATP is required in addition to NADPH+H⁺, the cell is able to channel the products of the regenerative part of the PPP (fructose 6-phosphate and glyceraldehyde 3-phosphate) into glycolysis. Further degradation is carried out via the tri-carboxylic acid cycle and the respiratory chain to CO₂ and water. Overall, the cell in this way obtains 12 mol NADPH+H⁺ and around 150 mol ATP from 6 mol glucose 6-phosphate. PPP activity is stimulated by insulin (see p. 388). This not only increases the rate of glucose degradation, but also produces additional NADPH+H⁺ for fatty acid synthesis (see p. 168).
A. Pentose phosphate pathway: oxidative part

Glucose 6-phosphate → NADP → NADPH + H

PPP – oxidative part → CO₂

B. Reactions

6-Ribulose 5-phosphate → 6 CO₂

Anabolic pathways:

6-Glucose 6-phosphate

6-Phosphogluconate → 6-Phosphogluconolactone

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Gluconeogenesis

Some tissues, such as brain and erythrocytes, depend on a constant supply of glucose. If the amount of carbohydrate taken up in food is not sufficient, the blood sugar level can be maintained for a limited time by degradation of hepatic glycogen (see p. 156). If these reserves are also exhausted, de-novo synthesis of glucose (gluconeogenesis) begins. The liver is also mainly responsible for this (see p. 310), but the tubular cells of the kidney also show a high level of gluconeogenic activity (see p. 328). The main precursors for gluconeogenesis are amino acids derived from muscle proteins. Another important precursor is lactate, which is formed in erythrocytes and muscle proteins when there is oxygen deficiency. Glycerol produced from the degradation of fats can also be used for gluconeogenesis. However, the conversion of fatty acids into glucose is not possible in animal metabolism (see p. 138). The human organism can synthesize several hundred grams of glucose per day by gluconeogenesis.

A. Gluconeogenesis

Many of the reaction steps involved in gluconeogenesis are catalyzed by the same enzymes that are used in glycolysis (see p. 150). Other enzymes are specific to gluconeogenesis and are only synthesized, under the influence of cortisol and glucagon when needed (see p. 158). Glycolysis takes place exclusively when needed in the cytoplasm, but gluconeogenesis also involves the mitochondria and the endoplasmic reticulum (ER). Gluconeogenesis consumes 4 ATP (3 ATP + 1 GTP) per glucose—i.e., twice as many as glycolysis produces.

[1] Lactate as a precursor for gluconeogenesis is mainly derived from muscle (see Cori cycle, p. 338) and erythrocytes. LDH (see p. 98) oxidizes lactate to pyruvate, with NADH formation.

[2] The first steps of actual gluconeogenesis take place in the mitochondria. The reason for this “detour” is the equilibrium state of the pyruvate kinase reaction (see p. 150). Even coupling to ATP hydrolysis would not be sufficient to convert pyruvate directly into phosphoenolpyruvate (PEP). Pyruvate derived from lactate or amino acids is therefore initially transported into the mitochondrial matrix, and—in a biotin-dependent reaction catalyzed by pyruvate carboxylase—is carboxylated there to oxaloacetate. Oxaloacetate is also an intermediate in the tricarboxylic acid cycle. Amino acids with breakdown products that enter the cycle or supply pyruvate can therefore be converted into glucose (see p. 180).

[3] The oxaloacetate formed in the mitochondrial matrix is initially reduced to malate, which can leave the mitochondria via inner membrane transport systems (see p. 212).

[4] In the cytoplasm, oxaloacetate is reformed and then converted into phosphoenolpyruvate by a GTP-dependent PEP carboxykinase. The subsequent steps up to fructose 1,6-bisphosphate represent the reverse of the corresponding reactions involved in glycolysis. One additional ATP per C3 fragment is used for the synthesis of 1,3-bisphosphoglycerate.

Two gluconeogenesis-specific phosphatases then successively cleave off the phosphate residues from fructose 1,6-bisphosphate. In between these reactions lies the isomerization of fructose 6-phosphate to glucose 6-phosphate—another glycolytic reaction.

[5] The reaction catalyzed by fructose 1,6-bisphosphatase is an important regulation point in gluconeogenesis (see p. 158).

[6] The last enzyme in the pathway, glucose 6-phosphatase, occurs in the liver, but not in muscle. It is located in the interior of the smooth endoplasmic reticulum. Specific transporters allow glucose 6-phosphate to enter the ER and allow the glucose formed there to return to the cytoplasm. From there, it is ultimately released into the blood.

Glycerol initially undergoes phosphorylation at C-3 [7]. The glycerol 3-phosphate formed is then oxidized by an NAD+-dependent dehydrogenase to form glycerone 3-phosphate [8] and thereby channeled into gluconeogenesis. An PEP-dependent mitochondrial enzyme is also able to catalyze this reaction (known as the “glycerophosphate shuttle”; see p. 212).
Glycogen metabolism

Glycogen (see p. 40) is used in animals as a carbohydrate reserve, from which glucose phosphates and glucose can be released when needed. Glucose storage itself would not be useful, as high concentrations within cells would make them strongly hypertonic and would therefore cause an influx of water. By contrast, insoluble glycogen has only low osmotic activity.

A. Glycogen balance

Animal glycogen, like amylpectin in plants, is a branched homopolymer of glucose. The glucose residues are linked by an α1→4-glycosidic bond. Every tenth or so glucose residue has an additional α1→6 bond to another glucose. These branches are extended by additional α1→4-linked glucose residues. This structure produces tree-shaped molecules consisting of up to 50000 residues (M > 1·10⁶ Da).

Hepatic glycogen is never completely degraded. In general, only the nonreducing ends of the “tree” are shortened, or—when glucose is abundant—elongated. The reducing end of the tree is linked to a special protein, glycogenin. Glycogenin carries out autocatalytic covalent bonding of the first glucose at one of its tyrosine residues and elongation of this by up to seven additional glucose residues. It is only at this point that glycogen synthase becomes active to supply further elongation.

[1] The formation of glycosidic bonds between sugars is endergonic. Initially, therefore, the activated form—UDP-glucose—is synthesized by reaction of glucose 1-phosphate with UTP (see p. 110).

[2] Glycogen synthase now transfers glucose residues one by one from UDP-glucose to the non-reducing ends of the available “branches.”

[3] Once the growing chain has reached a specific length (> 11 residues), the branching enzyme cleaves an oligosaccharide consisting of 6–7 residues from the end of it, and adds this into the interior of the same chain or a neighboring one with α1→6 linkage. These branches are then further extended by glycogen synthase.

[4] The branched structure of glycogen allows rapid release of sugar residues. The most important degradative enzyme, glycogen phosphorylase, cleaves residues from a non-reducing end one after another as glucose 1-phosphate. The larger the number of these ends, the more phosphorylase molecules can attack simultaneously. The formation of glucose 1-phosphate instead of glucose has the advantage that no ATP is needed to channel the released residues into glycolysis or the PPP. [5] [6] Due to the structure of glycogen phosphorylase, degradation comes to a halt four residues away from each branching point. Two more enzymes overcome this blockage. First, a glucomutase moves a trisaccharide from the side chain to the end of the main chain [5]. A 1,6-glucosidase [6] then cleaves the single remaining residue as a free glucose and leaves behind an unbranched chain that is once again accessible to phosphorylase.

The regulation of glycogen metabolism by interconversion, and the role of hormones in these processes, are discussed on p. 120.

B. Glycogen balance

The human organism can store up to 450 g of glycogen—one-third in the liver and almost all of the remainder in muscle. The glycogen content of the other organs is low.

Hepatic glycogen is mainly used to maintain the blood glucose level in the postresorptive phase (see p. 308). The glycogen content of the liver therefore varies widely, and can decline to almost zero in periods of extended hunger. After this, gluconeogenesis (see p. 154) takes over the glucose supply for the organism. Muscle glycogen serves as an energy reserve and is not involved in blood glucose regulation. Muscle does not contain any glucose 6-phosphatase and is therefore unable to release glucose into the blood. The glycogen content of muscle therefore does not fluctuate as widely as that of the liver.
A. Glycogen metabolism

1. UTP-glucose 1-phosphate uridyltransferase 2.7.7.9
2. Glycogen synthase 2.4.1.11
3. Glucan branching enzyme 2.4.1.18

UTP-glucose 1-phosphate → Glucose 1-phosphate → Glucose 6-phosphate

Reducing end → Glucose 1-phosphate → Glucose 6-phosphate

Further degradation

B. Glycogen balance

Liver glycogen → Glucose 1-phosphate → Glucose 6-phosphate → Glucose

Muscle glycogen → Glucose 1-phosphate → Glucose 6-phosphate → Glucose

Liver glycogen

Muscle glycogen

Blood glucose

Glucose 1-phosphate

Glucose 6-phosphate

Glucose

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Regulation

A. Regulation of carbohydrate metabolism

In all organisms, carbohydrate metabolism is subject to complex regulatory mechanisms involving hormones, metabolites, and coenzymes. The scheme shown here (still a simplified one) applies to the liver, which has central functions in carbohydrate metabolism (see p. 306). Some of the control mechanisms shown here are not effective in other tissues.

One of the liver’s most important tasks is to store excess glucose in the form of glycogen and to release glucose from glycogen when required (buffer function). When the glycogen reserves are exhausted, the liver can provide glucose by de novo synthesis (gluconeogenesis; see p. 154). In addition, like all tissues, the liver breaks glucose down via glycolysis. These functions have to be coordinated with each other. For example, there is no point in glycolysis and gluconeogenesis taking place simultaneously, and glycogen synthesis and glycogen degradation should not occur simultaneously either. This is ensured by the fact that two different enzymes exist for important steps in both pathways, each of which catalyzes only the anabolic or the catabolic reaction. The enzymes are also regulated differently. Only these key enzymes are shown here.

Hormones. The hormones that influence carbohydrate metabolism include the peptides insulin and glucagon; a glucocorticoid, cortisol; and a catecholamine, epinephrine (see p. 380). Insulin activates glycogen synthase ([1]; see p. 388), and induces several enzymes involved in glycolysis [3, 5, 7]. At the same time, insulin inhibits the synthesis of enzymes involved in gluconeogenesis (repression; [4, 6, 8, 9]). Glucagon, the antagonist of insulin, has the opposite effect. It induces gluconeogenesis enzymes [4, 6, 8, 9] and represses pyruvate kinase [7], a key enzyme of glycolysis. Additional effects of glucagon are based on the interconversion of enzymes and are mediated by the second messenger cAMP. This inhibits glycogen synthesis [1] and activates glycogenolysis [2]. Epinephrine acts in a similar fashion. The inhibition of pyruvate kinase [7] by glucagon is also due to interconversion.

Glucocorticoids—mainly cortisol (see p. 374)—induce all of the key enzymes involved in gluconeogenesis [4, 6, 8, 9]. At the same time, they also induce enzymes involved in amino acid degradation and thereby provide precursors for gluconeogenesis. Regulation of the expression of PEP carboxykinase, a key enzyme in gluconeogenesis, is discussed in detail on p. 244.

Metabolites. High concentrations of ATP and citrate inhibit glycolysis by allosteric regulation of phosphofructokinase. ATP also inhibits pyruvate kinase. Acetyl-CoA, an inhibitor of pyruvate kinase, has a similar effect. All of these metabolites arise from glucose degradation (feedback inhibition). AMP and ADP, signals for ATP deficiency, activate glycogen degradation and inhibit gluconeogenesis.

B. Fructose 2,6-bisphosphate

Fructose 2,6-bisphosphate (Fru-2,6-bp) plays an important part in carbohydrate metabolism. This metabolite is formed in small quantities from fructose 6-phosphate and has purely regulatory functions. It stimulates glycolysis by allosteric activation of phosphofructokinase and inhibits gluconeogenesis by inhibition of fructose 1,6-bisphosphatase.

The synthesis and degradation of Fru-2,6-bp are catalyzed by one and the same protein [10a, 10b]. If the enzyme is present in an unphosphorylated form [10a], it acts as a kinase and leads to the formation of Fru-2,6-bp. After phosphorylation by cAMP-dependent protein kinase A (PK-A), it acts as a phosphatase [10b] and now catalyzes the degradation of Fru-2,6-bp to fructose 6-phosphate. The equilibrium between [10a] and [10b] is regulated by hormones. Epinephrine and glucagon increase the cAMP level (see p. 120). As a result of increased PK-A activity, this reduces the Fru-2,6-bp concentration and inhibits glycolysis, while at the same time activating gluconeogenesis. Conversely, via [10a], insulin activates the synthesis of Fru-2,6-bp and thus glycolysis. In addition, insulin also inhibits the action of glucagon by reducing the cAMP level (see p. 120).
A. Regulation of carbohydrate metabolism

B. Fructose 2,6-bisphosphate

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Diabetes mellitus

*Diabetes mellitus* is a very common metabolic disease that is caused by absolute or relative insulin deficiency. The lack of this peptide hormone (see p. 76) mainly affects carbohydrate and lipid metabolism. Diabetes mellitus occurs in two forms. In type 1 diabetes (insulin-dependent diabetes mellitus, IDDM), the insulin-forming cells are destroyed in young individuals by an autoimmune reaction. The less severe type 2 diabetes (non-insulin-dependent diabetes mellitus, NIDDM) usually has its first onset in elderly individuals. The causes have not yet been explained in detail in this type.

**A. Insulin biosynthesis**

Insulin is produced by the B cells of the islets of Langerhans in the pancreas. As is usual with secretory proteins, the hormone’s precursor (proinsulin) carries a signal peptide that directs the peptide chain to the interior of the endoplasmic reticulum (see p. 210). Proinsulin is produced in the ER by cleavage of the signal peptide and formation of disulfide bonds. Proinsulin passes to the Golgi apparatus, where it is packed into vesicles—the β-granules. After cleavage of the C peptide, mature insulin is formed in the β-granules and is stored in the form of zinc-containing hexamers until secretion.

**B. Effects of insulin deficiency**

The effects of insulin on carbohydrate metabolism are discussed on p. 158. In simplified terms, they can be described as stimulation of glucose utilization and inhibition of gluconeogenesis. In addition, the transport of glucose from the blood into most tissues is also insulin-dependent (exceptions to this include the liver, CNS, and erythrocytes).

The lipid metabolism of adipose tissue is also influenced by the hormone. In these cells, insulin stimulates the reorganization of glucose into fatty acids. This is mainly based on activation of acetyl CoA carboxylase (see p. 162) and increased availability of NADPH+H+ due to increased PPP activity (see p. 152). On the other hand, insulin also inhibits the degradation of fat by hormone-sensitive lipases (see p. 162) and prevents the breakdown of muscle protein.

The effects of insulin deficiency on metabolism are shown by arrows in the illustration. Particularly noticeable is the increase in the glucose concentration in the blood, from 5 mM to 9 mM (90 mg dl⁻¹) or more (hyperglycemia, elevated blood glucose level). In muscle and adipose tissue—the two most important glucose consumers—glucose uptake and glucose utilization are impaired by insulin deficiency. Glucose utilization in the liver is also reduced. At the same time, gluconeogenesis is stimulated, partly due to increased proteolysis in the muscles. This increases the blood sugar level still further. When the capacity of the kidneys to resorb glucose is exceeded (at plasma concentrations of 9 mM or more), glucose is excreted in the urine (glucosuria).

The increased degradation of fat that occurs in insulin deficiency also has serious effects. Some of the fatty acids that accumulate in large quantities are taken up by the liver and used for lipoprotein synthesis (hyperlipidemia), and the rest are broken down into acetyl CoA. As the tricarboxylic acid cycle is not capable of taking up such large quantities of acetyl CoA, the excess is used to form ketone bodies (acetoacetate and β-hydroxybutyrate see p. 312). As H⁺ ions are released in this process, diabetics not receiving adequate treatment can suffer severe metabolic acidosis (diabetic coma). The acetone that is also formed gives these patients’ breath a characteristic odor. In addition, large amounts of ketone body anions appear in the urine (ketonuria).

*Diabetes mellitus* can have serious secondary effects. A constantly raised blood sugar level can lead in the long term to changes in the blood vessels (diabetic angiopathy), kidney damage (nephropathy) and damage to the nervous system (neuropathy), as well as to cataracts in the eyes.

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A. Insulin biosynthesis

B cells

Nucleus

Rough ER

β-Granules

Golgi apparatus

Exocytosis

Preproinsulin

Proinsulin

Insulin

H3N

84 AS

51 AS

DOC

Signal peptide

C peptide

Zn

Insulin hexamer

B. Effects of insulin deficiency

Muscle and other insulin-dependent tissues

Blood

Glucose uptake impaired

Adipose tissue

Hyperglycemia

Glucose

Lipolysis

Fatty acids

Maximal resorption capacity exceeded

Kidney

Hyperlipidemia

Fatty acids

Lipoproteins

Anions of ketone bodies

Liver

Pyruvate

Acetyl CoA

Ketone bodies

Metabolic acidosis

Urine

Glucose

Anions of ketone bodies

Water Electrolytes

Insulin deficiency

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Overview

A. Fat metabolism

Fat metabolism in adipose tissue (top). Fats (triacylglycerols) are the most important energy reserve in the animal organism. They are mostly stored in insoluble form in the cells of adipose tissue—the adipocytes—where they are constantly being synthesized and broken down again.

As precursors for the biosynthesis of fats (lipogenesis), the adipocytes use triacylglycerols from lipoproteins (VLDLs and chylomicrons; see p. 278), which are formed in the liver and intestines and delivered by the blood. Lipoprotein lipase [1], which is located on the inner surface of the blood capillaries, cleaves these triacylglycerols into glycerol and fatty acids, which are taken up by the adipocytes and converted back into fats.

The degradation of fats (lipolysis) is catalyzed in adipocytes by hormone-sensitive lipase [2]—an enzyme that is regulated by various hormones by cAMP-dependent interconversion (see p. 120). The amount of fatty acids released depends on the activity of this lipase; in this way, the enzyme regulates the plasma levels of fatty acids.

In the blood plasma, fatty acids are transported in free form—i.e., non-esterified. Only short-chain fatty acids are soluble in the blood; longer, less water-soluble fatty acids are transported bound to albumin.

Degradation of fatty acids in the liver (left). Many tissues take up fatty acids from the blood plasma in order to synthesize fats or to obtain energy by oxidizing them. The metabolism of fatty acids is particularly intensive in the hepatocytes in the liver.

The most important process in the degradation of fatty acids is β-oxidation—a metabolic pathway in the mitochondrial matrix (see p. 164). Initially, the fatty acids in the cytoplasm are activated by binding to coenzyme A into acyl CoA [3]. Then, with the help of a transport system (the carnitine shuttle [4]; see p. 164), the activated fatty acids enter the mitochondrial matrix, where they are broken down into acetyl CoA. The resulting acetyl residues can be oxidized to CO₂ in the tricarboxylic acid cycle, producing reduced coenzyme and ATP derived from it by oxidative phosphorylation. If acetyl CoA production exceeds the energy requirements of the hepatocytes—as is the case when there is a high level of fatty acids in the blood plasma (typical in hunger and diabetes mellitus)—then the excess is converted into ketone bodies (see p. 312). These serve exclusively to supply other tissues with energy.

Fat synthesis in the liver (right). Fatty acids and fats are mainly synthesized in the liver and in adipose tissue, as well as in the kidneys, lungs, and mammary glands. Fatty acid biosynthesis occurs in the cytoplasm—in contrast to fatty acid degradation. The most important precursor is glucose, but certain amino acids can also be used.

The first step is carboxylation of acetyl CoA to malonyl CoA. This reaction is catalyzed by acetyl-CoA carboxylase [5], which is the key enzyme in fatty acid biosynthesis. Synthesis into fatty acids is carried out by fatty acid synthase [6]. This multifunctional enzyme (see p. 168) starts with one molecule of acetyl-CoA and elongates it by adding malonyl groups in seven reaction cycles until palmitate is reached. One CO₂ molecule is released in each reaction cycle. The fatty acid therefore grows by two carbon units each time. NADPH+H⁺ is used as the reducing agent and is derived either from the pentose phosphate pathway (see p. 152) or from isocitrate dehydrogenase and malic enzyme reactions.

The elongation of the fatty acid by fatty acid synthase concludes at C₁₆, and the product, palmitate (16:0), is released. Unsaturated fatty acids and long-chain fatty acids can arise from palmitate in subsequent reactions. Fats are finally synthesized from activated fatty acids (acyl CoA) and glycerol 3-phosphate (see p. 170). To supply peripheral tissues, fats are packed by the hepatocytes into lipoprotein complexes of the VLDL type and released into the blood in this form (see p. 278).
A. Fat metabolism

- Lipoprotein
- Hormone-sensitive lipase
- Fatty acid-CoA ligase
- Carboxy-3-hydroxyl/trans-
terase 2.3.1.21

- CoA
- ATP
- AMP+
- HCO3
- NADP
- NADPH
+H
- ADP+
- ATP
- CO2
- 7x
- COO

- Blood
- Acetyl-CoA
- Fatty acid-CoA complex

- Adipocyte
- Free fatty acids

- Triacylglycerols
- Largest energy store

- Chylomicrons
- From the intestine

- Fatty acid-albumin complex
- Largest energy store

- Fatty acid-CoA
- Elongated fatty acids
- Unsaturated fatty acids

- Mitochondrion
- Ketone bodies
- Citrate
- Respiratory chain
- CO2+ATP

- Amino acid degradation
- Fatty acid biosynthesis

- Insulin
- Glucagon

- Amino acids
- Glucose

- Malonyl-CoA
- Acetyl-CoA
- ADP+Pi
- ATP

- Fatty acid degradation
- Fatty acid biosynthesis

- Citric acid cycle
- Respiratory chain

- Most important precursor

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Fatty acid degradation

A. Fatty acid degradation: β-oxidation

After uptake by the cell, fatty acids are activated by conversion into their CoA derivatives—acyl CoA is formed. This uses up two energy-rich anhydride bonds of ATP per fatty acid (see p. 162). For channeling into the mitochondria, the acyl residues are first transferred to carnitine and then transported across the inner membrane as acyl carnitine (see B).

The degradation of the fatty acids occurs in the mitochondrial matrix through an oxidative cycle in which C₂ units are successively cleaved off as acetyl CoA (activated acetic acid). Before the release of the acetyl groups, each CH₂ group at C-3 of the acyl residue (the β-C atom) is oxidized to the keto group—hence the term β-oxidation for this metabolic pathway. Both spatially and functionally, it is closely linked to the tricarboxylic acid cycle (see p. 136) and to the respiratory chain (see p. 140).

1. The first step is dehydrogenation of acyl CoA at C-2 and C-3. This yields an unsaturated Δ²-enoyl-CoA derivative with a trans-configured double bond. The two hydrogen atoms are initially transferred from FAD-containing acyl CoA dehydrogenase to the electron-transferring flavoprotein (ETF). ETF dehydrogenase [5] passes them on from ETF to ubiquinone (coenzyme Q), a component of the respiratory chain (see p. 140). Other ETF-containing mitochondrial dehydrogenases are also able to supply the respiratory chain with electrons in this fashion.

There are three isoenzymes (see p. 98) of acyl CoA dehydrogenase that are specialized for long-chain fatty acids (12–18 C atoms), medium-chain fatty acids (4–14), and short-chain fatty acids (4–8).

2. The next step in fatty acid degradation is the addition of a water molecule to the double bond of the enoyl CoA (hydration), with formation of β-hydroxyacyl CoA.

3. In the next reaction, the OH group at C-3 is oxidized to a carboxyl group (dehydrogenation). This gives rise to β-ketoacyl CoA, and the reduction equivalents are transferred to NAD⁺, which also passes them on to the respiratory chain.

[4] β-Ketoacyl-CoA is now broken down by an acyl transferase into acetyl CoA and an acyl CoA shortened by 2 C atoms (“thiolester cleavage”). Several cycles are required for complete degradation of long-chain fatty acids—eight cycles in the case of stearoyl-CoA (C₁₈:₀), for example. The acetyl CoA formed can then undergo further metabolism in the tricarboxylic acid cycle (see p. 136); or can be used for biosynthesis. When there is an excess of acetyl CoA, the liver can also form ketone bodies (see p. 312).

When oxidative degradation is complete, one molecule of palmitic acid supplies around 106 molecules of ATP, corresponding to an energy of 3300 kJ mol⁻¹. This high energy yield makes fats an ideal form of storage for metabolic energy. Hibernating animals such as polar bears can meet their own energy requirements for up to 6 months solely by fat degradation, while at the same time producing the vital water they need via the respiratory chain (“respiratory water”).

B. Fatty acid transport

The inner mitochondrial membrane has a group-specific transport system for fatty acids. In the cytoplasm, the acyl groups of activated fatty acids are transferred to carnitine by carnitine acyltransferase [1]. They are then channeled into the matrix by an acylcarnitine/carnitine antiport as acyl carnitine, in exchange for free carnitine. In the matrix, the mitochondrial enzyme carnitine acyltransferase catalyzes the return transfer of the acyl residue to CoA.

The carnitine shuttle is the rate-determining step in mitochondrial fatty acid degradation. Malonyl CoA, a precursor of fatty acid biosynthesis, inhibits carnitine acyltransferase (see p. 162), and therefore also inhibits uptake of fatty acids into the mitochondrial matrix.

The most important regulator of β-oxidation is the NAD⁺/NADH⁺ ratio. If the respiratory chain is not using any NADH⁺, then not only the tricarboxylic acid cycle (see p. 136) but also β-oxidation come to a standstill due to the lack of NAD⁺.
A. Fatty acid degradation: β-oxidation

- Electron transferring flavoprotein (ETF)
- β-Carbon
- Acyl-CoA
- (n - 2 carbons)
- Acyl-CoA
- dehydrogenase 1.3.99.3
- Acyl-CoA hydratase 4.2.1.17
- Hydroxy-acyl-CoA dehydrogenase 1.3.35
- Acetyl-CoA acyltransferase 2.3.1.16
- ETF dehydrogenase [FAD, Fe₄S₄] 1.5.5.1

B. Fatty acid transport

- Carnitine O-palmitoyltransferase 2.3.1.21
- Fat degradation
- Acyl carnitine
- β-Oxidation
- Acyl carnitine
- Acyl carnitine
- Acyl carnitine

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Minor pathways of fatty acid degradation

Most fatty acids are saturated and even-numbered. They are broken down via β-oxidation (see p.164). In addition, there are special pathways involving degradation of unsaturated fatty acids (A), degradation of fatty acids with an odd number of C atoms (B), α and ω oxidation of fatty acids, and degradation in peroxisomes.

A. Degradation of unsaturated fatty acids (A)

Unsaturated fatty acids usually contain a cis double bond at position 9 or 12—e.g., linoleic acid (18:2; 9,12). As with saturated fatty acids, degradation in this case occurs via β-oxidation until the C-9-cis double bond is reached. Since enoyl-CoA hydratase only accepts substrates with two double bonds, the corresponding enoyl-CoA is converted by an isomerase from the cis-Δ9, cis-Δ6 isomer into the trans-Δ9, cis-Δ6 isomer [1]. Degradation by β-oxidation can now continue until a shortened trans-Δ9, cis-Δ6 derivative occurs in the next cycle. This cannot be isomerized in the same way as before, and instead is reduced in an NADPH-dependent way to the trans-Δ9 compound [2]. After rearrangement by enoyl-CoA isomerase [1], degradation can finally be completed via normal β-oxidation.

B. Degradation of odd-numbered fatty acids (B)

Fatty acids with an odd number of C atoms are treated in the same way as "normal" fatty acids—i.e., they are taken up by the cell with ATP-dependent activation to acyl-CoA and are transported into the mitochondria with the help of the carnitine shuttle and broken down there by β-oxidation (see p.164). In the last step, propionyl-CoA arises instead of acetyl-CoA. This is first carboxylated by propionyl-CoA carboxylase into (5)-methylmalonyl-CoA [3], which—after isomerization into the (R) enantiomer (not shown; see p.411)—is isomerized into succinyl-CoA [4].

Various coenzymes are involved in these reactions. The carboxylase [3] requires biotin, and the mutase [4] is dependent on coenzyme B12 (5'-deoxyadenosyl) cobalamin; see p.108). Succinyl-CoA is an intermediate in the tricarboxylic acid cycle and is available for gluconeogenesis through conversion into oxaloacetate. Odd-numbered fatty acids from propionyl-CoA can therefore be used to synthesize glucose.

This pathway is also important for ruminant animals, which are dependent on symbiotic microorganisms to break down their food. The microorganisms produce large amounts of propionic acid as a degradation product, which the host can channel into the metabolism in the way described.

Further information

In addition to the degradation pathways described above, there are also additional special pathways for particular fatty acids found in food.

— Oxidation is used to break down methyl-branched fatty acids. It takes place through step-by-step removal of C1 residues, begins with a hydroxylation, does not require coenzyme A, and does not produce any ATP.

β Oxidation—i.e., oxidation starting at the end of the fatty acid—also starts with a hydroxylation catalyzed by a monooxygenase (see p.316), and leads via subsequent oxidation to fatty acids with two carboxyl groups, which can undergo β-oxidation from both ends until C4 or C6 dicarboxylic acids are reached, which can be excreted in the urine in this form.

Degradation of unusually long fatty acids.

An alternative form of β-oxidation takes place in hepatic peroxisomes, which are specialized for the degradation of particularly long fatty acids (n ≥ 20). The degradation products are acetyl-CoA and hydrogen peroxide (H2O2), which is detoxified by the catalase (see p.32) common in peroxisomes.

Enzyme defects are also known to exist in the minor pathways of fatty acid degradation. In Refsum disease, the methyl-branched phytanic acid (obtained from vegetable foods) cannot be degraded by α-oxidation. In Zellweger syndrome, a peroxisomal defect means that long-chain fatty acids cannot be degraded.
A. Degradation of unsaturated fatty acids

- Linoleoyl CoA (18:2; 9,12)
- Shift and isomerization of the marked double bond
- Reduction and shift of the marked double bonds

- β-Oxidation
- Reduction of the marked double bond

- Enoyl-CoA isomerase
- 5.3.3.8
- 2,4-Dienoyl-CoA reductase
- 1.3.1.34

B. Degradation of odd-numbered fatty acids

- Odd-numbered fatty acids
- β-Oxidation

- Propionyl-CoA carboxylase
- 6.4.1.3 [biotin]
- Methylmalonyl-CoA mutase
- 5.4.99.2 [cobamide]

- Tricarboxylic acid cycle

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Fatty acid synthesis

In the vertebrates, biosynthesis of fatty acids is catalyzed by fatty acid synthase, a multifunctional enzyme. Located in the cytoplasm, the enzyme requires acetyl CoA as a starter molecule. In a cyclic reaction, the acetyl residue is elongated by one C₂ unit at a time for seven cycles. NADPH+H⁺ is used as a reducing agent in the process. The end product of the reaction is the saturated C₁₆ acid, palmitic acid.

A. Fatty acid synthase

Fatty acid synthase in vertebrates consists of two identical peptide chains—i.e., it is a homodimer. Each of the two peptide chains, which are shown here as hemispheres, catalyzes all seven of the partial reactions required to synthesize palmitate. The spatial compression of several successive reactions into a single multifunctional enzyme has advantages in comparison with separate enzymes. Competing reactions are prevented, the individual reactions proceed in a coordinated way as if on a production line, and due to low diffusion losses they are particularly efficient.

Each subunit of the enzyme binds acetyl residues as thioesters at two different SH groups: at one peripheral cysteine residue (CysSH) and one central 4'-phosphopentenethione group (Pan-SH). Pan-SH, which is very similar to coenzyme A (see p. 12), is covalently bound to a protein segment of the synthase known as the acyl-carrier protein (ACP). This part functions like a long arm that passes the substrate from one reaction center to the next. The two subunits of fatty acid synthase cooperate in this process; the enzyme is therefore only capable of functioning as a dimer.

Spatially, the enzyme activities are arranged into three different domains. Domain 1 catalyzes the entry of the substrates acetyl CoA and malonyl CoA by [ACP]-S-acetyltransferase [1] and [ACP]-Smalonyl transferase [2] and subsequent condensation of the two partners by 3-oxoacyl-[ACP]-synthase [3]. Domain 2 catalyzes the conversion of the 3-oxo group to a CH₂ group by 3-oxoacyl-[ACP]-reductase [4], 3-hydroxyacyl-[ACP]-dehydratase [5], and enoyl-[ACP]-reductase [6]. Finally, domain 3 serves to release the finished product by acyl-[ACP]-hydrolase [7] after seven steps of chain elongation.

B. Reactions of fatty acid synthase

The key enzyme in fatty acid synthesis is acetyl CoA carboxylase (see p. 162), which precedes the synthase and supplies the malonyl-CoA required for elongation. Like all carboxylases, the enzyme contains covalently bound biotin as a prosthetic group and is hormone-dependently inactivated by phosphorylation or activated by dephosphorylation (see p. 120). The precursor citrate (see p. 138) is an allosteric activator, while palmitoyl-CoA inhibits the end product of the synthesis pathway.

[1] The first cycle (n = 1) starts with the transfer of an acetyl residue from acetyl CoA to the peripheral cysteine residue (Cys-SH). At the same time,

[2] a malonyl residue is transferred from malonyl CoA to 4-phosphopentenethione (Pan-SH).

[3] By condensation of the acetyl residue—or (in later cycles) the acyl residue—with the malonyl group, with simultaneous decarboxylation, the chain is elongated.

[4]–[6] The following three reactions (reduction of the 3-oxo group, dehydrogenation of the 3-hydroxyl derivative, and renewed reduction of it) correspond in principle to a reversal of β-oxidation, but they are catalyzed by other enzymes and use NADPH+H⁺ instead of NADH+H⁺ for reduction. They lead to an acyl residue bound at Pan-SH with 2n + 2 C atoms (n = the number of the cycle). Finally, depending on the length of the product,

[7] the acyl residue is transferred back to the peripheral cysteine, so that the next cycle can begin again with renewed loading of the ACP with a malonyl residue, or:

[7] After seven cycles, the completed palmitic acid is hydrolytically released.

In all, one acetyl-CoA and seven malonyl-CoA are converted with the help of 14 NADPH+H⁺ into one palmitic acid, 7 CO₂, 8 H₂O, 8 CoA and 14 NAD⁺. Acetyl CoA carboxylase also uses up seven ATP.
A. Fatty acid synthase

1. Substrate entry
2. Chain elongation
3. Reduction
4. Product release

B. Reactions of fatty acid synthesis

1. [ACP]-S-Acetyl-trans-Enoyl-3-Hydroxyacyl-[ACP] synthase 2.3.1.38
2. [ACP]-S-Malonyl-trans-Enoyl-3-OxOacyl-[ACP] synthase 2.3.1.39
3. 3-OxOacyl-[ACP] synthase 2.3.1.41
4. 3-OxOacyl-[ACP] reductase 1.1.1.100
5. 3-Hydroxypalmitoyl-[ACP] dehydratase 4.2.1.61
6. Enoyl-[ACP] reductase (NADPH) 1.3.1.10
7. Acyl-[ACP] hydrolase 3.1.2.14

All reactions catalyzed by enzymes as indicated.
Biosynthesis of complex lipids

A. Biosynthesis of fats and phospholipids

Complex lipids, such as neutral fats (triacylglycerols), phospholipids, and glycolipids, are synthesized via common reaction pathways. Most of the enzymes involved are associated with the membranes of the smooth endoplasmic reticulum.

The synthesis of fats and phospholipids starts with glycerol 3-phosphate. This compound can arise via two pathways:

1. By reduction from the glycolytic intermediate glycerone 3-phosphate (dihydroxyacetone 3-phosphate; enzyme: glycerol-3-phosphate dehydrogenase (NAD+). 1.1.1.8); or:
2. By phosphorylation of glycerol deriving from fat degradation (enzyme: glycerol kinase 2.7.1.30).

3. Esterification of glycerol 3-phosphate with a long-chain fatty acid produces a strongly amphipathic lyso phosphatidate (enzyme: glycerol-3-phosphate acyltransferase 2.3.1.51). In this reaction, an acyl residue is transferred from the activated precursor acyl-CoA to the hydroxy group at C-1.

4. A second esterification of this type leads to a phosphatidate (enzyme: 1-acylglycerol-3-phosphate acyltransferase 2.3.1.51). Unsaturated acyl residues, particularly oleic acid, are usually incorporated at C-2 of the glycerol. Phosphatidates (anions of phosphatidic acids) are the key molecules in the biosynthesis of fats, phospholipids, and glycolipids.

5. To biosynthesize fats (triacylglycerols), the phosphate residue is again removed by hydrolysis (enzyme: phosphatidate phosphatase 3.1.3.4). This produces diacylglycerols (DAG).

6. Transfer of an additional acyl residue to DAG forms triacylglycerols (enzyme: diacylglycerol acyltransferase 2.3.1.20). This completes the biosynthesis of neutral fats. They are packaged into VLDLs by the liver and released into the blood. Finally, they are stored by adipocytes in the form of insoluble fat droplets.

The biosynthesis of most phospholipids also starts from DAG.

7. Transfer of a phosphocholine residue to the free OH group gives rise to phosphatidylcholine (lecithin; enzyme: 1-alkyl-2-acetylglycerolcholine phosphotransferase 2.7.8.16). The phosphocholine residue is derived from the precursor CDP-choline (see p. 110). Phosphatidylethanolamine is similarly formed from CDP-ethanolamine and DAG. By contrast, phosphatidyserine is derived from phosphatidylethanolamine by an exchange of the amino alcohol. Further reactions serve to interconvert the phospholipids—e.g., phosphatidyserine can be converted into phosphatidylethanolamine by decarboxylation, and the latter can then be converted into phosphatidylcholine by methylation with S-adenosyl methionine (not shown; see also p. 409). The biosynthesis of phosphatidylinositol starts from phosphatidate rather than DAG.

8. In the lumen of the intestine, fats from food are mainly broken down into monoaclglycerols (see p. 270). The cells of the intestinal mucosa re-synthesize these into neutral fats. This pathway also passes via DAG (enzyme: acylglycerol alaminyl transferase 2.3.1.22).

9. Transfer of a CMP residue gives rise first to CDP-diacylglycerol (enzyme: phosphatidate phosphatidyl transferase 2.3.1.22).

10. Substitution of the CMP residue by inositol then provides phosphatidylinositol (PtdIns; enzyme: CDP-diacylglycerolinositol-3-phosphatidyl transferase 2.7.8.11).

11. An additional phosphorylation (enzyme: phosphatidylinositol-4-phosphate kinase 2.7.1.68) finally provides phosphatidylinositol-4,5-bisphosphate (PIP_2, PtdIns(4,5)_P_2). PIP_2 is the precursor for the second messengers 2.3-diacylglycerol (DAG) and inositol-1,4,5-trisphosphate (InsP_3; see p. 367).

The biosynthesis of the sphingolipids is shown in schematic form on p. 409.
Biosynthesis of cholesterol

Cholesterol is a major constituent of the cell membranes of animal cells (see p. 216). It would be possible for the body to provide its full daily cholesterol requirement (ca. 1 g) by synthesizing it itself. However, with a mixed diet, only about half of the cholesterol is derived from endogenous biosynthesis, which takes place in the intestine and skin, and mainly in the liver (about 50%). The rest is taken up from food. Most of the cholesterol is incorporated into the lipid layer of plasma membranes, or converted into bile acids (see p. 314). A very small amount of cholesterol is used for biosynthesis of the steroid hormones (see p. 376). In addition, up to 1 g cholesterol per day is released into the bile and thus excreted.

A. Cholesterol biosynthesis

Cholesterol is one of the isoprenoids, synthesis of which starts from acetyl CoA (see p. 52). In a long and complex reaction chain, the C27 sterol is built up from C7 components. The biosynthesis of cholesterol can be divided into four sections. In the first (1), mevalonate, a C10 compound, arises from three molecules of acetyl CoA. In the second part (2), mevalonate is converted into isopentenyl diphosphate, the “active isoprene.” In the third part (3), six of these C5 molecules are linked to produce squalene, a C30 compound. Finally, squalene undergoes cyclization, with three C atoms being removed, to yield cholesterol (4). The illustration only shows the most important intermediates in biosynthesis.

1) Formation of mevalonate. The conversion of acetyl CoA to acetoacetyl CoA and then to 3-hydroxy-3-methylglutaryl CoA (3-HMG CoA) corresponds to the biosynthetic pathway for ketone bodies (details on p. 312). In this case, however, the synthesis occurs not in the mitochondria as in ketone body synthesis, but in the smooth endoplasmic reticulum. In the next step, the 3-HMG group is cleaved from the CoA and at the same time reduced to mevalonate with the help of NADPH+H+. 3-HMG CoA reductase is the key enzyme in cholesterol biosynthesis. It is regulated by repression of transcription (effectors: oxysterols such as cholesterol) and by interconversion (effectors: hormones). Insulin and thyroxine stimulate the enzyme and glucagon inhibits it by cAMP-dependent phosphorylation. A large supply of cholesterol from food also inhibits 3-HMG-CoA reductase.

2) Formation of isopentenyl diphosphate. After phosphorylation, mevalonate is decarboxylated to isopentenyl diphosphate, with consumption of ATP. This is the component from which all of the isoprenoids are built (see p. 53).

3) Formation of squalene. Isopentenyl diphosphate undergoes isomerization to form dimethylallyl diphosphate. The two C5 molecules condense to yield geranyl diphosphate, and the addition of another isopentenyl diphosphate produces farnesyl diphosphate. This can then undergo dimerization, in a head-to-head reaction, to yield squalene. Farnesyl diphosphate is also the starting point for other polyisoprenoids, such as dolichol (see p. 230) and ubiquinone (see p. 52).

4) Formation of cholesterol. Squalene, a linear isoprenoid, is cyclized, with O2 being consumed, to form lanosterol, a C30 sterol. Three methyl groups are cleaved from this in the subsequent reaction steps, to yield the end product cholesterol. Some of these reactions are catalyzed by cytochrome P450 systems (see p. 318).

The endergonic biosynthetic pathway described above is located entirely in the smooth endoplasmic reticulum. The energy needed comes from the CoA derivatives used and from ATP. The reducing agent in the formation of mevalonate and squalene, as well as in the final steps of cholesterol biosynthesis, is NADPH+H+.

The division of the intermediates of the reaction pathway into three groups is characteristic: CoA compounds, diphosphates, and highly lipophilic, poorly soluble compounds (squalene to cholesterol), which are bound to sterol carriers in the cell.
A. Cholesterol biosynthesis

1. Mevalonate

2. Isopentenyl diphosphate

3. Squalene

4. Cholesterol

Acetyl CoA \[\rightarrow\] Mevalonate \[\rightarrow\] Isopentenyl diphosphate \[\rightarrow\] Squalene \[\rightarrow\] Cholesterol

Key enzyme

Insulin

Thyroxin

Glucagon

HMG-CoA reductase

1.1.1.34

Mevalonate

Mevalonyl diphosphate

Dimethylallyl diphosphate

Isopentenyl diphosphate

Ceranyl diphosphate

Farnesyl diphosphate

Squalene

O_{2} + \text{H}_{2}O \rightarrow \text{CO}_2 + \text{H}_2\text{O}

Multiple steps

Insulin

Thyroxin

Glucagon

Insulin

Thyroxin

Glucagon

Mevalonate

Mevalonyl diphosphate

Dimethylallyl diphosphate

Isopentenyl diphosphate

Ceranyl diphosphate

Farnesyl diphosphate

Squalene

O_{2} + \text{H}_{2}O \rightarrow \text{CO}_2 + \text{H}_2\text{O}

Multiple steps
Protein metabolism: overview

Quantitatively, proteins are the most important group of endogenous macromolecules. A person weighing 70 kg contains about 10 kg protein, with most of it located in muscle. By comparison, the proportion made up by other nitrogen-containing compounds is minor. The organism’s nitrogen balance is therefore primarily determined by protein metabolism. Several hormones—mainly testosterone and cortisol—regulate the nitrogen balance (see p. 374).

A. Protein metabolism: overview ●

In adults, the nitrogen balance is generally in equilibrium—i.e., the quantities of protein nitrogen taken in and excreted per day are approximately equal. If only some of the nitrogen taken in is excreted again, then the balance is positive. This is the case during growth, for example. Negative balances are rare and usually occur due to disease.

Proteins taken up in food are initially broken down in the gastrointestinal tract into amino acids, which are resorbed and distributed in the organism via the blood (see p. 266). The human body is not capable of synthesizing 8–10 of the 20 proteinogenic amino acids it requires (see p. 60). These amino acids are essential, and have to be supplied from food (see p. 184).

Proteins are constantly being lost via the intestine and, to a lesser extent, via the kidneys. To balance these inevitable losses, at least 30 g of protein have to be taken up with food every day. Although this minimum value is barely reached in some countries, in the industrial nations the protein content of food is usually much higher than necessary. As it is not possible to store amino acids, up to 100 g of excess amino acids per day are used for biosynthesis or degraded in the liver in this situation. The nitrogen from this excess is converted into urea (see p. 182) and excreted in the urine in this form. The carbon skeletons are used to synthesize carbohydrates or lipids (see p. 180), or are used to form ATP.

It is thought that adults break down 300–400 g of protein per day into amino acids (proteolysis). On the other hand, approximately the same amount of amino acids is reincorporated into proteins (protein biosynthesis). The body’s high level of protein turnover is due to the fact that many proteins are relatively short-lived. On average, their half-lives amount to 2–8 days. The key enzymes of the intermediary metabolism have even shorter half-lives. They are sometimes broken down only a few hours after being synthesized, and are replaced by new molecules. This constant process of synthesis and degradation makes it possible for the cells to quickly adjust the quantities, and therefore the activity, of important enzymes in order to meet current requirements. By contrast, structural proteins such as the histones, hemoglobin, and the components of the cytoskeleton are particularly long-lived.

Almost all cells are capable of carrying out biosynthesis of proteins (top left). The formation of peptide chains by translation at the ribosome is described in greater detail on pp. 250–253. However, the functional forms of most proteins arise only after a series of additional steps. To begin with, supported by auxiliary proteins, the biologically active conformation of the peptide chain has to be formed (folding; see pp. 74, 232). During subsequent “post-translational” maturation, many proteins remove part of the peptide chain again and attach additional groups—e.g., oligosaccharides or lipids. These processes take place in the endoplasmic reticulum and in the Golgi apparatus (see p. 223). Finally, the proteins have to be transported to their site of action (sorting; see p. 228).

Some intracellular protein degradation (proteolysis) takes place in the lysosomes (see p. 234). In addition, there are protein complexes in the cytoplasm, known as proteasomes, in which incorrectly folded or old proteins are degraded. These molecules are recognized by a special marking (see p. 176). The proteasome also plays an important part in the presentation of antigens by immune cells (see p. 296).
A. Protein metabolism: overview

Protein synthesis (300–400 g/day)
Proteolysis (300–400 g/day)
Proteasome
Lysosome
Protein synthesis (300–400 g/day)

Amino acid pool

Food
Protein secretion
Resorption
Digestion
Amino acids

Excess amino acids
Glucose
Lipids
Ketone bodies
2-Oxoacids
Urea
CO₂, H₂O
NH₃

Pyruvate
Phosphoenolpyruvate
3-Phosphoglycerate
2-Oxoacids
Sugar phosphates

De-novo synthesis
Degradation
Urea

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Proteolysis

A. Proteolytic enzymes

Combinations of several enzymes with different specificities are required for complete degradation of proteins into free amino acids. Proteinases and peptidases are found not only in the gastrointestinal tract (see p. 268), but also inside the cell (see below).

The proteolytic enzymes are classified into endopeptidases and exopeptidases, according to their site of attack in the substrate molecule. The endopeptidases or proteinases cleave peptide bonds inside peptide chains. They “recognize” and bind to short sections of the substrate’s sequence, and then hydrolyze bonds between particular amino acid residues in a relatively specific way (see p. 94). The proteinases are classified according to their reaction mechanism. In serine proteinases, for example (see C), a serine residue in the enzyme is important for catalysis, while in cysteine proteinases, it is a cysteine residue, and so on.

The exopeptidases attack peptides from their termini. Peptidases that act at the N terminus are known as aminopeptidases, while those that recognize the C terminus are called carboxypeptidases. The dipeptidases only hydrolyze dipeptides.

B. Proteasome

The functional proteins in the cell have to be protected in order to prevent premature degradation. Some of the intracellularly active proteolytic enzymes are therefore enclosed in lysosomes (see p. 234). The proteinases that act there are also known as cathepsins.

Another carefully regulated system for protein degradation is located in the cytoplasm. This consists of large protein complexes (mass 2 × 10^6 Da), the proteasomes. Proteasomes contain a barrel-shaped core consisting of 28 subunits that has a sedimentation coefficient (see p. 200) of 20 S. Proteolytic activity (shown here by the scissors) is localized in the interior of the 20-S core and is therefore protected. The openings in the barrel are sealed by 19-S particles with a complex structure that control access to the core.

Proteins destined for degradation in the proteasome (e.g., incorrectly folded or old molecules) are marked by covalent linkage with chains of the small protein ubiquitin. The ubiquitin is previously activated by the introduction of reactive thioester groups. Molecules marked with ubiquitin (“ubiquitinated”) are recognized by the 19S particle, unfolded using ATP, and then shifted into the interior of the nucleus, where degradation takes place. Ubiquitin is not degraded, but is reused after renewed activation.

C. Serine proteases

A large group of proteinases contain serine in their active center. The serine proteinases include, for example, the digestive enzymes trypsin, chymotrypsin, and elastase (see pp. 94 and 268), many coagulation factors (see p. 290), and the fibrinolytic enzyme plasmin and its activators (see p. 292).

As described on p. 270, pancreatic proteinases are secreted as proenzymes (zymogens). Activation of these is also based on proteolytic cleavages. This is illustrated here in detail using the example of trypsinogen, the precursor of trypsin (1). Activation of trypsinogen starts with cleavage of an N-terminal hexapeptide by enteropeptidase (enterokinase), a specific serine proteinase that is located in the membrane of the intestinal epithelium. The cleavage product (β-trypsin) is already catalytically active, and it cleaves additional trypsinogen molecules at the sites marked in red in the illustration (autocatalytic cleavage). The precursors of chymotrypsin, elastase, and carboxypeptidase A, among others, are also activated by trypsin.

The active center of trypsin is shown in Fig. 2. A serine residue in the enzyme (Ser-195), supported by a histidine residue and an aspartate residue (His-57, Asp-102), nucleophilically attacks the bond that is to be cleaved (red arrow). The cleavage site in the substrate peptide is located on the C-terminal side of a lysine residue, the side chain of which is fixed in a special “binding pocket” of the enzyme (left) during catalysis (see p. 94).
A. Proteolytic enzymes

- Amino peptidase 3.4.11.1
- Dipeptidase [Zn²⁺] 3.4.13.1
- Carboxypeptidase 3.4.14.7

B. Proteasome

- Folding protein
- Activated ubiquitin
- Ubiquitinated protein
- 19S particle
- 26S nucleus
- 19S particle

C. Serine proteases

- Enteropeptidase 3.4.21.9
- Trypsin: active center
- Trypsin 3.4.21.4
- Trypsinogen activation

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Transamination and deamination

Amino nitrogen accumulates during protein degradation. In contrast to protein, amino nitrogen is not suitable for oxidative energy production. If they are not being reused for biosynthesis, the amino groups of amino acids are therefore incorporated into urea (see p. 182) and excreted in this form.

A. Transamination and deamination

Among the \( \text{NH}_2 \) transfer reactions, transaminations (1) are particularly important. They are catalyzed by transaminases, and occur in both catabolic and anabolic amino acid metabolism. During transamination, the amino group of an amino acid (amino acid 1) is transferred to a 2-oxoacid (oxoacid 2). From the amino acid, this produces a 2-oxoacid (a), while from the original oxoacid, an amino acid is formed (b). The \( \text{NH}_2 \) group is temporarily taken over by enzyme-bound pyridoxal phosphate (PLP; see p. 106), which thus becomes pyridoxamine phosphate.

If the \( \text{NH}_2 \) is released as ammonia, the process is referred to as deamination. There are different mechanisms for this (see p. 180). A particularly important one is oxidative deamination (2). In this reaction, the \( \alpha \)-amino group is initially oxidized into an imino group (2a), and the reducing equivalents are transferred to \( \text{NAD}^+ \) or \( \text{NADP}^+ \). In the second step, the imino group is then cleaved by hydrolysis. As in transamination, this produces a 2-oxoacid (C). Oxidative deamination mainly takes place in the liver, where glutamate is broken down in this way into 2-oxoglutarate and ammonia, catalyzed by glutamate dehydrogenase. The reverse reaction initiates biosynthesis of the amino acids in the glutamate family (see p. 184).

B. Mechanism of transamination

In the absence of substrates, the aldehyde group of pyridoxal phosphate is covalently bound to a lysine residue of the transaminase (1). This type of compound is known as an aldmine or "Schiff’s base." During the reaction, amino acid 1 (A, 1a) displaces the lysine residue, and a new aldmine is formed (2). The double bond is then shifted by isomerization.

The ketamine (3) is hydrolyzed to yield the 2-oxoacid and pyridoxamine phosphate (4).

In the second part of the reaction (see A, 1b), these steps take place in the opposite direction: pyridoxamine phosphate and the second 2-oxoacid form a ketamine, which is isomerized into aldmine. Finally, the second amino acid is cleaved and the coenzyme is regenerated.

C. \( \text{NH}_3 \) metabolism in the liver

In addition to urea synthesis itself (see p. 182), the precursors \( \text{NH}_3 \) and aspartate are also mainly formed in the liver. Amino nitrogen arising in tissue is transported to the liver by the blood, mainly in the form of glutamine (Gln) and alanine (Ala; see p. 338). In the liver, Gln is hydrolytically deaminated by glutaminase [1] into glutamate (Glu) and \( \text{NH}_3 \). The amino group of the alanine is transferred by alanine transaminase [1] to 2-oxoglutarate (2-OG, formerly known as \( \alpha \)-ketoglutarate). This transamination (A) produces another glutamate. \( \text{NH}_3 \) is finally released from glutamate by oxidative deamination (A). This reaction is catalyzed by glutamate dehydrogenase [4], a typical liver enzyme. Aspartate (Asp), the second amino group donor in the urea cycle, also arises from glutamate. The aspartate transaminase [2] responsible for this reaction is found with a high level of activity in the liver, as is alanine transaminase [1].

Transaminases are also found in other tissues, from which they leak from the cells into the blood when injury occurs. Measurement of serum enzyme activity (serum enzyme diagnosis; see also p. 98) is an important method of recognizing and monitoring the course of such injuries. Transaminase activity in the blood is for instance important for diagnosing liver disease (e.g., hepatitis) and myocardial disease (cardiac infarction).
A. Transamination and deamination

1. Transamination

Amino acid 1

\[ \text{H}_2\text{N-CH}_2-\text{R} \]

Oxoid acid 1

\[ \text{H}_2\text{N-CH}_2-\text{R} \]

Pyridoxamine phosphate

2. Oxidative deamination

Amino acid 2

\[ \text{H}_2\text{N-CH}_2-\text{R} \]

Aldimine 2

Ketimine

B. Mechanism of transamination

1. Aldimine 2

2. Rearrangement

3. Ketimine

4. Pyridoxamine

C. NH₃ metabolism in the liver

From the blood

FAD

Glutamate dehydrogenase

2.6.1.2

Glutaminase

1.5.1.2

Aspartate transaminase

2.6.1.1

Alanine transaminase

2.6.1.2

TRANSACTIONS

Oxidative
deamination

Hydrolytic
deamination

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Amino acid degradation

A large number of metabolic pathways are available for amino acid degradation, and an overview of these is presented here. Further details are given on pp. 414 and 415.

A. Amino acid degradation: overview

During the degradation of most amino acids, the α-amino group is initially removed by transamination or deamination. Various mechanisms are available for this, and these are discussed in greater detail in B. The carbon skeletons that are left over after deamination undergo further degradation in various ways.

During degradation, the 20 proteinogenic amino acids produce only seven different degradation products (highlighted in pink and violet). Five of these metabolites (2-oxoglutarate, succinyl CoA, fumarate, oxaloacetate, and pyruvate) are precursors for gluconeogenesis and can therefore be converted into glucose by the liver and kidneys (see p. 154). Amino acids whose degradation supplies one of these five metabolites are therefore referred to as glucogenic amino acids. The first four degradation products listed are already intermediates in the tricarboxylic acid cycle, while pyruvate can be converted into oxaloacetate by pyruvate carboxylase and thus made available for gluconeogenesis (green arrow).

With two exceptions (lysine and leucine; see below), all of the proteinogenic amino acids are also glucogenic. Quantitatively, they represent the most important precursors for gluconeogenesis. At the same time, they also have an anaplerotic effect—i.e., they replenish the tricarboxylic acid cycle in order to feed the anabolic reactions that originate in it (see p. 138).

Two additional degradation products (acetoacetate and acetyl CoA) cannot be channeled into gluconeogenesis in animal metabolism, as there is no means of converting them into precursors of gluconeogenesis. However, they can be used to synthesize ketone bodies, fatty acids, and isoprenoids. Amino acids that supply acetyl CoA or acetoacetate are therefore known as ketogenic amino acids. Only leucine and lysine are purely ketogenic. Several amino acids yield degradation products that are both glucogenic and ketogenic. This group includes phenylalanine, tyrosine, tryptophan, and isoleucine.

Degradation of acetoacetate to acetyl CoA takes place in two steps (not shown). First, acetoacetate and succinyl CoA are converted into acetoacetyl CoA and succinate (enzyme: 2-oxosuccin-CoA transferase 2.8.1.5). Acetoacetyl CoA is then broken down by β-oxidation into two molecules of acetyl CoA (see p. 164), while succinate can be further metabolized via the tricarboxylic acid cycle.

B. Deamination

There are various ways of releasing ammonia (NH₃) from amino acids, and these are illustrated here using the example of the amino acids glutamine, glutamate, alanine, and serine.

1. In the branched-chain amino acids (Val, Leu, Ile) and also tyrosine and ornithine, degradation starts with a transamination. For alanine and aspartate, this is actually the only degradation step. The mechanism of transamination is discussed in detail on p. 178.

2. Oxidative deamination, with the formation of NADH⁺, only applies to glutamate in animal metabolism. The reaction mainly takes place in the liver and releases NH₃ for urea formation (see p. 178).

3. Two amino acids—asparagine and glutamine—contain acid-amide groups in the side chains, from which NH₃ can be released by hydrolysis (hydrolytic deamination). In the blood, glutamine is the most important transport molecule for amino nitrogen. Hydrolytic deamination of glutamine in the liver also supplies the urea cycle with NH₃.

4. Eliminating deamination takes place in the degradation of histidine and serine. H₂O is first eliminated here, yielding an unsaturated intermediate. In the case of serine, this intermediate is first rearranged into an imine (not shown), which is hydrolyzed in the second step into NH₃ and pyruvate, with H₂O being taken up. H₂O does not therefore appear in the reaction equation.
A. Amino acid degradation: overview

B. Deamination

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Urea cycle

Amino acids are mainly broken down in the liver. Ammonia is released either directly or indirectly in the process (see p. 178). The degradation of nucleobases also provides significant amounts of ammonia (see p. 186).

Ammonia (NH₃) is a relatively strong base, and at physiological pH values it is mainly present in the form of the ammonium ion NH₄⁺ (see p. 30). NH₃ and NH₄⁺ are toxic, and at higher concentrations cause brain damage in particular. Ammonia therefore has to be effectively inactivated and excreted. This can be carried out in various ways. Aquatic animals can excrete NH₄⁺ directly. For example, fish excrete NH₄⁺ via the gills (ammonotetic animals). Terrestrial vertebrates, including humans, hardly excrete any NH₄⁺, and instead, most ammonia is converted into urea before excretion (ureotelic animals). Birds and reptiles, by contrast, form uric acid, which is mainly excreted as a solid in order to save water (uricotelic animals).

The reasons for the neurotoxic effects of ammonia have not yet been explained. It may disturb the metabolism of glutamate and its precursor glutamine in the brain (see p. 356).

A. Urea cycle

Urea (H₂N–CO–NH₂) is the diamide of carbonic acid. In contrast to ammonia, it is neutral and therefore relatively non-toxic. The reason for the lack of basicity is the molecule’s mesomeric characteristics. The free electron pairs of the two nitrogen atoms are delocalized over the whole structure, and are therefore no longer able to bind protons. As a small, uncharged molecule, urea is able to cross biological membranes easily. In addition, it is easily transported in the blood and excreted in the urine.

Urea is produced only in the liver, in a cyclic sequence of reactions (the urea cycle) that starts in the mitochondria and continues in the cytoplasm. The two nitrogen atoms are derived from NH₄⁺ (the second has previously been incorporated into aspartate; see below). The keto group comes from hydrogen carbonate (HCO₃⁻), or CO₂ that is in equilibrium with HCO₃⁻.

[1] In the first step, carboxamyl phosphate is formed in the mitochondria from hydrogen carbonate (HCO₃⁻) and NH₄⁺, with two ATP molecules being consumed. In this compound, the carboxamyl residue (–O–CO–NH₂) is at a high chemical potential. In hepatic mitochondria, enzyme [1] makes up about 20% of the matrix proteins.

[2] In the next step, the carboxamyl residue is transferred to the non-proteinogenic amino acid ornithine, converting it into citrulline, which is also non-proteinogenic. This is passed into the cytoplasm via a transporter.

[3] The second NH₂ group of the later urea molecule is provided by aspartate, which condenses with citrulline into argininosuccinate. ATP is cleaved into AMP and diphosphate (PP₄) for this endergonic reaction. To shift the equilibrium of the reaction to the side of the product, diphosphate is removed from the equilibrium by hydrolysis.

[4] Cleavage of fumarate from argininosuccinate leads to the proteinogenic amino acid arginine, which is synthesized in this way in animal metabolism.

[5] In the final step, isourea is released from the guanidinium group of the arginine by hydrolysis (not shown), and is immediately rearranged into urea. In addition, ornithine is regenerated and returns via the ornithine transporter into the mitochondria, where it becomes available for the cycle once again.

The fumarate produced in step [4] is converted via malate to oxaloacetate [6, 7], from which aspartate is formed again by transamination [9]. The glutamate required for reaction [9] is derived from the glutamate dehydrogenase reaction [8], which fixes the second NH₂⁺ in an organic bond. Reactions [6] and [7] also occur in the tricarboxylic acid cycle. However, in urea formation they take place in the cytoplasm, where the appropriate isoenzymes are available.

The rate of urea formation is mainly controlled by reaction [1], N-acetyl glutamate, as an allosteric effector, activates carboxamyl-phosphate synthase. In turn, the concentration of acetyl glutamate depends on arginine and ATP levels, as well as other factors.
A. Urea cycle

1. Carboxyl phosphate synthase (NH$_3$) 6.3.4.16
2. Ornithine carboxyamidase 2.1.3.3
3. N-Acetyl glutamate
4. Argininosuccinate synthase 6.3.4.5
5. Argininosuccinate lyase 4.3.2.1
6. Arginase 3.5.3.1
7. Fumarate hydratase 4.2.1.2
8. Malate dehydrogenase 1.1.1.37
9. Glutamate dehydrogenase 1.4.1.2
10. Aspartate transaminase [PLP]

NH$_4$$\rightleftharpoons$Urea cycle

Urea

Ornithine

Citrulline

Arginine

Argininosuccinate

Fumarate

Glutamate

Aspartate

Fumarate hydratase 4.2.1.2

Malate dehydrogenase 1.1.1.37

Glutamate dehydrogenase 1.4.1.2

Aspartate transaminase [PLP]
Amino acid biosynthesis

A. Symbiotic nitrogen fixation

Practically unlimited quantities of elementary nitrogen (N\textsubscript{2}) are present in the atmosphere. However, before it can enter the natural nitrogen cycle, it has to be reduced to NH\textsubscript{3} and incorporated into amino acids (“fixed”). Only a few species of bacteria and bluegreen algae are capable of fixing atmospheric nitrogen. These exist freely in the soil, or in symbiosis with plants. The symbiosis between bacteria of the genus Rhizobium and legumes (Fabales)—such as clover, beans, and peas—is of particular economic importance. These plants are high in protein and are therefore nutritionally valuable.

In symbiosis with Fabales, bacteria live as endosymbionts in root nodules inside the plant cells. The plant supplies the bacteroids with nutrients, but it also benefits from the fixed nitrogen that the symbionts make available.

The N\textsubscript{2}-fixing enzyme used by the bacteria is nitrogenase. It consists of two components: an Fe protein that contains an [Fe\textsubscript{6}S\textsubscript{4}] cluster as a redox system (see p. 106), accepts electrons from ferredoxin, and donates them to the second component, the Fe–Mo protein. This molybdenum-containing protein transfers the electrons to N\textsubscript{2} and thus, via various intermediate steps, produces ammonia (NH\textsubscript{3}). Some of the reducing equivalents are transferred in a side-reaction to H\textsuperscript{+}. In addition to NH\textsubscript{3}, hydrogen is therefore always produced as well.

B. Amino acid biosynthesis: overview

The proteinogenic amino acids (see p. 60) can be divided into five families in relation to their biosynthesis. The members of each family are derived from common precursors, which are all produced in the tricarboxylic acid cycle or in catabolic carbohydrate metabolism. An overview of the biosynthetic pathways is shown here; further details are given on pp. 412 and 413.

Plants and microorganisms are able to synthesize all of the amino acids from scratch, but during the course of evolution, mammals have lost the ability to synthesize approximately half of the 20 proteinogenic amino acids. These essential amino acids therefore have to be supplied in food. For example, animal metabolism is no longer capable of carrying out de-novo synthesis of the aromatic amino acids (tyrosine is only non-essential because it can be formed from phenylalanine when there is an adequate supply available). The branched-chain amino acids (valine, leucine, isoleucine, and threonine) as well as methionine and lysine, also belong to the essential amino acids. Histidine and arginine are essential in rats; whether the same applies in humans is still a matter of debate. A supply of these amino acids in food appears to be essential at least during growth.

The nutritional value of proteins (see p. 360) is decisively dependent on their essential amino acid content. Vegetable proteins—e.g., those from cereals—are low in lysine and methionine, while animal proteins contain all the amino acids in balanced proportions. As mentioned earlier, however, there are also plants that provide high-value protein. These include the soy bean, one of the plants that is supplied with NH\textsubscript{3} by symbiotic N\textsubscript{2} fixers (A).

Non-essential amino acids are those that arise by transamination from 2-oxoacids in the intermediary metabolism. These belong to the glutamate family (Glu, Gln, Pro, Arg, derived from 2-oxoglutarate), the aspartate family (only Asp and Asn in this group, derived from oxalacetate), and alanine, which can be formed by transamination from pyruvate. The amino acids in the serine family (Ser, Gly, Cys) and histidine, which arise from intermediates of glycolysis, can also be synthesized by the human body.
A. Symbiotic nitrogen fixation

B. Amino acid biosynthesis: overview

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Nucleotide degradation

The nucleotides are among the most complex metabolites. Nucleotide biosynthesis is elaborate and requires a high energy input (see p. 188). Understandably, therefore, bases and nucleotides are not completely degraded, but instead mostly recycled. This is particularly true of the purine bases adenine and guanine. In the animal organism, some 90% of these bases are converted back into nucleoside monophosphates by linkage with phosphoribosyl diphosphate (PRPP) [enzymes 1 and 2]. The proportion of pyrimidine bases that are recycled is much smaller.

A. Degradation of nucleotides

The principles underlying the degradation of purines (1) and pyrimidines (2) differ. In the human organism, purines are degraded into uric acid and excreted in this form. The purine ring remains intact in this process. In contrast, the ring of the pyrimidine bases (uracil, thymine, and cytosine) is broken down into small fragments, which can be returned to the metabolism or excreted (for further details, see p. 419).

Purine (left). The purine nucleotide guanosine monophosphate (GMP, 1) is degraded in two steps—first to the guanosine and then to guanine (Gua). Guanine is converted by deamination into another purine base, xanthine. In the most important degradative pathway for adenosine monophosphate (AMP), it is the nucleotide that deaminated, and inosine monophosphate (IMP) arises. In the same way as in GMP, the purine base hypoxanthine is released from IMP. A single enzyme, xanthine oxidase [3], then both converts hypoxanthine into xanthine and xanthine into uric acid. An oxo group is introduced into the substrate in each of these reaction steps. The oxo group is derived from molecular oxygen; another reaction product is hydrogen peroxide (H₂O₂), which is toxic and has to be removed by peroxidases.

Almost all mammals carry out further degradation of uric acid with the help of aricase, with further opening of the ring to allantoin, which is then excreted. However, the pri-mates, including humans, are not capable of synthesizing allantoin. Uric acid is therefore the form of the purines excreted in these species. The same applies to birds and many reptiles. Most other animals continue purine degradation to reach allantoic acid or urea and glyoxylate.

Pyrimidine (right). In the degradation of pyrimidine nucleotides (2), the free bases uracil (Ura) and thymine (Thy) are initially released as important intermediates. Both are further metabolized in similar ways. The pyrimidine ring is first reduced and then hydrolytically cleaved. In the next step, β-alanine arises by cleavage of CO₂ and NH₃ as the degradation product of uracil. When there is further degradation, β-alanine is broken down to yield acetate, CO₂, and NH₃. Propionate, CO₂, and NH₃ arise in a similar way from 2-aminoisobutyrate, the degradation product of thymine (see p. 419).

B. Hyperuricemia

The fact that purine degradation in humans already starts at the uric acid stage can lead to problems, since—in contrast to allantoin—uric acid is poorly soluble in water. When large amounts of uric acid are formed or uric acid processing is disturbed, excessive concentrations of uric acid can develop in the blood (hyperuricemia). This can result in the accumulation of uric acid crystals in the body. Deposition of these crystals in the joints can cause very painful attacks of gout.

Most cases of hyperuricemia are due to disturbed uric acid excretion via the kidneys (1). A high-purine diet (e.g., meat) may also have unfavorable effects (2). A rare hereditary disease, Lesch-Nyhan syndrome, results from a defect in hypoxanthine phosphoribosyltransferase (A; enzyme [1]). The impaired re-cycling of the purine bases caused by this leads to hyperuricemia and severe neurological disorders.

Hyperuricemia can be treated with allopurinol, a competitive inhibitor of xan-thine oxidase. This substrate analogue differs from the substrate hypoxanthine only in the arrangement of the atoms in the 5-ring.
A. Degradation of nucleotides

1. Purine nucleotides

2. Pyrimidine nucleotides

B. Hyperuricemia (gout)

Causes:
1. Disturbed uric acid excretion
2. Elevated uric acid formation
   a) Unbalanced nutrition
   b) Impaired recycling of purine bases

Recycling reactions

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Purine and pyrimidine biosynthesis

The bases occurring in nucleic acids are derivatives of the aromatic heterocyclic compounds purine and pyrimidine (see p. 80). The biosynthesis of these molecules is complex, but is vital for almost all cells. The synthesis of the nucleobases is illustrated here schematically. Complete reaction schemes are given on pp. 417 and 418.

A. Components of nucleobases

The *pyrimidine ring* is made up of three components: the nitrogen atom N-1 and carbons C-4 to C-6 are derived from aspartate, carbon C-2 comes from HCO_3^-, and the second nitrogen (N-3) is taken from the amide group of glutamine.

The synthesis of the *purine ring* is more complex. The only major component is glycine, which donates C-4 and C-5, as well as N-7. All of the other atoms in the ring are incorporated individually. C-6 comes from HCO_3^- Amide groups from glutamine provide the atoms N-3 and N-9. The amino group donor for the inclusion of N-1 is aspartate, which is converted into fumarate in the process, in the same way as in the urea cycle (see p. 182). Finally, the carbon atoms C-2 and C-8 are derived from formyl groups in N^10-formyl-tetrahydrofolate (see p. 108).

B. Pyrimidine and purine synthesis

The major intermediates in the biosynthesis of nucleic acid components are the mononucleotides *uridine monophosphate* (UMP) in the pyrimidine series and *inosine monophosphate* (IMP, base: hypoxanthine) in the purines. The synthetic pathways for pyrimidines and purines are fundamentally different. For the pyrimidines, the pyrimidine ring is first constructed and then linked to ribose 5’-phosphate to form a nucleotide. By contrast, synthesis of the purines starts directly from ribose 5’-phosphate. The ring is then built up step by step on this carrier molecule.

The precursors for the synthesis of the pyrimidine ring are *carbamoyl phosphate*, which arises from glutamate and HCO_3^- (1a) and the amino acid aspartate. These two components are linked to *N-carbamoyl aspartate* (1b) and then converted into *dihydroorotate* by closure of the ring (1c). In mammals, steps 1a to 1c take place in the cytoplasm, and are catalyzed by a single multifunctional enzyme. In the next step (1d), dihydroorotate is oxidized to orotate by an FMN-dependent dehydrogenase. Orotate is then linked with *phosphoribosyl diphosphate* (PRPP) to form the nucleotide *orotidine 5’-monophosphate* (OMP). Finally, decarboxylation yields *uridine 5’-monophosphate* (UMP).

Purine biosynthesis starts with PRPP (the names of the individual intermediates are given on p. 417). Formation of the ring starts with transfer of an amino group, from which the later N-9 is derived (2a). Glycine and a formyl group from N^10-formyl-THF then supply the remaining atoms of the five-membered ring (2b, 2c). Before the five-membered ring is closed (in step 2f), atoms N-3 and C-6 of the later six-membered ring are attached (2d, 2e). Synthesis of the ring then continues with N-1 and C-2 (2g, 2i). In the final step (2j), the six-membered ring is closed, and *inosine 5’-monophosphate* arises. However, the IMP formed does not accumulate, but is rapidly converted into AMP and GMP. These reactions and the synthesis of the other nucleotides are discussed on p. 190.

Further information

The regulation of bacterial aspartate carbamoyltransferase by ATP and CTP has been particularly well studied, and is discussed on p. 116. In animals, in contrast to prokaryotes, it is not ACTase but carbamoylphosphate synthase that is the key enzyme in pyrimidine synthesis. It is activated by ATP and PRPP and inhibited by UTP.

The biosynthesis of the purines is also regulated by feedback inhibition. ADP and GDP inhibit the formation of PRPP from ribose-5’-phosphate. Similarly, step 2a is inhibited by AMP and GMP.
A. Components of nucleobases

![Diagram of nucleobase components]

B. Pyrimidine and purine synthesis

![Diagram of pyrimidine and purine synthesis]

Carbamoyl phosphate

Phosphoribosyl diphosphate

n-Carboxymethyl aspartate

Dihydro-orotate

Orotate 5'-monophosphate

Uridine 5'-monophosphate (UMP)

1. Pyrimidines

Aspartate

Glycine

5'-Phosphoribosyl residue

UMP

IMP

2. Purines

Inosine 5'-monophosphate (IMP)
Nucleotide biosynthesis

De novo synthesis of purines and pyrimidines yields the monophosphates IMP and UMP, respectively (see p. 188). All other nucleotides and deoxynucleotides are synthesized from these two precursors. An overview of the pathways involved is presented here; further details are given on p. 417. Nucleotide synthesis by recycling of bases (the salvage pathway) is discussed on p. 186.

A. Nucleotide synthesis: overview

The synthesis of purine nucleotides (1) starts from IMP. The base it contains, hypoxanthine, is converted in two steps each into adenine or guanine. The nucleoside monophosphates AMP and GMP that are formed are then phosphorylated by nucleoside phosphate kinases to yield the diphosphates ADP and GDP, and these are finally phosphorylated into the triphosphates ATP and GTP. The nucleoside triphosphates serve as components for RNA, or function as coenzymes (see p. 106). Conversion of the ribonucleotides into deoxyribo-nucleotides occurs at the level of the diphosphates and is catalyzed by nucleoside diphosphate reductase (B).

The biosynthetic pathways for the pyrimidine nucleotides (2) are more complicated. The first product, UMP, is phosphorylated first to the diphosphate and then to the triphosphate, UTP. CTP synthase then converts UTP into CTP. Since pyrimidine nucleotides are also reduced to deoxyribonucleotides at the diphosphate level, CTP first has to be hydrolyzed by a phosphatase to yield CDP before dCDP and dCTP can be produced.

The DNA component deoxythymidine triphosphate (dTTP) is synthesized from UDP in several steps. The base thymine, which only occurs in DNA (see p. 80), is formed by methylation of dUMP at the nucleoside monophosphate level. Thymidylate synthase and its helper enzyme dihydrofolate reductase are important target enzymes for cytostatic drugs (see p. 402).

B. Ribonucleotide reduction

2’-Deoxyribose, a component of DNA, is not synthesized as a free sugar, but arises at the diphosphate level by reduction of ribonucleo-

side diphosphates. This reduction is a complex process in which several proteins are involved. The reducing equivalents needed come from NADPH+H+. However, they are not transferred directly from the coenzyme to the substrate, but first pass through a redox series that has several steps (1).

In the first step, thioredoxin reductase reduces a small redox protein, thioredoxin, via enzyme-bound FAD. This involves cleavage of a disulfide bond in thioredoxin. The resulting SH groups in turn reduce a catalytically active disulfide bond in nucleoside diphosphate reductase (“ribonucleotide reductase”). The free SH groups formed in this way are the actual electron donors for the reduction of ribonucleotide diphosphates.

In eukaryotes, ribonucleotide reductase is a tetramer consisting of two R1 and two R2 subunits. In addition to the disulfide bond mentioned, a tyrosine radical in the enzyme also participates in the reaction (2). It initially produces a substrate radical (3). This cleaves a water molecule and thereby becomes radical cation. Finally, the deoxyribose residue is produced by reduction, and the tyrosine radical is regenerated.

The regulation of ribonucleotide reductase is complex. The substrate-specificity and activity of the enzyme are controlled by two allosteric binding sites (a and b) in the R1 subunits. ATP and dATP increase or reduce the activity of the reductase by binding at site a. Other nucleotides interact with site b, and thereby alter the enzyme’s specificity.
A. Nucleotide synthesis: overview

1. Purine nucleotides
   De novo synthesis
   - AMP ➔ IMP ➔ GMP
   - dADP ➔ dGDP
   - ATP ➔ CTP ➔ GTP
   - RNA ➔ DNA

2. Pyrimidine nucleotides
   De novo synthesis
   - UMP ➔ dUMP ➔ dTMP
   - UDP ➔ dUDP
   - dTDP ➔ dTTP

B. Ribonucleotide reduction

1. Overview
   - Ribonucleoside diphosphate reductase 1.17.4.1
   - CTP synthase 6.3.4.2
   - Thymidylate synthase 2.1.1.45
   - Nucleoside diphosphate kinase 2.7.4.6
   - Thio-redoxin (oxidized)
   - Thio-redoxin (reduced)
   - Thioredoxin reductase [FAD] 1.6.4.5

2. Reaction mechanism
   - 2e⁻, H⁺ ➔ NADPH
   - NADP⁺ ➔ NADPH
   - NADPH ➔ H⁺
   - H₂O ➔ H₂O
   - NDP ➔ dNDP
   - Radical ➔ H₂O
   - dNDP ➔ dNDP
   - dNDP ➔ dNDP

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Heme biosynthesis

Heme, an iron-containing tetrapyrrole pigment, is a component of O₂-binding proteins (see p. 106) and a coenzyme of various oxidoreductases (see p. 32). Around 85% of heme biosynthesis occurs in the bone marrow, and a much smaller percentage is formed in the liver. Both mitochondria and cytoplasm are involved in heme synthesis.

A. Biosynthesis of heme

Synthesis of the tetrapyrrole ring starts in the mitochondria.

[1] Succinyl CoA (upper left), an intermediate in the tricarboxylic acid cycle, undergoes condensation with glycine and subsequent decarboxylation to yield 5-aminolevulinate (ALA). The ALA synthase responsible for this step is the key enzyme of the whole pathway. Synthesis of ALA synthase is repressed and existing enzyme is inhibited by heme, the end product of the pathway. This is a typical example of end-product or feedback inhibition.

[2] 5-Aminolevulinate now leaves the mitochondria. In the cytoplasm, two molecules condense to form porphobilinogen, a compound that already contains the pyrrole ring. Porphobilinogen synthase is inhibited by lead ions. This is why acute lead poisoning is associated with increased concentrations of ALA in the blood and urine.

[3] The tetrapyrrole structure characteristic of the porphyrins is produced in the next steps of the synthetic pathway. Hydroxymethylbilane synthase catalyzes the linkage of four porphobilinogen molecules and cleavage of an NH₂ group to yield uroporphyrinogen III.

[4] Formation of this intermediate step requires a second enzyme, uroporphyrinogen III synthase. If this enzyme is lacking, the “wrong” isomer, uroporphyrinogen I, is formed.

The tetrapyrrole structure of uroporphyrinogen III is still very different from that of heme. For example, the central iron atom is missing, and the ring contains only eight of the 11 double bonds. In addition, the ring system only carries charged R side chains (four acetate and four propionate residues). As heme groups have to act in the apolar interior of proteins, most of the polar side chains have to be converted into less polar groups.

[5] Initially, the four acetate residues (R₁) are decarboxylated into methyl groups. The resulting coproporphyrinogen III returns to the mitochondria again. The subsequent steps are catalyzed by enzymes located either on or inside the inner mitochondrial membrane.

[6] An oxidase first converts two of the propionate groups (R₂) into vinyl residues. The formation of protoporphyrinogen IX completes the modification of the side chains.

[7] In the next step, another oxidation produces the conjugated π-electron system of protoporphyrin IX.

[8] Finally, a divalent iron is incorporated into the ring. This step also requires a specific enzyme, ferrochelatase. The heme b or Fe-protoporphyrin IX formed in this way is found in hemoglobin and myoglobin, for example (see p. 280), where it is noncovalently bound, and also in various oxidoreductases (see p. 106).

Further information

There are a large number of hereditary or acquired disturbances of porphyrin synthesis, known as porphyrias, some of which can cause severe clinical pictures. Several of these diseases lead to the excretion of heme precursors in feces or urine, giving them a dark red color. Accumulation of porphyrins in the skin can also occur, and exposure to light then causes disfiguring, poorly healing blisters. Neurological disturbances are also common in the porphyrias.

It is possible that the medieval legends about human vampires (“Dracula”) originated in the behavior of porphyria sufferers (avoidance of light, behavioral disturbances, and drinking of blood in order to obtain heme—which markedly improves some forms of porphyria).
A. Heme biosynthesis

Tricarboxylic acid cycle

1. 5-Aminolevulinate synthase [PLP] 2.3.1.37
2. Porphobilinogen synthase 4.2.1.24
3. Hydroxymethylbilane synthase 4.3.1.8
4. Uroporphyrinogen-III synthase 4.2.1.75

Mitochondrion

Cytoplasm

Fe²⁺

Protoperphyrin IX

Protoperphyrinogen IX

Coproporphyrinogen III

Heme
Heme degradation

A. Degradation of heme groups

Heme is mainly found in the human organism as a prosthetic group in erythrocyte hemoglobin. Around 100–200 million aged erythrocytes per hour are broken down in the human organism. The degradation process starts in reticuloendothelial cells in the spleen, liver, and bone marrow.

[1] After the protein part (globin) has been removed, the tetrapyrrole ring of heme is oxidatively cleaved between rings A and B by heme oxygenase. This reaction requires molecular oxygen and NADPH+H⁺, and produces green biliverdin, as well as CO (carbon monoxide) and Fe²⁺, which remains available for further use (see p. 286).

[2] In another redox reaction, biliverdin is reduced by biliverdin reductase to the orange-colored bilirubin. The color change from purple to green to yellow can be easily observed in vivo in a bruise or hematoma.

The color of heme and the other porphyrin systems (see p. 106) results from their numerous conjugated double bonds. Heme contains a cyclic conjugation (highlighted in pink) that is removed by reaction [1]. Reaction [2] breaks the π system down into two smaller separate systems (highlighted in yellow).

For further degradation, bilirubin is transported to the liver via the blood. As bilirubin is poorly soluble, it is bound to albumin for transport. Some drugs that also bind to albumin can lead to an increase in free bilirubin.

[3] The hepatocytes take up bilirubin from the blood and conjugate it in the endoplasmic reticulum with the help of UDP-glucuronic acid into the more easily soluble bilirubin monoglucuronides and diglucuronides. To do this, UDP-glucuronosyltransferase forms estertype bonds between the OH group at C-1 of glucuronic acid and the carboxyl groups in bilirubin (see p. 316). The glucuronides are then excreted by active transport into the bile, where they form what are known as the bile pigments.

Glucuronide synthesis is the rate-determining step in hepatic bilirubin metabolism. Drugs such as phenobarbital, for example, can induce both conjugate formation and the transport process.

Some of the bilirubin conjugates are broken down further in the intestine by bacterial β-glucuronidase. The bilirubin released is then reduced further via intermediate steps into colorless stercoobilinogen, some of which is oxidized again into orange to yellow-colored sterobilin. The end products of bile pigment metabolism in the intestine are mostly excreted in feces, but a small proportion is resorbed (enterohepatic circulation; see p. 334). When high levels of heme degradation are taking place, sterobilinogen appears as uroobilinogen in the urine, where oxidative processes darken it to form urobilin.

In addition to hemoglobin, other heme proteins (myoglobin, cytochromes, catalases, and peroxidases; see p. 32) also supply heme groups that are degraded via the same pathway. However, these contribute only about 10–15% to a total of ca. 250 mg of bile pigment formed per day.

Further information

Hyperbilirubinemia. An elevated bilirubin level (> 10 mg L⁻¹) is known as hyperbilirubinemia. When this is present, bilirubin diffuses from the blood into peripheral tissue and gives it a yellow color (jaundice). The easiest way of observing this is in the white conjunctiva of the eyes.

Jaundice can have various causes. If increased erythrocyte degradation (hemolysis) produces more bilirubin, it causes hemolytic jaundice. If bilirubin conjugation in the liver is impaired—e.g., due to hepatitis or liver cirrhosis—it leads to hepato cellular jaundice, which is associated with an increase in unconjugated (“indirect”) bilirubin in the blood. By contrast, if there is a disturbance of bile drainage (obstructive jaundice, due to gallstones or pancreatic tumors), then conjugated (“direct”) bilirubin in the blood increases. Neonatal jaundice (physiologic jaundice) usually resolves after a few days by itself. In severe cases, however, unconjugated bilirubin can cross the blood–brain barrier and lead to brain damage ( kernicterus).
A. Degradation of heme groups

1. Heme oxygenase (decycling) 1.14.99.3
2. Biliverdin reductase 1.3.1.24
3. Glucuronosyl transferase 2.4.1.17
Structure of cells

A. Comparison of prokaryotes and eukaryotes

Present-day living organisms can be divided into two large groups—the prokaryotes and eukaryotes. The prokaryotes are represented by bacteria (eubacteria and archaebacteria). These are almost all small unicellular organisms only a few microns (10^-6 m) in size. The eukaryotes include fungi, plants, and animals and comprise both unicellular and multicellular organisms. Multicellular eukaryotes are made up of a wide variety of cell types that are specialized for different tasks. Eukaryotic cells are much larger than prokaryotic ones (volume ratio approximately 2000 : 1). The most important distinguishing feature of these cells in comparison with the prokaryotes is the fact that they have a nucleus (karyon in Greek—hence the term).

In comparison with the prokaryotes, eukaryotic cells have greater specialization and complexity in their structure and functioning. Eukaryotic cells are structured into compartments (see below). The metabolism and synthesis of macromolecules are distributed through these reaction spaces and are separately regulated. In prokaryotes, these functions are organized in a simpler fashion and are spatially closely related.

Although the storage and transfer of genetic information function according to the same principle in the prokaryotes and eukaryotes, there are also differences. Eukaryotic DNA consists of very long, linear molecules with a total of 10^9 to more than 10^10 base pairs (bp), only a small fraction of which are used for genetic information. In eukaryotes, the genes (20000–50000 per genome) are usually interrupted by non-coding regions (introns). Eukaryotic DNA is located in the nucleus, where together with histones and other proteins it forms the chromatin (see p. 238).

In prokaryotes, by contrast, DNA is ring-shaped, much shorter (up to 5 10^6 bp), and located in the cytoplasm. Almost all of it is used for information storage, and it does not contain any introns.

B. Structure of an animal cell

In the human body alone, there are at least 200 different cell types. The illustration outlines the basic structures of an animal cell in an extremely simplified way. The details given regarding the proportion of the compartments relative to cell volume (highlighted in yellow) and their numbers per cell frequency (blue) refer to mammalian hepatocytes (liver cells). The figures can vary widely from cell type to cell type.

The eukaryotic cell is subdivided by membranes. On the outside, it is enclosed by a plasma membrane. Inside the cell, there is a large space containing numerous components in solution—the cytoplasm. Additional membranes divide the internal space into compartments (confined reaction spaces). Well-defined compartments of this type are known as organelles.

The largest organelle is the nucleus (see p. 208). It is easily recognized using the light microscope. The endoplasmic reticulum (ER), a closed network of shallow sacs and tubules (see pp. 226ff.), is linked with the outer membrane of the nucleus. Another membrane-bound organelle is the Golgi apparatus (see p. 228), which resembles a bundle of layered slices. The endosomes and exosomes are bubble-shaped compartments (vesicles) that are involved in the exchange of substances between the cell and its surroundings. Probably the most important organelles in the cell’s metabolism are the mitochondria, which are around the same size as bacteria (see pp. 210ff.). The lysosomes and peroxisomes are small, globular organelles that carry out specific tasks. The whole cell is traversed by a framework of proteins known as the cytoskeleton (see pp. 204ff.).

In addition to these organelles, plant cells (see p. 43) also have plastids—e.g., chloroplasts, in which photosynthesis takes place (see p. 128). In their interior, there is a large, fluid-filled vacuole. Like bacteria and fungi, plant cells have a rigid cell wall consisting of polysaccharides and proteins.
### A. Comparison of prokaryotes and eukaryotes

<table>
<thead>
<tr>
<th>Organisms</th>
<th>Prokaryotes</th>
<th>Eukaryotes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Form</td>
<td>Single-celled</td>
<td>Single or multi-cellular</td>
</tr>
<tr>
<td>Organelles, cytoskeleton, cell division apparatus</td>
<td>Missing</td>
<td>Present, complicated, specialized</td>
</tr>
<tr>
<td>DNA</td>
<td>Small, circular, no introns, plasmids</td>
<td>Large, in nucleus, many introns</td>
</tr>
<tr>
<td>RNA: Synthesis and maturation</td>
<td>Simple, in cytoplasm</td>
<td>Complicated, in nucleus</td>
</tr>
<tr>
<td>Protein: Synthesis and maturation</td>
<td>Simple, coupled with RNA synthesis</td>
<td>Complicated, in the cytoplasm and the rough endoplasmic reticulum</td>
</tr>
<tr>
<td>Metabolism</td>
<td>Anaerobic or aerobic, very flexible</td>
<td>Mostly aerobic, compartmented</td>
</tr>
<tr>
<td>Endocytosis and Exocytosis</td>
<td>no</td>
<td>yes</td>
</tr>
</tbody>
</table>

### B. Structure of an animal cell

- **Golgi complex**: 6% of cell volume, 1 µm in diameter.
- **Nucleus**: 6% of cell volume, 1 µm in diameter.
- **Rough endoplasmic reticulum**: 9% of cell volume, 1 µm in diameter, 22% of total protein synthesis.
- **Mitochondrion**: 22% of cell volume, ~2000 µm in length.
- **Peroxisome**: 1% of cell volume, 400 µm in length.
- **Cytoplasm**: 54% of cell volume, 1 µm in diameter.
- **Proportion of cell volume**: 10-30 µm.
- **Plasma membrane**: 1 µm.
- **Lysosome**: 1% of cell volume, 300 µm in length.
- **Endosome**: 1% of cell volume, 200 µm in length.
- **Free ribosomes**: 1 µm.
Cell fractionation

A. Isolation of cell organelles

To investigate the individual compartments of the cell (see p. 196), various procedures have been developed to enrich and isolate cell organelles. These are mainly based on the size and density of the various organelles.

The isolation of cell components starts with disruption of the tissue being examined and subsequent homogenization of it (breaking down the cells) in a suitable buffer (see below). Homogenization using the “Potter” (the Potter–Elvehjem homogenizer, a rotating Teflon pestle in a glass cylinder) is particularly suitable for animal tissue. This method is very gentle and is therefore used to isolate fragile structures and molecules. Other cell disruption procedures include enzymatic lysis with the help of enzymes that break down the cell wall, mechanical disruption by grinding frozen tissue, cutting or smashing with rotating knives, large pressure changes, osmotic shock, and repeated freezing and thawing.

To isolate intact organelles, it is important for the homogenization solution to be isotonic—i.e., the osmotic value of the buffer has to be the same as that of the interior of the cell. If hypotonic solutions were used, the organelles would take up water and burst, while in hypertonic solutions they would shrink.

Homogenization is followed by coarse filtration through gauze to remove intact cells and connective-tissue fragments. The actual fractionation of cellular components is then carried out by centrifugation steps, in which the gravitational force (given as multiples of the earth’s gravity, g = 9.81 m s⁻²) is gradually increased (differential centrifugation; see p. 200). Due to the different shapes and densities of the organelles, this leads to successive sedimentation of each type out of the suspension.

Nuclei already sediment at low accelerations that can be achieved with bench-top centrifuges. Decanting the residue (the “supernatant”) and carefully suspending the sediment (or “pellet”) in an isotonic medium yields a fraction that is enriched with nuclei. However, this fraction may still contain other cellular components as contaminants—e.g., fragments of the cytoskeleton.

Particles that are smaller and less dense than the nuclei can be obtained by step-by-step acceleration of the gravity on the supernatant left over from the first centrifugation. However, this requires very powerful centrifuges (high-speed centrifuges and ultracentrifuges). The sequence in which the fractions are obtained is: mitochondria, membrane vesicles, and ribosomes. Finally, the supernatant from the last centrifugation contains the cytosol with the cell’s soluble components, in addition to the buffer.

The isolation steps are carried out at low temperatures on principle (usually 0–5 °C), to slow down degradation reactions—e.g., due to released enzymes and other influencing factors. The addition of thiols and chelating agents protects functional SH groups from oxidation. Isolated cell organelles quickly lose their biological activity despite these precautions. Nevertheless, it is possible by working carefully to isolate mitochondria that will still take up substrates for a few hours in the test tube and produce ATP via oxidative phosphorylation.

B. Marker molecules

During cell fractionation, it is very important to analyze the purity of the fractions obtained. Whether or not the intended organelle is present in a particular fraction, and whether or not the fraction contains other components, can be determined by analyzing characteristic marker molecules. These are molecules that occur exclusively or predominately in one type of organelle. For example, the activity of organelle-specific enzymes (marker enzymes) is often assessed. The distribution of marker enzymes in the cell reflects the compartmentation of the processes they catalyze. These reactions are discussed in greater detail here under the specific organelles.
A. Isolation of cell organelles

1. Slice Tissue
2. Buffer
3. Potter homogenizer
4. Centrifuge

- **$g = 300,000$**
- **$g = 100,000$**
- **$g = 15,000$**
- **$g = 600$**

- **Cytosol**
- **Supernatant**
- **Pellets**

- **Ribosomes**
- **Viruses**
- **Macromolecules**

- **Golgi complex**
- **α-Mannosidase II**

- **Endoplasmic reticulum**
- **Glucose 6-phosphatase**
- **rRNA**

- **Mitochondrion**
- **Succinate dehydrogenase**
- **Cytochrome c oxidase**
- **1.9.3.7**

- **Peroxisome**
- **Catalase**
- **1.11.1.6**

- **Nucleus**
- **DNA**

- **Cytoskeleton**

- **Mitochondria**
- **Lysosomes**
- **Peroxisomes** (plants: chloroplasts)

- **Plasma membrane**

- **Ribosomes**
- **rRNA**

- **Microsomal fraction**

- **Whole cells, connective tissue**

**Cell fraction**

B. Marker molecules

- **Golgi complex**
- **α-Mannosidase II**

- **Endoplasmic reticulum**
- **Glucose 6-phosphatase**
- **rRNA**

- **Mitochondrion**
- **Succinate dehydrogenase**
- **Cytochrome c oxidase**
- **1.9.3.7**

- **Peroxisome**
- **Catalase**
- **1.11.1.6**

- **Nucleus**
- **DNA**

- **Cytoskeleton**

- **Mitochondria**
- **Lysosomes**
- **Peroxisomes** (plants: chloroplasts)

- **Plasma membrane**

- **Ribosomes**
- **rRNA**

- **Microsomal fraction**
Centrifugation

A. Principles of centrifugation

In a solution, particles whose density is higher than that of the solvent sink (sediment), and particles that are lighter than it float to the top. The greater the difference in density, the faster they move. If there is no difference in density (isopycnic conditions), the particles hover. To take advantage of even tiny differences in density to separate various particles in a solution, gravity can be replaced with the much more powerful "centrifugal force" provided by a centrifuge.

**Equipment.** The acceleration achieved by centrifugation is expressed as a multiple of the earth's gravitational force (g = 9.81 m s⁻²). Bench-top centrifuges can reach acceleration values of up to 15000 g, while high-speed refrigerated centrifuges can reach 500000 g and ultracentrifuges, which operate with refrigeration and in a vacuum, can reach 5000000 g. Two types of rotor are available in high-powered centrifuges: **fixed angle rotors** and **swingout rotors** that have movable bucket containers. The tubes or buckets used for centrifugation are made of plastic and have to be very precisely adjusted to avoid any imbalances that could lead to accidents.

**Theory.** The velocity (v) of particle sedimentation during centrifugation depends on the angular velocity (ω) of the rotor, its effective radius (rₑₑₑ, the distance from the axis of rotation), and the particle's sedimentation properties. These properties are expressed as the **sedimentation coefficient** S (1 Svedberg, = 10⁻¹³ s). The sedimentation coefficient depends on the mass M of the particle, its shape (expressed as the coefficient of friction, f), and its density (expressed as the reciprocal density v, "partial specific volume").

At the top right, the diagram shows the densities and sedimentation coefficients for biomolecules, cell organelles, and viruses. Proteins and protein-rich structures have densities of around 1.3 g cm⁻³, while nucleic acids show densities of up to 2 g cm⁻³. Equilibrium sedimentation of nucleic acids therefore requires high-density media—e.g., concentrated solutions of cesium chloride (CsCl).

To allow comparison of S values measured in different media, they are usually corrected to values for water at 20 °C ("S₂₀w").

B. Density gradient centrifugation

Density gradient centrifugation is used to separate macromolecules that differ only slightly in size or density. Two techniques are commonly used.

In **zonal centrifugation**, the sample being separated (e.g., a cell extract or cells) is placed on top of the centrifugation solution as a thin layer. During centrifugation, the particles move through the solution due to their greater density. The rate of movement basically depends on their molecular mass (see A, formulae). Centrifugation stops before the particles reach the bottom of the tube. Drilling a hole into the centrifugation tube and allowing the contents to drip out makes it possible to collect the different particles in separate fractions. During centrifugation, the solution tube is stabilized in the tube by a **density gradient**. This consists of solutions of carbohydrates or colloidal silica gel, the concentration of which increases from the surface of the tube to the bottom. Density gradients prevent the formation of convection currents, which would impair the separation of the particles.

**Isopycnic centrifugation**, which takes much longer, starts with a CsCl solution in which the sample material (e.g., DNA, RNA, or viruses) is homogeneously distributed. A density gradient only forms during centrifugation, as a result of sedimentation and diffusion processes. Each particle moves to the region corresponding to its own buoyant density. Centrifugation stops once equilibrium has been reached. The samples are obtained by fractionation, and their concentration is measured using the appropriate methods.

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A. Principles of centrifugation

Gravitational acceleration: \( g \)

Sedimentation velocity: \( v \) (cm \( \cdot \) s\(^{-1} \))

Angular velocity: \( \omega \) (rad \( \cdot \) s\(^{-1} \))

Effective radius: \( r_{\text{eff}} \) (cm)

\[
g = \omega^2 \cdot r_{\text{eff}}
\]

\[
v = \omega^2 \cdot r_{\text{eff}} \cdot S
\]

\[
s = \frac{M \cdot (1 - v \cdot r)}{f}
\]

\( s \): Sedimentation coefficient (\( S = 10^{-13} \) s

\( M \): Molecular mass

\( v \): Partial specific particle volume (cm\(^3\) \( \cdot \) g\(^{-1} \))

\( f \): Density of the solution (g \( \cdot \) cm\(^{-3} \))

\( r \): Coefficient of friction

B. Density gradient centrifugation

Particle migration according to S-value

Isopyknic centrifugation

Sucrose or CsCl density gradient

Concentration

Fraction

Detection

Fractionation

Zonal centrifugation

Particles distributed according to density

Centrifugation

Particulate sedimentation

Particle distribution

Centrifugation

Particles migrate according to S-value

Sucrose density gradient

After t = 0 0.5 1 2 h

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Cell components and cytoplasm

The Gram-negative bacterium *Escherichia coli* (*E. coli*) is a usually harmless symbiont in the intestine of mammals. The structure and characteristics of this organism have been particularly well characterized. *E. coli* is also frequently used in genetic engineering (see p. 258).

A. Components of a bacterial cell

A single *E. coli* cell has a volume of about 0.88 μm³. One-sixth of this consists of membranes and one-sixth is DNA (known as the “nucleoid”). The rest of the internal space of the cell is known as cytoplasm (not “cytosol”; see p. 198).

The main component of *E. coli*—as in all cells—is water (70%). The other components are macromolecules (proteins, nucleic acids, polysaccharides), small organic molecules, and inorganic ions. The majority of the macromolecules are proteins, which represent ca. 55% of the dry mass of the cell. When a number of assumptions are made about the distribution and size (average mass 40 kDa) of proteins, it can be estimated that there are approximately 250000 protein molecules in the cytoplasm of an *E. coli* cell. In eukaryotic cells, which are about a thousand times larger, it is estimated that the number of protein molecules is in the order of several billion.

B. Looking inside a bacterial cell

The illustration shows a schematic view inside the cytoplasm of *E. coli*, magnified approximately one million times. At this magnification, a single carbon atom would be the size of a grain of salt, and an ATP molecule would be as large as a grain of rice. The detail shown is 100 nm long, corresponding to about 1/600th of the volume of a cell in *E. coli*. To make the macromolecules clearer, small molecules such as water, cofactors, and metabolites have all been omitted from the illustration. The section of the cytoplasm shown contains:

- Several hundred macromolecules, which are needed for protein biosynthesis—i.e., 30 ribosomes, more than 100 protein fac-

tors, 30 aminoacyl-tRNA synthases, 340 tRNA molecules, 2–3 mRNAs (each of which is 10 times the length of the section shown), and six molecules of RNA polymerase.
- About 330 other enzyme molecules, including 130 glycolytic enzymes and 100 enzymes from the tricarboxylic acid cycle.
- 30000 small organic molecules with masses of 100–1000 Da—e.g., metabolites of the intermediary metabolism and coenzymes. These are shown at a magnification 10 times higher in the bottom right corner.
- And finally, 50000 inorganic ions. The rest consists of water.

The illustration shows that the cytoplasm of cells is a compartment densely packed with macromolecules and smaller organic molecules. The distances between organic molecules are small. They are only separated by a few water molecules.

All of the molecules are in motion. Due to constant collisions, however, they do not advance in a straight path but move in zigzags. Due to their large mass, proteins are particularly slow. However, they do cover an average of 3 nm in 1 ms—a distance approximately equal to their own length. Statistically, a protein is capable of reaching any point in a bacterial cell in less than a second.

C. Biochemical functions of the cytoplasm

In eukaryotes, the cytoplasm, representing slightly more than 50% of the cell volume, is the most important cellular compartment. It is the central reaction space of the cell. This is where many important pathways of the intermediary metabolism take place—e.g., glycolysis, the pentose phosphate pathway, the majority of gluconeogenesis, and fatty acid synthesis. Protein biosynthesis (translation; see p. 250) also takes place in the cytoplasm. By contrast, fatty acid degradation, the tricarboxylic acid cycle, and oxidative phosphorylation are located in the mitochondria (see p. 210).
A. Components of a bacterial cell

- Proteins (17%, 3,000)
- Water (70%, 1)
- RNA (8%)""
Cytoskeleton: components

The cytoplasm of eukaryotic cells is traversed by three-dimensional scaffolding structures consisting of filaments (long protein fibers), which together form the cytoskeleton. These filaments are divided into three groups, based on their diameters: microfilaments (6–8 nm), intermediate filaments (ca. 10 nm), and microtubules (ca. 25 nm). All of these filaments are polymers assembled from protein components.

A. Actin

Actin, the most abundant protein in eukaryotic cells, is the protein component of the microfilaments (actin filaments). Actin occurs in two forms—a monomolecular form (G actin, globular actin) and a polymer (F actin, filamentous actin). G actin is an asymmetrical molecule with a mass of 42 kDa, consisting of two domains. As the ionic strength increases, G actin aggregates reversibly to form F actin, a helical homopolymer. G actin carries a firmly bound ATP molecule that is slowly hydrolyzed in F actin to form ADP. Actin therefore also has enzyme properties (ATPase activity).

As individual G actin molecules are always oriented in the same direction relative to one another, F actin consequently has polarity. It has two different ends, at which polymerization takes place at different rates. If the ends are not stabilized by special proteins (as in muscle cells), then at a critical concentration of G actin the (+) end of F actin will constantly grow, while the (−) end simultaneously decays. These partial processes can be blocked by fungal toxins experimentally. Phalloidin, a toxin contained in the Amanita phalloides mushroom, inhibits decay by binding to the (−) end. By contrast, cytochalasins, mold toxins with cytostatic effects, block polymerization by binding to the (+) end.

Actin-associated proteins. The cytoplasm contains more than 50 different proteins that bind specifically to G actin and F actin. Their actin uptake has various different functions. This type of bonding can serve to regulate the G actin pool (example: profilin), influence the polymerization rate of G actin (villin), stabilize the chain ends of F actin (fuglin, β-actinin), attach filaments to one another or to other cell components (villin, α-actinin, spectrin), or disrupt the helical structure of F actin (gelonin). The activity of these proteins is regulated by protein kinases via Ca²⁺ and other second messengers (see p. 386).

B. Intermediate filaments

The components of the intermediate filaments belong to five related protein families. They are specific for particular cell types. Typical representatives include the cytokeratins, desmin, vimentin, glial fibrillary acidic protein (GFAP), and neurofilament. These proteins all have a rod-shaped basic structure in the center, which is known as a superhelix ("coiled coil"; see keratin, p. 70). The dimers are arranged in an antiparallel fashion to form tetramers. A staggered head-to-head arrangement produces protofilaments. Eight protofilaments ultimately form an intermediary filament.

Free protein monomers of intermediate filaments rarely occur in the cytoplasm, in contrast to microfilaments and microtubules. Their polymerization leads to stable polymers that have no polarity.

C. Tubulins

The basic components of the tube-shaped microtubules are α– and β-tubulin (53 and 55 kDa). These form αβ-heterodimers, which in turn polymerize to form linear protofilaments. Thirteen protofilaments form a ring-shaped complex, which then grows into a long tube as a result of further polymerization.

Like microfilaments, microtubules are dynamic structures with (+) and (−) ends. The (−) end is usually stabilized by bonding to the centrosome. The (+) end shows dynamic instability. It can either grow slowly or shorten rapidly, GTP, which is bound by the microtubules and gradually hydrolyzed into GDP, plays a role in this. Various proteins can also be associated with microtubules.
A. Actin

F-actin helical polymer microfilament (detail)

Phallolidin

(-) End: dissociation favored

Phallolidin

(+). End: polymerization favored

B. Intermediate filaments

Dimer

Tetramer

Protofilament

Intermediate filament

Superhelical structure

IF Proteins:
- Cytokeratins
- Desmin
- Vimentin
- Glial fibrillary acidic protein
- Neurofilaments
- Lamins

C. Tubulins

α β

Tubulin 53 and 55 kDa heterodimer

Microtubule (cylindrical polymer)

Plant alkaloids: Vinblastine, Vincristine, Colchicine

(-) End: stabilized by binding to the centromere

(+). End: grows or shortens

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Structure and functions

The cytoskeleton carries out three major tasks:

- It represents the cell's mechanical scaffold-
ing, which gives it its typical shape and
connects membranes and organelles to
each other. This scaffolding has dynamic
properties; it is constantly being synthe-
sized and broken down to meet the cell's
requirements and changing conditions.

- It acts as the motor for movement of animal
cells. Not only muscle cells (see p. 332), but
also cells of noncontractile tissues contain
many different motor proteins, which they
use to achieve coordinated and directed
movement. Cell movement, shape changes
during growth, cytoplasmic streaming, and
cell division are all made possible by com-
ponents of the cytoskeleton.

- It serves as a transport track within the cell.
Organelles and other large protein com-
plexes can move along the filaments with
the help of the motor proteins.

A. Microfilaments and intermediate
filaments

The illustration schematically shows a detail
of the microvilli of an intestinal epithelial cell
as an example of the structure and function of
the components of the cytoskeleton (see also
CT).

Microfilaments of F actin traverse the mi-
crovilli in ordered bundles. The microfila-
ments are attached to each other by actin-as-
associated proteins, particularly fimbrin and vil-
lin. Calmodulin and a myosin-like ATPase con-
nect the microfilaments laterally to the
plasma membrane. Fodrin, another microfila-
ment-associated protein, anchors the actin
fibers to each other at the base, as well as
attaching them to the cytoplasmic membrane
and to a network of intermediate filaments. In
this example, the microfilaments have a
mainly static function. In other cases, actin is
also involved in dynamic processes. These in-
clude muscle contraction (see p. 332), cell
movement, phagocytosis by immune cells,
the formation of microspikes and lamellipo-
dia (cellular extensions), and the acrosomal
process during the fusion of sperm with the
egg cell.

B. Microtubules

Only the cell's microtubules are shown here.
They radiate out in all directions from a center
near the nucleus, the centrosome. The tube-
shaped microtubules are constantly being
synthesized and broken down at their (+) ends.
In the centriole, the (-) end is blocked
by associated proteins (see p. 204). The (+) end
can also be stabilized by associated pro-
teins—e.g., when the microtubules have
reached the cytoplasmic membrane.

The microtubules are involved in defining
the shape of the cell and also serve as guiding
tracks for the transport of organelles. To-
gether with associated proteins (dynein, kine-
sin), microtubules are able to carry out me-
chanical work—e.g., during the transport of
mitochondria, the movement of cilia (hair-
like cell protrusions in the lungs, intestinal
epithelium, and oviduct) and the beating of
the flagella of sperm. Microtubules also play a
special role in the mitotic period of cell divi-
sion (see p. 394).

C. Architecture

The complex structure and net-like density of
the cytoskeleton is illustrated here using
three examples in which the cytoskeletal
components are visualized with the help of
antibodies.

1. The border of an intestinal epithelial cell
is seen here (see also B). There are micro-
filaments (a) passing from the interior of the
cell out into the microvilli. The filaments are
firmly held together by spectrin (b), an asso-
ciated protein, and they are anchored to in-
termediate filaments (c).

2. Only microtubules are seen in this fibro-
blast cell. They originate from the microtubule
organizing center (centrosome) and radiate
out as far as the plasma membrane.

3. Keratin filaments are visible here in an
epithelial cell. Keratin fibers belong to the
group of intermediate filaments (see pp. 70,
204; d = nucleus).
A. Microfilaments and intermediate filaments

B. Microtubules

C. Architecture
Nucleus

A. Nucleus

The nucleus is the largest organelle in the eukaryotic cell. With a diameter of about 10 μm, it is easily recognizable with the light microscope. This is the location for storage, replication, and expression of genetic information.

The nucleus is separated from the cytoplasm by the nuclear envelope, which consists of the outer and inner nuclear membranes. Each of the two nuclear membranes has two layers, and the membranes are separated from each other by the perinuclear space. The outer nuclear membrane is continuous with the rough endoplasmic reticulum and is covered with ribosomes. The inner side of the membrane is covered with a protein layer (the nuclear lamina), in which the nuclear structures are anchored.

The nucleus contains almost all of the cell’s DNA (around 1% of which is mitochondrial DNA). Together with histones and structural proteins, the nuclear DNA forms the chromatin (see p. 238). It is only during cell division that chromatin condenses into chromosomes, which are also visible with the light microscope. During this phase, the nuclear membrane temporarily disintegrates.

During the phase between cell divisions, the interphase, it is possible to distinguish between the more densely packed heterochromatin and loose euchromatin using an electron microscope. Active transcription of DNA into mRNA takes place in the region of the euchromatin. A particularly electron-dense region is noticeable in many nuclei—the nucleolus (several nucleoli are sometimes present). The DNA in the nucleolus contains numerous copies of the genes for rRNAs (see p. 242). They are constantly undergoing transcription, leading to a high local concentration of RNA.

B. Nuclear pores

The exchange of substances between the nucleus and the cytoplasm is mediated by pore complexes with complicated structures, which traverse the nuclear membrane. The nuclear pores consist of numerous proteins that form several connected rings of varying diameter. Low-molecular structures and small proteins can enter the nucleus without difficulty. By contrast, larger proteins (over 40 kDa) can only pass through the nuclear pores if they carry a nuclear localization sequence consisting of four successive basic amino acids inside their peptide chains (see p. 228). mRNAs and tRNAs formed in the nucleus cross the pores into the cytoplasm as complexes with proteins (see below).

C. Relationships between the nucleus and cytoplasm

Almost all of the RNA in the cell is synthesized in the nucleus. In this process, known as transcription, the information stored in DNA is transcribed into RNA (see p. 242). As mentioned above, ribosomal RNA (rRNA) is mainly produced in the nucleolus, while messenger and transfer RNA (mRNA and tRNA) are formed in the region of the euchromatin. Enzymatic duplication of DNA—replication—also only takes place in the nucleus (see p. 240).

The nucleotide components required for transcription and replication have to be imported into the nucleus from the cytoplasm. Incorporation of these components into RNA leads to primary products, which are then altered by cleavage, excision of introns, and the addition of extra nucleotides (RNA maturation; see p. 242). It is only once these processes have been completed that the RNA molecules formed in the nucleus can be exported into the cytoplasm for protein synthesis (translation; see p. 250).

The nucleus is not capable of synthesizing proteins. All of the nuclear proteins therefore have to be imported—the histones with which DNA is associated in chromatin, and also the so-called non-histone proteins (DNA polymerases and RNA polymerases, auxiliary and structural proteins, transcription factors, and ribosomal proteins). Ribosomal RNA (rRNA) already associates with proteins in the nucleolus to form ribosome precursors.

A special metabolic task carried out by the nucleus is biosynthesis of NAD⁺. The immediate precursor of this coenzyme, nicotinamide mononucleotide (NMN⁺), arises in the cytoplasm and is then transported into the nucleolus, where it is enzymatically converted into the dinucleotide NAD⁺. Finally, NAD⁺ then returns to the cytoplasm.
Structure and functions

A. Mitochondrial structure

Mitochondria are bacteria-sized organelles (about 1 × 2 μm in size), which are found in large numbers in almost all eukaryotic cells. Typically, there are about 2000 mitochondria per cell, representing around 25% of the cell volume. Mitochondria are enclosed by two membranes—a smooth outer membrane and a markedly folded or tubular inner mitochondrial membrane, which has a large surface and encloses the matrix space. The folds of the inner membrane are known as cristae, and tube-like protrusions are called tubules. The intermembrane space is located between the inner and the outer membranes.

The number and shape of the mitochondria, as well as the numbers of cristae they have, can differ widely from cell type to cell type. Tissues with intensive oxidative metabolism—e.g., heart muscle—have mitochondria with particularly large numbers of cristae. Even within one type of tissue, the shape of the mitochondria can vary depending on their functional status. Mitochondria are mobile, pliable organelles.

Mitochondria probably developed during an early phase of evolution from aerobic bacteria that entered into symbiosis with prot-eval anaerobic eukaryotes. This endosymbiotic theory is supported by many findings. For example, mitochondria have a ring-shaped DNA (four molecules per mitochondrion) and have their own ribosomes. The mitochondrial genome became smaller and smaller during the course of evolution. In humans, it still contains 16 569 base pairs, which code for two rRNAs, 22 tRNAs, and 13 proteins. Only these 13 proteins (mostly subunits of respiratory chain complexes) are produced in the mitochondrion. All of the other mitochondrial proteins are coded by the nuclear genome and have to be imported into the mitochondria after translation in the cytoplasm (see p. 228). The mitochondrial envelope consisting of two membranes also supports the endosymbiotic theory. The inner membrane, derived from the former symbiont, has a structure reminiscent of prokaryotes. It contains the unusual lipid cardiolipin (see p. 50), but hardly any cholesterol (see p. 216).

Both mitochondrial membranes are very rich in proteins. Porins (see p. 214) in the outer membrane allow small molecules (< 10 kDa) to be exchanged between the cytoplasm and the intermembrane space. By contrast, the inner mitochondrial membrane is completely impermeable even to small molecules (with the exception of O₂, CO₂, and H₂O). Numerous transporters in the inner membrane ensure the import and export of important metabolites (see p. 212). The inner membrane also transports respiratory chain complexes, ATP synthase, and other enzymes. The matrix is also rich in enzymes (see B).

B. Metabolic functions

Mitochondria are also described as being the cell’s biochemical powerhouse, since—through oxidative phosphorylation (see p. 112)—they produce the majority of cellular ATP. Pyruvate dehydrogenase (PDH), the tricarboxylic acid cycle, β-oxidation of fatty acids, and parts of the urea cycle are located in the matrix. The respiratory chain, ATP synthesis, and enzymes involved in heme biosynthesis (see p. 192) are associated with the inner membrane.

The inner membrane itself plays an important part in oxidative phosphorylation. As it is impermeable to protons, the respiratory chain—which pumps protons from the matrix into the intermembrane space via complexes I, III, and IV—establishes a proton gradient across the inner membrane, in which the chemical energy released during NADH oxidation is conserved (see p. 126). ATP synthase then uses the energy stored in the gradient to form ATP from ADP and inorganic phosphate. Several of the transport systems are also dependent on the H⁺ gradient.

In addition to the endoplasmic reticulum, the mitochondria also function as an intracellular calcium reservoir. The mitochondria also play an important role in “programmed cell death”—apoptosis (see p. 396).
A. Mitochondrial structure

2 µm
NH₃
HCO₃
CO₂
H₂O
O₂
ATP
N A
A
P P P
A
P P P
H + H + H +
P P
A
P
H +
H +
–
Ca²⁺
Ca²⁺
ETF
P

B. Metabolic functions

Pyruvate
Acyl CoA
Carnitine shuttle
Inter-membrane space

Cytoplasmic calcium ions
Pyrurate
Acetyl CoA
β-Oxidation
Urea cycle

ATP synthesis

O₂

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Transport systems

Mitochondria are surrounded by an inner and an outer membrane (see p. 210). The outer membrane contains porins, which allow smaller molecules up to 10 kDa in size to pass. By contrast, the inner membrane is also impermeable to small molecules (with the exception of water and the gases O₂, CO₂, and NH₃). All of the other substrates of mitochondrial metabolism, as well as its products, therefore have to be moved through the inner membrane with the help of special transporters.

A. Transport systems

The transport systems of the inner mitochondrial membrane use various mechanisms. Metabolites or ions can be transported alone (uniport, U), together with a second substance (symport, S), or in exchange for another molecule (antiport, A). Active transport—i.e., transport coupled to ATP hydrolysis—does not play an important role in mitochondria. The driving force is usually the proton gradient across the inner membrane (blue star) or the general membrane potential (red star; see p. 126).

The pyruvate (left) formed by glycolysis in the cytoplasm is imported into the matrix in antiport with OH⁻. The OH⁻ ions react in the intermembrane space with the H⁺ ions abundantly present there to form H₂O. This maintains a concentration gradient of OH⁻. The import of phosphate (H₃PO₄) is driven in a similar way. The exchange of the ATP formed in the mitochondrial for ADP via an adenine nucleotide translocase (center) is also dependent on the H⁺ gradient. ATP with a quadruple negative charge is exchanged for ADP with a triple negative charge, so that overall one negative charge is transported into the H⁺-rich intermembrane space. The import of malate by the tri carbonylate transporter, which is important for the malate shuttle (see B) is coupled to the export of citrate, with a net export of one negative charge to the exterior again. In the opposite direction, malate can leave the matrix in antiport for phosphate. When Ca²⁺ is imported (right), the metal cation follows the membrane potential. An electron-neutral antiport for two H⁺ or two Na⁺ serves for Ca²⁺ export.

B. Malate and glycerophosphate shuttles

Two systems known as “shuttles” are available to allow the import of reducing equivalents that arise from glycolysis in the cytoplasm in the form of NADH⁺H⁺. There is no transporter in the inner membrane for NADH⁺H⁺ itself.

In the malate shuttle (left)—which operates in the heart, liver, and kidneys, for example—oxaloacetic acid is reduced to malate by malate dehydrogenase (MDH, [2a]) with the help of NADH⁺H⁺. In antiport for 2-oxogluta rate, malate is transferred to the matrix, where the mitochondrial isoenzyme for MDH [2b] regenerates oxaloacetic acid and NADH⁺H⁺. The latter is reoxidized by complex I of the respiratory chain, while oxaloacetic acid, for which a transporter is not available in the inner membrane, is first transaminated to aspartate by aspartate aminotransferase (AST, [3a]). Aspartate leaves the matrix again, and in the cytoplasm once again supplies oxaloacetate for step [2a] and glutamate for return transport into the matrix [3b]. On balance, only NADH⁺H⁺ is moved from the cytoplasm into the matrix; ATP is not needed for this.

The glycerophosphate shuttle (right) was discovered in insect muscle, but is also active in the skeletal musculature and brain in higher animals. In this shuttle, NADH⁺H⁺ formed in the cytoplasm is used to reduce glycero 3-phosphate, an intermediate of glycolysis (see p. 150) to glycerol 3-phos phate. Via porins, this enters the intermembrane space and is oxidized again there on the exterior side of the inner membrane by the flavin enzyme glycerol 3-phosphate dehydrogenase back into glycero 3-phosphate. The reducing equivalents are passed on to the respiratory chain via ubiquinone (coenzyme Q).

The carnitine shuttle for transporting acyl residues into the mitochondrial matrix is dis cussed on p. 164.
**A. Transport systems**

Driving force: Membrane potential

Proton gradient

H₂O

H₂O

Ca²⁺

Ca²⁺

HPO₄²⁻

HPO₄²⁻

Malate shuttle

2-Oxoglutarate/citrate

ADP

ADP

O₂

O₂

NADH + H⁺

NADH + H⁺

Complex I

Complex III

Ubiquinone

Complex IV

H₂O

1,3-Bisphosphoglycerate

Glycerophosphate shuttle

Glyceraldehyde 3-phosphate dehydrogenase 1.1.1.37

Glucose 6-phosphate

Fructose 1,6-bisphosphate

Glyceraldehyde 3-phosphate dehydrogenase 1.1.1.8

Aspartate transaminase 2.6.1.1

Glycerol 3-phosphate dehydrogenase 1.1.1.8

Glyceraldehyde 3-phosphate DH (FAD) 1.1.99.5

B. Malate and glycerophosphate shuttle

Cytoplasm

Mitochondrial membrane

Matrix

Glu

Asp

Malate shuttle

2-Oxoglutarate

Oxaloacetate

2-Oxoglutarate

Malate

Glycerol 3-phosphate

Glycerol 3-phosphate DH (FAD) 1.1.99.5

Glycerol 3-phosphate dehydrogenase 1.1.1.8
Structure and components

A. Structure of the plasma membrane

All biological membranes are constructed according to a standard pattern. They consist of a continuous bilayer of amphipathic lipids approximately 5 nm thick, into which proteins are embedded. In addition, some membranes also carry carbohydrates (mono- and oligo-saccharides) on their exterior, which are bound to lipids and proteins. The proportions of lipids, proteins, and carbohydrates differ markedly depending on the type of cell and membrane (see p. 216).

Membrane lipids are strongly amphipathic molecules with a polar hydrophilic “head group” and an apolar hydrophobic “tail.” In membranes, they are primarily held together by the hydrophobic effect (see p. 28) and weak Van der Waals forces, and are therefore mobile relative to each other. This gives membranes a more or less fluid quality.

The fluidity of membranes primarily depends on their lipid composition and on temperature. At a specific transition temperature, membranes pass from a semicrystalline state to a more fluid state. The double bonds in the alky chains of unsaturated acyl residues in the membrane lipids disturb the semicrystalline state. The higher the proportion of unsaturated lipids present, therefore, the lower the transition temperature. The cholesterol content also influences membrane fluidity. While cholesterol increases the fluidity of semicrystalline, closely-packed membranes, it stabilizes fluid membranes that contain a high proportion of unsaturated lipids.

Like lipids, proteins are also mobile within the membrane. If they are not fixed in place by special mechanisms, they float within the lipid layer as if in a two-dimensional liquid; biological membranes are therefore also described as being a “fluid mosaic.”

Lipids and proteins can shift easily within one layer of a membrane, but switching between the two layers (“flip/flop”) is not possible for proteins and is only possible with difficulty for lipids (with the exception of cholesterol). To move to the other side, phospholipids require special auxiliary proteins (translocators, “flipases”).

B. Membrane lipids

The illustration shows a model of a small section of a membrane. The phospholipids are the most important group of membrane lipids. They include phosphatidylcholine (lecithin), phosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, and sphingomyelin (for their structures, see p. 50). In addition, membranes in animal cells also contain cholesterol (with the exception of inner mitochondrial membranes). Glycolipids (a ganglioside is shown here) are mainly found on the outside of the plasma membrane. Together with the glycoproteins, they form the exterior coating of the cell (the glycoalyx).

C. Membrane proteins

Proteins can be anchored in or on membranes in various ways. Integral membrane proteins cross right through the lipid bilayer. The sections of the peptide chains that lie within the bilayer usually consist of 20 to 25 mainly hydrophobic amino acid residues that form a right-handed α-helix.

Type I and II membrane proteins only contain one transmembrane helix of this type, while type III proteins contain several. Rarely, type I and II polypeptides can aggregate to form a type IV transmembrane protein. Several groups of integral membrane proteins—e.g., the porins (see p. 212)—penetrate the membrane with antiparallel β-sheet structures. Due to its shape, this tertiary structure is known as a “β-barrel.”

Type V and VI proteins carry lipid anchors. These are fatty acids (palmitic acid, myristic acid), isoprenoids (e.g., farnesol), or glycolipids such as glycosyl phosphatidylinositol (GPI) that are covalently bound to the peptide chain.

Peripheral membrane proteins are associated with the head groups of phospholipids or with another integral membrane protein (not shown).
A. Structure of the plasma membrane

B. Membrane lipids

C. Membrane proteins

1. α-Helical
2. β-Barrel

Polar
Apolar
Outer leaflet
Inner leaflet
Lipid bilayer

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Functions and composition

The most important membranes in animal cells are the plasma membrane, the inner and outer nuclear membranes, the membranes of the endoplasmic reticulum (ER) and the Golgi apparatus, and the inner and outer mitochondrial membranes. Lysosomes, peroxisomes, and various vesicles are also separated from the cytoplasm by membranes. In plants, additional membranes are seen in the plastids and vacuoles. All membranes show polarity—i.e., there is a difference in the composition of the inner layer (facing toward the cytoplasm) and the outer layer (facing away from it).

A. Functions of membranes

Membranes and their components have the following functions:

1. Enclosure and insulation of cells and organelles. The enclosure provided by the plasma membrane protects cells from their environment both mechanically and chemically. The plasma membrane is essential for maintaining differences in the concentration of many substances between the intracellular and extracellular compartments.

2. Regulated transport of substances, which determines the internal milieu and is a precondition for homeostasis—i.e., the maintenance of constant concentrations of substances and physiological parameters. Regulated and selective transport of substances through pores, channels, and transporters (see p. 218) is necessary because the cells and organelles are enclosed by membrane systems.

3. Reception of extracellular signals and transfer of these signals to the inside of the cell (see pp. 384ff.), as well as the production of signals.

4. Enzymatic catalysis of reactions. Important enzymes are located in membranes at the interface between the lipid and aqueous phases. This is where reactions with apolar substrates occur. Examples include lipid biosynthesis (see p. 170) and the metabolism of apolar xenobiotics (see p. 316). The most important reactions in energy conversion—i.e., oxidative phosphorylation (see p. 140) and photosynthesis (see p. 128)—also occur in membranes.

5. Interactions with other cells for the purposes of cell fusion and tissue formation, as well as communication with the extracellular matrix.

6. Anchoring of the cytoskeleton (see p. 204) to maintain the shape of cells and organelles and to provide the basis for movement processes.

B. Composition of membranes

Biological membranes consist of lipids, proteins, and carbohydrates (see p. 214). These components occur in varying proportions (left). Proteins usually account for the largest proportion, at around half. By contrast, carbohydrates, which are only found on the side facing away from the cytoplasm, make up only a few percent. An extreme composition is seen in myelin, the insulating material in nerve cells, three-quarters of which consists of lipids. By contrast, the inner mitochondrial membrane is characterized by a very low proportion of lipids and a particularly high proportion of proteins.

When the individual proportions of lipids in membranes are examined more closely (right part of the illustration), typical patterns for particular cells and tissues are also found. The illustration shows the diversity of the membrane lipids and their approximate quantitative composition. Phospholipids are predominant in membrane lipids in comparison with glycolipids and cholesterol. Triacylglycerols (neutral fats) are not found in membranes.

Cholesterol is found almost exclusively in eukaryotic cells. Animal membranes contain substantially more cholesterol than plant membranes, in which cholesterol is usually replaced by other sterols. There is no cholesterol at all in prokaryotes (with a few exceptions). The inner mitochondrial membrane of eukaryotes is also low in cholesterol, while it is the only membrane that contains large amounts of cardiolipin. These facts both support the endosymbiotic theory of the development of mitochondria (see p. 210).
A. Functions of membranes

B. Composition of membranes

Membrane components

Relative proportion of lipids

Nerve cell: Plasma membrane

Erythrocyte: Plasma membrane

Liver cell: Plasma membrane

Mitochondrion

Cardiolipin

Inner membrane

Both membranes

Lipids
Carbohydrates
Proteins
Phospholipids
Phosphatidylcholine
Phosphatidylethanolamine
Phosphatidylserine
Sphingomyelin
Glycolipids
Cholesterol
Other lipids

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Transport processes

A. Permeability

Only small, uncharged molecules such as gases, water, ammonia, glycerol, or urea are able to pass through biological membranes by free diffusion. With increasing size, even compounds of this type are no longer able to pass through. Membranes are impermeable to glucose and other sugars, for example.

The polarity of a molecule is also important. Apolar substances, such as benzene, ethanol, diethyl ether, and many narcotic agents are able to enter biological membranes easily. By contrast, membranes are impermeable to strongly polar compounds, particularly those that are electrically charged. To be able to take up or release molecules of this type, cells have specialized channels and transporters in their membranes (see below).

B. Passive and active transport

Free diffusion is the simplest form of membrane transport. When it is supported by integral membrane proteins, it is known as facilitated diffusion (or facilitated transport).

1. Channel proteins have a polar pore through which ions and other hydrophilic compounds can pass. For example, there are channels that allow selected ions to pass (ion channels; see p. 222) and porins that allow molecules below a specific size to pass in a more or less nonspecific fashion (see p. 212).

2. Transporters recognize and bind the molecules to be transported and help them to pass through the membrane as a result of a conformational change. These proteins (permeases) are thus comparable with enzymes—although with the difference that they "catalyze" vectorial transport rather than an enzymatic reaction. Like enzymes, they show a certain affinity for each molecule transported (expressed as the dissociation constant, \( K_d \) in \( \text{mol} \cdot L^{-1} \)) and a maximum transport capacity (\( V \)).

Free diffusion and transport processes facilitated by ion channels and transport proteins always follow a concentration gradient—i.e., the direction of transport is from the site of higher concentration to the site of lower concentration. In ions, the membrane potential also plays a role; the processes are summed up by the term "electrochemical gradient" (see p. 126). These processes therefore involve passive transport, which runs "downhill" on the slope of a gradient.

By contrast, active transport can also run "uphill"—i.e., against a concentration or charge gradient. It therefore requires an input of energy, which is usually supplied by the hydrolysis of ATP (see p. 124). The transporter first binds its "cargo" on one side of the membrane. ATP-dependent phosphorylation then causes a conformational change that releases the cargo on the other side of the membrane (see p. 220). A non-spontaneous transport process can also take place through coupling to another active transport process (known as secondary active transport; see p. 220).

Using the transport systems in the membranes, cells regulate their volume, internal pH value, and ionic environment. They concentrate metabolites that are important for energy metabolism and biosynthesis, and exclude toxic substances. Transport systems also serve to establish ion gradients, which are required for oxidative phosphorylation and stimulation of muscle and nerve cells, for example (see p. 350).

C. Transport processes

Another classification of transport processes is based on the number of particles transported and the direction in which they move. When a single molecule or ion passes through the membrane with the help of a channel or transporter, the process is described as a uniport (example: the transport of glucose into liver cells). Simultaneous transport of two different particles can take place either as a symport (example: the transport of amino acids or glucose together with \( \text{Na}^+ \) ions into intestinal epithelial cells) or as an antiport. Ions are often transported in an antiport in exchange for another similarly charged ion. This process is electroneutral and therefore more energetically favorable (example: the exchange of \( \text{HCO}_3^- \) for \( \text{Cl}^- \) at the erythrocyte membrane).
### A. Permeability of membranes

- **Small molecules**
  - Apolar: \( \text{O}_2, \text{N}_2 \)
  - Polar, uncharged: \( \text{H}_2\text{O}, \text{Urea}, \text{Glycerol}, \text{CO}_2, \text{N}_2\text{O} \)

- **Large molecules**
  - Polar, uncharged: e.g., glucose

- **Ions**
  - \( \text{H}^+, \text{Na}^+, \text{K}^+, \text{Mg}^{2+}, \text{Ca}^{2+}, \text{NH}_4^+ \)
  - \( \text{HCO}_3^-, \text{CO}_3^{2-}, \text{H}_2\text{PO}_4^- \)

- **Amino acids**
- **Nucleotides**

- **Free diffusion**
- **Facilitated diffusion**
- **No membrane passage**

### B. Passive and active transport

- **Electrochemical gradient**
- **Charge gradient**

- **Low**
- **No**

- **High**

- **Pore**
  - Channel protein
  - Free diffusion

- **Facilitated diffusion**

- **Transporter**
  - Conformational change

- **Active transport**

### C. Transport processes

- **Uniport**
  - Glucose
  - Na

- **Symport**
  - \( \text{CF}^+ \)
  - \( \text{HCO}_3^- \)

- **Antiport**
  - \( \text{CF}^+ \)
  - \( \text{HCO}_3^- \)
Transport proteins

Illustrations B–D show transporters whose structure has been determined experimentally or established on analogy with other known structures. They all belong to group III of the α-helical transmembrane proteins (see p. 214).

A. Transport mechanisms

Some cells couple the “pure” transport forms discussed on p. 218—i.e., passive transport (1) and active transport (2)—and use this mechanism to take up metabolites. In secondary active transport (3), which is used for example by epithelial cells in the small intestine and kidney to take up glucose and amino acids, there is a symport (5) located on the luminal side of the membrane, which takes up the metabolite M together with an Na⁺ ion. An ATP-dependent Na⁺ transporter (Na⁺/K⁺ ATPase; see p. 350) on the other side keeps the intracellular Na⁺ concentration low and thus indirectly drives the uptake of M. Finally, a uniport (U) releases M into the blood.

B. Glucose transporter Glut-1

The glucose transporters (Glut) are a family of related membrane proteins with varying distribution in the organs. Glut-1 and Glut-3 have a relatively high affinity for glucose (Kₘ ≈ 1 mM). They occur in nearly all cells, and ensure continuous glucose uptake. Glut-2 is found in the liver and pancreas. This form has a lower affinity (Kₘ = 15–20 mM). The rate of glucose uptake by Glut-2 is therefore strongly dependent on the blood glucose level (normally 4–8 mM). Transport by Glut-4 (Kₘ = 5 mM), which is mainly expressed in muscle and fat cells, is controlled by insulin, which increases the number of transporters on the cell surface (see p. 388). Glut-5 mediates secondary active resorption of glucose in the intestines and kidney (see A).

Glut-1 consists of a single peptide chain that spans the membrane with 12 α-helices of different lengths. The glucose is bound by the peptide loops that project on each side of the membrane.

C. Aquaporin-1

Aquaporins help water to pass through biological membranes. They form hydrophilic pores that allow H₂O molecules, but not hydrated ions or larger molecules, to pass through. Aquaporins are particularly important in the kidney, where they promote the reuptake of water (see p. 328). Aquaporin-2 in the renal collecting ducts is regulated by antidiuretic hormone (ADH, vasopressin), which via cAMP leads to shifting of the channels from the ER into the plasma membrane. Aquaporin-1, shown here, occurs in the proximal tubule and in Henle’s loop. It contains eight transmembrane helices with different lengths and orientations. The yellow-colored residues form a narrowing that only H₂O molecules can overcome.

D. Sarcoplasmic Ca²⁺ pump

Transport ATPases transport cations—they are “ion pumps.” ATPases of the F type—e.g., mitochondrial ATP synthase (see p. 142)—use H⁺ transport for ATP synthesis. Enzymes of the V type, using up ATP, “pump” protons into lysosomes and other acidic cell compartments (see p. 234). P type transport ATPases are particularly numerous. These are ATP-driven cation transporters that undergo covalent phosphorylation during the transport cycle.

The Ca²⁺ ATPase shown also belongs to the P type. In muscle, its task is to pump the Ca²⁺ released into the cytoplasm to trigger muscle contraction back into the sarcoplasmic reticulum (SR; see p. 334). The molecule (1) consists of a single peptide chain that is folded into various domains. In the transmembrane part, which is formed by numerous α-helices, there are binding sites for two Ca²⁺ ions (blue) ATP is bound to the cytoplasmic N domain (green). Four different stages can be distinguished in the enzyme’s catalytic cycle (2). First, binding of ATP to the N domain leads to the uptake of two Ca²⁺ into the transmembrane part (a). Phosphorylation of an aspartate residue in the P domain (b) and dissociation of ADP then causes a conformation change that releases the Ca²⁺ ions into the SR (c). Finally, dephosphorylation of the aspartate residue restores the initial conditions (d).
A. Transport mechanisms

1. Facilitated diffusion
2. Active transport
3. Secondary active transport

B. Glucose transporter Glut-1

Blood
Plasma membrane
Cytoplasm
Glucose

C. Aquaporin-1

Tubular lumen
Plasma membrane
Tubule cell

D. Sarcoplasmic Ca^{2+}pump

Binding site for ATP
Cytoplasm
“stalk”
Binding sites for Ca^{2+}
Transmembrane domain

1. Structure
2. Catalytic cycle

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Ion channels

Ion channels facilitate the diffusion of ions through biological membranes. Some ion channels open and close depending on the membrane potential ([voltage-gated channels, A] or in response to specific ligands [ligand-gated channels, B]. Other channels operate passively. In these cases, transport depends only on the concentration gradient (C).

A. Voltage-gated Na⁺ channel

Voltage-gated Na⁺ channels play a decisive part in the conduction of electrical impulses in the nervous system (see p. 350). These channels open when the membrane potential in their environment reverses. Due to the high equilibrium potential for Na⁺ (see p. 126), an inflow of Na⁺ ions takes place, resulting in local depolarization of the membrane, which propagates by activation of neighboring voltage-dependent Na⁺ channels. A spreading depolarization wave of this type is known as an action potential (see p. 350). Externally directed K⁺ channels are involved in the repolarization of the membrane. In their functioning, these resemble the much more simply structured K⁺ channels shown in C. The Ca²⁺ channels that trigger exocytosis of vesicles (see p. 228) are also controlled by the action potential.

The voltage-gated Na⁺ channels in higher animals are large complexes made up of several subunits. The α-subunit shown here mediates Na⁺ transport. It consists of a very long peptide chain (around 2000 amino acid residues), which is folded into four domains, each with six transmembrane helices (left). The 56 helices of all the domains (blue) together form a centrally located hydrophilic pore which can be made narrow or wide depending on the channel’s functional status. The six 54 helices (green) function as voltage sensors.

The current conception of the way in which the opening and closing mechanism functions is shown in a highly simplified form on the right. For the sake of clarity, only one of the four domains (domain IV) is shown. The 54 helices contain several positively charged residues. When the membrane is polarized (α), the surplus negative charges on the inner side keep the helix in the membrane. If this attraction is removed as a result of local depolarization, the 54 helices are thought to snap upwards like springs and thus open the central pore (b).

B. Nicotinic acetylcholine receptor

Many receptors for neurotransmitters function as ligand-gated channels for Na⁺, K⁺ and/or Ca²⁺ ions (see p. 354). The ones that have been studied in the greatest detail are the nicotinic receptors for acetylcholine (see p. 352). These consist of five separate but structurally closely related subunits. Each forms four transmembrane helices, the second of which is involved in the central pore in each case. The type of monomer and its arrangement in the complex is not identical in all receptors of this type. In the neuromuscular junction (see p. 334), the arrangement of α is found (1).

In the interior of the structure, acetylcholine binds to the two α-subunits and thus opens the pore for a short time (1–2 ms). Negatively charged residues are arranged in three groups in a ring shape inside it. They are responsible for the receptor’s ion specificity. It is thought that binding of the neurotransmitter changes the position of the subunits in such a way that the pore expands (3). The bound acetylcholine dissociates again and is hydrolytically inactivated (see p. 356). The receptor is thus able to function again.

C. K⁺ channel in Streptomyces lividans

The only detailed structures of ion channels established so far are those of potassium channels like that of an outwardly directed K⁺ channel in the bacterium Streptomyces lividans. It consists of four identical subunits (blue, yellow, green, and red), each of which contains two long α-helices and one shorter one. In the interior of the cell (bottom), the K⁺ ions (violet) enter the structure’s central channel. Before they are released to the outside, they have to pass through what is known as a “selectivity filter.” In this part of the channel, several C=O groups in the peptide chain form a precisely defined opening that is only permeable to non-hydrated K⁺ ions.
A. Voltage-gated Na\textsuperscript{+} channel

1. Structure

- Voltage-sensitive helix (helix 4)
- Membrane polarized, helix 4 in position 1
- Membrane depolarized, helix 4 in position 2

2. Mechanism

B. Nicotinic acetylcholine receptor

1. Structure

- Subunits

2. Pore

- Acetylcholine

3. Mechanism

C. K\textsuperscript{+} channel in Streptomyces lividans

- Membrane
- Homotetramer

- Narrow pore
- Wide pore

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Membrane receptors

To receive and pass on chemical or physical signals, cells are equipped with receptor proteins. Many of these are integral membrane proteins in the plasma membrane, where they receive signals from their surroundings. Other receptor proteins are located in intercellular membranes. The receptors for lipophilic hormones are among the few that function in a soluble form. They regulate gene transcription in the nucleus (see p. 378).

A. Principle of receptor action

Membrane-located receptors can be divided into three parts, which have different tasks. The receptor domain reacts specifically to a given signal. Signals of this type can be of a purely physical nature. For example, many organisms react to light. In this way, plants adapt growth and photosynthesis to light conditions, while animals need light receptors for visual processing (C, see p. 358). Mechanoreceptors are involved in hearing and in pressure regulation, among other things. Channels that react to action potentials (see p. 350) can be regarded as receptors for electrical impulses.

However, most receptors do not react to physical stimuli, but rather to signal molecules. Receptors for these chemical signals contain binding sites in the receptor domain that are complementary to each ligand. In this respect, they resemble enzymes (see p. 94). As the effector domain of the receptor is usually separated by a membrane, a mechanism for signal transfer between the domains is needed. Little is yet known regarding this. It is thought that conformation changes in the receptor protein play a decisive part. Some receptors dimerize after binding of the ligand, thereby bringing the effector domains of two molecules into contact (see p. 392).

The way in which the effector works differs from case to case. By binding or interconversion, many receptors activate special mediator proteins, which then trigger a signal cascade (signal transduction; see p. 384). Other receptors function as ion channels. This is particularly widespread in receptors for neurotransmitters (see p. 354).

B. Insulin receptor

The receptor for the hormone insulin (see p. 76) belongs to the family of 1-helix receptors.

These molecules span the membrane with only one α-helix. The subunits of the dimeric receptor (red and blue) each consist of two polypeptides (α and β) bound by disulfide bonds. The α-chains together bind the insulin, while the β-chains contain the transmembrane helix and, at the C-terminus, domains with tyrosine kinase activity. In the activated state, the kinase domains phosphorylate themselves and also mediator proteins (receptor substrates) that set in motion cascades of further phosphorylations (see pp. 120 and 388).

C. 7-helix receptors

A large group of receptors span the membrane with α-helices seven times. These are known as 7-helix receptors. Via their effector domains, they bind and activate trimeric proteins, which in turn bind and hydrolyze GTP and are therefore called G proteins. Most G proteins, in turn, activate or inhibit enzymes that create secondary signaling molecules (second messengers; see p. 386). Other G proteins regulate ion channels. The illustration shows the complex of the light receptor rhodopsin, with the associated G protein transducin (see p. 358). The GTP-binding α-subunit (green) and the γ-subunit (purple) of transducin are anchored in the membrane via lipids (see p. 214). The β-subunit is shown in detail on p. 72.

D. T-cell receptor

The cells of the immune system communicate with each other particularly intensively. The T-cell receptor plays a central role in the activation of T lymphocytes (see p. 296). The cell at the top has been infected with a virus, and it indicates this by presenting a viral peptide (violet) with the help of a class I MHC protein (yellow and green). The combination of the two molecules is recognized by the dimeric T-cell receptor (blue) and converted into a signal that activates the T cell (bottom) and thereby enhances the immune response to the virus.
A. Principle of receptor action

Chemical signals
- Metabolites
- Hormones
- Neurotransmitters
- Mediators
- Odorants
- Tastants
- Other molecules
- Inorganic ions

Physical signals
- Light
- Electrical impulses
- Mechanical stimuli

Activator
- Protein kinase
- Ion channel

G-protein receptor substrate

Protein activated by ions

Cellular response

B. Insulin receptor

Insulin

α2

α1

Adaptor protein

Protein kinase

Cellular response

Protein activated by ions

C. 7-Helix receptors

Lipid anchor

α-Subunit

GTP

β-Subunit

γ-Subunit

Signaling substance

G protein

Activated receptor

GDP

GTP

Precursor

Second messenger

D. T-cell receptor

Antigen-presenting cell

MHC protein (class I)

β2-Microglobulin

Viral peptide

β2-Microglobulin

G protein

Effector enzyme

T-helper cell

Signal recipient

Transmitter

Effector

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ER: structure and function

The endoplasmic reticulum (ER) is an extensive closed membrane system consisting of tubular and saccular structures. In the area of the nucleus, the ER turns into the external nuclear membrane. Morphologically, a distinction is made between the rough ER (rER) and the smooth ER (sER). Large numbers of ribosomes are found on the membranes of the rER, which are lacking on the sER. On the other hand, the sER is rich in membrane-bound enzymes, which catalyze partial reactions in the lipid metabolism as well as biotransformations.

A. Rough endoplasmic reticulum and the Golgi apparatus

The rER (1) is a site of active protein biosynthesis. This is where proteins destined for membranes, lysosomes, and export from the cell are synthesized. The remaining proteins are produced in the cytoplasm on ribosomes that are not bound to membranes.

Proteins synthesized at the rER (1) are folded and modified after translation (protein maturation; see p. 230). They remain either in the rER as membrane proteins, or pass with the help of transport vesicles (2) to the Golgi apparatus (3). Transport vesicles are formed by budding from existing membranes, and they disappear again by fusing with them (see p. 228).

The Golgi apparatus (3) is a complex network, also enclosed, consisting of flattened membrane saccules ("cisterns"), which are stacked on top of each other in layers. Proteins mature here and are sorted and packed. A distinction is made between the cis, medial, and trans Golgi regions, as well as a trans Golgi network (tGN). The post-translational modification of proteins, which starts in the ER, continues in these sections.

From the Golgi apparatus, the proteins are transported by vesicles to various targets in the cells—e.g., to lysosomes (4), the plasma membrane (6), and secretory vesicles (5) that release their contents into the extracellular space by fusion with the plasma membrane (exocytosis; see p. 228). Protein transport can either proceed continuously (constitutive), or it can be regulated by chemical signals. The decision regarding which pathway a protein will take and whether its transport will be constitutive or regulated depends on the signal sequences or signal structures that proteins carry with them like address labels (see p. 228). In addition to proteins, the Golgi apparatus also transports membrane lipids to their targets.

B. Smooth endoplasmic reticulum

Regions of the ER that have no bound ribosomes are known as the smooth endoplasmic reticulum (sER). In most cells, the proportion represented by the sER is small. A marked sER is seen in cells that have an active lipid metabolism, such as hepatocytes and Leydig cells. The sER is usually made up of branching, closed tubules.

Membrane-located enzymes in the sER catalyze lipid synthesis. Phospholipid synthesis (see p. 170) is located in the sER, for example, and several steps in cholesterol biosynthesis (see p. 172) also take place there. In endocrine cells that form steroid hormones, a large proportion of the reaction steps involved also take place in the sER (see p. 376). In the liver's hepatocytes, the proportion represented by the sER is particularly high. It contains enzymes that catalyze so-called biotransformations. These are reactions in which apolar foreign substances, as well as endogenous substances—e.g., steroid hormones—are chemically altered in order to inactivate them and/or prepare them for conjugation with polar substances (phase I reactions; see p. 316). Numerous cytochrome P450 enzymes are involved in these conversions (see p. 318) and can therefore be regarded as the major molecules of the sER.

The sER also functions as an intracellular calcium store, which normally keeps the Ca²⁺ level in the cytoplasm low. This function is particularly marked in the sarcoplasmic reticulum, a specialized form of the sER in muscle cells (see p. 334). For release and uptake of Ca²⁺, the membranes of the sER contain signal-controlled Ca²⁺ channels and energy-dependent Ca²⁺ ATPases (see p. 220). In the lumen of the sER, the high Ca²⁺ concentration is buffered by Ca²⁺-binding proteins.
A. Rough endoplasmic reticulum and Golgi apparatus

1. rER
2. Transport vesicle
3. Golgi complex
4. Lysosome
5. Secretory vesicle
6. Cytoplasmic membrane

Biochemical processes
1. Transport
2. Protein synthesis and folding
   - Signal peptide cleavage
   - Formation of disulfide bonds
   - N-Glycosylation folding
3. cis:
   - Phosphorylation
   - Sugar cleavage
   - Addition of GlcNAc
   - Addition of Gal and NeuAc
   - Sorting
4. Hydrolysis of macromolecules
5. Proteolysis
6. Exocytosis

B. Smooth endoplasmic reticulum

- Phospholipids
- Cholesterol
- Steroid hormones

Calcium store

Enzyme systems of the lipid metabolism

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Protein sorting

A. Protein sorting

The biosynthesis of all proteins starts on free ribosomes (top). However, the paths that the proteins follow soon diverge, depending on which target they are destined for. Proteins that carry a signal peptide for the ER (1) follow the secretory pathway (right); Proteins that do not have this signal follow the cytoplasmic pathway (left).

Secretory pathway. Ribosomes that synthesize a protein with a signal peptide for the ER settle on the ER (see p. 226). The peptide chain is transferred into the lumen of the rER. The presence or absence of other signal sequences and signal regions determines the subsequent transport pathway.

Proteins that have stop-transfer sequences (4) remain as integral membrane proteins in the ER membrane. They then pass into other membranes via vesicular transport (see p. 226). From the rER, their pathway then leads to the Golgi apparatus and then on to the plasma membrane. Proteins destined to remain in the rER—e.g., enzymes—find their way back from the Golgi apparatus to the rER with the help of a retention signal (2). Other proteins move from the Golgi apparatus to the lysosomes (3; see p. 234), to the cell membrane (integral membrane proteins or constitutive exocytosis), or are transported out of the cell (9; signal-regulated exocytosis) by secretory vesicles (8).

Cytoplasmic pathway. Proteins that do not have a signal peptide for the ER are synthesized in the cytoplasm on free ribosomes, and remain in that compartment. Special signals mediate further transport into the mitochondria (5; see p. 232), the nucleus (6; see p. 208) or peroxisomes (7).

B. Translocation signals

Signal peptides are short sections at the N or C terminus, or within the peptide chain. Areas on the protein surface that are formed by various sections of the chain or by various chains are known as signal regions. Signal peptides and signal regions are structural signals that are usually recognized by receptors on organelles (see A). They move the proteins, with the help of additional proteins, into the organelles (selective protein transfer). Structural signals can also activate enzymes that modify the proteins and thereby determine their subsequent fate. Examples include lysosomal proteins (see p. 234) and membrane proteins with lipid anchors (see p. 214).

After they have been used, signal peptides at the N terminus are cleaved off by specific hydrolases (symbol: scissors). In proteins that contain several successive signal sequences, this process can expose the subsequent signals. By contrast, signal peptides that have to be read several times are not cleaved.

C. Exocytosis

Exocytosis is a term referring to processes that allow cells to expel substances (e.g., hormones or neurotransmitters) quickly and in large quantities. Using a complex protein machinery, secretory vesicles fuse completely or partially with the plasma membrane and release their contents. Exocytosis is usually regulated by chemical or electrical signals. As an example, the mechanism by which neurotransmitters are released from synapses (see p. 348) is shown here, although only the most important proteins are indicated.

The decisive element in exocytosis is the interaction between proteins known as SNAREs that are located on the vesicular membrane (v-SNAREs) and on the plasma membrane (t-SNAREs). In the resting state (1), the v-SNARE synaptobrevin is blocked by the vesicular protein synaptogamin. When an action potential reaches the presynaptic membrane, voltage-gated Ca\(^{2+}\) channels open (see p. 348). Ca\(^{2+}\) flows in and triggers the machinery by conformational changes in proteins. Contact takes place between synaptobrevin and the t-SNARE synaptotagmin (2). Additional proteins known as SNAPs bind to the SNARE complex and allow fusion between the vesicle and the plasma membrane (3). The process is supported by the hydrolysis of GTP by the auxiliary protein Rab.

The toxin of the bacterium *Clostridium botulinum*, one of the most poisonous substances there is, destroys components of the exocytosis machinery in synapses through enzymatic hydrolysis, and in this way blocks neurotransmission.
A. Protein sorting

B. Translocation signals

1. Signal peptide (secretory pathway)
2. Signal sequence (ER proteins)
3. Signal group (lysosomal proteins)
4. Stop-transfer sequence (membrane proteins)
5. Signal peptide (mitochondrial proteins)
6. Signal sequence (nuclear proteins)
7. Signal sequence (peroxisomes)
8. Signal region (secretory vesicle)

C. Exocytosis

1. Synaptic cleft
2. Membrane fusion
3. SNARE complex
Protein synthesis and maturation

A. Protein synthesis in the rER

With all proteins, protein biosynthesis (Translation; for details, see p. 250) starts on free ribosomes in the cytoplasm (1). Proteins that are exported out of the cell or into lysosomes, and membrane proteins of the ER and the plasma membrane, carry a signal peptide for the ER at their N-terminus. This is a section of 15–60 amino acids in which one or two strongly basic residues (Lys, Arg) near the N-terminus are followed by a strongly hydrophobic sequence of 10–15 residues (see p. 228).

As soon as the signal peptide (red) appears on the surface of the ribosome (2), an RNA-containing signal recognition particle (SRP, green) binds to the sequence and initially interrupts translation (3). The SRP then binds to an SRP receptor in the rER membrane, and in this way attaches the ribosome to the ER (4). After this, the SRP dissociates from the signal peptide and from the SRP receptor and is available again for step 3. This endergonic process is driven by GTP hydrolysis (5). Translation now resumes. The remainder of the protein, still unfolded, is gradually introduced into a channel (the translocon) in the lumen of the rER (6), where a signal peptidase located in the inner ER membrane cleaves the signal peptide while translation is still taking place (7). This converts the preproteins into a propeptide, from which the mature protein finally arises after additional post-translational modifications (8) in the ER and in the Golgi apparatus.

If the growing polypeptide contains a stop-transfer signal (see p. 228), then this hydrophobic section of the chain remains stuck in the membrane outside the translocon, and an integral membrane protein arises. In the course of translation, an additional signal sequence can re-start the transfer of the chain through the translocon. Several repetitions of this process produce integral membrane proteins with several transmembrane helices (see p. 214).

All plasma proteins with the exception of albumin are glycosylated. Together with glycolipids, numerous glycoproteins on the cell surface form the glycocalyx. Inside the ER, the carbohydrate parts of the glycoproteins are cotranslationally transferred to the growing chain, and are then converted into their final form while passing through the ER and Golgi apparatus.

N-bound oligosaccharides (see p. 44) are always bound to the acid-amide group of asparagine residues. If a glycosylation sequence (Asn-Asp-Thr-, where X can be any amino acid) appears in the growing peptide chain, then a transglycosylase in the ER membrane (1) transfers a previously produced core oligosaccharide consisting of 14 hexose residues en-bloc from the carrier molecule dolichol diphosphate to the peptide.

Dolichol is a long-chain isoprenoid (see p. 52) consisting of 10–20 isoprene units, which is embedded in the ER membrane. A hydroxyl group at the end of the molecule is bound to diphosphate, on which the nuclear oligosaccharide is built up in an extended reaction sequence (not shown here in detail). The core structure consists of two residues of N-acetylgalactosamine (GlcNAc), a branched group of nine mannose residues (Man) and three terminal glucose residues (Glc).

As the proprotein passes through the ER, glycosidases (2) remove the glucose residues completely and the mannoses partially (“trimming”), thereby producing the mannos-rich type of oligosaccharide residues. Subsequently, various glycosyltransferases (3) transfer additional monosaccharides (e.g., GlcNAc, galactose, fucose, and N-acetylneuraminic acid; see p. 38) to the mannos-rich intermediate and thereby produce the complex type of oligosaccharide. The structure of the final oligosaccharide depends on the type and activity of the glycosyltransferases present in the ER of the cell concerned, and is therefore genetically determined (although indirectly).

B. Protein glycosylation

Most extracellular proteins contain covalently bound oligosaccharide residues. For example,
A. Protein synthesis in the rough endoplasmic reticulum

1. mRNA
2. Signal peptide
3. SRP
4. ER-lumen
5. Signal peptidase
6. Pro-transl. modification

B. Protein glycosylation

1. Ribosome
2. Dolichol (Dol)
3. Core structure
4. Mannose-rich type
5. Complex type

- Protein glycosyltransferase 2.4.1.19
- O-glycosidases 3.2.1.n
- Glycosyltransferases 2.4.1.n

- Glucose
- N-acetylglucosamine
- Mannose
- Galactose
- N-acetyleneuraminic acid

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Protein maturation

After translation, proteins destined for the secretory pathway (see p. 228) first have to fold into their native conformation within the rER (see p. 230). During this process they are supported by various auxiliary proteins.

A. Protein folding in the ER

To prevent incorrect folding of the growing protein during protein biosynthesis, chaperones (see Chapter 8) in the lumen of the rER bind to the peptide chain and stabilize it until translation has been completed. Binding protein (BIP) is an important chaperone in the ER.

Many secretory proteins—e.g., pancreatic ribonuclease (RNase; see p. 74)—contain several disulfide bonds that are only formed oxidatively from SH groups after translation. The eight cysteine residues of the RNase can in principle form 105 different pairings, but only the combination of the four disulfide bonds shown on p. 75 provides active enzyme. Incorrect pairings can block further folding or lead to unstable or insoluble conformations. The enzyme protein disulfide isomerase [1] accelerates the equilibration between paired and unpaired cysteine residues, so that incorrect pairs can be quickly split before the protein finds its final conformation.

Most peptide bonds in proteins take on the trans conformation (see p. 66). Only bonds with proline residues (−X-Pro−) can be present in both cis and trans forms.

In the protein's native conformation, every X-Pro bond has to have the correct conformation (cis or trans). As the uncatalyzed transition between the two forms is very slow, there is a proline cis-trans isomerase [2] in the ER that accelerates the conversion.

B. Chaperones and chaperonins

Most proteins fold spontaneously into their native conformation, even in the test tube. In the cell, where there are very high concentrations of proteins (around 350 g L−1), this is more difficult. In the unfolded state, the apolar regions of the peptide chain (yellow) tend to aggregate due to the hydrophobic effect (see p. 28)—with other proteins or with each other to form insoluble products (2). In addition, unfolded proteins are susceptible to proteases. To protect partly folded proteins, there are auxiliary proteins called chaperones because they guard immature proteins against damaging contacts. Chaperones are formed increasingly during temperature stress and are therefore also known as heat-shock proteins (hsp). Several classes of hsp are distinguished. Chaperones of the hsp70 type (Dna K in bacteria) are common, as are type hsp60 chaperonins (GroEL/ES in bacteria). Class hsp90 chaperones have special tasks (see p. 378).

While small proteins can often reach their native conformation without any help (1), larger molecules require hsp70 proteins for protection against aggregation which bind as monomers and can dissociate again, dependent on ATP (3). By contrast, type hsp60 chaperonins form large, barrel-shaped complexes with 14 subunits in which proteins can fold independently while shielded from their environment (4). The function of hsp60 has been investigated in detail in the bacterial chaperonin GroEL (right). The barrel has two chambers, which are closed with a lid (GroES) during folding of the guest protein. Driven by ATP hydrolysis, the chambers open and close alternately, i.e., the release of the fully folded protein from one chamber is coupled to the uptake of an unfolded peptide in the second chamber.

C. Protein import in mitochondria

Class hsp70 chaperones are also needed for translocation of nuclear-coded proteins from the cytoplasm into the mitochondria (see p. 228). As two membranes have to be crossed to reach the matrix, there are two translocator complexes: TOM (“transport outer membrane”) and TIM (“transport inner membrane”). For transport, proteins are unfolded in the cytoplasm and protected by hsp70. TOM recognizes the positively charged signal sequence at the protein's N terminus (see p. 228) and with the help of the membrane potential threads the chains through the central pores of the two complexes. Inside TIM, further hsp70 molecules bind and pull the chain completely into the matrix. As with import into the ER, the signal peptide is proteolytically removed by a signal peptidase during translocation.
A. Protein folding in the rER

1. Protein disulfide isomerase 5.3.4.7
2. Peptidyl proline cis-trans-isomerase 5.2.1.8

B. Chaperones and chaperonins

1. Folded protein
2. Small protein
3. Aggregation
4. hsp 70 (chaperone)
5. Insoluble precipitate or degradation
6. Folded protein

C. Protein import in mitochondria

1. Signal peptide for mitochondrial import
2. Nuclear-coded mitochondrial protein
3. hsp 70

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Lysosomes

A. Structure and contents

Animal lysosomes are organelles with a diameter of 0.2–2.0 µm with various shapes that are surrounded by a single membrane. There are usually several hundred lysosomes per cell. ATP-driven V-type proton pumps are active in their membranes (see p. 220). As these accumulate H+ in the lysosomes, the content of lysosomes with pH values of 4.5–5 is much more acidic than the cytoplasm (pH 7.0–7.5).

The lysosomes are the cell’s “stomachs,” serving to break down various cell components. For this purpose, they contain some 40 different types of hydrolyses, which are capable of breaking down every type of macromolecule. The marker enzyme of lysosomes is acid phosphatase. The pH optimum of lysosomal enzymes is adjusted to the acid pH value and is also in the range of pH 5. At neutral pH, as in the cytoplasm, lysosomal enzymes only have low levels of activity. This appears to be a mechanism for protecting the cells from digesting themselves in case lysosomal enzymes enter the cytoplasm at any time. In plants and fungi, the cell vacuoles (see p. 43) have the function of lysosomes.

B. Functions

Lysosomes serve for enzymatic degradation of macromolecules and cell organelles, which are supplied in various ways. The example shows the degradation of an averaged mitochondrial autophagy. To accomplish this, the lysosome encloses the organelle (1). During this process, the primary lysosome converts into a secondary lysosome, in which the hydrolytic degradation takes place (2). Finally, residual bodies contain the indigestible residues of the lysosomal degradation process. Lysosomes are also responsible for the degradation of macromolecules and particles taken up by cells via endocytosis and phagocytosis—e.g., lipoproteins, proteohormones, and bacteria (heterophagy). In the process, lysosomes fuse with the endosomes (3) in which the endocytosed substances are supplied.

C. Synthesis and transport of lysosomal proteins

Primary lysosomes arise in the region of the Golgi apparatus. Lysosomal proteins are synthesized in the rough endoplasmic reticulum and are glycosylated there as usual (1; see p. 228). The next steps are specific for lysosomal proteins (right part of the illustration). In a two-step reaction, terminal mannose residues (Man) are phosphorylated at the C-6 position of the mannose. First, N-acetylglucosamine 1-phosphate is transferred to the OH group at C-6 in a terminal mannose residue, and N-acetylglucosamine is then cleaved again. Lysosomal proteins therefore carry a terminal mannose 6-phosphate (Man(6−P)2).

The membranes of the Golgi apparatus contain receptor molecules that bind Man 6−P. They recognize lysosomal proteins by this residue and bind them (3). With the help of clathrin, the receptors are concentrated locally. This allows the appropriate membrane sections to be pinched off and transported to the endolysosomes with the help of transport vesicles (4), from which primary lysosomes arise through maturation (5). Finally, the phosphate groups are removed from Man 6−P (6).

The Man 6−P receptors are reused. The fall in the pH value in the endolysosomes releases the receptors from the bound proteins (7) which are then transported back to the Golgi apparatus with the help of transport vesicles.

Further information

Many hereditary diseases are due to genetic defects in lysosomal enzymes. The metabolism of glycogen (→ glycogenoses), lipids (→ lipidoses), and proteoglycans (→ mucopolysaccharidoses) is particularly affected. As the lysosomal enzymes are indispensable for the intracellular breakdown of macromolecules, unmetabolized macromolecules or degradation products accumulate in the lysosomes in these diseases and lead to irreversible cell damage over time. In the longer term, enlargement takes place, and in severe cases there may be failure of the organ affected—e.g., the liver.
A. Structure and contents

- Approx. 40 different hydrolases with acidic pH optima
- Lysosome pH = 4.5 - 5.0
- Nucleases
- Proteases
- Glycosidases
- Lipases
- Phosphatases
- Sulfatases
- Phospholipases

Cytoplasm

pH = 7.0 - 7.3

H^+ ATPase

B. Functions

1. Overaged mitochondrion
2. Enzymatic degradation
3. Acid hydrolases
4. Primary lysosome
5. Endosome
6. Residual body
7. Endocytotic vesicle
8. Secondary lysosome
9. Endocytosis or phagocytosis

C. Synthesis and transport of lysosomal proteins

1. rER Protein biosynthesis
2. N-Glycosylation
3. cis-Golgi apparatus
4. Phosphorylation
5. trans-Golgi network
6. Binding to Man-6-P receptor
7. Sorting
8. Sealing
9. Vesicular transport
10. Endolysosome
11. Acidification
12. Dissociation of the receptor-protein complex
13. Primary lysosome
14. Phosphate cleavage

Low pH triggers conformational change

Terminal mannose

GlcNAc-phosphoryltransferase 2.7.3.17
GlcNAc-phosphoglycosidase 1.1.4.45

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Molecular genetics: overview

Nucleic acids (DNA and various RNAs) are of central importance in the storage, transmission, and expression of genetic information. The decisive factor involved is their ability to enter into specific base pairings with each other (see p. 84). The individual processes involved, which are summed up in an overview here, are discussed in more detail on the following pages.

A. Expression and transmission of genetic information

Storage. The genetic information of all cells is stored in the base sequence of their DNA (RNA only occurs as a genetic material in viruses; see p. 404). Functional sections of DNA that code for inheritable structures or functions are referred to as genes. The 30,000–40,000 human genes represent only a few percent of the genome, which consists of approximately 5 × 10^9 base pairs (bp). Most genes code for proteins—i.e., they contain the information for the sequence of amino acid residues of a protein (its sequence). Every amino acid residue is represented in DNA by a code word (a codon) consisting of a sequence of three base pairs (a triplet). At the level of DNA, codons are defined as sequences of the sense strand read in the 5'→3' direction (see p. 84). A DNA codon for the amino acid phenylalanine, for example, is thus TTC (2).

Replication. During cell division, all of the genetic information has to be passed on to the daughter cells. To achieve this, the whole of the DNA is copied during the S phase of the cell cycle (see p. 394). In this process, each strand serves as a matrix for the synthesis of a complementary second strand (1; see p. 240).

Transcription. For expression of a gene—i.e., synthesis of the coded protein—the DNA sequence information has to be converted into a protein sequence. As DNA itself is not involved in protein synthesis, the information is transferred from the nucleus to the site of synthesis in the cytoplasm. To achieve this, the template strand in the relevant part of the gene is transcribed into an RNA (hnRNA). The sequence of this RNA is thus complementary to that of the template strand (3), but—with the exception of the exchange of thy-
A. Expression and transmission of genetic information

1. Replication

2. Transcription

3. RNA maturation

4. Translation

5. Expression and transmission of genetic information
Genome

A. Chromatin

In the nuclei of eukaryotes (see p. 196), DNA is closely associated with proteins and RNA. These nucleoprotein complexes, with a DNA proportion of approximately one-third, are known as chromatin. It is only during cell division (see p. 354) that chromatin condenses into chromosomes that are visible under light microscopy. During interphase, most of the chromatin is loose, and in these conditions a morphological distinction can be made between tightly packed heterochromatin and the less dense euchromatin. Euchromatin is the site of active transcription.

The proteins contained in chromatin are classified as either histone or non-histone proteins. Histones (8) are small, strongly basic proteins that are directly associated with DNA. They contribute to the structural organization of chromatin, and their basic amino acids also neutralize the negatively charged phosphate groups, allowing the dense packing of DNA in the nucleus. This makes it possible for the 46 DNA molecules of the diploid human genome, with their 5 × 10^9 base pairs (bp) and a total length of about 2 m, to be accommodated in a nucleus with a diameter of only 10 μm. Histones also play a central role in regulating transcription (see p. 244).

Two histone molecules each of types H2A (blue), H2B (green), H3 (yellow), and H4 (red) form an octameric complex, around which 146 bp of DNA are wound in 1.8 turns. These particles, with a diameter of 7 nm, are referred to as nucleosomes. Another histone (H1) binds to DNA segments that are not directly in contact with the histone octamers (“linker” DNA). It covers about 20 bp and supports the formation of spirally wound superstructures with diameters of 30 nm, known as solenoids. When chromatin condenses into chromosomes, the solenoids form loops about 200 nm long, which already contain about 80 000 bp. The loops are bound to a protein framework (the nuclear scaffold), which in turn organizes some 20 loops to form minibands. A large number of stacked minibands finally produces a chromosome. In the chromosome, the DNA is so densely packed that the smallest human chromosome already contains more than 50 million bp.

The non-histone proteins are very heterogeneous. This group includes structural proteins of the nucleus, as well as many enzymes and transcription factors (see p. 118), which selectively bind to specific segments of DNA and regulate gene expression and other processes.

B. Histones

The histones are remarkable in several ways. With their high proportions of lysine and arginine (blue shading), they are strongly basic, as mentioned above. In addition, their amino acid sequence has hardly changed at all in the course of evolution. This becomes clear when one compares the histone sequences in mammals, plants, and fungi (yeasts are single-celled fungi; see p. 148). For example, the H4 histones in humans and wheat differ only in a single amino acid residue, and there are only a few changes between humans and yeast. In addition, all of these changes are “conservative”—i.e., the size and polarity barely differ. It can be concluded from this that the histones were already “optimized” when the last common predecessor of animals, plants, and fungi was alive on Earth (more than 700 million years ago). Although countless mutations in histone genes have taken place since, almost all of these evidently led to the extinction of the organisms concerned.

The histones in the octamer carry N-terminal mobile “tails” consisting of some 20 amino acid residues that project out of the nucleosomes and are important in the regulation of chromatin structure and in controlling gene expression (see A2: only two of the eight tails are shown in full length). For example, the condensation of chromatin into chromosomes is associated with phosphorylation (P) of the histones, while the transcription of genes is initiated by acetylation (A) of lysine residues in the N-terminal region (see p. 244).
A. Chromatin

1. Organization of chromatin

- Nuclear scaffold
- DNA double helix
- Nucleosome

Histone-Octamer
(H₂A · H₂B₂(H₃ · H₄)₂)

Histone molecules

N-terminal tail (H₂B)

N-terminal tail (H₃)

H₂A
H₂B
H₃
H₄

2. Nucleosome

B. Histone

<table>
<thead>
<tr>
<th>Acetylation</th>
<th>Phosphorylation</th>
<th>Methylation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Animals</td>
<td>Plants</td>
<td>Yeast</td>
</tr>
<tr>
<td>H₂A</td>
<td>H₂B</td>
<td>H₃</td>
</tr>
<tr>
<td>H₂A</td>
<td>H₂B</td>
<td>H₄</td>
</tr>
</tbody>
</table>

Amino acid sequence of histone H₄

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Replication

For genetic information to be passed on during cell division, a complete copy of the genome has to be produced before each mitosis. This process is known as DNA replication.

A. Mechanism of DNA polymerases

Replication is catalyzed by DNA-dependent DNA polymerases. These enzymes require a single strand of DNA, known as the template. Beginning at a short starting sequence of RNA (the primer), they synthesize a second complementary strand on the basis of this template, and thus create a complete DNA double helix again. The substrates of the DNA polymerases are the four deoxynucleoside triphosphates dATP, dGTP, dCTP, and dTTP. In each step, base pairing first binds the nucleotide that is complementary to the current base in the template strand. The α-phosphate residue of the newly bound nucleoside triphosphate is then subjected to nucleophilic attack by the 3′–OH group of the nucleotide incorporated immediately previously. This is followed by the elimination of diphosphate and the formation of a new phosphoric acid diester bond. These steps are repeated again for each nucleotide. The mechanism described means that the matrix can only be read in the 3′→5′ direction. In other words, the newly synthesized strand always grows in the 5′→3′ direction. The same mechanism is also used in transcription by DNA-dependent RNA polymerases (see p. 242). Most DNA and RNA polymerases consist of more than 10 subunits, the role of which is still unclear to some extent.

B. Replication in E. coli

Although replication in prokaryotes is now well understood, many details in eukaryotes are still unclear. However, it is certain that the process is in principle similar. A simplified scheme of replication in the bacterium Escherichia coli is shown here.

In bacteria, replication starts at a specific point in the circular DNA—the origin of replication—and proceeds in both directions. This results in two diverging replication forks, in which the two strands are replicated simultaneously. Numerous proteins are involved in the processes taking place in this type of fork, and only the most important are shown here. The two strands of the initial DNA (1) are shown in blue and violet, while the newly formed strands are pink and orange.

Each fork (2) contains two molecules of DNA polymerase III and a number of helper proteins. The latter include DNA topoisomerasers and single-strand-binding proteins. Topoisomerases are enzymes that unwind the superhelical DNA double strand (gyrase, topoisomerase II) and then separate it into the two individual strands (helicase, topoisomerase I). Since the template strand is always read from 3′ to 5′ (see above), only one of the strands (known as the leading strand; violet/pink) can undergo continuous replication. For the lagging strand (light blue), the reading direction is the opposite of the direction of movement of the fork. In this matrix, the new strand is first synthesized in individual pieces, which are known as Okazaki fragments after their discoverer (green/orange).

Each fragment starts with a short RNA primer (green), which is necessary for the functioning of the DNA polymerase and is synthesized by a special RNA polymerase ("primase," not shown). The primer is then extended by DNA polymerase III (orange). After 1000–2000 nucleotides have been included, synthesis of the fragment is interrupted and a new one is begun, starting with another RNA primer that has been synthesized in the interim. The individual Okazaki fragments are initially not bound to one another and still have RNA at the 5′ end (3). At some distance from the fork, DNA polymerase I therefore starts to remove the RNA primer and replace it with DNA components. Finally, the gaps still remaining are closed by a DNA ligase. In DNA double helices formed in this way, only one of the strands has been newly synthesized—i.e., replication is semiconservative.

In bacteria, some 1000 nucleotides are replicated per second. In eukaryotes, replication takes place more slowly (about 50 nucleotides s⁻¹) and the genome is larger. Thousands of replication forks are therefore active simultaneously in eukaryotes.
A. Mechanism of DNA polymerases

B. Replication in E. coli

1. DNA polymerase III
2. Auxiliary proteins
   - DNA helicase 5.99.1.2
   - DNA gyrase 5.99.1.3
3. DNA polymerase I
4. Replication is semiconservative
Transcription

For the genetic information stored in DNA to become effective, it has to be rewritten (transcribed) into RNA. DNA only serves as a template and is not altered in any way by the transcription process. Transcribable segments of DNA that code for a defined product are called genes. It is estimated that the mammalian genome contains 30,000–40,000 genes, which together account for less than 5% of the DNA.

A. Transcription and maturation of RNA: overview

Transcription is catalyzed by DNA-dependent RNA polymerases. These act in a similar way to DNA polymerases (see p. 240), except that they incorporate ribonucleotides instead of deoxyribonucleotides into the newly synthesized strand; also, they do not require a primer. Eukaryotic cells contain at least three different types of RNA polymerase. RNA polymerase I synthesizes an RNA with a sedimentation coefficient of 45 S, which serves as precursor for three ribosomal RNAs. The products of RNA polymerase II are hnRNAs, from which mRNAs later develop, as well as precursors for snRNAs. Finally, RNA polymerase III transcribes genes that code for tRNAs, 5S RNA, and certain snRNAs. These precursors give rise to functional RNA molecules by a process called RNA maturation (see p. 246). Polymerases II and III are inhibited by α-amanitin, a toxin in the Amanita phalloides mushroom.

B. Organization of the PEP-CK gene

The way in which a typical eukaryotic gene is organized is illustrated here using a gene that codes for a key enzyme in gluconeogenesis (see p. 154)—the phosphoenolpyruvate carboxykinase (PEP-CK).

In the rat, the PEP-CK gene is nearly 7 kbp (kilobase pairs) long. Only 1863 bp, distributed over 10 coding segments (exons, dark blue) carry the information for the protein’s 621 amino acids. The remainder is allotted to the promoter (pink) and intervening sequences (introns, light blue). The gene’s promoter region (approximately 1 kbp) serves for regulation (see p. 188). Transcription starts at the 3’ end of the promoter (“transcription start”) and continues until the polyadenylation sequence (see below) is reached. The primary transcript (hnRNA) still has a length of about 6.2 kbp. During RNA maturation, the noncoding sequences corresponding to the introns are removed, and the two ends of the hnRNA are modified. The translatable mRNA still has half the length of the hnRNA and is modified at both ends (see p. 246).

In many eukaryotic genes, the proportion of introns is even higher. For example, the gene for dihydrofolate reductase (see p. 402) is over 30 kbp long. The information is distributed over six exons, which together have a length of only about 6 kbp.

C. Transcription process

As mentioned above, RNA polymerase II (green) binds to the 3’ end of the promoter region. A sequence that is important for this binding is known as the TATA box—a short A–T–rich sequence that varies slightly from gene to gene. A typical base sequence (“consensus sequence”) is ...TAT... Numerous proteins known as basal transcription factors are necessary for the interaction of the polymerase with this region. Additional factors can promote or inhibit the process (transcriptional control; see p. 244). Together with the polymerase, they form the basal transcription complex.

At the end of initiation (2), the polymerase is repeatedly phosphorylated, frees itself from the basal complex, and starts moving along the DNA in the 3’ direction. The enzyme separates a short stretch of the DNA double helix into two single strands. The complementary nucleoside triphosphates are bound by base pairing in the template strand and are linked step by step to the hnRNA as it grows in the 5’→3’ direction (3). Shortly after the beginning of elongation, the 5’ end of the transcript is protected by a “cap” (see p. 246). Once the polyadenylation sequence has been reached (typical sequence: ...AATAA...), the transcript is released (4). Shortly after this, the RNA polymerase stops transcribing and dissociates from the DNA.
A. Transcription and maturation of RNA: overview

ATP, GTP, CTP, UTP

Transcription

Polymerase I

28S RNA

18S RNA

5.8S RNA

mRNA

5S RNA

tRNA

snRNA

B. Organization of the PEP-CK gene

Transcription start

Translation start (ATG)

100 Bases

Promoter region

DNA

hnRNA

Poly-A sequence

mRNA

C. Process of transcription

1. Basal transcription complex

2. RNA Polymerase II

Elongation

Template strand

3. Cap

4. Termination

hnRNA

UAA

AATAA

Polyadenylation sequence

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Transcriptional control

Although all cells contain the complete genome, they only use a fraction of the information in it. The genes known as “housekeeping genes,” which code for structural molecules and enzymes of intermediate metabolism, are the only ones that undergo constant transcription. The majority of genes are only active in certain cell types, in specific metabolic conditions, or during differentiation. Which genes are transcribed and which are not is regulated by transcriptional control (see also p. 118). This involves control elements (cis-active elements) in the gene’s promoter region and gene-specific regulatory proteins (transcription factors, trans-active factors), which bind to the control elements and thereby activate or inhibit transcription.

A. Initiation of transcription

In the higher organisms, DNA is blocked by histones (see p. 238) and is therefore not capable of being transcribed without special positive regulation. In eukaryotes, it is therefore histones that play the role of repressors (see p. 118). For transcription to be set in motion at all, the chromatin first has to be restructured.

In the resting state, the lysine residues in the N-terminal “tail” of the histones (see p. 238) are not acetylated. In this state, which can be produced by histone deacetylases [1], the nucleosomes are stable. It is only the interaction of activator and regulator proteins with their control elements that allows the binding of coactivator complexes that have histone acetylase activity [2]. They acetylate the histone tails and thereby loosen the nucleosome structure sufficiently for the basal transcription complex to form.

This consists of DNA-dependent RNA polymerase II and basal transcription factors (TFIIK, X = A - H). First, the basal factor TFIIID binds to the promoter. TFIIID, a large complex of numerous proteins, contains TATA box-binding protein (TBP) and so-called TAFs (TBP-associated factors). The polymerase is attached to this core with the help of TFIIIB. Before transcription starts, additional TFs have to bind, including TFIIH, which has helicase activity and separates the two strands of DNA during elongation. In all, some 35 different proteins are involved in the basal complex. This alone, however, is still not sufficient for transcription to start. In addition, positive signals have to be emitted by more distant trans-active factors, integrated by the coactivator/mediator complex, and passed on to the basal complex (see B).

The actual signal for starting elongation consists of the multiple phosphorylation of a domain in the C-terminal region of the polymerase. In phosphorylated form, it releases itself from the basal complex along with a few TFs and starts to synthesize hnRNA.

B. Regulation of PEP-CK transcription

Phosphoenolpyruvate carboxykinase (PEP-CK), a key enzyme in gluconeogenesis, is regulated by several hormones, all of which affect the transcription of the PEP-CK gene. Cortisol, glucagon, and thyroxin induce PEP-CK, while insulin inhibits its induction (see p. 158).

More than ten control elements (dark red), distributed over approximately 1 kbp, have so far been identified in the promoter of the PEP-CK gene (top). These include response elements for the glucocorticoid receptor (GRE; see p. 378), for the thyroxin receptor (TR), and for the steroid-like retinoic acid (AF-1). Additional control elements (CRE, CAMP-responsive element) bind the transcription factor C/EBP, which is activated by cAMP-dependent protein kinase A through phosphorylation. This is the way in which glucagon, which raises the CAMP level (see p. 158), works. Control element P1 binds the hormone-independent factor NF-1 (nuclear factor-1). All proteins that bind to the control elements mentioned above are in contact with a coactivator/mediator complex (CBP/p300), which integrates their input like a computer and transmits the result in the form of stronger or weaker signals to the basal transcription complex. Inhibition of PEP-CK transcription by insulin is mediated by an insulin-responsive element (IRE) in the vicinity of the GRE. Binding of an as yet unknown factor takes place here, inhibiting the binding of the glucocorticoid receptor to the GRE.
A. Initiation of transcription

- Histone deacetylase
- Activator protein
- Coactivator complex (histone acetylase)

B. Regulation of PEP-CK transcription

- Control element
- Transcription factor
- Coactivator complex
- Mediator complex
- RNA polymerase II

Receptors for retinoate, cortisol, thyroid, and glucagon

HRE – hormone response element
TAFs – TBP-associated factors
TBP – TATA box-binding protein
A–H – basal transcription factors

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RNA maturation

Before the snRNA produced by RNA polymerase II (see p. 242) can leave the nucleus in order to serve as a template for protein synthesis in the cytoplasm, it has to undergo several modifications first. Even during transcription, the two ends of the transcript have additional nucleotides added (A). The sections that correspond to the intervening gene sequences in the DNA (introns) are then cut out (splicing; see B). Other transcripts—e.g., the 45 S precursor of rRNA formed by polymerase I (see p. 242)—are broken down into smaller fragments by nucleases before export into the cytoplasm.

A. 5’ and 3’ modification of mRNA

Shortly after transcription begins in eukaryotes, the end of the growing RNA is blocked in several reaction steps by a structure known as a “cap.” In hnRNAs, this consists of a GTP residue that is methylated at N-7 of the guanine ring. The β-phosphate residue of the cap is linked to the free 5’-OH group of the terminal ribose via an ester bond. After the “polyadenylation signal” has been reached (typical sequence: ...AUAAG... see p. 242), a polyadenylate “tail” consisting of up to 200 AMP nucleotides is also added at the free 3’ end of the transcript. This reaction is catalyzed by a special polyadenylate polymerase. It is only at this point that the mRNA leaves the nucleus as a complex with RNA-binding proteins.

Both the cap and the poly-A tail play a vital part in initiating eukaryotic translation (see p. 250). They help position the ribosome correctly on the mRNA near to the starting codon. The protection which the additional nucleotides provide against premature enzymatic degradation appears to be of lesser importance.

B. Splicing of hnRNA

Immediately after transcription, the hnRNA introns are removed and the exons are linked to form a continuous coding sequence. This process, known as splicing, is supported by complicated RNA–protein complexes in the nucleus, the so-called spliceosomes. The components of these macromolecular machines are called snRNPs (small nuclear ribonucleoprotein particles, pronounced “snurps”). SnRNPs occur in five different forms (U1, U2, U4, U5, and U6). They consist of numerous proteins and one molecule of snRNA each (see p. 82).

To ensure that the RNA message is not destroyed, splicing has to take place in a very precise fashion. The start and end of the hnRNA introns are recognized by a characteristic sequence (...)AGC... at the 5’ end or ...(CUJAGC... at the 3’ end). Another important structure is the so-called branching point inside the intron. Its sequence is less conserved than the terminal splicing sites, but it always contains one adenosine residue (A).

During splicing, the 2’-OH group of this residue—supported by the spliceosome (see C)—attacks the phosphoric acid diester bond at the 5’ end of the intron and cleaves it (b). Simultaneously, an unusual 2’→5’ bond is formed inside the intron, which thereby takes on a lasso shape (e; see formula). In the second step of the splicing process, the free 3’-OH group at the end of the 5’ terminal exon attacks the A→G bond at the 3’ end of the intron. As a result, the two exons are linked and the intron is released, still in a lasso shape (d).

C. Spliceosome

As described above, it is residues of the snRNA that carry out bond cleavage and bond formation during the splicing process. It is therefore not a protein enzyme that acts as a catalyst here, but rather an RNA. Catalytic RNAs of this type are called ribozymes (see also p. 88). The task of the spliceosomes is to fix and orientate the reacting groups by establishing base pairings between snRNAs and segments of the hnRNA. The probable situation before the adenosine attack at the branching point on the 5’ splicing site (see B, Fig. b) is shown schematically on the right side of the illustration. In this phase, the U1 snRNA fixes the 5’ splicing site, U2 fixes the branching site, and U5 fixes the ends of the two exons.
A. 5' and 3' modification of mRNA

B. Splicing of hnRNA: mechanism

C. Spliceosome

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Amino acid activation

A. The genetic code

Most of the genetic information stored in the genome codes for the amino acid sequences of proteins. For these proteins to be expressed, a text in “nucleic acid language” therefore has to be translated into “protein language.” This is the origin of the use of the term translation to describe protein biosynthesis. The dictionary used for the translation is the genetic code.

As there are 20 proteinogenic amino acids (see p. 60), the nucleic acid language has to contain at least as many words (codons). However, there are only four letters in the nucleic acid alphabet (A, G, C, and U or T). To obtain 20 different words from these, each word has to be at least three letters long (with two letters, there would only be 4^2 = 16 possibilities). And in fact the codons do consist of three sequential bases (triplets).

Figure 1 shows the standard code in “DNA language” (i.e., as a sequence of triplets in the sense strand of DNA, read in the 5’-→3’ direction; see p. 84), represented as a circular diagram. The scheme is read from the inside to the outside. For example, the triplet CAT codes for the amino acid histidine. With the exception of the exchange of U for T, the DNA codons are identical to those of mRNA.

As the genetic code provides 4^3 = 64 codons for the 20 amino acids, there are several synonymous codons for most amino acids—the code is degenerate. Three triplets do not code for amino acids, but instead signal the end of translation (stop codons). Another special codon, the start codon, marks the start of translation. The code shown here is almost universally applicable; only the mitochondria (see p. 210) and a few microorganisms deviate from it slightly.

As an example of the way in which the code is read, Fig. 2 shows small sections from the normal and a mutated form of the β-globin gene (see p. 280), as well as the corresponding mRNA and protein sequences. The point mutation shown, which is relatively frequent, leads to replacement of a glutamate residue in position 6 of the β-chain by valine (GAG → GTG). As a consequence, the mutated hemoglobin tends to aggregate in the deoxy- genated form. This leads to sickle-shaped distortions of the erythrocytes and disturbances of O₂ transport (sickle-cell anemia).

B. Amino acid activation

Some 20 different amino acid tRNA ligases in the cytoplasm each bind one type of tRNA (see p. 82) with the corresponding amino acid. This reaction, known as amino acid activation, is endergonic and is therefore coupled to ATP cleavage in two steps.

First, the amino acid is bound by the enzyme and reacts there with ATP to form diphosphate and an “energy-rich” mixed acid anhydride (aminoacyl adenylate). In the second step, the 3’-OH group (in other ligases it is the 2’-OH group) of the terminal ribose residue of the tRNA takes over the amino acid residue from the aminoacyl adenylate.

In aminoacyl tRNAs, the carboxyl group of the amino acid is therefore esterified with the ribose residue of the terminal adenosine of the sequence ...CCA-3’.

The accuracy of translation primarily depends on the specificity of the amino acid tRNA ligases, as incorrectly incorporated amino acid residues are not recognized by the ribosome later. A “proofreading mechanism” in the active center of the ligase therefore ensures that incorrectly incorporated amino acid residues are immediately removed again. On average, an error only occurs once every 1300 amino acid residues. This is a surprisingly low rate considering how similar some amino acids are—e.g., leucine and iso- leucine.

C. Asp–tRNA ligase (dimer)

The illustration shows the ligase responsible for the activation of aspartate. Each subunit of the dimeric enzyme (protein parts shown in orange) binds one molecule of tRNAAsp (blue). The active centers can be located by the bound ATP (green). They are associated with the 3’ end of the tRNA. Another domain in the protein (upper left) is responsible for “recognition” of the tRNA anticodon.
A. The genetic code

B. Amino acid activation

C. Asp-tRNA-Ligase (Dimer)
Translation I: initiation

Like amino acid activation (see p. 248), protein biosynthesis (translation) takes place in the cytoplasm. It is catalyzed by complex nucleoprotein particles, the ribosomes, and mainly requires GTP to cover its energy requirements.

A. Structure of the eukaryotic ribosome

Ribosomes consist of two subunits of different size, made up of ribosomal RNA (rRNA) and nearly 80 proteins (the number of proteins varies at different stages). It is customary to give the sedimentation coefficient (see p. 200) of ribosomes and their components instead of their masses. For example, the eukaryotic ribosome has a sedimentation coefficient of 80 Svedberg units (80 S), while the sedimentation coefficient of its subunits are 40 S and 60 S (S values are not additive).

The smaller 40 S subunit consists of one molecule of 18 S rRNA and 33 protein molecules. The larger 60 S subunit contains three types of rRNA with sedimentation coefficients of 5 S, 5.8 S, and 28 S and 47 proteins. In the presence of mRNA, the subunits assemble to form the complete ribosome, with a mass about 650 times larger than that of a hemoglobin molecule.

The arrangement of the individual components of a ribosome has now been determined for prokaryotic ribosomes. It is known that filamentous mRNA passes through a cleft between the two subunits near the characteristic “horn” on the small subunit. tRNAs also bind near this site. The illustration shows the size of a tRNA molecule for comparison.

Prokaryotic ribosomes have a similar structure, but are somewhat smaller than those of eukaryotes (sedimentation coefficient 70 S for the complete ribosome, 30 S and 50 S for the subunits). Mitochondrial and chloroplast ribosomes are comparable to prokaryotic ones.

B. Polysomes

In cells that are carrying out intensive protein synthesis, ribosomes are often found in a linear arrangement like a string of pearls; these are known as polysomes. This arrangement arises because several ribosomes are translating a single mRNA molecule simultaneously. The ribosome first binds near the start codon (AUG; see p. 248) at the 5’ end of the mRNA (top). During translation, the ribosome moves in the direction of the 3’ end until it reaches a stop codon (UAA, UAG, or UGA). At this point, the newly synthesized chain is released, and the ribosome dissociates again into its two subunits.

C. Initiation of translation in E. coli

Protein synthesis in prokaryotes is in principle the same as in eukaryotes. However, as the process is simpler and has been better studied in prokaryotes, the details involved in translation are discussed here and on p. 252 using the example of the bacterium Escherichia coli.

The first phase of translation, initiation, involves several steps. First, two proteins, initiation factors IF–1 and IF–3, bind to the 30 S subunit (1). Another factor, IF–2, binds as a complex with GTP (2). This allows the subunit to associate with the mRNA and makes it possible for a special tRNA to bind to the start codon (3). In prokaryotes, this starter tRNA carries the substituted amino acid N-formylmethionine (fMet), in eukaryotes, it carries an unsubstituted methionine. Finally, the 50 S subunit binds to the above complex (4). During steps 3 and 4, the initiation factors are released again, and the GTP bound to IF–2 is hydrolyzed to GDP and P

In the 70 S initiation complex, formylmethionine tRNA is initially located at a binding site known as the peptidyl site (P). A second binding site, the acceptor site (A), is not yet occupied during this phase of translation. Sometimes, a third tRNA binding site is defined as an exit site (E), from which uncharged tRNAs leave the ribosome again (see p. 252; not shown).
A. Structure of eukaryotic ribosomes

49 Proteins + 28S RNA (4718 nt)

33 Proteins + 18S RNA (1874 nt)

Large subunit (60S) 2.8 · 10^6 Da

Small subunit (40S) 1.4 · 10^6 Da

Ribosome (80S) 4.2 · 10^6 Da

mRNA

C. Initiation of translation in E. coli

1. Start codon [AUG]

2. Ribosome (80S) complex

3. GTP

4. f-Met

5. mRNA

Termination

Elongation

40S

50S

70S

Initiation complex

Stop codon (UAA, UAG, or UGA)

Protein

Formyl-methionine

mRNA (165)

GTP

f-Met

mRNA

B. Polysome

Start codon [AUG]

mRNA

mRNA

Direction of ribosomal movement

Growing peptide chain

Protein

60S

40S

N

N

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Translation II: elongation and termination

After translation has been initiated (see p. 250), the peptide chain is extended by the addition of further amino acid residues (elongation) until the ribosome reaches a stop codon on the mRNA and the process is interrupted (termination).

A. Elongation and termination of protein biosynthesis in E. coli

Elongation can be divided into four phases:

1] Binding of aminoacyl tRNA. First, the peptidyl site (P) of the ribosome is occupied by a tRNA that carries at its 3’ end the complete peptide chain formed up to this point (top left). A second tRNA, loaded with the next amino acid (Val-tRNA\(^{\text{Val}}\) in the example shown), then binds via its complementary anticodon (see p. 82) to the mRNA codon exposed at the acceptor site (in this case GUC). The tRNA binds as a complex with a GTP-containing protein, the elongation factor Tu (EF–Tu) (1a). It is only after the bound GTP has been hydrolyzed to GDP and phosphate that EF–Tu dissociates again (1b). As the binding of the tRNA to the mRNA is still loose before this, GTP hydrolysis acts as a delaying factor, making it possible to check whether the correct tRNA has been bound. A further protein, the elongation factor Ts (EF–Ts), later catalyzes the exchange of GDP for GTP and in this way regenerates the EF–Tu GTP complex. EF–Tu is related to the G proteins involved in signal transduction (see p. 384).

2] Synthesis of the peptide bond takes place in the next step. Ribosomal peptidyltransferase catalyzes (without consumption of ATP or GTP) the transfer of the peptide chain from the tRNA at the P site to the NH\(_2\) group of the amino acid residue of the tRNA at the A site. The ribosome’s peptidyltransferase activity is not located in one of the ribosomal proteins, but in the 28s tRNA. Catalytically active RNAs of this type are known as ribozymes (cf. p. 246). It is thought that the few surviving ribozymes are remnants of the “RNA world”–an early phase of evolution in which proteins were not as important as they are today.

3] After the transfer of the growing peptide to the A site, the free tRNA at the P site dissociates and another GTP–containing elongation factor (EF–G GTP) binds to the ribosome. Hydrolysis of the GTP in this factor provides the energy for translocation of the ribosome. During this process, the ribosome moves three bases along the mRNA in the direction of the 3’ end. The tRNA carrying the peptide chain is stationary relative to the mRNA and reaches the ribosome’s P site during translocation, while the next mRNA codon (in this case GUC) appears at the A site.

4] The uncharged Val-tRNA then dissociates from the E site. The ribosome is now ready for the next elongation cycle.

When one of the three stop codons (UAA, UAG, or UGA) appears at the A site, termination starts.

5] There are no complementary tRNAs for the stop codons. Instead, two releasing factors bind to the ribosome. One of these factors (RF–1) catalyzes hydrolytic cleavage of the ester bond between the tRNA and the C–terminus of the peptide chain, thereby releasing the protein.

6] Hydrolysis of GTP by factor RF–3 supplies the energy for the dissociation of the whole complex into its component parts.

Energy requirements in protein synthesis are high. Four energy-rich phosphoric acid anhydride bonds are hydrolyzed for each amino acid residue. Amino acid activation uses up two energy-rich bonds per amino acid (ATP → AMP + PP; see p. 248), and two GTPs are consumed per elongation cycle. In addition, initiation and termination each require one GTP per chain.

Further information

In eukaryotic cells, the number of initiation factors is larger and initiation is therefore more complex than in prokaryotes. The cap at the 5’ end of mRNA and the polyA tail (see p. 246) play important parts in initiation. However, the elongation and termination processes are similar in all organisms. The individual steps of bacterial translation can be inhibited by antibiotics (see p. 254).
A. Elongation and termination of protein biosynthesis in *E. coli*

- **Elongation**
  - Peptidyl transferase
  - GTP
  - EF-G
  - GTP
  - EF-G
  - GDP
  - EF-Tu
  - GTP

- **Termination**
  - Stop codon
  - Termination factors
  - RF-1
  - RF-3
  - 30S subunit
  - 50S subunit
  - mRNA
  - Protein

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Antibiotics

A. Antibiotics: overview

Antibiotics are substances which, even at low concentrations, inhibit the growth and reproduction of bacteria and fungi. The treatment of infectious diseases would be inconceivable today without antibiotics. Substances that only restrict the reproduction of bacteria are described as having bacteriostatic effects (or fungistatic for fungi). If the target cells are killed, then the term bactericidal (or fungicidal) is used. Almost all antibiotics are produced by microorganisms—mainly bacteria of the genus Streptomyces and certain fungi. However, there are also synthetic antibacterial substances, such as sulfonamides and gyrase inhibitors.

A constantly increasing problem in antibiotic treatment is the development of resistant pathogens that no longer respond to the drugs available. The illustration shows a few of the therapeutically important antibiotics and their sites of action in the bacterial metabolism.

Substances known as intercalators, such as rifampicin and actinomycin D (bottom) are deposited in the DNA double helix and thereby interfere with replication and transcription (B). As DNA is the same in all cells, intercalating antibiotics are also toxic for eukaryotes, however. They are therefore only used as cytostatic agents (see p. 402). Synthetic inhibitors of DNA topoisomerase II (see p. 240), known as gyrase inhibitors (center), restrict replication and thus bacterial reproduction.

A large group of antibiotics attack bacterial ribosomes. These inhibitors of translation (left) include the tetracyclines—broad-spectrum antibiotics that are effective against a large number of different pathogens. The aminoglycosides, of which streptomycin is the best-known, affect all phases of translation. Erythromycin impairs the normal functioning of the large ribosomal subunit. Chloramphenicol, one of the few natural nitro compounds, inhibits ribosomal peptidyldetransferase. Finally, puromycin mimics an aminoacyl tRNA and therefore leads to premature interruption of elongation.

The β-lactam antibiotics (bottom right) are also frequently used. The members of this group, the penicillins and cephalosporins, are synthesized by fungi and have a reactive β-lactam ring. They are mainly used against Gram-positive pathogens, in which they inhibit cell wall synthesis (C).

The first synthetic antibiotics were the sulfonamides (right). As analogues of p-aminobenzoic acid, these affect the synthesis of folic acid, an essential precursor of the coenzyme THF (see p. 108). Transport antibiotics (top center) have the properties of ion channels (see p. 222). When they are deposited in the plasma membrane, it leads to a loss of ions that damages the bacterial cells.

B. Intercalators

The effects of intercalators (see also p. 262) are illustrated here using the example of the daunomycin–DNA complex, in which two daunomycin molecules (red) are inserted in the double helix (blue). The antibiotic’s ring system inserts itself between G/C base pairs (bottom), while the sugar moiety occupies the minor groove in the DNA (above). This leads to a localized change of the DNA conformation that prevents replication and transcrip-tion.

C. Penicillin as a “suicide substrate”

The site of action in the β-lactam antibiotics is muramoylpentapeptide carboxypeptidase, an enzyme that is essential for cross-linking of bacterial cell walls. The antibiotic resembles the substrate of this enzyme (a peptide with the C-terminal sequence D-Ala–D-Ala) and is therefore reversibly bound in the active center. This brings the β-lactam ring into proximity with an essential serine residue of the enzyme. Nucleophilic substitution then results in the formation of a stable covalent bond between the enzyme and the inhibitor, blocking the active center (see p. 96). In dividing bacteria, the loss of activity of the enzyme leads to the formation of unstable cell walls and eventually death.
A. Antibiotics: overview

B. Intercalators

C. Penicillin as “suicide substrate”

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Mutation and repair

Genetic information is set down in the base sequence of DNA. Changes in the DNA bases or their sequence therefore have mutagenic effects. Mutagens often also damage growth regulation in cells, and they are then also carcinogenic (see p. 400). Gene alterations (mutations) are one of the decisive positive factors in biological evolution. On the other hand, an excessive mutation frequency would threaten the survival of individual organisms or entire species. For this reason, every cell has repair mechanisms that eliminate most of the DNA changes arising from mutations (C).

A. Mutagenic agents

Mutations can arise as a result of physical or chemical effects, or they can be due to accidental errors in DNA replication and recombination.

The principal physical mutagen is ionizing radiation (α, β, and γ radiation, X-rays). In cells, it produces free radicals (molecules with unpaired electrons), which are extremely reactive and can damage DNA. Short-wavelength ultraviolet light (UV light) also has mutagenic effects, mainly in skin cells (sunburn). The most common chemical change due to UV exposure is the formation of thymine dimers, in which two neighboring thymine bases become covalently linked to one another (2). This results in errors when the DNA is read during replication and transcription.

Only a few examples of the group of chemical mutagens are shown here. Nitrous acid (HNO₂; salt: nitrite) and hydroxylamine (NH₂OH) both deaminate bases; they convert cytosine to uracil and adenine to inosine.

Alkylation compounds carry reactive groups that can form covalent bonds with DNA bases (see also p. 402). Methyl nitrosamines (3) release the reactive methyl cation (CH₃⁺), which methylates OH and NH₂ groups in DNA. The dangerous carcinogen benzo[a]pyrene is an aromatic hydrocarbon that is only converted into the active form in the organism (4; see p. 316). Multiple hydroxylation of one of the rings produces a reactive epoxide that can react with NH₂ groups in guanine residues, for example. Free radicals of benzo[a]pyrene also contribute to its toxicity.

B. Effects

Nitrous acid causes point mutations (1). For example, C is converted to U, which in the next replication pairs with A instead of G. The alteration thus becomes permanent. Mutations in which a number of nucleotides not divisible by three are inserted or removed lead to reading errors in whole segments of DNA, as they move the reading frame (frameshift mutations). This is shown in Fig. 2 using a simple example. From the inserted C onwards, the resulting mRNA is interpreted differently during translation, producing a completely new protein sequence.

C. Repair mechanisms

An important mechanism for the removal of DNA damage is excision repair (1). In this process, a specific excision endonuclease removes a complete segment of DNA on both sides of the error site. Using the sequence of the opposite strand, the missing segment is then replaced by a DNA polymerase. Finally, a DNA ligase closes the gaps again.

Thymine dimers can be removed by photoreactivation (2). A specific photolyase binds at the defect and, when illuminated, cleaves the dimer to yield two single bases again.

A third mechanism is recombination repair (3, shown in simplified form). In this process, the defect is omitted during replication. The gap is closed by shifting the corresponding sequence from the correctly replicated second strand. The new gap that results is then filled by polymerases and ligases. Finally, the original defect is corrected by excision repair as in Fig. 1 (not shown).
A. Mutagenic agents

1. Ionizing radiation
2. Alkylating compounds
3. UV radiation
4. Free radicals
5. Chemical modification of bases
6. Desamination
7. Formation of pyrimidine dimers
8. Base exchange
9. Spontaneous loss of bases
10. Chemical modification of bases
11. Reactive methyl group

B. Effects

1. Point mutation
2. Frameshift mutation
3. Insertion
4. Deletions or insertions due to faulty recombination

C. Repair mechanisms

1. Excision repair
2. Recombinational repair
3. Photoreactivation
4. Repair mechanisms

Thymine dimer

Excision endonuclease

Defect-binding protein

Single-strand binding proteins

DNA polymerase

DNA ligase

Repairod DNA

Photo-lyase

Light

Epoxide

Desamination

Deletions or insertions due to faulty recombination

Point mutation

Frameshift mutation

Insertion

A. Mutagenic agents

B. Effects

C. Repair mechanisms

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DNA cloning

The growth of molecular genetics since 1970 has mainly been based on the development and refinement of methods of analyzing and manipulating DNA. Genetic engineering has practical applications in many fields. For example, it has provided new methods of diagnosing and treating diseases, and it is now also possible to create targeted changes in specific characteristics of organisms. Since biological risks cannot be completely ruled out with these procedures, it is particularly important to act responsibly when dealing with genetic engineering. A short overview of important methods involved in genetic engineering is provided here and on the following pages.

A. Restriction endonucleases

In many genetic engineering procedures, defined DNA fragments have to be isolated and then newly combined with other DNA segments. For this purpose, enzymes are used that can cut DNA and join it together again inside the cell. Of particular importance are restriction endonucleases—a group of bacterial enzymes that cleave the DNA double strand in a sequence-specific way. The numerous restriction enzymes known are named using abbreviations based on the organism from which they originate. The example used here is EcoRI, a nuclease isolated from the bacterium Escherichia coli.

Like many other restriction endonucleases, EcoRI cleaves DNA at the site of a palindromic—i.e., a short segment of DNA in which both the strand and counter-strand have the same sequence (each read in the 5’→3’ direction). In this case, the sequence is 5’→GAATTC→3’. EcoRI, a homodimer, cleaves the phosphoric acid diester bonds in both strands between G and A. This results in the formation of complementary overhanging or “sticky” ends (AAAT), which are held together by base pairing. However, they are easily separated—e.g. by heating. When the fragments are cooled, the overhanging ends hybridize again in the correct arrangement. The cleavage sites can then be sealed again by a DNA ligase.

B. DNA cloning

Most DNA segments—e.g., genes—occur in very small quantities in the cell. To be able to work with them experimentally, a large number of identical copies (“clones”) first have to be produced. The classic procedure for cloning DNA takes advantage of the ability of bacteria to take up and replicate short, circular DNA fragments known as plasmids.

The segment to be cloned is first cut out of the original DNA using restriction endonucleases (see above; for the sake of simplicity, cleavage using EcoRI alone is shown here, but in practice two different enzymes are usually used). As a vehicle (“vector”), a plasmid is needed that has only one EcoRI cleavage site. The plasmid rings are first opened by cleavage with EcoRI and then mixed with the isolated DNA fragments. Since the fragment and the vector have the same overhanging ends, some of the molecules will hybridize in such a way that the fragment is incorporated into the vector DNA. When the cleavage sites are now closed again using DNA ligase, a newly combined (“recombinant”) plasmid arises.

By pretreating a large number of host cells, one can cause some of them to take up the plasmid (a process known as transformation) and replicate it along with their own genome when reproducing. To ensure that only host bacteria that contain the plasmid replica, plasmids are used that give the host resistance to a particular antibiotic. When the bacteria are incubated in the presence of this antibiotic, only the cells containing the plasmid will replicate. The plasmid is then isolated from these cells, cleaved with EcoRI again, and the fragments are separated using agarose gel electrophoresis (see p. 262). The desired fragment can be identified using its size and then extracted from the gel and used for further experiments.
A. Restriction endonucleases

B. DNA cloning

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DNA sequencing

A. Gene libraries

It is often necessary in genetic engineering to isolate a DNA segment when its details are not fully known—e.g., in order to determine its nucleotide sequence. In this case, one can use what are known as DNA libraries. A DNA library consists of a large number of vector DNA molecules containing different fragments of foreign DNA. For example, it is possible to take all of the mRNA molecules present in a cell and transcribe them into DNA. These DNA fragments (known as cDNA or dDNA) are then randomly introduced into vector molecules.

A library of genomic DNA can be established by cleaving the total DNA from a cell into small fragments using restriction endonucleases (see p. 258), and then incorporating these into vector DNA. Suitable vectors for gene libraries include bacteriophages, for example (“phages” for short). Phages are viruses that only infect bacteria and are replicated by them (see p. 404). Gene libraries have the advantage that they can be searched for specific DNA segments, using hybridization with oligonucleotides.

The first step is to strongly dilute a small part of the library (10^7–10^9 phages in a small volume), mix it with host bacteria, and plate out the mixture onto nutrient medium. The bacteria grow and form a continuous cloudy layer of cells. Bacteria infected by phages grow more slowly. In their surroundings, the bacterial “lawn” is less dense, and a clearer circular zone known as a plaque forms. The bacteria in this type of plaque exclusively contain the offspring of a single phage from the library.

The next step is to make an impression of the plate on a plastic foil, which is then heated. This causes the phage DNA to adhere to the foil. When the foil is incubated with a DNA fragment that hybridizes to the DNA segment of interest (a gene probe), the probe binds to the sites on the imprint at which the desired DNA is attached. Binding of the gene probe can be detected by prior radioactive or other labeling of the probe. Phages from the positive plaques in the original plate are then isolated and replicated. Restriction cleavage finally provides large amounts of the desired DNA.

B. Sequencing of DNA

The nucleotide sequence of DNA is nowadays usually determined using the so-called chain termination method. In single-strand sequencing, the DNA fragment (a) is cloned into the DNA of phage M13 (see p. 404), from which the coded single strand can be easily isolated. This is hybridized with a primer— a short, synthetically produced DNA fragment that binds to 3’ end of the introduced DNA segment (b).

Based on this hybrid, the missing second strand can now be generated in the test tube by adding the four deoxynucleoside triphosphates (dNTP) and a suitable DNA polymerase (c). The trick lies in also adding small amounts of deoxynucleoside triphosphates (ddNTP). Incorporating a ddNTP leads to the termination of second-strand synthesis. This can occur whenever the corresponding dNTP ought to be incorporated. The illustration shows this in detail using the example of ddGTP. In this case, fragments are obtained that each include the primer plus three, six, eight, 13, or 14 additional nucleotides. Four separate reactions, each with a different ddNTP, are carried out (c), and the products are placed side by side on a supporting material. The fragments are then separated by gel electrophoresis (see p. 76), in which they move in relation to their length.

Following visualization (d), the sequence of the fragments in the individual lanes is simply read from bottom to top (e) to directly obtain the nucleotide sequence. A detail from such a sequencing gel and the corresponding protein sequence are shown in Fig. 2.

In a more modern procedure, the four ddNTPs are covalently marked with fluorescent dyes, which produce a different color for each ddNTP on laser illumination. This allows the sequence in which the individual fragments appear at the lower end of the gel to be continuously recorded and directly stored in digital form.
A. Gene libraries

Gene library in phages

Host cell

Imprint on plastic membrane

Plate with phage plaques

Positive plaque

Gene probe

Washing, detection of the gene probe

Cloned gene

DNA isolation

Restriction

Phage replications

B. Sequencing of DNA

Synthetic primer

Single-stranded preparation

Hybridization

+ dGTP + dATP + dCTP + ddTTP

Example: G = ddG

Gel electrophoresis

Visualization of the fragments

Reading off (→): ACATG...

2. Sequence pattern

DNA sequence

Protein sequence
PCR and protein expression

A. Polymerase chain reaction (PCR)

The polymerase chain reaction (PCR) is an important procedure in genetic engineering that allows any DNA segment to be replicated (amplified) without the need for restriction enzymes, vectors, or host cells (see p. 258). However, the nucleotide sequence of the segment to be amplified; also needed are sufficient quantities of the four deoxyribonucleoside triphosphates and a special heat-tolerant DNA polymerase. The primers are produced by chemical synthesis, and the polymerase is obtained from thermostable bacteria.

First, the starter is heated to around 90 °C to separate the DNA double helix into single strands (a; cf. p. 84). The mixture is then cooled to allow hybridization of the primers (b). Starting from the primers, complementary DNA strands are now synthesized in both directions by the polymerase (c). This cycle (cycle 1) is repeated 20–30 times with the same reaction mixture (cycle 2 and subsequent cycles). The cyclic heating and cooling are carried out by computer-controlled thermostats.

After only the third cycle, double strands start to form with a length equal to the distance between the two primers. The proportion of these approximately doubles during each cycle, until almost all of the newly synthesized segments have the correct length.

B. DNA electrophoresis

The separation of DNA fragments by electrophoresis is technically simpler than protein electrophoresis (see p. 78). The mobility of molecules in an electrical field of a given strength depends on the size and shape of the molecules, as well as their charge. In contrast to proteins, in which all three factors vary, the ratio of mass to charge in nucleic acids is constant, as all of the nucleotide components have similar masses and carry one negative charge. When electrophoresis is carried out in a wide-meshed support material that does not separate according to size and shape, the mobility of the molecules depends on their mass alone. The supporting material generally used in genetic engineering is a gel of the polysaccharide agarose (see p. 40). Agarose gels are not very stable and are therefore poured horizontally into a plastic chamber in which they are used for separation (top).

To make the separated fragments visible, after running the procedure the gels are placed in solutions of ethidium bromide. This is an intercalator (see p. 254) that shows strong fluorescence in UV light after binding to DNA, although it barely fluoresces in an aqueous solution. The result of separating two PCR amplificates (lanes 1 and 2) is shown in the lower part of the illustration. Comparing their distances with those of polynucleotides of known lengths (lane 3; bp = base pairs) yields lengths of approximately 800 bp for fragment 1 and 1800 bp for fragment 2. After staining, the bands can be cut out of the gel and the DNA can be extracted from them and used for further experiments.

C. Overexpression of proteins

To treat some diseases, proteins are needed that occur in such small quantities in the organism that isolating them on a large scale would not be economically feasible. Proteins of this type can be obtained by overexpression in bacteria or eukaryotic cells. To do this, the corresponding gene is isolated from human DNA and cloned into an expression plasmid as described on p. 258. In addition to the gene itself, the plasmid also has to contain DNA segments that allow replication by the host cell and transcription of the gene. After transformation and replication of suitable host cells, induction is used in a targeted fashion to trigger efficient transcription of the gene. Translation of the mRNA formed in the host cell then gives rise to large amounts of the desired protein. Human insulin (see p. 76), plasminogen activators for dissolving blood clots (see p. 292), and the growth hormone somatotropin are among the proteins produced in this way.
A. Polymerase chain reaction (PCR)

1. Heat
2. Hybridize

B. DNA electrophoresis

1. Electrophoresis chamber
2. Sample
3. Power supply unit
4. Agarose gel
5. Ethidium bromide

C. Overexpression of proteins

1. Transformations
2. Propagation
3. Induction
4. Overexpression protein
5. Protein purification
6. Cell lysis

Ribosome binding site
Inducible promoter
Gene for antibiotic resistance
Origin of replication
Expression plasmid
Host cell
Gene to be expressed

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Genetic engineering in medicine

Genetic engineering procedures are becoming more and more important in medicine for diagnostic purposes (A–C). New genetic approaches to the treatment of severe diseases are still in the developmental stage (*gene therapy*, D).

A. DNA fingerprinting

DNA fingerprinting is used to link small amounts of biological material—e.g., traces from the site of a crime—to a specific person. The procedure now used is based on the fact that the human genome contains non-coding repetitive DNA sequences, the length of which varies from individual to individual. Short tandem repeats (STRs) thus exist in which dinucleotides (e.g., T–T—X—) are frequently repeated. Each STR can occur in five to 15 different lengths (alleles), of which one individual possesses only one or two. When the various allele combinations for several STRs are determined after PCR amplification of the DNA being investigated, a "genetic fingerprint" of the individual from whom the DNA originates is obtained. Using comparative material—e.g., saliva samples—definite identification is then possible.

B. Diagnosis of sickle-cell anemia using RFLP

This example illustrates a procedure for diagnosing a point mutation in the β-globin gene that leads to sickle-cell anemia (see p. 248). The mutation in the first exon of the gene destroys a cleavage site for the restriction endonuclease MstII (see p. 258). When the DNA of healthy and diseased individuals is cleaved with MstII, different fragments are produced in the region of the β-globin gene, which can be separated by electrophoresis and then demonstrated using specific probes (see p. 260). In addition, heterozygotic carriers of the sickle-cell gene can be distinguished from homozygotic ones.

C. Identification of viral DNA using RT-PCR

In viral infections, it is often difficult to determine the species of the pathogen precisely. RT-PCR can be used to identify RNA viruses. In this procedure, reverse transcriptase (see p. 404) is used to transcribe the viral RNA into dsDNA, and then PCR is employed to amplify a segment of this DNA with virus-specific primers. In this way, an ampiclitate with a characteristic length can be obtained for each pathogen and identified using gel electrophoresis as described above.

D. Gene therapy

Many diseases, such as hereditary metabolic defects and tumors, can still not be adequately treated. About 10 years ago, projects were therefore initiated that aimed to treat diseases of this type by transferring genes into the affected cells (gene therapy). The illustration combines conceivable and already implemented approaches to gene therapy for metabolic defects (left) and tumors (right). None of these procedures has yet become established in clinical practice.

If a mutation leads to failure of an enzyme E1 (left), its substrate B will no longer be converted into C and will accumulate. This can lead to cell damage by B itself or by a toxic product formed from it. Treatment with intact E1 is not possible, as the proteins are not capable of passing through the cell membrane. By contrast, it is in principle possible to introduce foreign genes into the cell using viruses as vectors (adenoviruses or retroviruses are mainly used). Their gene products could replace the defective E1 or convert B into a harmless product. Another approach uses the so-called antisense DNA (bottom right). This consists of polynucleotides that hybridize with the mRNA for specific cellular proteins and thereby prevent their translation. In the case shown, the synthesis of E2 could be blocked, for example.

The main problem in chemotherapy for tumors is the lack of tumor-specificity in the highly toxic cytostatic agents used (see p. 402). Attempts are therefore being made to introduce into tumor cells genes with products that are only released from a precursor to form active cytostatics once they have reached their target (left). Other gene products are meant to force the cells into apoptosis (see p. 396) or make them more susceptible to attack by the immune system. To steer the viral vectors to the tumor (targeting), attempts are being made to express proteins on the virus surface that are bound by tumor-specific receptors. Fusion with a tumor-specific promoter could also help limit the effect of the foreign gene to the tumor cells.
B. Diagnosis of sickle-cell anemia using RFLP

- **DNA** extraction
- **PCR** amplification
- **Agarose gel** analysis

<table>
<thead>
<tr>
<th>Locus 1</th>
<th>Locus 2</th>
<th>Locus 3</th>
</tr>
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<tr>
<td>Alleles</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1/3</td>
<td>1/4</td>
<td></td>
</tr>
<tr>
<td>2/4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3/3</td>
<td>3/5</td>
<td></td>
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</tbody>
</table>

**Mutation**

- 1 Normal (A/A)
- 2 Heterozygotic (A/S)
- 3 Homozygotic (S/S)

C. Evidence of viral DNA using RT-PCR

- **Viral vector** with foreign DNA
- **Transcription**
- **Cell death**

D. Gene therapy

1. For metabolic defects
   - Normal body cell
   - Harmless product
   - Accumulates
   - Toxic product
   - Antisense DNA
   - Apoptosis

2. For tumors
   - Tumor cell DNA
   - Cytostatic agent
   - Cell proliferation
   - Immune system
Digestion: overview

Most components of food (see p. 360) cannot be resorbed directly by the organism. It is only after they have been broken down into smaller molecules that the organism can take up the essential nutrients. Digestion refers to the mechanical and enzymatic breakdown of food and the resorption of the resulting products.

A. Hydrolysis and resorption of food components

Following mechanical fragmentation of food during chewing in the mouth, the process of enzymatic degradation starts in the stomach. For this purpose, the chyme is mixed with digestive enzymes that occur in the various digestive secretions or in membrane-bound form on the surface of the intestinal epithelium (see p. 268). Almost all digestive enzymes are hydrolases (class 3 enzymes; see p. 88): they catalyze the cleavage of composite bonds with the uptake of water.

Proteins are first denatured by the stomach’s hydrochloric acid (see p. 270), making them more susceptible to attack by the endopeptidases (proteinases) present in gastric and pancreatic juice. The peptides released by endopeptidases are further degraded into amino acids by exopeptidases. Finally, the amino acids are resorbed by the intestinal mucosa in cotransport with Na⁺ ions (see p. 220). There are separate transport systems for each of the various groups of amino acids.

Carbohydrates mainly occur in food in the form of polymers (starches and glycogen). They are cleaved by pancreatic amylase into oligosaccharides and are then hydrolyzed by glycosidases, which are located on the surface of the intestinal epithelium, to yield monosaccharides. Glucose and galactose are taken up into the enterocytes by secondary active cotransport with Na⁺ ions (see p. 220). In addition, monosaccharides also have passive transport systems in the intestine.

Nucleic acids are broken down into their components by nucleases from the pancreas and small intestine (ribonucleases and deoxyribonucleases). Further breakdown yields the nucleobases (purine and pyrimidine derivatives), pentoses (ribose and deoxyribose), phosphate, and nucleosides (nucleobase–pentose). These cleavage products are resorbed by the intestinal wall in the region of the jejunum.

Lipids are a special problem for digestion, as they are not soluble in water. Before enzymatic breakdown, they have to be emulsified by bile salts and phospholipids in the bile (see p. 314). At the water–lipid interface, pancreatic lipase then attacks monoglycerols with the help of colipase (see p. 270). The cleavage products include fatty acids, 2-monoacylglycerols, glycerol, and phosphate from phospholipid breakdown. After resorption into the epithelial cells, fats are resynthesized from fatty acids, glycerol and 2-monoacylglycerols and passed into the lymphatic system (see p. 272). The lipids in milk are more easily digested, as they are already present in emulsion; on cleavage, they mostly provide short-chain fatty acids.

Inorganic components such as water, electrolytes, and vitamins are directly absorbed by the intestine.

High-molecular-weight indigestible components, such as the fibrous components of plant cell walls, which mainly consist of cellulose and lignin, pass through the bowel unchanged and form the main component of feces, in addition to cells shed from the intestinal mucosa. Dietary fiber makes a positive contribution to digestion as a bulk material by binding water and promoting intestinal peristalsis.

The food components resorbed by the epithelial cells of the intestinal wall in the region of the jejunum and ileum are transported directly to the liver via the portal vein. Fats, cholesterol, and lipid-soluble vitamins are exceptions. These are first released by the enterocytes in the form of chylomicrons (see p. 278) into the lymph system, and only reach the blood via the thoracic duct.
A. Hydrolysis and resorption of dietary constituents

**Nutrients**
- Proteins
- Carbohydrates
- Nucleic acids
- Lipids
- Vitamins
- Inorganic substances

**Cleavage products**
- Bile salts
- Phospholipids
- 2-Monoacylglycerol
- Fatty acids
- Cholesterol

**Transport**
- Hydrophilic
- Lipophilic

**Enzymatic hydrolysis**
- Portal vessel
- Lymph system
- Liver
- Blood
- Feces

**Resorption**
- Resorption by active transport

*Wilhelm Busch*
Digestive secretions

A. Digestive juices

Saliva. The salivary glands produce a slightly alkaline secretion which—in addition to water and salts—contains glycoproteins (mucins) as lubricants, antibodies, and enzymes. α-Amylase attacks polysaccharides, and a lipase hydrolyzes a small proportion of the neutral fats. α-Amylase and lipase, a mucin-cleaving enzyme (see p. 40), probably serve to regulate the oral bacterial flora rather than for digestion (see p. 340).

Gastric juice. In the stomach, the chyme is mixed with gastric juice. Due to its hydrochloric acid content, this secretion of the gastric mucosa is strongly acidic (pH 1–3; see p. 270). It also contains mucus (mainly glycoproteins known as mucins), which protects the mucosa from the hydrochloric acid, salts, and pepsinogen—the proenzyme ("zymogen") of the aspartate proteinase pepsin (see pp. 176, 270). In addition, the gastric mucosa secretes what is known as "intrinsic factor"—a glycoprotein needed for resorption of vitamin B₁₂ ("extrinsic factor") in the bowel.

In the stomach, pepsin and related enzymes initiate the enzymatic digestion of proteins, which takes 1–3 hours. The acidic gastric contents are then released into the duodenum in batches, where they are neutralized by alkaline pancreatic secretions and mixed with cystic bile.

Pancreatic secretions. In the acinar cells, the pancreas forms a secretion that is alkaline due to its HCO₃⁻ content, the buffer capacity of which is sufficient to neutralize the stomach's hydrochloric acid. The pancreatic secretion also contains many enzymes that catalyze the hydrolysis of high-molecular-weight food components. All of these enzymes are hydrolyses with pH optima in the neutral or weakly alkaline range. Many of them are formed and secreted as proenzymes and are only activated in the bowel lumen (see p. 270).

Trypsin, chymotrypsin, and elastase are endopeptidases that belong to the group of serine proteinases (see p. 176). Trypsin hydrolyzes specific peptide bonds on the C side of the basic amino acids Arg and Lys, while chymotrypsin prefers peptide bonds of the apolar amino acids Tyr, Trp, Phe, and Leu (see p. 94). Elastase mainly cleaves on the C side of the aliphatic amino acids Gly, Ala, Val, and Ile. Smaller peptides are attacked by carboxypeptidases, which as exopeptidases cleave individual amino acids from the C-terminal end of the peptides (see p. 176).

β-Amylase, the most important endoglycosidase in the pancreas, catalyzes the hydrolysis of α₁→4 bonds in the polymeric carbohydrates starch and glycogen. This releases maltose, maltriose, and a mixture of other oligosaccharides.

Various pancreatic enzymes hydrolyze lipids, including lipase with its auxiliary protein colipase (see p. 270), phospholipase A₂, and sterol esterase. Bile salts activate the lipid-cleaving enzymes through micelle formation (see below).

Several hydrolases—particularly ribonuclease (RNAse) and deoxyribonuclease (DNAse)—break down the nucleic acids contained in food.

Bile. The liver forms a thin secretion (bile) that is stored in the gallbladder after water and salts have been extracted from it. From the gallbladder, it is released into the duodenum. The most important constituents of bile are water and inorganic salts, bile acids and bile salts (see p. 314), phospholipids, bile pigments, and cholesterol. Bile salts, together with phospholipids, emulsify insoluble food lipids and activate the lipases. Without bile, fats would be inadequately cleaved, if at all, resulting in "fatty stool" (steatorrhea). Resorption of fat-soluble vitamins would also be affected.

Small-intestinal secretions. The glands of the small intestine (the Lieberkühn and Brunner glands) secrete additional digestive enzymes into the bowel. Together with enzymes on the microvilli of the intestinal epithelium (peptidases, glycosidases, etc.), these enzymes ensure almost complete hydrolysis of the food components previously broken down by the endoenzymes.
### A. Digestive juices

#### Pancreatic secretions

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<th>Function</th>
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<td>Oligo-1,6-glucosidase (3.2.1.10)</td>
</tr>
<tr>
<td>β-Galactosidase (3.2.1.23)</td>
</tr>
<tr>
<td>Sucrose-α-glucosidase (3.2.1.48)</td>
</tr>
<tr>
<td>α, α-Trehalase (3.2.1.28)</td>
</tr>
<tr>
<td>Alkaline phosphatase (3.1.3.1)</td>
</tr>
<tr>
<td>Polyphosphatases (3.1.3.n)</td>
</tr>
<tr>
<td>Nucleotidases (3.2.2.n)</td>
</tr>
<tr>
<td>Phospholipases (3.1.n.n)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Saliva</th>
</tr>
</thead>
<tbody>
<tr>
<td>Daily secretion 1.0–1.5 l</td>
</tr>
<tr>
<td>pH 7</td>
</tr>
<tr>
<td>Water</td>
</tr>
<tr>
<td>Salts</td>
</tr>
<tr>
<td>Antibodies</td>
</tr>
<tr>
<td>α-Amylases (3.2.1.1)</td>
</tr>
<tr>
<td>α-Lactalbumin (3.2.1.7)</td>
</tr>
<tr>
<td>Lysozyme (3.2.1.17)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Bile</th>
</tr>
</thead>
<tbody>
<tr>
<td>Daily secretion 0.6 l</td>
</tr>
<tr>
<td>pH 6.5–7.7</td>
</tr>
<tr>
<td>Water</td>
</tr>
<tr>
<td>Salts</td>
</tr>
<tr>
<td>Bile salts</td>
</tr>
<tr>
<td>Phospholipids</td>
</tr>
<tr>
<td>Bile pigments</td>
</tr>
<tr>
<td>Cholesterol</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Gastric juice</th>
</tr>
</thead>
<tbody>
<tr>
<td>Daily secretion 2–3 l</td>
</tr>
<tr>
<td>pH 1</td>
</tr>
<tr>
<td>Water</td>
</tr>
<tr>
<td>Salts</td>
</tr>
<tr>
<td>HCl</td>
</tr>
<tr>
<td>Antacid</td>
</tr>
<tr>
<td>Mucus</td>
</tr>
<tr>
<td>Pepsins (3.4.21.1)</td>
</tr>
<tr>
<td>Chymosin (3.4.21.4)</td>
</tr>
<tr>
<td>Triacylglycerol lipase (3.1.1.3)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Secretions of the small intestine</th>
</tr>
</thead>
<tbody>
<tr>
<td>Daily secretion unknown</td>
</tr>
<tr>
<td>pH 6.5–7.8</td>
</tr>
<tr>
<td>Aminopeptidases (3.4.11.n)</td>
</tr>
<tr>
<td>Dipeptidases (3.4.13.n)</td>
</tr>
<tr>
<td>α-Glucosidase (3.2.1.20)</td>
</tr>
<tr>
<td>Oligo-1,6-glucosidase (3.2.1.10)</td>
</tr>
<tr>
<td>β-Galactosidase (3.2.1.23)</td>
</tr>
<tr>
<td>Sucrose-α-glucosidase (3.2.1.48)</td>
</tr>
<tr>
<td>α, α-Trehalase (3.2.1.28)</td>
</tr>
<tr>
<td>Alkaline phosphatase (3.1.3.1)</td>
</tr>
<tr>
<td>Polyphosphatases (3.1.3.n)</td>
</tr>
<tr>
<td>Nucleotidases (3.2.2.n)</td>
</tr>
<tr>
<td>Phospholipases (3.1.n.n)</td>
</tr>
</tbody>
</table>

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Digestive processes

Gastric juice is the product of several cell types. The parietal cells produce hydrochloric acid, chief cells release pepsinogen, and accessory cells form a mucin-containing mucus.

A. Formation of hydrochloric acid

The secretion of hydrochloric acid (H⁺ and Cl⁻) by the parietal cells is an active process that uses ATP and takes place against a concentration gradient (in the gastric lumen, with a pH of 1, the H⁺ concentration is some 10⁶ times higher than in the parietal cells, which have a pH of 7).

The precursors of the exported H⁺ ions are carbon dioxide (CO₂) and water (H₂O). CO₂ diffuses from the blood into the parietal cells, and in a reaction catalyzed by carbonic dehydratase (carbonic anhydrase [2]), it reacts with H₂O to form H⁺ and hydrogen carbonate (HCO₃⁻). The H⁺ ions are transported into the gastric lumen in exchange for K⁺ by a membrane-bound H⁺/K⁺-exchanging ATPase [1] (a transport ATPase of the P type; see p. 220).

The remaining hydrogen carbonate is released into the interstitium in electroneutral antiport in exchange for chloride ions (Cl⁻), and from there into the blood. The Cl⁻ ions follow the secreted protons through a channel into the gastric lumen.

The hydrochloric acid in gastric juice is important for digestion. It activates pepsinogen to form pepsin (see below) and creates an optimal pH level for it to take effect. It also denatures food proteins so that they are more easily attacked by proteinases, and it kills micro-organisms.

Regulation. HCl secretion is stimulated by the peptide hormone gastrin, the mediator histamine (see p. 380), and—via the neurotransmitter acetylcholine—by the autonomous nervous system. The peptide somatostatin and certain prostaglandins (see p. 390) have inhibitory effects. Together with cholecystokinin, secretin, and other peptides, gastrin belongs to the group of gastrointestinal hormones (see p. 370). All of these are formed in the gastrointestinal tract and mainly act in the vicinity of the site where they are formed—i.e., they are paracrine hormones (see p. 372).

While gastrin primarily enhances HCl secretion, cholecystokinin and secretin mainly stimulate pancreatic secretion and bile release.

B. Zymogen activation

To prevent self-digestion, the pancreas releases most proteolytic enzymes into the duodenum in an inactive form as proenzymes (zymogens). Additional protection from the effects of premature activation of pancreatic proteinases is provided by proteinase inhibitors in the pancreatic tissue, which inactivate active enzymes by complex formation (right). Trypsinogen plays a key role among the proenzymes released by the pancreas. In the bowel, it is proteolytically converted into active trypsin (see p. 176) by enteropeptidase, a membrane enzyme on the surface of the enterocytes. Trypsin then autocatalytically activates additional trypsinogen molecules and the other proenzymes (left).

C. Fat digestion

Due to the "hydrophobic effect" (see p. 28), water-insoluble neutral fats in the aqueous environment of the bowel lumen would aggregate into drops of fat in which most of the molecules would not be accessible to pancreatic lipase. The amphipathic substances in bile (bile acids, bile salts, phospholipids) create an emulsion in which they occupy the surface of the droplets and thereby prevent them from coalescing into large drops. In addition, the bile salts, together with the auxiliary protein colipase, mediate binding of tracylglycerol lipase [1] to the emulsified fat droplets. Activation of the lipase is triggered by a conformation change in the C-terminal domain of the enzyme, which uncovers the active center.

During passage through the intestines, the active lipase breaks down the triacylglycerols in the interior of the droplets into free fatty acids and amphipathic monoaoylglycerols. Over time, smaller micelles develop (see p. 28), in the envelope of which monoaoylglycerols are present in addition to bile salts and phospholipids. Finally, the components of the micelles are resorbed by the enterocytes in ways that have not yet been explained.

Monaoylglycerols and fatty acids are reassembled into fats again (see p. 272), while the bile acids return to the liver (enterohepatic circulation; see p. 314).
A. Formation of hydrochloric acid

B. Zymogen activation

C. Fat digestion

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Resorption

Enzymatic hydrolysis in the digestive tract breaks down foodstuffs into their resorbable components. Resorption of the cleavage products takes place primarily in the small intestine. Only ethanol and short-chain fatty acids are already resorbed to some extent in the stomach.

The resorption process is facilitated by the large inner surface of the intestine, with its brush-border cells. Lipophilic molecules penetrate the plasma membrane of the mucosal cells by simple diffusion, whereas polar molecules require transporters (facilitated diffusion; see p. 218). In many cases, carrier-mediated cotransport with Na⁺ ions can be observed. In this case, the difference in the concentration of the sodium ions (high in the intestinal lumen and low in the mucosal cells) drives the import of nutrients against a concentration gradient (secondary active transport; see p. 220). Failure of carrier systems in the gastrointestinal tract can result in diseases.

A. Monosaccharides

The cleavage of polymeric carbohydrates by α-amylase [1] leads to oligosaccharides, which are broken down further by exoglycosidases (oligosaccharidases and disaccharidases [2]) on the membrane surface of the brush border. The monosaccharides released in this way then pass with the help of various sugar-specific transporters into the cells of intestinal epithelium. Secondary active transport serves for the uptake of glucose and galactose, which are transported against a concentration gradient into cotransport with Na⁺. The Na⁺ gradient is maintained on the basolateral side of the cells by Na⁺/K⁺-ATPase [3]. Another passive transporter then releases glucose and galactose into the blood.

Fructose is taken up by a special type of transporter using facilitated diffusion.

Amino acids (not illustrated)

Protein degradation is initiated by proteases—by pepsins in the stomach and by trypsin, chymotrypsin, and elastase in the small intestine. The resulting peptides are then further hydrolyzed by various peptidases into amino acids. Individual amino acid groups have group-specific amino acid transporters, some of which transport the amino acids into the enterocytes in cotransport with Na⁺ ions (secondary active transport), while others transport them in an Na⁺-independent manner through facilitated diffusion. Small peptides can also be taken up.

B. Lipids

Fats and other lipids are poorly soluble in water. The larger the accessible surface is—i.e., the better the fat is emulsified—the easier it is for enzymes to hydrolyze it (see p. 270). Due to the special properties of milk, milk fats already reach the gastrointestinal tract in emulsified form. Digestion of them therefore already starts in the oral cavity and stomach, where lipases in the saliva and gastric juice are available. Lipids that are less accessible—e.g., from roast pork—are emulsified in the small intestine by bile salts and bile phospholipids. Only then are they capable of being attacked by pancreatic lipase [4] (see p. 270).

Fats (triacylglycerols) are mainly attacked by pancreatic lipase at positions 1 and 3 of the glycerol moiety. Cleavage of two fatty acid residues gives rise to fatty acids and 2-monoglycerides, which are quantitatively the most important products. However, a certain amount of glycerol is also formed by complete hydrolysis. These cleavage products are resorbed by a non-ATP-dependent process that has not yet been explained in detail.

In the mucosal cells, long-chain fatty acids are resynthesized by an ATP-dependent ligase [5] to form acyl-CoA and then triacylglycerols (fats; see p. 170). The fats are released into the lymph in the form of chylomicrons (see p. 278) and, bypassing the liver, are deposited in the thoracic duct—i.e., the blood system. Cholesterol also follows this route.

By contrast, short-chain fatty acids (with chain lengths of less than 12 C atoms) pass directly into the blood and reach the liver via the portal vein. Resorbed glycerol can also take this path.
A. Monosaccharides

- Poly-saccharides
  - α-Amylase
  - Glucose
  - Galactose
  - Fructose
  - Other monosaccharides
- Oligo-saccharides

B. Lipids

- Triacylglycerol
  - Act as "fuel" for fat synthesis
- Diglycerol
- 2-Mono-acylglycerol
  - Stimulated by bile salts, phosphatidic acid, and Ca^{2+}
- Glycerol

Fat synthesis

Secondary-active transport
- Facilitated diffusion

ATPase

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Blood: composition and functions

Human blood constitutes about 8% of the body’s weight. It consists of cells and cell fragments in an aqueous medium, the blood plasma. The proportion of cellular elements, known as hematocrit, in the total volume is approximately 45%.

A. Functions of the blood ●

The blood is the most important transport medium in the body. It serves to keep the “internal milieu” constant (homeostasis) and it plays a decisive role in defending the body against pathogens.

Transport. The gases oxygen and carbon dioxide are transported in the blood. The blood mediates the exchange of substances between organs and takes up metabolic end products from tissues in order to transport them to the lungs, liver, and kidney for excretion. The blood also distributes hormones throughout the organism (see p. 370).

Homeostasis. The blood ensures that a balanced distribution of water is maintained between the vascular system, the cells (intracellular space), and the extracellular space. The acid–base balance is regulated by the blood in combination with the lungs, liver, and kidneys (see p. 288). The regulation of body temperature also depends on the controlled transport of heat by the blood.

Defense. The body uses both non-specific and specific mechanisms to defend itself against pathogens. The defense system includes the cells of the immune system and certain plasma proteins (see p. 294).

Self-protection. To prevent blood loss when a vessel is injured, the blood has systems for stanching blood flow and coagulating the blood (hemostasis; see p. 290). The dissolution of blood clots (fibrinolysis) is also managed by the blood itself (see p. 292).

B. Cellular elements ●

The solid elements in the blood are the erythrocytes (red blood cells), leukocytes (white blood cells), and thrombocytes (platelets).

The erythrocytes provide for gas transport in the blood. They are discussed in greater detail on pp. 280–285.

The leukocytes include various types of granulocyte, monocyte, and lymphocyte. All of these have immune defense functions (see p. 294). The neutrophil granulocytes, monocytes, and the macrophages derived from monocytes are phagocytes. They can ingest and degrade invading pathogens. The lymphocytes are divided into two groups, B lymphocytes and T lymphocytes. B lymphocytes produce antibodies, while T lymphocytes regulate the immune response and destroy virus-infected cells and tumor cells. Eosinophilic and basophilic granulocytes have special tasks for defense against animal parasites.

Thrombocytes are cell fragments that arise in the bone marrow from large precursor cells, the megakaryocytes. Their task is to promote hemostasis (see p. 290).

C. Blood plasma: composition ●

The blood plasma is an aqueous solution of electrolytes, nutrients, metabolites, proteins, vitamins, trace elements, and signaling substances. The fluid phase of coagulated blood is known as blood serum. It differs from the plasma in that it lacks fibrin and other coagulation proteins (see p. 290).

Laboratory assessment of the composition of the blood plasma is often carried out in clinical chemistry. Among the electrolytes, there is a relatively high concentration of Na⁺, Ca²⁺, and Cl⁻ ions in the blood in comparison with the cytoplasm. By contrast, the concentrations of K⁺, Mg²⁺, and phosphate ions are higher in the cells. Proteins also have a higher intracellular concentration. The electrolyte composition of blood plasma is similar to that of seawater, due to the evolution of early forms of life in the sea. The solution known as “physiological saline” (NaCl at a concentration of 0.15 mol L⁻¹) is almost isotonic with blood plasma.

A list of particularly important metabolites in the blood plasma is given on the right.
A. Functions of the blood

Transport

Homeostasis

Defense

Water balance

Acid-base balance

Blood gases:

\( \text{H}_2\text{O} \)

\( \text{O}_2 \)

\( \text{CO}_2 \)

Nutrients

Metabolites

Metabolic wastes

Hormones

B. Cellular elements

Erythrocyte

Neutrophilic granulocyte

Monocyte

Small lymphocyte

Large lymphocyte

Eosinophilic granulocyte

Basophilic granulocyte

Leukocytes

Thrombocytes

C. Blood plasma: composition

<table>
<thead>
<tr>
<th>Metabolite</th>
<th>Concentration (mM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glucose</td>
<td>3.6 – 6.1</td>
</tr>
<tr>
<td>Lactate</td>
<td>0.4 – 1.8</td>
</tr>
<tr>
<td>Pyruvate</td>
<td>0.07 – 0.11</td>
</tr>
<tr>
<td>Urea</td>
<td>3.5 – 9.0</td>
</tr>
<tr>
<td>Uric acid</td>
<td>0.18 – 0.54</td>
</tr>
<tr>
<td>Creatinin</td>
<td>0.06 – 0.13</td>
</tr>
<tr>
<td>Amino acids</td>
<td>2.3 – 4.0</td>
</tr>
<tr>
<td>Ammonia</td>
<td>0.02 – 0.06</td>
</tr>
<tr>
<td>Lipids (total)</td>
<td>5.5 – 6.0 g \cdot l^{-1}</td>
</tr>
<tr>
<td>Triglycerides</td>
<td>1.0 – 1.3 g \cdot l^{-1}</td>
</tr>
<tr>
<td>Cholesterol</td>
<td>1.7 – 2.1 g \cdot l^{-1}</td>
</tr>
</tbody>
</table>
Plasma proteins

Quantitatively, proteins are the most important part of the soluble components of the blood plasma. With concentrations of between 60 and 80 g L\(^{-1}\), they constitute approximately 4% of the body’s total protein. Their tasks include transport, regulation of the water balance, hemostasis, and defense against pathogens.

A. Plasma proteins

Some 100 different proteins occur in human blood plasma. Based on their behavior during electrophoresis (see below), they are broadly divided into five fractions: albumins and α1-, α2-, β-, and γ-globulins. Historically, the distinction between the albumins and globulins was based on differences in the proteins’ solubility—albumins are soluble in pure water, whereas globulins only dissolve in the presence of salts.

The most frequent protein in the plasma, at around 45 g L\(^{-1}\), is albumin. Due to its high concentration, it plays a crucial role in maintaining the blood’s colloid osmotic pressure and represents an important amino acid reserve for the body. Albumin has binding sites for apolar substances and therefore functions as a transport protein for long-chain fatty acids, bilirubin, drugs, and some steroid hormones and vitamins. In addition, serum albumin binds Ca\(^{2+}\) and Mg\(^{2+}\) ions. It is the only important plasma protein that is not glycosylated.

The albumin fraction also includes transthyretin (prealbumin), which together with other proteins transports the hormone thyroxine and its metabolites.

The table also lists important globulins in blood plasma, with their mass and function. The α- and β-globulins are involved in the transport of lipids (lipoproteins; see p. 278), hormones, vitamins, and metal ions. In addition, they provide coagulation factors, protease inhibitors, and the proteins of the complement system (see p. 298). Soluble antibodies (immunoglobulins; see p. 300) make up the γ-globulin fraction.

Synthesis and degradation. Most plasma proteins are synthesized by the liver. Exceptions to this include the immunoglobulins, which are secreted by B lymphocytes known as plasma cells (see p. 302) and peptide hormones, which derive from endocrine gland cells.

With the exception of albumin, almost all plasma proteins are glycoproteins. They carry oligosaccharides in N- and O-glycosidic bonds (see p. 44). N-acetyliminuramic acid (sialic acid; see p. 38) often occurs as a terminal carbohydrate among sugar residues. Neuraminidases (sialidases) on the surface of the vascular endothelia gradually cleave the sialic acid residues and thereby release galactose units on the surfaces of the proteins. These asialoglycoproteins (“asialo” = without sialic acid) are recognized and bound by galactose receptors on hepatocytes. In this way, the liver takes up aged plasma proteins by endocytosis and breaks them down. The oligosaccharides on the protein surfaces thus determine the half-life of plasma proteins, which is a period of days to weeks.

In healthy individuals, the concentration of plasma proteins is constant. Diseases in organs that are involved in protein synthesis and breakdown can shift the protein pattern. For example, via cytokines (see p. 392), severe injuries trigger increased synthesis of acute-phase proteins, which include C-reactive protein, haptoglobin, fibrinogen, complement factor C-3, and others. The concentrations of individual proteins are altered in some diseases (known as dysproteinemias).

B. Carrier electrophoresis

Proteins and other electrically charged macromolecules can be separated using electrophoresis (see also pp. 78, 262). Among the various procedures used, carrier electrophoresis on cellulose acetate foil (CAF) is particularly simple. Using this method, serum proteins—which at slightly alkaline pH values all move towards the anode, due to their excess of negative charges—can be separated into the five fractions mentioned. After the proteins have been stained with dyes, the resulting bands can be quantitatively assessed using densitometry.
### A. Plasma proteins

<table>
<thead>
<tr>
<th>Group</th>
<th>Protein</th>
<th>Mr in kDa</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Albumins:</td>
<td>Transthryrin</td>
<td>50-66</td>
<td>Transport of thyroxin and triiodothyronin</td>
</tr>
<tr>
<td></td>
<td>Albumin: 45 g · l⁻¹</td>
<td>67</td>
<td>Maintenance of osmotic pressure; transport of fatty acids, bilirubin, bile acids, steroid hormones, pharmaceuticals and inorganic ions.</td>
</tr>
<tr>
<td>α₁-Globulins</td>
<td>Antitrypsin</td>
<td>51</td>
<td>Inhibition of trypsin and other proteases</td>
</tr>
<tr>
<td></td>
<td>Antichymotrypsin</td>
<td>58-68</td>
<td>Inhibition of chymotrypsin</td>
</tr>
<tr>
<td></td>
<td>Lipoprotein (HDL)</td>
<td>200-400</td>
<td>Transport of lipids</td>
</tr>
<tr>
<td></td>
<td>Prothrombin</td>
<td>72</td>
<td>Coagulation factor II, thrombin precursor (J.4.21.5)</td>
</tr>
<tr>
<td></td>
<td>Transcortin</td>
<td>51</td>
<td>Transport of cortisol, corticosteroids and progesterone</td>
</tr>
<tr>
<td></td>
<td>Acid glycoprotein</td>
<td>44</td>
<td>Transport of progesterone</td>
</tr>
<tr>
<td></td>
<td>Thyroxin-binding globulin</td>
<td>54</td>
<td>Transport of thyroxin and triiodothyronin</td>
</tr>
<tr>
<td>α₂-Globulins</td>
<td>Ceruloplasmin</td>
<td>135</td>
<td>Transport of copper ions</td>
</tr>
<tr>
<td></td>
<td>Antithrombin III</td>
<td>58</td>
<td>Inhibition of blood clotting</td>
</tr>
<tr>
<td></td>
<td>Haptoglobin</td>
<td>100</td>
<td>Binding of hemoglobin</td>
</tr>
<tr>
<td></td>
<td>Cholinesterase (1.1.1.8)</td>
<td>ca. 350</td>
<td>Cleavage of choline esters</td>
</tr>
<tr>
<td></td>
<td>Plasminogen</td>
<td>90</td>
<td>Precursor of plasmin (J.4.21.7), breakdown of blood clots</td>
</tr>
<tr>
<td></td>
<td>Macroglobulin</td>
<td>725</td>
<td>Binding of proteases, transport of zinc ions</td>
</tr>
<tr>
<td></td>
<td>Retinol-binding protein</td>
<td>21</td>
<td>Transport of vitamin A</td>
</tr>
<tr>
<td></td>
<td>Vitamin D-binding protein</td>
<td>52</td>
<td>Transport of calcicols</td>
</tr>
<tr>
<td>β-Globulins:</td>
<td>Lipoprotein (LDL)</td>
<td>2.000-4.500</td>
<td>Transport of lipids</td>
</tr>
<tr>
<td></td>
<td>Transferrin</td>
<td>80</td>
<td>Transport of iron ions</td>
</tr>
<tr>
<td></td>
<td>Fibrinogen</td>
<td>340</td>
<td>Coagulation factor I</td>
</tr>
<tr>
<td></td>
<td>Sex hormone-binding globulin</td>
<td>65</td>
<td>Transport of testosterone and estradiol</td>
</tr>
<tr>
<td></td>
<td>Transcobalamin</td>
<td>38</td>
<td>Transport of vitamin B₁₂</td>
</tr>
<tr>
<td></td>
<td>C-reactive protein</td>
<td>110</td>
<td>Complement activation</td>
</tr>
<tr>
<td>γ-Globulins:</td>
<td>IgG</td>
<td>150</td>
<td>Late antibodies</td>
</tr>
<tr>
<td></td>
<td>IgA</td>
<td>162</td>
<td>Mucosa-protecting antibodies</td>
</tr>
<tr>
<td></td>
<td>IgM</td>
<td>980</td>
<td>Early antibodies</td>
</tr>
<tr>
<td></td>
<td>IgD</td>
<td>172</td>
<td>B-lymphocyte receptors</td>
</tr>
<tr>
<td></td>
<td>IgE</td>
<td>196</td>
<td>Reagins</td>
</tr>
</tbody>
</table>

### B. Electrophoresis

[Diagram showing electrophoresis process]

- Buffer-saturated strip of filter paper
- Cellulose-acetate sheet soaked with buffer
- Serum sample
- Anode
- Electrophoresis
- Staining
- Densitometry
- Cellulose-acetate sheet

**Graph:**

- Anodes: α₁, α₂, β, γ-Globulins
- Light absorption:
  - 52-58%
  - 2.4-4.4%
  - 6.1-10.1%
  - 8.5-14.5%
  - 10-21%
Lipoproteins

Most lipids are barely soluble in water, and many have amphipathic properties. In the blood, free triacylglycerols would coalesce into drops that could cause fat embolisms. By contrast, amphipathic lipids would be deposited in the blood cells’ membranes and would dissolve them. Special precautions are therefore needed for lipid transport in the blood. While long-chain fatty acids are bound to albumin and short-chain ones are dissolved in the plasma (see p. 276), other lipids are transported in lipoprotein complexes, of which there several types in the blood plasma, with different sizes and composition.

A. Composition of lipoprotein complexes

Lipoproteins are spherical or discoid aggregates of lipids and apoproteins. They consist of a nucleus of apolar lipids (triacylglycerols and cholesterol esters) surrounded by a single-layered shell approximately 2 nm thick of amphipathic lipids (phospholipids and cholesterol; the example shown here is LDL). The shell, in which the apoproteins are also deposited, gives the surfaces of the particles polar properties and thereby prevents them from aggregating into large particles. The larger the lipid nucleus of a lipoprotein is—i.e., the larger the number of apolar lipids it contains—the lower its density is.

Lipoproteins are classified into five groups. In order of decreasing size and increasing density, these are: chylomicrons, VLDLs (very-low-density lipoproteins), IDLs (intermediate-density lipoproteins), LDLs (low-density lipoproteins), and HDLs (high-density lipoproteins). The proportions of apoproteins range from 1% in chylomicrons to over 50% in HDLs. These proteins serve less for solubility purposes, but rather function as recognition molecules for the membrane receptors and enzymes that are involved in lipid exchange.

B. Transport functions

The classes of lipoproteins differ not only in their composition, but also in the ways in which they originate and function.

The chylomicrons take care of the transport of triacylglycerols from the intestine to the tissues. They are formed in the intestinal mu- cosa and reach the blood via the lymphatic system (see p. 266). In the peripheral vessels—particularly in muscle and adipose tissue—lipoprotein lipase [1] on the surface of the vascular endothelia hydrolyzes most of the triacylglycerols. Chylomicron breakdown is activated by the transfer of apoproteins E and C from HDL. While the fatty acids released and the glycerol are taken up by the cells, the chylomicrons gradually become converted into chylomicron remnants, which are ultimately removed from the blood by the liver.

VLDLs, IDLs, and LDLs are closely related to one another. VLDLs formed in the liver (see p. 312) transport triacylglycerols, cholesterol, and phospholipids to other tissues. Like chylomicrons, they are gradually converted into IDL and LDL under the influence of lipoprotein lipase [1]. This process is also stimulated by HDL. Cells that have a demand for cholesterol bind LDL through an interaction between their LDL receptor and ApoB-100, and then take up the complete particle through receptor-mediated endocytosis. This type of transport is mediated by depressions in the membrane (“coated pits”), the interior of which is lined with the protein clathrin. After LDL binding, clathrin promotes invagination of the pits and pinching off of vesicles (“coated vesicles”). The clathrin then dissociates off and is reused. After fusion of the vesicle with lysosomes, the LDL particles are broken down (see p. 234), and cholesterol and other lipids are used by the cells.

The HDLs also originate in the liver. They return the excess cholesterol formed in the tissues to the liver. While it is being transported, cholesterol is acylated by lecithin cholesterol acyltransferase (LCAT). The cholesterol esters formed are no longer amphipathic and can be transported in the core of the lipoproteins. In addition, HDLs promote chylomicron and VLDL turnover by exchanging lipids and apoproteins with them (see above).
A. Composition of lipoprotein complexes

<table>
<thead>
<tr>
<th>Lipoprotein Complexes</th>
<th>Apoprotein</th>
<th>Free Cholesterol</th>
<th>Phospholipid</th>
<th>Cholesterol Ester</th>
<th>Triacylglycerols</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chylomicrons</td>
<td>C-II, B-48, C-II, C-III, E, A-I</td>
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<tr>
<td>LDL</td>
<td>B-100</td>
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<tr>
<td>HDL</td>
<td>A-I, A-III, C-II</td>
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</table>

B. Transport functions

1. **Dietary lipids**
   - Liver
   - Cholesterol
   - Fats
   - Chylomicrons
   - Chylomicron remnants
   - Adipose tissue

2. **Indigenous lipids**
   - Liver
   - Cholesterol return
   - HDL
   - Free fatty acids

3. **Extrahepatic**
   - Exchange of lipids and apoproteins

- **Lecithin-cholesterol acyltransferase (LCAT)** 2.3.1.43
- **Lipoprotein lipase** 1.2.9.3
Hemoglobin

The most important task of the red blood cells (erythrocytes) is to transport molecular oxygen ($O_2$) from the lungs into the tissues, and carbon dioxide ($CO_2$) from the tissues back into the lungs. To achieve this, the higher organisms require a special transport system, since $O_2$ is poorly soluble in water. For example, only around 3.2 mL $O_2$ is soluble in 1 L blood plasma. By contrast, the protein hemoglobin (Hb), contained in the erythrocytes, can bind a maximum of 220 mL $O_2$ per liter—70 times the physically soluble amount.

The Hb content of blood, at 140–180 g L$^{-1}$ in men and 120–160 g L$^{-1}$ in women, is twice as high as that of the plasma proteins (50–80 g L$^{-1}$). Hb is therefore also responsible for the majority of the blood proteins’ pH buffer capacity (see p. 288).

A. Hemoglobin: structure

In adults, hemoglobin (HbA; see below) is a heterotetramer consisting of two $\alpha$-chains and two $\beta$-chains, each with masses of 16 kDa. The $\alpha$- and $\beta$-chains have different sequences, but are similarly folded. Some 80% of the amino acid residues form $\alpha$-helices, which are identified using the letters A–H.

Each subunit carries a heme group (formula on p. 106), with a central bivalent iron ion. When $O_2$ binds to the heme iron (Oxygenation of Hb) and when $O_2$ is released (Deoxygenation), the oxidation stage of the iron does not change. Oxidation of Fe$^{2+}$ to Fe$^{3+}$ only occurs occasionally. The oxidized form, methemoglobin, is then no longer able to bind $O_2$. The proportion of Met-Hb is kept low by reduction (see p. 284) and usually amounts to only 1–2%.

Four of the six coordination sites of the iron in hemoglobin are occupied by the nitrogen atoms of the pyrrol rings, and another is occupied by a histidine residue of the globin (the proximal histidine). The iron’s sixth site is coordinated with oxygen in oxyhemoglobin and with $H_2O$ in deoxyhemoglobin.

B. Hemoglobin: allosteric effects

Like aspartate carbamoyltransferase (see p. 116), Hb can exist in two different states (conformations), known as the T form and the R form. The T form (tense; left) and has a much lower $O_2$ affinity than the R form (relaxed; right).

Binding of $O_2$ to one of the subunits of the T form leads to a local conformational change that weakens the association between the subunits. Increasing $O_2$ partial pressure thus means that more and more molecules convert to the higher-affinity R form. This cooperative interaction between the subunits increases the $O_2$ affinity of Hb with increasing $O_2$ concentrations—i.e., the $O_2$ saturation curve is sigmoidal (see p. 282).

Various allosteric effectors influence the equilibrium between the T and R forms and thereby regulate the $O_2$ binding behavior of hemoglobin (yellow arrows). The most important effectors are $CO_2$, H$, and 2,3-bisphosphoglycerate (see p. 282).

Further information

As mentioned above, hemoglobin in adults consists of two $\alpha$- and two $\beta$-chains. In addition to this main form (HbA, $\alpha_2\beta_2$), adult blood also contains small amounts of a second form with a higher $O_2$ affinity in which the $\beta$-chains are replaced by $\delta$-chains (HbA$, \alpha_2\delta_2$). Two other forms occur during embryonic and fetal development. In the first three months, embryonic hemoglobins are formed, with the structure $\zeta_2\delta_2$ and $\alpha_2\epsilon_2$. Up to the time of birth, fetal hemoglobin then predominates (Hbf, $\alpha_2\gamma_2$), and it is gradually replaced by HbA during the first few months of life. Embryonic and fetal hemoglobins have higher $O_2$ affinities than HbA, as they have to take up oxygen from the maternal circulation.
A. Hemoglobin: structure

Hemoglobin A (α2 β2) M: 65 kDa

Proximal histidine
Distal histidine

F helix
Heme
E helix

B. Hemoglobin: allosteric effects

4 O2 + HbT · BPG

HbR · (O2)4 + H+ → BPG

O2 bond
weakens
association

O2 affinity 70
times higher
than in T form

Deoxyhemoglobin
T form

Oxyhemoglobin
R form

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Gas transport
Most tissues are constantly dependent on a supply of molecular oxygen (O₂) to maintain their oxidative metabolism. Due to its poor solubility, O₂ is bound to hemoglobin for transport in the blood (see p. 280). This not only increases the oxygen transport capacity, but also allows regulation of O₂ uptake in the lungs and O₂ release into tissues.

A. Regulation of O₂ transport
When an enzyme reacts to effectors (substrates, activators, or inhibitors) with conformational changes that increase or reduce its activity, it is said to show allosteric behavior (see p. 116). Allosteric enzymes are usually oligomers with several subunits that mutually influence each other.

Although hemoglobin is not an enzyme (it releases the bound oxygen without changing it), it has all the characteristics of an allosteric protein. Its effectors include oxygen, which as a positive homotropic effector promotes its own binding. The O₂ saturation curve of hemoglobin is therefore markedly sigmoidal in shape (2, curve 2). The non-sigmoidal saturation curve of the muscular protein myoglobin is shown for comparison (curve 1). The structure of myoglobin (see p. 336) is similar to that of a subunit of hemoglobin, but as a monomer it does not exhibit any allosteric behavior.

O₂, H⁺, and a special metabolite of erythrocytes—2,3-bisphosphoglycerate (BPG)—act as heterotropic effectors of hemoglobin. BPG is synthesized from 1,3-bisphosphoglycerate, an intermediate of glycolysis (see p. 150), and it can be returned to glycolysis again by breakdown into 2-phosphoglycerate (1), with loss of an ATP.

BPG binds selectively to deoxy–Hb, thereby increasing its amount of equilibrium. The result is increased O₂ release at constant pO₂. In the diagram, this corresponds to a right shift of the saturation curve (2, curve 3). CO₂ and H⁺ act in the same direction as BPG. Their influence on the position of the curve has long been known as the Bohr effect.

The effects of CO₂ and BPG are additive. In the presence of both effectors, the saturation curve of isolated Hb is similar to that of whole blood (curve 4).

B. Hemoglobin and CO₂ transport
Hemoglobin is also decisively involved in the transport of carbon dioxide (CO₂) from the tissues to the lungs.

Some 5% of the CO₂ arising in the tissues is covalently bound to the N terminus of hemoglobin and transported as carbaminohemoglobin (not shown). About 90% of the CO₂ is first converted in the periphery into hydrogen carbonate (HCO₃⁻), which is more soluble (bottom). In the lungs (top), CO₂ is regenerated again from HCO₃⁻ and can then be exhaled.

These two processes are coupled to the oxygenation and deoxygenation of Hb. Deoxy–Hb is a stronger base than oxy–Hb. It therefore binds additional protons (about 0.7 H⁺ per tetramer), which promotes the formation of HCO₃⁻ from CO₂ in the peripheral tissues. The resulting HCO₃⁻ is released into the plasma via an antipporter in the erythrocyte membrane in exchange for Cl⁻, and passes from the plasma to the lungs. In the lungs, the reactions described above then proceed in reverse order: deoxy–Hb is oxygenated and releases protons. The protons shift the HCO₃⁻/CO₂ equilibrium to the left and thereby promote CO₂ release.

O₂ binding to Hb is regulated by H⁺ ions (i.e., by the pH value) via the same mechanism. High concentrations of CO₂, such as those in tissues with intensive metabolism locally increase the H⁺ concentration and thereby reduce hemoglobin’s O₂ affinity (Bohr effect; see above). This leads to increased O₂ release and thus to an improved oxygen supply.

The adjustment of the equilibrium between CO₂ and HCO₃⁻ is relatively slow in the uncatalyzed state. It is therefore accelerated in the erythrocytes by carbonic anhydrase (carbonic anhydrase) (1)—an enzyme that occurs in high concentrations in the erythrocytes.
A. Regulation of \( \text{O}_2 \) transport

1. BPG metabolism

2. Saturation curves

D. Hemoglobin and \( \text{CO}_2 \) transport
Erythrocyte metabolism

Cells living in aerobic conditions are dependent on molecular oxygen for energy production. On the other hand, O₂ constantly gives rise to small quantities of toxic substances known as reactive oxygen species (ROS). These substances are powerful oxidation agents or extremely reactive free radicals (see p. 32), which damage cellular structures and functional molecules. Due to their role in O₂ transport, the erythrocytes are constantly exposed to high concentrations of O₂ and are therefore particularly at risk from ROS.

A. Reactive oxygen species

The dioxygen molecule (O₂) contains two unpaired electrons—i.e., it is a diradical. Despite this, O₂ is relatively stable due to its special electron arrangement. However, if the molecule takes up an extra electron (a), the highly reactive superoxide radical (O₂⁻) arises. Another reduction step (b) leads to the peroxide anion (O₂²⁻), which easily binds protons and thus becomes hydrogen peroxide (H₂O₂). Inclusion of a third electron (c) leads to cleavage of the molecule into the ions O²⁻ and O²⁻. While O₂⁻ can form water by taking up two protons, protonation of O²⁻ provides the extremely dangerous hydroxyl radical (OH). A fourth electron transfer and subsequent protonation also converts O²⁻ into water.

The synthesis of ROS can be catalyzed by iron ions, for example. Reaction of O₂ with FMN or FAD (see p. 32) also constantly produces ROS. By contrast, reduction of O₂ by cytochrome c-oxidase (see p. 140) is “clean,” as the enzyme does not release the intermediates. In addition to antioxidants (b), enzymes also provide protection against ROS: superoxide dismutase [1] breaks down (“disproportionates”) two superoxide molecules into O₂ and the less damaging H₂O₂. The latter is in turn disproportionate into O₂ and H₂O by heme-containing catalase [2].

B. Biological antioxidants

To protect them against ROS and other radicals, all cells contain antioxidants. These are reducing agents that react easily with oxidative substances and thus protect more important molecules from oxidation. Biological antioxidants include vitamins C and E (see pp. 364, 368), coenzyme Q (see p. 104), and several carotenoids (see pp. 132, 364), Bilirubin, which is formed during heme degradation (see p. 194), also serves for protection against oxidation.

Glutathione, a tripeptide that occurs in high concentrations in almost all cells, is particularly important. Glutathione (sequence: Glu-Cys-Gly) contains an atypical γ-peptide bond between Glu and Cys. The thiol group of the cysteine residue is redox-active. Two molecules of the reduced form (GSH, top) are bound to the disulfide (GSSG, bottom) during oxidation.

C. Erythrocyte metabolism

Erythrocytes also have systems that can inactivate ROS (superoxide dismutase, catalase, GSH). They are also able to repair damage caused by ROS. This requires products that are supplied by the erythrocytes' maintenance metabolism, which basically only involves anaerobic glycolysis (see p. 150) and the pentose phosphate pathway (PPP; see p. 152).

The ATP formed during glycolysis serves mainly to supply NAD⁻/NAD⁺-ATPase, which maintains the erythrocytes' membrane potential. The allosteric effector 2,3-BPG (see p. 282) is also derived from glycolysis. The PPP supplies NADPH⁺, which is needed to regenerate glutathione (GSH) from GSSG with the help of glutathione reductase [3]. GSH, the most important antioxidant in the erythrocytes, serves as a coenzyme for glutathione peroxidase [5]. This selenium-containing enzyme detoxifies H₂O₂ and hydroperoxides, which arise during the reaction of ROS with unsaturated fatty acids in the erythrocyte membrane. The reduction of methemoglobin (Hb Fe⁺⁺⁺) to Hb (Hb Fe⁺⁺, [4]) is carried out by GSH or ascorbate by a non-enzymatic pathway; however, there are also NAD(P)H-dependent Met-Hb reductases.
### A. Reactive oxygen species

<table>
<thead>
<tr>
<th>Molecular oxygen</th>
<th>Superoxide radical</th>
<th>Hydroxyl radical</th>
</tr>
</thead>
<tbody>
<tr>
<td>$O_2$</td>
<td>$O_2^-$</td>
<td>$O_2^-$</td>
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<tr>
<td>$e^-$</td>
<td>$e^-$</td>
<td>$e^-$</td>
</tr>
<tr>
<td>Disproportionation</td>
<td>Hydrogen peroxide</td>
<td>Water</td>
</tr>
<tr>
<td>$O_2$</td>
<td>$2H^+$</td>
<td>$2H^+$</td>
</tr>
<tr>
<td>$O_2^-$</td>
<td>Hydrogen peroxide</td>
<td>Water</td>
</tr>
<tr>
<td>$e^-$</td>
<td></td>
<td>$2H^+$</td>
</tr>
</tbody>
</table>

1. Superoxide dismutase 1.15.3.1
2. Catalase 1.11.1.6

### B. Biological antioxidants

<table>
<thead>
<tr>
<th>Quinols and enols</th>
<th>α-Tocopherol (vitamin E)</th>
<th>Ubiquinol (coenzyme Q)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Ascorbic acid (vitamin C)</td>
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</table>

<table>
<thead>
<tr>
<th>Carotenoids</th>
<th>β-Carotin</th>
<th>Lycopin</th>
</tr>
</thead>
<tbody>
<tr>
<td>Others</td>
<td>Glutathione</td>
<td>Bilirubin</td>
</tr>
</tbody>
</table>

1. Examples

<table>
<thead>
<tr>
<th>Glu</th>
<th>Cys</th>
<th>Gly</th>
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2. Glutathione

### C. Erythrocyte metabolism

<table>
<thead>
<tr>
<th>Glutathione reductase</th>
<th>Methemoglobin reductase</th>
<th>Glutathione peroxidase</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glucose</td>
<td>Glucose 6-phosphate</td>
<td>Pentose phosphate pathway</td>
</tr>
<tr>
<td>Glucose 6-phosphate</td>
<td>Glucose</td>
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<tr>
<td>Hydrophobic ATPase</td>
<td>3 Na^+</td>
<td>3 Na^+</td>
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<td>2 K^+</td>
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<td>Glucose 6-phosphate</td>
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<td>2 Glutathione</td>
</tr>
</tbody>
</table>

Molecular oxygen

Superoxide radical

Hydroxyl radical

Hydrogen peroxide

Water

Ozone

Superoxide dismutase 1.15.3.1

Catalase 1.11.1.6

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Iron metabolism

A. Distribution of iron
Iron (Fe) is quantitatively the most important trace element (see p. 362). The human body contains 4–5 g iron, which is almost exclusively present in protein-bound form. Approximately three-quarters of the total amount is found in heme proteins (see pp. 106, 192), mainly hemoglobin and myoglobin. About 1% of the iron is bound in iron-sulfur clusters (see p. 106), which function as cofactors in the respiratory chain, in photosynthesis, and in other redox chains. The remainder consists of iron in transport and storage proteins (transferrin, ferritin; see B).

B. Iron metabolism
Iron can only be resorbed by the bowel in bivalent form (i.e., as Fe²⁺). For this reason, reducing agents in food such as ascorbate (vitamin C; see p. 368) promote iron uptake. Via transporters on the luminal and basal side of the enterocytes, Fe²⁺ enters the blood, where it is bound by transferrin. Part of the iron that is taken up is stored in the bowel in the form of ferritin (see below); Heme groups can also be resorbed by the small intestine.

Most of the resorbed iron serves for the formation of red blood cells in the bone marrow (erythropoiesis, top). As discussed on p. 192, it is only in the final step of hem biosynthesis that Fe³⁺ is incorporated by ferrochelatase into the previously prepared tetrapyrol framework.

In the blood, 2.5–3.0 g of hemoglobin iron circulates as a component of the erythrocytes (top right). Over the course of several months, the flexibility of the red blood cells constantly declines due to damage to the membrane and cytoskeleton. Old erythrocytes of this type are taken up by macrophages in the spleen and other organs and broken down. The organic part of the heme is oxidized into bilirubin (see p. 194), while the iron returns to the plasma pool. The quantity of heme iron recycled per day is much larger than the amount resorbed by the intestines.

Transferrin, a β-globulin with a mass of 80 kDa, serves to transport iron in the blood. This monomeric protein consists of two similar domains, each of which binds an Fe²⁺ ion very tightly. Similar iron transport proteins are found in secretions such as saliva, tears, and milk; these are known as lactoferrins (bottom right). Transferrin and the lactoferrins maintain the concentration of free iron in body fluids at values below 10⁻¹⁰ mol L⁻¹. This low level prevents bacteria that require free iron as an essential growth factor from proliferating in the body. Like LDLs (see p. 278), transferrin and the lactoferrins are taken up into cells by receptor-mediated endocytosis.

Excess iron is incorporated into ferritin and stored in this form in the liver and other organs. The ferritin molecule consists of 24 subunits and has the shape of a hollow sphere (bottom left). It takes up Fe²⁺ ions, which in the process are oxidized to Fe³⁺ and then deposited in the interior of the sphere as ferriferydrite. Each ferritin molecule is capable of storing several thousand iron ions in this way. In addition to ferritin, there is another storage form, hemosiderin, the function of which is not yet clear.

Further information
Disturbances of the iron metabolism are frequent and can lead to severe disease pictures. Iron deficiency is usually due to blood loss, or more rarely to inadequate iron uptake. During pregnancy, increased demand can also cause iron deficiency states. In severe cases, reduced hemoglobin synthesis can lead to anemia (“iron-deficiency anemia”). In these patients, the erythrocytes are smaller and have less hemoglobin. As their membrane is also altered, they are prematurely eliminated in the spleen.

Disturbances resulting from raised iron concentrations are less frequent. Known as hemochromatosis, these conditions can have genetic causes, or may be due to repeated administration of blood transfusions. As the body has practically no means of excreting iron, more and more stored iron is deposited in the organs over time in patients with untreated hemochromatosis, ultimately leading to severe disturbances of organ function.
### A. Distribution of iron

<table>
<thead>
<tr>
<th>Oxygenated heme</th>
<th>Heme enzyme (&lt;1%)</th>
<th>Myoglobin (6%)</th>
<th>Hemo-globin (66%)</th>
<th>Transport and storage forms (26%)</th>
<th>Fe₃⁺-Cluster</th>
</tr>
</thead>
</table>

1. Heme iron

2. Non-heme iron

### B. Iron metabolism

- **120 – 150 mg**
  - Erythropoiesis
  - Bone marrow

- **2500 – 3000 mg**
  - Erythrocytes
  - Concentration of free iron in the blood < 10⁻¹⁰ mol l⁻¹

- **30 mg.d⁻¹**
  - Iron

- **150 – 200 mg**
  - Ferritin

- **2500 – 3000 mg**
  - Hemosiderin

- **3 mg.d⁻¹**
  - Intestine

- **4 mg**
  - Ferritin

- **1 mg.d⁻¹**
  - Fe₃⁺-S₄-Cluster

- **5 mg.d⁻¹**
  - Blood serum

- **5 mg.d⁻¹**
  - Lactic acid

- **5 mg.d⁻¹**
  - Insoluble

- **150 – 200 mg**
  - Ferritin

- **150 – 200 mg**
  - Storage tissue (liver, etc.)
Acid–base balance

A. Hydrogen ion concentration in the blood plasma

The $H^+$ concentration in the blood and extracellular space is approximately $40 \text{ nM}$ ($4 \times 10^{-9} \text{ mol L}^{-1}$). This corresponds to a pH of 7.40. The body tries to keep this value constant, as large shifts in pH are incompatible with life.

The pH value is kept constant by buffer systems that cushion minor disturbances in the acid–base balance (C). In the longer term, the decisive aspect is maintaining a balanced equilibrium between $H^+$ production and uptake and $H^+$ release. If the blood’s buffering capacity is not sufficient, or if the acid–base balance is not in equilibrium—e.g., in kidney disease or during hyperventilation or hyperventilation—shifts in the plasma pH value can occur. A reduction by more than 0.03 units is known as acidosis, and an increase is called alkalosis.

B. Acid–base balance

Protons are mainly derived from two sources: free acids in the diet and sulfur-containing amino acids. Acids taken up with food—e.g., citric acid, ascorbic acid, and phosphoric acid—already release protons in the alkaline pH of the intestinal tract. More important for proton balance, however, are the amino acids methionine and cysteine, which arise from protein degradation in the cells. Their S atoms are oxidized in the liver to form sulfuric acid, which supplies protons by dissociation into sulfate.

During anaerobic glycolysis in the muscles and erythrocytes, glucose is converted into lactate, releasing protons in the process (see p. 338). The synthesis of the ketone bodies acetocacetic acid and 2-hydroxybutyric acid in the liver (see p. 312) also releases protons. Normally, the amounts formed are small and of little influence on the proton balance. If acids are formed in large amounts, however (e.g., during starvation or in diabetes mellitus; see p. 180), they strain the buffer systems and can lead to a reduction in pH (metabolic acidoses; lactic acidosis or ketoacidosis).

Only the kidney is capable of excreting protons in exchange for Na$^+$ ions (see p. 326). In the urine, the $H^+$ ions are buffered by NH$_3$ and phosphate.

C. Buffer systems in the plasma

The buffering capacity of a buffer system depends on its concentration and its $pK_a$ value. The strongest effect is achieved if the pH value corresponds to the buffer system’s $pK_a$ value (see p. 30). For this reason, weak acids with $pK_a$ values of around 7 are best suited for buffering purposes in the blood.

The most important buffer in the blood is the CO$_2$/bicarbonate buffer. This consists of water, carbon dioxide (CO$_2$, the anhydride of carbonic acid H$_2$CO$_3$), and hydrogen carbonate (HCO$_3^-$, bicarbonate). The adjustment of the balance between CO$_2$ and HCO$_3^-$ is accelerated by the zinc-containing enzyme carbonic anhydrase (carbonic anhydrase [1]; see also p. 282). At the pH value of the plasma, HCO$_3^-$ and CO$_2$ are present in a ratio of about 20 : 1. However, the CO$_2$ in solution in the blood is in equilibrium with the gaseous CO$_2$ in the pulmonary alveoli. The CO$_2$/HCO$_3^-$ system is therefore a powerful open buffer system, despite having a not entirely optimal $pK_a$ value of 6.1. Faster or slower respiration increases or reduces CO$_2$ release in the lungs. This shifts the CO$_2$/HCO$_3^-$ ratio and thus the plasma pH value (respiratory acidosis or alkalosis). In this way, respiration can compensate to a certain extent for changes in plasma pH values. However, it does not lead to the excretion of protons.

Due to their high concentration, plasma proteins—and hemoglobin in the erythrocytes in particular—provide about one-quarter of the blood’s buffering capacity. The buffering effect of proteins involves contributions from all of the ionizable side chains. At the pH value of blood, the acidic amino acids (Asp, Glu) and histidine are particularly effective.

The second dissociation step in phosphate (H$_2$PO$_4^-$/HPO$_4^{2-}$) also contributes to the buffering capacity of the blood plasma. Although the $pK_a$ value of this system is nearly optimal, its contribution remains small due to the low total concentration of phosphate in the blood (around 1 mM).
A. Hydrogen ion concentration in the blood plasma

B. Acid–base balance

C. Buffer systems in the plasma

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Blood clotting

Following injury to blood vessels, hemostasis ensures that blood loss is minimized. Initially, thrombocyte activation leads to contraction of the injured vessel and the formation of a loose clot consisting of thrombocytes (hemostasis). Slightly later, the action of the enzyme thrombin leads to the formation and deposition in the thrombus of polymeric fibrin (coagulation, blood clotting). The coagulation process is discussed here in detail.

A. Blood clotting

The most important reaction in blood clotting is the conversion, catalyzed by thrombin, of the soluble plasma protein fibrinogen (factor I) into polymeric fibrin, which is deposited as a fibrous network in the primary thrombus. Thrombin (factor IIa) is a serine proteinase (see p. 176) that cleaves small peptides from fibrinogen. This exposes binding sites that spontaneously allow the fibrin molecules to aggregate into polymers. Subsequent covalent cross-linking of fibrin by a transglutaminase (factor XIII) further stabilizes the thrombus.

Normally, thrombin is present in the blood as an inactive proenzyme (see p. 270). Prothrombin is activated in two different ways, both of which represent cascades of enzymatic reactions in which inactive proenzymes (zymogens, symbol: circle) are proteolytically converted into active proteinases (symbol: sector of a circle). The proteinases activate the next proenzyme in turn, and so on. Several steps in the cascade require additional protein factors (factors III, Va and VIIIa) as well as anionic phospholipids (PL; see below) and Ca\(^{2+}\) ions. Both pathways are activated by injuries to the vessel wall.

In the extravascular pathway (right), tissue thromboplastin (factor III), a membrane protein in the deeper layers of the vascular wall, activates coagulation factor VII. The activated form of this (VIIa) autocatalytically promotes its own synthesis and also generates the active factors IXa and Xa from their precursors. With the aid of factor VIIIa, PL, and Ca\(^{2+}\), factor IXa produces additional Xa, which finally—with the support of Va, PL, and Ca\(^{2+}\)—releases active thrombin.

The intravascular pathway (left) is probably also triggered by vascular injuries. It leads in five steps via factors XIIa, Xla, IXa, and Xa to the activation of prothrombin. The significance of this pathway in vivo has been controversial since it was found that a genetic deficiency in factor XII does not lead to coagulation disturbances.

Both pathways depend on the presence of activated thrombocytes, on the surface of which several reactions take place. For example, the prothrombinase complex (left) forms when factors Xa and II, with the help of Va, bind via Ca\(^{2+}\) ions to anionic phospholipids in the thrombocyte membrane. For this to happen, factors II and X have to contain the non-proteinogenic amino acid γ-carboxyglutamate (Gla; see p. 62), which is formed in the liver by post-translational carboxylation of the factors. The Gla residues are found in groups in special domains that create contacts to the Ca\(^{2+}\) ions. Factors VII and IX are also linked to membrane phospholipids via Gla residues.

Substances that bind Ca\(^{2+}\) ions (e.g., citrate) prevent Gla-containing factors from attaching to the membrane and therefore inhibit coagulation. Antagonists of vitamin K, which is needed for synthesis of the Gla residues (see p. 364) also have anticoagulatory effects. These include dicumarol, for example. Active thrombin not only converts fibrinogen into fibrin, but also indirectly promotes its own synthesis by catalyzing the activation of factors V and VIII. In addition, it catalyzes the activation of factor XIII and thereby triggers the cross-linking of the fibrin.

Regulation of blood clotting (not shown). To prevent the coagulation reaction from becoming excessive, the blood contains a number of anticoagulant substances, including highly effective proteinase inhibitors. For example, antithrombin III binds to various serine proteinases in the cascade and thereby inactivates them. Heparin, an anticoagulant glycosaminoglycan (see p. 346), potentiates the effect of antithrombin III. Thrombomodulin, which is located on the vascular endothelium, also inactivates thrombin. A glycoprotein known as Protein C ensures proteolytic degradation of factors V and VIII. As it is activated by thrombin, coagulation is shut down in this way.
A. Blood clotting

Coagulation factors
- Fibrinogen
- Prothrombin * 3.4.21.5
- Tissue factor/thromboplastin
- Ca²⁺
- Proaccelerin
- Proconvertin * 3.4.21.21
- Antihemophilic factor A
- Christmas factor * 3.4.21.22
- Stuart-Prower factor * 3.4.21.6
- Plasma thromboplastin antecedent * (PTA) 3.4.21.27
- Hageman factor * 3.4.21.38
- Fibrin-stabilizing factor * 2.3.2.13

Function unclear

Prothrombinase complex

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Fibrinolysis, blood groups

A. Fibrinolysis

The fibrin thrombus resulting from blood clotting (see p. 290) is dissolved again by plasmin, a serine proteinase found in the blood plasma. For this purpose, the precursor plasminogen first has to be proteolytically activated by enzymes from various tissues. This group includes the plasminogen activator from the kidney (urokinase) and tissue plasminogen activator (t-PA) from vascular endothelia. By contrast, the plasma protein α2-antiplasmin, which binds to active plasmin and thereby inactivates it, inhibits fibrinolysis.

Urokinase, t-PA, and streptokinase, a bacterial proteinase with similar activity, are used clinically to dissolve thrombs following heart attacks. All of these proteinases are expressed recombinantly in bacteria (see p. 262).

B. Blood groups: the ABO system

During blood transfusions, immune reactions can occur that destroy the erythrocytes transfused from the donor. These reactions result from the formation of antibodies (see p. 300) directed to certain surface structures on the erythrocytes. Known as blood group antigens, these are proteins or oligosaccharides that can differ from individual to individual. More than 20 different blood group systems are now known. The ABO system and the Rh system are of particular clinical importance.

In the ABO system, the carbohydrate parts of glycoproteins or glycolipids act as antigens. In this relatively simple system, there are four blood groups (A, B, AB, and O). In individuals with blood groups A and B, the antigens consist of tetrascarharides that only differ in their terminal sugar (galactose or N-acetylgalactosamine). Carriers of the AB blood group have both antigens (A and B). Blood group 0 arises from an oligosaccharide (the H antigen) that lacks the terminal residue of antigens A and B. The molecular cause for the differences between blood groups are mutations in the glycosyl transferases that transfer the terminal sugar to the core oligosaccharide.

Antibodies are only formed against antigens that the individual concerned does not possess. For example, carriers of blood group A form antibodies against antigen B (“anti-B”), while carriers of group B form antibodies against antigen A (“anti-A”). Individuals with blood group 0 form both types, and those with blood group AB do not form any of these antibodies.

If blood from blood group A is transfused into the circulation of an individual with blood group B, for example, then the anti-A present in the B erythrocytes binds to the A antigens. The donor erythrocytes marked in this way are recognized and destroyed by the complement system (see p. 298). In the test tube, agglutination of the erythrocytes can be observed when donor and recipient blood are incompatible.

The recipient’s serum should not contain any antibodies against the donor erythrocytes, and the donor serum should not contain any antibodies against the recipient’s erythrocytes. Donor blood from blood group 0 is unproblematic, as its erythrocytes do not possess any antibodies and therefore do not react with anti-A or anti-B in the recipient’s blood. Conversely, blood from the AB group can only be administered to recipients with the AB group, as these are the only ones without antibodies.

In the Rh system (not shown), proteins on the surface of the erythrocytes act as antigens. These are known as “rhesus factors,” as the system was first discovered in rhesus monkeys.

The rhesus D antigen occurs in 84% of all white individuals, who are therefore “Rh-positive.” If an Rh-negative mother, fetal erythrocytes can enter the mother’s circulation during birth and lead to the formation of antibodies (IgG) against the D antigen. This initially has no acute effects on the mother or child. Complications only arise when there is a second pregnancy with an Rh-positive child, as maternal anti-D antibodies cross the placenta to the fetus even before birth and can trigger destruction of the child’s Rh-positive erythrocytes (fetal erythroblastosis).
A. Fibrinolysis

B. Blood groups: the ABO system

<table>
<thead>
<tr>
<th>Blood group</th>
<th>A</th>
<th>B</th>
<th>AB</th>
<th>0</th>
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<tbody>
<tr>
<td>Genotypes</td>
<td>AA and A0</td>
<td>BB and B0</td>
<td>AB</td>
<td>00</td>
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<tr>
<td>Antigens</td>
<td>A</td>
<td>B</td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>Antibodies in blood</td>
<td>anti-B</td>
<td>anti-A</td>
<td>-</td>
<td>anti-A</td>
</tr>
<tr>
<td>Frequency in central Europe</td>
<td>40%</td>
<td>16%</td>
<td>4%</td>
<td>40%</td>
</tr>
</tbody>
</table>

GP Glycoprotein with oligosaccharide
- N-acetyl-D-glucosamine
- D-Galactose
- D-Fucose
- N-acetyl-D-galactosamine

1. Fucosyltransferase 2.4.1.69/152
2. N-acetyl-galactosaminyl transferase 2.4.1.49
3. Galactosyltransferase 2.4.1.37

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Immune response

Viruses, bacteria, fungi, and parasites that enter the body of vertebrates of are recognized and attacked by the immune system. Endogenous cells that have undergone alterations—e.g., tumor cells—are also usually recognized as foreign and destroyed. The immune system is supported by physiological changes in infected tissue, known as inflammation. This reaction makes it easier for the immune cells to reach the site of infection.

Two different systems are involved in the immune response. The **innate immune system** is based on receptors that can distinguish between bacterial and viral surface structures or foreign proteins (known as antigens) and those that are endogenous. With the help of these receptors, phagocytes bind to the pathogens, absorb them by endocytosis, and break them down. The complement system (see p. 298) is also part of the innate system.

The **acquired (adaptive) immune system** is based on the ability of the lymphocytes to form highly specific antigen receptors “on suspicion,” without ever having met the corresponding antigen. In humans, there are several billion different lymphocytes, each of which carries a different antigen receptor. If this type of receptor recognizes “its” cognate antigen, the lymphocyte carrying it is activated and then plays its special role in the immune response.

In addition, a distinction is made between cellular and humoral immune responses. The **lymphocytes (T cells)** are responsible for cellular immunity. They are named after the thymus, in which the decisive steps in their differentiation take place. Depending on their function, another distinction is made between cytotoxic T cells (green) and helper T cells (blue). **Humoral immunity** is based on the activity of the **B lymphocytes** (B cells, light brown), which mature in the bone marrow. After activation by T cells, B cells are able to release soluble forms of their specific antigen receptors, known as **antibodies** (see p. 300), into the blood plasma. The immune system’s “memory” is represented by memory cells. These are particularly long-lived cells that can arise from any of the lymphocyte types described.

A. Simplified diagram of the immune response

Pathogens that have entered the body—e.g., viruses (top)—are taken up by **antigen-presenting cells** (APCs) and proteolytically degraded (1). The viral fragments produced in this way are then presented on the surfaces of these cells with the help of special membrane proteins (MHC proteins; see p. 296) (2). The APCs include B lymphocytes, macrophages, and dendritic cells such as the skin’s Langerhans cells.

The complexes of MHC proteins and viral fragments displayed on the APCs are recognized by T cells that carry a receptor that matches the antigen (“T-cell receptors”; see p. 296) (3). Binding leads to activation of the T cell concerned and selective replication of it (4, “clonal selection”). The proliferation of immune cells is stimulated by **interleukins** (IL). These are a group of more than 20 signaling substances belonging to the cytokine family (see p. 392), with the help of which immune cells communicate with each other. For example, activated macrophages release IL-1 (5), while T cells stimulate their own replication and that of other immune cells by releasing IL-2 (6).

Depending on their type, activated T cells have different functions. **Cytotoxic** T cells (green) are able to recognize and bind virus-infected body cells or tumor cells (7). They then drive the infected cells into apoptosis (see p. 396) or kill them with perforin, a protein that perforates the target cell’s plasma membrane (8).

**B lymphocytes**, which as APCs present viral fragments on their surfaces, are recognized by **helper T cells** (blue) or their T cell receptors (9). Stimulated by interleukins, selective clonal replication then takes place of B cells that carry antigen receptors matching those of the pathogen (10). These mature into **plasma cells** (11) and finally secrete large amounts of soluble **antibodies** (12).
A. Simplified scheme of the immune response
T-cell activation

For the selectivity of the immune response (see p. 294), the cells involved must be able to recognize foreign antigens and proteins on other immune cells safely and reliably. To do this, they have antigen receptors on their cell surfaces and co-receptors that support recognition.

A. Antigen receptors

Many antigen receptors belong to the immunoglobulin superfamily. The common characteristic of these proteins is that they are made up from “immunoglobulin domains.” These are characteristically folded substructures consisting of 70–110 amino acids, which are also found in soluble immunoglobulins (Ig; see p. 300). The illustration shows schematically a few of the important proteins in the Ig superfamily. They consist of constant regions (brown or green) and variable regions (orange). Homologous domains are shown in the same colors in each case. All of the receptors have transmembrane helices at the C terminus, which anchor them to the membranes. Intramolecular and intermolecular disulfide bonds are also usually found in proteins belonging to the Ig family.

Immunoglobulin M (IgM), a membrane protein on the surface of B lymphocytes, serves to bind free antigens to the B cells. By contrast, T cell receptors only bind antigens when they are presented by another cell as a complex with an MHC protein (see below). Interaction between MHC-bound antigens and T cell receptors is supported by co-receptors. This group includes CD8, a membrane protein that is typical in cytotoxic T cells. T helper cells use CD4 as a co-receptor instead (not shown). The abbreviation “CD” stands for “cluster of differentiation.” It is the term for a large group of proteins that are all located on the cell surface and can therefore be identified by antibodies. In addition to CD4 and CD8, there are many other co-receptors on immune cells (not shown).

The MHC proteins are named after the “major histocompatibility complex”—the DNA segment that codes for them. Human MHC proteins are also known as HLA antigens (“human leukocyte-associated” antigens). Their polymorphism is so large that it is unlikely that any two individuals carry the same set of MHC proteins—except for monozygotic twins.

Class I MHC proteins occur in almost all nucleated cells. They mainly interact with cytotoxic T cells and are the reason for the rejection of transplanted organs. Class I MHC proteins are heterodimers (αβ). The β subunit is also known as β2-microglobulin.

Class II MHC proteins also consist of two peptide chains, which are related to each other. MHC II molecules are found on all antigen-presenting cells in the immune system. They serve for interaction between these cells and CD4-carrying T helper cells.

B. T-cell activation

The illustration shows an interaction between a virus-infected body cell (bottom) and a CD8-carrying cytotoxic T lymphocyte (top). The infected cell breaks down viral proteins in its cytoplasm (1) and transports the peptide fragments into the endoplasmic reticulum with the help of a special transporter (TAP) (2). Newly synthesized class I MHC proteins on the endoplasmic reticulum are loaded with one of the peptides (3) and then transferred to the cell surface by vesicular transport (4). The viral peptides are bound on the surface of the α2 domain of the MHC protein in a depression formed by an insertion as a “floor” and two helices as “walls” (see smaller illustration).

Supported by CD8 and other co-receptors, a T cell with a matching T cell receptor binds to the MHC peptide complex (5; cf. p. 224). This binding activates protein kinases in the interior of the T cell, which trigger a chain of additional reactions (signal transduction; see p. 388). Finally, destruction of the virus-infected cell by the cytotoxic T lymphocytes takes place.
The diagram illustrates the immune response, specifically focusing on the activation of T cells. The process begins with viral peptide presentation by the MHC (major histocompatibility complex) class I proteins on the surface of virus-infected cells. These peptides are generated through proteolysis and transported into the endoplasmic reticulum by TAP (transporter associated with antigen processing). The MHC class I proteins present the viral peptides to CD8+ T cells. The T cell receptor (TCR) on the T cell recognizes the viral peptide-MHC complex, initiating T cell activity. This activation is further facilitated by the interaction of the TCR with costimulatory molecules on the T cell surface. The diagram also highlights the characteristic domain of the superfamily, involving the α and β chains of the T cell receptor, with their respective molecular weights and domains such as Ig domain, C terminus, and β2 microglobulin.
Complement system

The complement system is part of the innate immune system (see p. 294). It supports non-specific defense against microorganisms. The system consists of some 30 different proteins, the “complement factors,” which are found in the blood and represent about 4% of all plasma proteins there. When inflammatory reactions occur, the complement factors enter the infected tissue and take effect there.

The complement system works in three different ways:

Chemotaxis. Various complement factors attract immune cells that can attack and phagocytose pathogens.

Opsonization. Certain complement factors (“opsonins”) bind to the pathogens and thereby mark them as targets for phagocytosing cells (e.g., macrophages).

Membrane attack. Other complement factors are deposited in the bacterial membrane, where they create pores that lyse the pathogen (see below).

A. Complement activation

The reactions that take place in the complement system can be initiated in several ways. During the early phase of infection, lipopolysaccharides and other structures on the surface of the pathogens trigger the alternative pathway (right). If antibodies against the pathogens become available later, the antigen–antibody complexes formed activate the classic pathway (left). Acute-phase proteins (see p. 276) are also able to start the complement cascade (lectin pathway, not shown).

Factors C1 to C4 (for “complement”) belong to the classic pathway, while factors B and D form the reactive components of the alternative pathway. Factors C5 to C9 are responsible for membrane attack. Other components not shown here regulate the system.

As in blood coagulation (see p. 290), the early components in the complement system are serine proteinases, which mutually activate each other through limited proteolysis. They create a self-reinforcing enzyme cascade. Factor C3, the products of which are involved in several functions, is central to the complement system.

The classic pathway is triggered by the formation of factor C1 at IgG or IgM on the surface of microorganisms (left). C1 is an 18-part molecular complex with three different components (C1q, C1r, and C1s). C1q is shaped like a bunch of tulips, the “flowers” of which bind to the Fc, region of antibodies (left). This activates C1r, a serine proteinase that initiates the cascade of the classic pathway. First, C4 is proteolytically activated into C4b, which in turn cleaves C2 into C2a and C2b. C4b and C2a together form C3 convertase [1], which finally catalyzes the cleavage of C3 into C3a and C3b. Small amounts of C3b also arise from non-enzymatic hydrolysis of C3.

The alternative pathway starts with the binding of factors C3b and B to bacterial lipopolysaccharides (endotoxins). The formation of this complex allows cleavage of B by factor D, giving rise to a second form of C3 convertase (C3bBb).

Proteolytic cleavage of factor C3 provides two components with different effects. The reaction exposes a highly reactive thioester group in C3b, which reacts with hydroxyl or amino groups. This allows C3b to bind covalently to molecules on the bacterial surface (opsonization, right). In addition, C3b initiates a chain of reactions leading to the formation of the membrane attack complex (see below).

Together with C4a and C5a (see below), the smaller product C3a promotes the inflammatory reaction and has chemotactic effects. The “late” factors C5 to C9 are responsible for the development of the membrane attack complex (bottom). They create an ion-permeable pore in the bacterial membrane, which leads to lysis of the pathogen. This reaction is triggered by C5 convertase [2]. Depending on the type of complement activation, this enzyme has the structure C4b2a3b or C3bBb3b, and it cleaves C5 into C5a and C5b. The complex of C5b and C6 allows deposition of C7 in the bacterial membrane. C8 and numerous C9 molecules—which form the actual pore—then bind to this core.
A. Complement activation

Immune complex

Pathogen surface Lipopolysaccharide

Classic pathway

Alternative pathway

Membrane attack complex

C3/C5 convertase 3.4.21.43/47

Structure of the membrane attack complex
Antibodies

Soluble antigen receptors, which are formed by activated B cells (plasma cells; see p. 294) and released into the blood, are known as antibodies. They are also members of the immunoglobulin family (Ig; see p. 296). Antibodies are an important part of the humoral immune defense system. They have no antimicrobial properties themselves, but support the cellular immune system in various ways:

1. They bind to antigens on the surface of pathogens and thereby prevent them from interacting with body cells (neutralization; see p. 404, for example).
2. They link single-celled pathogens into aggregates (immune complexes), which are more easily taken up by phagocytes (agglutination).
3. They activate the complement system (see p. 298) and thereby promote the innate immune defense system (opsonization).

In addition, antibodies have become indispensable aids in medical and biological diagnosis (see p. 304).

A. Domain structure of immunoglobulin G

Type G immunoglobulins (IgG) are quantitatively the most important antibodies in the blood, where they form the fraction of γ-globulins (see p. 276). IgGs (mass 150 kDa) are tetramers with two heavy chains (H chains; red or orange) and two light chains (L chains; yellow). Both H chains are glycosylated (violet; see also p. 43).

The proteinase papain cleaves IgG into two Fα fragments and one Fβ fragment. The Fα (“antigen-binding”) fragments, which each consist of one L chain and the N-terminal part of an H chain, are able to bind antigens. The Fβ (“crystallizable”) fragment is made up of the C-terminal halves of the two H chains. This segment serves to bind IgG to cell surfaces, for interaction with the complement system and antibody transport.

Immunoglobulins are constructed in a modular fashion from several immunoglobulin domains (shown in the diagram on the right in Ω form). The H chains of IgG contain four of these domains (VH, CH1, CH2, and CH3) and the L chains contain two (CL and VL).

The letters C and V designate constant or variable regions.

Disulfide bonds link the two heavy chains to each other and also link the heavy chains to the light chains. Inside the domains, there are also disulfide bonds that stabilize the tertiary structure. The domains are approximately 110 amino acids (AA) long and are homologous with each other. The antibody structure evidently developed as a result of gene duplication. In its central region, known as the “hinge” region, the antibodies are highly mobile.

B. Classes of immunoglobulins

Human immunoglobulins are divided into five classes, IgA (with two subgroups), IgD, IgE, IgG (with four subgroups), and IgM are defined by their H chains, which are designated by the Greek letters α, δ, ε, γ, and μ. By contrast, there are only two types of L chain (κ and λ). IgD and IgE (like IgG) are tetramers with the structure H2L2. By contrast, soluble IgA and IgM are multimers that are held together by disulfide bonds and additional J peptides (joining peptides).

The antibodies have different tasks. IgMs are the first immunoglobulins formed after contact with a foreign antigen. Their early forms are located on the surface of B cells (see p. 296), while the later forms are secreted from plasma cells as pentamers. Their action targets microorganisms in particular. Quantitatively, IgGs are the most important immunoglobulins (see the table showing serum concentrations). They occur in the blood and interstitial fluid. As they can pass the placenta with the help of receptors, they can be transferred from mother to fetus. IgAs mainly occur in the intestinal tract and in body secretions. IgEs are found in low concentrations in the blood. As they can trigger degranulation of mast cells (see p. 380), they play an important role in allergic reactions. The function of IgDs is still unexplained. Their plasma concentration is also very low.
A. Domain structure of immunoglobulin G

- Heavy chain (450 AA)
  - Variable domain
  - "Hinge" region
  - C-terminal end
  - Fc fragment

- Light chain (212 AA)
  - Variable domain
  - Antigen-binding site
  - "Hinge" region
  - C-terminal end
  - Fab fragment

- Fc fragment
  - Oligosaccharide
  - Disulfide bond

- Cleavage site for papain 3.4.22.2

B. Classes of immunoglobulins

<table>
<thead>
<tr>
<th>Class</th>
<th>Molecular Weight (kDa)</th>
</tr>
</thead>
<tbody>
<tr>
<td>IgA</td>
<td>360-720</td>
</tr>
<tr>
<td>IgD</td>
<td>172</td>
</tr>
<tr>
<td>IgE</td>
<td>196</td>
</tr>
<tr>
<td>IgG</td>
<td>150</td>
</tr>
<tr>
<td>IgM</td>
<td>935</td>
</tr>
</tbody>
</table>

Chain:

- Heavy chain (H)
  - α, δ, ε, γ, μ
- Light chain (L)
  - κ or λ

Structures:

- IgA: [2κδμ]n
- IgD: [2κδ]n
- IgE: [2κδμ]n
- IgG: [2κδμ]n
- IgM: [2κδμ]n
  \( n = 1, 2 \) or 3

Serum concentration (g · l⁻¹):

- IgA: 3.5
- IgD: 0.03
- IgE: 0.00005
- IgG: 1.3
- IgM: 1.5

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Antibody biosynthesis

The acquired (adaptive) immune system (see p. 294) is based on the ability of the lymphocytes to keep an extremely large repertoire of antigen receptors and soluble antibodies ready for use, so that even infections involving new types of pathogen can be combated. The wide range of immunoglobulins (Ig) are produced by genetic recombination and additional mutations during the development and maturation of the individual lymphocytes.

A. Variability of immunoglobulins

It is estimated that more than $10^6$ different antibody variants occur in every human being. This variability affects both the heavy and the light chains of immunoglobulins.

There are five different types of heavy (H) chain, according to which the antibody classes are defined (α, δ, ε, γ, μ), and two types of light (L) chain (κ and λ; see p. 300). The various Ig types that arise from combinations of these chains are known as isotypes. During immunoglobulin biosynthesis, plasma cells can switch from one isotype to another ("gene switch"). Idiotype variation is based on the existence of various alleles of the same gene—i.e., genetic differences between individuals. The term idiotype variation refers to the fact that the antigen binding sites in the Feγ fragments can be highly variable. Idiotype variation affects the variable domains (shown here in pink) of the light and heavy chains. At certain sites—known as the hypervariable regions (shown here in red)—variation is particularly wide; these sequences are directly involved in the binding of the antigen.

B. Causes of antibody variety

There are three reasons for the extremely wide variability of antibodies:

1. Multiple genes. Various genes are available to code for the variable protein domains. Only one gene from among these is selected and expressed.

2. Somatic recombination. The genes are divided into several segments, of which there are various versions. Various ("untidy") combinations of the segments during lymphocyte maturation give rise to randomly combined new genes ("mosaic genes").

3. Somatic mutation. During differentiation of B cells into plasma cells, the coding genes mutate. In this way, the "primordial" germ-line genes can become different somatic genes in the individual B cell clones.

C. Biosynthesis of a light chain

We can look at the basic features of the genetic organization and synthesis of immunoglobulins using the biosynthesis of a mouse κ chain as an example. The gene segments for this light chain are designated L, V, J, and C. They are located on chromosome 6 in the germ-line DNA (on chromosome 2 in humans) and are separated from one another by introns (see p. 242) of different lengths.

Some 150 identical L segments code for the signal peptide ("leader sequence," 17–20 amino acids) for secretion of the product (see p. 230). The V segments, of which there are 150 different variants, code for most of the variable domains (95 of the 108 amino acids). L and V segments always occur in pairs—in tandem, so to speak. By contrast, there are only five variants of the J segments (joining segments) at most. These code for a peptide with 13 amino acids that links the variable part of the κ chains to the constant part. A single C segment codes for the constant part of the light chain (84 amino acids).

During the differentiation of B lymphocytes, individual V/J combinations arise in each B cell. One of the 150 L/V tandem segments is selected and linked to one of the five J segments. This gives rise to a somatic gene that is much smaller than the germline gene. Transcription of this gene leads to the formation of the mRNA for the κ chain, from which introns and surplus J segments are removed by splicing (see p. 246). Finally, the completed mRNA still contains one each of the L–V–J–C segments and after being transported into the cytoplasm is available for translation. The subsequent steps in Ig biosynthesis follow the rules for the synthesis of membrane-bound or secretory proteins (see p. 230).
**A. Variability of immunoglobulins**

- **Isotypic**
- **Allotypic**
- **Idiotypic**

**B. Origins of antibody variety**

1. Multiple genes
   - DNA
   - Protein

2. Somatic recombination
   - Germ line DNA
   - Somatic DNA in B cell
   - Protein

3. Somatic mutation
   - Germ line DNA
   - Somatic DNA
   - Protein

**C. Biosynthesis of a light chain**

- **V/J Recombination**
- **Transcription**
- **Splicing**
- **Translation**
- **Protein**
Monoclonal antibodies, immunoassay

A. Monoclonal antibodies

Monoclonal antibodies (MABs) are secreted by immune cells that derive from a single antibody-forming cell (from a single cell clone). This is why each MAB is directed against only one specific epitope of an immunogenic substance, known as an "antigenic determinant." Large molecules contain several epitopes, against which various antibodies are formed by various B cells. An antiserum containing a mixture of all of these antibodies is described as being polyclonal.

To obtain MABs, lymphocytes isolated from the spleen of immunized mice (1) are fused with mouse tumor cells (myeloma cells, 2). This is necessary because antibody-secreting lymphocytes in culture have a lifespan of only a few weeks. Fusion of lymphocytes with tumor cells gives rise to cell hybrids, known as hybridomas, which are potentially immortal.

Successful fusion (2) is a rare event, but the frequency can be improved by adding polyethylene glycol (PEG). To obtain only successfully fused cells, incubation is required for an extended period in a primary culture with HAT medium (3), which contains hypoxanthine, aminopterin, and thymidine. Aminopterin, an analogue of dihydrofolic acid, competitively inhibits dihydrofolate reductase and thus inhibits the synthesis of dTMP (see p. 402). As dTMP is essential for DNA synthesis, myeloma cells cannot survive in the presence of aminopterin. Although spleen cells are able to circumvent the inhibitory effect of aminopterin by using hypoxanthine and thymidine, they have a limited lifespan and die. Only hybridomas survive culture in HAT medium, because they possess both the immortality of the myeloma cells and the spleen cells' metabolic side pathway.

Only a few fused cells actually produce antibodies. To identify these cells, the hybridomas have to be isolated and replicated by cloning (4). After the clones have been tested for antibody formation, positive cultures are picked out and selected by further cloning (5). This results in hybridomas that synthesize monoclonal antibodies. Finally, MAB production is carried out in vitro using a bioreactor, or in vivo by producing ascites fluid in mice (6).

B. Immunoassay

Immunoassays are semiquantitative procedures for assessing substances with low concentrations. In principle, immunoassays can be used to assay any compound against which antibodies are formed.

The basis for this procedure is the antigen-antibody "reaction"—i.e., specific binding of an antibody to the molecule being assayed. Among the many different immunoassay techniques that have been developed—e.g., radioimmunoassay (RIA), and chemiluminescence immunoassay (CIA)—a version of the enzyme-linked immunoassay (ELISA) is shown here.

The substance to be assayed—e.g., the hormone thyroxine in a serum sample—is pipetted into a microtitration plate (1), the walls of which are coated with antibodies that specifically bind the hormone. At the same time, a small amount of thyroxine is added to the incubation to which an enzyme known as the "tracer" (1) has been chemically coupled. The tracer and the hormone being assayed compete for the small number of antibody binding sites available. After binding has taken place (2), all of the unbound molecules are rinsed out. The addition of a substrate solution for the enzyme (a chromogenic solution) then triggers an indicator reaction (3), the products of which can be assessed using photometry (4).

The larger the amount of enzyme that can bind to the antibodies on the container’s walls, the larger the amount of dye that is produced. Conversely, the larger the amount of the substance being assayed that is present in the sample, the smaller the amount of tracer that can be bound by the antibodies. Quantitative analysis can be carried out through parallel measurement using standards with a known concentration.
### A. Monoclonal antibodies

1. **Immunization**
   - Immunized mouse
   - Antigen
   - Spleen cells
   - Myeloma cells
2. **Cell fusion**
   - Fusion
   - Primary culture
3. **Antibody test**
   - Positive cultures
4. **Selection**
   - Selection of positive clones
5. **Subcloning**
6. **Production of monoclonal antibodies**
   - Mouse with ascites
   - Culture of a selected clone
   - Myeloma cells
   - Hybridoma cells

### B. Immunoassay

1. **Sample preparation**
   - Sample
   - Antibodies
2. **Incubation**
   - Tracer
   - Microtiter plate
3. **Wash step**
   - Substrate: H$_2$O$_2$
   - Chromogen: C
4. **Detection**
   - Peroxidase
   - Dye + H$_2$O

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Liver: functions

Weighing 1.5 kg, the liver is one of the largest organs in the human body. Although it only represents 2–3% of the body's mass, it accounts for 25–30% of oxygen consumption.

A. Diagram of a hepatocyte ●

The 3 \(10^{13}\) cells in the liver—particularly the hepatocytes, which make up 90% of the cell mass—are the central location for the body's intermediary metabolism. They are in close contact with the blood, which enters the liver from the portal vein and the hepatic arteries, flows through capillary vessels known as sinusoids, and is collected again in the central veins of the hepatic lobes. Hepatocytes are particularly rich in endoplasmic reticulum, as they carry out intensive protein and lipid synthesis. The cytoplasm contains granules of insoluble glycogen. Between the hepatocytes, there are bile capillaries through which bile components are excreted.

B. Functions of the liver ●

The most important functions of the liver are:
1. Uptake of nutrients supplied by the intestines via the portal vein.
2. Biosynthesis of endogenous compounds and storage, conversion, and degradation of them into excretable molecules (metabolism).
   In particular, the liver is responsible for the biosynthesis and degradation of almost all plasma proteins.
3. Supply of the body with metabolites and nutrients.
4. Detoxification of toxic compounds by biotransformation.
5. Excretion of substances with the bile.

C. Hepatic metabolism ●

The liver is involved in the metabolism of practically all groups of metabolites. Its functions primarily serve to cushion fluctuations in the concentration of these substances in the blood, in order to ensure a constant supply to the peripheral tissues (homeostasis).

Carbohydrate metabolism. The liver takes up glucose and other monosaccharides from the plasma. Glucose is then either stored in the form of the polysaccharide glycogen or converted into fatty acids. When there is a drop in the blood glucose level, the liver releases glucose again by breaking down glycogen. If the glycogen store is exhausted, glucose can also be synthesized by gluconeogenesis from lactate, glycerol, or the carbon skeleton of amino acids (see p. 310).

Lipid metabolism. The liver synthesizes fatty acids from acetate units. The fatty acids formed are then used to synthesize fats and phospholipids, which are released into the blood in the form of lipoproteins. The liver’s special ability to convert fatty acids into ketone bodies and to release these again is also important (see p. 312).

Like other organs, the liver also synthesizes cholesterol, which is transported to other tissues as a component of lipoproteins. Excess cholesterol is converted into bile acids in the liver or directly excreted with the bile (see p. 314).

Amino acid and protein metabolism. The liver controls the plasma levels of the amino acids. Excess amino acids are broken down. With the help of the urea cycle (see p. 182), the nitrogen from the amino acids is converted into urea and excreted via the kidneys. The carbon skeleton of the amino acids enters the intermediary metabolism and serves for glucose synthesis or energy production. In addition, most of the plasma proteins are synthesized or broken down in the liver (see p. 276).

Biotransformation. Steroid hormones and bilirubin, as well as drugs, ethanol, and other xenobiotics are taken up by the liver and inactivated and converted into highly polar metabolites by conversion reactions (see p. 316).

Storage. The liver not only stores energy reserves and nutrients for the body, but also certain mineral substances, trace elements, and vitamins, including iron, retinol, and vitamins A, D, K, folic acid, and B₁₂.
A. Diagram of a hepatocyte

B. Functions of the liver

C. Liver metabolism

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Buffer function in organ metabolism

All of the body’s tissues have a constant requirement for energy substrates and nutrients. The body receives these metabolites with food, but the supply is irregular and in varying amounts. The liver acts here along with other organs, particularly adipose tissue, as a balancing buffer and storage organ.

In the metabolism, a distinction is made between the absorptive state (well-fed state) immediately after a meal and the postabsorptive state (state of starvation), which starts later and can merge into hunger. The switching of the organ metabolism between the two phases depends on the concentration of energy-bearing metabolites in the blood (plasma level). This is regulated jointly by hormones and by the autonomic nervous system.

A. Absorptive state

The absorptive state continues for 2–4 hours after food intake. As a result of food digestion, the plasma levels of glucose, amino acids, and fats (triacylglycerols) temporarily increase.

The endocrine pancreas responds to this by altering its hormone release—there is an increase in insulin secretion and a reduction in glucagon secretion. The increase in the insulin/glucagon quotient and the availability of substrates trigger an anabolic phase in the tissues—particularly liver, muscle, and adipose tissues.

The liver forms increased amounts of glycogen and fats from the substrates supplied. Glycogen is stored, and the fat is released into the blood in very low density lipoproteins (VLDLs).

Muscle also refills its glycogen store and synthesizes proteins from the amino acids supplied.

Adipose tissue removes free fatty acids from the lipoproteins, synthesizes triacylglycerols from them again, and stores these in the form of insoluble droplets.

During the absorptive state, the heart and neural tissue mainly use glucose as an energy source, but they are unable to establish any substantial energy stores. Heart muscle cells are in a sense “omnivorous,” as they can also use other substances to produce energy (fatty acids, ketone bodies). By contrast, the central nervous system (CNS) is dependent on glucose. It is only able to utilize ketone bodies after a prolonged phase of hunger (B).

B. Postabsorptive state

When the food supply is interrupted, the postabsorptive state quickly sets in. The pancreatic A cells now release increased amounts of glucagon, while the B cells reduce the amount of insulin they secrete. The reduced insulin/glucagon quotient leads to switching of the intermediary metabolism. The body now falls back on its energy reserves. To do this, it breaks down storage substances (glycogen, fats, and proteins) and shifts energy-supplying metabolites between the organs.

The liver first empties its glycogen store (glycogenolysis; see p.156). It does not use the released glucose itself, however, but supplies the other tissues with it. In particular, the brain, adrenal gland medulla, and erythrocytes depend on a constant supply of glucose, as they have no substantial glucose reserves themselves. When the liver’s glycogen reserves are exhausted after 12–24 hours, gluconeogenesis begins (see p. 154). The precursors for this are derived from the muscle lature (amino acids) and adipose tissue (glycerol from fat degradation). From the fatty acids that are released (see below), the liver starts to form ketone bodies (ketogenesis; see p.312). These are released into the blood and serve as important energy suppliers during the hunger phase. After 1–2 weeks, the CNS also starts to use ketone bodies to supply part of its energy requirements, in order to save glucose.

In muscle, the extensive glycogen reserves are exclusively used for the muscles’ own requirements (see p.320). The slowly initiated protein breakdown in muscle supplies amino acids for gluconeogenesis in the liver.

In adipose tissue, glucagon triggers lipolysis, releasing fatty acids and glycerol. The fatty acids are used as energy suppliers by many types of tissue (with the exception of brain and erythrocytes). An important recipient of the fatty acids is the liver, which uses them for ketogenesis.
A. Absorptive state

Liver
Intestine
Muscle
Nervous tissue
Heart

Do not have energy reserves
Ketone bodies
Glucose
Gluconeogenesis
Amino acids
Fat
Adipose tissue
Pancreas

High blood glucose level
Storage compound

B. Postabsorptive state

Liver
Intestine
Muscle
Nervous tissue
Heart

Do not have energy reserves
Ketone bodies
Fat
Adipose tissue
Pancreas

Glucose
Amino acids
Gluconeogenesis
Proteins
Triacylglycerols
Insulin
Glucagon

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Carbohydrate metabolism

Besides fatty acids and ketone bodies, glucose is the body's most important energy supplier. The concentration of glucose in the blood (the “blood glucose level”) is maintained at 4–6 mM (0.8–1.0 g L⁻¹) by precise regulation of glucose-supplying and glucose-utilizing processes. Glucose suppliers include the intestines (glucose from food), liver, and kidneys. The liver plays the role of a "glucostat" (see p. 308).

The liver is also capable of forming glucose by converting other sugars—e.g., fructose and galactose—or by synthesizing from other metabolites. The conversion of lactate to glucose in the Cori cycle (see p. 338) and the conversion of alanine to glucose with the help of the ornithine cycle (see p. 338) are particularly important for the supply of erythrocytes and muscle cells.

Transporters in the plasma membrane of hepatocytes allow insulin-independent transport of glucose and other sugars in both directions. In contrast to muscle, the liver possesses the enzyme glucose-6-phosphatase, which can release glucose from glucose-6-phosphate.

A. Gluconeogenesis overview

Regeneration of glucose (up to 250 g per day) mainly takes place in the liver. The tubule cells of the kidney are also capable of carrying out gluconeogenesis, but due to their much smaller mass, their contribution only represents around 10% of total glucose formation. Gluconeogenesis is regulated by hormones. Cortisol, glucagon, and epinephrine promote gluconeogenesis, while insulin inhibits it (see pp. 158, 244).

The main precursors of gluconeogenesis in the liver are lactate from anaerobically working muscle cells and from erythrocytes, glucogenic amino acids from the digestive tract and muscles (mainly alanine), and glycerol from adipose tissue. The kidney mainly uses amino acids for gluconeogenesis (Glu, Gin; see p. 328).

In mammals, fatty acids and other suppliers of acetyl CoA are not capable of being used for gluconeogenesis, as the acetyl residues formed during β-oxidation in the tricarboxylic acid cycle (see p. 132) are oxidized to CO₂ and therefore cannot be converted into oxaloacetic acid, the precursor for gluconeogenesis.

B. Fructose and galactose metabolism

Fructose is mainly metabolized by the liver, which channels it into glycolysis (left half of the illustration).

A special ketohexokinase [1] initially phosphorylates fructose into fructose 1-phosphate. This is then cleaved by an aldolase [2], which is also fructose-specific, to yield glycerone 3-phosphate (dihydroxyacetone phosphate) and glyceraldehyde. Glycerone 3-phosphate is already an intermediate of glycolysis (center), while glyceraldehyde can be phosphorylated into glyceraldehyde 3-phosphate by triokinase [3].

To a smaller extent, glyceraldehyde is also reduced to glycerol [4] or oxidized to glyceraldehyde, which can be channeled into glycolysis following phosphorylation (not shown). The reduction of glyceraldehyde [4] uses up NAD⁺. As the rate of degradation of alcohol in the hepatocytes is limited by the supply of NAD⁺, fructose degradation accelerates alcohol degradation (see p. 320).

Outside of the liver, fructose is channeled into the sugar metabolism by reduction at C-2 to yield sorbitol and subsequent dehydration at C-1 to yield glucose (the polyol pathway; not shown).

Galactose is also broken down in the liver (right side of the illustration). As is usual with sugars, the metabolism of galactose starts with a phosphorylation to yield galactose 1-phosphate [5]. The connection to the glucose metabolism is established by C-4 epimerization to form glucose 1-phosphate. However, this does not take place directly. Instead, a transferase [6] transfers a uridine 5'-monophosphate (UMP) residue from uridine diphosphogalactose (UDP-galactose) to galactose 1-phosphate. This releases glucose 1-phosphate, while galactose 1-phosphate is converted into uridine diphosphogalactose (UDP-galactose). This then is isomerized into UDP-glucose. The biosynthesis of galactose also follows this reaction pathway, which is freely reversible up to reaction [5]. Genetic defects of enzymes [5] or [6] can lead to the clinical picture of galactosemia.
A. Gluconeogenesis: overview

B. Fructose and galactose metabolism

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Lipid metabolism

The liver is the most important site for the formation of fatty acids, fats (triacylglycerols), ketone bodies, and cholesterol. Most of these products are released into the blood. In contrast, the triacylglycerols synthesized in adipose tissue are also stored there.

A. Lipid metabolism

Lipid metabolism in the liver is closely linked to the carbohydrate and amino acid metabolism. When there is a good supply of nutrients in the resorptive (fed) state (see p. 308), the liver converts glucose via acetyl CoA into fatty acids. The liver can also take up fatty acids from chylomicrons, which are supplied by the intestine, or from fatty acid–albumin complexes (see p. 162). Fatty acids from both sources are converted into fats and phospholipids. Together with apoproteins, they are packed into very-low-density lipoproteins (VLDLs; see p. 278) and then released into the blood by exocytosis. The VLDLs supply extrahepatic tissue, particularly adipose tissue and muscle.

In the postresorptive state (see p. 292)–particularly during fasting and starvation—the lipid metabolism is readjusted and the organism falls back on its own reserves. In these conditions, adipose tissue releases fatty acids. They are taken up by the liver and are mainly converted into ketone bodies (B).

Cholesterol can be derived from two sources—food or endogenous synthesis from acetyl-CoA. A substantial percentage of endogenous cholesterol synthesis takes place in the liver. Some cholesterol is required for the synthesis of bile acids (see p. 314). In addition, it serves as a building block for cell membranes (see p. 216), or can be esterified with fatty acids and stored in lipid droplets. The rest is released together into the blood in the form of lipoprotein complexes (VLDLs) and supplies other tissues. The liver also contributes to the cholesterol metabolism by taking up from the blood and breaking down lipoproteins that contain cholesterol and cholesteryl esters (HDLs, IDLs, LDLs; see p. 278).

B. Biosynthesis of ketone bodies

At high concentrations of acetyl-CoA in the liver mitochondria, two molecules condense to form acetoacetyl CoA [1]. The transfer of another acetyl group [2] gives rise to 3-hydroxy-3-methylglutaryl-CoA (HMG CoA), which after release of acetyl CoA [3] yields free acetoacetate (Krebs cycle). Acetoacetate can be converted to 3-hydroxybutyrate by reduction [4], or can pass into acetone by nonenzymatic decarboxylation [5]. These three compounds are together referred to as "ketone bodies," although in fact 3-hydroxybutyrate is not actually a ketone. As reaction [3] releases an H⁺ ion, metabolic acidosis can occur as a result of increased ketone body synthesis (see p. 288).

The ketone bodies are released by the liver into the blood, in which they are easily soluble. Blood levels of ketone bodies therefore rise during periods of hunger. Together with free fatty acids, 3-hydroxybutyrate and acetoacetate are then the most important energy suppliers in many tissues (including heart muscle). Acetone cannot be metabolized and is exhaled via the lungs or excreted with urine.

To channel ketone bodies into the energy metabolism, acetoacetate is converted with the help of succinyl CoA into succinic acid and acetoacetyl CoA, which is broken down by β-oxidation into acetyl CoA (not shown; see p. 180).

If the production of ketone bodies exceeds the demand for them outside the liver, there is an increase in the concentration of ketone bodies in the plasma (ketonemia) and they are also eventually excreted in the urine (ketonuria). Both phenomena are observed after prolonged starvation and in inadequately treated diabetes mellitus. Severe ketonuria with ketoacidosis can cause electrolyte shifts and loss of consciousness, and is therefore life-threatening (ketoacidotic coma).
**A. Lipid metabolism**

Intestine → Glucose → Acetyl CoA → Ketone bodies → Fatty acids → Adipose tissue

Muscle → Fatty acids → Ketone bodies

Muscle → Fats → Cholesterol → Chylomicron residues → VLDL → HDL, IDL, LDL → Peripheral tissues

Muscle → Adipose tissue → Fatty acids

**A. Biosynthesis of ketone bodies**

1. Acetyl-CoA-C-acyltransferase 2.3.1.16
2. Hydroxymethylglutaryl-CoA synthase 4.1.3.5
3. Hydroxymethylglutaryl-CoA lyase 4.1.3.4
4. 3-Hydroxybutyrate dehydrogenase 1.1.1.30
5. Nonenzymatic reaction

3-Hydroxybutyrate → Acetyl CoA → Acetacetate → Acetone
Bile acids

Bile is an important product released by the hepatocytes. It promotes the digestion of fats from food by emulsifying them in the small intestine (see p. 2770). The emulsifying components of bile, apart from phospholipids, mainly consist of bile acids and bile salts (see below). The bile also contains free cholesterol, which is excreted in this way (see p. 312).

A. Bile acids and bile salts

Bile acids are steroids consisting of 24 C atoms carrying one carboxylate group and several hydroxyl groups. They are formed from cholesterol in the liver via an extensive reaction pathway (top). Cytochrome P450 enzymes in the ER of hepatocytes are involved in many of the steps (see p. 318). Initially, the cholesterol double bond is removed. Monoxygenases then introduce one or two additional OH groups into the sterane framework. Finally, the side chain is shortened by three C atoms, and the terminal C atom is oxidized to a carboxylate group.

It is important that the arrangement of the A and B rings is altered from trans to cis during bile acid synthesis (see p. 54). The result of this is that all of the hydrophilic groups in the bile acids lie on one side of the molecule. Cholesterol, which is weakly amphipathic (top), has a small polar “head” and an extended apolar “tail.” By contrast, the much more strongly amphipathic bile acid molecules (bottom) resemble disks with polar top sides and apolar bottom sides. At physiological pH values, the carboxyl groups are almost completely dissociated and therefore negatively charged.

Cholic acid and chenodeoxycholic acid, known as the primary bile acids, are quantitatively the most important metabolites of cholesterol. After being biosynthesized, they are mostly activated with coenzyme A and then conjugated with glycine or the non-proteinogenic amino acid taurine (see p. 62). The acid amides formed in this way are known as conjugated bile acids or bile salts. They are even more amphipathic than the primary products.

Deoxycholic acid and lithocholic acid are only formed in the intestine by enzymatic cleavage of the OH group at C-7 (see B). They are therefore referred to as secondary bile acids.

B. Metabolism of bile salts

Bile salts are exclusively synthesized in the liver (see A). The slowest step in their biosynthesis is hydroxylation at position 7 by a 7-α-hydroxylase. Cholic acid and other bile acids inhibit this reaction (end-product inhibition). In this way, the bile acids present in the liver regulate the rate of cholesterol utilization.

Before leaving the liver, a large proportion of the bile acids are activated with CoA and then conjugated with the amino acids glycine or taurine (2; cf. A). In this way, cholic acid gives rise to glycocholic acid and taurocholic acid. The liver bile secreted by the liver becomes denser in the gallbladder as a result of the removal of water (bladder bile; 3).

Intestinal bacteria produce enzymes that can chemically alter the bile salts (4). The acid amide bond in the bile salts is cleaved, and dehydroxylation at C-7 yields the corresponding secondary bile acids from the primary bile acids (5). Most of the intestinal bile acids are resorbed again in the ileum (6) and returned to the liver via the portal vein (enterohepatic circulation). In the liver, the secondary bile acids give rise to primary bile acids again, from which bile salts are again produced. Of the 15–30 g bile salts that are released with the bile per day, only around 0.5 g therefore appears in the feces. This approximately corresponds to the amount of daily de novo synthesis of cholesterol.

Further information

The cholesterol excreted with the bile is poorly water-soluble. Together with phospholipids and bile acids, it forms micelles (see p. 270), which keep it in solution. If the proportions of phospholipids, bile acids and cholesterol shift, gallstones can arise. These mainly consist of precipitated cholesterol (cholesterol stones), but can also contain Ca²⁺ salts of bile acids and bile pigments (pigment stones).
A. Bile acids and bile salts

Bile acids

<table>
<thead>
<tr>
<th>Bile acids</th>
<th>HO– in position</th>
</tr>
</thead>
<tbody>
<tr>
<td>Primary bile acids</td>
<td></td>
</tr>
<tr>
<td>— Cholic acid</td>
<td>C-3 C-7 C-12</td>
</tr>
<tr>
<td>— Chenodeoxycholic acid</td>
<td>C-3 C-7 -</td>
</tr>
<tr>
<td>Secondary bile acids</td>
<td></td>
</tr>
<tr>
<td>— Deoxycholic acid</td>
<td>C-3 - C-12</td>
</tr>
<tr>
<td>— Lithocholic acid</td>
<td>C-3 - -</td>
</tr>
</tbody>
</table>

Bile salts

- Glycocholic acid
- Taurocholic acid

Bile salts = conjugated bile acids

B. Metabolism of bile salts

1. Cholesterol
2. Primary bile acids
3. Bile salts
4. Gallbladder
5. Intestine
6. Bile salts breakdown
7. Secondary bile acids
8. Primary bile acids
9. Resorption
10. Feces

Enterohpatic circulation

15 – 30 g

0.5 g
Biotransformations

The body is constantly taking up foreign substances (xenobiotics) from food or through contact with the environment, via the skin and lungs. These substances can be natural in origin, or may have been synthetically produced by humans. Many of these substances are toxic, particularly at high concentrations. However, the body has effective mechanisms for inactivating and then excreting foreign substances through biotransformations. The mechanisms of biotransformation are similar to those with which endogenous substances such as bile pigments and steroid hormones are enzymatically converted. Biotransformations mainly take place in the liver.

A. Biotransformations

Phase I reactions (interconversion reactions). Type I reactions introduce functional groups into inert, apolar molecules or alter functional groups that are already present. In many cases, this is what first makes it possible for foreign substances to conjugate with polar molecules via phase II reactions (see below). Phase I reactions usually reduce the biological activity or toxicity of a substance (“detoxification”). However, some substances only become biologically active as a result of the interconversion reaction (see, for example, benzo[α]pyrene, p. 256) or become more toxic after interconversion than the initial substance (“toxicification”).

Important phase I biotransformation reactions include:

- **Hydrolitic cleavages** of ether, ester, and peptide bonds. Example (1) shows hydrolysis of the painkiller acetylsalicylic acid.

- **Oxidations.** Hydroxylations, epoxide formation, sulfide formation, dealkylation, deamination. For example, benzene is oxidized into phenol, and toluene (methylbenzene) is oxidized into benzoic acid.

- **Reductions.** Reduction of carbonyl, azo-, or nitro- compounds, dehalogenation.

- **Methylations.** Example (2) illustrates the inactivation of the catecholamine norepinephrine by methylation of a phenolic OH group (see p. 334).

- **De sulfurations.** The reactions take place in the hepatocytes on the smooth endoplasmic reticulum.

Most oxidation reactions are catalyzed by cytochrome P450 systems (see p. 318). These monooxygenases are induced by their substrates and show wide specificity. The substrate-specific enzymes of the steroid metabolism (see p. 376) are exceptions to this.

Phase II reactions (conjugate formation). Type II reactions couple their substrates (bilirubin, steroid hormones, drugs, and products of phase I reactions) via ester or amide bonds to highly polar negatively charged molecules. The enzymes involved are transferases, and their products are known as conjugates.

The most common type of conjugate formation is coupling with glucuronate (GlCUA) as an O- or N-glucuronide. The enzyme for the reaction is uridine diphosphate glucuronate, the “active glucuronate” (see p. 110). Coupling with the polar glucuronate makes an apolar (hydrophobic) molecule more strongly polar, and it becomes sufficiently water-soluble and capable of being excreted. Example (3) shows the glucuronidation of tetrahydrocortisol, a metabolite of the glucocorticoid cortisol (see p. 374).

The biosynthesis of sulfate esters with the help of phosphoadenosine phosphosulfate (PAPS), the “active sulfate” (see p. 110) and amide formation with glycine and glutamine also play a role in conjugation. For example, benzoic acid is conjugated with glycine to form the more soluble and less toxic hippuric acid (N-benzoxylglycine; see p. 124).

In contrast with unconjugated compounds, the conjugates are much more water-soluble and capable of being excreted. The conjugates are eliminated from the liver either by the biliary route—i.e., by receptor-mediated excretion into the bile—or by the renal route, via the blood and kidneys by filtration.

Further information

To detoxify heavy metals, the liver contains metallothioneins, a group of cysteine-rich proteins with a high af nity for divalent metal ions such as Cd\(^{2+}\), Cu\(^{2+}\), Hg\(^{2+}\), and Zn\(^{2+}\). These metal ions also induce the formation of metallothioneins via a special metal-regulating element (MRE) in the gene’s promoter (see p. 244).

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A. Biotransformations

Foreign substances:
- Drugs
- Preservatives
- Plasticizers
- Pigments
- Pesticides etc.

Endogenous substances:
- Steroid hormones
- Other low molecular weight substances
- Bile pigments

Substrate induction

Phase I reactions:
- Hydrolytic cleavage
- Epoxide formation
- Dealkylation
- Deamination
- Reduction
- Methylation
- Desulfuration

Transformation products:

Phase II reactions:

Conjugate formation:
- Glucuronidation
- Esterification with sulfate
- Amidation with Gly and Glu

Water soluble, inactive, non-toxic

Conjugate

Bile

Urine

Poorly soluble, biologically active, some toxic

Transformation product

Transformation of a drug

1. Hydrolysis of a drug

Acetylsaliclyc acid

2. Methylation of a hormone/neurotransmitter

Norepinephrine

3. Glucuronidation of a hormone

Acetysaliclyc acid

Salicylate

S-adenosyl methionine

S-adenosyl homocysteine

Norepinephrine

O-methyl norepinephrine

S-adenosyl homocysteine

Tetrahydrocortisol glucuronide

Arylesterase 3.1.1.2

Catechol O-methyltransferase 2.1.1.6

Glucuronosyltransferase 2.4.1.17

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Cytochrome P450 systems

During the first phase of biotransformation in the liver, compounds that are weakly chemically reactive are enzymatically hydroxylated (see p. 316). This makes it possible for them to be conjugated with polar substances. The hydroxylating enzymes are generally monoxygenases that contain a heme as the redox-active coenzyme (see p. 106). In the reduced form, the heme can bind carbon monoxide (CO), and it then shows characteristic light absorption at 450 nm. This was what led to this enzyme group being termed cytochrome P450 (Cyt P450).

Cyt P450 systems are also involved in many other metabolic processes—e.g., the biosynthesis of steroid hormones (see p. 172), bile acids (see p. 314), and eicosanoids (see p. 390), as well as the formation of unsaturated fatty acids (see p. 409). The liver’s reddish-brown color is mainly due to the large amounts of P450 enzymes it contains.

A. Cytochrome P450-dependent monoxygenases: reactions

Cyt P450-dependent monoxygenases catalyze reductive cleavage of molecular oxygen (O2). One of the two oxygen atoms is transferred to the substrate, while the other is released as a water molecule. The necessary reducing equivalents are transferred to the actual monoxygenase by an FAD-containing auxiliary enzyme from the coenzyme NADPH+H+.

Cyt P450 enzymes occur in numerous forms in the liver, steroid-producing glands, and other organs. The substrate specificity of liver enzymes is low. Apolar compounds containing aliphatic or aromatic rings are particularly easily converted. These include endogenous substances such as steroid hormones, as well as medical drugs, which are inactivated by phase I reactions. This is why Cyt P450 enzymes are of particular interest in pharmacology. The degradation of ethanol in the liver is also partly catalyzed by Cyt P450 enzymes (the “micromodal ethanol-oxidizing system”; see p. 304). As alcohol and drugs are broken down by the same enzyme system, the effects of alcoholic drinks and medical drugs can sometimes be mutually enhancing—even sometimes to the extent of becoming life-threatening.

Only a few examples of the numerous Cyt P450-dependent reactions are shown here. Hydroxylation of aromatic rings (a) plays a central part in the metabolism of medicines and steroids. Aliphatic methyl groups can also be oxidized to hydroxyl groups (b). Epoxidation of aromatics (c) by Cyt P450 yields products that are highly reactive and often toxic. For example, the mutagenic effect of benzo[a]pyrene (see p. 244) is based on this type of interconversion in the liver. In Cyt P450 dependent dealkylations (d), alkyl substituents of O, N, or S atoms are released as aldehydes.

B. Reaction mechanism

The course of Cyt P450 catalysis is in principle well understood. The most important function of the heme group consists of converting molecular oxygen into an especially reactive atomic form, which is responsible for all of the reactions described above.

1. In the resting state, the heme iron is trivalent. Initially, the substrate binds near the heme group.

2. Transfer of an electron from FADH2 reduces the iron to the divalent form that is able to bind an O2 molecule (2).

3. Transfer of a second electron and a change in the valence of the iron reduce the bound O2 to the peroxide.

4. A hydroxyl ion is now cleaved from this intermediate. Uptake of a proton gives rise to H2O and the reactive form of oxygen mentioned above. In this ferryl radical, the iron is formally tetravalent.

5. The activated oxygen atom inserts itself into a C-H bond in the substrate, thereby forming an OH group.

6. Dissociation of the product returns the enzyme to its initial state.
A. Cytochrome P450-dependent monooxygenases: reactions

1. **Hydroxylation**
   - a) Hydroxylation of aromatic compounds
   - b) Hydroxylation of aliphatic compounds
   - c) Epoxidation
   - d) Dealkylation

B. Reaction mechanism

1. **Resting state**
   - Cyt P450 reductase
   - Substrate

2. **Activated oxygen**
   - Product

3. **Oxygenation**
   - "Activated oxygen"

4. **Deactivation**
   - Cyt P450 reductase
   - Substrate

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Ethanol metabolism

A. Blood ethanol level

Ethanol (EtOH, “alcohol”) naturally occurs in fruit in small quantities. Alcoholic drinks contain much higher concentrations. Their alcohol content is usually given as percent by volume. To estimate alcohol uptake and the blood alcohol level, it is useful to convert the amount to grams of ethanol (density 0.79 kg \( \text{L}^{-1} \)). For example, a bottle of beer (0.5 L at 4\% v/v alcohol) contains 20 mL = 16 g of ethanol, while a bottle of wine (0.7 L at 12\% v/v alcohol) contains 84 mL = 66 g ethanol.

Ethanol is membrane-permeable and is quickly resorbed. The maximum blood level is already reached within 60–90 min after drinking. The resorption rate depends on various conditions, however. An empty stomach, a warm drink (e.g., mulled wine), and the presence of sugar and carbonic acid (e.g., in champagne) promote ethanol resorption, whereas a heavy meal reduces it. Ethanol is rapidly distributed throughout the body. A large amount is taken up by the muscles and brain, but comparatively little by adipose tissue and bones. Roughly 70% of the body is accessible to alcohol. Complete resorption of the ethanol contained in one bottle of beer (16 g) by a person weighing 70 kg (distribution in 70 kg \( \times 70/100 = 49 \) kg) leads to a blood alcohol level of 0.33 per thousand (7.2 mM). The lethal concentration of alcohol is approximately 3.5 per thousand (76 mM).

B. Ethanol metabolism

The major site of ethanol degradation is the liver, although the stomach is also able to metabolize ethanol. Most ethanol is initially oxidized by alcohol dehydrogenase to form ethanal (acetaldehyde). A further oxidation, catalyzed by aldehyde dehydrogenase, leads to acetate. Acetate is then converted with the help of acetate-CoA ligase to form acetyl-CoA, using ATP and providing a link to the intermediary metabolism. In addition to cytoplasmic alcohol dehydrogenase, catalase and inducible microsomal alcohol oxidase (“MEOS”; see p. 318) also contribute to a lesser extent to ethanol degradation. Many of the enzymes mentioned above are induced by ethanol.

The rate of ethanol degradation in the liver is limited by alcohol dehydrogenase activity. The amount of NAD+ available is the limiting factor. As the maximum degradation rate is already reached at low concentrations of ethanol, the ethanol level therefore declines at a constant rate (zero-order kinetics). The calorific value of ethanol is 29.4 \( \text{kJ g}^{-1} \). Alcoholic drinks—particularly in alcoholics—can therefore represent a substantial proportion of dietary energy intake.

C. Liver damage due to alcohol

Alcohol is a socially accepted drug of abuse in Western countries. Due to the high potential for addiction to develop, however, it is actually a “hard” drug and has a much larger number of victims than the opiate drugs, for example. In the brain, ethanol is deposited in membranes due to its amphipathic properties, and it influences receptors for neurotransmitters (see p. 352). The effect of GABA is enhanced, while that of glutamate declines.

High ethanol consumption over many years leads to liver damage. For a healthy man, the limit is about 60 g per day, and for a woman about 50 g. However, these values are strongly dependent on body weight, health status, and other factors.

Ethanol-related high levels of NADH+H+ and acetyl-CoA in the liver lead to increased synthesis of neutral fats and cholesterol. However, since the export of these in the form of VLDLs (see p. 278) is reduced due to alcohol, storage of lipids occurs (fatty liver). This increase in the fat content of the liver (from less than 5% to more than 50% of the dry weight) is initially reversible. However, in chronic alcoholism the hepatocytes are increasingly replaced by connective tissue. When liver cirrhosis occurs, the damage to the liver finally reaches an irreversible stage, characterized by progressive loss of liver functions.
A. Blood ethanol level

- Cognac
- Whiskey
- Corn liquor
- Cherry brandy
- Advocat
- Red wine
- White wine
- Strong beer
- Beer
- Water

B. Ethanol metabolism

- Alcohol dehydrogenase 1.1.1.1 [Zn²⁺]
- Aldehyde dehydrogenase 1.2.1.3
- Acetate-CoA ligase 6.2.1.1

C. Liver damage due to alcohol

- Healthy liver
- Fatty liver
- Cirrhotic liver
- Death

- Vol.% 10
- 0.0
- 0.5
- 1.0
- Maximum after 60 - 90 min
- Constant decline ca. 0.015 % · h⁻¹
- Rapid increase due to easy resorption

- Vodka (55 Vol.%) 0.75 g EtOH · kg⁻¹

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Kidney: functions

A. Functions of the kidneys

The kidneys’ main function is excretion of water and water-soluble substances (1). This is closely associated with their role in regulating the body’s electrolyte and acid–base balance (homeostasis, see pp. 326 and 328). Both excretion and homeostasis are subject to hormonal control. The kidneys are also involved in synthesizing several hormones (3; see p. 315). Finally, the kidneys also play a role in the intermediary metabolism (4), particularly in amino acid degradation and gluconeogenesis (see p. 154).

The kidneys are extremely well-perfused organs, with about 1200 L of blood flowing through them every day. Approximately 180 L of primary urine is filtered out of this. Removal of water leads to extreme concentration of the primary urine (to approximately one-hundredth of the initial volume). As a result, only a volume of 0.5–2.0 L of final urine is excreted per day.

B. Urine formation

The functional unit of the kidney is the nephron. It is made up of the Malpighian bodies or renal corpuscles (consisting of Bowman’s capsules and the glomerulus), the proximal tubule, Henle’s loop, and the distal tubule, which passes into a collecting duct. The human kidney contains around one million nephrons. The nephrons form urine in the following three phases.

Ultrafiltration. Ultrafiltration of the blood plasma in the glomerulus gives rise to primary urine, which is isotonic with plasma. The pores in the glomerular basement membrane, which are made up of type IV collagen (see p. 344), have an effective mean diameter of 2.9 nm. This allows all plasma components with a molecular mass of up to about 15 kDa to pass through unhindered. At increasing masses, molecules are progressively held back; at masses greater than 65 kDa, they are completely unable to enter the primary urine. This applies to almost all plasma proteins—which in addition, being anions, are repelled by the negative charge in the basal membrane.

Resorption. All low-molecular weight plasma components enter the primary urine via glomerular filtration. Most of these are transported back into the blood by resorption, to prevent losses of valuable metabolites and electrolytes. In the proximal tubule, organic metabolites (e.g., glucose and other sugars, amino acids, lactate, and ketone bodies) are recovered by secondary active transport (see p. 220). There are several group-specific transport systems for resorbing amino acids, with which hereditary diseases can be associated (e.g., cystinuria, glycinuria, and Hartnup’s disease). HCO₃⁻, Na⁺, phosphate, and sulfate are also resorbed by ATP-dependent (active) mechanisms in the proximal tubule. The later sections of the nephron mainly serve for additional water recovery and regulated resorption of Na⁺ and Cl⁻ (see pp. 326, 328). These processes are controlled by hormones (aldosterone, vasopressin).

Secretion. Some excretible substances are released into the urine by active transport in the renal tubules. These substances include H⁺ and K⁺ ions, urea, and creatinine, as well as drugs such as penicillin.

Clearance. Renal clearance is used as a quantitative measure of renal function. It is defined as the plasma volume cleared of a given substance per unit of time. Inulin, a fructose polysaccharide with a mass of ca. 6 kDa (see p. 40) that is neither actively excreted nor resorbed but is freely filtered, has a clearance of 120 mL · min⁻¹ in healthy individuals.

Further information

Concentrating urine and transporting it through membranes are processes that require large amounts of energy. The kidneys therefore have very high energy demands. In the proximal tubule, the ATP needed is obtained from oxidative metabolism of fatty acids, ketone bodies, and several amino acids. To a lesser extent, lactate, glycerol, and citric acid are also used. In the distal tubule and Henle’s loop, glucose is the main substrate for the energy metabolism. The endothelial cells in the proximal tubule are also capable of gluconeogenesis. The substrates for this are mainly the carbohydrate skeletons of amino acids. Their amino groups are used as ammonia for buffering urine (see p. 311). Enzymes for peptide degradation and the amino acid metabolism occur in the kidneys at high levels of activity (e.g., amino acid oxidases, amine oxidases, glutaminase).

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A. Functions of the kidneys

1. Excretion
   - Water
   - Salts
   - Metabolic wastes
   - Foreign substances

2. Homeostasis
   - Acid-base balance
   - Electrolyte balance

3. Hormone synthesis
   - Erythropoietin
   - Calcitriol

4. Metabolism
   - Glucose
   - Amino acids
   - Gluconeo- genesis
   - NH₃

B. Urine formation

Renal corpuscle

- Ultrafiltration
  - All solute plasma components smaller than 3 nm – 15 kDa
- Secretion
  - H⁺
  - K⁺
  - Drugs
  - Uric acid
  - Creatinine
- Resorption
  - Glucose
  - Lactate
  - 2-Oxoacids
  - Amino acids
  - Na⁺, K⁺, Ca²⁺, Mg²⁺, Cl⁻, SO₄²⁻, HPO₄²⁻, HCO₃⁻
  - Water, etc.

Final urine

Proximal tubule

Distal tubule

Collecting duct

Henle’s loop

Regulated secretion

Regulated resorption of H₂O
Urine

A. Urine
Water and water-soluble compounds are excreted with the urine. The volume and composition of urine are subject to wide variation and depend on food intake, body weight, age, sex, and living conditions such as temperature, humidity, physical activity, and health status. As there is a marked circadian rhythm in urine excretion, the amount of urine and its composition are usually given relative to a 24-hour period.

A human adult produces 0.5–2.0 L urine per day, around 95% of which consists of water. The urine usually has a slightly acidic pH value (around 5.8). However, the pH value of urine is strongly affected by metabolic status. After ingestion of large amounts of plant food, it can increase to over 7.

B. Organic components
Nitrogen-containing compounds are among the most important organic components of urine. Urea, which is mainly synthesized in the liver (urea cycle; see p. 182), is the form in which nitrogen atoms from amino acids are excreted. Breakdown of pyrimidine bases also produces a certain amount of urea (see p. 190). When the nitrogen balance is constant, as much nitrogen is excreted as is taken up (see p. 174), and the amount of urea in the urine therefore reflects protein degradation: 70 g protein in food yields approximately 30 g urea in the urine.

Uric acid is the end product of the purine metabolism. When uric acid excretion via the kidneys is disturbed, gout can develop (see p. 190). Creatinine is derived from the muscle metabolism, where it arises spontaneously and irreversibly by cyclization of creatine and creatine phosphate (see p. 336). Since the amount of creatinine in an individual excretes per day is constant (it is directly proportional to muscle mass), creatinine as an endogenous substance can be used to measure the glomerular filtration rate. The amount of amino acids excreted in free form is strongly dependent on the diet and on the efficiency of liver function. Amino acid derivatives are also found in the urine (e.g., hippurate, a detoxification product of benzoic acid).

Modified amino acids, which occur in special proteins such as hydroxyproline in collagen and 3-methylhistidine in actin and myosin, can be used as indicators of the degradation of these proteins.

Other components of the urine are conjugates with sulfuric acid, glucuronic acid, glycine, and other polar compounds that are synthesized in the liver by biotransformation (see p. 316). In addition, metabolites of many hormones (catecholamines, steroids, serotinin) also appear in the urine and can provide information about hormone production. The proteohormone chorionic gonadotropin (hCG, mass ca. 36 kDa), which is formed at the onset of pregnancy, appears in the urine due to its relatively small size. Evidence of hCG in the urine provides the basis for an immunological pregnancy test.

The yellow color of urine is due to urochromes, which are related to the bile pigments produced by hemoglobin degradation (see p. 194). If urine is left to stand long enough, oxidation of the urochromes may lead to a darkening in color.

C. Inorganic components
The main inorganic components of the urine are the cations Na⁺, K⁺, Ca²⁺, Mg²⁺, and NH₄⁺ and the anions Cl⁻, SO₄²⁻, and HPO₄²⁻, as well as traces of other ions. In total, Na⁺ and Cl⁻ represent about two-thirds of all the electrolytes in the final urine. Calcium and magnesium occur in the feces in even larger quantities. The amounts of the various inorganic components of the urine also depend on the composition of the diet. For example, in acidosis there can be a marked increase in the excretion of ammonia (see p. 326). Excretion of Na⁺, K⁺, Ca²⁺, and phosphate via the kidneys is subject to hormonal regulation (see p. 330).

Further information
Shifts in the concentrations of the physiological components of the urine and the appearance of pathological urine components can be used to diagnose diseases. Important examples are glucose and ketone bodies, which are excreted to a greater extent in diabetes mellitus (see p. 160).
A. Urine

- Unic acid: 0.3-2.0 g from purine degradation
- Urea: 20-35 g from proteins and amino acids
- Creatinine: 1.0-1.5 g from creatine and creatine phosphate

B. Organic constituents

- Glucose: <0.36 g
- Ketone bodies: <3 g
- Proteins: <0.35 g
- Amino acids: 1-3 g
- Urea: 20-35 g from proteins and amino acids
- Uric acid: 0.3-2.0 g from purine degradation
- Creatinine: 1.0-1.5 g from creatine and creatine phosphate

C. Inorganic constituents

- Dissociation dependent on pH
- Daily excretion (mmol)

- Na+: 100-150
- K+: 60-80
- Mg²⁺: 4-11
- Ca²⁺: 2-6
- Cl⁻: 120-240
- HPO₄²⁻: 10-40
- SO₄²⁻: 30-60
- NH₄⁺: 30-50
- Daily excretion (mmol)

- Volume: 0.5-2 l/day
- pH: 5.8 (4.8-7.6)
- Density: 1.015 ± 0.002 kg/l
- Osmolarity: 60-1300 mmol/1kg solids: 50-72 g/day
Functions in the acid–base balance

Along with the lungs, the kidneys are particularly involved in keeping the pH value of the extracellular fluid constant (see p. 288). The contribution made by the kidneys particularly involves resorbing HCO₃⁻ and actively excreting protons.

A. Proton excretion

The renal tubule cells are capable of secreting protons (H⁺) from the blood into the urine against a concentration gradient, despite the fact that the H⁺ concentration in the urine is up to a thousand times higher than in the blood. To achieve this, carbon dioxide (CO₂) is taken up from the blood and—together with water (H₂O) and with the help of carbonic anhydrase (carbonic anhydrase, [1])—converted into hydrogen carbonate (“bicarbonate,” HCO₃⁻) and one H⁺. Formally, this yields carbonic acid H₂CO₃ as an intermediate, but it is not released during the reaction.

The hydrogen carbonate formed in carbonic anhydrase returns to the plasma, where it contributes to the blood’s base reserve. The proton is exported into the urine by secondary active transport in antiport for Na⁺ (bottom right). The driving force for proton excretion, as in other secondary active processes, is the Na⁺ gradient established by the ATPase involved in the Na⁺/K⁺ exchange (“Na⁺/K⁺ ATPase”, see p. 220). This integral membrane protein on the basal side (towards the blood) of tubule cells keeps the Na⁺ concentration in the tubule cell low, thereby maintaining Na⁺ inflow. In addition to this secondary active H⁺ transport mechanism, there is a V-type H⁺-transporting ATPase in the distal tubule and collecting duct (see p. 220).

An important function of the secreted H⁺ ions is to promote HCO₃⁻ resorption (top right). Hydrogen carbonate, the most important buffering base in the blood, passes into the primary urine quantitatively, like all ions. In the primary urine, HCO₃⁻ reacts with H⁺ ions to form water and CO₂, which returns by free diffusion to the tubule cells and from there into the blood. In this way, the kidneys also influence the CO₂/HCO₃⁻ buffering balance in the plasma.

B. Ammonia excretion

Approximately 60 mmol of protons are excreted with the urine every day. Buffering systems in the urine catch a large proportion of the H⁺ ions, so that the urine only becomes weakly acidic (down to about pH 4.8).

An important buffer in the urine is the hydrogen phosphate/dihydrogen phosphate system ([HPO₄²⁻/H₂PO₄⁻]). In addition, ammonia also makes a vital contribution to buffering the secreted protons.

Since plasma concentrations of free ammonia are low, the kidneys release NH₃ from glutamine and other amino acids. At 0.5–0.7 mM, glutamine is the most important amino acid in the plasma and is the preferred form for ammonia transport in the blood. The kidneys take up glutamine, and with the help of glutaminase [4], initially release NH₃ from the amide bond hydrolytically. From the glutamate formed, a second molecule of NH₃ can be obtained by oxidative deamination with the help of glutamate dehydrogenase [5] (see p. 178). The resulting 2-oxoglutarate is further metabolized in the tricarboxylic acid cycle. Several other amino acids—alanine in particular, as well as serine, glycine, and aspartate—can also serve as suppliers of ammonia.

Ammonia can diffuse freely into the urine through the tubule membrane, while the ammonium ions that are formed in the urine are charged and can no longer return to the cell. Acidic urine therefore promotes ammonia excretion, which is normally 30–50 mmol per day. In metabolic acidosis (e.g., during fasting or in diabetes mellitus), after a certain time increased induction of glutaminase occurs in the kidneys, resulting in increased NH₃ excretion. This in turn promotes H⁺ release and thus counteracts the acidosis. By contrast, when the plasma pH value shifts towards alkaline values (alkalosis), renal excretion of ammonia is reduced.
A. Proton secretion

Blood plasma

\[ \text{CO}_2 \rightarrow \text{H}_2\text{O} \rightarrow \text{H}_2\text{O} \rightarrow \text{CO}_2 \]

Tubule cell

\[ \text{CO}_2 \rightarrow \text{H}_2\text{O} \rightarrow \text{H}_2\text{O} \rightarrow \text{CO}_2 \]

Urine

\[ \text{HCO}_3^- \rightarrow \text{H}^+ \rightarrow \text{CO}_2 \rightarrow \text{CO}_2 \]

Secondary active transport of \( \text{H}^+ \)

3.6. 1.3

B. Ammonia excretion

Glutamine

Amino acid with the highest plasma concentration

\[ \text{Glutamine} \rightarrow \text{Glutamate} \rightarrow \text{2-Oxoglutarate} \]

\[ \text{Tricarboxylic acid cycle} \]

Excretion of 30 – 50 mmol/day

3.5. 1.2

Glutaminase

Glutamate Dehydrogenase 3.4.1.2

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Electrolyte and water recycling

A. Electrolyte and water recycling

Electrolytes and other plasma components with low molecular weights enter the primary urine by ultrafiltration (right). Most of these substances are recovered by energy-dependent resorption (see p. 322). The extent of the resorption determines the amount that ultimately reaches the final urine and is excreted. The illustration does not take into account the zoning of transport processes in the kidney (physiology textbooks may be referred to for further details).

Calcium and phosphate ions. Calcium (Ca\(^{2+}\)) and phosphate ions are almost completely resorbed from the primary urine by active transport (i.e., in an ATP-dependent fashion). The proportion of Ca\(^{2+}\) resorbed is over 99%, while for phosphate the figure is 80–90%. The extent to which these two electrolytes are resorbed is regulated by the three hormones parathyrin, calcitonin, and calcium.

The peptide hormone parathyrin (PTH), which is produced by the parathyroid gland, stimulates Ca\(^{2+}\) resorption in the kidneys and at the same time inhibits the resorption of phosphate. In conjunction with the effects of this hormone in the bones and intestines (see p. 344), this leads to an increase in the plasma level of Ca\(^{2+}\) and a reduction in the level of phosphate ions.

Calcitonin, a peptide produced in the C cells of the thyroid gland, inhibits the resorption of both calcium and phosphate ions. The result is an overall reduction in the plasma level of both ions. Calcitonin is thus a parathyrin antagonist relative to Ca\(^{2+}\).

The steroid hormone calcitriol, which is formed in the kidneys (see p. 304), stimulates the resorption of both calcium and phosphate ions and thus increases the plasma level of both ions.

Sodium ions. Controlled resorption of Na\(^{+}\) from the primary urine is one of the most important functions of the kidney. Na\(^{+}\) resorption is highly effective, with more than 97% being resorbed. Several mechanisms are involved: some of the Na\(^{+}\) is taken up passively in the proximal tubule through the junctions between the cells (paracellularly). In addition, there is secondary active transport together with glucose and amino acids (see p. 322). These two pathways are responsible for 60–70% of total Na\(^{+}\) resorption. In the ascending part of Henle’s loop, there is another transporter (shown at the bottom right), which functions electroneutrally and takes up one Na\(^{+}\) ion and one K\(^{+}\) ion together with two Cl\(^{−}\) ions. This symport is also dependent on the activity of Na\(^{+}/K\(^{+}\) ATPase [2], which pumps the Na\(^{+}\) resorbed from the primary urine back into the plasma in exchange for K\(^{+}\).

The steroid hormone aldosterone (see p. 55) increases Na\(^{+}\) reuptake, particularly in the distal tubule, while atrial natriuretic peptide (ANF) originating from the cardiac atrium reduces it. Among other effects, aldosterone induces Na\(^{+}/K\(^{+}\) ATPase and various Na\(^{+}\) transporters on the luminal side of the cells.

Water. Water resorption in the proximal tubule is a passive process in which water follows the osmotically active particles, particularly the Na\(^{+}\) ions. Fine regulation of water excretion (diuresis) takes place in the collecting ducts, where the peptide hormone vasopressin (antidiuretic hormone, ADH) operates. This promotes recovery of water by stimulating the transfer of aquaporins (see p. 220) into the plasma membrane of the tubule cells via V_2 receptors. A lack of ADH leads to the disease picture of diabetes insipidus, in which up to 30 L of final urine is produced per day.

B. Gluconeogenesis

Apart from the liver, the kidneys are the only organs capable of producing glucose by neosynthesis (gluconeogenesis; see p. 154). The main substrate for gluconeogenesis in the cells of the proximal tubule is glutamine. In addition, other amino acids and also lactate, glycerol, and fructose can be used as precursors. As in the liver, the key enzymes for gluconeogenesis are induced by cortisol (see p. 374). Since the kidneys also have a high level of glucose consumption, they only release very little glucose into the blood.
Renal hormones

A. Renal hormones

In addition to their involvement in excretion and metabolism, the kidneys also have endocrine functions. They produce the hormones erythropoietin and calcitriol and play a decisive part in producing the hormone angiotensin II by releasing the enzyme renin. Renal prostaglandins (see p. 390) have a local effect on Na+ resorption.

Calcitriol (vitamin D hormone, 1α,25-dihydroxycholecalciferol) is a hormone closely related to the steroids that is involved in Ca2+ homeostasis (see p. 342). In the kidney, it is formed from calcidiol by hydroxylation at C-1. The activity of calcitriol-1-monoxygenase [1] is enhanced by the hormone parathyroid (PTH).

Erythropoietin is a peptide hormone that is formed predominantly by the kidneys, but also by the liver. Together with other factors known as “colony-stimulating factors” (CSF; see p. 392), it regulates the differentiation of stem cells in the bone marrow.

Erythropoietin release is stimulated by hypoxia (low pO2). Within hours, the hormone ensures that erythrocyte precursor cells in the bone marrow are converted to erythrocytes, so that their numbers in the blood increase. Renal damage leads to reduced erythropoietin release, which in turn results in anemia. Forms of anemia with renal causes can now be successfully treated using erythropoietin produced by genetic engineering techniques. The hormone is also administered to dialysis patients. Among athletes and sports professionals, there have been repeated cases of erythropoietin being misused for doping purposes.

B. Renin–angiotensin system

The peptide hormone angiotensin II is not synthesized in a hormonal gland, but in the blood. The kidneys take part in this process by releasing the enzyme renin.

Renin [2] is an aspartate proteinase (see p. 176). It is formed by the kidneys as a precursor (prorenin), which is proteolytically activated into renin and released into the blood. In the blood plasma, renin acts on angiotensinogen, a plasma glycoprotein in the α2-globulin group (see p. 276), which like almost all plasma proteins is synthesized in the liver. The decapptide cleaved off by renin is called angiotensin I. Further cleavage by peptidyl dipeptidase A (angiotensin-converting enzyme, ACE), a membrane enzyme located on the vascular endothelium in the lungs and other tissues, gives rise to the octapeptide angiotensin II [3], which acts as a hormone and neurotransmitter. The lifespan of angiotensin II in the plasma is only a few minutes, as it is rapidly broken down by other peptidases (angiotensinases [4]), which occur in many different tissues. The plasma level of angiotensin II is mainly determined by the rate at which renin is released by the kidneys. Renin is synthesized by juxtaglomerular cells, which release it when sodium levels decline or there is a fall in blood pressure.

Effects of angiotensin II. Angiotensin II has effects on the kidneys, brain stem, pituitary gland, adrenal cortex, blood vessel walls, and heart via membrane-located receptors. It increases blood pressure by triggering vasoconstriction (narrowing of the blood vessels). In the kidneys, it promotes the retention of Na+ and water and reduces potassium secretion. In the brain stem and at nerve endings in the sympathetic nervous system, the effects of angiotensin II lead to increased toxicity (neurotransmitter effect). In addition, it triggers the sensation of thirst. In the pituitary gland, angiotensin II stimulates vasopressin release (antidiuretic hormone) and corticotropic (ACTH) release. In the adrenal cortex, it increases the biosynthesis and release of aldosterone, which promotes sodium and water retention in the kidneys. All of the effects of angiotensin II lead directly or indirectly to increased blood pressure, as well as increased sodium and water retention. This important hormonal system for blood pressure regulation can be pharmacologically influenced by inhibitors at various points:

- Using angiotensinogen analogs that inhibit renin.
- Using angiotensin I analogs that competitively inhibit the enzyme ACE [3].
- Using hormone antagonists that block the binding of angiotensin II to its receptors.

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A. Renal hormones

- Calcitriol
- Parathyrin
- Calcitrol from liver

B. Renin angiotensin system

- Angiotensinogen from liver
- Enzyme
- Peptidases 3.4.13
- Peptidyl-dipeptidase-A (Zn\textsuperscript{2+}) 3.4.15.1 (ACE)

Effects

- Blood pressure
- Blood vessels: Vasoconstriction
- Blood pressure↑
- Adrenal: Aldosterone production↑
- Brain: Release of vasopressin, angiotensin, Thirst
- Kidneys: Na\textsuperscript{+} retention, H\textsubscript{2}O retention

Octapeptide DRVYIHPF

Calcitriol 1-monooxygenase (heme P450) 1.14.13.15
Renin 3.4.23.15
Peptidyl-dipeptidase A (Zn\textsuperscript{2+}) 3.4.15.1 (ACE)
Muscle contraction

The musculature is what makes movements possible. In addition to the skeletal muscles, which can be contracted voluntarily, there are also the autonomically activated heart muscle and smooth muscle, which is also involuntary. In all types of muscle, contraction is based on an interplay between the proteins actin and myosin.

A. Organization of skeletal muscle

Striated muscle consists of parallel bundles of muscle fibers. Each fiber is a single large multinucleate cell. The cytoplasm in these cells contains myofibrils 2–3 μm thick that can extend over the full length of the muscle fiber. The striation of the muscle fibers is characteristic of skeletal muscle. It results from the regular arrangement of molecules of differing density. The repeating contractile units, the sarcomeres, are bounded by Z lines from which thin filaments of F-actin (see p. 204) extend on each side. In the A bands, there are also thick parallel filaments of myosin. The H bands in the middle of the A bands only contain myosin, while only actin is found on each size of the Z lines.

Myosin is quantitatively the most important protein in the myofibrils, representing 65% of the total. It is shaped like a golf club (bottom right). The molecule is a hexamer consisting of two identical heavy chains (2 x 223 kDa) and four light chains (each about 20 kDa). Each of the two heavy chains has a globular “head” at its amino end, which extends into a “tail” about 150 nm long in which the two chains are intertwined to form a superhelix. The small subunits are attached in the head area. Myosin is present as a bundle of several hundred stacked molecules in the form of a thick myosin filament. The head portion of the molecule acts as an ATPase, the activity of which is modulated by the small subunits.

Actin (42 kDa) is the most important component of the “thin filaments.” It represents ca. 20–25% of the muscle proteins. F-actin is also an important component of the cytoskeleton (see p. 204). This filamentous polymer is held in equilibrium with its monomer, G-actin. The other protein components of muscle include tropomyosin and troponin.

B. Mechanism of muscle contraction

The sliding filament model describes the mechanism involved in muscle contraction. In this model, sarcomeres become shorter when the thin and thick filaments slide alongside each other and telescope together, with ATP being consumed. During contraction, the following reaction cycle is repeated several times:

[1] In the initial state, the myosin heads are attached to actin. When ATP is bound, the heads detach themselves from the actin (the “plasticizing” effect of ATP).
[2] The myosin head hydrolyzes the bound ATP to ADP and P, but initially withholds the two reaction products. ATP cleavage leads to allosteric tension in the myosin head.
[4] The actin causes the release of the P, and shortly afterwards release of the ADP as well. This converts the allosteric tension in the myosin head into a conformational change that acts like a rowing stroke.

The cycle can be repeated for as long as ATP is available, so that the thick filaments are constantly moving along the thin filaments in the direction of the Z disk. Each rowing stroke of the 500 or so myosin heads in a thick filament produces a contraction of about 10 nm. During strong contraction, the process is repeated about five times per second. This leads to the whole complex of thin filaments moving together; the H band becomes shorter and the Z lines slide closer together.
A. Organization of striated muscle

- Bundle of muscle fibers
- Sarcomere
- H zone
- A band
- I band
- Thick myosin filament
- Thin actin filament
- Troponin
- Actin
- Tropomyosin

B. Mechanism of muscle contraction

- Center of the sarcomere
- Myosin head relaxed
- Power stroke
- Contact
- Myosin head contracted
- ATP
- H₂O
- Small subunits
- Globular head
- Myosin molecule
Control of muscle contraction

A. Neuromuscular junction

Muscle contraction is triggered by motor neurons that release the neurotransmitter acetylcholine (see p. 332). The transmitter diffuses through the narrow synaptic cleft and binds to nicotinic acetylcholine receptors on the plasma membrane of the muscle cell (the sarcolemma), thereby opening the ion channels integrated into the receptors (see p. 222). This leads to an inflow of Na⁺, which triggers an action potential (see p. 350) in the sarcolemma. The action potential propagates from the end plate in all directions and constantly stimulates the muscle fiber. With a delay of a few milliseconds, the contractile mechanism responds to this by contracting the muscle fiber.

B. Sarcomplasmic reticulum (SR)

The action potential (A) produced at the neuromuscular junction is transferred in the muscle cell into a transient increase in the Ca²⁺ concentration in the cytoplasm of the muscle fiber (the sarcomplasm).

In the resting state, the Ca²⁺ level in the sarcomplasm is very low (less than 10⁻⁷ M). By contrast, the sarcomplasmic reticulum (SR), which corresponds to the ER, contains Ca²⁺ ions at a concentration of about 10⁻⁴ M. The SR is a branched organelle that surrounds the myofibrils like a net stocking inside the muscle fibers (illustrated at the top using the example of a heart muscle cell). The high Ca²⁺ level in the SR is maintained by Ca²⁺-transporting ATPases (see p. 220). In addition, the SR also contains calsequestrin, a protein (55 kDa) that is able to bind numerous Ca²⁺ ions via acidic amino acid residues.

The transfer of the action potential to the SR is made possible by transverse tubules (T tubules), which are open to the extracellular space and establish a close connection with the SR. There is a structure involved in the contact between the T tubule and the SR that was formerly known as the “SR foot” (it involves parts of the ryanodine receptor; see p. 386).

At the point of contact with the SR, the action potential triggers the opening of the Ca²⁺ channels on the surface of the sarcolemma. Calcium ions then leave the SR and enter the sarcomplasm, where they lead to a rapid increase in Ca²⁺ concentrations. This in turn causes the myofibrils to contract (C).

C. Regulation by calcium ions

In relaxed skeletal muscle, the complex consisting of troponin and tropomyosin blocks the access of the myosin heads to actin (see p. 332). Troponin consists of three different subunits (T, C, and I). The rapid increase in cytoplasmic Ca²⁺ concentrations caused by opening of the calcium channels in the SR leads to binding of Ca²⁺ to the C subunit of troponin, which closely resembles calmodulin (see p. 386). This produces a conformational change in troponin that causes the whole troponin–tropomyosin complex to slip slightly and expose a binding site for myosin (red). This initiates the contraction cycle. After contraction, the sarcomplasmic Ca²⁺ concentration is quickly reduced again by active transport back into the SR. This results in troponin losing the bound Ca²⁺ ions and returning to the initial state, in which the binding site for myosin on actin is blocked. It is not yet clear whether the mechanism described above is the only one that triggers binding of myosin to actin.

When triggering of contraction in striated muscle occurs, the following sequence of processes thus takes place:

1. The sarcolemma is depolarized.
2. The action potential is signaled to Ca²⁺ channels in the SR.
3. The Ca²⁺ channels open and the Ca²⁺ level in the sarcomplasm increases.
4. Ca²⁺ binds to troponin C and triggers a conformational change.
5. Troponin causes tropomyosin to slip, and the myosin heads bind to actin.
6. The actin–myosin cycle takes place and the muscle fibers contract.

Conversely, at the end of contraction, the following processes take place:

1. The Ca²⁺ level in the sarcomplasm declines due to transport of Ca²⁺ back into the SR.
2. Troponin C loses Ca²⁺ and tropomyosin returns to its original position on the actin molecule.
3. The actin–myosin cycle stops and the muscle relaxes.
A. Neuromuscular junction

- Action potential
- End plate
- Nucleus
- Muscle fiber

B. Sarcoplasmatic reticulum (SR)

- Transverse tubule
- Sarcolemmal reticulum
- Calsequestrin
- SR foot
- Ca\(^{2+}\) channels
- Extracellular space
- Cytosol
- SR
- Myosin-binding site on actin blocked

C. Regulation by calcium ions

- Myosin head
- Actin
- Troponin
- Cyp250
- Cyp250 exposes myosin-binding site on actin
Muscle metabolism I

Muscle contraction is associated with a high level of ATP consumption (see p. 332). Without constant resynthesis, the amount of ATP available in the resting state would be used up in less than 1 s of contraction.

A. Energy metabolism in the white and red muscle fibers

Muscles contain two types of fibers, the proportions of which vary from one type of muscle to another. Red fibers (type I fibers) are suitable for prolonged effort. Their metabolism is mainly aerobic and therefore depends on an adequate supply of O₂. White fibers (type II fibers) are better suited for fast, strong contractions. These fibers are able to form suf cient ATP even when there is little O₂ available. With appropriate training, athletes and sports participants are able to change the proportions of the two fiber types in the musculature and thereby prepare themselves for the physiological demands of their disciplines in a targeted fashion. The expression of functional muscle proteins can also change during the course of training.

Red fibers provide for their ATP requirements mainly (but not exclusively) from fatty acids, which are broken down via ß-oxidation, the tricarboxylic acid cycle, and the respiratory chain (right part of the illustration). The red color in these fibers is due to the monomeric heme protein myoglobin, which they use as an O₂ reserve. Myoglobin has a much higher af nity for O₂ than hemoglobin and therefore only releases its O₂ when there is a severe drop in O₂ partial pressure (cf. p. 282).

At a high level of muscular effort—e.g., during weightlifting or in very fast contractions such as those carried out by the eye muscles—the O₂ supply from the blood quickly becomes inadequate to maintain the aerobic metabolism. White fibers (left part of the illustration) therefore mainly obtain ATP from anaerobic glycolysis. They have supplies of glycogen from which they can quickly release glucose-1-phosphate when needed (see p. 156). By isomerization, this gives rise to glucose-6-phosphate, the substrate for glycolysis. The NADH+H⁺ formed during glycolysis has to be reoxidized into NAD⁺ in order to maintain glucose degradation and thus ATP formation. If there is a lack of O₂, this is achieved by the formation of lactate, which is released into the blood and is resynthesized into glucose in the liver (Cori cycle; see p. 338).

Muscle-specific auxiliary reactions for ATP synthesis exist in order to provide additional ATP in case of emergency. Creatine phosphate (see B) acts as a buffer for the ATP level. Another ATP-supplying reaction is catalyzed by adenylate kinase [1] (see also p. 72). This disproportionates two molecules of ADP into ATP and AMP. The AMP is deaminated into IMP in a subsequent reaction [2] in order to shift the balance of the reversible reaction [1] in the direction of ATP formation.

B. Creatine metabolism

Creatine (N-methylguanidoacetic acid) and its phosphorylated form creatine phosphate (a guanidophosphate) serve as an ATP buffer in muscle metabolism. In creatine phosphate, the phosphate residue is at a similarly high chemical potential as in ATP and is therefore easily transferred to ADP. Conversely, when there is an excess of ATP, creatine phosphate can arise from ATP and creatine. Both processes are catalyzed by creatine kinase [5].

In resting muscle, creatine phosphate forms due to the high level of ATP. If there is a risk of a severe drop in the ATP level during contraction, the level can be maintained for a short time by synthesis of ATP from creatine phosphate and ADP. In a nonenzymatic reaction [6], small amounts of creatine and creatine phosphate cyclize constantly to form creatinine, which can no longer be phosphorylated and is therefore excreted with the urine (see p. 324).

Creatine does not derive from the muscles themselves, but is synthesized in two steps in the kidneys and liver (left part of the illustration). Initially, the guanidino group of arginine is transferred to glycine in the kidneys, yielding guanidino acetate [3]. In the liver, N-methylation of guanidino acetate leads to the formation of creatine from this [4]. The coenzyme in this reaction is S-adenosyl methionine (SAM; see p.110).
### A. Energy metabolism in the white and red muscle fibers

<table>
<thead>
<tr>
<th>White (slow) fibers, anaerobic</th>
<th>Red (fast) fibers, aerobic</th>
</tr>
</thead>
</table>

- **Glycogen** → ADP → ATP → Myoglobin
- **Creatine phosphate** → ADP → NADH + H⁺ → Acetyl CoA
- **Pyruvate** → Lactate
- **Glycolysis** → **Tricarboxylic acid cycle**
- **β-Oxidation** → Ketone bodies
- **Respiratory chain** → O₂
- **O₂** → **Creatine**

### B. Creatine metabolism

- **5-adenosyl homocysteine** → **Creatine** → **Creatine phosphate** → **Creatinine**
- **Guanidinoacetate methyltransferase** 2.1.1.2
- **Creatine kinase** 2.7.3.2
- **Not-enzymatic**

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Muscle metabolism II

A. Cori and alanine cycle

White muscle fibers (see p. 336) mainly obtain ATP from anaerobic glycolysis—i.e., they convert glucose into lactate. The lactate arising in muscle and, in smaller quantities, its precursor pyruvate are released into the blood and transported to the liver, where lactate and pyruvate are resynthesized into glucose again via gluconeogenesis, with ATP being consumed in the process (see p. 154). The glucose newly formed by the liver returns via the blood to the muscles, where it can be used as an energy source again. This circulation system is called the Cori cycle, after the researchers who first discovered it. There is also a very similar cycle for erythrocytes, which do not have mitochondria and therefore produce ATP by anaerobic glycolysis (see p. 284).

The muscles themselves are not capable of gluconeogenesis. Nor would this be useful, as gluconeogenesis requires much more ATP than is supplied by glycolysis. As O₂ deficiencies do not arise in the liver even during intensive muscle work, there is always sufficient energy there available for gluconeogenesis.

There is also a corresponding circulation system for the amino acid alanine. The alanine cycle in the liver not only provides alanine as a precursor for gluconeogenesis, but also transports to the liver the amino nitrogen arising in muscles during protein degradation. In the liver, it is incorporated into urea for excretion.

Most of the amino acids that arise in muscle during proteolysis are converted into glutamate and 2-oxo acids by transamination (not shown; cf. p. 180). Again by transamination, glutamate and pyruvate give rise to alanine, which after glutamine is the second important form of transport for amino nitrogen in the blood. In the liver, alanine and 2-oxo-glutarate are resynthesized into pyruvate and glutamate (see p. 178). Glutamate supplies the urea cycle (see p. 182), while pyruvate is available for gluconeogenesis.

B. Protein and amino acid metabolism

The skeletal muscle is the most important site for degradation of the branched-chain amino acids (Val, Leu, Ile; see p. 414), but other amino acids are also broken down in the muscles. Alanine and glutamine are resynthesized from the components and released into the blood. They transport the nitrogen that arises during amino acid breakdown to the liver (alanine cycle; see above) and to the kidneys (see p. 328).

During periods of hunger, muscle proteins serve as an energy reserve for the body. They are broken down into amino acids, which are transported to the liver. In the liver, the carbon skeletons of the amino acids are converted into intermediates in the tricarboxylic acid cycle or into acetoacetyl-CoA (see p. 175). These amphiphilic metabolites are then available to the energy metabolism and for gluconeogenesis. After prolonged starvation, the brain switches to using ketone bodies in order to save muscle protein (see p. 356).

The synthesis and degradation of muscle proteins are regulated by hormones. Cortisol leads to muscle degradation, while testosterone stimulates protein formation. Synthetic anabolics with a testosterone-like effect have repeatedly been used for doping purposes or for intensive muscle-building.

Further information

Smooth muscle differs from skeletal muscle in various ways. Smooth muscles—which are found, for example, in blood vessel walls and in the walls of the intestines—do not contain any muscle fibers. In smooth-muscle cells, which are usually spindle-shaped, the contractile proteins are arranged in a less regular pattern than in striated muscle. Contraction in this type of muscle is usually not stimulated by nerve impulses, but occurs in a largely spontaneous way. Ca²⁺ (in the form of Ca²⁺-calmodulin; see p. 386) also activates contraction in smooth muscle; in this case, however, it does not affect tropomysin, but activates a protein kinase that phosphorylates the light chains in myosin and thereby increases myosin’s ATPase activity. Hormones such as epinephrine and angiotensin II (see p. 330) are able to influence vascular tonicity in this way, for example.
A. Cori and alanine cycle

1. Glycolysis
2. Transamination
3. Lactate dehydrogenase
4. Gluconeogenesis

B. Protein and amino acid metabolism

Val: 0.25 mM
Leu: 0.16 mM
Ile: 0.08 mM
Ala: 0.42 mM
Gln: 0.66 mM

Plasma concentration

Ala, Gln

Amino acids

Testosterone, Anabolic agents

[\(\text{NH}_2\)]

Synthesis
Degradation

Energy gain

Energy reserve in prolonged hunger

Muscle

Muscle breaks down branched-chain amino acids

Protein

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Bone and teeth

The family of connective-tissue cells includes fibroblasts, chondrocytes (cartilage cells), and osteoblasts (bone-forming cells). They are specialized to secrete extracellular proteins, particularly collagens, and mineral substances, which they use to build up the extracellular matrix (see p. 346). By contrast, osteoclasts dissolve bone matter again by secreting H+ and collagenases (see p. 342).

A. Bone

Bone is an extremely dense, specialized form of connective tissue. In addition to its supportive function, it serves to store calcium and phosphate ions. In addition, blood cells are formed in the bone marrow. The most important mineral component of bone is apatite, a form of crystalline calcium phosphate.

Apatites are complexes of cationic Ca2+ matched by HPO42-, CO32-, OH-, or F- as anions. Depending on the counter-ion, apatite can occur in the forms carbonate apatite Ca10(OH)2(PO4)6, as hydroxyapatite Ca10(PO4)6(OH)2, or fluoroapatite Ca10(PO4)6F2. In addition, alkaline earth carbonates also occur in bone. In adults, more than 1 kg calcium is stored in bone.

Osteoblast and osteoclast activity is constantly incorporating Ca2+ into bone and removing it again. There are various hormones that regulate these processes: calcitonin increases deposition of Ca2+ in the bone matrix, while parathyroid hormone (PTH) promotes the mobilization of Ca2+, and calcitriol improves mineralization (for details, see p. 342).

The most important organic components of bone are collagens (mainly type I; see p. 344) and proteoglycans (see p. 346). These form the extracellular matrix into which the apatite crystals are deposited (biomineralization). Various proteins are involved in this not yet fully understood process of bone formation, including collagens and phosphatases. Alkaline phosphatase is found in osteoblasts and acid phosphatase in osteoclasts. Both of these enzymes serve as marker enzymes for bone cells.

B. Teeth

The illustration shows a longitudinal section through an incisor, one of the 32 permanent teeth in humans. The majority of the tooth consists of dentine. The crown of the tooth extends beyond the gums, and it is covered in enamel. By contrast, the root of the tooth is coated in dental cement.

Cement, dentin, and enamel are bone-like substances. The high proportion of inorganic matter they contain (about 97% in the dental enamel) gives them their characteristic hardness. The organic components of cement, dentin, and enamel mainly consist of collagens and proteoglycans; their most important mineral component is apatite, as in bone (see above).

A widespread form of dental disease, caries, is caused by acids that dissolve the mineral part of the teeth by neutralizing the negatively charged counter-ions in apatite (see A). Acids occur in food, or are produced by microorganisms that live on the surfaces of the teeth (e.g., Streptococcus mutans).

The main product of anaerobic degradation of sugars by these organisms is lactic acid. Other products of bacterial carbohydrate metabolism include extracellular dextrans (see p. 40)—insoluble polymers of glucose that help bacteria to protect themselves from their environment. Bacteria and dextrans are components of dental plaque, which forms on inadequately cleaned teeth. When Ca2+ salts and other minerals are deposited in plaque as well, tartar is formed.

The most important form of protection against caries involves avoiding sweet substances (foods containing saccharose, glucose, and fructose). Small children in particular should not have very sweet drinks freely available to them. Regular removal of plaque by cleaning the teeth and hardening of the dental enamel by fluoridization are also important. Fluoride has a protective effect because fluorapatite (see A) is particularly resistant to acids.
Connective tissue

**A. Bone**

- **Functions**: Mechanical support, Storage for Ca\(^{2+}\) and phosphate, Synthesis of blood cells, Maturation of B cells
- **Hormones of the calcium metabolism**
  - Parathyroid hormone
  - Calcitonin
  - Calcitriol
- **Composition**: Inorganic, Organic, Apatite, Type I collagen, Carbonate, Proteoglycans, Phosphatases
- **Hydroxyapatite**: Ca\(_{10}\)(PO\(_4\)\(_6\))(OH\(_2\)\)

**Absence leads to rickets**

**B. Teeth**

- **Hardest substance in the body**: Dental enamel
- **97%**
  - Dental enamel
  - Dentin
  - Cement
  - Jawbone
- **Dental plaque**: 70%, 65%, 45%
- **Inorganic components**
- **Dextran**
- **Plaque**
- **Bacterium**
- **Dental enamel**
- **Protect bacteria**
- **Sugar**
  - Saccharose
  - Glucose
  - Fructose
- **Anaerobic metabolism**
  - Bacterium E.g. Streptococcus mutans
- **Attack apatite**
  - Acids
  - Lactic acid
  - Propionic acid
  - Acrylic acid
  - Butyric acid
  - Calcium salts
- **Demineralization**

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Calcium metabolism

A. Functions of calcium

The human body contains 1–1.5 kg Ca\(^{2+}\), most of which (about 98%) is located in the mineral substance of bone (see p. 362).

In addition to its role as a bone component, calcium functions as a signaling substance. Ca\(^{2+}\) ions act as second messengers in signal transduction pathways (see p. 396), they trigger exocytosis (see p. 228) and muscle contraction (see p. 334), and they are indispensable as cofactors in blood coagulation (see p. 290). Many enzymes also require Ca\(^{2+}\) for their activity. The intracellular and extracellular concentrations of Ca\(^{2+}\) are strictly regulated in order to make these functions possible (see B, C, and p. 388).

Proteins bind Ca\(^{2+}\) via oxygen ligands, particularly carboxylate groups and carbonyl groups of peptide bonds. This also applies to the structure illustrated here, in which a Ca\(^{2+}\) ion is coordinated by the oxygen atoms of carboxylic and acid amide groups.

B. Bone remodeling

Deposition of Ca\(^{2+}\) in bone (mineralization) and Ca\(^{2+}\) mobilization from bone are regulated by at least 15 hormones and hormone-like signaling substances. These mainly influence the maturation and activity of bone cells. Osteoblasts (top) deposit collagen, as well as Ca\(^{2+}\) and phosphate, and thereby create new bone matter, while osteoclasts (bottom) secrete H\(^{+}\) ions and collagenases that locally dissolve bone (bone remodeling). Osteoblasts and osteoclasts mutually activate each other by releasing cytokines (see p. 392) and growth factors. This helps keep bone formation and bone breakdown in balance.

The Ca\(^{2+}\)-selective hormones calcitriol, parathyroid hormone, and calcitonin influence this interaction in the bone cells. Parathyroid hormone promotes Ca\(^{2+}\) release by promoting the release of cytokines by osteoblasts. In turn, the cytokines stimulate the development of mature osteoclasts from precursor cells (bottom). Calcitonin inhibits this process. At the same time, it promotes the development of osteoblasts (top). Osteoporosis, which mainly occurs in women following the menopause, is based (at least in part) on a reduction in estrogen levels. Estrogens normally inhibit the stimulation of osteoclast differentiation by osteoblasts. If the effects of estrogen decline, the osteoclasts predominate and excess bone removal occurs.

The effects of the steroid hormone calcitriol (see p. 330) in bone are complex. On the one hand, it promotes bone formation by stimulating osteoblast differentiation (top). This is particularly important in small children, in whom calcitriol deficiency can lead to mineralization disturbances (rickets; see p. 364). On the other hand, calcitriol increases blood Ca\(^{2+}\) levels through increased Ca\(^{2+}\) mobilization from bone. An overdose of vitamin D (cholecalciferol), the precursor of calcitriol, can therefore have unfavorable effects on the skeleton similar to those of vitamin deficiency (hypervitaminosis; see p. 364).

C. Calcium homeostasis

Ca\(^{2+}\) metabolism is balanced in healthy adults. Approximately 1 g Ca\(^{2+}\) is taken up per day, about 300 mg of which is resorbed. The same amount is also excreted again. The amounts of Ca\(^{2+}\) released from bone and deposited in it per day are much smaller. Milk and milk products, especially cheese, are particularly rich in calcium.

Calcitriol and parathyroid hormone, on the one hand, and calcitonin on the other, ensure a more or less constant level of Ca\(^{2+}\) in the blood plasma and in the extracellular space (80–110 mg 2.0–2.6 mM). The peptide parathyroid hormone (PTH; 84 AA) and the steroid calcitriol (see p. 374) promote direct or indirect processes that raise the Ca\(^{2+}\) level in blood. Calcitriol increases Ca\(^{2+}\) resorption in the intestines and kidneys by inducing transporters. Parathyroid hormone supports these processes by stimulating calcitriol biosynthesis in the kidneys (see p. 330). In addition, it directly promotes resorption of Ca\(^{2+}\) in the kidneys (see p. 328) and Ca\(^{2+}\) release from bone (see B). The PTH antagonist calcitonin (32 AA) counteracts these processes.
Collagens
Collagens are quantitatively the most abundant of animal proteins, representing 25% of the total. They form insoluble tensile fibers that occur as structural elements of the extracellular matrix and connective tissue throughout the body. Their name (which literally means “glue-producers”) is derived from the gels that appear as a decomposition product when collagen is boiled.

A. Structure of collagens

Nineteen different collagens are now known, and they are distinguished using roman numerals. They mostly consist of a dextro-rotatory triple helix made up of three polypeptides (α-chains) (see p. 70).

The triplet Gly-X-Y is constantly repeated in the sequence of the triple-helical regions—i.e., every third amino acid in such sequences is a glycine. Proline (Pro) is frequently found in positions X or Y; the Y position is often occupied by 4-hydroxyproline (4Hyp), although 3-hydroxyproline (3Hyp) and 5-hydroxylysine (5Hyl) also occur. These hydroxylated amino acids are characteristic components of collagens. They are only produced after protein biosynthesis by hydroxylation of the amino acids in the peptide chain (see p. 62).

The formation of Hyp and Hyl residues in procollagen is catalyzed by iron-containing oxygenases (“proline and lysine hydroxylase,” EC 1.14.11.1/2). Ascorbate is required to maintain their function. Most of the symptoms of the vitamin C deficiency disease scurvy (see p. 368) are explained by disturbed collagen biosynthesis.

The hydroxyproline residues stabilize the triple helix by forming hydrogen bonds between the α-chains, while the hydroxyl groups of hydroxylysine are partly glycosylated with a disaccharide (→Glc–Gal).

The various types of collagen consist of different combinations of α-chains (α1 to α3 and other subtypes). Types I, II, and III represent 90% of collagens. The type I collagen shown here has the structure [α1(1)]2α2(1).

Numerous tropocollagen molecules (mass 285 kDa, length 400 nm) aggregate extracellularly into a defined arrangement, forming cylindrical fibrils (20–500 nm in diameter). Under the electron microscope, these fibrils are seen to have a characteristic banding pattern of elements that are repeated every 64–67 nm.

Tropocollagen molecules are firmly linked together, particularly at their ends, by covalent networks of altered lysine side chains. The number of these links increases with age. Type IV collagens form networks with a defined mesh size. The size-selective filtering effect of the basal membranes in the renal glomeruli is based on this type of structure (see p. 322).

B. Biosynthesis

The precursor molecule of collagen (procollagen), formed in the rER, is subject to extensive post-translational modifications (see p. 232) in the ER and Golgi apparatus.

Cleavage of the signal peptide gives rise to procollagen, which still carries large propeptides at each end [1]. During this phase, most proline residues and some lysine residues of procollagen are hydroxylated [2]. The procollagen is then glycosylated at hydroxyllysine residues [3]. Intramolecular and intermolecular disulfide bonds form in the propeptides [4], allowing correct positioning of the peptide strands to form a triple helix [5]. It is only after these steps have been completed that procollagen is secreted into the extracellular space by exocytosis. This is where the N- and C-terminal propeptides are removed proteolytically [6], allowing the staggered aggregation of the tropocollagen molecules to form fibrils [7]. Finally, several ε-amino groups in lysine residues are oxidatively converted into aldehyde groups [8]. Covalent links between the molecules then form as a result of condensation [9]. In this way, the fibrils reach their final structure, which is characterized by its high tensile strength and protease resistance.
A. Structure of collagens

- Basic unit

- Special amino acids: 4-Hydroxyproline (4Hyp) 5-Hydroxylysine (5Hyl)

- Primary structure

- Type I tropocollagen ~285 kDa

- Overlap D = 64–67 nm

- Gap All nm

- Diameter 1.5 nm

- Length 400 nm

- Collagen fibril (section)

B. Biosynthesis

- Transcription

- Translation

- Pre-procollagen

- Intracellular protein modification

- Exocytosis

- Collagen fibril

- Removal of the prepeptide
- Hydroxylation of Pro and Lys residues
- Glycosylation of SHyl and Asn
- Oxidation of Cys in propeptides
- Assemblage to form triple helix
- Removal of the propeptide
- Staggered deposition to form fibrils
- Oxidation of Lys and SHyl to aldehydes
- Cross-linking to form supramolecules

- Procollagen-proline 4-dioxygenase 1.14.11.2 [ascorbate, Fe]
- Procollagen-lysine 5-dioxygenase 1.14.11.4 [ascorbate, Fe]
- Protein-lysine 6-oxidase 1.4.3.13 [Cu]

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Extracellular matrix

A. Extracellular matrix

The space between the cells (the interstitium) is occupied by a substance with a complex composition known as the extracellular matrix (ECM). In many types of tissue—e.g., muscle and liver—the ECM is only a narrow border between the cells, while in others it forms a larger space. In connective tissue, cartilage, and bone, the ECM is particularly strongly marked and is actually the functional part of the tissue (see p. 340). The illustration shows the three main constituents of the extracellular matrix in a highly schematic way: collagen fibers, network-forming adhesive proteins, and space-filling proteoglycans.

The ECM has a very wide variety of functions: it establishes mechanical connections between cells; it creates structures with special mechanical properties (as in bone, cartilage, tendons, and joints); it creates filters (e.g., in the basal membrane in the renal corpuscles; see p. 322); it separates cells and tissues from each other (e.g., to allow the joints to move freely); and it provides pathways to guide migratory cells (important for embryonic development). The chemical composition of the ECM is just as diverse as its functions.

Collagens (see p. 344), of which there are at least 19 different varieties, form fibers, fibrils, networks, and ligaments. Their characteristic properties are tensile strength and flexibility. Elastin is a fiber protein with a high degree of elasticity.

Adhesive proteins provide the connections between the various components of the extracellular matrix. Important representatives include laminin and fibronectin (see B). These multifunctional proteins simultaneously bind to several other types of matrix component. Cells attach to the cell surface receptors in the ECM with the help of the adhesive proteins.

Due to their polarity and negative charge, proteoglycans (see C) bind water molecules and cations. As a homogenous “cement,” they fill the gaps between the ECM fibers.

B. Fibronectins

Fibronectins are typical representatives of adhesive proteins. They are filamentous dimers consisting of two related peptide chains (each with a mass of 250 kDa) linked to each other by disulfide bonds. The fibronectin molecules are divided into different domains, which bind to cell-surface receptors, collagens, fibrin, and various proteoglycans. This is what gives fibronectins their “molecular glue” characteristics.

The domain structure in fibronectins is made up of a few types of peptide module that are repeated numerous times. Each of the more than 50 modules is coded for by one exon in the fibronectin gene. Alternative splicing (see p. 246) of the hnRNA transcript of the fibronectin gene leads to fibronectins with different compositions. The module that causes adhesion to cells contains the characteristic amino acid sequence—Arg–Gly–Asp–Ser—. It is these residues that enable fibronectin to bind to cell-surface receptors, known as integrins.

C. Proteoglycans

Proteoglycans are giant molecule complexes consisting of carbohydrates (95%) and proteins (5%), with masses of up to 2 × 10^6 Da. Their bottlebrush-shaped structure is produced by an axis consisting of hyaluronate. This thread-like polysaccharide (see p. 44), has proteins attached to it, from which in turn long polysaccharide chains emerge. Like the central hyaluronate, these terminal polysaccharides belong to the glycosaminoglycan group (see p. 44).

The glycosaminoglycans are made up of repeating disaccharide units, each of which consists of one uronic acid (glucuronic acid or iduronic acid) and one amino sugar (N-acetylgalosamine or N-acetylglactosamine) (see p. 38). Many of the amino sugars are also esterified with sulfuric acid (sulfated), further increasing their polarity. The proteoglycans bind large amounts of water and fill the gaps between the fibrillar components of the ECM in the form of a hydrated gel. This inhibits the spread of pathogens in the ECM, for example.
A. Extracellular matrix

Collagens
(at least
19 different
forms)

Cell surface
receptors
(Integrins)

Adhesive
proteins:
Elastin, laminin,
fibronectin

Proteoglycans
and
hyaluronic acid

B. Fibronectins

Heparan sulfate
Fibers

Collagens

Domains

Integrins

Heparan sulfate
Fibers

Peptide modules

Variable peptides

C. Proteoglycans

Disaccharide units

IduUA = Iduronate
GlcUA = Glucuronate
GalNAc = N-Acetyl-
galactosamine
GlcNAc = N-Acetyl-
glucosamine

Dermatan
sulfate

Heparan
sulfate

Heparin

Keratan
sulfate

Chondroitin
6-sulfate

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Signal transmission in the CNS

A. Structure of nerve cells

Nerve cells (neurons) are easily excitable cells that produce electrical signals and can react to such signals as well. Their structure is markedly different from that of other types of cell. Numerous branching processes project from their cell body (soma). Neurons are able to receive signals via dendrites and to pass them on via axons. The axons, which can be up to 1 m long, are usually surrounded by Schwann cells, which cover them with a lipid-rich myelin sheath to improve their electrical insulation.

The transfer of stimuli occurs at the synapses, which link the individual neurons to each other as well as linking neurons functionally to muscle fibers. Neutrotransmitters (see p. 352) are stored in the axonal nerve endings. These signaling substances are released in response to electrical signals in order to excite neighboring neurons (or muscle cells). It is estimated that each neuron in the brain is in contact via synapses with approximately 10,000 other neurons.

There is a noticeably high proportion of lipids in the composition of nerve cells, representing about 50% of their dry weight. In particular, there is a very wide variety of phospholipids, glycolipids, and sphingolipids (see p. 216).

B. Neurotransmitters and neurohormones

Neurosecretions are classed into two groups: neurotransmitters are released into the synaptic cleft in order to influence neighboring cells (C). They have a short range and a short lifespan. By contrast, neurohormones are released into the blood, allowing them to cover larger distances. However, the distinction between the two groups is a fluid one; some neurotransmitters simultaneously function as neurohormones.

C. Synaptic signal transmission

All chemical synapses function according to a similar principle. In the area of the synapse, the surface of the signaling cell (presynaptic membrane) is separated from the surface of the receiving cell (postsynaptic membrane) only by a narrow synaptic cleft. When an action potential (see p. 350) reaches the presynaptic membrane, voltage-gated Ca2+ channels integrated into the membrane open and trigger exocytosis of the neurotransmitter stored in the presynaptic cell (for details, see p. 228).

Each neuron usually releases only one type of neurotransmitter. Neurons that release dopamine are referred to as “dopaminergic,” for example, while those that release acetylcholine are “cholinergic,” etc. The transmitters that are released diffuse through the synaptic cleft and bind on the other side to receptors on the postsynaptic membrane. These receptors are integral membrane proteins that have binding sites for neurotransmitters on their exterior (see p. 224).

The receptors for neurotransmitters are divided into two large groups according to the effect produced by binding of the transmitter (for details, see p. 354).

Ionotropic receptors (bottom left) are ligand-gated ion channels. When they open as a result of the transmitter’s influence, ions flow in due to the membrane potential (see p. 126). If the inflowing ions are cations (Na+, K+, Ca2+), depolarization of the membrane occurs and an action potential is triggered on the surface of the postsynaptic cell. This is the way in which stimulatory transmitters work (e.g., acetylcholine and glutamate). By contrast, if anions flow in (mainly Cl−), the result is hyperpolarization of the postsynaptic membrane, which makes the production of a postsynaptic action potential more difficult. The action of inhibitory transmitters such as glycine and GABA is based on this effect.

A completely different type of effect is observed in metabotropic receptors (bottom right). After binding of the transmitter, these interact on the inside of the postsynaptic membrane with G proteins (see p. 384), which in turn activate or inhibit the synthesis of second messengers. Finally, second messengers activate or inhibit protein kinases, which phosphorylate cellular proteins and thereby alter the behavior of the postsynaptic cells (signal transduction; see p. 380).
A. Structure of nerve cells

B. Neurotransmitters and neurohormones

C. Synaptic signal transmission

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Resting potential and action potential

A. Resting potential

A characteristic property of living cells is the uneven distribution of positively and negatively charged ions on the inside and outside of the plasma membrane. This gives rise to a membrane potential (see p. 126)—i.e., there is electrical voltage between the two sides of the membrane, which can only balance out when ion channels allow the unevenly distributed ions to move.

At rest, the membrane potential in most cells is −60 to −90 mV. It mainly arises from the activity of Na⁺/K⁺ transporting ATPase (“Na⁺/K⁺ ATPase”), which occurs on practically all animal cells. Using up ATP, this P-type enzyme (see p. 220) “pumps” three Na⁺ ions out of the cell in exchange for two K⁺ ions. Some of the K⁺ ions, following the concentration gradient, leave the cell again through potassium channels. As the protein anions that predominate inside the cell cannot follow them, and inflow of Cl⁻ ions from the outside is not possible, the result is an excess of positive charges outside the cell, while anions predominate inside it.

An equilibrium potential exists for each of the ions involved. This is the value of the membrane potential at which there is no net inflow or outflow of the ions concerned. For K⁺ ions, the resting potential lies in the range of the membrane potential, while for Na⁺ ions it is much higher at −70 mV. At the first opportunity, Na⁺ ions will therefore spontaneously flow into the cell. The occurrence of action potentials is based on this (see B).

Nerve cell membranes contain ion channels for Na⁺, K⁺, Cl⁻, and Ca²⁺. These channels are usually closed and open only briefly to let ions pass through. They can be divided into channels that are regulated by membrane potentials (“voltage-gated”—e.g., fast Na⁺ channels; see p. 222) and those regulated by ligands (“ligand-gated”—e.g., nicotinic acetylcholine receptors; see p. 222).

B. Action potential

Action potentials are special signals that are used to transmit information in the nervous system. They are triggered by chemical stim-
A. Resting potential

B. Action potential

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Neurotransmitters

Neurotransmitters in the strict sense are substances that are produced by neurons, stored in the synapses, and released into the synaptic cleft in response to a stimulus. At the postsynaptic membrane, they bind to special receptors and affect their activity.

A. Important neurotransmitters

Neurotransmitters can be classified into several groups according to their chemical structure. The table lists the most important representatives of this family, which has more than 100 members.

Acetylcholine, the acetic acid ester of the cationic alcohol choline (see p. 50) acts at neuromuscular junctions, where it triggers muscle contraction (see p. 334), and in certain parts of the brain and in the autonomous nervous system.

Several proteinogenic amino acids (see p. 60) have neurotransmitter effects. A particularly important one is glutamate, which acts as a stimulatory transmitter in the CNS. More than half of the synapses in the brain are glutamnergic. The metabolism of glutamate and that of the amine GABA synthesized from it (see below) are discussed in more detail on p. 356. Glycine is an inhibitory neurotransmitter with effects in the spinal cord and in parts of the brain.

Biogenic amines arise from amino acids by decarboxylation (see p. 62). This group includes 4-aminobutyrate (γ-aminobutyric acid, GABA), which is formed from glutamate and is the most important inhibitory transmitter in the CNS. The catecholamines norepinephrine and epinephrine (see B), serotonin, which is derived from tryptophan, and histamine also belong to the biogenic amine group. All of them additionally act as hormones or mediators (see p. 380).

Peptides make up the largest group among the neurosecretions. Many peptide hormones—e.g., thyrotropin (TRH) and angiotensin II—simultaneously act as transmitters. Most neuropeptides are small (3–15 AA). At their N-terminus, many of them have a glutamate residue that has been cyclized to form pyroglutamate (5-oxoproline, <G), while the C-terminus is often an acid amide (–NH₂).

This provides better protection against breakdown by peptidases.

Endorphins, dynorphins, and enkephalins are a particularly interesting group of neuropeptides. They act as “endogenous opiates” by producing analgetic, sedative, and euphorant effects in extreme situations. Drugs such as morphine and heroin activate the receptors for these peptides (see p. 354).

Purine derivatives with neurotransmitter function are all derived from adenine-containing nucleotides or nucleosides. ATP is released along with acetylcholine and other transmitters, and among other functions it regulates the emission of transmitters from its synapse of origin. The stimulatory effect of caffeine is mainly based on the fact that it binds to adenosine receptors.

B. Biosynthesis of catecholamines

The catecholamines are biogenic amines that have a catechol group. Their biosynthesis in the adrenal cortex and CNS starts from tyrosine.

1) Hydroxylation of the aromatic ring initially produces dopa (3,4-dihydroxyphenylalanine). This reaction uses the usual coenzyme tetrahydrobiopterin (THB). Dopa (cf. p. 6) is also used in the treatment of Parkinson's disease.

2) Decarboxylation of dopa yields dopamine, an important transmitter in the CNS. In dopaminergic neurons, catecholamine synthesis stops at this point.

3) The adrenal gland and adrenergic neurons continue the synthesis by hydroxylating dopamine into norepinephrine (noradrenaline). Ascorbic acid (vitamin C; see p. 368) acts as a hydrogen-transferring coenzyme here.

4) Finally, N-methylation of norepinephrine yields epinephrine (adrenaline). The coenzyme for this reaction is S-adenosylmethionine (SAM; see p. 110).

The physiological effects of the catecholamines are mediated by a large number of different receptors that are of particular interest in pharmacology. Norepinephrine acts in the autonomic nervous system and certain areas of the brain. Epinephrine is also used as a transmitter by some neurons.
A. Important neurotransmitters

B. Biosynthesis of the catecholamines

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Receptors for neurotransmitters

Like all signaling substances, neurotransmitters (see p. 352) act via receptor proteins. The receptors for neurotransmitters are integrated into the membrane of the postsynaptic cell, where they trigger ion inflow or signal transduction processes (see p. 348).

A. Receptors for neurotransmitters

A considerable number of receptors for neurotransmitters are already known and new ones are continuing to be discovered. The table only lists the most important examples. They are classified into two large groups according to their mode of action.

- **Ionotropic receptors** are ligand-gated ion channels (left half of the table). The receptors for stimulatory transmitters (indicated in the table by a ♂) mediate the inflow of cations (mainly Na⁺). When these open after binding of the transmitter, local depolarization of the postsynaptic membrane occurs. By contrast, inhibitory neurotransmitters (GABA and glycine) allow Cl⁻ to flow in. This increases the membrane’s negative resting potential and hinders the action of stimulatory transmitters (hyperpolarization, ♀).

- **Metabotropic receptors** (right half of the table) are coupled to G proteins (see p. 386), through which they influence the synthesis of second messengers. Receptors that work with type G₁ proteins (see p. 386) increase the cAMP level in the postsynaptic cell ([cAMP]↑), while those that activate G₃ proteins reduce it ([cAMP]↓). Via type G₂ proteins, other receptors increase the intracellular Ca²⁺ concentration ([Ca²⁺]↑).

There are several receptor subtypes for most neurotransmitters. These are distinguished numerically (e.g., D₁ to D₅) or are named after their agonists—i.e., after molecules experimentally found to activate the receptor. For example, one specific subtype of glutamate receptors reacts to NMDA (N-methyl-D-aspartate), while another subtype reacts to the compound AMPA, etc.

The nicotinic ACh receptor responds to the alkaloid nicotine contained in tobacco (many of the physiological effects of nicotine are based on this). The nicotinic receptor is ionotropic. Its properties are discussed in greater detail on p. 222.

The muscarinic ACh receptors (of which there are at least five subtypes) are metabotropic. Their name is derived from the alkaloid muscarine, which is found in the fly agaric mushroom (Amanita muscaria), for example. Like ACh, muscarine is bound at the receptor, but in contrast to ACh (see ♂), it is not broken down and therefore causes permanent stimulation of muscle.

The muscarinic ACh receptors influence the cAMP level in the postsynaptic cells (M₁, M₃ and M₄ increase it, while subtypes M₂ and M₅ reduce it).

C. Metabolism of acetylcholine

Acetylcholine is synthesized from acetyl-CoA and choline in the cytoplasm of the presynaptic axon [1] and is stored in synaptic vesicles, each of which contains around 1000–10 000 ACh molecules. After it is released by exocytosis (see p. 228), the transmitter travels by diffusion to the receptors on the postsynaptic membrane. Catalyzed by acetylcholinesterase, hydrolysis of ACh to acetate and choline immediately starts in the synaptic cleft [2], and within a few milliseconds, the ACh released has been eliminated again. The cleavage products choline and acetate are taken up again by the presynaptic neuron and reused for acetylcholine synthesis [3].

Substances that block the serine residue in the active center of acetylcholinesterase [2]—e.g., the neurotoxin E605 and other organophosphates—prevent ACh degradation and thus cause prolonged stimulation of the postsynaptic cell. This impairs nerve conduction and muscle contraction. Curare, a paralyzing arrow-poison used by South American Indians, competitively inhibits binding of ACh to its receptor.

B. Acetylcholine receptors

Acetylcholine (ACH) was the neurotransmitter first discovered, at the beginning of the last century. It binds to two types of receptor.
### A. Receptors for neurotransmitters

<table>
<thead>
<tr>
<th>Receptor</th>
<th>Transmitter</th>
<th>Ion(s)</th>
<th>Effect</th>
<th>Receptor</th>
<th>Transmitter</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acetylcholine (nicotinic)</td>
<td>Acetylcholine</td>
<td>Na⁺</td>
<td>Open</td>
<td>Acetylcholine (muscarinic)</td>
<td>M1, M3, M5, M2, M4</td>
<td>[Ca²⁺][AMP] ↑</td>
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<tr>
<td>SHT3</td>
<td>Serotonin</td>
<td>Na⁺</td>
<td>Open</td>
<td>Serotonin</td>
<td>SHT₁, SHT₂, SHT₄</td>
<td>[Ca²⁺][AMP] ↑</td>
</tr>
<tr>
<td>GABAa</td>
<td>GABA</td>
<td>Cl⁻</td>
<td>Closed</td>
<td>α₁</td>
<td>Norepinephrine</td>
<td>[Ca²⁺][AMP] ↑</td>
</tr>
<tr>
<td>Glycine</td>
<td>Glycine</td>
<td>Cl⁻</td>
<td>Closed</td>
<td>β₁, β₂, β₃</td>
<td>Norepinephrine</td>
<td>[Ca²⁺][AMP] ↑</td>
</tr>
<tr>
<td>AMPA</td>
<td>Glutamate</td>
<td>Na⁺</td>
<td>Open</td>
<td>Glutamate</td>
<td>D₁, D₂, D₃, D₄</td>
<td>Dopamine</td>
</tr>
<tr>
<td>NMDA</td>
<td>Glutamate</td>
<td>Na⁺</td>
<td>Open</td>
<td>Glutamate</td>
<td>NMDA</td>
<td>Dopamine</td>
</tr>
<tr>
<td>Kainate</td>
<td>Glutamate</td>
<td>Na⁺</td>
<td>Open</td>
<td>Glutamate</td>
<td>K⁺</td>
<td>Opioids</td>
</tr>
</tbody>
</table>

### B. Acetylcholine receptors

1. Nicotinic receptor
2. Muscarinic receptors

### C. Metabolism of acetylcholine

- Acetylcholine
- Choline acetyltransferase
- Acetylcholinesterase
- Acetyl-CoA ligase

1. Re-uptake
2. Storage
3. Release
4. Neurotoxins
5. Curare

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Metabolism

The brain and other areas of the central nervous system (CNS) have high ATP requirements. Although the brain only represents about 2% of the body’s mass, it consumes around 20% of the metabolized oxygen and ca. 60% of the glucose. The neurons’ high energy requirements are mainly due to ATP-dependent ion pumps (particularly Na+/K+ ATPase) and other active transport processes that are needed for nerve conduction (see p. 350).

A. Energy metabolism of the brain

Glucose is normally the only metabolite from which the brain is able to obtain adequate amounts of ATP through aerobic glycolysis and subsequent terminal oxidation to CO$_2$ and H$_2$O. Lipids are unable to pass the blood–brain barrier, and amino acids are also only available in the brain in limited quantities (see B). As neurons only have minor glycogen reserves, they are dependent on a constant supply of glucose from the blood. A severe drop in the blood glucose level—as can occur after insulin overdosage in diabetics, for example—rapidly leads to a drop in the ATP level in the brain. This results in loss of consciousness and neurological deficits that can lead to death. Oxygen deficiency (hypoxia) also first affects the brain. The effects of a brief period of hypoxia are still reversible, but as time progresses irreversible damage increasingly occurs and finally complete loss of function (“brain death”).

During periods of starvation, the brain after a certain time acquires the ability to use ketone bodies (see p. 312) in addition to glucose to form ATP. In the first weeks of a starvation period, there is a strong increase in the activities of the enzymes required for this in the brain. The degradation of ketone bodies in the CNS saves glucose and thereby reduces the breakdown of muscle protein that maintains gluconeogenesis in the liver during starvation. After a few weeks, the extent of muscle breakdown therefore declines to one-third of the initial value.

B. Glutamate, glutamine, and GABA

The proteinogenic amino acid glutamate (Glu) and the biogenic amine 4-aminobutyrate derived from it are among the most important neurotransmitters in the brain (see p. 352). They are both synthesized in the brain itself. In addition to the neurons, which use Glu or GABA as transmitters, neuroglia are also involved in the metabolism of these substances.

Since glutamate and GABA as transmitters must not appear in the extracellular space in an unregulated way, the cells of the neuroglia (center) supply “glutaminergic” and “GABAergic” neurons with the precursor glutamine (Gln), which they produce from glutamate with the help of glutamine synthetase [1].

GABA neurons (left) and glutamate neurons (right) initially hydrolyze glutamine with the help of glutaminase [1] to form glutamate again. The glutamate neurons store this in vesicles and release it when stimulated. The GABA neurons continue the degradation process by using glutamate decarboxylase [3] to convert glutamate into the transmitter GABA.

Both types of neuron take up their transmitter again. Some of it also returns to the neuroglia, where glutamate is amidated back into glutamine.

Glutamate can also be produced again from GABA. The reaction sequence needed for this, known as the GABA shunt, is characteristic of the CNS. A transaminase [4] first converts GABA and 2-oxoglutarate into glutamate and succinate semialdehyde (\(-\text{OOC-CH}_2-\text{CH}_2-\text{CHO}\)). In an NAD$^+$-dependent reaction, the aldehyde is oxidized to succinic acid [5], from which 2-oxoglutarate can be regenerated again via tricarboxylic acid cycle reactions.

The function of glutamate as a stimulatory transmitter in the brain is the cause of what is known as the “Chinese restaurant syndrome.” In sensitive individuals, the monosodium glutamate used as a flavor enhancer in Chinese cooking can raise the glutamate level in the brain to such an extent that transient mild neurological disturbances can occur (dizziness, etc.).
A. Energy metabolism of the brain

B. Glutamate, glutamine, and GABA

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Sight

Two types of photoreceptor cell are found in the human retina—rods and cones. Rods are sensitive to low levels of light, while the cones are responsible for color vision at higher light intensities.

Signaling substances and many proteins are involved in visual processes. Initially, a light-induced cis-trans isomerization of the pigment retinal triggers a conformational change in the membrane protein rhodopsin. Via the G protein transducin, which is associated with rhodopsin, an enzyme is activated that breaks down the second messenger cGMP. Finally, the cGMP deficiency leads to hyperpolarization of the light-sensitive cell, which is registered by subsequent neurons as reduced neurotransmitter release.

A. Photoreceptor

The cell illustrated opposite, a rod, has a structure divided by membrane discs into which the 7-helix receptor rhodopsin is integrated (see p. 224). In contrast to other receptors in the 7-helix class (see p. 384), rhodopsin is a light-sensitive chromoprotein. Its protein part, opsin, contains the aldehyde retinal (see p. 364)—an isorenoid which is bound to the ε-amino group of a lysine residue as an aldime.

The light absorption of rhodopsin is in the visible range, with a maximum at about 500 nm. The absorption properties of the visual pigment are thus optimally adjusted to the spectral distribution of sunlight.

Absorption of a photon triggers isomerization from the 11-cis form of retinal to all-trans-retinal (top right). Within milliseconds, this photochemical process leads to an alloteric conformational change in rhodopsin. The active conformation (rhodopsin*) binds and activates the G protein transducin. The signal cascade (B) that now follows causes the rod cells to release less neurotransmitter (glutamate) at their synapses. The adjoining bipolar neurons register this change and transmit it to the brain as a signal for light.

There are several different rhodopsins in the cones. All of them contain retinal molecules as light-sensitive components, the absorption properties of which are modulated by the different proportions of opsin they contain in such a way that colors can also be perceived.

B. Signal cascade

Dark (bottom left). Rod cells that are not exposed to light contain relatively high concentrations (70 μM) of the cyclic nucleotide cGMP (3’-5’-cycloGMP; cf. cAMP, p. 386), which is synthesized by a guanylate cyclase ([2], see p. 388). The cGMP binds to an ion channel in the rod membrane (bottom left) and thus keeps it open. The inflow of cations (Na⁺, Ca²⁺) depolarizes the membrane and leads to release of the neurotransmitter glutamate at the synapse (see p. 356).

Light (bottom right). When the G protein transducin binds to light-activated rhodopsin* (see A, on the structure of the complex; see p. 224), it leads to the GTP that is bound to the transducin being exchanged for GTP. In transducin* that has been activated in this way, the GTP-containing α-subunit breaks off from the rest of the molecule and in turn activates a membrane cGMP phosphodiesterase [1]. This hydrolyzes cGMP to GMP and thus reduces the level of free cGMP within milliseconds. As a consequence, the cGMP bound at the ion channel dissociates off and the channel closes. As cations are constantly being pumped out of the cell, the membrane potential falls and hyperpolarization of the cell occurs, which interrupts glutamate release.

Regeneration. After exposure to light, several processes restore the initial conditions:

1. The α-subunit of transducin* inactivates itself by GTP hydrolysis and thus terminates the activation of cGMP esterase.
2. The reduced Ca²⁺ concentration causes activation of guanylate cyclase, which increases the cGMP level until the cation channels reopen.
3. An isomerase [3] transfers all-trans-retinal to the 11-cis form, in which it is available for the next cycle. A dehydrogenase [4] can also allow retinal to be supplied from vitamin A (retinol).
A. Photoreceptor

Light (hν) → Membrane discs → Rhodopsin → Interlamellar space → Decreased release of neurotransmitter

B. Signal cascade

Light → Rhodopsin → Retinal → 11-cis-Retinal

1. cGMP esterase 3.7.4.35
2. Guanylate cyclase 4.6.1.2
3. Retinal isomerase 5.2.7.3
4. Retinal dehydrogenase 1.1.1.105

GTP → cGMP → cGMP esterase → GMP

Closes due to lack of cGMP

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Organic substances

A balanced human diet needs to contain a large number of different components. These include proteins, carbohydrates, fats, minerals (including water), and vitamins. These substances can occur in widely varying amounts and proportions, depending on the type of diet. As several components of the diet are essential for life, they have to be regularly ingested with food. Recommended daily minimums for nutrients have been published by the World Health Organization (WHO) and a number of national expert committees.

A. Energy requirement

The amount of energy required by a human is expressed in kJ d\(^{-1}\) (kilojoule per day). An older unit is the kilocalorie (kcal; 1 kcal = 4.187 kJ). The figures given are recommended values for adults with a normal body weight. However, actual requirements are based on age, sex, body weight, and in particular on physical activity. In those involved in competitive sports, for example, requirements can increase from 12 000 to 17 000 kJ d\(^{-1}\).

It is recommended that about half of the energy intake should be in the form of carbohydrates, a third at most in the form of fat, and therest as protein. The fact that alcoholic beverages can make a major contribution to daily energy intake is often overlooked. Ethanol has a caloric value of about 30 kJ g\(^{-1}\) (see p. 320).

B. Nutrients

Proteins provide the body with amino acids, which are used for endogenous protein biosynthesis. Excess amino acids are broken down to provide energy (see p. 174). Most amino acids are glucogenic—i.e., they can be converted into glucose (see p. 180).

Proteins are essential components of the diet, as they provide essential amino acids that the human body is not capable of producing on its own (see the table). Some amino acids, including cysteine and histidine, are not absolutely essential, but promote growth in children. Some amino acids are able to substitute for each other in the diet. For example, humans can form tyrosine, which is actually essential, by hydroxylation from phenylalanine, and cysteine from methionine.

The minimum daily requirement of protein is 37 g for men and 29 g for women, but the recommended amounts are about twice these values. Requirements in pregnant and breast-feeding women are even higher. Not only the quantity, but also the quality of protein is important. Proteins that lack several essential amino acids or only contain small quantities of them are considered to be of low value, and larger quantities of them are therefore needed. For example, pulses only contain small amounts of methionine, while wheat and corn proteins are poor in lysine. In contrast to vegetable proteins, most animal proteins are high-value (with exceptions such as collagen and gelatin).

Carbohydrates serve as a general and easily available energy source. In the diet, they are present as monosaccharides in honey and fruit, or as disaccharides in milk and in all foods sweetened with sugar (sucrose). Metabolically usable polysaccharides are found in vegetable products (starch) and animal products (glycogen). Carbohydrates represent a substantial proportion of the body’s energy supply, but they are not essential.

Fats are primarily important energy suppliers in the diet. Per gram, they provide more than twice as much energy as proteins and carbohydrates. Fats are essential as suppliers of fat-soluble vitamins (see p. 364) and as sources of polyunsaturated fatty acids, which are needed to biosynthesize eicosanoids (see pp. 48, 390).

Mineral substances and trace elements, a very heterogeneous group of essential nutrients, are discussed in more detail on p. 362. They are usually divided into macro- and microminerals. Vitamins are also indispensable components of the diet. The animal body requires them in very small quantities in order to synthesize coenzymes and signaling substances (see pp. 364–369).
### A. Energy requirement

| Daily requirement (average) | 9,200 kJ (2,200 kcal) | 12,600 kJ (3,000 kcal) |

### B. Nutrients

<table>
<thead>
<tr>
<th>Quantity in body (kg)</th>
<th>Energy content (kJ/g)</th>
<th>Daily requirement (g)</th>
<th>General function in metabolism</th>
<th>Essential constituents</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Proteins</strong></td>
<td>10</td>
<td>17 (41)</td>
<td>37 55 92</td>
<td>Supplier of amino acids (Cys, Met)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Energy source</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Daily requirement in mg per kg body weight</td>
</tr>
<tr>
<td><strong>Carbohydrates</strong></td>
<td>1</td>
<td>17 (41)</td>
<td>0 390 240-310</td>
<td>General source of energy (glucose) (energy reserve (glycogen), roughage (cellulose))</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Supporting substances (bones, cartilage, mucus)</td>
</tr>
<tr>
<td><strong>Fats</strong></td>
<td>10-15</td>
<td>39 (93)</td>
<td>10 80 130</td>
<td>General energy source (most important energy reserve, solvent of vitamins) (solvent of essential fatty acids)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Baker of vitamins (essential fatty acids)</td>
</tr>
<tr>
<td><strong>Water</strong></td>
<td>35-40</td>
<td>0</td>
<td>2,400 –</td>
<td>Solvent (cellular building block, electrolytes) (dielectric reaction partner, temperature regulator)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Macrominerals (microminerals)</td>
</tr>
<tr>
<td><strong>Minerals</strong></td>
<td>3</td>
<td>0</td>
<td></td>
<td>Building blocks (electrolytes, cofactors of enzymes)</td>
</tr>
<tr>
<td><strong>Vitamins</strong></td>
<td>–</td>
<td>–</td>
<td></td>
<td>Often precursors of coenzymes (lipid-soluble vitamins)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Water-soluble vitamins</td>
</tr>
</tbody>
</table>

**a:** Minimum daily requirement  
**b:** Recommended daily intake  
**c:** Actual daily intake in industrialized nations
Minerals and trace elements

A. Minerals

Water is the most important essential inorganic nutrient in the diet. In adults, the body has a daily requirement of 2–3 L of water, which is supplied from drinks, water contained in solid foods, and from the oxidation water produced in the respiratory chain (see p. 140). The special role of water for living processes is discussed in more detail elsewhere (see p. 26).

The elements essential for life can be divided into macroelements (daily requirement > 100 mg) and microelements (daily requirement < 100 mg). The macroelements include the electrolytes sodium (Na), potassium (K), calcium (Ca), and magnesium (Mg), and the nonmetals chlorine (Cl), phosphorus (P), sulfur (S), and iodine (I).

The essential microelements are only required in trace amounts (see also p. 2). This group includes iron (Fe), zinc (Zn), manganese (Mn), copper (Cu), cobalt (Co), chromium (Cr), selenium (Se), and molybdenum (Mo). Fluorine (F) is not essential for life, but does promote healthy bones and teeth. It is still a matter of controversy whether vanadium, nickel, tin, boron, and silicon also belong to the essential trace elements.

The second column in the table lists the average amounts of mineral substances in the body of an adult weighing 65 kg. The daily requirements listed in the fourth column also apply to an adult, and are average values. Children, pregnant and breast-feeding women, and those who are ill generally have higher mineral requirements relative to body weight than men.

As the human body is able to store many minerals, deviations from the daily ration are balanced out over a given period of time. Minerals stored in the body include water, which is distributed throughout the whole body; calcium, stored in the form of apatite in the bones (see p. 340); iodine, stored as thyroglobulin in the thyroid; and iron, stored in the form of ferritin and hemosiderin in the bone marrow, spleen, and liver (see p. 286). The storage site for many trace elements is the liver. In many cases, the metabolism of minerals is regulated by hormones—for example, the uptake and excretion of H2O, Na+, Ca2+, and phosphate (see p. 328), and storage of Fe2+ and I.

Resorption of the required mineral substances from food usually depends on the body's requirements, and in several cases also on the composition of the diet. One example of dietary influence is calcium (see p. 342). Its resorption as Ca2+ is promoted by lactate and citrate, but phosphate, oxalic acid, and phytol inhibit calcium uptake from food due to complex formation and the production of insoluble salts.

Mineral deficiencies are not uncommon and can have quite a variety of causes—e.g., an unbalanced diet, resorption disturbances, and diseases. Calcium deficiency can lead to rickets, osteoporosis, and other disturbances. Chloride deficiency is observed as a result of severe Cl− losses due to vomiting. Due to the low content of iodine in food in many regions of central Europe, iodine deficiency is widespread there and can lead to goiter. Magnesium deficiency can be caused by digestive disorders or an unbalanced diet—e.g., in alcoholism. Trace element deficiencies often result in a disturbed blood picture—i.e., forms of anemia.

The last column in the table lists some of the functions of minerals. It should be noted that almost all of the macroelements in the body function either as nutrients or electrolytes. Iodine (as a result of its incorporation into iodothyronines) and calcium act as signaling substances. Most trace elements are cofactors for proteins, especially for enzymes. Particularly important in quantitative terms are the iron proteins hemoglobin, myoglobin, and the cytochromes (see p. 286), as well as more than 300 different zinc proteins.

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<table>
<thead>
<tr>
<th>Mineral</th>
<th>Content (g)</th>
<th>Major source</th>
<th>Daily requirement (g)</th>
<th>Functions/Occurrence*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Water</td>
<td>35 000-40 000</td>
<td>Drinks, Water in solid foods, From metabolism 300g</td>
<td>1.200  900</td>
<td>Solvent, cellular building block, dielectric, coolant, medium for transport, reaction partner</td>
</tr>
<tr>
<td><strong>Macroelements (daily requirement &gt;100 mg)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Na</td>
<td>100</td>
<td>Table salt</td>
<td>1.1-3.3</td>
<td>Osmoregulation, membrane potential, mineral metabolism</td>
</tr>
<tr>
<td>K</td>
<td>150</td>
<td>Vegetables, fruit, cereals</td>
<td>1.9-5.6</td>
<td>Membrane potential, mineral metabolism</td>
</tr>
<tr>
<td>Ca</td>
<td>1300</td>
<td>Milk, milk products</td>
<td>0.8</td>
<td>Bone formation, blood clotting, signal molecule</td>
</tr>
<tr>
<td>Mg</td>
<td>20</td>
<td>Green vegetables</td>
<td>0.35</td>
<td>Bone formation, cofactor for enzymes</td>
</tr>
<tr>
<td>Cl</td>
<td>100</td>
<td>Table salt</td>
<td>1.7-5.1</td>
<td>Mineral metabolism</td>
</tr>
<tr>
<td>P</td>
<td>650</td>
<td>Meat, milk, cereals, vegetables</td>
<td>0.8</td>
<td>Bone formation, energy metabolism, nucleic acid metabolism</td>
</tr>
<tr>
<td>S</td>
<td>200</td>
<td>S-containing amino acids (Cys and Met)</td>
<td>0.2</td>
<td>Lipid and carbohydrate metabolism, conjugate formation</td>
</tr>
<tr>
<td><strong>Microelements (trace elements)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fe</td>
<td>4-5</td>
<td>Meat, liver, eggs, vegetables, potatoes, cereals</td>
<td>10</td>
<td>Hemoglobin, myoglobin, cytochromes, Fe/S clusters</td>
</tr>
<tr>
<td>Zn</td>
<td>2-3</td>
<td>Meat, liver, cereals</td>
<td>15</td>
<td>Zinc enzymes</td>
</tr>
<tr>
<td>Mn</td>
<td>0.02</td>
<td>Found in many foodstuffs</td>
<td>2-5</td>
<td>Enzymes</td>
</tr>
<tr>
<td>Cu</td>
<td>0.1-0.2</td>
<td>Meat, vegetables, fruit, fish</td>
<td>2-3</td>
<td>Oxidases</td>
</tr>
<tr>
<td>Co</td>
<td>&lt;0.01</td>
<td>Meat</td>
<td>Traces</td>
<td>Vitamin B&lt;sub&gt;12&lt;/sub&gt;</td>
</tr>
<tr>
<td>Cr</td>
<td>&lt;0.01</td>
<td></td>
<td>0.05-0.2</td>
<td>Not clear</td>
</tr>
<tr>
<td>Mo</td>
<td>0.02</td>
<td>Cereals, nuts, legumes</td>
<td>0.15-0.5</td>
<td>Redox enzymes</td>
</tr>
<tr>
<td>Se</td>
<td></td>
<td>Vegetables, meat</td>
<td>0.05-0.2</td>
<td>Selenium enzymes</td>
</tr>
<tr>
<td>I</td>
<td>0.03</td>
<td>Seafood, iodized salt, drinking water</td>
<td>0.15</td>
<td>Thyroxin</td>
</tr>
</tbody>
</table>

**Requirement not known**

| F | Drinking water (fluoridated), tea, milk | 0.0015-0.004 | Bones, dental enamel |

* Content in the body of a 65 kg adult
Lipid-soluble vitamins

Vitamins are essential organic compounds that the animal organism is not capable of forming itself, although it requires them in small amounts for metabolism. Most vitamins are precursors of coenzymes; in some cases, they are also precursors of hormones or act as antioxidants. Vitamin requirements vary from species to species and are influenced by age, sex, and physiological conditions such as pregnancy, breast-feeding, physical exercise, and nutrition.

A. Vitamin supply

A healthy diet usually covers average daily vitamin requirements. By contrast, malnutrition, malnourishment (e.g., an unbalanced diet in older people, malnourishment in alcoholics, ready meals), or resorption disturbances lead to an inadequate supply of vitamins from which hypovitaminosis, or in extreme cases avitaminosis, can result. Medical treatments that kill the intestinal flora—e.g., antibiotics—can also lead to vitamin deficiencies (K, B₁₂, H) due to the absence of bacterial vitamin synthesis.

Since only a few vitamins can be stored (A, D, E, B₁₂), a lack of vitamins quickly leads to deficiency diseases. These often affect the skin, blood cells, and nervous system. The causes of vitamin deficiencies can be treated by improving nutrition and by administering vitamins in tablet form. An overdose of vitamins only leads to hypervitaminoses, with toxic symptoms, in the case of vitamins A and D. Normally, excess vitamins are rapidly excreted with the urine.

B. Lipid-soluble vitamins

Vitamins are classified as either lipid-soluble or water-soluble. The lipid-soluble vitamins include vitamins A, D, E, and K, all of which belong to the isoprenoids (see p. 52).

Vitamin A (retinol) is the parent substance of the retinoids, which include retinal and retinoic acid. The retinoids also can be synthesized by cleavage from the provitamin β-carotene. Retinoids are found in meat-containing diets, whereas β-carotene occurs in fruits and vegetables (particularly carrots). Retinal is involved in visual processes as the pigment of the chromoprotein rhodopsin (see p. 358). Retinoic acid, like the steroid hormones, influences the transcription of genes in the cell nucleus. It acts as a differentiation factor in growth and development processes. Vitamin A deficiency can result in night blindness, visual impairment, and growth disturbances.

Vitamin D (calcitriol, cholecalciferol) is the precursor of the hormone calcitriol (1α₂5-di-hydroxycholecalciferol; see p. 320). Together with two other hormones (parathyroid and calcitonin), calcitriol regulates the calcium metabolism (see p. 342). Calcitriol can be synthesized in the skin from 7-dehydrocholesterol, an endogenous steroid, by a photochemical reaction. Vitamin D deficiencies only occur when the skin receives insufficient exposure to ultraviolet light and vitamin D is lacking in the diet. Deficiency is observed in the form of rickets in children and osteomalacia in adults. In both cases, bone mineralization is disturbed.

Vitamin E (tocopherol) and related compounds only occur in plants (e.g., wheat germ). They contain what is known as a chroman ring. In the lipid phase, vitamin E is mainly located in biological membranes, where as an antioxidant it protects unsaturated lipids against ROS (see p. 284) and other radicals.

Vitamin K (phyloquinone) and similar substances with modified side chains are involved in carboxylating glutamate residues of coagulation factors in the liver (see p. 290). The form that acts as a cofactor for carboxylase is derived from the vitamin by enzymatic reduction. Vitamin K antagonists (e.g., coumarin derivatives) inhibit this reduction and consequently carboxylation as well. This fact is used to inhibit blood coagulation in prophylactic treatment against thrombosis. Vitamin K deficiency occurs only rarely, as the vitamin is formed by bacteria of the intestinal flora.
A. Vitamin supply

B. Lipid-soluble vitamins

* Adult daily requirement

Provitamin

Vegetables

Fruit

1

Milk

Liver

Egg yolk

uv

0.01

Cod liver oil

Milk

Egg yolk

β-Carotene

Retinol

1

Retinoic acid

Calcitriol

Tocopherols

Phylloquinones

Healthy nutrition

Vitamin requirement satisfied

Poor nutrition

Malnutrition

Antibiotics

Disturbed resorption

Diseases

Hypovitaminosis

Vitamin intake

Vitamin poisoning

Vitamin A and D

Overdose

Excess vitamins

Urine

Vitamin intake

Provitamin

Vegetables

Fruit

1

Milk

Liver

Egg yolk

β-Carotene

Retinol

1

Retinoic acid

Calcitriol

Tocopherols

Phylloquinones

Reducing agent

Blood clotting (carboxylation of plasma proteins)

Important for

Sight

Sugars transport

Development

Differentiation

Calcium metabolism

Antioxidant


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Water-soluble vitamins I

The B group of vitamins covers water-soluble vitamins, all of which serve as precursors for coenzymes. Their numbering sequence is not continuous, as many substances that were originally regarded as vitamins were not later confirmed as having vitamin characteristics.

A. Water-soluble vitamins I 

**Vitamin B1** (thiamine) contains two heterocyclic rings—a pyrimidine ring (a six-membered aromatic ring with two Ns) and a thiazole ring (a five-membered aromatic ring with N and S), which are joined by a methylene group. The active form of vitamin B1 is thiamine diphosphate (TDP), which contributes as a coenzyme to the transfer of hydroxylaldehyde residues (active aldehyde groups). The most important reactions of this type are oxidative deamination of 2-oxoacids (see p. 134) and the transketolase reaction in the pentose phosphate pathway (see p. 152). Thiamine was the first vitamin to be discovered, around 100 years ago. Vitamin B1 deficiency leads to beriberi, a disease with symptoms that include neurological disturbances, cardiac insufficiency, and muscular atrophy.

**Vitamin B2** is a complex of several vitamins: riboflavin, folate, nicotinate, and pantothenic acid.

Riboflavin (from the Latin flavius, yellow) serves in the metabolism as a component of the redox coenzymes flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD; see p. 104). As prosthetic groups, FMN and FAD are cofactors for various oxidoreductases (see p. 32). No specific disease due to a deficiency of this vitamin is known.

Folate, the anion of folic acid, is made up of three different components—a pteridine derivative, 4-aminobenzoate, and one or more glutamate residues. After reduction to tetrahydrofolate (THF), folate serves as a coenzyme in the C1 metabolism (see p. 418). Folate deficiency is relatively common, and leads to disturbances in nucleotide biosynthesis and thus cell proliferation. As the precursors for blood cells divide particularly rapidly, disturbances of the blood picture can occur, with increased amounts of abnormal precursors for megalocytes (megaloblastic anemia). Later, general damage ensues as phospholipid synthesis and the amino acid metabolism are affected.

In contrast to animals, microorganisms are able to synthesize folate from their own components. The growth of microorganisms can therefore be inhibited by sulfonamides, which competitively inhibit the incorporation of 4-aminobenzoate into folate (see p. 254). Since folate is not synthesized in the animal organism, sulfonamides have no effect on animal metabolism.

Nicotinate and nicotinamide, together referred to as “niacin,” are required for biosynthesis of the coenzymes nicotinamide adenine dinucleotide (NAD+) and nicotinamide adenine dinucleotide phosphate (NADP+). These both serve in energy and nutrient metabolism as carriers of hydride ions (see pp. 32, 104). The animal organism is able to convert tryptophan into nicotinate, but only with a poor yield. Vitamin deficiency therefore only occurs when nicotinate, nicotinamide, and tryptophan are all simultaneously lacking in the diet. It manifests in the form of skin damage (pellagra), digestive disturbances, and depression.

Pantothenic acid is an acid amide consisting of β-alanine and 2,4-dihydroxy-3,3'-dimethylbutyrate (pantoic acid). It is a precursor of coenzyme A, which is required for activation of acyl residues in the lipid metabolism (see pp. 12, 106). Acyl carrier protein (ACP; see p. 168) also contains pantothenic acid as part of its prosthetic group. Due to the widespread availability of pantothenic acid in food (Greek pantothén = “from everywhere”), deficiency diseases are rare.

Further information

The requirement for vitamins in humans and other animals is the result of mutations in the enzymes involved in biosynthetic coenzymes. As intermediates of coenzyme biosynthesis, vitamin anions are available in sufficient amounts in the diet of heterotrophic animals (see p. 112). The lack of endogenous synthesis cannot have unfavorable effects for them. Microorganisms and plants whose nutrition is mainly autotrophic have to produce all of these compounds themselves in order to survive.
## A. Water-soluble vitamins I

<table>
<thead>
<tr>
<th>Vitamin</th>
<th>Active form: coenzyme</th>
<th>Function in metabolism</th>
</tr>
</thead>
<tbody>
<tr>
<td>Thiamine</td>
<td>Thiamine diphosphate</td>
<td>Transfer of hydroxy-alkyl residues</td>
</tr>
<tr>
<td>B1</td>
<td>CoA</td>
<td></td>
</tr>
<tr>
<td>B2</td>
<td>Riboflavin</td>
<td>Hydrogen transfer</td>
</tr>
<tr>
<td></td>
<td>FAD</td>
<td></td>
</tr>
<tr>
<td>Folate</td>
<td>Tetrahydrofolate</td>
<td>C1- metabolism</td>
</tr>
<tr>
<td></td>
<td>4-Aminobenzoate residue</td>
<td></td>
</tr>
<tr>
<td>Nicotinate</td>
<td>Nicotinamide</td>
<td>Hydride transfer</td>
</tr>
<tr>
<td></td>
<td>20 mg*</td>
<td></td>
</tr>
<tr>
<td></td>
<td>(or 1.2 g tryptophan)</td>
<td></td>
</tr>
<tr>
<td>Pantothenate</td>
<td>CoA</td>
<td>Activation of carboxylic acids</td>
</tr>
<tr>
<td></td>
<td>7 mg*</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Widely distributed</td>
<td></td>
</tr>
</tbody>
</table>

* Adult daily requirement

---

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Water-soluble vitamins II

A. Water-soluble vitamins II

Vitamin B₆ consists of three substituted pyridines—pyridoxal, pyridoxamine, and pyridoxamine. The illustration shows the structure of pyridoxal, which carries an aldehyde group (−CHO) at C-4. Pyridoxol is the corresponding alcohol (−CH₂OH), and pyridoxamine the amine (−CH₄NH₂).

The active form of vitamin B₆, pyridoxal phosphate, is the most important coenzyme in the amino acid metabolism (see p. 106). Almost all conversion reactions involving amino acids require pyridoxal phosphate, including transaminations, decarboxylations, dehydrogenations, etc. Glycogen phosphorylase, the enzyme for glycogen degradation, also contains pyridoxal phosphate as a cofactor. Vitamin B₆ deficiency is rare.

Vitamin B₁₂ (cobalamin) is one of the most complex low-molecular-weight substances occurring in nature. The core of the molecule consists of a tetrapyrryl system (corrin), with cobalt as the central atom (see p. 108). The vitamin is exclusively synthesized by microorganisms. It is abundant in liver, meat, eggs, and milk, but not in plant products. As the intestinal flora synthesizes vitamin B₁₂ strict vegetarians usually also have an adequate supply of the vitamin.

Cobalamin can only be resorbed in the small intestine when the gastric mucosa secretes what is known as intrinsic factor—a glycoprotein that binds cobalamin (the extrinsic factor) and thereby protects it from degradation. In the blood, the vitamin is bound to a special protein known as transcobalamin. The liver is able to store vitamin B₁₂ in amounts sufficient to last for several months. Vitamin B₁₂ deficiency is usually due to an absence of intrinsic factor and the resulting resorption disturbance. This leads to a disturbance in blood formation known as pernicious anemia.

In animal metabolism, derivatives of cobalamin are mainly involved in rearrangement reactions. For example, they act as coenzymes in the conversion of methylmalonyl-CoA to succinyl-CoA (see p. 166), and in the formation of methionine from homocysteine (see p. 418). In prokaryotes, cobalamin derivatives also play a part in the reduction of ribonucleotides.

Vitamin C is L-ascorbic acid (chemically: 2-oxogulonolactone). The two hydroxyl groups have acidic properties. By releasing a proton, ascorbic acid therefore turns into its anion, ascorbate. Humans, apes, and guinea pigs require vitamin C because they lack the enzyme L-gulonolactone oxidase (∇/3.3.1), which catalyzes the final step in the conversion of glucose into ascorbate.

Vitamin C is particularly abundant in fresh fruit and vegetables. Many soft drinks and foodstuffs also have synthetic ascorbic acid added to them as an antioxidant and flavor enhancer. Boiling slowly destroys vitamin C. In the body, ascorbic acid serves as a reducing agent in variations reactions (usually hydroxylations). Among the processes involved are collagen synthesis, tyrosine degradation, catecholamine synthesis, and bile acid biosynthesis. The daily requirement for ascorbic acid is about 60 mg, a comparatively large amount for a vitamin. Even higher doses of the vitamin have a protective effect against infections. However, the biochemical basis for this effect has not yet been explained. Vitamin C deficiency only occurs rarely nowadays; it becomes evident after a few months in the form of scaly, with connective-tissue damage, bleeding, and tooth loss.

Vitamin H (biotin) is present in liver, egg yolk, and other foods; it is also synthesized by the intestinal flora. In the body, biotin is covalently attached via a lysine side chain to enzymes that catalyze carboxylation reactions. Biotin-dependent carboxylases include pyruvate carboxylase (see p. 154) and acetyl-CoA carboxylase (see p. 162). CO₂ binds, using up ATP, to one of the two N atoms of biotin, from which it is transferred to the acceptor (see p. 108).

Biotin binds with high affinity (Kₐ = 10⁻¹⁵ M) and specificity to avidin, a protein found in egg white. Since boiling denatures avidin, biotin deficiency only occurs when egg whites are eaten raw.
# A. Water-soluble vitamins II

<table>
<thead>
<tr>
<th>Vitamin</th>
<th>Active form: coenzyme</th>
<th>Function in metabolism</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>B6</strong></td>
<td>Pyridoxal Pyridoxol Pyridoxamine PLP</td>
<td>Activation of amino acids</td>
</tr>
<tr>
<td></td>
<td>2 mg*</td>
<td>Meat, Vegetables, Grain products</td>
</tr>
<tr>
<td><strong>B12</strong></td>
<td>Cobalamin 5-Deoxy-adenosyl cobalamin</td>
<td>Isomerization e.g.</td>
</tr>
<tr>
<td></td>
<td>0.002 mg*</td>
<td>Meat, Liver, Milk, Eggs</td>
</tr>
<tr>
<td><strong>C</strong></td>
<td>Ascorbic acid Ascorbate</td>
<td>Stabilization of enzyme systems, coenzyme, antioxidant</td>
</tr>
<tr>
<td></td>
<td>60 mg*</td>
<td>Fruit, Vegetables</td>
</tr>
<tr>
<td><strong>H</strong></td>
<td>Biotin</td>
<td>Transfer of carboxyl groups</td>
</tr>
<tr>
<td></td>
<td>0.1 mg*</td>
<td>Yeast products, Legumes, Nuts</td>
</tr>
</tbody>
</table>
Basics

Hormones are chemical signaling substances. They are synthesized in specialized cells that are often associated to form endocrine glands. Hormones are released into the blood and transported with the blood to their effector organs. In the organs, the hormones carry out physiological and biochemical regulatory functions. In contrast to endocrine hormones, tissue hormones are only active in the immediate vicinity of the cells that secrete them.

The distinctions between hormones and other signaling substances (mediators, neurotransmitters, and growth factors) are fluid. Mediators is the term used for signaling substances that do not derive from special hormone-forming cells, but are formed by many cell types. They have hormone-like effects in their immediate surroundings. Histamine (see p. 352) and prostaglandins (see p. 390) are important examples of these substances. Neurohormones and neurotransmitters are signaling substances that are produced and released by nerve cells (see p. 348). Growth factors and cytokines mainly promote cell proliferation and cell differentiation (see p. 392).

A. Hormones: overview

The animal organism contains more than 100 hormones and hormone-like substances, which can be classified either according to their structure or according to their function. In chemical terms, most hormones are amino acid derivatives, peptides or proteins, or steroids. Hormones regulate the following processes:

- Growth and differentiation of cells, tissues, and organs
  These processes include cell proliferation, embryonic development, and sexual differentiation—i.e., processes that require a prolonged time period and involve proteins de novo synthesis. For this reason, mainly steroid hormones which function via transcription regulation are active in this field (see p. 244).

- Metabolic pathways
  Metabolic regulation requires rapidly acting mechanisms. Many of the hormones involved therefore regulate interconversion of enzymes (see p. 120). The main processes subject to hormonal regulation are the uptake and degradation of storage substances (glycogen, fat), metabolic pathways for biosynthesis and degradation of central metabolites (glucose, fatty acids, etc.), and the supply of metabolic energy.

- Digestive processes
  Digestive processes are usually regulated by locally acting peptides (paracrine; see p. 372), but mediators, biogenic amines, and neuropeptides are also involved (see p. 270).

- Maintenance of ion concentrations (homeostasis)
  Concentrations of Na+, K+, and Cl− in body fluids, and the physiological variables dependent on these (e.g. blood pressure), are subject to strict regulation. The principal site of action of the hormones involved is the kidneys, where hormones increase or reduce the resorption of ions and recovery of water (see pp. 326–331). The concentrations of Ca²⁺ and phosphate, which form the mineral substance of bone and teeth, are also precisely regulated. Many hormones influence the above processes only indirectly by regulating the synthesis and release of other hormones (hormonal hierarchy; see p. 372).

B. Hormonal regulation system

Each hormone is the center of a hormonal regulation system. Specialized glandular cells synthesize the hormone from precursors, store it in many cases, and release it into the bloodstream when needed (biosynthesis). For transport, the poorly water-soluble lipophilic hormones are bound to plasma proteins known as hormone carriers. To stop the effects of the hormone again, it is inactivated by enzymatic reactions, most of which take place in the liver (metabolism). Finally, the hormone and its metabolites are expelled via the excretory system, usually in the kidney (excretion). All of these processes affect the concentration of the hormone and thus contribute to regulation of the hormonal signal.

In the effector organs, target cells receive the hormone’s message. These cells have hormone receptors for the purpose, which bind the hormone. Binding of a hormone passes information to the cell and triggers a response (effect).
A. Hormones: overview

- Peptide Protein
- Steroid
- Amino acid derivative

Sexual hormones
Retinoic acid

Hormones

Proliferation Growth Development

Cytokines
Growth factors
Somatotropin

Parathyroid hormone
Calcitonin
ANF
Aldosterone
Calcitriol

Insulin
Glucagon
Cor
Tisol
Thyroxin
Epinephrine

Water, electrolytes, etc.

Hormonal system

A. Hormonal regulation system

Gland cell
Circulatory system
Target cell

Biosynthesis
Transport
Response
Excretion

Digestion
Gastrin
Secretin
CCK
eetc.

Metabolism
Insulin
Glucagon
Cortisol
Thyroxin
Epinephrine

Hormones: overview

- Hormone precursor
- Hormone metabolite
- Hormone carrier

M Hormone
P Hormone precursor
H Hormone

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Plasma levels and hormone hierarchy

A. Endocrine, paracrine, and autocrine hormone effects

Hormones transfer signals by migrating from their site of synthesis to their site of action. They are usually transported in the blood. In this case, they are said to have an endocrine effect (1; example: insulin). By contrast, tissue hormones, the target cells for which are in the immediate vicinity of the glandular cells that produce them, are said to have a paracrine effect (2; example: gastrointestinal tract hormones). When signal substances also pass effects back to the cells that synthesize them, they are said to have an autocrine effect (3; example: prostaglandins). Autocrine effects are often found in tumor cells (see p. 406), which stimulate their own proliferation in this way.

Insulin, which is formed in the B cells of the pancreas, has both endocrine and paracrine effects. As a hormone with endocrine effects, it regulates glucose and fat metabolism. Via a paracrine mechanism, it inhibits the synthesis and release of glucagon from the neighboring A cells.

B. Dynamics of the plasma level

Hormones circulate as signaling substances in the blood at very low concentrations ($10^{-12}$ to $10^{-7}$ mol L$^{-1}$). These values change periodically in rhythms that depend on the time of day, month, or year, or on physiological cycles. The first example shows the circadian rhythm level. As an activator of gluconeogenesis (see p. 158), cortisol is mainly released in the early morning, when the liver’s glycogen stores are declining. During the day, the plasma cortisol level declines. Many hormones are released into the blood in a spasmodic and irregular manner. In this case, their concentrations change in an episodic or pulsatile fashion. This applies, for instance, to luteinizing hormone (LH, lutein). Concentrations of other hormones are event-regulated. For example, the body responds to increased blood sugar levels after meals by releasing insulin. Regulation of hormone synthesis, release, and degradation allows the blood concentrations of hormones to be precisely adjusted. This is based either on simple feedback control or on hierarchically structured regulatory systems.

C. Closed-loop feedback control

The biosynthesis and release of insulin by the pancreatic B cells (see p. 160) is stimulated by high blood glucose levels (> 5 mM). The insulin released then stimulates increased uptake and utilization of glucose by the cells of the muscle and adipose tissues. As a result, the blood glucose level falls back to its normal value, and further release of insulin stops.

D. Hormone hierarchy

Hormone systems are often linked to each other, giving rise in some cases to a hierarchy of higher-order and lower-order hormones. A particularly important example is the pituitary–hypothalamic axis, which is controlled by the central nervous system (CNS). Nerve cells in the hypothalamus react to stimulatory or inhibitory signals from the CNS by releasing activating or inhibiting factors, which are known as liberins (“releasing hormones”) and statins (“inhibiting hormones”). These neurohormones reach the adenohypophysis by short routes through the bloodstream. In the adenohypophysis, they stimulate (liberins) or inhibit (statins) the biosynthesis and release of tropines. Tropines (glandotropic hormones) in turn stimulate peripheral glands to synthesize glandular hormones. Finally, the glandular hormone acts on its target cells in the organism. In addition, it passes effects back to the higher-order hormone systems. This (usually negative) feedback influences the concentrations of the higher-order hormones, creating a feedback loop.

Many steroid hormones are regulated by this type of axis—e.g., thyroidin, cortisol, estradiol, progesterone, and testosterone. In the case of the glucocorticoids, the hypothalamus releases corticoprotein-releasing hormone (CRH or corticulin), a peptide consisting of 41 amino acids), which in turn releases corticoprotein (ACTH, 39 AAs) in the pituitary gland. Corticoprotein stimulates synthesis and release of the glandular steroid hormone cortisol in the adrenal cortex.
A. Endocrine, paracrine and autocrine hormone effects

1. Endocrine
2. Paracrine
3. Autocrine

B. Plasma level dynamics

C. Regulatory circuit

D. Hormone hierarchy

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Lipophilic hormones

Classifying hormones into hydrophilic and lipophilic molecules indicates the chemical properties of the two groups of hormones and also reflects differences in their mode of action (see p. 120).

A. Lipophilic hormones

Lipophilic hormones, which include steroid hormones, thyrothyrinones, and retinoic acid, are relatively small molecules (300–800 Da) that are poorly soluble in aqueous media. With the exception of the thyrothyrinones, they are not stored by hormone-forming cells, but are released immediately after being synthesized. During transport in the blood, they are bound to specific carriers. Via intracellular receptors, they mainly act on transcription (see p. 358). Other effects of steroid hormones—e.g., on the immune system—are not based on transcriptional control. Their details have not yet been explained.

Steroid hormones

The most important steroid hormones in vertebrates are listed on p. 57. Calcitriol (vitamin D hormone) is also included in this group, although it has a modified steroid structure. The most important steroid hormone in invertebrates is ecdysone.

Progesterone is a female sexual steroid belonging to the progestin (gestagen) family. It is synthesized in the corpus luteum of the ovaries. The blood level of progesterone varies with the menstrual cycle. The hormone prepares the uterus for a possible pregnancy. Following fertilization, the placenta also starts to synthesize progesterone in order to maintain the pregnant state. The development of the mammary glands is also stimulated by progesterone.

 Estradiol is the most important of the estrogens. Like progesterone, it is synthesized by the ovaries and, during pregnancy, by the placenta as well. Estradiol controls the menstrual cycle. It promotes proliferation of the uterine mucosa, and is also responsible for the development of the female secondary sexual characteristics (breast, fat distribution, etc.).

Testosterone is the most important of the male sexual steroids (androgens). It is synthesized in the Leydig interstitial cells of the testes, and controls the development and functioning of the male gonads. It also determines secondary sexual characteristics in men (muscles, hair, etc.).

Cortisol, the most important glucocorticoid, is synthesized by the adrenal cortex. It is involved in regulating protein and carbohydrate metabolism by promoting protein degradation and the conversion of amino acids into glucose. As a result, the blood glucose level rises (see p. 152). Synthetic glucocorticoids (e.g., dexamethasone) are used in drugs due to their anti-inflammatory and immunosuppressant effects.

Aldosterone, a mineralocorticoid, is also synthesized in the adrenal gland. In the kidneys, it promotes Na⁺ resorption by inducing Na⁺/K⁺ ATPase and Na⁺ channels (see p. 328). At the same time, it leads to increased K⁺ excretion. In this way, aldosterone indirectly increases blood pressure.

Calcitriol is a derivative of vitamin D (see p. 364). On exposure to ultraviolet light, a precursor of the hormone can also arise in the skin. Calcitriol itself is synthesized in the kidneys (see p. 330). Calcitriol promotes the resorption of calcium in the intestine and increases the Ca²⁺ level in the blood.

Iodothyronines

The thyroid hormone thyroxine (tetraiodothyronine, T₄) and its active form triiodothyronine (T₃) are derived from the amino acid tyrosine. The iodine atoms at positions 3 and 5 of the two phenol rings are characteristic of them. Post-translational synthesis of thyroxine takes place in the thyroid gland from tyrosine residues of the protein thyroglobulin, from which it is proteolytically cleaved before being released. Iodothyronines are the only organic molecules in the animal organism that contain iodine. They increase the basal metabolic rate, partly by regulating mitochondrial ATP synthesis. In addition, they promote embryonic development.
<table>
<thead>
<tr>
<th>Hormone</th>
<th>Site of formation</th>
<th>Sites of action</th>
<th>Actions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ovaries</td>
<td>Progesterone</td>
<td></td>
<td>Maintenance of pregnancy †</td>
</tr>
<tr>
<td>Uterus</td>
<td></td>
<td></td>
<td>Development of mammary glands †</td>
</tr>
<tr>
<td>Ovaries</td>
<td>Estradiol</td>
<td></td>
<td>Menstrual cycle</td>
</tr>
<tr>
<td>Uterus and other organs</td>
<td></td>
<td></td>
<td>Bone development †</td>
</tr>
<tr>
<td>Testes</td>
<td>Testosterone</td>
<td></td>
<td>Development of secondary female sex characteristics e.g., fat distribution, breasts, body hair †</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Protein synthesis †</td>
</tr>
<tr>
<td>Adrenal glands (cortex)</td>
<td>Cortisol</td>
<td></td>
<td>Proteolysis †</td>
</tr>
<tr>
<td>Adrenal glands (cortex)</td>
<td>Aldosterone</td>
<td></td>
<td>Protein synthesis †</td>
</tr>
<tr>
<td>Kidneys</td>
<td>Calcitriol</td>
<td></td>
<td>Gluconeogenese †</td>
</tr>
<tr>
<td>Thyroid gland</td>
<td>Thyrxine</td>
<td></td>
<td>Activity of the immune system ↓</td>
</tr>
</tbody>
</table>

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Metabolism of steroid hormones

A. Biosynthesis of steroid hormones

All steroid hormones are synthesized from cholesterol. The gonane core of cholesterol consists of 19 carbon atoms in four rings (A–D). The D ring carries a side chain of eight C atoms (see p. 54).

The cholesterol required for biosynthesis of the steroid hormones is obtained from various sources. It is either taken up as a constituent of LDL lipoproteins (see p. 278) into the hormone-synthesizing glandular cells, or synthesized by glandular cells themselves from acetyl-CoA (see p. 172). Excess cholesterol is stored in the form of fatty acid esters in lipid droplets. Hydrolysis allows rapid mobilization of the cholesterol from this reserve again.

**Biosynthetic pathways.** Only an overview of the synthesis pathways that lead to the individual hormones is shown here. Further details are given on p. 410.

Among the reactions involved, hydroxylations (H) are particularly numerous. These are catalyzed by specific *monooxygenases* ("hydroxylases") of the cytochrome P450 family (see p. 318). In addition, there are NADPH-dependent and NADP⁺-dependent *dehydrogenations* (Y) and dehydrogenations (D), as well as clevage and isomerization reactions (S, I). The estrogens have a special place among the steroid hormones, as they are the only ones that contain an aromatic A ring. When this is formed, catalyzed by aromatase, the angular methyl group (C-19) is lost.

**Pregnenolone** is an important intermediate in the biosynthesis of most steroid hormones. It is identical to cholesterol with the exception of a shortened and oxidized side chain. Pregnenolone is produced in three steps by hydroxylation and cleavage in the side chain. Subsequent dehydrogenation of the hydroxyl group at C-3 (b) and shifting of the double bond from C-5 to C-4 results in the gestagen progesterone.

With the exception of calcitriol, all steroid hormones are derived from progesterone. Hydroxylations of progesterone at C atoms 17, 21, and 11 lead to the glucocorticoid cortisol. Hydroxylation at C-17 is omitted during synthesis of the mineralocorticoid aldosterone. Instead, the angular methyl group (C-18) is oxidized to the aldehyde group. During synthesis of the androgen testosterone from progesterone, the side chain is completely removed. Aromatization of the A ring, as mentioned above, finally leads to estradiol.

On the way to calcitriol (vitamin D hormone; see p. 342), another double bond in the B ring of cholesterol is first introduced. Under the influence of UV light on the skin, the B ring is then photochemically cleaved, and the secosteroid cholecalciferol arises (vitamin D₃; see p. 364). Two Cytr P450-dependent hydroxylations in the liver and kidneys produce the active vitamin D hormone (see p. 330).

B. Inactivation of steroid hormones

The steroid hormones are mainly inactivated in the liver, where they are either reduced or further hydroxylated and then conjugated with glucuronic acid or sulfate for excretion (see p. 316). The *reduction reactions* attack oxo groups and the double bond in ring A. A combination of several inactivation reactions gives rise to many different steroid metabolites that have lost most of their hormonal activity. Finally, they are excreted with the urine and also partly via the bile. Evidence of steroids and steroid metabolites in the urine is used to investigate the hormone metabolism.

Further information

Congenital defects in the biosynthesis of steroid hormones can lead to severe developmental disturbances. In the *adrenogenital syndrome* (AGS), which is relatively common, there is usually a defect in 21-hydroxylase, which is needed for synthesis of cortisol and aldosterone from progesterone. Reduced synthesis of this hormone leads to increased formation of testosterone, resulting in masculinization of female fetuses. With early diagnosis, this condition can be avoided by providing the mother with hormone treatment before birth.
A. Biosynthesis of steroid hormones

- **C27**: Cholesterol → Calcitriol
- **C21**: Pregnenolone → Cortisol
- **C19**: Progesterone
- **C18**: Estradiol

B. Inactivation of steroid hormones

- **Cortisol**
  - Oxidative cleavage
  - Conjugate formation
  - Oxidation
  - Conjugate formation

- **Estradiol**
  - Hydrasilation
  - Conjugate formation

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Mechanism of action

A. Mechanism of action of lipophilic hormones

Lipophilic signaling substances include the steroid hormones, calcitriol, the iodothyronines (T3 and T4), and retinoic acid. These hormones mainly act in the nucleus of the target cells, where they regulate gene transcription in collaboration with their receptors and with the support of additional proteins (known as coactivators and mediators; see p. 244). There are several effects of steroid hormones that are not mediated by transcription control. These alternative pathways for steroid effects have not yet been fully explained.

In the blood, there are a number of transport proteins for lipophilic hormones (see p. 276). Only the free hormone is able to penetrate the membrane and enter the cell. The hormone encounters its receptor in the nucleus (and sometimes also in the cytoplasm).

The receptors for lipophilic hormones are rare proteins. They occur in small numbers (10^2–10^5 molecules per cell) and show marked specificity and high affinity for the hormone (Kd = 10^-9–10^-10 M). After binding to the hormone, the steroid receptors are able to bind as homodimers or heterodimers to control elements in the promoters of specific genes, from where they can influence the transcription of the affected genes—i.e., they act as transcription factors.

The illustration shows the particularly well-investigated mechanism of action for cortisol, which is unusual to the extent that the hormone-receptor complex already arises in the cytoplasm. The free receptor is present in the cytoplasm as a monomer in complex with the chaperone hsp90 (see p. 232). Binding of cortisol to the complex leads to an allosteric conformational change in the receptor, which is then released from the hsp90 and becomes capable of DNA binding as a result of dimerization.

In the nucleus, the hormone-receptor complex binds to nucleotide sequences known as hormone response elements (HREs). These are short palindromic DNA segments that usually promote transcription as enhancer elements (see p. 244). The illustration shows the HRE for glucocorticoids (GRE; “n” stands for any nucleotide). Each hormone receptor only recognizes its “own” HRE and therefore only influences the transcription of genes containing that HRE. Recognition between the receptor and HRE is based on interaction between the amino acid residues in the DNA-binding domain (B) and the relevant bases in the HRE (emphasized in color in the structure illustrated).

As discussed on p. 244, the hormone receptor does not interact directly with the RNA polymerase, but rather—along with other transcription factors—with a coactivator/mediator complex that processes all of the signals and passes them on to the polymerase. In this way, hormonal effects lead within a period of minutes to hours to altered levels of mRNAs for key proteins in cellular processes (“cellular response”).

B. Steroid receptors

The receptors for lipophilic signaling substances all belong to one protein superfamily. They are constructed in a modular fashion from domains with various lengths and functions. Starting from the N terminal, these are: the regulatory domain, the DNA-binding domain, a nuclear localization sequence (see p. 228), and the hormone-binding domain (see p. 73D).

The homology among receptors is particularly great in the area of the DNA-binding domain. The proteins have cysteine-rich sequences here that coordinatively bind zinc ions (A, Cys shown in yellow, Zn^2+ in light blue). These centers, known as “zinc fingers” or “zinc clusters,” stabilize the domains and support their dimerization, but do not take part in DNA binding directly. As in other transcription factors (see p. 118), “recognition helices” are responsible for that.

In addition to the receptors mentioned in A, the family of steroid receptors also includes the product of the oncogene erb-A (see p. 398), the receptor for the environmental toxin dioxin, and other proteins for which a distinct hormone ligand has not been identified (known as “orphan receptors”). Several steroid receptors—e.g., the retinoic acid receptor—form functional heterodimers with orphan receptors.
A. Mechanism of action of lipophilic hormones

- Hormone interacts with the receptor
- Heat-shock protein (hsp 90)
- Nucleus
- DNA-binding domain (dimer)
- Hormone response element (HRE)

B. Receptors of lipophilic hormones

- Receptor gene
  - A/B
  - C
  - D
  - E
- Variable length domains
  - Domain A/B: 100 – 600 aa
  - Domain D: 100 – 600 aa
  - Domain E: ~250 aa
  - Domain C: ~70 aa
- Interactions:
  - Binds ligand
  - DNA-binding domain
  - Nuclear-targeting sequence
  - Interaction with other nuclear components

- Steroid hormone
- T3, T4
- Calcitriol
- Retinoic acid
Hydrophilic hormones

The hydrophilic hormones are derived from amino acids, or are peptides and proteins composed of amino acids. Hormones with endocrine effects are synthesized in glandular cells and stored there in vesicles until they are released. As they are easily soluble, they do not need carrier proteins for transport in the blood. They bind on the plasma membrane of the target cells to receptors that pass the hormonal signal on (signal transduction; see p. 384). Several hormones in this group have paracrine effects—i.e., they only act in the immediate vicinity of their site of synthesis (see p. 372).

A. Signaling substances derived from amino acids

Histamine, serotonin, melatonin, and the catecholamines dopamine, epinephrine, and norepinephrine are known as “biogenic amines.” They are produced from amino acids by decarboxylation and usually act not only as hormones, but also as neurotransmitters.

Histamine acts as a mediator (local signaling substance) and neurotransmitter, is mainly stored in tissue mast cells and basophilic granulocytes in the blood. It is involved in inflammatory and allergic reactions. “Histamine liberators” such as tissue hormones, type E immunoglobulins (see p. 330), and drugs can release it. Histamine acts via various types of receptor. Binding to H1 receptors promotes contraction of smooth muscle in the bronchial system and dilates the capillary vessels and increases their permeability. Via H2 receptors, histamine slows down the heart rate and promotes the formation of HCl in the gastric mucosa. In the brain, histamine acts as a neurotransmitter.

Epinephrine is a hormone synthesized in the adrenal glands from tyrosine (see p. 352). Its release is subject to neuronal control. This “emergency hormone” mainly acts on the blood vessels, heart, and metabolism. It constricts the blood vessels and thereby increases blood pressure (via α1 and α2 receptors); it increases cardiac function (via β1 receptors); it promotes the degradation of glycogen into glucose in the liver and muscles (via β2 receptors); and it dilates the bronchia (also via β2 receptors).

B. Examples of peptide hormones and proteohormones

Numerically the largest group of signaling substances, these arise by protein biosynthesis (see p. 382). The smallest peptide hormone, thyroliberin (362 Da), is a tripeptide. Proteohormones can reach masses of more than 20 kDa—e.g., thyrotropin (28 kDa). Similarities in the primary structures of many peptide hormones and proteohormones show that they are related to one another. They probably arose from common predecessors in the course of evolution.

Thyroliberin (thyrotropin-releasing hormone, TRH) is one of the neurohormones of the hypothalamus (see p. 330). It stimulates pituitary gland cells to secrete thyrotropin (TSH). TRH consists of three amino acids, which are modified in characteristic ways (see p. 353).

Thyrotropin (thyroid-stimulating hormone, TSH) and the related hormones lutropin (luteinizing hormone, LH) and folliculotropin (follicle-stimulating hormone, FSH) originate in the adenohypophysis. They are all dimeric glycoproteins with masses of around 28 kDa. Thyrotropin stimulates the synthesis and secretion of thyroxin by the thyroid gland.

Insulin (for the structure, see p. 70) is produced and released by the B cells of the pancreas and is released when the glucose level rises. Insulin reduces the blood sugar level by promoting processes that consume glucose—e.g., glycolysis, glycogen synthesis, and conversion of glucose into fatty acids. By contrast, it inhibits gluconeogenesis and glycogen degradation. The transmission of the insulin signal in the target cells is discussed in greater detail on p. 398.

Glucagon, a peptide of 29 amino acids, is a product of the A cells of the pancreas. It is the antagonist of insulin and, like insulin, mainly influences carbohydrate and lipid metabolism. Its effects are each opposite to those of insulin. Glucagon mainly acts via the second messenger cAMP (see p. 384).
A. Signaling substances derived from amino acids

<table>
<thead>
<tr>
<th>Hormone</th>
<th>Sites of formation</th>
<th>Sites of action</th>
<th>Actions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Thyroliberin (TRH)</td>
<td>3 AA</td>
<td>Hypothalamus</td>
<td>Thyrotropin secretion ↑</td>
</tr>
<tr>
<td>Thyrotropin (TSH)</td>
<td>α chain 92 AA</td>
<td>Pituitary</td>
<td>Synthetic action and secretion of thyroxine↑</td>
</tr>
<tr>
<td></td>
<td>β chain 112 AA</td>
<td>Brain</td>
<td></td>
</tr>
<tr>
<td>Epinephrine</td>
<td></td>
<td>Adrenal glands</td>
<td>Cardiac output ↑</td>
</tr>
<tr>
<td></td>
<td>mast cell</td>
<td>(medulla)</td>
<td>Width of blood vessels↓</td>
</tr>
<tr>
<td>Histamine</td>
<td>Basophilic</td>
<td>Lungs</td>
<td>Capillaries: width↑</td>
</tr>
<tr>
<td></td>
<td>granulocyte</td>
<td>Stomach</td>
<td>permeability↑</td>
</tr>
<tr>
<td>Epinephrine</td>
<td></td>
<td>Adipose tissue</td>
<td>Gastric acid secretion by parietal cells↑</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Liver</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Muscle</td>
<td></td>
</tr>
</tbody>
</table>

B. Examples of peptide hormones and proteohormones

<table>
<thead>
<tr>
<th>Hormone</th>
<th>Sites of formation</th>
<th>Sites of action</th>
<th>Actions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Insulin A</td>
<td>Pancreas</td>
<td>Glucose</td>
<td>Glucose uptake by cells↑</td>
</tr>
<tr>
<td></td>
<td>A chain 21 AA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glucagon 29</td>
<td>Pancreas</td>
<td>Glucose</td>
<td>Glucose uptake by cells↑</td>
</tr>
<tr>
<td></td>
<td>AA</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>A cells</td>
<td>Glucose</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Proteins</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Fats</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ketone bodies</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Metabolism of peptide hormones

Hydrophilic hormones and other water-soluble signaling substances have a variety of biosynthetic pathways. Amino acid derivatives arise in special metabolic pathways (see p. 352) or through post-translational modification (see p. 374). Proteohormones, like all proteins, result from translation in the ribosome (see p. 250). Small peptide hormones and neuropeptides, most of which only consist of 3–30 amino acids, are released from precursor proteins by proteolytic degradation.

A. Biosynthesis

The illustration shows the synthesis and processing of the precursor protein proopiomelanocortin (POMC) as an example of the biosynthesis of small peptides with signaling functions. POMC arises in cells of the adeno-hypophysis, and after processing in the rER and Golgi apparatus, it supplies the opioid-like peptides met-enkephalin and β-endorphin (implying “opio-“; see p. 352), three melanocyte-stimulating hormones (α-, β- and γ-MSH, implying “melano-“), and the glandotropic hormone corticotropin (ACTH, implying “¬cortin“). Additional products of POMC degradation include two lipotropins with catabolic effects in the adipose tissue (β- and γ-LPH).

Some of the peptides mentioned are overlapping in the POMC sequence. For example, additional cleavage of ACTH gives rise to α-MSH and corticotropin-like intermediary peptide (CLIP). Proteolytic degradation of β-LPH provides γ-LPH and β-endorphin. The latter can be further broken down to yield met-enkephalin, while γ-LPH can still give rise to β-MSH (not shown). Due to the numerous derivative products with biological activity that it has, POMC is also known as a polypeptide. Which end product is formed and in what amounts depends on the activity of the proteases in the ER that catalyze the individual cleavages.

The principles underlying protein synthesis and protein maturation (see pp. 230–233) can be summed up once again using the example of POMC:

1. As a result of transcription of the POMC gene and maturation of the hnrNA, a mature mrNA consisting of some 1100 nucleotides arises, which is modified at both ends (see p. 246). This mRNA codes for prepro-POMC—i.e., a POMC protein that still has a signal peptide for the ER at the N terminus (see p. 230).

2. Prepro-POMC arises through translation in the rough endoplasmic reticulum (rER). The growing peptide chain is introduced into the ER with the help of a signal peptide.

3. Cleavage of the signal peptide and other modifications in the ER (formation of disulfide bonds, glycosylation, phosphorylation) give rise to the mature prohormone (“pro-POMC“).

4. The neuropeptides and hormones mentioned are now formed by limited proteolysis and stored in vesicles. Release from these vesicles takes place by exocytosis when needed.

The biosynthesis of peptide hormones and proteohormones, as well as their secretion, is controlled by higher-order regulatory systems (see p. 372). Calcium ions are among the substances involved in this regulation as second messengers; an increase in calcium ions stimulates synthesis and secretion.

B. Degradation and inactivation

Degradation of peptide hormones often starts in the blood plasma or on the vascular walls; it is particularly intensive in the kidneys.

Several peptides that contain disulfide bonds (e.g., insulin) can be inactivated by reductive cleavage of the disulfide bonds (1). Peptides and proteins are also cleaved by peptidases, starting from one end of the peptide by exopeptidases (2), or in the middle of it by peptidases (endopeptidases, 3). Proteolysis gives rise to a variety of hormone fragments, several of which are still biologically active. Some peptide hormones and proteohormones are removed from the blood by binding to their receptors with subsequent endocytosis of the hormone–receptor complex (4). They are then broken down in the lysosomes. All of the degradation reactions lead to amino acids, which become available to the metabolism again.
A. Biosynthesis

1. Transcription
2. Translation
3. Cleavage of signal peptide
4. Limited proteolysis

Prohormone

Human chromosome with POMC gene

DNA

Transcription

Splicing

mRNA

Translation

Pro-Androctin

Cleavage of signal peptide

Prohormone

Limited proteolysis

Prohormone modification

Storage

Secretion

Hormone

B. Degradation and inactivation

1. Cleavage of disulfide bonds by reductases
2. Degradation by exopeptidases
3. Degradation by prolines

Extracellular degradation:

Intracellular degradation:

1. Cleavage of desulfide bonds by reductases
2. Degradation by exopeptidases
3. Degradation by prolensases

4. Binding to membrane receptors

Endocytosis

Degradation in lysosomes

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Mechanisms of action

The messages transmitted by hydrophilic signaling substances (see p. 380) are sent to the interior of the cell by membrane receptors. These bind the hormone on the outside of the cell and trigger a new second signal on the inside by altering their conformation. In the interior of the cell, this secondary signal influences the activity of enzymes or ion channels. Via further steps, switching of the metabolism, changes in the cytoskeleton, and activation or inhibition of transcription factors can occur (“signal transduction”) can occur.

A. Mechanisms of action

Receptors are classified into three different types according to their structure (see also p. 224):

1. **1-Helix receptors** (left) are proteins that span the membrane with only one α-helix. On their intracellular side, they have domains with allosterically activatable enzyme activity. In most cases, these are tyrosine kinases.

   Insulins (see p. 388), growth factors, and cytokines (see p. 392), for example, act via 1-helix receptors. Binding of the signaling substance leads to activation of internal kinase activity (in some cases, dimerization of the receptor is needed for this). The activated kinase phosphorylates itself using ATP (auto-phosphorylation), and also phosphorylates tyrosine residues of other proteins (known as receptor substrates). Adaptor proteins that recognize the phosphotyrosine residues bind to the phosphorylated proteins (see pp. 388, 392). They pass the signal on to other protein kinases.

2. **Ion channels** (center). These receptors contain ligand-gated ion channels. Binding of the signaling substance opens the channels for ions such as Na⁺, K⁺, Ca²⁺, and Cl⁻. This mechanism is mainly used by neurotransmitters such as acetylcholine (nicotinic receptor; see p. 224) and GABA (A receptor; see p. 354).

3. **7-Helix receptors** (serpentine receptors, right) represent a large group of membrane proteins that transfer the hormone or transmitter signal, with the help of G proteins (see below), to effector proteins that alter the concentrations of ions and second messengers (see B).

B. Signal transduction by G proteins

G proteins transfer signals from 7-helix receptors to effector proteins (see above). G protein are heterotrimers consisting of three different types of subunit (α, β, and γ; see p. 224). The α-subunit can bind GDP or GTP (hence the name “G protein”) and has GTPase activity. Receptor-coupled G proteins are related to other GTP-binding proteins such as Ras (see pp. 388, 398) and EF-Tu (see p. 252).

G proteins are divided into several types, depending on their effects. Stimulatory G proteins (G₁) are widespread. They activate adenylate cyclases (see below) or influence ion channels. Inhibitory G proteins (Gᵢ) inhibit adenylate cyclase. G proteins in the G₄ family activate another effector enzyme—phospholipase C (see p. 386).

Binding of the signaling substance to a 7-helix receptor alters the receptor conformation in such a way that the corresponding G protein can attach on the inside of the cell. This causes the α-subunit of the G protein to exchange bound GDP for GTP (1). The G protein then separates from the receptor and dissociates into an α-subunit and a βγ-unit. Both of these components bind to other membrane proteins and alter their activity; ion channels are opened or closed, and enzymes are activated or inactivated.

In the case of the βγ-catecholamine receptor (illustrated here), the α-subunit of the G₁ protein, by binding to adenylate cyclase, leads to the synthesis of the second messenger cAMP. cAMP activates protein kinase A, which in turn activates or inhibits other proteins (2; see p. 120).

The βγ-unit of the G protein stimulates a kinase (βARK, not shown), which phosphorylates the receptor. This reduces its affinity for the hormone and leads to binding of the blocking protein arrestin. The internal GTase activity of the α-subunit hydrolyzes the bound GTP to GDP within a period of seconds to minutes, and thereby terminates the action of the G protein on the adenylate cyclase (3).
A. Mechanisms of action

1. 1-Helix receptor
   Hydrophilic signaling substance
   Tyrosine kinase
   ATP → ADP
   Receptor substrate
   Other enzymes
   phosphorylate
   Transcription factors
   Nucleus
   Transcription

2. Ion channel
   Membrane
   Increase
   G-protein
   7 Transmembrane helices
   Effector enzyme
   Adenylate cyclase
   Guanylate cyclase
   Phospholipase C

3. 7-Helix receptor
   Second messenger
   CAMP, DAG, InsP3
   Signal transduction
   Protein kinases (PKs)
   Protein phosphatases
   Enzymes
   regulate
   modulate
   Metabolism
   Cytoskeleton

B. Signal transduction by G proteins

1. Substrate
   GS
   GDP → GTP
   Activated 7-helix receptor
   βγ-unit

2. Second messenger
   GTP → ATP
   cAMP
   CGMP

3. Arrestin
   Antagonist
   G-protein
   CGDP
   Adenylate cyclase 4.6.1.3

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Second messengers

Second messengers are intracellular chemical signals, the concentration of which is regulated by hormones, neurotransmitters, and other extracellular signals (see p. 384). They arise from easily available substrates and only have a short half-life. The most important second messengers are cAMP, cGMP, Ca²⁺, inositol trisphosphate (InsP₃), diacylglycerol (DAG), and nitrogen monoxide (NO).

A. Cyclic AMP

Metabolism. The nucleotide cAMP (adenosine 3',5'-cyclic monophosphate) is synthesized by membrane-bound adenylate cyclases [1] on the inside of the plasma membrane. The adenylate cyclases are a family of enzymes that cyclize ATP to cAMP by cleaving diphosphate (P₂). The degradation of cAMP to AMP is catalyzed by phosphodiesterases [2], which are inhibited by methylxanthines such as caffeine, for example. By contrast, insulin activates the esterase and thereby reduces the cAMP level (see p. 388).

Adenylate cyclase activity is regulated by G proteins (G₁ and G₂), which in turn are controlled by extracellular signals via 7-helix receptors (see p. 384). Ca²⁺-calmodulin (see below) also activates specific adenylate cyclases.

Action. cAMP is an allosteric effector of protein kinase A (PK-A, [3]). In the inactive state, PK-A is a heterotetramer (G₁R₂), the catalytic subunits of which (C) are blocked by regulatory units (R; autoinhibition). When cAMP binds to the regulatory units, the C units separate from the R units and become enzymatically active. Active PK-A phosphorlates serine and threonine residues of more than 100 different proteins, enzymes, and transcription factors. In addition to cAMP, cGMP also acts as a second messenger. It is involved in sight (see p. 358) and in the signal transduction of NO (see p. 388).

B. Inositol 1,4,5-trisphosphate and diacylglycerol

Type G₂ G proteins activate phospholipase C [4]. This enzyme creates two second messengers from the double-phosphorylated membrane phosphatidylphosphatidylinositol bisphosphate (PtdIns(4,5)₂), i.e., inositol 1,4,5-trisphosphate (InsP₃), which is soluble, and diacylglycerol (DAG). InsP₃ migrates to the endoplasmic reticulum (ER), where it opens Ca²⁺ channels that allow Ca²⁺ to flow into the cytoplasm (see C). By contrast, DAG, which is lipophilic, remains in the membrane, where it activates type C protein kinases, which phosphorylate proteins in the presence of Ca²⁺ ions and thereby pass the signal on.

C. Calcium ions

Calcium level. Ca²⁺ (see p. 342) is a signaling substance. The concentration of Ca²⁺ ions in the cytoplasm is normally very low (10–100 nM), as it is kept down by ATP-driven Ca²⁺ pumps and Na⁺/Ca²⁺ exchangers. In addition, many proteins in the cytoplasm and organelles bind calcium and thus act as Ca²⁺ buffers.

Specific signals (e.g., an action potential or second messenger such as InsP₃ or cAMP) can trigger a sudden increase in the cytoplasmic Ca²⁺ level to 500–1000 nM by opening Ca²⁺ channels in the plasma membrane or in the membranes of the endoplasmic or sarcoplasmic reticulum. Ryanodine, a plant substance, acts in this way on a specific channel in the ER. In the cytoplasm, the Ca²⁺ level always only rises very briefly (Ca²⁺ “spikes”), as prolonged high concentrations in the cytoplasm have cytotoxic effects.

Calcium effects. The biochemical effects of Ca²⁺ in the cytoplasm are mediated by special Ca²⁺-binding proteins (“calcium sensors”). These include the annexins, calmodulin, and troponin C in muscle (see p. 334). Calmodulin is a relatively small protein (17 kDa) that occurs in all animal cells. Binding of four Ca²⁺ ions (light blue) converts it into a regulatory element. Via a dramatic conformational change (cf. 2a and 2b), Ca²⁺-calmodulin enters into interaction with other proteins and modulates their properties. Using this mechanism, Ca²⁺ ions regulate the activity of enzymes, ion pumps, and components of the cytoskeleton.
A. Cyclic AMP

- Adenylate cyclase 4.6.1.1
- Phosphodiesterase 3.1.4.17
- Protein kinase A 2.7.1.37

B. Inositol 1,4,5-trisphosphate and diacylglycerol

C. Calcium ions

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Signal cascades

The signal transduction pathways that mediate the effects of the metabolic hormone insulin are of particular medical interest (see A). The mediator nitrogen monoxide (NO) is also clinically important, as it regulates vascular caliber and thus the body’s perfusion with blood (see B).

A. Insulin: signal transduction O

The diverse effects of insulin (see p. 160) are mediated by protein kinases that mutually activate each other in the form of enzyme cascades. At the end of this chain there are kinases that influence gene transcription in the nucleus by phosphorylating target proteins, or promote the uptake of glucose and its conversion into glycogen. The signal transduction pathways involved have not yet been fully explained. They are presented here in a simplified form.

The insulin receptor (top) is a dimer with subunits that have activatable tyrosine kinase domains in the interior of the cell (see p. 224). Binding of the hormone increases the tyrosine kinase activity of the receptor, which then phosphorylates itself and other proteins (receptor substrates) at various tyrosine residues. Adaptor proteins, which conduct the signal further, bind to the phosphoryrosine residues.

The effects of insulin on transcription are shown on the left of the illustration. Adaptor proteins Grb-2 and SOS (“son of sevenless”) bind to the phosphorylated IRS (insulin-receptor substrate) and activate the G protein Ras (named after its gene, the oncogene ras; see p. 398). Ras activates the protein kinase Raf (another oncogene product). Raf sets in motion a phosphorylation cascade that leads via the kinases MEK and ERK (also known as MAPK, “mitogen-activated protein kinase”) to the phosphorylation of transcription factors in the nucleus.

Some of the effects of insulin on the carbohydrate metabolism (right part of the illustration) are possible without protein synthesis. In addition to Grb-2, another dimeric adaptor protein can also bind to phosphorylated IRS. This adaptor protein thereby acquires phosphatidylinositol-3-kinase activity (PI3K) and, in the membrane, phosphorylates phospholipids from the phosphatidylinositol group (see p. 50) at position 3. Protein kinase PDK-1 binds to these reaction products, becoming activated itself and in turn activating protein kinase B (PK-B).

This has several effects. In a manner not yet fully understood, PK-B leads to the fusion with the plasma membrane of vesicles that contain the glucose transporter Glut-4. This results in inclusion of Glut-4 in the membrane and thus to increased glucose uptake into the muscles and adipose tissue (see p. 160). In addition, PK-B inhibits glycogen synthase kinase 3 (GSK-3) by phosphorylation. As GSK-3 in turn inhibits glycogen synthase by phosphorylation (see p. 120), its inhibition by PK-B leads to increased glycogen synthesis. Protein phosphatase-1 (PP-1) converts glycogen synthase into its active form by dephosphorylation (see p. 120). PP-1 is also activated by insulin.

B. Nitrogen monoxide (NO) as a mediator O

Nitrogen monoxide (NO) is a short-lived radical that functions as a locally acting mediator (see p. 370). In a complex reaction, NO arises from arginine in the endothelial cells of the blood vessels [1]. The trigger for this is Ca2+-calmodulin (see p. 386), which forms when there is an increase in the cytoplasmic Ca2+ level.

NO diffuses from the endothelium into the underlying vascular muscle cells, where it leads, as a result of activation of guanylate cyclase [2], to the formation of the second messenger cGMP (see pp. 358, 384). Finally, by activating a special protein kinase (PK-G), cGMP triggers relaxation of the smooth muscle and thus dilution of the vessels. The effects of atrial natriuretic peptide (ANP; see p. 328) in reducing blood pressure are also mediated by cGMP-induced vasodilation. In this case, cGMP is formed by the guanylate cyclase activity of the ANP receptor.

Further information

The drug nitroglycerin (glyceryl trinitrate), which is in the treatment of angina pectoris, releases NO in the bloodstream and thereby leads to better perfusion of cardiac muscle.
A. Insulin: signal transduction

B. Nitrogen monoxide (NO) as a mediator

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Eicosanoids

The eicosanoids are a group of signaling substances that arise from the C-20 fatty acid arachidonic acid and therefore usually contain 20 C atoms (Greek eicos = 20). As mediators, they influence a large number of physiological processes (see below). Eicosanoid metabolism is therefore an important drug target. As short-lived substances, eicosanoids only act in the vicinity of their site of synthesis (paracrine effect; see p. 372).

A. Eicosanoids

Biochemistry. Almost all of the body’s cells form eicosanoids. Membrane phospholipids that contain the polyunsaturated fatty acid arachidonic acid (20:4; see p. 48) provide the starting material.

Initially, phospholipase A₁ [1] releases the arachidonate moiety from these phospholipids. The activity of phospholipase A₁ is strictly regulated. It is activated by hormones and other signals via G proteins. The arachidonate released is a signaling substance itself. However, its metabolites are even more important.

Two different pathways lead from arachidonate to prostaglandins, prostacyclins, and thromboxanes, on the one hand, or leukotrienes on the other. The key enzyme for the first pathway is prostaglandin synthase [2]. Using up Gₛ, it catalyzes in a two-step reaction the cyclization of arachidonate to prostaglandin H₂, the parent substance for the prostaglandins, prostacyclins, and thromboxanes. Acetylsalicylic acid (aspirin) irreversibly acetylates a serine residue near the active center of prostaglandin synthase, so that access for substrates is blocked (see below).

As a result of the action of lipooxygenases [3], hydroxyfatty acids and hydroperoxyl fatty acids are formed from arachidonate, from which elimination of water and various conversion reactions give rise to the leukotrienes. The formulae only show one representative from each of the various groups of eicosanoids.

Effects. Eicosanoids act via membrane receptors in the immediate vicinity of their site of synthesis, both on the synthesizing cell itself (autocrine action) and on neighboring cells (paracrine action). Many of their effects are mediated by the second messengers cAMP and cGMP.

The eicosanoids have a very wide range of physiological effects. As they can stimulate or inhibit smooth-muscle contraction, depending on the substance concerned, they affect blood pressure, respiration, and intestinal and uterine activity, among other properties. In the stomach, prostaglandins inhibit HCl secretion via Gₛ proteins (see p. 270). At the same time, they promote mucus secretion, which protects the gastric mucosa against the acid. In addition, prostaglandins are involved in bone metabolism and in the activity of the sympathetic nervous system. In the immune system, prostaglandins are important in the inflammatory reaction. Among other things, they attract leukocytes to the site of infection. Eicosanoids are also deci-

Metabolism. Eicosanoids are inactivated within a period of seconds to minutes. This takes place by enzymatic reduction of double bonds and dehydrogenation of hydroxyl groups. As a result of this rapid degradation, their range is very limited.

Further information

Acetylsalicylic acid and related non-steroidal anti-inflammatory drugs (NSAIDs) selectively inhibit the cyclooxygenase activity of prostaglandin synthase [2] and consequently the synthesis of most eicosanoids. This explains their analgesic, antipyretic, and anti-inflammatory effects. Frequent side effects of NSAIDs also result from inhibition of eicosanoid synthesis. For example, they impair hemostasis because the synthesis of thromboxanes by thrombo-

cytes is inhibited. In the stomach, NSAIDs increase HCl secretion and at the same time inhibit the formation of protective mucus. Long-term NSAID use can therefore damage the gastric mucosa.
### A. Eicosanoids

**Essential fatty acids:**
- Linoleic acid
- Linolenic acid
- Arachidonic acid

**Inclusion in:**
- Phospholipid

**Hormones and other signals**

**Lysophospholipid**

**Arachidonic acid**

**Prostaglandin synthase**

**Lipoxygenase**

**Hydroxy- and hydroperoxy fatty acids**

**Prostaglandin H2**

**Leukotrienes**

**Prostacyclins**

**Prostaglandins**

**Thromboxanes**

**Acetylsalicylic acid**

**Effects:**
- Stimulation of contraction of smooth muscle
- Biosynthesis of steroid hormones
- Gastric juice secretion
- Hormone-controlled lipases
- Thromboctye aggregation
- Pain production
- Inflammatory response

**Phospholipase A2** 3.1.1.4

**Prostaglandin H-synthase [heme]** (dioxygenase + peroxidase) 1.14.99.1

**Arachidonate lipoxygenases** 1.13.11. n
Cytokines

A. Cytokines

Cytokines are hormone-like peptides and proteins with signaling functions, which are synthesized and released by cells of the immune system and other cell types. Their numerous biological functions operate in three areas: they regulate the development and homeostasis of the immune system; they control the hematopoietic system; and they are involved in non-specific defense, influencing inflammatory processes, blood coagulation, and blood pressure. In general, cytokines regulate the growth, differentiation, and survival of cells. They are also involved in regulating apoptosis (see p. 396).

There is an extremely large number of cytokines; only the most important representatives are listed opposite. The cytokines include interleukins (IL), lymphokines, monokines, chemokines, interferons (IFN), and colony-stimulating factors (CSF). Via interleukins, immune cells stimulate the proliferation and activity of other immune cells (see p. 294). Interferons are used medically in the treatment of viral infections and other diseases.

Although cytokines rarely show structural homologies with each other, their effects are often very similar. The cytokines differ from hormones (see p. 370) only in certain respects: they are released by many different cells, rather than being secreted by defined glands, and they regulate a wider variety of target cells than the hormones.

B. Signal transduction in the cytokines

As peptides or proteins, the cytokines are hydrophilic signaling substances that act by binding to receptors on the cell surface (see p. 380). Binding of a cytokine to its receptor (1) leads via several intermediate steps (2-5) to the activation of transcription of specific genes (6).

In contrast to the receptors for insulin and growth factors (see p. 388), the cytokine receptors (with a few exceptions) have no tyrosine kinase activity. After binding of cytokine (1), they associate with one another to form homodimers, join together with other signal transduction proteins (STPs) to form dimers, or promote dimerization of other STPs (2). Class I cytokine receptors interact with three different STPs (gp130, βc, and γc). The STPs themselves do not bind cytokines, but conduct the signal to tyrosine kinases (3). The fact that different cytokines can activate the same STP via their receptors explains the overlapping biological activity of some cytokines.

As an example of the signal transduction pathway in cytokines, the illustration shows the way in which the IL-6 receptor, after binding its ligand IL-6 (1), induces the dimerization of the STP gp130 (2). The dimeric gp130 binds cytoplasmic tyrosine kinases from the jak family ("Janus kinases," with two kinase centers) and activates them (3). The Janus kinases phosphorylate cytokine receptors, STPs, and various cytoplasmic proteins that conduct the signal further. In addition, they phosphorylate transcription factors known as STATs ("signal transducers and activators of transcription"). STATs are among the proteins that have an SH2 domain and are able to bind phosphorylated residues (see p. 388). They therefore bind to cytokine receptors that have been phosphorylated by Janus kinases. When STATs are then also phosphorylated themselves (4), they are converted into their active form and become dimers (5). After transfer to the nucleus, they bind—along with auxiliary proteins as transcription factors—to the promoters of inducible genes and in this way regulate their transcription (6).

The activity of the cytokine receptors is terminated by protein phosphatases, which hydrolytically cleave the phosphotyrosine residues. Several cytokine receptors are able to lose their ligand-binding extracellular domain by proteolysis (not shown). The extracellular domain then appears in the blood, where it competes for cytokines. This reduces the effective cytokine concentration.
A. Cytokines

<table>
<thead>
<tr>
<th>IL-1</th>
<th>Interleukin 1</th>
<th>G-CSF</th>
<th>Granulocyte colony-stimulating factor</th>
</tr>
</thead>
<tbody>
<tr>
<td>IL-2</td>
<td>Interleukin 2</td>
<td>GM-CSF</td>
<td>Granulocyte/macrophage colony-stimulating factor</td>
</tr>
<tr>
<td>IL-3</td>
<td>Interleukin 3</td>
<td>MIF</td>
<td>Macrophage migration inhibitory factor</td>
</tr>
<tr>
<td>IL-4</td>
<td>Interleukin 4</td>
<td>IL-1</td>
<td>Interleukin 5</td>
</tr>
<tr>
<td>IL-6</td>
<td>Interleukin 6</td>
<td>TNFα</td>
<td>Tumor necrosis factor-α</td>
</tr>
<tr>
<td>IFN-α</td>
<td>Interferon α</td>
<td>TNFβ</td>
<td>Tumor necrosis factor-β</td>
</tr>
<tr>
<td>IFN-β</td>
<td>Interferon β</td>
<td>and others</td>
<td></td>
</tr>
</tbody>
</table>

- **Immune system**
- **Hematopoietic system**
- **Non-specific defense**
- **Secretion by individual cells**
- **Signal peptide or signal protein**
- **Effects on many cell types**

B. Signal transduction in the cytokines

1. Cytokine
2. Secretion by individual cells
3. Signal peptide or signal protein
4. Effects on many cell types

**Dimerization of STAT**

- **SH2 domain can bind phosphotyrosine residues**
- **Phosphotyrosine residue**
- **STAT dimer**
- **Phosphorylation Dimenization**

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Cell cycle

A. Cell cycle

Proliferating cells undergo a cycle of division (the cell cycle), which lasts approximately 24 hours in mammalian cells in cell culture. The cycle is divided into four different phases (G₁, S, G₂, and M—in that sequence).

Fully differentiated animal cells only divide rarely. These cells are in the so-called G₀ phase, in which they can remain permanently. Some G₀ cells return to the G₁ phase again under the influence of mitogenic signals (growth factors, cytokines, tumor viruses, etc.), and after crossing a control point (G₁ to S), enter a new cycle. DNA is replicated (see p. 240) during the S phase, and new chromatin is formed. Particularly remarkable in morphological terms is the actual mitosis (M phase), in which the chromosomes separate and two daughter cells are formed. The M and S phases are separated by two segments known as the G₁ and G₂ phases (the G stands for “gap”). In the G₁ phase, the duration of which can vary, the cell grows by de novo synthesis of cell components. Together, the G₁, G₂, S, and G₀ phases are referred to as the interphase, which alternates in the cell cycle with the short M phase.

B. Control of the cell cycle

The progression of the cell cycle is regulated by interconversion processes. In each phase, special Ser/Thr-specific protein kinases are formed, which are known as cyclin-dependent kinases (CDKs). This term is used because they have to bind an activator protein (cyclin) in order to become active. At each control point in the cycle, specific CDKs associate with equally phase-specific cyclins. If there are no problems (e.g., DNA damage), the CDK–cyclin complex is activated by phosphorylation and/or dephosphorylation. The activated complex in turn phosphorylates transcription factors, which finally lead to the formation of the proteins that are required in the cell cycle phase concerned (enzymes, cytoskeleton components, other CDKs, and cyclins). The activity of the CDK–cyclin complex is then terminated again by proteolytic cyclin degradation

The above outline of cell cycle progression can be examined here in more detail using the G₁–M transition as an example.

Entry of animal cells into mitosis is based on the “mitosis-promoting factor” (MPF). MPF consists of CDK₁ (cdc2) and cyclin B. The intracellular concentration of cyclin B increases constantly until mitosis starts, and then declines again rapidly (top left). MPF is initially inactive, because CDK₁ is phosphorylated and cyclin B is dephosphorylated (top center). The M phase is triggered when a protein phosphatase [1] dephosphorylates the CDK while cyclin B is phosphorylated by a kinase [2]. In its active form, MPF phosphorylates various proteins that have functions in mitosis—e.g., histone H1 (see p. 238), components of the cytoskeleton such as the lamins in the nuclear membrane, transcription factors, mitotic spindle proteins, and various enzymes.

When mitosis has been completed, cyclin B is marked with ubiquitin and broken down proteolytically by proteasomes (see p. 176). Protein phosphatases then regain control and dephosphorylate the proteins involved in mitosis. This returns the cell to the interphase.

Further information

The G₁–S transition (not shown) is particularly important for initiating the cell cycle. It is triggered by the CDK4–cyclin D complex, which by phosphorylating the protein pRb releases the transcription factor E2F previously bound to pRb. This activates the transcription of genes needed for DNA replication. If the DNA is damaged by mutagens or ionizing radiation, the protein p53 initially delays entry into the S phase. If the DNA repair system (see p. 256) does not succeed in removing the DNA damage, p53 forces the cell into apoptosis (see p. 396). The genes coding for pRb and p53 belong to the tumor-suppressor genes (see p. 398). In many tumors (see p. 400), these genes are in fact damaged by mutation.
A. Cell cycle

**M phase**
- Mitosis
- Chromosome separation
- Cell division

**G<sub>2</sub> phase**
- Preparation for mitosis

**S phase**
- DNA replication
- Histone synthesis
- Centrosome formed
- Chromosome duplication

**G<sub>1</sub> phase**
- RNA and protein synthesis
- Cell growth

**G<sub>0</sub> phase**
- No cell division
- Restriction point

---

B. Control of the cell cycle

**Cyclin B concentration**

<table>
<thead>
<tr>
<th>Time</th>
<th>M</th>
<th>M</th>
<th>M</th>
<th>M</th>
<th>M</th>
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</thead>
<tbody>
<tr>
<td>0 h</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6 h</td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

**Cyclin-dependent protein kinases**
- CDK 1–6
- Cyclin
- Cyclins A–E

**Cyclin B**
- Regulatory subunit
- Catalytic subunit

**Cyclin-dependent protein kinase (CDK1)**
- Inactive protein kinase
- Active protein kinase

**Interphase**
- Proteolysis
- Spindle formation
- Chromosome condensation
- Disappearance of nuclear membrane
- Transcription stop
- Cyclin degradation

**Mitosis**
- Active protein kinase
- Phosphoprotein phosphatase
- Protein kinase

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Apoptosis

A. Cell proliferation and apoptosis

The number of cells in any tissue is mainly regulated by two processes—cell proliferation and physiological cell death, apoptosis. Both of these processes are regulated by stimulatory and inhibitory factors that act in solute form (growth factors and cytokines) or are presented in bound form on the surface of neighboring cells (see below).

Apoptosis is genetically programmed cell death, which leads to “tidy” breakdown and disposal of cells. Morphologically, apoptosis is characterized by changes in the cell membrane (with the formation of small blebs known as “apoptotic bodies”), shrinking of the nucleus, chromatin condensation, and fragmentation of DNA. Macrophages and other phagocytic cells recognize apoptotic cells and remove them by phagocytosis without inflammatory phenomena developing.

Cell necrosis (not shown) should be distinguished from apoptosis. In cell necrosis, cell death is usually due to physical or chemical damage. Necrosis leads to swelling and bursting of the damaged cells and often triggers an inflammatory response.

The growth of tissue (or, more precisely, the number of cells) is actually regulated by apoptosis. In addition, apoptosis allows the elimination of unwanted or superfluous cells—e.g., during embryonic development or in the immune system. The contraction of the uterus after birth is also based on apoptosis. Diseased cells are also eliminated by apoptosis—e.g., tumor cells, virus-infected cells, and cells with irreparably damaged DNA. An everyday example of this is the peeling of the skin after sunburn.

B. Regulation of apoptosis

Apoptosis can be triggered by a number of different signals that use various transmission pathways. Other signaling pathways prevent apoptosis.

At the center of the apoptotic process lies a group of specialized cysteine-containing aspartate proteinases (see p. 176), known as caspases. These mutually activate one another, creating an enzyme cascade resembling the cascade involved in blood coagulation (see p. 290). Other enzymes in this group, known as effector caspases, cleave cell components after being activated—e.g., laminin in the nuclear membrane and snRNPs proteins (see p. 246)—or activate special DNases which then fragment the nuclear DNA.

An important trigger for apoptosis is known as the Fas system. This is used by cytotoxic T cells, for example, which eliminate infected cells in this way (top left). Most of the body’s cells have Fas receptors (CD 95) on their plasma membrane. If a T cell is activated by contact with an MHC presenting a viral peptide (see p. 296), binding of its Fas ligands occurs on the target cell’s Fas receptors. Via the mediator protein FADD (“Fas-associated death domain”), this activates caspase-8 inside the cell, setting in motion the apoptotic process.

Another trigger is provided by tumor necrosis factor-α (TNF-α), which acts via a similar protein (TRADD) and supports the endogenous defense system against tumors by inducing apoptosis.

Caspase-8 activates the effector caspases either directly, or indirectly by promoting the cytochrome c (see p. 140) from mitochondria. Once in the cytoplasm, cytochrome c binds to and activates the protein Apaf-1 (not shown) and thus triggers the caspase cascade. Apoptotic signals can also come from the cell nucleus. If irreparable DNA damage is present, the p53 protein (see p. 394)—the product of a tumor suppressor gene—promotes apoptosis and thus helps eliminate the defective cell.

There are also inhibitory factors that oppose the signals that activate apoptosis. These include bcl-2 and related proteins. The genomes of several viruses include genes for this type of protein. The genes are expressed by the host cell and (to the benefit of the virus) prevent the host cell from being prematurely eliminated by apoptosis.
A. Cell proliferation and apoptosis

Factors

Cell proliferation → Apoptosis

Constant cell number

Changes in membranes

Dissolution of nuclear structure

Shrinking of cytoplasm

Condensation of chromatin

Fragmentation of DNA

Apoptotic cell

B. Regulation of apoptosis

Cytotoxic T cell

Fas ligand

Fas receptor

TNF-α

TNF receptor type I

Caspase 8

Cytochrome c

Effector caspases

p53 protein

bcl-2 protein

Other proteins

snRNA proteins

Laminin

Caspase-activated DNases

DNA with irradiation damage

Apoptosis

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Oncogenes

Oncogenes are cellular genes that can trigger uncontrolled cell proliferation if their sequence is altered or their expression is incorrectly regulated. They were first discovered as viral (+)-oncogenes in retroviruses that cause tumors (tumor viruses). Viruses of this type (see p. 404) sometimes incorporate genes from the host cell into their own genome. If these genes are reincorporated into the host DNA again during later infection, tumors can then be caused in rare cases. Although virus-related tumors are rare, research into them has made a decisive contribution to our understanding of oncogenes and their functioning.

A. Proto-oncogenes: biological role

The cellular form of oncogenes (known as c-oncogenes or proto-oncogenes) code for proteins involved in controlling growth and differentiation processes. They only become oncogenes if their sequence has been altered by mutations (see p. 256), deletions, and other processes, or when excessive amounts of the gene products have been produced as a result of overexpression.

Overexpression can occur when amplification leads to numerous functional copies of the respective gene, or when the gene falls under the influence of a highly active promoter (see p. 244). If the control of oncogene expression by tumor suppressor genes (see p. 394) is also disturbed, transformation and unregulated proliferation of the cells can occur. A single activated oncogene does not usually lead to a loss of growth control. It only occurs when over the course of time mutations and regulation defects accumulate in one and the same cell. If the immune system does not succeed in eliminating the transformed cell, it can over the course of months or years grow into a macroscopically visible tumor.

B. Oncogene products: biochemical functions

A feature common to all oncogenes is the fact that they code for proteins involved in signal transduction processes. The genes are designated using three-letter abbreviations that usually indicate the origin of the viral gene and are printed in italics (e.g., myc for myelocytomatosis, a viral disease in birds). Oncogene products can be classified into the following groups according to their functions.

1. Ligands such as growth factors and cytokines, which promote cell proliferation.
2. Membrane receptors of the 1-helix type with tyrosine kinase activity, which can bind growth factors and hormones (see p. 394).
3. GTP-binding proteins. This group includes the G proteins in the strict sense and related proteins such as Ras (see p. 388), the product of the oncogene c-ras.
4. Receptors for lipophilic hormones mediate the effects of steroid hormones and related signaling substances. They regulate the transcription of specific genes (see p. 378). The products of several oncogenes (e.g., erbA) belong to this superfamily of ligand-controlled transcription factors.
5. Nuclear tumor suppressors inhibit return to the cell cycle in fully differentiated cells. The genes that code for these proteins are referred to as anti-oncogenes due to this function. On the role of p53 and pRb, see p. 394.
6. DNA-binding proteins. A whole series of oncogenes code for transcription factors. Particularly important for cell proliferation are myc, as well as fos and jun. The protein products of the latter two genes form the transcription factor AP-1 as a heterodimer (see p. 244).
7. Protein kinases play a central role in intracellular signal transduction. By phosphorylating proteins, they bring about alterations in biological activity that can only be reversed again by the effects of protein phosphatases. The interplay between protein phosphorylation by protein kinases and dephosphorylation by protein phosphatases (interconversion) serves to regulate the cell cycle (see p. 394) and other important processes. The protein kinase Raf is also involved in the signal transduction of insulin (see p. 388).
A. Proto-oncogenes: biological role

B. Oncogene products: biochemical functions

- Ligands: sis, hst, int-2, wnt-1
- Receptors: fms, trk, int-2, mas, neu, erbB
- GTP-binding proteins: H-ras, N-ras, K-ras
- Nuclear hormone receptors: erbA, MIF-1
- Nuclear tumor suppressors: p53, wt1, DCC, APC
- DNA-binding proteins: jun, fos, myc, N-myc, mbl, fra1, egr-1, rel
- Protein kinases: src, yes, fak, abl, met, mos, rap

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Tumors

A. Division behavior of cells

The body's cells are normally subject to strict "social" control. They only divide until they come into contact with neighboring cells; cell division then ceases due to contact inhibition. Exceptions to this rule include embryonic cells, cells of the intestinal epithelium (where the cells are constantly being replaced), cells in the bone marrow (where formation of blood cells takes place), and tumor cells. Uncontrolled cell proliferation is an important indicator of the presence of a tumor. While normal cells in cell culture only divide 20–60 times, tumor cells are potentially immortal and are not subject to contact inhibition.

In medicine, a distinction is made between benign and malignant tumors. Benign tumors consist of slowly growing, largely differentiated cells. By contrast, malignant tumors show rapid, invasive growth and tend to form metastases (dissemination of daughter lesions). The approximately 100 different types of tumor that exist are responsible for more than 20% of deaths in Europe and North America.

B. Transformation

The transition of a normal cell into a tumor cell is referred to as transformation. Normal cells have all the characteristics of fully differentiated cells specialized for a particular function. Their division is inhibited and they are usually in the G0 phase of the cell cycle (see p. 394). Their external shape is variable and is determined by a strongly structured cytoskeleton.

In contrast, tumor cells divide without inhibition and are often de-differentiated—i.e., they have acquired some of the properties of embryonic cells. The surface of these cells is altered, and this is particularly evident in a disturbance of contact inhibition by neighboring cells. The cytoskeleton of tumor cells is also restructured and often reduced, giving them a rounded shape. The nuclei of tumor cells can be atypical in terms of shape, number, and size.

Tumor markers are clinically important for detecting certain tumors. These are proteins that are formed with increasing frequency by tumor cells (group 1) or are induced by them in other cells (group 2). Group 1 tumor markers include tumor-associated antigens, secreted hormones, and enzymes. The table lists a few examples.

The transition from a normal to a transformed state is a process involving several steps.

1. Tumor initiation. Almost every tumor begins with damage to the DNA of an individual cell. The genetic defect is almost always caused by environmental factors. These can include tumor-inducing chemicals (carcinogens—e.g., components of tar from tobacco), physical processes (e.g., UV light, X-ray radiation; see p. 256), or in rare cases tumor viruses (see p. 398). Most of the approximately 1014 cells in the human body probably suffer this type of DNA damage during the average lifespan, but it is usually repaired again (see p. 256). It is mainly defects in proto-oncogenes (see p. 398) that are relevant to tumor initiation; these are the decisive cause of transformation. Loss of an anti-oncogene (a tumor-suppressor gene) can also contribute to tumor initiation.

2. Tumor promotion is preferential proliferation of a cell damaged by transformation. It is a very slow process that can take many years. Certain substances are able to strongly accelerate it—e.g., phorbol esters. These occur in plants (e.g., Euphorbia species) and act as activators of protein kinase C (see p. 386).

3. Tumor progression finally leads to a macroscopically visible tumor as a result of growth. When solid tumors of this type exceed a certain size, they form their own vascular network that supplies them with blood (angiogenesis). Collagenases (matrix metalloproteinases, MMPs) play a special role in the metastatic process, by loosening surrounding connective tissue and thereby allowing tumor cells to disseminate and enter the bloodstream. New approaches to combating tumors have been aimed at influencing tumor angiogenesis and metastatic processes.
A. Division behavior of cells

- Growth inhibition due to contacts with adjacent cells
- Uncontrolled cell proliferation

Nutrient medium

Normal cells | Tumor cells

B. Transformation

Tumor initiators
- Viruses
- Carcinogenic chemicals
- Physical processes

Tumor promoters
- e.g. Esters of phorbol
- Hormones
- Phorbol

Tumor markers (examples)
- Tumor-associated antigens
  - CEA - Carcinoembryonic antigen
  - AFP - α-Fetoprotein
  - Hormones
  - Enzymes
  - Acid phosphatase

Tumor initiation: Genetic damage

Tumor progression: Preferential propagation

Tumor progression: Acquisition of malignancy

Normal cell

Interruptions:
- Differentiated
- Defined form

Indicators:
- De-differentiated
- Uncontrolled cell division
- Altered cell surface
- Altered cytoskeleton and nucleus

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Cytostatic drugs

Tumors (see p. 400) arise from degenerated (transformed) cells that grow in an uncontrolled way as a result of genetic defects. Most transformed cells are recognized by the immune system and eliminated (see p. 294). If endogenous defense is not sufficiently effective, rapid tumor growth can occur. Attempts are then made to inhibit growth by physical or chemical treatment.

A frequently used procedure is targeted irradiation with γ-rays, which block cell reproduction due to their mutagenic effect (see p. 256). Another approach is to inhibit cell growth by chemotherapy. The growth-inhibiting substances used are known as cytostatic drugs. Unfortunately, neither radiotherapy nor chemotherapy act selectively—i.e., they damage normal cells as well, and are therefore often associated with severe side effects.

Most cytostatic agents directly or indirectly inhibit DNA replication in the S phase of the cell cycle (see p. 394). The first group (A) leads to chemical changes in cellular DNA that impede transcription and replication. A second group of cytostatic agents (B) inhibit the synthesis of DNA precursors.

A. Alkylating agents, anthracyclines

Alkylating agents are compounds capable of reacting covalently with DNA bases. If a compound of this type contains two reactive groups, intramolecular or intermolecular crosslinking of the DNA double helix and “bending” of the double strand occurs. Examples of this type shown here are cyclophosphamide and the inorganic complex cisplatin. Anthracyclines such as doxorubicin (adriamycin) insert themselves non-covalently between the bases and thus lead to local alterations in the DNA structure (see p. 254 B).

B. Antimetabolites

Antimetabolites are enzyme inhibitors (see p. 96) that selectively block metabolic pathways. The majority of clinically important cytostatic drugs act on nucleotide biosynthesis. Many of these are modified nucleobases or nucleotides that competitively inhibit their target enzymes (see p. 96). Many are also incorporated into the DNA, thereby preventing replication.

The cytostatic drugs administered (indicated by a syringe in the illustration) are often not active themselves but are only converted into the actual active agent in the metabolism. This also applies to the adenine analogue 6-mercaptopurine, which is initially converted to the mononucleotide tIMP (thioguanine monophosphate). Via several intermediate steps, tIMP gives rise to tGTP, which is incorporated into the DNA and leads to cross-links and other anomalies in it. The second effective metabolite of 6-mercaptopurine is S-methylated tIMP, an inhibitor of amidophosphoribosyl transferase (see p. 188). Hydroxurea selectively inhibits ribonucleotide reductase (see p. 190). As a radical scavenger, it removes the tyrosine radicals that are indispensable for the functioning of the reductase.

Two other important cytostatic agents target the synthesis of DNA-typical thymine, which takes place at the level of the deoxynucleoside (see p. 190). The deoxynucleoside formed by 5-fluorouracil or the corresponding nucleoside inhibits thymidylate synthase. This inhibition is based on the fact that the fluorine atom in the pyrimidine ring cannot be substituted by a methyl group. In addition, the fluorine analogue is also incorporated into the DNA.

Dihydrofolate reductase acts as an auxiliary enzyme for thymidylate synthase. It is involved in the regeneration of the coenzyme N\textsuperscript{5},N\textsuperscript{10}-methylene-THF, initially reducing DHF to THF with NADPH as the reductant (see p. 418). The folate acid analogue methotrexate, a frequently used cytostatic agent, is an extremely effective competitive inhibitor of dihydrofolate reductase. It leads to the depletion of N\textsuperscript{5},N\textsuperscript{10}-methylene-THF in the cells and thus to cessation of DNA synthesis.

Further information

To reduce the side effects of cytostatic agents, new approaches are currently being developed on the basis of gene therapy (see p. 264). Attempts are being made, for example, to administer drugs in the form of precursors (known as produgs), which only become active in the tumor itself (“tumor targeting”).

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### A. Alkylating agents, anthracyclines

**Cyclophosphamide**

**Adriamycin**

**Cisplatin**

**5-fluorouracil**

**5-fluoro-2'-deoxyuridine**

**Hydroxyurea**

**5-fluorodeoxyuridine monophosphate**

**S-10-mercaptopurine**

**S-10-mercaptopurine ribonucleoside diphosphate reductase**

**Thymidylate synthase**

**Dihydrofolate reductase**

**Thiopurine methyltransferase**

**Hypoxanthine phosphoribosyltransferase**

**Amidophosphoribosyltransferase**

**Ribonucleoside diphosphate reductase**

**N5,N10-methylene-THF**

**Methotrexate**

**Thymidylate synthase**

**Dihydrofolate reductase**

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Viruses

Viruses are parasitic nucleoprotein complexes. They often consist of only a single nucleic acid molecule (DNA or RNA, never both) and a protein coat. Viruses have no metabolism of their own, and can therefore only replicate themselves with the help of host cells. They are therefore not regarded as independent organisms. Viruses that damage the host cell when they replicate are pathogens. Diseases caused by viruses include AIDS, rabies, polio-myelitis, measles, German measles, smallpox, influenza, and the common cold.

A. Viruses: examples

Only a few examples from the large number of known viruses are illustrated here. They are all shown on the same scale.

Viruses that only replicate in bacteria are known as bacteriophages (or “phages” for short). An example of a phage with a simple structure is M13. It consists of a single-stranded DNA molecule (ssDNA) of about 7000 bp with a coat made up of 2700 helically arranged protein subunits. The coat of a virus is referred to as a capsid, and the complete structure as a nucleocapsid. In genetic engineering, M13 is important as a vector for foreign DNA (see p. 258).

The phage T4 (bottom left), one of the largest viruses known, has a much more complex structure with around 170,000 base pairs (bp) of double-stranded DNA (dsDNA) contained within its “head.”

The tobacco mosaic virus (center right), a plant pathogen, has a structure similar to that of M13, but contains ssRNA instead of DNA. The poliovirus, which causes poliomyelitis, is also an RNA virus. In the influenza virus, the pathogen that causes viral flu, the nucleocapsid is additionally surrounded by a coat derived from the plasma membrane of the host cell (C). The coat carries viral proteins that are involved in the infection process.

B. Capsid of the rhinovirus

Rhinoviruses cause the common cold. In these viruses, the capsid is shaped like an icosahedron—i.e., an object made up of 20 equilateral triangles. Its surface is formed from three different proteins, which associate with one another to form pentamers and hexamers. In all, 60 protein molecules are involved in the structure of the capsid.

C. Life cycle of HIV

The human immunodeficiency virus (HIV) causes the immunodeficiency disease known as AIDS (acquired immune deficiency syndrome). The structure of this virus is similar to that of the influenza virus (A).

The HIV genome consists of two molecules of ssRNA (each 9.2 kb). It is enclosed by a double-layered capsid and a protein-containing coating membrane. HIV mainly infects T helper cells (see p. 294) and can thereby lead to failure of the immune system in the longer term.

During infection (1), the virus’s coating membrane fuses with the target cell’s plasma membrane, and the core of the nucleocapsid enters the cytoplasm (2). In the cytoplasm, the viral RNA is initially transcribed into an RNA/DNA hybrid (3) and then into dsDNA (4). Both of these reactions are catalyzed by reverse transcriptase, an enzyme deriving from the virus. The dsDNA formed is integrated into the host cell genome (5), where it can remain in an inactive state for a long time.

When viral replication occurs, the DNA segment corresponding to the viral genome is first transcribed by host cell enzymes (6). This gives rise not only to viral ssRNA, but also to transcription of mRNAs for precursors of the viral proteins (7). These precursors are integrated into the plasma membrane (8, 9) before undergoing proteolytic modification (10). The cycle is completed by the release of new virus particles (11).

The group of RNA viruses to which HIV belongs are called retroviruses, because DNA is produced from RNA in their replication cycle—the reverse of the usual direction of transcription (DNA → RNA).
A. Viruses: examples

1. Bacteriophages

- Phage M13: ssDNA 7 kb, Helical Coat
- T4-Phage: dsDNA 170 kbp, complex structure
- Helical

2. Plant and animal pathogenic viruses

- Influenza virus: ssRNA (8 molecules) 3.6 kb, Nucleocapsid with coat
- Helical

- Tobacco mosaic virus: ssRNA 6.4 kb, Helical

- Poliovirus: ssRNA 7 kb, Eicosahedral capsid

B. Capsid of the rhinovirus

1. Structure

- Pentamer
- Hexamer
- Eicosahedron of 180 monomers

2. Diagram

C. Life cycle of the human immunodeficiency virus (HIV)

1. Infection

2. Reverse transcriptase

3. Ribonuclease H

4. Viral RNA

5. Translation

6. Transcription

7. mRNA

8. Viral RNA

9. Precursors of core proteins and enzymes

10. Mature virus particle

11. Reverse transcriptase

12. Ribonuclease H

13. gp120

14. Core

15. Membrane

16. Other enzymes

17. Nucleus

18. Host DNA

19. Cytoplasm

20. Nucleus

21. Host DNA

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Metabolic charts

Explanations

The following 13 plates (pp. 407–419) provide a concise schematic overview of the most important metabolic pathways. Explanatory text is deliberately omitted from them.

These "charts":

- Contain details of metabolic pathways that are only shown in outline in the main text for reasons of space. This applies in particular to the synthesis and degradation of the amino acids and nucleotides, and for some aspects of carbohydrate and lipid metabolism.
- Offer a quick overview of a specific pathway, the metabolites that arise in it, and the enzymes involved.
- Can be used for reference purposes and for revising material previously learned.

The most important intermediates are shown with numbers in the charts. The corresponding compounds can be identified using the table on the same page.

In addition, at each step the four-figure EC number (see p. 88) for the enzyme responsible for a reaction is given in italics. The enzyme name and its systematic classification in the system used by the Enzyme Catalogue are available in the following annotated enzyme list (pp. 420–430), in which all of the enzymes mentioned in this book are listed according to their EC number. The book’s index is helpful when looking for a specific enzyme in the text.

In reactions that involve coenzymes, the coenzyme names are also given (sometimes in simplified form). Particularly important starting, intermediate, or end products are given with the full name, or as formulae.

Example

On p. 407, the initial step of the dark reactions in plant photosynthesis (in the Calvin cycle) is shown at the top left.

In this reaction, one molecule of ribulose-1,5-bisphosphate (metabolite 1) and one molecule of CO₂ (metabolite 2) give rise to two molecules of 3-phosphoglycerate (metabolite 3). The enzyme responsible has the EC number 4.1.1.39. The annotated enzyme list shows that this refers to ribulose bisphosphate carboxylase ("rubisco" for short). Rubisco belongs to enzyme class 4 (the lyases) and, within that group, to subclass 4.1 (the carboxy-lyases). It contains copper as a cofactor ([Cu]).
A. Carbohydrate metabolism

1. Glycogen
2. UDP-Glucose
3. Glucose 1-phosphate
4. Glucose
5. Glucose 6-phosphate
6. Gluconolactone 6-
7. Gluconate 6-phosphate
8. Ribulose 5-phosphate
9. Ribose 5-phosphate
10. Xylulose 5-phosphate
11. Sedoheptulose 7-phosphate
12. Glyceraldehyde 3-phosphate
13. Erythrose 4-phosphate
14. Fructose 6-phosphate
15. Fructose 1,6-bisphosphate
16. Glycerone-3-phosphate
17. 1,3-Bisphosphoglycerate
18. 3-Phosphoglycerate
19. 2-Phosphoglycerate
20. Phosphoenolpyruvate
21. Pyruvate
22. Lactate
23. Glycerol
24. Glycerol 3-phosphate

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A. Synthesis of ketone bodies and steroids

1. Pyruvate
2. Acetyl CoA
3. 3-Hydroxy-3-methylglutaryl CoA
4. Acetoacetate
5. Acetoacetate
6. 3-Hydroxybutyrate
7. Palmitate
8. Palmitoyl CoA
9. Stearoyl CoA
10. Oleyl CoA
11. Mevalonate
12. Mevalonate 5-diphosphate
13. Isopentenyl diphosphate
14. Geranyl diphosphate
15. Farnesyl diphosphate
16. Squalene
17. Cholesterol
18. pregnenolone
19. 17-OH-Pregnenolone
20. Dehydroepiandrosterone
21. Androstene-3,17-dione
22. Testosterone
23. Estradiol
24. Progesterone
25. 17-OH-Progesterone
26. 11-Deoxycortisol
27. Cortisol
28. 11-Deoxy corticosterone
29. Aldosterone

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A. Degradation of fats and phospholipids

1. Triacylglycerol
2. Diaclylglycerol
3. Monoacylglycerol
4. Glycerol
5. Glycerol 3-phosphate
6. Glycerone 3-phosphate
7. Phospholipid
8. Free fatty acid
9. Acyl CoA
10. Shortened acyl CoA
11. Acyl carnitine
12. 2,3-Dehydroacyl CoA
13. 3-Hydroxyacyl CoA
14. 3-Oxoacyl CoA
15. Acetyl CoA
16. Propionyl CoA
17. (S)-Methylmalonyl CoA
18. (R)-Methylmalonyl CoA
19. Succinyl CoA

From uneven-numbered fatty acids

Phospholipases
A1 3.1.1.32
A2 3.1.1.4
C 3.1.4.3
D 3.1.4.4

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A. Biosynthesis of the essential amino acids

1. Pyruvate
2. 2-Oxobutyrate
3. 2-Aceto-2-hydroxybutyrate
4. 2-Oxo-4-methylvalerate
5. 2-Acetolactate
6. 2-Oxoisovalerate
7. 2-Oxoisocaproate
8. Phosphoribosyl diphosphate
9. Aspartate
10. Aspartyl 4-phosphate
11. Aspartate 4-semialdehyde
12. Homoserine
13. Phosphohomoserine
14. Phosphoenolpyruvate
15. Erythrose 4-phosphate
16. 2-Oxo-3-deoxyarabinohexulosonate 7-phosphate
17. Chorismate
18. Phenylpyruvate
19. Anthranilate
20. N-(Phosphoribosyl)anthranilate

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A. Biosynthesis of the non-essential amino acids

1. 3-Phosphoglycerate
2. 3-Phosphohydroxybutyrate
3. 3-Phosphoserine
4. Glycine
5. Cystathionine
6. Homocysteine
7. 2-Oxobutyrate
8. Pyruvate
9. Oxaloacetate
10. Aspartate
11. Asparagine
12. 2-Oxoglutarate
13. Glutamate
14. γ-Glutamyl phosphate
15. Δ1-Pyrroline-5-carboxylate
16. N-Acetylglutamate
17. N-Acetylglutamate 5-phosphate
18. N-Acetylglutamate semialdehyde
19. N-Acetylmethionine
20. Ornithine
21. Arginine
A. Amino acid degradation II

1. 5-Adenosylmethionine
2. Homocysteine
3. Cystathionine
4. 2-Oxobutyrate
5. Propionyl CoA
6. Succinyl CoA
7. Fumarate
8. Aspartate
9. Acetyl CoA
10. Oxaloacetate
11. Cysteine sulfinic acid
12. 3-Sulfinylpyruvate
13. 2-Oxoadipate
14. Crotonyl CoA
15. 4-Hydroxyphenylpyruvate
16. Homogentisate
17. Pyruvate
18. ATP
19. Serine
20. Adenosine
21. [CH3]
22. H2O
23. SO2
24. OG
25. O2
26. Glu
27. NADH
28. NAD
29. NADP
30. NADPH
31. Glutamate
32. Ascorbate
33. Dehydroascorbate
34. Tryptophan
35. Lysine
36. CO2
37. H2O
38. 4-Maleylacetoacetate
39. Fumarylacetoacetate
40. Homogentisate
41. Acetoacetate
42. Glutamate 4-semialdehyde
43. Ornithine
44. 2-Oxoglutarate
45. ATP

Non-enzymatic reaction

β-Oxidation

Tricarboxylic acid cycle

[CH3]
A. Ammonia metabolism

Nitrogen donor in synthesis of purine bases, cytosine, GlcNAc, His, and Trp

Neutral, non-toxic Urea

Kidney

Pyruvate 2-Oxoglutarate Oxaloacetate Carboxamidopropyl phosphate Malate

Fumarate Ornithine Citrulline Argininosuccinate Arginine
A. Biosynthesis of purine nucleotides

1. Ribose 5-phosphate
2. Phosphoribosyl diphosphate (PRPP)
3. PR-amine
4. PR-glycineamide
5. PR-formylglycine-amidine
6. PR-formylglycine-amidine
7. PR-5-aminoimidazole
8. PR-4-carboxy-5-aminoimidazole
9. PR-5-amino-4-imidazolecarboxamide
10. PR-5-formamidinoimidazole-4-carboxamide
11. Inosine 5’-monophosphate
12. Adenylosuccinic acid

PR = 5’-Phosphoribosyl-
A. Biosynthesis of the pyrimidine nucleotides and C₃ metabolism

1. HCO₃⁻
2. Carboxylase
3. Carbamoyl aspartate
4. Dihydroorotate
5. Orotate
6. Phosphoribosyl diphosphate
7. Orotate 5'-monophosphate

---

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A. Nucleotide degradation

1. Hypoxanthine (Hyp)
2. Xanthine (Xan)
3. Allantoin
4. Allantoic acid
5. Glyoxylate
6. Urea
7. Dihydrothymine
8. Carbamoyl-β-aminoisobutyrate
9. β-Aminoisobutyrate
10. 2-Methyl-3-oxopropionate
11. Dihydouracil
12. Carboxamyl-β-alanine
13. β-alanine
14. 3-oxopropionate
Annotated enzyme list

Only the enzymes mentioned in this atlas are listed here, from among the more than 2000 enzymes known. The enzyme names are based on the IUBMB’s official Enzyme nomenclature 1992. The additions shown in round brackets belong to the enzyme name, while prosthetic groups and other cofactors are enclosed in square brackets. Common names of enzyme groups are given in italics, and trivial names are shown in quotation marks.

Class 1: Oxidoreductases (catalyze reduction-oxidation reactions)

Subclass 1.n: What is the electron donor?
Sub-subclass 1.n.n: What is the electron acceptor?

1.1 A –CH–OH group is the donor

1.1.1 NAD(P)⁺ is the acceptor (dehydrogenases, reductases)

1.1.1.1 Alcohol dehydrogenase [Zn⁺]

1.1.1.3 Homoserine dehydrogenase

1.1.1.8 Glycerol 3-phosphate dehydrogenase (NAD⁺)

1.1.1.21 Aldehyde reductase

1.1.1.27 Lactate dehydrogenase

1.1.1.30 3-Hydroxybutyrate dehydrogenase

1.1.1.31 3-Hydroxyisobutyrate dehydrogenase

1.1.1.34 Hydroxymethylglutaryl-CoA reductase (NADPH)

1.1.1.35 3-Hydroxyacyl-CoA dehydrogenase

1.1.1.37 Malate dehydrogenase

1.1.1.40 Malate dehydrogenase (oxaloacetate-decarboxylating, NADP⁺)—“malic enzyme”

1.1.1.41 Isocitrate dehydrogenase (NAD⁺)

1.1.1.42 Isocitrate dehydrogenase (NADP⁺)

1.1.1.44 Phosphogluconate dehydrogenase (decarboxylating)

1.1.1.49 Glucose 6-phosphate 1-dehydrogenase

1.1.1.51 3-(or 17β)-Hydroxysteroid dehydrogenase

1.1.1.95 Phosphoglycerate dehydrogenase

1.1.1.100 3-Oxoacyl-[ACP] reductase

1.1.1.101 Acylglycerone phosphate reductase

1.1.1.105 Retinol dehydrogenase

1.1.1.145 3β-Hydroxy-delta-steroid dehydrogenase

1.1.1.205 IMP dehydrogenase

1.1.3 Molecular oxygen is the acceptor (oxidases)

1.1.3.4 Glucose oxidase [FAD]

1.1.3.8 L-Gulonolactone oxidase

1.1.3.22 Xanthine oxidase [Fe, Mo, FAD]

1.1.99.5 Glycero1-3-phosphate dehydrogenase (FAD)

1.2 An aldehyde or keto group is the donor

1.2.1 NAD(P)⁺ is the acceptor (dehydrogenases)

1.2.1.3 Aldehyde dehydrogenase (NAD⁺)

1.2.1.11 Aspartate semialdehyde dehydrogenase

1.2.1.12 Glyceraldehyde 3-phosphate dehydrogenase

1.2.1.13 Glyceraldehyde 3-phosphate dehydrogenase (NADP⁺) (phosphorylating)

1.2.1.24 Succinate semialdehyde dehydrogenase

1.2.1.25 2-Oxoisovalerate dehydrogenase (acylating)

1.2.1.38 N-Acetyl-γ-glutamylphosphate reductase

1.2.4.1 Glutamylphosphate reductase
1.2.4 A disulfide is the acceptor
1.2.4.1 Pyruvate dehydrogenase (lipoamide) [TPP]
1.2.4.2 Oxoglutarate dehydrogenase (lipoamide) [TPP]

1.2.7 An Fe/S protein is the acceptor
1.2.7.2 2-Oxobutyrate synthase

1.3 A –CH–CH– group is the donor
1.3.1.10 Enoyl-[ACP] reductase (NADPH)
1.3.1.24 Biliverdin reductase
1.3.1.34 2,4-Dienoyl-CoA reductase
1.3.5.1 Succinate dehydrogenase (ubiquinone) [FAD, Fe,S₂, Fe,S₄]; “complex II”
1.3.99.3 Acyl-CoA dehydrogenase [FAD]
1.3.99.11 Dihydroorotate dehydrogenase [FMN]

1.4 A –CH-NH₂ group is the donor
1.4.1.2 Glutamate dehydrogenase
1.4.3.4 Amine oxidase [FAD], “monoamine oxidase (MAO)”
1.4.3.13 Protein lysine 6-oxidase [Cu]
1.4.4.2 Glycine dehydrogenase (decarboxylating) [PLP]

1.5 A –CH-NH group is the donor
1.5.1.2 Pyrrole-5-carboxylate reductase
1.5.1.3 Dihydrofolate reductase
1.5.1.5 Methylenetetrahydrofolate dehydrogenase (NADP⁺)
1.5.1.12 1-Pyrrole-5-carboxylate dehydrogenase
1.5.1.20 Methylenetetrahydrofolate reductase (NADPH) [FAD]
1.5.1.5 Electron-transfering flavoprotein (ETF) dehydrogenase [Fe,S₄]
1.5.99.8 Proline dehydrogenase [FAD]

1.6 NAD(P)H is the donor
1.6.4.2 Glutathione reductase (NADPH) [FAD]
1.6.4.5 Thioredoxin reductase (NADPH) [FAD]
1.6.5.3 NADH dehydrogenase (ubiquinone) [FAD, Fe,S₂, Fe,S₄]; “complex I”

1.8 A sulfur group is the donor
1.8.1.4 Dihydriodiolamine dehydrogenase [FAD]

1.9 A heme group is the donor
1.9.3.1 Cytochrome c oxidase [heme, Cu, Zn] – “cytochrome oxidase,” “complex IV”

1.10 A diphenol is the donor
1.10.2.2 Ubiquinol cytochrome c reductase [heme, Fe,S₂, Fe,S₄]; “complex III”

1.11 A peroxide is the acceptor (peroxidases)
1.11.1.6 Catalase [heme]
1.11.1.7 Peroxidase [heme]
1.11.1.12 Lipid hydroperoxide glutathione peroxidase [Se]

1.13 Molecular oxygen is incorporated into the electron donor (oxygenases)
1.13.11 One donor, both O atoms are incorporated (dioxygenases)
1.13.11.5 Homogentisate 1,2-dioxygenase [Fe]
1.13.11.20 Cysteine dioxygenase [Fe]
1.13.11.27 4-Hydroxyphenylpyruvate dioxygenase [ascorbate]
1.13.11.n Arachidonate lipooxygenases

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Annotated enzyme list

1.4 Two donors, one O atom is incorporated into both \( \text{monooxygenases, hydroxylases} \)
1.4.1.2 Procollagen proline 4-dioxygenase [Fe, ascorbate]—“proline hydroxylase”
1.4.1.4 Procollagen lysine 5-dioxygenase [Fe, ascorbate]—“lysine hydroxylase”
1.4.13.13 C provocative 1-monoxygenase [heme]
1.4.15.4 Steroid 11ß-monoxygenase [heme]
1.4.15.6 Cholesterol monoxygenase (side-chain-cleaving) [heme]
1.4.16.1 Phenylalanine 4-monoxygenase [Fe, tetrahydrobiopterin]
1.4.16.2 Tyrosine 3-monoxygenase [Fe, tetrahydrobiopterin]
1.4.17.1 Dopamine 3ß-monoxygenase [Cu]
1.4.99.1 Prostaglandin H-synthase [heme]
1.4.99.3 Heme oxygenase (decycling) [heme]
1.4.99.5 Stearyl-CoA desaturase [heme]
1.4.99.9 Steroid 17ß-monoxygenase [heme]
1.4.99.10 Steroid 21-monoxygenase [heme]
1.5 A superoxide radical is the acceptor
1.5.1.1 Superoxide dismutase
1.7 A –CH\(_2\) group is the donor
1.7.4.1 Ribonucleoside diphosphate reductase [Fe]—“ribonucleotide reductase”
1.8 Reduced ferredoxin is the donor
1.8.1.2 Ferredoxin-NAD\(^{+}\) reductase [FAD]
1.8.6.1 Nitrogenase [Fe, Mo, Fe\(_{\text{d}}\)]

Class 2: Transferases (catalyze the transfer of groups from one molecule to another)

Subclass 2.a: Which group is transferred?

2.1 A C\(_1\) group is transferred

2.1.1 A methyl group
2.1.1.2 Guanidinoacetate N-methyltransferase
2.1.1.6 Catechol O-methyltransferase
2.1.1.13 5-Methyltetrahydrofolate-homocysteine 5-methyltransferase
2.1.1.28 Phenylethanolamine N-methyltransferase
2.1.1.45 Thymidylate synthase
2.1.1.67 Thiourimine methyltransferase

2.1.2 A formyl group
2.1.2.1 Glycine hydroxymethyltransferase [PLP]
2.1.2.2 Phosphoribosylglycinamide formyltransferase
2.1.2.3 Phosphoribosylaminomimidazolecarboxamid formyltransferase
2.1.2.5 Glutamate formimino transferase [PLP]
2.1.2.10 Aminomethyltransferase

2.1.3 A carbamoyl group
2.1.3.2 Aspartate carbamoyltransferase [Zn\(^{2+}\)]
2.1.3.3 Ornithine carbamoyltransferase

2.1.4 An amidino group
2.1.4.1 Glycine amidinotransferase

2.2 An aldehyde or ketone residue is transferred
2.2.1.1 Transketolase [TPP]
2.2.1.2 Transaldolase

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2.3 An acyl group is transferred

2.3.1 With acyl-CoA as donor

2.3.1.1 Amino acid N-acyltransferase

2.3.1.2 Choline O-acyltransferase

2.3.1.12 Dihydrolipoamide acetyltransferase [lipoamide]

2.3.1.15 Glycerol 3-phosphate O-acyltransferase

2.3.1.16 Acetyl-CoA acetyltransferase

2.3.1.20 Diacylglycerol O-acyltransferase

2.3.1.21 Carnitine O-palmitoyltransferase

2.3.1.22 Acylglycerol O-palmitoyltransferase

2.3.1.24 Sphingosine N-acyltransferase

2.3.1.37 3-Aminolevulinate synthase [PLP]

2.3.1.38 [ACP] S-acyltransferase

2.3.1.39 [ACP] S-malonyltransferase

2.3.1.41 3-Oxoadyl-[ACP] synthase

2.3.1.42 Glycerone phosphate O-acyltransferase

2.3.1.43 Phosphatidylcholine-sterol acyltransferase—“lecithin-cholesterol acyltransferase (LCAT)"

2.3.1.51 Acylglycerol-3-phosphate O-acyltransferase

2.3.1.61 Dihydrolipoamide succinyltransferase

2.3.1.85 Fatty-acid synthase

2.3.2 An aminoacyl group is transferred

2.3.2.2 γ-glutamyltransferase

2.3.2.12 Peptidyltransferase (a ribozyme)

2.3.2.13 Protein-glutamine γ-glutamyltransferase [Ca]—“fibrin-stabilizing factor”

2.4 A glycosyl group is transferred

2.4.1 A hexose residue

2.4.1.1 Phosphorylase [PLP]—“glycogen (starch) phosphorylase”

2.4.1.11 Glycogen (starch) synthase

2.4.1.17 Glucuronosyltransferase

2.4.1.18 1,4-α-Glucan branching enzyme

2.4.1.25 4-α-Glucanotransferase

2.4.1.47 N-Acylsphingosine galactosyltransferase

2.4.1.119 Protein glycosyltransferase

2.4.2 A pentose residue

2.4.2.7 Adenine phosphoribosyltransferase

2.4.2.8 Hypoxanthine phosphoribosyltransferase

2.4.2.10 Orotate phosphoribosyltransferase

2.4.2.14 Amimidophosphoribosyl transferase

2.5 An alkyl or aryl group is transferred

2.5.1.1 Dimethylallyltransferase

2.5.1.6 Methionine adenosyltransferase

2.5.1.10 Geranyltransferase

2.5.1.21 Farnesyldiphosphate farnesyltransferase

2.6 A nitrogen-containing group is transferred

2.6.1 An amino group (transaminases)

2.6.1.1 Aspartate transaminase [PLP]—“GOT”

2.6.1.2 Alanine transaminase [PLP]—“GPT”
<table>
<thead>
<tr>
<th>Enzyme Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cysteine transaminase [PLP]</td>
<td></td>
</tr>
<tr>
<td>Tyrosine transaminase [PLP]</td>
<td></td>
</tr>
<tr>
<td>Leucine transaminase [PLP]</td>
<td></td>
</tr>
<tr>
<td>Acetyloinithione transaminase [PLP]</td>
<td></td>
</tr>
<tr>
<td>Ornithine transaminase [PLP]</td>
<td></td>
</tr>
<tr>
<td>4-Aminobutyrate transaminase [PLP]</td>
<td></td>
</tr>
<tr>
<td>Branched-chain amino acid transaminase [PLP]</td>
<td></td>
</tr>
<tr>
<td>Phosphoserine transaminase [PLP]</td>
<td></td>
</tr>
</tbody>
</table>

2.7 **A phosphorus-containing group is transferred** *(kinases)*

2.7.1 **With –OH–OH as acceptor**

<table>
<thead>
<tr>
<th>Enzyme Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hexokinase</td>
<td></td>
</tr>
<tr>
<td>Ketohexokinase</td>
<td></td>
</tr>
<tr>
<td>Galactokinase</td>
<td></td>
</tr>
<tr>
<td>6-Phosphofructokinase</td>
<td></td>
</tr>
<tr>
<td>Phosphoribulokinase</td>
<td></td>
</tr>
<tr>
<td>Triokinase (triosekinase)</td>
<td></td>
</tr>
<tr>
<td>Glycerol kinase</td>
<td></td>
</tr>
<tr>
<td>Choline kinase</td>
<td></td>
</tr>
<tr>
<td>Mevalonate kinase</td>
<td></td>
</tr>
<tr>
<td>Protein kinase</td>
<td></td>
</tr>
<tr>
<td>Phosphorylase kinase</td>
<td></td>
</tr>
<tr>
<td>Homoserine kinase</td>
<td></td>
</tr>
<tr>
<td>Pyruvate kinase</td>
<td></td>
</tr>
<tr>
<td>1-Phosphatidylinositol-4-kinase</td>
<td></td>
</tr>
<tr>
<td>1-Phosphatidylinositol 4-phosphate kinase</td>
<td></td>
</tr>
<tr>
<td>Ethanolamine kinase</td>
<td></td>
</tr>
<tr>
<td>[Pyruvate dehydrogenase] kinase</td>
<td></td>
</tr>
<tr>
<td>6-Phosphofructo-2-kinase</td>
<td></td>
</tr>
<tr>
<td>Protein tyrosine kinase</td>
<td></td>
</tr>
</tbody>
</table>

2.7.2 **With –CO–OH as acceptor**

<table>
<thead>
<tr>
<th>Enzyme Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phosphoglycerate kinase</td>
<td></td>
</tr>
<tr>
<td>Aspartate kinase</td>
<td></td>
</tr>
<tr>
<td>Acetylglutamate kinase</td>
<td></td>
</tr>
<tr>
<td>Glutamate 5-kinase</td>
<td></td>
</tr>
</tbody>
</table>

2.7.3 **With a nitrogen-containing group as acceptor**

<table>
<thead>
<tr>
<th>Enzyme Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Creatine kinase</td>
<td></td>
</tr>
</tbody>
</table>

2.7.4 **With a phosphate group as acceptor**

<table>
<thead>
<tr>
<th>Enzyme Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phosphomevalonate kinase</td>
<td></td>
</tr>
<tr>
<td>Adenylyl kinase</td>
<td></td>
</tr>
<tr>
<td>Nucleoside phosphate kinase</td>
<td></td>
</tr>
<tr>
<td>Nucleoside diphosphate kinase</td>
<td></td>
</tr>
</tbody>
</table>

2.7.6 **A diphosphate residue is transferred**

<table>
<thead>
<tr>
<th>Enzyme Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ribose phosphate pyrophosphokinase</td>
<td></td>
</tr>
</tbody>
</table>

2.7.7 **A nucleotide is transferred**

<table>
<thead>
<tr>
<th>Enzyme Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DNA-directed RNA polymerase—&quot;RNA polymerase&quot;</td>
<td></td>
</tr>
<tr>
<td>DNA-directed DNA polymerase—&quot;DNA polymerase&quot;</td>
<td></td>
</tr>
<tr>
<td>UTP-glucose-1-phosphate uridylytransferase</td>
<td></td>
</tr>
<tr>
<td>Hexose-1-phosphate uridylytransferase</td>
<td></td>
</tr>
<tr>
<td>Ethanolamine phosphate cytidylytransferase</td>
<td></td>
</tr>
</tbody>
</table>

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2.7.7.15 Choline phosphate cytidylyltransferase
2.7.7.41 Phosphatidate cytidylyltransferase
2.7.7.49 RNA-directed DNA polymerase—"reverse transcriptase"

2.7.8 Another substituted phosphate is transferred
2.7.8.1 Ethanolaminephosphotransferase
2.7.8.2 Diacylglycerol cholinephosphotransferase
2.7.8.11 CDP-diacylglycerol-inositol 3-phosphatidylyltransferase
2.7.8.16 1-Alkyl-2-acetylglycerol cholinephosphotransferase
2.7.8.17 N-Acetylgalactosaminephosphotransferase

Class 3: Hydrolases (catalyze bond cleavage by hydrolysis)

Subclass 3.n: What kind of bond is hydrolyzed?

3.1 An ester bond is hydrolyzed (esterases)

3.1.1 In carboxylic acid esters
3.1.1.2 Arylesterase
3.1.1.3 Triacylglycerol lipase
3.1.1.4 Phospholipase A₂
3.1.1.7 Acylcholesterase
3.1.1.13 Cholesterol esterase
3.1.1.17 Glucorolactonase
3.1.1.32 Phospholipase A₁
3.1.1.34 Lipoprotein lipase, diacylglycerol lipase

3.1.2 In thioesters 3.1.2.4 3-Hydroxyisobutryl-CoA hydrolase
3.1.2.14 Acyl-[ACP] hydrolase

3.1.3 In phosphoric acid monoesters (phosphatases)
3.1.3.1 Alkaline phosphatase [Zn²⁺]
3.1.3.2 Acid phosphatase
3.1.3.4 Phosphatidate phosphatase
3.1.3.9 Glucose 6-phosphatase
3.1.3.11 Fructose bisphosphatase
3.1.3.13 Bisphosphoglycerate phosphatase
3.1.3.16 Phosphoprotein phosphatase
3.1.3.37 Sedoheptulose bisphosphatase
3.1.3.43 [Pyrurate dehydrogenase] phosphatase
3.1.3.46 Fructose-2,6-bisphosphatase
3.1.3.n Polynucleotidases

3.1.4 In phosphoric acid diesters (phosphodiesterases)
3.1.4.1 Phosphodiesterase
3.1.4.3 Phospholipase C
3.1.4.4 Phospholipase D
3.1.4.17 3’:5’-cCMP phosphodiesterase
3.1.4.35 3’:5’-cGMP phosphodiesterase
3.1.4.45 N-Acetylglucosaminyl phosphodiesterase

3.1.21 In DNA
3.1.21.1 Deoxyribonuclease I
3.1.21.4 Site-specific deoxyribonuclease (type II)—"restriction endonuclease"

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### Annoted enzyme list

<table>
<thead>
<tr>
<th>Enzyme ID</th>
<th>Enzyme Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>3.10.26–7</td>
<td>In RNA</td>
</tr>
<tr>
<td>3.12.6.4</td>
<td>Ribonuclease H</td>
</tr>
<tr>
<td>3.12.7.5</td>
<td>Pancreatic ribonuclease</td>
</tr>
<tr>
<td>3.2</td>
<td>A glycosidic bond is hydrolyzed (glycosidases)</td>
</tr>
<tr>
<td>3.2.1</td>
<td>In O-glycosides</td>
</tr>
<tr>
<td>3.2.1.1</td>
<td>α-Amylase</td>
</tr>
<tr>
<td>3.2.1.10</td>
<td>Oligo-1,6-glucosidase</td>
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<tr>
<td>3.2.1.17</td>
<td>Lysozyme</td>
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<td>3.2.1.18</td>
<td>Neuraminidase</td>
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<td>3.2.1.20</td>
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<td>β-Galactosidase</td>
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<td>α-Mannosidase</td>
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<td>3.2.1.26</td>
<td>β-Fructofuranosidase—“saccharase,” “invertase”</td>
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<td>3.2.1.28</td>
<td>α,α-Trehalase</td>
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<td>3.2.1.33</td>
<td>Amylo-1,6-glucosidase</td>
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<td>Sucrose α-glucosidase</td>
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<td>3.3</td>
<td>An ether bond is hydrolyzed</td>
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<td>3.3.1.1</td>
<td>Adenosylhomocysteinase</td>
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<td>3.4</td>
<td>A peptide bond is hydrolyzed (peptidases)</td>
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<td>3.4.4.11</td>
<td>Aminopeptidases (N-terminal exopeptidases)</td>
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<td>3.4.4.11.n</td>
<td>Various aminopeptidases [Zn²⁺]</td>
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<td>3.4.4.13</td>
<td>Dipeptidases (act on dipeptides only)</td>
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<td>3.4.4.13.n</td>
<td>Various dipeptidases [Zn²⁺]</td>
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<td>3.4.4.15</td>
<td>Peptidyl dipeptidases (C-terminal exopeptidases, releasing dipeptides)</td>
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<td>3.4.4.15.1</td>
<td>Peptidyl-dipeptidase A [Zn²⁺]—“angiotensin-converting enzyme (ACE)”</td>
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<td>Carboxypeptidases (C-terminal exopeptidases)</td>
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<td>Carboxypeptidase A [Zn²⁺]</td>
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<td>Carboxypeptidase B [Zn²⁺]</td>
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<td>Muramoylpentapeptide carboxypeptidase</td>
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<td>Serine proteinases (endopeptidases)</td>
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<td>Coagulation factor Xα—“Stuart–Prower factor”</td>
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<td>3.4.2.19</td>
<td>Enteropeptidase—“enterokinase”</td>
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<td>Coagulation factor VIIα—“proconvertin”</td>
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<td>3.4.2.22</td>
<td>Coagulation factor IXα—“Christmas factor”</td>
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<td>Coagulation factor Xα—“plasma thromboplastin antecedent”</td>
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<td>3.4.2.35</td>
<td>Tissue kalikrein</td>
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<td>3.4.2.36</td>
<td>Elastase</td>
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<td>3.4.2.38</td>
<td>Coagulation factor XIIα—“Hageman factor”</td>
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<td>C3/C5 convertase (complement—classical pathway)</td>
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<td>3.4.2.47</td>
<td>C3/C5 convertase (complement—alternative pathway)</td>
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</table>
Annotated enzyme list

3.4.21.68  Plasminogen activator (tissue)—“tissue plasminogen activator (t-PA)”
3.4.21.73  Plasminogen activator (urine)—“urokinase”

3.4.22  Cysteine proteinases (endopeptidases)
3.4.22.2  Papain

3.4.23  Aspartate proteinases (endopeptidases)
3.4.23.1  Pepsin A
3.4.23.2  Pepsin B
3.4.23.3  Gastricin (pepsin C)
3.4.23.4  Chymosin
3.4.23.15  Renin

3.4.24  Metalloproteinases (endopeptidases)
3.4.24.7  Collagenase

3.4.99  Other peptidases
3.4.99.36  Signal peptidase

3.5  Another amide bond is hydrolyzed (amidases)
3.5.1.1  Asparaginase
3.5.1.2  Glutaminase
3.5.1.16  Acetylornithine deacetylase [Zn++]
3.5.2.3  Dihydroorotase
3.5.2.7  Imidazolonepropionase
3.5.3.1  Arginase
3.5.4.6  AMP deaminase
3.5.4.9  Methylenetetrahydrofolate cyclohydrolase
3.5.4.10  IMP cyclohydrolase

3.6  An anhydride bond is hydrolyzed
3.6.1.6  Nucleoside diphosphatase
3.6.1.32  Myosin ATPase
3.6.1.34  H+-transporting ATP synthase—“ATP synthase;” “complex V”
3.6.1.35  H+-transporting ATPase
3.6.1.36  H+/K+-exchanging ATPase
3.6.1.37  Na+/K+-exchanging ATPase—“Na+/K+-ATPase”
3.6.1.38  Ca2+-transporting ATPase

3.7  A C-C bond is hydrolyzed
3.7.1.2  Fumarilacetacetase

Class 4: Lyases (cleave or form bonds without oxidative or hydrolytic steps)

Subclass 4.n: What kind of bond is formed or cleaved?

4.1  A C-C bond is formed or cleaved

4.1.1  Carboxy-lyases (carboxylases, decarboxylases)
4.1.1.1  Pyruvate decarboxylase [TPP]
4.1.1.15  Glutamate decarboxylase [PLP]
4.1.1.21  Phosphoribosylaminomimidazole carboxylase
4.1.1.23  Orotidine-5’-phosphate decarboxylase
4.1.1.28  Aromatic L-amino acid decarboxylase [PLP]
4.1.1.32  Phosphoenolpyruvate carboxykinase (GTP)
4.1.1.39  Ribulose bisphosphate carboxylase [Cu]—“rubisco”

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Annotated enzyme list

4.1.2 Acting on aldehydes or ketones
4.1.2.5 Threonine aldolase [PLP]
4.1.3.4 Hydroxymethylglutaryl-CoA lyase
4.1.3.5 Hydroxymethylglutaryl-CoA synthase
4.1.3.7 Citrate synthase
4.1.3.8 ATP-citrate lyase
4.1.3.18 Acetolactate synthase [TPP, flavin]

4.1.99 Other C–C lyases
4.1.99.3 Deoxyribofibririmidine photolyase [FAD]—“photolyase”

4.2 A C–O bond is formed or cleaved

4.2.1 Hydrolyases (hydratases, dehydratases)
4.2.1.1 Carbonate dehydratase [Zn2+]—“carbonic anhydrase”
4.2.1.2 Fumarate hydratase—“fumarase”
4.2.1.3 Aconitate hydratase [Fe;S4]—“aconitase”
4.2.1.11 Phosphopyruvate hydratase—“enolase”
4.2.1.13 Serine dehydratase
4.2.1.17 Enol-CoA hydratase
4.2.1.18 Methylglutaryl-CoA hydratase
4.2.1.22 Cystathionine β-synthase [PLP]
4.2.1.24 Porphobilinogen synthase
4.2.1.49 Urocanate hydratase
4.2.1.61 3-Hydroxyacyl-CoA dehydratase
4.2.1.75 Uroporphyrinogen III synthase

4.2.99 Other C–O lyases
4.2.99.2 Threonine synthase [PLP]

4.3 A C–N bond is formed or cleaved

4.3.1 Ammonia lyases 4.3.1.3
4.3.1.8 Hydroxymethylbilane synthase

4.3.2 Amidase lyases 4.3.2.1
4.3.2.2 Arginosuccinate lyase

4.4 A C–S bond is formed or cleaved
4.4.1.1 Cystathionine γ-lyase [PLP]

4.6 A P–O bond is formed or cleaved
4.6.1.1 Adenylyl cyclase
4.6.1.2 Guanylate cyclase

Class 5: Isomerases (catalyze changes within one molecule)

Subclass 5.a: What kind of isomerization is taking place?

5.1 A racemization or epimerization (epimerases)
5.1.3.1 Ribulose phosphate 3-epimerase
5.1.3.2 UDPglucose 4-epimerase
5.1.3.4 L-Ribulose phosphate 4-epimerase
5.1.99.1 Methylmalonyl-CoA epimerase

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5.2  A cis–trans isomerization
5.2.1.2 Maleylacetacetate isomerase
5.2.1.3 Retinal isomerase
5.2.1.8 Peptidyl proline cis–trans-isomerase

5.3  An intramolecular electron transfer
5.3.1.1 Triose phosphate isomerase
5.3.1.6 Ribose 5-phosphate isomerase
5.3.1.9 Glucose 6-phosphate isomerase
5.3.3.1 Steroid 5-isomerase
5.3.3.8 Enoyl-CoA isomerase
5.3.4.1 Protein disulfide isomerase

5.4  An intramolecular group transfer (mutases)
5.4.2.1 Phosphoglycerate mutase
5.4.2.2 Phosphoglucomutase
5.4.2.4 Bisphosphoglycerate mutase
5.4.99.2 Methylmalonyl-CoA mutase [cobamide]

5.99  Another kind of isomerization
5.99.1.2 DNA topoisomerase (type I)—“DNA helicase”
5.99.1.3 DNA topoisomerase (ATP-hydrolyzing, type II)—“DNA gyrase”

Class 6: Ligases (join two molecules with hydrolysis of an “energy-rich” bond)

Subclass 6.1: What kind of bond is formed?

6.1  A C–O bond is formed
6.1.1n (Amino acid)-tRNA ligases (aminoacyl-tRNA synthetases)

6.2  A C–S bond is formed
6.2.1.1 Acetate-CoA ligase
6.2.1.3 Long-chain fatty-acid-CoA ligase
6.2.1.4 Succinate-CoA ligase (GDP-forming)—“thiokinase”

6.3  A C–N bond is formed
6.3.1.2 Glutamate-NH₂ ligase—“glutamine synthetase”
6.3.2.6 Phosphoribosylaminomimidazole-succinocarboxamide synthase (sorA)
6.3.3.1 Phosphoribosylformylglycinamidine cyclase
6.3.3.2 5-Formyltetrahydrofolate cyclase
6.3.4.2 CTP synthase
6.3.4.4 Adenosuccinate synthase
6.3.4.5 Argininosuccinate synthase
6.3.4.13 Phosphoribosylamine glycine ligase
6.3.4.16 Carbamoylphosphate synthase (NH₃)
6.3.5.2 GMP synthase (glutamine-hydrolyzing)
6.3.5.3 Phosphoribosylformylglycinamidine synthase
6.3.5.4 Asparagine synthase (glutamine-hydrolyzing)
6.3.5.5 Carbamoylphosphate synthase (glutamine-hydrolyzing)

6.4  A C–C bond is formed
6.4.1.1 Pyruvate carboxylase [biotin]
6.4.1.2 Acetyl-CoA carboxylase [biotin]
6.4.1.3 Propionyl-CoA carboxylase [biotin]
6.4.1.4 Methylcrotonyl-CoA carboxylase [biotin]

6.5  A P–O bond is formed
6.5.1.1 DNA ligase (ATP)
### Abbreviations

Abbreviations for amino acids, p. 60  
For bases and nucleosides, p. 80  
For monosaccharides, p. 38

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
<th>Abbreviation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>Amino acid</td>
<td>FAD</td>
<td>Flavin adenine dinucleotide</td>
</tr>
<tr>
<td>ACE</td>
<td>Angiotensin-converting enzyme (peptidyl-dipeptidase A)</td>
<td>Fd</td>
<td>Ferredoxin</td>
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<tr>
<td>ACP</td>
<td>Acyl carrier protein</td>
<td>FFA</td>
<td>Free fatty acid</td>
</tr>
<tr>
<td>ACTH</td>
<td>Adrenocorticotropic hormone (corticotropin)</td>
<td>FMN</td>
<td>Flavin mononucleotide</td>
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<tr>
<td>ADH</td>
<td>Antidiuretic hormone (aduretin, vasopresxin)</td>
<td>Fp</td>
<td>Flavoprotein (containing FMN or FAD)</td>
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<tr>
<td>ADP</td>
<td>Adenosine 5’-diphosphate</td>
<td>GABA</td>
<td>γ-Aminobutyric acid</td>
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<td>AIDS</td>
<td>Acquired immunodeficiency syndrome</td>
<td>GDP</td>
<td>Guanosine 5’-diphosphate</td>
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<td>ALA</td>
<td>3-Aminolevulinic acid</td>
<td>Glut</td>
<td>Glucose transporter</td>
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<tr>
<td>AMP</td>
<td>Adenosine 5’-monophosphate</td>
<td>GMP</td>
<td>Guanosine 5’-monophosphate</td>
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<td>ANF</td>
<td>Atrial natriuretic factor</td>
<td>GTP</td>
<td>Guanosine 5’-triphosphate</td>
</tr>
<tr>
<td>ANP</td>
<td>Atrial natriuretic peptide (~ ANF)</td>
<td>h</td>
<td>hour</td>
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<td>ATP</td>
<td>Adenosine 5’-triphosphate</td>
<td>HAT medium</td>
<td>Medium containing hypoxanthine, aminopterin, and thymidine</td>
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<td>AVP</td>
<td>Arginine vasopressin</td>
<td>Hb</td>
<td>Hemoglobin</td>
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<tr>
<td>b</td>
<td>Base</td>
<td>HDL</td>
<td>High-density lipoprotein</td>
</tr>
<tr>
<td>bp</td>
<td>Base pair</td>
<td>HIV</td>
<td>Human immunodeficiency</td>
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<tr>
<td>BPG</td>
<td>2,3-Bisphosphoglycerate</td>
<td>HLA</td>
<td>Human leukocyte-associated antigen</td>
</tr>
<tr>
<td>cAMP</td>
<td>Cyclic AMP</td>
<td>HMG-CoA</td>
<td>3-Hydroxy-3-methylglutaryl-CoA</td>
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<td>CAP</td>
<td>Catabolite activator protein</td>
<td>CoA</td>
<td>Hexose monophosphate pathway</td>
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<tr>
<td>CDK</td>
<td>Cyclin-dependent protein kinase (in cell cycle)</td>
<td>CoA</td>
<td>Homogeneous nuclear ribonucleic acid</td>
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<tr>
<td>CDNA</td>
<td>Complementary DNA</td>
<td>CoA</td>
<td>Human leukocyte-associated antigen</td>
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<tr>
<td>CDP</td>
<td>Cytidine 5’-diphosphate</td>
<td>CoA</td>
<td>Human leukocyte-associated antigen</td>
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<td>3’,5’-Cyclic GMP</td>
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<td>Hexose monophosphate pathway</td>
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<td>CIA</td>
<td>Chemoluminescence immunassay</td>
<td>hnRNA</td>
<td>Heterogeneous nuclear ribonucleic acid</td>
</tr>
<tr>
<td>CMP</td>
<td>Cytidine 5’-monophosphate</td>
<td>HPLC</td>
<td>High-performance liquid chromatography</td>
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<tr>
<td>CoA</td>
<td>Coenzyme A</td>
<td>IF</td>
<td>Intermediary filament</td>
</tr>
<tr>
<td>CoQ</td>
<td>Coenzyme Q (ubiquinone)</td>
<td>IFN</td>
<td>Interferon</td>
</tr>
<tr>
<td>CSF</td>
<td>Colony-stimulating factor</td>
<td>Ig</td>
<td>Immunoglobulin</td>
</tr>
<tr>
<td>CTP</td>
<td>Cytidine 5’-triphosphate</td>
<td>IL</td>
<td>Interleukin</td>
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<td>d</td>
<td>Deoxy-</td>
<td>Inositol</td>
<td>Inositol 1,4,5-trisphosphate</td>
</tr>
<tr>
<td>Da</td>
<td>Dalton (atomic mass unit)</td>
<td>IPR</td>
<td>Isopropylthiogalactoside</td>
</tr>
<tr>
<td>DAc</td>
<td>Dicarboxylic acid</td>
<td>IRS</td>
<td>Insulin-receptor substrate</td>
</tr>
<tr>
<td>dd</td>
<td>Dideoxy-</td>
<td>kDa</td>
<td>Kilodalton (10^3 atomic mass units)</td>
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<td>DH</td>
<td>Dehydrogenase</td>
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<tr>
<td>dsDNA</td>
<td>Double-stranded DNA</td>
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<tr>
<td>EA</td>
<td>Ethanolamine</td>
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<td>EIA</td>
<td>Enzyme-linked immunoassay</td>
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<td>ER</td>
<td>Endoplasmic reticulum</td>
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</tr>
<tr>
<td>LDH</td>
<td>Lactate dehydrogenase</td>
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<td>LDL</td>
<td>Low-density lipoprotein</td>
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<tr>
<td>M</td>
<td>Molarity (mol L⁻¹)</td>
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<td>Mab</td>
<td>Monoclonal antibody</td>
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<tr>
<td>MAP kinase</td>
<td>Mitogen-activated protein kinase</td>
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<td>MHC</td>
<td>Major histocompatibility complex</td>
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<td>MPF</td>
<td>Maturation-promoting factor</td>
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<td>mRNA</td>
<td>Messenger ribonucleic acid</td>
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<td>N</td>
<td>Nucleotide with any base</td>
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<td>Oxidized nicotinamide adenine dinucleotide</td>
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<td>ODH</td>
<td>2-Oxoglutarate dehydrogenase</td>
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<td>Polyacrylamide gel electrophoresis</td>
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<tr>
<td>Pan</td>
<td>Panthenine</td>
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<tr>
<td>PAPS</td>
<td>Phosphoadenosine phosphosulfate</td>
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<td>PCB</td>
<td>Polymerase chain reaction</td>
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<td>RER</td>
<td>Rough endoplasmic reticulum</td>
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<td>Reticuloendothelial system</td>
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<td>RFLP</td>
<td>Restriction fragment length polymorphism</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RIA</td>
<td>Radioimmunoassay</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RNA</td>
<td>Ribonucleic acid</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ROS</td>
<td>Reactive oxygen species</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RP</td>
<td>Reversed phase (of silica gel)</td>
<td></td>
<td></td>
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<tr>
<td>rRNA</td>
<td>Ribosomal ribonucleic acid</td>
<td></td>
<td></td>
</tr>
<tr>
<td>S</td>
<td>Svedberg (unit of sedimentation coefficient)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SAP</td>
<td>S-adenosyl L-homocysteine</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SDS</td>
<td>Sodium dodecylsulfate</td>
<td></td>
<td></td>
</tr>
<tr>
<td>sER</td>
<td>Smooth endoplasmic reticulum</td>
<td></td>
<td></td>
</tr>
<tr>
<td>sn</td>
<td>Stereospecific numbering</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ssDNA</td>
<td>Single-stranded DNA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TBG</td>
<td>Thyroxine-binding globulin</td>
<td></td>
<td></td>
</tr>
<tr>
<td>THB</td>
<td>Tetrahydrobiotin</td>
<td></td>
<td></td>
</tr>
<tr>
<td>THF</td>
<td>Tetrahydrofolate</td>
<td></td>
<td></td>
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<tr>
<td>TLC</td>
<td>Thin-layer chromatography</td>
<td></td>
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</tr>
<tr>
<td>TIP</td>
<td>Thiamine diphosphate</td>
<td></td>
<td></td>
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<tr>
<td>TRH</td>
<td>Thyrotropin-releasing hormone (thyrotropin)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tris</td>
<td>Tris(hydroxymethyl)aminomethane</td>
<td></td>
<td></td>
</tr>
<tr>
<td>tRNA</td>
<td>Transfer ribonucleic acid</td>
<td></td>
<td></td>
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<tr>
<td>TSH</td>
<td>Thyroid-stimulating hormone (thyrotropin)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>UDP</td>
<td>Uridine 5′-diphosphate</td>
<td></td>
<td></td>
</tr>
<tr>
<td>UMP</td>
<td>Uridine 5′-monophosphate</td>
<td></td>
<td></td>
</tr>
<tr>
<td>UTP</td>
<td>Uridine 5′-triphosphate</td>
<td></td>
<td></td>
</tr>
<tr>
<td>UV</td>
<td>Ultraviolet radiation</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Vmax</td>
<td>Maximal velocity (of an enzyme)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>VLDL</td>
<td>Very-low-density lipoprotein</td>
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## Quantities and units

### 1. SI base units

<table>
<thead>
<tr>
<th>Quantity</th>
<th>SI unit</th>
<th>Symbol</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>Length</td>
<td>Meter</td>
<td>m</td>
<td>1 yard (yd) = 0.9144 m</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1 inch (in) = 0.0254 m</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1 Å = 10⁻¹⁰ m = 0.1 nm</td>
</tr>
<tr>
<td>Mass</td>
<td>Kilogram</td>
<td>kg</td>
<td></td>
</tr>
<tr>
<td>Time</td>
<td>Second</td>
<td>s</td>
<td>1 pound (lb) = 0.4536 kg</td>
</tr>
<tr>
<td>Current strength</td>
<td>Ampere</td>
<td>A</td>
<td></td>
</tr>
<tr>
<td>Temperature</td>
<td>Kelvin</td>
<td>K</td>
<td>°C (degree Celsius) = K - 273.2</td>
</tr>
<tr>
<td>Light</td>
<td>Candela</td>
<td>cd</td>
<td>Fahrenheit: °F = °C × 9/5 + 32</td>
</tr>
<tr>
<td>Amount of substance</td>
<td>Mol</td>
<td>mol</td>
<td></td>
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### 2 Derived units

<table>
<thead>
<tr>
<th>Quantity</th>
<th>Unit</th>
<th>Symbol</th>
<th>Derivation</th>
<th>Remarks</th>
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<tr>
<td>Frequency</td>
<td>Hertz</td>
<td>Hz</td>
<td>s⁻¹</td>
<td></td>
</tr>
<tr>
<td>Volume</td>
<td>Liter</td>
<td>L</td>
<td>10⁻³ m³</td>
<td>1 U.S. gallon (gal) = 3.785 L</td>
</tr>
<tr>
<td>Force</td>
<td>Newton</td>
<td>N</td>
<td>kg m s⁻²</td>
<td></td>
</tr>
<tr>
<td>Pressure</td>
<td>Pascal</td>
<td>Pa</td>
<td>N m⁻²</td>
<td>1 bar = 10⁵ Pa</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1 mmHg = 133.3 Pa</td>
</tr>
<tr>
<td>Energy, work, heat</td>
<td>Joule</td>
<td>J</td>
<td>N m</td>
<td>1 calorie (cal) = 4.1868 J</td>
</tr>
<tr>
<td>Power</td>
<td>Watt</td>
<td>W</td>
<td>J s⁻¹</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Volt</td>
<td>V</td>
<td>W A⁻²</td>
<td></td>
</tr>
<tr>
<td>Voltage</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Concentration</td>
<td>Molarity</td>
<td>M</td>
<td>mol L⁻¹</td>
<td></td>
</tr>
<tr>
<td>Molecular mass</td>
<td>Dalton</td>
<td>Da</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Molar mass</td>
<td>–</td>
<td>g</td>
<td>–</td>
<td>Nondimensional</td>
</tr>
<tr>
<td>Molecular weight</td>
<td>–</td>
<td>Mₐ</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Reaction rate</td>
<td>v</td>
<td>mol s⁻¹</td>
<td>–</td>
<td></td>
</tr>
<tr>
<td>Catalytic activity</td>
<td>Katal</td>
<td>kat</td>
<td>mol s⁻¹</td>
<td>1 unit (U) = 1.67 × 10⁻¹⁸ kat</td>
</tr>
<tr>
<td>Specific activity</td>
<td>–</td>
<td>kat (kg enzyme)⁻¹</td>
<td>Usually: U (mg enzyme)⁻¹</td>
<td></td>
</tr>
<tr>
<td>Sedimentation coefficient</td>
<td>Svedberg</td>
<td>S</td>
<td>10⁻¹³ s</td>
<td></td>
</tr>
<tr>
<td>Radioactivity</td>
<td>Becquerel</td>
<td>Bq</td>
<td>Decays s⁻¹</td>
<td>1 curie (Ci) = 3.7 × 10⁹ Bq</td>
</tr>
</tbody>
</table>

### 3 Multiples and fractions

<table>
<thead>
<tr>
<th>Factor</th>
<th>Prefix</th>
<th>Symbol</th>
<th>Example</th>
<th>General gas constant, R</th>
<th>( R = 8.314 ) J mol⁻¹ K⁻¹</th>
</tr>
</thead>
<tbody>
<tr>
<td>10⁶</td>
<td>Giga</td>
<td>G</td>
<td>GHz = 10⁶ hertz</td>
<td>Loschmidt (Avogadro) number, N</td>
<td>N = 6.0225 × 10²³</td>
</tr>
<tr>
<td>10³</td>
<td>Mega</td>
<td>M</td>
<td>MPa = 10⁶ pascal</td>
<td>(number of particles per mol)</td>
<td></td>
</tr>
<tr>
<td>10⁻³</td>
<td>Milli</td>
<td>m</td>
<td>mJ = 10⁻³ joule</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10⁻⁶</td>
<td>Micro</td>
<td>µ</td>
<td>µJ = 10⁻⁶ volt</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10⁻¹²</td>
<td>Nano</td>
<td>n</td>
<td>nJ = 10⁻¹² joule</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10⁻¹⁵</td>
<td>Pico</td>
<td>p</td>
<td>pm = 10⁻¹⁵ meter</td>
<td></td>
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</tr>
</tbody>
</table>

### 4 Important constants

- Faraday constant \( F = 96480 \) C mol⁻¹
Further reading

Textbooks

Reference works

Selected periodicals (journals and yearbooks)
Annual Review of Biochemistry. Annual Reviews, Inc., Palo Alto, CA, USA [the most important collection of biochemical reviews].
Current Biology, Current Opinion in Cell Biology, Current Opinion in Structural Biology, and related journals in this series. Current Biology, Ltd. London [short up-to-date reviews].
Trends in Biochemical Sciences. Elsevier Trends Journals, Cambridge, United Kingdom [the "newspaper" for biochemists; official publication of the International Union of Biochemistry and Molecular Biology (IUBMB)].
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<table>
<thead>
<tr>
<th>Page</th>
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<tr>
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<td>A</td>
<td>Beckman Instruments, Munich, Bulletin no. DS-555A, p. 6, Fig. 6</td>
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<td>203</td>
<td>B</td>
<td>Goodsell DS, Trends Biochem Sci 1991; 16: 203–6; Figs. 1a and 1b</td>
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<td>Stryer L. Biochemistry. New York: Freeman, 1988, p. 945, Fig. 36–47</td>
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<td>Alberts B, et al. The molecular biology of the cell. New York: Garland, 1989, p. 663, Fig. 11–73B and p. 634, Fig. 11–36</td>
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<td>279</td>
<td>A, B</td>
<td>Voet D, Voet JG. Biochemistry. New York: Wiley, 1990, p. 305, Fig. 11–45 and p. 396, Fig. 11–47</td>
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<td>295</td>
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<td>Voet D, Voet JG. Biochemistry. New York: Wiley, 1990, p. 1097, Fig. 34–13</td>
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<td>Voet D, Voet JG. Biochemistry. New York: Wiley, 1990, p. 1112, Fig. 34–33</td>
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<td>297</td>
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<td>Janeway CA, Travers P. Immunology. Heidelberg, Germany: Spektrum, 1994, p. 164, Fig. 4.3.c</td>
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<td>Voet D, Voet JG. Biochemistry. New York: Wiley, 1990, p. 1126, Fig. 34–55</td>
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<td>335</td>
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<td>Darnell J, et al. Molecular cell biology. 2nd ed. New York: Freeman, 1990, p. 923, Fig. 23–26</td>
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</table>
Index

Numbers in italics indicate figures.
acetylglutaryl-0-palmitoyltransferase 170, 171, 423
acetylglutaryl-3-phosphate
O-acetyltransferase 170,
171, 423
acetylglucuronate phosphate
reductase 420
N-acetylglucosamine galacto-
syntransferase 423
adapted immune system
294
adaptor proteins 388
Grb-2 388
SOS 388
additions 14, 15
adenine 12, 13, 80, 81
phosphoribosyltransferase
187, 423
adenosine 80, 81, 123
5'-diphosphate (ADP) see
ADP
5'-monophosphate
(AMP) see AMP
5'-triphosphate (ATP) see
ATP
5'-adenosyl-l-homocysteine
(SAH) III
5'-adenosyl-l-methionine
(SAM) 110, 111
adenosylcobalamin 108
adenosylhomocysteinase
426
denylate
cyclase 120, 121, 384, 385,
386, 387, 428
kinase 72, 73, 336, 337,
424
denylcyclase
lyase 428
synthase 429
ADH see antiuretic hor-
mone
adhesive proteins 346
adipocytes 46
adipose tissue 160, 161, 162,
308
adiuretin see antiuretic hor-
mone
ADP 190, 191, 212
adrenaline see epinephrine
adrenocorticotropic hor-
mone (ACTH)
adriamycin see doxorubicin
aerobic glycolysis 150
aerobic metabolism 122
aerobic oxidation 146, 147
agarase 40, 41, 262
agents, alkyllating 256, 402,
403
AIDS 404
air 29
ALA see 5-aminovaleric
acid
alanine 60, 61, 178, 184, 185
β-alanine 12, 13, 62, 63, 106
degradation 186
cycle 338, 339
seryl 65, 66, 67
transaminase 178, 179,
181, 423
albumins 194, 195, 277
alcohol 10
blood 321
dehydrogenase 64, 420
fermentation 148, 149
liver damage 320, 321
primary 11
secondary 11
alcohol dehydrogenase 65,
320, 321
fermentation 148, 149
alcohols 15
sugar 38, 39
aldehydes 11
dehydrogenase 320, 321,
420
reductase 310, 311, 420
aldehydes 10, 15
aldimines 10
aldimine 10, 108, 178, 179
aldose 34, 38
D-glucose see D-glucose
aldolase see fructose bis-
phosphate aldolase
aldolases 38
see also L-arabinose;
D-ribose; D-xylene
aldoses 39
aldoztetone 56, 57, 374, 376
aliphatic amino acids 60
alkaline phosphatase 425
alkanes 46, 47
alkanols 46
alkenes 15
1-alkyl-2-acetylglucocerebro-
side phosphotransferase
170, 171, 425
alkylating agents 256, 402,
403
allantoic acid 187
allantoic acid 186, 187
alloactone 110
allopurinol 186, 187
allosteric effects 2-3, 114,
115, 116
BP 28, 284
hemoglobin 116, 280
allosteric enzymes 92, 93,
96, 116
allosteric inhibitors 96
allosteric proteins 72
allozymic variation 302
α-amanitin 242
α, α'-globulins 276
α, β-globulins 276
α-keratin 71
alternative pathway,
complement 298
Amanita phalloides 242
amidases 89, 427
amidine lyases 428
amidophosphoribosyl
transferase 402, 403, 423
amine oxidase 62, 421
amines 10
biogenic 62, 63, 352
primary 11
secondary 11
tertiary 11
Amanita phalloides 204
amino acid N-acetylan-
transferase 423
D-amino acid oxidase 58
amino acid tRNA ligases 248
amino acids (AA) 35, 58-63,
146
activation 236, 248-9, 249
aromatic 60, 184
biosynthesis 184-5, 185,
412-13
branched chain 184, 185
charge 58
degradation 180-1, 181,
414-15
essential see essential
amino acids
excretion 324
function 58, 59
glucogenic 186
glucoconogenesis 154
ketogenic 180
metabolism 306, 338
neurotransmitters 352
optical activity 58, 59

Koolman, Color Atlas of Biochemistry, 2nd edition © 2005 Thiem All rights reserved. Usage subject to terms and conditions of license.
proteinogenic 58, 60-1, 61
non-proteinogenic 62-3
resorption 272
signaling 380, 381
translation 60
amino sugars 39, 44
aminonacyl
dehydrogenase 248, 249
tRNAs 248, 249, 252
4-aminobutyrate transami-
nase 356, 357, 424
aminopeptidases 425
aminoglycosides 254
β-aminosobutyrate 186, 187
5-aminolevulinate 192, 193
synthase 192, 193, 423
aminomethyltransferase
422
aminopeptidases 176, 177, 426
aminopropanol 63
aminopterin 304
aminotransferases 89
ammonia II
bases 30, 31
degradation 112
excretion 326, 327
lyases 428
metabolism 178, 179, 416
urea cycle 182, 183
ammonium ions (NH₄⁺) 31, 182, 183, 326
ammonotelic animals 182
AMP 158, 186, 190, 191
deaminase 336, 337, 427
amphibolic function 136
amphibolic pathways 112, 113
amphipathic molecules 28, 29
amphipathic molecules 28
ampicillin 255
amplification 398
DNA 262
amyloses α-amylase 268, 269, 272, 273, 426
brewing 148, 149
amylase 156, 157, 426
amylopectin 41, 42, 43
amyloplasts 42
amylose 41, 42, 43
anabolic pathways 112, 113, 138, 139, 338
anaerobic conditions 112, 146
anaerobic glycolysis 150, 336, 338
anaerobic oxidation 146, 147
analogogues
substrates 96, 97
transition states 97
analysis
analyzers 36
biochemical 102, 103
proteins 78
apoptotic effect 180
apoptotic pathways 139
anchors, lipid 214
anemia 286
sickle-cell 249, 264, 265
ANF see atrial natriuretic factor
angiotensin 330, 331
angiotensin-converting en-
yzme (ACE) 426
anhydrides mixed II
phosphoric acid II
animals
cells 197
types of 182
anions 15, 27
ammonium 36
ANP see atrial natriuretic peptide
antenna pigments 132
anthracenes 402, 403
antioxidants 400
antibiotics 225, 254-5, 255
antibodies 300-3, 303
monoclonal 304-5, 305
plasma cells 294
antidroms 82, 86, 236, 248, 249
antidiuretic hormone (ADH)
220
antigen-presenting cells (APCs) 294
antigens
blood groups 292
receptors 296, 297
antihypertensive factor A 291
antimetabolites 402, 403
antioxidants 104, 284, 285, 364
antiparallel pleated sheet 68
antiport 212, 218
antisense DNA 264
apatites 340, 341
APC see antigen-presenting
cells
apoferitin 287
apolar molecules 28
apo-proteins 278
apo-onp 210, 396-7, 397
aquaporin-1 220, 221
arabinan 41
L-arabinose 38, 39, 42
arachidonate lipoxigenases 390, 391, 421
arachidonic acid 48, 49, 390
arginase 183, 427
arginine 60, 61, 182, 183
lactate dehydrogenase 100
vasopressin (AVP) see
antidiuretic hormone
argininosuccinate 182, 183
lyase 183, 428
synthase 183, 429
aromatic amino acids 60, 184
l-aminolevulinate synthase 182, 183
carbamoyltransferase
(ACTase) 116, 117, 188, 422
family 184, 185
kinase 424
kinetic 117
proteinases 177, 427
purine ring 188, 189
pyrimidine ring 188, 189
semialdehyde dehydro-
genase 420
transaminase 178, 179, 183, 212, 213, 423
aspartic acid 60, 61
atomic oxygen 25
 ATP 35, 112, 122-3, 123
ATP, charge density 123
dATP 240
energetic coupling 16,
122, 124
exchange 212
formation 122, 123
glucose oxidation 147
hydrolysis 122, 123
nucleotide biosynthesis
190, 191
oxidative
phosphorylation 123
phosphate transfer 123
structure 122
synthase see ATP synthase
synthesis 112, 122, 142-5,
210
NADH+H+ 142, 143
proton driven 126, 127
ATP synthase 122, 126, 142,
143, 210
catalytic units 142, 143
H+-transporting 140, 141,
143, 427
light reactions 128, 129
proton channels 142, 143
respiratory control 144,
145
ATP-citrate lyase 428
ATP-dependent phosphorylation
114
ATPases
Ca++ 220
F type 220
H+-transporting 427
H++-exchanging 427
P type 220
V type 220
atrial natriuretic factor
(ANF), receptor 388, 389
atrial natriuretic peptide
(ANP) 388, 389
autocrine effects
eicosanoids 390
hormones 372, 373
avtrophs 112
AVP see arginine vasopres-
sin
axial (a) position 34
axons 348
B
B cell 161, 274, 275, 294
B-DNA 84, 87
Bacteria
bacterial membranes 157
bacterial toxins 151
bacteriophages 260, 404
bacteriorhodopsin 126, 127
bacteroids 184, 185
ball-and-stick models 6
basal transcription complex
242, 244, 245
base pairs (bp) 84
bases (b) 30-1, 31, 80-1
ammonia 30, 31, 182
chloride ions 31
conjugated 18, 30
DNA ratios 84
hydroxyl ions 31
water 31
basic amino acids 60, see
also individual amino
acids
bcl-2 396
beet 148, 149
Beer-Lambert law 102
behemic acid 49
dent-shaped curves 94, 95
benzene 4, 5
benz(o)pyrenes 256, 257
β-hexosaminidase 33
β-granules 160, 161
β-turns 69
β-oxidation 210
β-configurations 12
β-globulins 276, 286
bicarbonate, resorption 326
bile 194, 268, 289
pigments 194
salts 314, 315
bile acids 56, 57, 172, 312
conjugated 314
primary 56, 314-15
secondary 56, 314-15
bilirubin 194, 195, 287
digluconorides 194, 195
monoglucuronides 194
biliverdin 194, 195
reductase 194, 195, 421
binding sites 250
aminoacyl tRNA 252
biogenic amines 12, 62, 63,
352
biomolecules 10-13
biosynthesis
heme 192-3, 193, 210
NAD+ 208
biotin see vitamin H
biotransformations 226,
306, 316-17, 317
BIP 233
1,3-bisphosphoglycerate
124, 125, 150, 151, 155,
282, 283
2,3-bisphosphoglycerate see
BPG
bisphosphoglycerate
mutase 283, 429
phosphatase 283, 425
bisubstrate kinetics 95
blood
alcohol 321
cells 274, 275
clotting 290-1, 291
composition 274
ethanol 320, 321
function 274, 275
groups 292-3, 293
metabolites 274
plasma 31
serum 274
blood—brain barrier 356
boat conformation 54, 55
bodies, residual 234
Böhr effect 282
bonds
acid—amide 13
acid—anhydride 150
angles 7
chemical see chemical
bonds
disulfides 62, 72, 73, 106,
190
double 4
electron 6
hydrogen 72
lengths 7
peptide 66-7
phosphoric acid 122
polarity 6, 7
single 4
bone 340, 341
calcium 342
remodeling 342, 343
Bowman’s capsule 323
BPG 282, 283
brain 356, 357
gluconeogenesis 154
branched-chain amino acid transaminase 424
brewing 349
Brunner glands 268
buffers 30, 31
blood plasma 288, 289
capacity 30, 288
dialysis 78, 79
function, organ metabolism 308-9
building blocks, lipids 46
1,3-butadiene 4, 5
butyric acid 49

C
C peptide, insulin 76, 77, 160, 161
C segment 302
C state 116
C terminus 66
c-oncogenes see proto-oncogenes
C-peptides 76
C1
metabolism 418
transferrases 89
cæsium chloride 201
calcidol 1-monoxygenase 330, 331, 422
calcii see vitamin D
calcitonin 342, 343
calcitriol 56, 57, 330, 342, 374, 376
calcium
ATPase 220
bone 342
functions 342, 343
homeostasis 342, 343
ions 328, 334, 335, 386, 387
metabolism 342-3
reservoir 210
sarcoplasmic pump 220
signaling 342

store 226
calcium-transporting ATPase 427
calmodulin 386, 387
calorimetry 20, 21
Calvin cycle 128, 129, 130, 131, 407
cAMP 120, 380, 384, 386, 387
lactose operon 119
phosphodiesterase 120, 121
camphor 52, 53
CAP see catabolite activator protein
cap, RNA modification 246
capacity factor 16
capric acid 49
caproic acid 49
capsids, rhinovirus 404
N-carbamoyl aspartate 188, 189
carbamoyl phosphate 182, 183, 188, 189
synthase 182, 183, 188, 429
carbohydrate metabolism 160, 306, 310-11, 388
metabolic charts 408, 409
regulation 158-9, 159
carbohydrates 34-45, 35
bacteria 35
disaccharides see disaccharides
hydrolysis 266
membranes 216
metabolism see carbohydrate metabolism
monosaccharides see monosaccharides
nutrients 360
oligosaccharides see oligosaccharides
polysaccharides see polysaccharides
reserve 156
resorption 266
see also glycolipids; glycoproteins

hemoglobin 280, 282
carbonic anhydrase 270, 271, 283, 289, 428
proton secretion 326, 327
carbonic anhydrase see carbonic anhydrase
carbonium ions 15
carbonyl groups II
carboxy-lyases 427
N-carboxybiotin 108
γ-carboxylglutamate 62, 290
carboxyl groups II
carboxylases see carboxy-lyases
γ-carboxylation 62, 290
carboxylic acid 10, 11, 15, 48, 49
activated 106
amides 10, 11
ester 10, 11
carboxypeptidases 176, 177, 425-6
caries 340
carnitine 164, 165
carotene 46, 47
β-carotene 132, 133
carrageenan 40, 41
carrier electrophoresis 276
caspases 396
catabolic pathways 112, 113, 138, 139
catabolite activator protein (CAP) 64, 65, 118, 119
catalase 24, 25, 166, 284, 285, 421
catalysis 24-5, 25
acid-base 90
covalent 90
cycles 100, 143, 221
enzymes 90-1
hydrogen peroxide 25
iodide 25
lactate dehydrogenase 100
membranes 216
catalysts 88, 92, see also enzymes
catalytic units, ATP synthase 142, 143
catechol O-methyltransferase 316, 317, 422
catecholamines 352, 353

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cathepsins 176
cations 27
CD 296
CD 296
cdc2 see cyclin-dependent
gene 1 (CDK1)
CDK see cyclin-dependent
protein kinase
cDNA 260
CDP 190, 191
choline 110, 111
diaclyglycerol 170, 171
diaclyglycerol-inositol 3-
phosphatidyl transfer-
ase 170, 171, 425
cell bodies 348
cell cycle 394-5, 395
cells
animal 196
antigen-presenting
(ACPs) 294
division 400, 401
fractionation 198-9
inhibition 402
interaction 216
movement 206
necrosis 396
organelles 196, 198
plant 196
proliferation 396, 297
structure 196-7
transformation 401
transport 206
vacuoles 234
cellular immunity 294
cellulose 34, 41, 42, 43
hemicellulose 43
cement 340
centers
active 74, 90
reaction 132
central nervous system see
CNS
centrifugation 201
density gradient 200, 201
equipment 200
isopycnic 200
principles 200-1
steps 198
zonal 200
centrosome 206
cephalin see phosphatidyl-
ethanolamine
cephalosporins 254, 255
cerebrosides 46, 47, 51
galactosyl S
N-glucosylceramide 50, 51
cGMP 386
esterase 358, 359
phosphodiesterase 425
photoreceptors 358
chain termination method
260
chains
respiratory 106, 112, 126,
140-1, 210
side 76, 77
conformation 34, 54, 55
channels
ion 126, 218, 222-4, 350,
384
K+ 222
ligand-gated 222
passive 222
protein 218
voltage-gated Na+ 222
chaperones 232, 233
chaperonins 232, 233
charge 59
chemical bonds 4-7, 5
chemical energy 112, 122
chemical potential 12, 16, 22
chemical reactions 14-15
chemical work 17
chemokines 392
chemoluminescent immu-
noassay (CIA)
chemotaxis 298
chenodeoxycholic acid 56,
57, 314
chiral center 8, 12, 35, 49
chitin 40, 41
chloramphenicol 254, 255
chloride ions, bases 31
chlorophylls 128, 129, 132,
133
cholorplasts 196, 407, 407
lumen 128, 129
cholcalciferol see vitamin D
cholecystokinin 270
cholstane 54, 55
cholsterol 54, 55
cholsterol 52, 53, 56, 67,
71, 315
biosynthesis 172, 173
esterase 425
membranes 214, 215
monooxygenase 422
van der Waals models 54,
55
cholic acid 56, 57, 314, 315
choline 50, 51, 141, 354
kinase 424
O-acetyltansferase 354,
355, 423
phosphate cytidyltrans-
ferase 425
chondroitin 6-sulfate 347
Christmas factor 291
chromatin 208, 238, 239
chromatography 55, 78
chromosomes 238
chylomicrons 163, 272, 278
chymosin 427
cytomtrypsin 94, 95, 268,
269, 426
CIA see chemoluminesence
immunoassay
circadian rhythm 372
cirrhosis 320
cis—-trans isomerases 89
cis—-trans isomers 8, 9, 54,
55, 429
cisplatin 402
citrato 9, 137, 158
fat metabolism 163
lyase 139
synthase 136, 137, 138,
428
tricarboxylic acid cycle
144, 145
citric acid 136
cycle 141, 147
citonellal 52, 53
citrulline 62, 63, 182, 183
classic pathway, complement
298
clathrae, structure 28, 29
cleavage, homolytic 108
clones 258, 304
closed-loop feedback con-
trol 372
clotting 290-1, 291
CNP 187
3’5’-cGMP phosphodiester-
ase 423
CNS, signal transmission
348-9
co-lipase 268, 269
co-receptors 296
CO2 see carbon dioxide
CoA see acetyl CoA; coen-
yzme A
coactivator/mediator com-
plex 244
coagulation factors 291, 426
cobalamin see vitamin B₁₂
cobalt 108, 109
coding strands 85
codogenic strands 85
codons 236
antidroms 82, 86, 236, 248, 249
start 248, 250
stop 248, 250
coenzyme A (CoA) 106, 107, 134
acetyl CoA see acetyl CoA
coenzyme Q (CoQ) 104, 136, 140, 212
ATP synthesis 142, 143
isoprenoid anchors 52, 53
oxidized 212
redox systems 105
reduced 147
cytochrome c reductase complex 141, 421
coenzymes 104-11, 105
availability 114
coenzyme A see coenzyme A
coenzyme Q see coenzyme Q
definition 104
energetic coupling 106, 107
flavin see flavin
group-transferring 106-7, 107, 108-9, 109
heme 106, 107
NAD see NAD
nucleotide triphosphates 110, 122-3
redox 104, 105, 106-7, 107
soluble 104
vitamins 364
cofactors 46, 104
collagenase 427
collagens 64, 70, 71, 346
biosynthesis 344, 345
bone 340
helix 65, 68, 69, 344
procollagen 344
structure 344, 345
tropocollagen 344
collision complexes 90
colony-stimulating factors (CSF) 392
combustion 21
competitive inhibitors 96, 97
complement 298-9
activation 298, 299
alternative pathway 298
C₁–C₉ 298, 299
C₃/C₅ convertase 298, 299, 426
C₅ convertase 298, 299
classic pathway 298
factors 298
complementary DNA (cDNA) see cDNA
glycoproteins 45
complex I 140
complex II see succinate dehydrogenase
complex III 140
complex IV 140
complex V see ATP synthase, H⁺-translocating
complexes
complex lipids 170-1
complex oligosaccharides 44, 230
complex
basal transcription 242, 244, 245
coactivator/mediator 244
daunomycin—DNA 254
enzyme—substrate 92
enzymes 91, 95
fatty acid—albumin 163
formation 72
initiation 705 250
lipoprotein 312
membrane attack 298
multienzyme 134
oxoglutarate dehydrogenase 144, 145
poles 208
prothrombinase 291
repressor—allo lactose 119
translocator 232
vitamin B₁₂ 366
compounds 77
concentration
gradients 126, 127
substrates 97, 116
and velocity 93, 97
condensation, chromosomal 238
cones 358
conformation 8, 9, 35
A 86
cis—trans 8, 9, 54, 55, 429
enzymes 92
native 72, 74
R 117, 280, 281
ring 54, 55
space 66
stabilizing interactions 72, 73
T 177, 280, 281
zigzag (Z) 86
conjugates 316
steroid hormones 110
conservation
differences 98
energy 106, 126-7, 127
constitution 6
contraction
muscles 332-3
control 334-5
control elements 118
transcription 244
copper ions (Cu) 132, 133, 142, 143
coproorphyrinogen III 192, 193
CoQ see coenzyme Q
core oligosaccharide 230
core structures 44
Cori cycle 318, 339
corin 108
corticotropin see adreno-corticotropic hormone
cortisol 56, 57, 159, 338, 374, 376, 378
glucocorticoid 120, 121, 154
cosubstrates 104
cotton fibers 42
coupling
energetic 16, 18, 106, 112
ATP 16, 122, 124, 125
covalency 6, 90, 108
creatine 324
kinase 98, 336, 337, 424
metabolism 336, 337
phosphate 122, 336
creatinine 336
cristae 210
CSF see colony-stimulating factor
CTP 190, 191
dCTP 190, 191, 240
synthase 190, 191, 429
cultures, primary 304
curves, bell-shaped 94, 95
cyanobacteria, photosystem (PS) I 122
cycles, catalytic 100, 143
3′-cyclic AMP see cAMP

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dolichol 53, 53
diphosphate 230
domains
dimers 116
receptors 224
SH2 392
steroid receptors 378

donors 6
electrons 88
dopa 6, 63, 352
l-dopa 6, 7, 63

dopamine 62, 63, 352
β-monoxygenase 352, 353, 422
double helix 84, 86
double stranded (dsDNA)
see dsDNA
donor, acceptor 402

drugs, cytostatic 402-3
dTMP 80, 81, 187, 191
dTTP 190, 191, 240
dUMP 190

dynamics, proteins 72, 73

dehydrogenase 164, 165, 421
diabetes 198

dissociation curves 58
dissolution 20, 21
disulfides 10-11
bonds 62, 72, 73, 106, 190, 300
dithiol 106

diuresis 328
DNA 80, 84-5
amplification 262
antisense 264
B-DNA 84, 86
cDNA 260
cloning 258-9, 259
conformation 86-7, 87
electrophoresis 262, 263
fingerprinting 264, 265
genetic coding 84
germline 302

gyrase see DNA topoisomerase (ATP-hydrolyzing, type II)

helicase see DNA topoisomerase (type I)
libraries 260, 261
ligase 256, 257, 429
nucleus 208
polymerases 240, 241
see also individual polymerases
primers 240
proteins 65
sequencing 260-1, 261
structure 84, 85
templates 240
zig-zag 86
DNA K 232
DNA polymerases 240, 241
repair 256, 257
DNA topoisomerases 240
(−)ATP-hydrolyzing, type II)
240, 429
(type I) 240, 245, 429
DNA-binding proteins, oncogenes 398
DNA-dependent DNA polymerases 240, 242
DNA-directed DNA polymerases 424
DNA-directed RNA polymerases 240, 242, 243, 245, 424

DNP 144
dNTPs 260, 261, 262

Electron transfer flavoprotein (ETF) 164

dehydrogenase 164, 165, 421
electron acceptors 88
configurations 2, 3
donors 88
excitation 128, 129
oxidized forms 32
p 4
pairs 6
potential 18, 19
reduced forms 32
reducing equivalent 33
singlet state 130
transfers 33
transport chain 128, 140

electrophoresis 263, 277
carrier 276
DNA 262, 263
lactate dehydrogenase (LDH) 99
SDS gel 78, 79

elementary fibrils 42, 43
elements 3
eliminations 14, 15
eliminative deamination 180

elongation 242
Escherichia coli 251
factors 252
elution, proteins 78, 79

embryo, hemoglobin 280
emulsions 28, 270
enamel 340
emotions 8
enclosure, membranes 216
endocytosis 234, 235
receptor-mediated 278
endonucleases, restriction 258, 259, 425

endopeptidases see metalloproteases
endoplasmic reticulum (ER) 196, 226, 227


gluconeogenesis 154
protein folding 232, 233
protein synthesis 231
rough (rER) 226, 223

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smooth (seR) 172, 173, 226, 227
endomes 196, 234
endosymbiotic theory 210
endothermic reactions 20
energetic coupling 18, 17, 18, 112, 124-5, 125
ATP 16, 122, 124
coenzymes 106, 107
energetics 16-17, 17
coupling see energetic coupling
protein folding 74, 75
energy
activation 25
chemical 112, 122
conservation 106, 126-7, 127
definition 16
metabolism 336, 356
requirements 360, 361
engineering, genetic 258
enhancers 118
enol phosphate 124
endoase see phosphopru-
vate hydratase
enol-[ACP] reductase 168, 169, 421
enol-CoA
hydratase 165, 166, 428
isomerase 166, 167, 429
enterohypertonic circulation 194, 314
enteropeptidase (enteroki-
nase) 176, 270, 426
enthalpy 20-1, 21
folding 74
free 142, 143
entropy 20-1, 21
everoploleation 54, 55
enzyme—substrate com-
ples 92
enzyme-catalyzed reactions 90, 93
enzyme-linked immunoas-
say (EIA) 304
enzymes
activating 114
active centers 95
activity 88, 89
allosteric 92, 93
analysis 102-3
basics 88-9
catalysis 90-1, 216
classes 88, 89
see also individual classes
complement cascade 298
complexes 91, 95
conformations 92
glucose determination 102, 103
inhibitors see inhibitors
interconversion 114
isoenzymes 98, 99
isocitric 92, 93
kinetics 92-5
markers 198
nomenclature 420-30
pH 94, 95
polyol 177
reaction specificity 88
regulatory mechanisms 114
serum diagnosis 98, 178
substrate specificity 88
temperature 94, 95
turnover 88, 89
watersplitting 130
see also individual en-
zymes
epimerase 36
epimerases 89, 428
epipimerization 36, 37
epinephrine 159, 163, 352, 380
episodic release 372
equilibrium 16, 17, 18-19
constant (K) 18, 19
nitrogen 174, 175
potential 126, 350
equitorial (e) position 34
ER see endoplasmic reticu-
um
eggesterol 56, 57
ERK see MAPK
eric acid 49
erthrocites 274
glucocorticogenesis 154
metabolism 284-5, 285
erthromycin 254, 255
erthrophytes 286
erthropoietin 330
erythrose-4-phosphate 153
Escherichia coli
aspartate carbamoyl-
transferase 116
cell components 202-3
elongation 251
lactose operon 118
protein biosynthesis 251
pyruvate dehydrogenase 134, 135
replication 240, 241
termination 251
translation 251
essential amino acids (EAA) 60, 174, 360
active centers 99
biosynthesis 184, 185, 410, 412
non-essential 184, 413
essential fatty acids 46, 48
ester bonds 12
esterases 89
esterification 36, 37
esters 15, 47
estradiol 56, 57, 374, 376
estrogen 342
receptor 72, 73
ethanol 320
ethanol 27, 320-1, 321
ethanamine (EA) 50, 51, 62, 63
kinase 424
phosphate cytidytrans-
ferase 424
phosphotransferase 425
ethers 10, 11
ethidium bromide 262, 263
euchromatin 208, 238
eukaryotes 196, 197, 250, 251
event-regulated hormones 372
excision repair 256
excitation, electrons 128, 129
excretion
ammonia 326, 327
hormones 370
kidneys 322
liver 306
protons 326
exergonic processes 16, 17, 18, 112
exocytosis 226, 228, 229
neurotransmitters 348
exons 242, 243
exopeptidases 176, 177
exosomes 196
exothermic reactions 20
expression plasmids 262
extensin 42, 43
extracellular matrix (ECM) 346–7, 347
F
F type ATPase 220
F-actin 64, 65, 332
Fabes 184
Fad 346
factors, intrinsic 268, 269
FAO see flavin adenine dinucleotide
Faraday constant 19
farnesol 52, 53
farnesyl diphosphate 173
farnesyltransferase 423
Fas system 396
fat-soluble vitamins 46
fats 47, 48–9
biosynthesis 171, 409
brown 144, 145
degradation 410–11
digestion 270, 271
metabolism 162–3, 163, 312
nutrients 360
structure 48, 49, 51
synthesis, liver 162
uncouplers 144, 145
fatty acid synthase 12, 168, 169, 423
fat metabolism 162, 163
fatty acid–albumin complex 163
fatty acid-CoA ligase 163, 272, 273
fatty acids 46, 47, 48–9, 146, 312
degradation 163, 164–5, 165, 166–7
esential 46, 48
liver 162
long 166
muscle fibers 336
odd-numbered 166, 167
resorption 272
synthesis 113, 163, 168–9, 169
transport 164, 165
unsaturated 48, 166, 167
fatty liver 320
Fd see ferredoxin
Fe protein 184–5
Fe–Mo protein 184, 185
Fe-protoporphyrin IX 192
feedback inhibition 114, 115, 158
purines 188
fermentation 112, 146, 148–9, 149
ferredoxin 184, 185
ferredoxin-NADP+ reductase 422
ferritins 286, 287
ferrodoxin (Fd) 128, 129
fetal hemoglobin 280
FFA see free fatty acids
fibers
cotton 42
muscle 332, 337
red muscle 336
resorption 266
white muscle 336
fibrils 42, 344
elementary 42, 43
fibrin stabilizing factor 291
fibrin-stabilizing factor see protein-glutamine γ-glutamyltransferase
fibrinogen 291
fibrinolysis 292–3, 293
fibroin 70
fibroectins 346, 347
filaments
intermediate 70, 71, 204, 205, 206, 207
keratin 70, 71, 206
microfilaments 204, 206, 207
proteofilaments 71, 204
films
amphipathic 28
surface 29
filtration
cell 198
ultrafiltration 322
first-order reactions 22, 23
Fischer projections 9, 35, 59
fixation, carbon dioxide 130
flavin 104, 140
redox systems 33
flavin adenine dinucleotide (FAD) 32, 81, 104
pyruvate dehydrogenase 134
flavin mononucleotide (FMN) 32, 104, 105
ATP synthesis 142, 143
flavodoxin 72, 73
flavoprotein (Fp) 5-fluorouracil 402
fMet see N-formylmethionine folate 366
folic acid 254, 255
food 34, 266, 360
foreign genes 264
forks, replication 240
formate 4, 5
formic acid 49
N-formylmethionine (fMet)
250, 251
5-formyltetrahydrofolate cycligase 429
Fp see flavoprotein
fragments, Okazaki 240
frameshift mutation 257
free diffusion 218
free electron pairs 6
free enthalpy (G) 16, 142, 143
free fatty acids (FFA) 48
free radicals 32, 190, 256
fructose-1,6-bisphosphate 151
β-fructofuranosidase 38, 426
fructose
1,6-bisphosphatase 154, 155
bisphosphate 425
1,6-bisphosphate 150, 154, 159
2,6-bisphosphate 158, 159
2,6-bisphosphate 2-bisphosphatase 425
bisphosphate, adolase 310, 311, 428
t-fructose 36, 37, 39
1-phosphate 38, 310
6-phosphate 150, 151, 153, 155, 159
fructoses
gluconeogenesis 328
metabolism 310, 311
uptake 272
fucose 34, 44
l-fucose 39
fucolipidtransferase 292, 293
fuel, lipids 46
fumarate 136, 137, 182, 183, 189
dehydrogenase 136, 137
hydratase (fumarase) 183,
permeation chromatography 78
expression 236–7 foreign 264
libreries 260, 261
multiple 302 probes 260
regulation 118 structural 118
therapy 264, 265, 402
geenetics, molecular 236–65
geenomes 236, 238–9
geometric isomers 8
geraniol 52, 53
geranyl diphasate 173
eranyltransferase 423
germ-line DNA 302
Gibbs–Helmholtz equation
20, 21
 glandular hormones 372
GlcNAc see N-acetyl-β-glucosamine; N-acetyl-
glucosamine Glc, see β-glucuronic acid
globular proteins 72–3
globulins 276, 277
β-globulins 286
glucon 163, 308, 380
gluconeogenesis 154, 158, 159
glucon receptor 121
1,4-α-glucan, branching
enzyme 157, 423
α,1-4-glucan, chain 157
4-α-glucanotransferase 157, 423
β-glucuronafuranose 35
glycogen 120
gluconeogenesis 35, 113, 310, 311
amino acids 138, 154, 155, 180
cortisol 120, 121
 glucon 154, 158, 159
insulin 160, 161
recycling 328, 329
 gluconic acid 36
gluconolactonase 152, 425
 gluconolactone 37, 103
β-glucopyranose 34, 35
glucose 34, 35, 65, 146, 162
diabetic tissue 160, 161
brain 356
chain 35
β-glucose 34, 36, 39, 44
enzymic determination 102, 103
 gluconeogenesis 154, 155
 glycogen 156, 157
 glycocalyx 150, 151
insulin 121, 158, 159, 160, 161
kidney 160, 161
lactose operon 118
liver 160, 161
metabolism 120, 121
muscle 160, 161
oxidase 102, 103, 420
oxidation 36, 146, 147
reduction 36
transporter Glut-1 220, 221
uptake 272
glucose oxidation, hexokinase 147
glucose 1-phosphate 156,
157, 159, 310
glucose 6-phosphate 154, 155, 157, 425
glucose 6-phosphate 37,
150, 157, 152, 157, 159
dehydrogenase 152, 153,
420
 gluconeogenesis 154, 155
 isomerase 151, 429
pentose phosphate
pathway 153
α-glucosidase 224
glucoside formation 36
glucosuria 180
 glucosylceramide 50
 glucuronate 37
 glucuronic acid 36, 44
 β-glucuronidases 194
 glucuronosyltransferase
194, 195, 316, 317, 423
glutamate 178, 326, 357
 δ-kinase 424
decarboxylase 356, 357,
427
dehydrogenase 178, 179,
181, 183, 326, 327, 421
family 184, 185

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formiminotransferase 422
neurotransmitters 356
glutamate-NH₃ ligase 429
glutamic acid 60, 61
glutaminase 178, 179, 181, 327, 356, 357, 427
glutamine 60, 61, 178, 326, 357
brain 356
gluconeogenesis 328
muscle metabolism 338
purine biosynthesis 188, 189
pyrimidine biosynthesis 188, 189
synthase 64
synthetase 65, 124, 125, 356, 357, 429
glutamylphosphate reductase 420
glutathione 106, 284, 285
disulfide bonds 72
oxidized
peroxidase 284, 285, 421
reductase 284, 285, 421
glycer-3-phosphate dehydrogenase 212, 213
glycerol 5-phosphate 153
glyceroldehyde 310
α-glycerolphosphate 34
glycerolphosphate 3-phosphate 150, 151, 153, 155
glycerolphosphate dehydrogenase 124, 125, 420
glucose oxidation 147
α-glycerolphosphate shuttle 212, 213
glycolysis 150, 151
glycerol 27, 48, 49, 154, 170, 171
gluconeogenesis 328
kinase 155, 170, 171, 424
glycerol 3-phosphate 154, 155, 170, 171
dehydrogenase 155, 170, 171, 212, 213, 420
α-acyltransferase 170, 171, 423
glycerol phosphate O-acyltransferase 423
glycerol 1-phosphate 310
glycerol 3-phosphate 151, 154, 170, 171
α-glycerolphosphate 148
α-glycerolphosphate shuttle 212, 213
glycine 60, 61, 192, 193, 314
aminotransferase 336, 337, 422
collagen 70
dehydrogenase 421
hydroxymethyltransferase 422
glycinuria 322
glycogen 34, 35, 40, 41, 120, 127
balance 157
liver 156
metabolism 156-7, 157
muscle 156, 336
polymer 41
(starch) phosphorylase
see phosphorylase (starch) synthase 423
synthase 120, 121, 156, 157, 158, 159
kinase 3 (GSK-3) 388
glycogenin 34, 35, 156
glycolipids 35, 46, 47, 50-1
membranes 214
structure 50, 51
glycolysis 35, 113, 146, 150-9, 151, 336, 338
glycoproteins 35, 230
complex 45
forms 45, 45
mannose-rich 45
O-linked 45
glycaminoglycans 44-5, 346
N-glycosidic bonds 80
glycosidases 89, 426
O-glycosidases 231
N-glycosides 36, 37
N-glycosidic bonds 12, 13, 44, 123
N-glycosidic links 44
O-glycosidic links 44
glycosylation 62, 230
collagen 344
proteins 230, 231
sequence 230
glycosylceramide 50, 51
glycosyltransferases 89, 231
glyoxylic acid cycle 138
GMP 186, 187, 190, 191
synthase 429
Golgi apparatus 196, 226, 227
gonane 54, 55
GOT see aspartate transaminase
gout 186, 187
gpt130 392
GPT see alanine transaminase
gran 128, 129
granulocytes 274, 275
Grb-2 388
GroEl 232, 233
GroES 232, 233
grooves, strands 86
group transfer
coenzymes 106-7, 107, 108-9, 109
potential 12, 19
reactions 18, 19
group X 108
groups
hydroxyalkyl 106
leaving 14
prosthetic 104, 134, 142
growth factors 342
hormones 370
GSH see glutathione, reduced
GSK-3 see glycosynthase kinase-3
GSSG see glutathione, oxidized
GTP 136, 190, 191
dCp 240
GTP-binding proteins 398
guanidine
2′-O-methylguanidine 82, 83
7-methylguanidine 82, 83
guanidinoacetate 336
N-methyltransferase 336, 337, 422
guanine 80, 81, 186, 187
guanosine 80, 81, 186
5′-diphosphate (GDP) see GDP
5′-monophosphate (GMP) see GMP

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5'-triphosphate (GTP) see GTP
guanulate cyclase 358, 359, 388, 389, 428
l-gulonolactone oxidase 420
gyrase 240
inhibitors 254

H

H⁺ see hydronium ions
(H⁺O⁺); protons
H⁺-transporting ATP
synthase see ATP synthase, H⁺-transporting
H⁺-transporting ATPase 427
H⁺/K⁺-exchanging ATPase 270, 271, 427
Hageman factor 291
hair 70
Hartnup's disease 322
HAT medium 304
Haworth projections 34, 35
Hb see hemoglobin
HCO₃⁻ resorption 326
HDL 278
heart
absorptive state 308
muscle 332
heat
loss 20
c of reaction 20, 21
heat-shock proteins (hsp) 232, 378
heavy chains, IgG 300
helix 240
helices
1-helix receptors 384
7-helix receptors 225, 384
α-helix 67, 68, 69, 71
α-keratin 70, 71
collagen 68, 70, 344
DNA 84, 86
double 84, 86
left-handed 86
pitch 86
superhelix 70, 71
triple helix 70, 71, 344
helper T cells 294
heme
ATP synthase 142, 143
b 192
biosynthesis 192-3, 193,
210
catalase 25
coenzymes 106, 107, 140,
141
degradation 194-5, 195
groups 280
iron 286
monoxygenases 318
oxidase 194, 195, 422
oxidized 287
hemiacetals 10, 71, 34
hemicellulose 42
hemochromatosis 286
hemoglobin (Hb) 64, 65,
280-1, 281
allosteric effect 116, 280
buffers 288
transport 282, 283
hemoglobin 286, 287
Henderson–Haselbalch
equation 18, 19
heparin 290, 347
hepatic glycogen 156
hepatic metabolism 306
hepatocytes 163, 306, 307
heterochromatin 208, 238
heterogenous nuclear ribo-
nucleic acid (hnRNA) see
hnRNA
heterologous 40
heterotrophs 112, 128
Hevea brasiliensis 52
hexokinase 147, 159, 424
hexose monophosphate
pathway (HMP) see pen-
tose phosphate pathway
hexose-1-phosphate uridy-
lytransferase 310, 311, 424
hexoses 39
high-density lipoprotein
(HDL) see HDL
high-performance liquid
chromatography (HPLC)
Hill coef cient (H) 116
lupurrate 324
histidine 270, 380
histidine 59, 60, 61, 63, 184,
185
ammonia lyase 428
dissociation curves 58
lactate dehydrogenase
100
histone
acetyl transferase 244,
245
decaylase 244, 245
decaylases 64, 238, 239
non-histone proteins 238
phosphorylation 238
HIV 404, 405
HMG-CoA 172, 173, 312
dehydrogenase 420
lyase 312, 313, 428
reductase 172, 173
synthase 312, 313, 428
HMP see hexose mono-
phosphate pathway
hnRNA 236, 242
immunoglobulins 302
splicing 246, 247
homeostasis 322, 326, 328
blood 274
calcium 342, 343
cytokines 392
hormones 370
see also acid—base bal-
cance
homocysteine 110
homogenization 198
homogentisate 1,2-dioxo-
genase 421
homoglycans 40
homoserine
dehydrogenase 420
kinase 424
honey 38
hops 148
hormone response ele-
ments (HREs) 245, 378
hormone-sensitive lipase
162, 163
hormones 315, 322, 370-1,
371
action 120, 121, 378-9
biosynthesis 370, 382
carbohydrate metabolism 138
closed-loop feedback
control 372
degradation 383
differentiation 370
digestive processes 370
effects 370, 372, 373
episodic release 372
event-regulated 372
excretion 370
gastrointestinal 270
glandular 372
glucose metabolism 121
growth 370
hierarchy 372, 373
homeostasis 370
hydrophilic 120, 121, 380-9
inactivation 383
ion concentrations 370
juvenile 52, 53
lipophilic 120, 374-5, 375, 379
lipophilic see lipophilic hormones
metabolism 120-1, 370
neurohormones 348, 349
peptide 380, 381, 382-3
plasma levels 372-3, 373
protein hormones 380, 381
proteolysis 382
pulsatile release 372
receptors 120
regulation 120, 370, 371
renal 330-1, 331
second messengers 386-7
signal cascades 388-9
steroid see steroid hormones
tissue 370
transport 370
vitamins 364
HPLC see high performance liquid chromatography
HRE see hormone response elements
hsp see heat-shock proteins
human body 31
immunodeficiency virus (HIV) see HIV
humoral immunity 294
hyaluronic acid 346, 347
hyaluronic acid 41, 44, 45
hybridomas 304
hydration 26, 27, 44
shell 90
hydrite ions 32, 33, 104
hydrocarbons 46, 47
hydrochloric acid 266, 270, 271
hydrogen atoms 33
bonds 6, 7, 26, 68, 72
carbonate 182
chloride 30, 31
ions 288, 289
peroxide 24, 186, 284
catalysis 25
redox systems 33
reducing equivalents 33
sulfide 31
hydrolyses 88, 89, 234, 425
hydrolysis 266, 267
G of 38
hydrolytic cleavage 316
hydrolytic deamination 179, 180
hydrolyzable lipids 46
non-hydrolyzable 46
hydroxyl ions (H₂O⁺) 30, 31
hydroperoxyl radical 33
hydrophilic hormones 120, 121, 380-9, 385
hydrophilic molecules 26, 28
hydrophilic signaling substances 392
hydrophobic effects 72
hydrophobic molecules 26, 28
hydroquinone 33, 104
hydroxy radicals 284
3-hydroxy-3-methylglutararyl-CoA see HMG-CoA
3β-hydroxy-Δ5-steroid dehydrogenase 420
β-hydroxycarbonyl-CoA 164
3-hydroxyperoxyl-CoA dehydrogenase 165, 420
hydroxyl groups 106
hydroxyl thiamine diphosphate 135
3-hydroxybutyrate 141, 312
dehydrogenase 420
β-hydroxybutyric acid 160
3-hydroxyisobutyrate dehydrogenase 312, 313, 420
3-hydroxyisobutyryl-CoA dehydrogenase 425
hydroxyl ions (OH⁻) 30, 31
3-hydroxyacyl-CoA 141
dehydroxylation 62, 70
collagen 344
hydroxymethylbilane synthase 192, 193, 428
hydroxymethylglutaryl-CoA see HMG-CoA
3-hydroxypropionyl-[ACP] dehydratase 168, 169, 428
4-hydroxyphenylpyruvate dioxygenase 421
hydroxyproline, collagen 70
3β-hydroxysteroid dehydrogenase 420
17β-hydroxysteroid dehydrogenase 420
5-hydroxytryptophan 63
hydroxyurea 402
hyperhidrosis 194
hyperbolic plots 93, 97
hyperglycemia 160, 161
hyperlipidemia 160, 161
hyperpolarization 348
hyperuricemia 186, 187
hypervitaminosis 364
hypoidode 25
hypovitaminosis 364
hypoxanthine 186, 187, 304
phosphoribosyltransferase 186, 187, 402, 403, 423

ice 26, 27
idiotypic variation 302
IDIL 278
iduronic acid 44
IF see intermediary filaments
IFN see interferons
Ig see immunoglobulins
II see interleukins
imidazolonepropionase 427
imino acids 179
immune response 294-5, 295
immune system acquired 294
cytokines 392
inate 294
immunoassays 304, 305
immunoglobulins (Ig) classes 301
domains 300
heavy chains 302
IgA 300
IgD 300
IgE 300
IgG 44, 45, 64, 65
domains 300, 301
IgM 296, 300
light chains 302, 303
superfamily 296
variability 302, 303
IMP 186, 187
biosynthesis 188, 189

All rights reserved. Usage subject to terms and conditions of license.
proinsulin 76, 160, 161
receptor see insulin receptor
signal transduction 388, 389
insulin receptor 121, 224, 225, 388
substrate (IRS) 388
intensity factor 16
intercalators 225, 254
daunomycin—DNA complex 254
interconversion 134
enzymes 114, 115
processes 144, 394
pyruvate dehydrogenase 134
regulation 118, 120
interferons (IFN) 392
interleukins (IL) 392
IL-6 receptor 392
intermediary metabolism 112, 322
intermediate filaments (IF) 204, 205, 206, 207
α-keratin 70, 71
intermediate-density lipoprotein see IDL intermediates 142, 143
intermembrane space 210
international units (U) 88
interphase 394
intestines, pH 31
intramolecular transferases 89
intrinsic factor 268, 269
introns 242, 243
insulin 40, 41
invertase see β-fructofuranosidase
iodide catalysis 25
hypoiiodide 25
iodothyronines 374
ion channels 65, 126, 218, 222–4, 350, 384
see also individual receptors
ionic strength 78
ionizing radiation 256
ionotropic receptors 348, 354
ions calcium 328, 386
hormone concentrations 370
inorganic 202
products 30
IPTG see isopropylthiogalactoside
iron deficiency 286
distribution 287
ion, hemoglobin 280
metabolism 286–7, 287
protein 184–5
uptake 286
iron—sulfur centers 140, 141, 142, 143
iron—sulfur clusters 106, 107, 286, 287
iron–protoporphyrin IX 192
IRS see insulin—receptor substrate
islets of Langerhans 160
isovaloxazine see flavin (2R,3S)-isocitrate 9, 127
isocitrate 134, 141
dehydrogenase 136, 137, 420
glucose oxidation 147
tricarboxylic cycle 144, 145
isoelectric point 58, 59
isoenzymes 99
pattern 98
isolation, proteins 78
isoleucine 60, 61
isomerases 88, 89, 428
cis—trans-isomerases 89
coenzymes 108
isomerization, light-induced 358
isomers geometric 8
isomerism 8–9
isopentenyl diphosphate 52, 53, 172
isopentenyl-AMP 53
isoprenoids 52–3, 53, 172
isoprenylation 52
isopropylthiogalactoside (IPTG)
isosteric enzymes 92, 93
isotypes 302
isopylic centrifugation 200

All rights reserved. Usage subject to terms and conditions of license.
J

J segments 302
Janus kinases (JAK) 392
jaundice 194
joules 16, 17
juvenile hormone 52, 53

K

K⁺ channels 223
K systems 116
katal 88
keratan sulfate 247
keratin
filaments 206
α-keratin 70, 71
keratinus 194
ketamine 179
ketocidosis 288
ketocidotic coma 312
β-ketocyl-CoA 164
ketogenic amino acids 180
α-ketoglutarate see 2-oxo-glutarate
ketohexokinase 310, 311, 424
ketohexoses 38
β-fructose see β-fructose
ketone bodies 160, 161, 162, 163, 172
acid—base balance 288
biosynthesis 312, 313
brain 356
synthesis 410
ketonemia 312
ketones 10, 11, 162
ketonuria 160, 312
ketopentoses 38
β-ribulose see β-ribulose
ketoses 39
kidney, glucose 160, 161
kidneys 154, 288, 322-3, 323
kinetics
allosteric enzymes 116
aspartate 117
bisubstrate 94, 95
enzymes 92-3
inhibition 96, 97
see also reaction kinetics
Kₘ see Michaelis constant
Knall-gas 20
reaction see oxyhydrogen reaction

L

L segments 302
lac-repressor 118, 119
lactacidosis 288
β-lactam antibiotics 254
lactate 98, 99, 154, 155, 288
dehydrogenase see lactate dehydrogenase
gluconeogenesis 328
muscle 338
redox reactions 19
lactate dehydrogenase (LDH) 99, 420
activity 102, 103
catalytic cycle 100, 101
Cori cycle 338, 339
fermentation 148, 149
gel electrophoresis 99
gluconeogenesis 155
glucose oxidation 147
isoenzymes 98
structure 98
lactic acid 8, 9, 149
Lactobacillus 148, 149
lactoferrin 286, 287
lactose 38, 39
allo lactose 119
lactose operon 118
opera 118, 119
laminin 346
lanosterol 173
lattices
hexagonal 27
ice 26
lauric acid 49
LDH see lactate dehydrogenase
LDL 278
receptor 278
leaving groups 14
lecithin see phosphatidylcholine
lecithin-cholesterol acyltransferase (LCAT) see phosphatidylcholine-sterol acyltransferase
left-handed α-helix (α₁₁) 68
Lesch—Nyhan syndrome 186
leucine 60, 61
transaminase 424
leukocytes 274
leukotrienes 390
liberins 372
libraries
DNA 260, 261
genes 260, 261
Lieberkühn glands 268
life cycle, HIV 404
ligand-gated channels 222
nicotinic acetylcholine receptor 222
ligands 118, 119
modulation 114, 115
oncogenes 398
ligases 88, 89, 106, 429
light
absorption 102, 103, 128, 129
monochromatic 102
ultraviolet 256
light chains
biosynthesis 302
IgG 300
light-induced isomerization 358
lignoceric acid 49
Lineweaver–Burk plots 92, 93, 96
linoleic acid 48, 49
linolenic acid 48, 49
lipase 268, 269
lipid 46-57
alcohols 46
anchors 214
classification 47
complex 170-1
hydrolysis 266
hydroperoxide glutathione peroxidase 421
lipoproteins 278
membranes 214, 215, 216
metabolism 160, 306, 312-13, 313
resorption 272, 273
role 46, 47
synthesis 226
lipid-soluble vitamins 46, 364-5, 365
lipamide 106, 107, 134
arm 134, 135
lipogenesis 162
lipoic acid 62, 106
lipolysis 162
lipophilic hormones 120, 374-5, 375, 378, 379
receptors 378, 398
lipoprotein 278-9, 279
lipase 162, 163, 278, 279,
lithocholic acid 56, 57, 314
liver absorbptive state 308
alcohol 320
cirrhosis 320
damage, alcohol 321
liver, fat synthesis 162
fatty 320
fatty acids 162
functions 306-7, 307
glucose 160, 161
glycogen 156
metabolism see liver metabolism
postabsorptive state 308
postresorption 309
resorption 309
urea 182
liver metabolism 306, 307
ammonia 178, 179
glucose 120, 121
long-chain fatty-acid-CoA ligase 429
loops chromosomes 238
mobile 99
peptides 98
low-density lipoprotein see LDL
lumen, chloroplasts 128, 129
lyases 88, 89, 427-8
lymphocytes 161, 274, 275, 294
monoclonal antibodies 304
lymphokines 392
lysinen cycle 312
lysine 60, 61, 184
hydroxyase see procollagen lysine 5-dioxygenase
lysines, acetylation 238
lyso phosphatidate 170, 171
lyso phospholipid 50, 51
lysosomes 196, 234-5, 235
pH 31
lysozyme 42

M phase 394
M13 phage 260, 404
mAb see monoclonal anti-

membrane receptors 224-5, 398
membranes
attack complex 298
carbohydrates 216
cell interaction 216
composition 216
cytoskeletal anchors 216
depolarization 348
electrochemical gradients 126
energy conservation 126-7
functions 216-17
hyperpolarization 348
lips 214, 216, 409
micones 28
mitochondrial 210
nuclear 208
permeability 218, 219
plasma 196, 214-15
potential 126, 127, 350
proteins 214, 216
proton gradients 126, 127
receptors see membrane receptors
semipermeable 78
transport 216-19
uncouplers 144, 145
vesicles 28, 198
menaquinone 52, 53
menthol 52, 53
6-mercaptouridine 402
messenger RNA see mRNA messengers, second see second messengers
metabolic acidoses 160, 161, 268, 326
metabolic charts 406-10
metabolic defects, gene therapy 265
metabolic pathways 88
hormones 370
metabolism 356-7
acetylcholine 354, 355
antimetabolites 402, 403
buffer function 308-9
calcium 342-3
carbohydrate 388
creatine 336
dependence, brain 356
glycogen 157
hormones 120-1, 370, 376-7
intermediary 112, 113, 322
Index

455

All rights reserved. Usage subject to terms and conditions of license.
myofibrils 332
myoglobin 72, 73, 282, 336
myosin 64, 65, 332
ATPase 427
tropomyosin 64, 65, 332, 334
myristic acid 49

N
N terminus 66
N-bound oligosaccharides 230
Na’/K’-ATPase 126, 127, 272, 273, 326, 327, 350, 351, 427
NAD’ 99, 101, 104, 366
NADH ratio 144
biosynthesis 208
gluconeogenesis 155
redox reactions 19
NADH 101
dehydration 141, 421
glucose oxidation 147
NADH+H+ 142, 143
ATP synthesis 142
NADPH 33, 104, 105, 366
photosynthesis 128, 129, 131
NADPH+H+ 33, 152, 190, 191, 264
photosynthesis 128, 129
native conformation 72
nephron 322
Nernst equation 126, 127
nerve cells 348, 349
nervonic acid 49
net charge, amino acids 59
net outcome 136
NeuAc see N-acetyllneuraminic acid
neural synapses 349
neural tissue 308
neuraminidases 276, 426
neurohormones 348, 349
neuropeptides, proteolysis 382
neurotransmitters 62, 63, 348, 349, 352-3, 353
GABA 62, 63, 356
glutamate 356
receptors 354-5, 355
neutral amino acids 60
urea 182
niacin 366
nicotinamide 366
adenine dinucleotide oxidized see NAD’ reduced see NADH adenine dinucleotide phosphate oxidized see NADP’ reduced see NADPH nicotinate 366
nicotinic acetylcholine receptor 223
nitric oxide synthase 388, 389
nitrogen 11
balance 174
fixation 184, 185
monoxide (NO) 388, 389
nitrigenase 184, 185, 422
norepinephrine 145, 163, 317, 352
nuclear localization sequence 208
nuclear pores 208, 209
nuclear tumor suppressors 398
nucleic acids
bases 80, 81
genetic information 236
hydrolysis 266
see also individual nucleic acids
nucleobases
components 188, 189
see also purine ring; pyrimidine ring
nucleolus 208
nucleophilic substitutions 14, 15
nucleosides 426
nucleoside 80, 81
diphosphatase 427
diphosphate kinase 190, 191, 424
phosphate 106, 107
kinase 190, 191, 424
nucleoside diphosphate reductase 190, 191
nucleosomes 65, 238
nucleotides 80-1, 81
biosynthesis 190-1, 191, 417-18
degradation 186-7, 187,

419

dinucleotides 80
nucleotide triphosphates 110, 122
see also individual nucleotides
nucleus 196, 208-9, 209
and cytoplasm 208, 209
fractionation 198
localization sequence 208
membrane 208
poles 208, 209
scaffolding 238
tumor suppressors 398
nutrients 112, 306, 360, 361

O2 see oxygen
core rule 2
ODH see 2-oxoglutarate dehydrogenase
OH- see hydroxyl ions (OH-) oil
drop effect 28, 29
emulsions 28
Okazaki fragments 240
oleic acid 49
oligo-1,6-glucosidase 426
oligonucleotides 80, 81
oligosaccharides 44, 45, 230, 272, 273
OMP 188, 189
oncogenes 398-9, 399, 400
one-helix receptors 224
operators 118
opsin 358
opsonization 298
optical activity 8
optical isomers 8, 9
optical rotation 36
orbitals 2, 4, 5
organ metabolism 308-9
organelles 196, 198, 199
organic compounds 2
organic substances 360-1
organisms
heterotrophic 128
phototrophic 128
orientation, substrates 90, 100
origin of replication 240
ornithine 62, 63, 182, 183
carbamoyltransferase
periplasm 35
permeability, membranes 218, 219
peroxidases 119
peroxidases 89, 102, 103, 106, 305, 421
peroxide anions 284
pH 18
cells 30, 31
enzymes 94, 95
fermentation 148
pH, gradient 127
membrane difference 126
neutral 30
phages see bacteriophages
phagocytosis 234, 235
phallolidin 204
phenobarbital 194
phenylalanine 60, 61
4-monoxygenase 422
phenylethanolamine N-
methyltransferase 352, 353, 422
phosphinhyrin 130, 131
phosphates 12
ATP transfer 123
buffers 288
ions 328
residues 12
transport 213
phosphatases 47, 50, 51,
170, 171
cytohydrolase 170, 171, 425
lysophosphatidate 170, 171
phosphatase 170, 171, 425
phosphatidic acids 46
phosphatidylcholine 50, 51,
170, 212, 213
sterol acyltransferase 278, 279, 423
phosphatidyethanolamine 50,
170, 171, 212, 213
phosphatidylinositol 50,
170, 171, 212, 213
phosphatidylinositol 4, 5-
biphosphate (PIP2) 170, 171
phosphatidylinositol 4-
phosphate kinase 170, 171
phosphatidylycerine 50, 170, 171, 212, 213
phospho-a-yenosine phospho-
phosphat (PAPS) 110, 111
phosphodiesterase 120, 121,
386, 387, 425
phosphoeylpyruvate see
phosphoenolpyruvate
phosphoenolpyruvate
phosphokinase see PEP
phosphofructokinase 158,
159
glucone oxidation 147
glycolysis 150, 151
phosphoglucomutase 429
phosphoglucosamine
phosphogluconate 6,
phosphogluconate 152,
153
dehydrogenase 153, 420
phosphogluconolactone
phosphoglycerate 2,
phosphoglycerate 125,
150, 151, 153
3-phosphoglycerate 150,
151, 155
dehydrogenase 420
kinase 131, 147, 424
phospholipases
A1, 425
A2, 268, 390, 391, 425
C, 386, 387, 423
D, 425
phospholipids 46, 47, 50-1,
51
biosynthesis 171
blood clotting 290
degradation 411
lipid metabolism 312
lysophospholipids 50
membranes 214
structure 51
phosphomevalonate kinase
phosphopantetheine 12
phosphoprotein
phosphatase 394, 395,
425
phosphates 120, 121
phosphopyruvate hydratase
124, 428
5-phosphoribosyl 1-diphos-
phate (PRPP) 188, 189
phosphoribosylamine gly-
cine ligase 429
phosphoribosylaminomoi-
dazole
phosphoramidon
phosphoribosylformylglyci-
namidase syn hyse 429
phosphoribosylglycinamidase
formyltransferase 422
phosphoribosylformyltransferase
phosphoribosylformyltransferase 422
phosphoribulosine 131
phosphoric acid, esters 10,
11, 80
phosphoric acid, anhydride
11, 80
phosphoric acid—ester,
bonds 12, 13, 122, 123
phosphoric acid—ester
phosphorus II
phosphorylation 120, 121, 423
carbohydrate metabolism
159
glycogen metabolism
156, 157
kinase 424
phosphorylation 62, 106
ATP-dependent 114
cyclic 130, 131
dephosphorylation 114
histones 238
oxidative 112, 122, 140,
210
protein kinase A 120, 121
substrate-level 122, 124,
150
phosphoenine transami-
nase 424
phosphatidylinositol
1-phosphatidylinositol-
4-kinase 424
1-phosphatidylinositol
4-phosphate kinase
424
phosphatidylinositol
phosphatidylinositol (PtdIns) 170
phosphatidylinositol-3-
kinase (PI3K) 388
phosphatidylinositol-4, 5-
biphosphate (PIP2, Ptd
InsP2) 170
phosphotransferases 89
photolyase see deoxyribodi-
pyrimidine photolyase
<table>
<thead>
<tr>
<th>Index</th>
</tr>
</thead>
<tbody>
<tr>
<td>propionyl-CoA 166, 167</td>
</tr>
<tr>
<td>carboxylase 166, 167, 429</td>
</tr>
<tr>
<td>proprotein 230</td>
</tr>
<tr>
<td>prostacyclins 390</td>
</tr>
<tr>
<td>prostaglandins 390</td>
</tr>
<tr>
<td>prostaglandin H-syn- thase 390, 391, 422</td>
</tr>
<tr>
<td>prosthetic groups 104, 134, 142</td>
</tr>
<tr>
<td>proteasomes 176, 177</td>
</tr>
<tr>
<td>protein disulfide isomerase 233, 429</td>
</tr>
<tr>
<td>glycoryltransferase 231, 423</td>
</tr>
<tr>
<td>lysine 6-oxidase 344, 345, 421</td>
</tr>
<tr>
<td>phosphatases 114, 144, 145, 392</td>
</tr>
<tr>
<td>tyrosine kinase 424</td>
</tr>
<tr>
<td>see also proteins</td>
</tr>
<tr>
<td>protein folding 72, 74-5, 75, 174</td>
</tr>
<tr>
<td>endoplasmic reticulum 233</td>
</tr>
<tr>
<td>energetics 74</td>
</tr>
<tr>
<td>rough endoplasmic reticulum 232</td>
</tr>
<tr>
<td>protein kinases (PK) 114, 394, 395, 424</td>
</tr>
<tr>
<td>ERK 388</td>
</tr>
<tr>
<td>inactivating 144</td>
</tr>
<tr>
<td>MEK 388</td>
</tr>
<tr>
<td>oncogenes 398</td>
</tr>
<tr>
<td>PDK-1 388</td>
</tr>
<tr>
<td>PK-A 120, 121, 386, 387</td>
</tr>
<tr>
<td>PK-B 388</td>
</tr>
<tr>
<td>Raf 388</td>
</tr>
<tr>
<td>second messengers 348</td>
</tr>
<tr>
<td>protein metabolism 174-5, 175, 306</td>
</tr>
<tr>
<td>muscle 338, 339</td>
</tr>
<tr>
<td>protein-glutamine γ-gluta- myltransferase 423</td>
</tr>
<tr>
<td>proteinases 176, 290</td>
</tr>
<tr>
<td>proteinogenic amino acids 60-1, 61</td>
</tr>
<tr>
<td>non-proteinogenic 62-3 proteins 64-5, 63</td>
</tr>
<tr>
<td>adaptor 388</td>
</tr>
<tr>
<td>adhesive 346</td>
</tr>
<tr>
<td>allosteric 72</td>
</tr>
<tr>
<td>analysis 78</td>
</tr>
<tr>
<td>biosynthesis 174</td>
</tr>
<tr>
<td>catalysis 64</td>
</tr>
<tr>
<td>channels 218</td>
</tr>
<tr>
<td>clotting factors 290</td>
</tr>
<tr>
<td>defense 64</td>
</tr>
<tr>
<td>denaturation 74, 75</td>
</tr>
<tr>
<td>dynamics 72, 73</td>
</tr>
<tr>
<td>elution 78</td>
</tr>
<tr>
<td>Escherichia coli 251</td>
</tr>
<tr>
<td>folding see protein folding</td>
</tr>
<tr>
<td>globular 72-3</td>
</tr>
<tr>
<td>glycosylation 230, 231</td>
</tr>
<tr>
<td>gradients 127</td>
</tr>
<tr>
<td>heat-shock (hsp) 232</td>
</tr>
<tr>
<td>hyaluronate 346</td>
</tr>
<tr>
<td>hydrolysis 266</td>
</tr>
<tr>
<td>isolation 78</td>
</tr>
<tr>
<td>lysosomal 234, 235</td>
</tr>
<tr>
<td>marking 174</td>
</tr>
<tr>
<td>maturation 230-3</td>
</tr>
<tr>
<td>mediator 224</td>
</tr>
<tr>
<td>membranes 214, 215, 216</td>
</tr>
<tr>
<td>metabolism see protein metabolism</td>
</tr>
<tr>
<td>mitochondrial import 232, 233</td>
</tr>
<tr>
<td>motive force 127</td>
</tr>
<tr>
<td>movement 64</td>
</tr>
<tr>
<td>non-histone 238</td>
</tr>
<tr>
<td>nutrients 360</td>
</tr>
<tr>
<td>overexpression 262, 263</td>
</tr>
<tr>
<td>plasma 277</td>
</tr>
<tr>
<td>polyproteins 382</td>
</tr>
<tr>
<td>post-translational modification 62, 174</td>
</tr>
<tr>
<td>preprotein 230</td>
</tr>
<tr>
<td>proprotein 230</td>
</tr>
<tr>
<td>regulation 64</td>
</tr>
<tr>
<td>regulatory 114, 119</td>
</tr>
<tr>
<td>resorption 266</td>
</tr>
<tr>
<td>ribosomal 250</td>
</tr>
<tr>
<td>single-strand-binding 240</td>
</tr>
<tr>
<td>sorting 174, 228-9, 229</td>
</tr>
<tr>
<td>stabilization 74</td>
</tr>
<tr>
<td>storage 64</td>
</tr>
<tr>
<td>structure 64, 68-71</td>
</tr>
<tr>
<td>synthesis 230-1, 231</td>
</tr>
<tr>
<td>transport 64, 220-1</td>
</tr>
<tr>
<td>proteoglycans 34, 35, 340, 346, 347</td>
</tr>
<tr>
<td>proteohormones 380, 381</td>
</tr>
<tr>
<td>proteolysis 174, 176-7</td>
</tr>
<tr>
<td>enzymes 177</td>
</tr>
<tr>
<td>hormones 382</td>
</tr>
<tr>
<td>neuropeptides 382</td>
</tr>
<tr>
<td>prothrombin 291</td>
</tr>
<tr>
<td>prothrombinase complex 291</td>
</tr>
<tr>
<td>proto-oncogenes 398, 399, 400</td>
</tr>
<tr>
<td>protofilaments 70, 204</td>
</tr>
<tr>
<td>proton channels, ATP synthase 142, 143</td>
</tr>
<tr>
<td>proton gradients 126, 140, 210, 212</td>
</tr>
<tr>
<td>membranes 126, 127</td>
</tr>
<tr>
<td>protons</td>
</tr>
<tr>
<td>excretion 326</td>
</tr>
<tr>
<td>gradient see proton gradient</td>
</tr>
<tr>
<td>motive force (P) 126</td>
</tr>
<tr>
<td>pumps 126, 127</td>
</tr>
<tr>
<td>secretion 227</td>
</tr>
<tr>
<td>transfer 14, 18, 19</td>
</tr>
<tr>
<td>protoporphyrin IX 192, 193</td>
</tr>
<tr>
<td>protoporphyrinogen IX 192, 193</td>
</tr>
<tr>
<td>proximity, substrates 90, 100</td>
</tr>
<tr>
<td>PRPP see 5-phosphoribosyl-1-diphosphate</td>
</tr>
<tr>
<td>pseudouridine 82, 83</td>
</tr>
<tr>
<td>PTH see parathyroid hor- mone</td>
</tr>
<tr>
<td>pulsatile release, hormones 372</td>
</tr>
<tr>
<td>purines 80, 81</td>
</tr>
<tr>
<td>biosynthesis 188-9, 189</td>
</tr>
<tr>
<td>190, 417</td>
</tr>
<tr>
<td>degradation 186, 187</td>
</tr>
<tr>
<td>derivatives 352</td>
</tr>
<tr>
<td>ring 188, 189</td>
</tr>
<tr>
<td>pyranoses 34</td>
</tr>
<tr>
<td>pyridine nucleotides 32, see also NAD+, NADP⁺</td>
</tr>
<tr>
<td>pyridoxal 368</td>
</tr>
<tr>
<td>phosphate (PLP) 62, 178, 358, 368</td>
</tr>
<tr>
<td>transamination 108, 109</td>
</tr>
<tr>
<td>see also vitamin B₆ complex</td>
</tr>
<tr>
<td>pyridoxamine 179, 368</td>
</tr>
<tr>
<td>phosphate 108, 178, 179</td>
</tr>
<tr>
<td>pyridoxol 368</td>
</tr>
<tr>
<td>pyrimidines 80, 81</td>
</tr>
<tr>
<td>biosynthesis 188-9, 189, 190, 418</td>
</tr>
<tr>
<td>degradation 186, 187</td>
</tr>
<tr>
<td>ring 188, 189</td>
</tr>
</tbody>
</table>
pyrrolines 421
1-pyrroline-5-carboxylate dehydrogenase 421
pyrrole-5-carboxylate reductase 421
pyruvate 35, 39, 154, 155, 338
2-oxoglutarate 141
carboxylase 159, 429
decarboxylase 427
dehydrogenase see pyruvate dehydrogenase
glycolysis 150, 151
kinase 151, 159, 424
redox reactions 19, 101
transport 212
pyruvate carboxylase 138, 139, 155
pyruvate decarboxylase, fermentation 148, 149
pyruvate dehydrogenase (PDH) 210, 421
Escherichia coli 134, 135
glucose oxidation 147
kinase 424
tricarboxylic cycle 144, 145
pyruvate kinase 147
glucagon 158, 159
glycolysis 150, 151

Q
Q see coenzyme Q, oxidized (ubiquinone)
Q cycle 126, 127
QH2 see coenzyme Q, reduced (ubiquinol);
plastoquinone quaternary structure 76
quinol system 32
quinones 104, 131
hydroquinone 33, 104
redox systems 33
semiquinone radical 32, 33, 104
system 32
see also plastoquinone

R
R conformation 117
hemoglobin 280, 281
R state 116
R/S system 8
radiation 256
radicals 32, 256
hydroperoxyl 33
hydroxyl 33, 264
semiquinone 32, 33, 130, 131
superoxide 284
tyrosine 190, 191
radioimmunoassays (RIA) 388
Ramachandran plot 66
Ras 388
rate constants 22, 23
reaction centers 132, 133
P50 130, 131
heat of 20, 21
reactions catalyzed 25
dergonomic 112
enzyme specificity 88, 89
genome-catalyzed 90, 93
exergonomic 112
first-order 22, 23
kinetics 22-3
order 22, 23
rates 22, 23, 88
second-order 22, 23
specificity 88, 89
spontaneous 18
substrate specificity 88, 89
uncatalyzed 90
reactive oxygen species (ROS) 33, 284, 285
reagents 102, 103
modifying 97
rearrangements 14
see also isomerizations
receptor signaling 216
recognition particle (SRP) 230
signal transfer 224
receptor-mediated endocytosis 278
receptors 1-helix 224, 384
7-helix 224, 384
acetylcholine 354
antigen 296, 297
co-receptors 296
cytokines 392
domain 224
effects of 225
glucagon 121
hormones 120
insulin 224, 225, 388
ion channels 126, 218, 222-4, 350, 384
ionotropic 348, 354
lipophilic hormones 378, 398
membrane 216, 224-5
metabotropic 348, 354
neurotransmitters 354-5, 355
nicotinic acetylcholine 222
oncogenes 398
photoreceptors 358, 359
signaling see receptor signaling
steroid 378
substrates 388
synapses 348
T-cell 224
see also individual receptors
reciprocal velocity 93
recombination repairs 256
somatic 302, 303
recycling 328-9, 329
redox coenzymes 104, 105, 106-7, 107, 140
see also flavins; heme groups; iron—sulfur centers
potential (E) 18, 19, 32
processes 32-3
reactions see redox reactions
series 32, 130, 131, 142
systems see redox systems
redox reactions 14, 15, 32, 33
lactate 19, 100, 101
NAD+ 18, 19, 101
pyruvate 19
redox systems 32
biological 32, 33
coenzyme Q (CoQ) 105
flavin 33
hydrogen peroxide 33
respiratory chain 142, 143
reduced forms, electrons 32
reducing agents 32
reductases 89
reduction 316
equivalents 32, 33, 212
glucose 36, 37
refsum disease 166
regions, signal 228
regulation 114-21, 144-5
allosteric 116
carbohydrate metabolism 158-9
gene 118
glycogen metabolism 156
interconversion 120
transcription 118-20, 244
tricarboxylic cycle 144
regulatory proteins 114, 118, 119
relative velocity 25
renal hormones 330-1, 331
renin 330, 331, 427
renin—angiotensin system 330, 337
repair, mutations 256, 257
replication 208
DNA polymerases 240
Escherichia coli 240, 241
forks 240
genetic information 236, 240-1
origin of 240
repolarization 350
repression, transcription 114
repressors 118
rER see rough endoplasmic reticulum
RES see reticuloendothelial system
residual bodies 234
resonance 4, 5, 32, 66, 67
resorption 266, 267, 272-3, 273
HCO3 326
liver 309
minerals 362
urine 322
respiration 144, 145, 146-7
respiratory chain 106, 112, 126, 140-1, 210
ATP synthesis 142
components 132, 140, 141
redox systems 142, 143
respiratory control, ATP synthase 144, 145
resting potential 126, 350, 351
restriction endonucleases 258, 259, 264, 425
restriction fragment length polymorphisms see RFLP
reticuloendothelial system (RES) 358, 359, 429
retinol 52, 53
retinoic acid 364
retinoic acid 359, 420
retroviruses 404
reverse transcriptase see RNA-directed DNA polymerase
RFLP 265
sickle-cell anemia 262, 264
rhesus (Rh) blood groups 292
rhinovirus 404, 405
Rhizobium 184
rhodopsin 224, 358
RNA see radioimmunoassay
riboflavin 366
ribonucleic acid,
transcription 243
ribonuclease A 14, 75
H 404, 405, 426
ribonuclease 426
ribonucleic acid (RNA) see RNA
ribonucleoside diphosphate reductase 190, 191, 403, 422
ribonucleotide reductase see ribonucleoside diphosphate reductase
reduction 191
ribose 12, 123
phosphate pyrophosphokinase 424
ribose 34, 38, 39
ribose 5-phosphate 152, 153, 429
ribosomal RNA see RNA ribosomes 82, 236
eukaryotes 250, 251
fractionation 198
proteins 250
ribonucleases see ribonucleic acid,
riboneses 82, 236
ribuloses 39, 128, 152
ribulose phosphate 3-epimerase 428
ribulose 5-phosphate 152, 153
ribulose bisphosphate, carboxylase 130, 131, 427
Richardson diagrams 72, 73
rifamycin 254, 255
righthanded helix
α-helix (αh) 68
double 86
RNA 80, 81, 82-3, 83, 87
conformation 86
InRNA 236, 246, 247, 302
immunoglobulins 302
maturaton 208, 236, 242, 243, 246-7
transcription 242, 243
translation 83
see also mRNA; rRNA; snRNA; tRNA
RNA polymerase see DNA-directed RNA polymerase
RNA-binding proteins 82
RNA-directed DNA polymerase 404, 405, 425
cells 358
root nodules 184, 185
ROS see reactive oxygen species
rotation 67
rough endoplasmic reticulum (rER) 226, 227, 231, 232
rougshage 42, 273
rRNA 82
SS-rRNA 86, 87
RT-PCR 264, 265
rubber 52, 53
rubisco see ribulase bisphosphate carboxylase
S see Svedberg units
S phase 394
saccharase see β-fructofuranosidase
Saccharomyces cerevisiae 148, 149
SAH see S-adenosyl-L-homocysteine
salicylate 317
saliva 268, 269
salt, precipitation 78, 79
SAM see S-adenosyl-L-methionine
sarcomeres 332
sarcoplasmic Ca\(^{2+}\) pump 220, 221
sarcoplasmic reticulum (SR) 334, 335
scaffolding
 cytoskeletal 206
 nuclear 238
 Schiff’s base 108
 SDS gel electrophoresis 78, 79
 second messengers 224, 348
 glycolipids 50
 hormones 120, 121, 384, 386–7
 see also individual messengers
 second-order reactions 22, 23
 secondary structure 68–9, 76
 secretin 270
 secretions
 kidney 322
 pancreas 268–9
 small intestines 268–9
 secretory pathway 228
 sedimentation coefficient 200
 sedoheptulose bisphosphatase 425
 sedoheptulose 153
 selenocysteine 6, 63
 self-protection, blood 274
 semiquinone radical 32, 130, 131
 sense strands 84
 separation, spontaneous 29
 sequences
 glycosylation 230
 nuclear localization 208
 peptides 86
 sequencing 261
 sequential mechanisms 90, 91, 94, 95
 sER see smooth endoplasmic reticulum
 serine 50, 51, 60, 61, 63
dehydratase 181, 428
 family 184, 185
 proteases 176, 177, 298
 proteinases 177, 425
 serotonin 62, 63
 serum 274
 enzyme diagnosis 98, 178
 seryl alanine 65, 66, 67
 seven-helix receptors 224
 SH2 domain 392
 short tandem repeats (STRs) 264
 shuttles 212
 sialic acid see N-acetylneuraminic acid
 sickle-cell anemia 249, 264, 265
 sight 358–9
 sigmoidal substrate saturation curves 116
 signal
 cascades see signal cascades
 peptidase 427
 peptides 228, 230, 231
 receptor transfer 224
 regions 228
 signaling see signaling
 SRP see signal recognition particle
 stop-transfer 230
 transduction see signal transduction
 translocation 228, 229
 transmission see signal transmission
 signal cascades
 hormones 388–9
 photoreceptors 358, 359
 signal recognition particle (SRP) 230, 231
 receptor 230
 signal transducers and activators of transcription see STAT
 signal transduction 120
 cytokines 392, 393
 G proteins 384, 385
 insulin 388, 389
 oncogenes 398
 proteins (STPs) 392
 signal transmission
 CNS 348–9
 synaptic 348
 signaling amino acids 380, 381
 calcium 342
 cytokines 392–3
 eicosanoids 46, 390–1
 hydrophilic substances 392
 membranes 216
 second messengers 224
 steroids 46
 silencers 118
 silk 70, 71
 single–strand-binding proteins 240
 single-stranded DNA (ssDNA)
site-specific deoxyribonuclease see restriction endonucleases
 β-sitosterol 56, 57
 size, molecular 218
 skeletal muscles 332
 small intestines 31, 268, 269
 small nuclear ribonucleoprotein particles (snRNPs) 246
 small nuclear RNA (snRNA) 82
 smooth endoplasmic reticulum (sER) 172, 173, 226, 227
 smooth muscle 332, 338
 sn see stereospecific numbering
 SNAREs 228, 229
 snRNA, splicing 83
 snRNPs (snurps) 246
 soap bubbles 28, 29
 sodium chloride dissolution 21
 dodecylsulfate see SDS
 ions 328
 voltage-gated channel 221, 223
 solenoids 238
 solubility 28, 29
 soluble coenzymes 104
 solvents 26–7, 94
 somatic mutation 302

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somatic recombination 302
somatotropin 64, 65
receptor 64
son of sevenless see SOS
sorbitol 36, 37
α-sorbitol 39
sorting, proteins 174, 228-9, 229
SOS, adaptor proteins 388
space
space, intermembrane 210
matrix 210
spectrin 206
spectrophotometry 102, 103
sphingolipids 46, 47, 51, 170
sphingomyelin 214, 215
sphingophospholipid 51
sphingosine 51
N-acetyltransferase 423
spliceosomes 246, 247
splicing
hnRNA 246, 247
snRNA 83
spontaneous separation 29
squalene 52, 53, 172, 173
SR see sarcoplasmic reticulum
ssDNA see single-stranded DNA
stabilization
catalysis 90
transition states 100, 101
starches 40, 42, 43
brewing 148, 149
start codons 240, 250
STAT 392
statins 372
stationary phase 54
stearic acid 49
stearoyl-CoA desaturase 422
stercobilin 195
stercobilinogen 194, 195
stereospecific numbering (sn)
stereospecificity 8
steroid alcohols see sterols
steroid hormones 56, 57, 172, 374, 377
biosynthesis 376
conjugates 110
inactivation 376
metabolism 376-7, 377
see also individual hormones
steroids 46, 52, 53, 54-7, 55
hormones see steroid hormones
receptors 378
signaling 46
steroid 11β-monooxyge-
nase 422
steroid 17α-monooxyge-
nase 422
steroid 21-monooxyge-
nase 422
steroid -isomerase 429
structure 54
synthesis 410
sterol esterase 268, 269
sterol esters 47
sterols 46, 54, 55, 56, 57
see also cholesterol;
ergosterol; farnesol;
sterol; stigmasterol
stearylgllycerols,
tristearylglycerol 49
stigmasterol 56, 57
stop codons 240, 250
stop-transfer signal 230
storage, liver 306
STP see signal transduction protein
strands
double 85
grooves 86
matrix 85
sense 85
Streptococcus 148, 149
Streptomyces lividus 222, 223
streptomyacin 254
striated muscle 333
stroma 128, 129
STRs see short tandem repeats
structural genes 118
structure 6
dimers 116
isomers 8
polysaccharides 40
primary 76
proteins 68, 70-1
secondary 76
tertiary 76
quaternary 76
Stuart–Prower factor see coagulation factor X
Stuart–Prower factor 291
substitution, nucleophilic 14
substrate-level phosphory-
lization 150
substrates
activity 95
analogs 96, 97
bisubstrate kinetics 94, 95
coenzymes 105
concentration 97, 116
cosubstrates 104
enzymes 94
insulin 388
orientation 90, 100
phosphorylation 122,
124, 125
proximity 90, 100
receptors 388
specificity 88, 89, 94
suicide 96, 97
sucinate 136, 137
dehydrogenase 136, 137,
140, 421
glucose oxidation 147
semialdehyde dehydro-
genase 356, 357, 420
succinate-CoA ligase 136,
137, 147
(GDP-forming) 429
succinic acid 8, 9
succinyl phosphate 125
succinyl-CoA 136, 137, 166,
167
heme biosynthesis 192,
193
ligase 124, 125
sucrose 38, 39
α-glucosidase 426
density gradients 201
sugar 38
alcohols 38, 39
see also mannitol; sorbitol
amino 44
suicide substrates 96, 97
sulfathiazole 255
sulfates 50, 51
sulfides, disulfide 11
sulfonamides 254, 255
sulfur 11
sulfur-containing amino acids 60
superoxide dismutase 284, 285, 422
radicals 284
surface films 29
Svedberg unit (S)
sweat 31

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symbiosis
endosymbiotic theory
210
nitrogen fixation 184, 185
symport 212, 218, 220
synapses 348
receptors 348
signal transmission 348, 349
vesicles 354
synaptobrevin 228, 229
synaptogamin 228, 229
Synechococcus elongatus
130, 132
syntaxin 228, 229
synthases see lysases
synthetases see ligases

T cell 274, 275, 294
activation 296–7, 297
receptor 224, 225
T form 117
hemoglobin 280, 281
T state 116
T4 phage 404
TAFs see TATA box, binding protein, associated factors (TAFs)
tail, polyadenylate 246
TATA box 242, 243
binding protein (TBP) 244, 245
associated factors (TAFs) 244, 245
taurine 314
taurocholic acid 314, 315
TBG see thyroxine-binding globulin
TBP see TATA box, binding protein
teeth 340, 341
temperature, enzymes 94, 95
templates 84, 240
terminal oxidation 136
termination, Escherichia coli
251
terpenes 52, 53
tertiary structure 76
testosterone 56, 57, 338, 574, 576
tetracyclines 254
tetrahydrobiopterin (THB)
tetrahydrocortisol 317
tetrahydrofolate (THF) 108, 110
N1-formyl-THF 108
N5-methyl-THF 108
N5-methylene-THF 108
N10-formyl-THF 108
tetradiodothyronine see thyroid
tetramers 99
tetrapyroles 128, 129
THB see tetrahydrobiopterin
Thermodynamics, Second Law of 20
thermogenin (UCP-1) 144, 145
THF see tetrahydrofolate
thiamine
thiamine diphosphate (TPP) 106,
107, 366
pyruvate dehydrogenase 134, 135
see also vitamin B1
thiazole ring 106
thin-layer chromatography (TLC) 54, 55
thioesters 10, 11, 106, 125
bonds 12, 13
thioethers 10
thiokinase see succinate-CoA ligase (GDP-forming); succinyl-CoA ligase
thiols 10, 11
thiopurine methyltransferase 402, 403, 422
thioredoxin 190, 191
reductase 190, 191, 421
threonine 60, 61, 63
aldolase 428
synthase 428
thrombin 290, 426
thrombocytes 274, 290
thromboplastin 291
thromboxanes 390
thylakoids 128, 129, 133
thymidine 80, 81, 82, 304
thymidylate synthase 190,
191, 402, 403, 422
thymine 81, 84, 186, 187
dimers 256
thyroid-stimulating hormone (TSH) see thyrotropin
thyrotrpin 380
thyrotropin-releasing hormone (TRH) see thyrotropin
thyroxine 62, 374
thyroxine-binding globulin (TBG) 172, 232
tissue kallikrein 426
tissue plasminogen activator (tPA) see plasminogen activator (tissue)
tissues
disruption 198
hormones 370
titin 332
titration curves 30
TLC see thin-layer chromatography
TMP, dTMP 80, 81, 187
TNF-a see tumor necrosis factor-a
tobacco mosaic virus 404
tocopherol see vitamin E
TOM 232
topoisomerases 240, 245, 429
toxicity, urea 182
TPP see thiamine diphosphate
trace elements 2, 360, 362–3
TRADD 396
transducin 224
transferrin 286
transacetylation 119
transaldolase 152, 153, 422
transaminases 94, 176, 177
transamination 134, 178–9, 179, 180
pyridoxal phosphate 108, 109
transcription 208, 242–5,
243
control 114, 115, 118–20,
244–5
factors 114, 118, 119, 392,
394
regulatory information 236
initiation 244, 245
PP, CK 244, 245
regulation 244
RNA 242, 243
transducin 72, 73, 358
transfer RNA see tRNA
transferases 88, 89
C₁-transferases 89
intermolecular 89
transferrin 287
transformation 258, 398, 401
bio 226, 317
tumors 400
transition states 15, 90, 100
analogues 97
stabilization 100, 101
transketolase 152, 153, 422
translation 174, 208
amino acids 60
elongation 252-3
Escherichia coli 250, 251, 252, 253
gene information 236, 248, 250-3
inhibitors 254
initiation 250-1
RNA 83
termination 252-3
translocation 252
signals 228, 229
translocator complexes
TIM 232
TOM 232
translocan 230
transmembrane helix 214
transport
active 218
antibiotics 254
antiparallel 212, 218
blood 274
CO₂ 282, 283
hemoglobin 282, 283
hormones 370
lipoproteins 279
mechanisms 220
membrane regulation
216
mitochondrial 212-13
O₂ 282-3, 283
passive 218
plasma membranes 219
processes 218-19
proteins 220-1
secondary 220
symport 212, 218, 220
uniporl 212, 218
transporters 35, 210, 212, 218, 220
transhydrogenin 64, 65, 276
transverse tubules 314
α, α-trehalase 426
triacylglycerol 48, 49, 163, 170, 171
lipase 270, 271, 272, 273, 425
tricarboxylic acid cycle 113, 136-9, 137, 139, 210
and amino acid biosynthesis 185
regulation 144, 145
triiodothyronine 374
see also thyroxine
triokinase 310, 311, 424
triose phosphate isomerase 150, 151, 429
Tris(hydroxymethyl)aminomethane
tristearylglycerol, van der Waals model 49
rRNA™ 82, 83, 86, 87
aminoacyl 248
gene information 236
tropines 372
tropomyosin 64, 65, 332, 334
tropinin 332, 334
trypsin 94, 85, 177, 268, 269, 426
trypsinogen 176, 177, 270
tryptophan 60, 61
TSH see thyroid-stimulating hormone
tubules 210, 221
microtubules 204, 206, 207
transverse 334
tubulins 204, 205
tumor necrosis factor-α (TNF-α) 396
tumor-suppressor genes 394, 398
tumors 400-1, 401
genome therapy 264, 265
monoclonal antibodies 302
turnover
enzymes 88, 89
number 92
β-turns 68
type 1 diabetes 160
type 2 diabetes 150
tyrosine 60, 61, 352
kinases 224, 392
radical 190, 191
transaminase 424
tyrosine-3-monoxygenase 352, 353, 422
ubiquinol see coenzyme Q,
reduced
ubiquinone see coenzyme Q,
oxidized
ubiquitin 62, 176, 177, 394
UCP-1 see thermogenin
UDP glucose 110, 111, 156
4-epimerase 310, 311, 428
UDP glucose 1-phosphate uridylyltransferase 157
UDP glucuronic acid 194
UDP-glucuronosyltransferase 194
ultrafiltration 322
ultraviolet radiation (UV) 256
UMP 187, 188, 189, 190
uncouplers 144, 145
uniporl 212, 218
units, international (U) 88
unsaturated fatty acids 48
uracil 80, 81, 84, 186, 187
urea 324
cycle 113, 182-3, 183
degradation 112
liver 182
ureotelic animals 182
uric acid 186, 187, 324
uricase 186
uricotelic animals 182
uridine 80, 81
5'-diphosphate see UDP
5'-monophosphate see UMP
5'-triphosphate see UTP
dihydridouridine 82, 83
pseudouridine 82, 83
urine 31, 322, 323, 324-5, 325
urobilin 194, 195
urobilinogen 194, 195
urocanate hydratase 428
uropikase see plasminogen
activator (urine)
uroporphyrinogen III 192, 193
synthase 192, 193, 428
UTP 190
UDP-glucose-1-phosphate uridylyltransferase 424
UV see ultraviolet radiation

V segments 302
V systems 116
V type ATPase 220
V/J recombination 302, 303
vacuoles 43, 196, 234
valerianic acid 49
valine 60, 61
van der Waals models 6, 7
acetyl-CoA 13
cholesterol 54, 55
triolein 49
variability, immunoglobulins 302
variation
allotypic 302
idiotypic 302
vasopressin see antidiuretic hormone (ADH)
vectors 258, 259
velocity
and concentration 93, 97
maximum 92, 93
reciprocal 93
relative 25
very-low-density lipoprotein see VLDL
vesicles 28, 29
fractionation 198
synaptic 354
vitamin 332
viruses 404, 405
DNA 264, 265
rhinovirus 404, 405
vitamins 365
A (retinol) 52, 53, 364, 365
antioxidants 364
B₁ (thiamine) 366, 367
B₂ complex 366, 367
B₆ complex 368, 369
B₁₂ (cobalamine) 108, 368, 369
C (l-ascorbic acid) 104, 105, 368, 369
coenzymes 364
D (calcio, choleciferol) 52, 53, 364, 365
deficiency diseases 364
E (tocopherol) 32, 52, 53, 104, 364, 365
H (biotin) 62, 108, 109, 368, 369
hormones 364
K (phylloquinone) 52, 53, 104, 364, 365
lipid-soluble 46, 364-5, 365
nutrients 360
water-soluble 366-9, 367, 369
VLDL 163, 278, 312
Vmax see maximum velocity

tension-gated Na⁺ channels 222

VLDL

water 11, 27, 65, 296
acids 31
bacterial cells 202
degradation 112
emulsions 28
exclusion of 90
excretion 322
hydrophobic interactions 28-9
nutrients 362
O₂ 284
recycling 328-9, 329
solvents 26-7
structure 26
water-soluble vitamins 366-9, 367, 369
waterbinding polysaccharides 40
watersplitting enzyme 130
wavelength, constant 102, 103
waxes 47
work 17
energy 16
wort 148, 149

X

xanthine 187
oxidase 186, 187, 420
xyloglucan 41
D-xylene 38, 39, 42
xylulose 5-phosphate 153

Y

yeasts 148, 149

Z