Blood

Neighboring cell

Golgi apparatus
and membrane system

Magnification 50.000x
1cm=200nm

Nucleases, Glucosidases, Phospholipases, Proteases, Lysosome, Export of the building blocks from disassembled molecules, Glycocalyx as protection against self digestion, Recycling in metabolism, Phagosome, Receptor-recycling, Bacteria, Microvilli, Actin-filaments, Nude scaffold in microvilli with Fimbrin cross-crosslinking, Fimbrin, Dynamin, Clathrin mediated Endocytosis of LDL particles, Stripping from Clathrin, early Endosome, late Endosome, Sorting of proteins, Vesicle-Stock, Exocytosis on stimulus, Lysosomal Vesicles, Secretory Vesicles, direct Exocytosis, Membrane-protein Vesicle, Vesicle transport with different sheath proteins, COP1, anterograde Vesicle transport, retrograde Vesicle transport, COP2, Autophagosome, Digestion of defective cellular organelles, Modification of proteins, Glycolysis, Phosporylation, Sulfation, Modifications

Cell membrane

Magnification 400.000x
1cm=25nm

Glycocalyx, MHCI receptor with cytosolic antigen, Peptide bonds, α-Helix through Membrane, Amino acid-residues, Identify the cell towards the immune system, Transport protein (albumin), Rezeptor-Tyrosinkinasen, Insulin EGF VEGF, hydrophobic hormone (e.g. cortisol, estrogen, vitamin D), cytosolic transporter, Change in protein synthesis slow (Hours to days), Auto-phosphorylation on tyrosine residues, Ras; MAPkinase pathway, Triggering of complex signal cascades; Reaction time different, Protein kinase A signaling pathway, inhibiting, activating, Norepinephrine (α-2) Acetylcholine (M2 & M4) (M1 & M3), Glucagon Adrenaline (β-1, -2, -3) 1 molecule, Stimulation 10 molecules, Inhibition, Adenylate cyclase, cyclic Adenosine-monophosphate, cAMP 200 molecules, Active protein kinase A, 100 molecules (2cAMPnecessary), Change of the protein function through phosphorylation fast (seconds to minutes), 1000 molecules Active phosphorylase B, Ankerprotein, Verankerung der Membran an das Cytoskelett, Fettströpfchen, VLDL-Particles, Lipoprotein lipase, Fat, Triacylglycerols Cholesterol, Amino acids, Sugar, Glucose Galactose Fructose, Membrane transport, sec. active, active, passive, Other Molecules, Na+, Na/K-ATPase, 3x Na+, 2x K+, ATP, ADP+P, Diaphragm movement, Lateral Diffusion, Diffraction, Rotation, Flip-Flop, Membrane Channel through β-Barrel, asymmetrical distribution of the membrane lipids, Drive: Concentration gradient Na+, maintained by ATP, ATP, Concentration gradient

Blood electrolytes in [mmol/L]				pH: 7.4	+	−
K^+	4	Proteins	2			
Na^+	142	Cl	102			
Mg^{2+}	0.9	HCO_3	25			
Ca^{2+}	2.5	Organic phosphates and acids				
Other						

Cell electrolytes in [mmol/L]				pH: 7.5	+	−
K^+	155	Proteine	6			
Na^+	10	Cl	8			
Mg^{2+}	15	HCO_3	10			
Ca^{2+}	<0,0002	Organic phosphates and acids				
Other						

rough ER
(endoplasmic reticulum)

Magnification 200.000x
1cm=50nm

Trans-Golgi Network, Middle Region, Cis-Golgi Network, Vesicle, Dyneine, Kinesine, Centrosome, Microtubules, Protein folding Chaperones, faulty folding, Chaperone, proper folding, Export & Degradation in the proteasome, Ubiquitination, Ubiquitin-chain, Ubiquitin, Ubiquitin ligase, several Cycles, Proteasome, For degradation Tagged protein, 5 proteins Minute, Amino acid-pieces, Transmembrane-proteins, Glycosylation, N-gylcosidic via Asparagine O-glycosidic via serine, Translocation in membrane, ready Transmembrane protein, Signal sequence for membrane Protein, Translation via channel protein into the ER Lumen, Signal sequence for further translation in the rough ER, SRP (signal-recognition-particle), Loading of the tRNA, large molecules need shuttle, small molecules can pass like this, Ran-GDP, Ran-GTP, Core pore, Core lamina from Intermediate Filaments, Anchor proteins, core-specific amino acid sequence, Export with with the help of Shuttle proteins, ca 10⁶ Ribosomes/cell, 10⁵-10⁶ mRNAs/cell

Cytosol

Magnification 400.000x
1cm=25nm

Amino acid specific Aminoacyl-RNAsynthetase, Selection through specific interactions, Selective binding site for an amino acid, Amino acid-loaded tRNA, Amino-terminus, Carboxy-terminus, Peptide bond, 20 amino acids Second, Coding Sequence, Polysome Proteins for: - Cytosol - Peroxisomes - Nucleus - Mitochondria, STOP No matching tRNA, Stopcodon: UAA/UAG/UGA, Start codon: AUG = methionine, START, wobble Position, Anticodon, finished protein, Glycogen(granulum), 100.000 molecules, Glucose-1-phosphate, Galactose-1-phosphate, Glucose-6-phosphate, Fructose-6-phosphate, Fructose-1,6-bisphosphate, Fructose-1,6-bisphosphate, Dihydroxyacetonphosphate, Glyceraldehyd-3-phosphate, 1,3-Bisphosphoglycerate, 3-Phosphoglycerate, 2-Phosphoglycerate, Phosphoenolpyruvate, Pyruvate, Lactate, Ribose-5-phosphate, Glucose, Mannose, Saccarose, Lactose, Glycogenin, α-1,4-glycosidic Binding, α-1,6-glycosidic Binding, Glucose-Units, Glycogen-Synthase*, UDP-Glucose, UDP galactose, Active glycogen Phosphorylase*, Glucose-6-phosphatase* (in the smooth ER), Glucose-6-phosphate-dehydrogenase*, Hexokinase*, Phosphofructokinase 1*, Fructose 1,6-bisphosphatase, PRPP-Synthase, Glycerin-3-phosphate, Glycerin-3-phosphate, Acyl-CoA, Malonyl-CoA, Acetyl-CoA-Carboxylase*, Fatty acid-Synthase, repeated, Mevalonate, HMG-CoA reductase*, Cholesterol, Lanosterol, Squalene, Dolichol, Ubichinon Ceramid, Pyrimidine, Purine, Phosphoribosyl-Pyrophosphate (PRPP), 5-Phosphoribosylamin, IMP Inosinmonophosphate, HGPRT, Pentose phosphate pathway, Synthesis of Membrane lipids, Flippase, Glycerophospholipids, CMP Serine / Inositol / Choline, CDPdiacylglycerol, Triacylglycerin, Diacylglycerin, Phosphatidate, Lysophosphatidate, Acyl-transferase, Fatty Acid Shuttle (Carnitine Shuttle), Acyl-Carnitine, Carnitine, Fatty acids, Fat droplets, TAG-Lipase*, Eicosanoid synthesis, Phospholipase A2, Prostaglandin-Synthase, Cyclo-oxygenase, Arachidonic acid, Lipoxy-genase, Leukotrienes, Prostaglandins, Thromboxane, Prostacycline, Hydroc-peroxidase, Synthesis of unsaturated fatty acids, Extension of Fatty acids, Peroxisome, Catalase, Substrate-H₂, Substrate-O₂, Farnesyl PP, Geranyl PP, Isopentenyl PP, Fusion and Division

Balance degradation of an glucose	
4x ATP	à 1 ATP
2x NADH+	à 5 ATP
2x Acetyl-CoA	à 10 ATP
	34 ATP
Glucose division	-2 ATP
	32 ATP

Balance degradation of an acetyl-CoA	
1x GTP	à 1 ATP
3x NADH+H+	à 2,5 ATP
1x $FADH_2$	à 1,5 ATP
	10 ATP

Balance degradation C16 fatty acid	
8x Acetyl CoA	à 10 ATP
7x $FADH_2$	à 1,5 ATP
7x NADH+	à 2,5 ATP
	108 ATP
Transport	-2 ATP
	106 ATP

Mitochondrion

Magnification 300.000x
1cm=33nm

Mitochondrial DNA, ring-shaped; approx. 16,500 base pairs encode 37 genes (the majority of of mitochondrial proteins is produced in the cytosol), rRNA, tRNA, Control region, Replication: DNA-Polymerase γ, Protein genes: NADH dehydrogenase Cytochrome c oxidase ATP synthase, ATP transport, Cytosol, Intermembrane space, Mitochondrial Matrix pH ~8, pH ~7, Heat, UCP, Cyt. c, Amino acid, Pyridoxal-phosphate, Pyridoxamin-phosphate, α-keto acid, Transaminase, α-ketoglutarate, Glutamate, Glutamine Histidine Arginine Proline, Succinyl-CoA, Succinyl-CoA-Synthetase, Succinate, Succinate-Dehydrogenase, Phenylalanine Tyrosine, Fumarate, Fumarate-Hydratase, Malate, Malate-Dehydrogenase, Oxaloacetate, α-Ketoglutarate, Aspartate amino Transferase (AST or GOT), Aspartate, Asparagine Aspartate, Isocitrat, Isocitrat-Dehydrogenase*, Citrate, Citrate-Synthase*, Aconitase, Acetyl-CoA, Pyruvate, Pyruvate-Dehydrogenase*, Pyruvate-Carboxylase*, Pyruvate-Kinase*, Pyruvate-Dehydrogenase*, Lactate-Dehydrogenase*, Lactate, Serine Alanine Cysteine Glycine threonine Tryptophan, Phenylalanine Tyrosine Isoleucine Lysine Leucine Tryptophan, Methionine Valine Isoleucine Threonine, Glutamine Histidine Arginine Proline, Citrulline, Arginine, Ornithine, Carbamoyl-phosphate, Urea, Arginino-succinate, Citrulline, Aspartate, Fumarate, Oxaloacetate, Malate, Acetoacetyl-CoA, Acetoacetate, Acetone, β-Hydroxybutyrat, Citrate, Oxaloacetate, Malate, Citrate, Oxaloacetate, Acetyl-CoA, Malonyl-CoA, Acetoacetyl-CoA, Special feature for unsaturated fatty acids, normal further, trans-form, cis-form, Fatty acids, Acyl-Carnitine, Carnitine, Acyl-CoA, Glycerin-3-phosphate, Acyl-CoA (Palmityl-CoA), Malonyl-CoA, Acetyl-CoA-Carboxylase*, Fatty acid-Synthase, repeated, Mevalonate, HMG-CoA reductase*, Succinyl-CoA-Synthetase, Succinate-Dehydrogenase, Fumarate-Hydratase, Malate-Dehydrogenase, Citrate-Synthase*, Isocitrat-Dehydrogenase*, α-Ketoglutarate-Dehydrogenase*, Pyruvate-Dehydrogenase*, Pyruvate-Carboxylase*, Acetyl-CoA-Carboxylase*, Fatty acid-Synthase, repeated, Citrate, Malate, Oxaloacetate, Acetyl-CoA, Malonyl-CoA, Acetoacetyl-CoA, Acyl-Carnitine, Carnitine, Acyl-CoA, Fatty acids, Glycerin-3-phosphate, Acyl-CoA (Palmityl-CoA), Malonyl-CoA, Acetoacetyl-CoA, Mevalonate, HMG-CoA

Nucleus

Magnification 400.000x
1cm=25nm

Splicing and Regulation of: - Gene expression - cell cycle - cell death, t(transfer) RNA, m(essenger) RNA, r(ibosomal) RNA, Other RNA Types - snoRNA - miRNA - snRNA - siRNA - ..., Modifications, Protein binding to DNAvia α-helices (leucine zipper motif), Hormone binds to regulatory domain, Splicing, enzymatic active RNA, Spliceosome from snRNA, Protection from Degradation, 5' cap, 3' Poly-A tail, Transcription-bubble, 60 Nucleotide second, Start complex, Mediator, Chromatin-Remodeling-Complex, Histone modifying enzymes, Rna polymerase, Start sequence (TATAbox), DNA Template, RNA-Strand, Separation of the DNAstrands, RNA Polymerase, Nucleotides are added to the 3' end of the RNA, Transcribed RNA, DNAlesions, in particular Chemo-therapeutics, Single strand break due to Base loss, Base changes (e.g. depurination, depyrimidation), Double strand Break, DNA-Crosslinking, Nucleosomes, not transcribable highly condensed DNA = Heterochromatin, 30nm, transcribable loosened DNA = Euchromatin, Histones Octamer, Repair of mismatch (0-30 mutations/replication), Detection of mismatch by repair system, Generous cutting through exonuclease, Filling the gap by polymerase α, Connecting the strands by ligase, Replication origin (ori), Replication fork, SSB proteins to stabilize the separated single strands, DNAextension from 5' to 3', 50-100 Nucleotides/second, Okazaki fragments 5' (100-200 nucleotides), Removal of the RNAprimer by nucleases, Filling up the created gap, Ligation of the unlinked bases, Loosening the torsions and torsion forces by induced single strand break with subsequent ligation, Separation of the DNAstrands, DNAtemplate, Helicase, RNAprimer with uracil, Topoisomerase, DNApolymerase α, DNA polymerase δ, Nucleasen, DNA-Polymerase α, DNA-Ligase 1, DNA polymerase ε, Folding of the chromosome in the nucleus, approx. 5 megabases, Chromosome, p-arm, q-arm, Centromere, Telomeres

Cell-Cell-contacts

Magnification 200.000x
1cm=50nm

Spontaneous Particle movement, Diffusion barrier, Claudin, Occludin, Tight-Junctions, Gap-Junctions Material exchange between cells, Intermediate filaments, Desmosomes Adhesive contacts for fixing the cells to each other, Cadherine, Adherens contacts Adhesive contacts for fixing the cells to each other, Actin filaments, DNAdouble helix, ca. 2 nm, Cytosin, Adenin, Thymin, large furrow, small furrow, Direction of rotation of helix: right, Bases / Winding: 10, Rise / Winding: 3.4nm, Genome size: 3.2 billion bases, Protein Coding genes: approx. 21,000, Sugar phosphate Backbone

Cell-matrix contacts

Magnification 250.000x
1cm=40nm

Collagen fibril, 50 nm, Collagen molecule, Collagen-tripelhelix, Basal-membrane, Actin-filaments, Integrin Alpha + Beta Unit, Laminin, Collagen, Proteoglycans, Aggrecan, Linkage protein, Hyaluron-molecule, Chondroitin-sulfates and Other sugars, Stretched, Relaxed, Cross-connection, single elastin molecule, elastic fibers

smooth ER
(endoplasmic reticulum)

Magnification 200.000x
1cm=50nm

Phase 1 reaction, Cytochrome P-450 Oxigenases, Dehydrogenases & peroxidases, Toxic Substance, -SH / -OH / -NH, Attachment of a functional group, Phase 2 reaction, Glucuronic acid / Sulfuric acid / Acetyl-CoA Amino acids / Methyl groups, Conjugation with water soluble radical, Water soluble residue, Excretion via kidney and bile, Ca2+ homeostasis, Calcium storage, SERCA, Ryanoidin-Receptor, IP3, [Calcium], Proliferation/ Fertilization, Exocytosis, Contraction, Transcription, Regulation, Glucocorticoids (cortisol), Mineralcorticoids (aldosterone), Androgens, Estrogens, Aromatase, Progesterone, Pregnenolone, Vitamin D_3

Mitosis

Chromosome set, Gene copy number, Prophase, Prometaphase, Metaphase, Anaphase, Telophase, Cytokinesis

Interphase

Cell cycle, DNAdamage? DNAreplication successful? Good environmental factors?, All chromosomes connected with spindle?, Good environmental factors? DNAdamage?, G2 phase Preparation of cell division, e.g. synthesis of cell division-specific proteins, S Phase Duplication of DNA (replication), production of histones and regulatory proteins, G1 Phase RNA& protein synthesis, no DNAsynthesis, G0 Phase Working state / resting state of the cell

Meiosis

Meiosis I Mating and segregation homologous chromosomes diploid chromosome set, Meiosis II Separation of the sister chromatids haploid chromosome set, Fertilization Fusion of female and male germ cell (mitochondria only from female germ cell)

Cell death

Phagocytosis, Fragmentation, Shrinkage, Apoptosis Ordered cell death induced by external or internal signals, Phagocyte, Cell fragments are taken up by scavenger cells, Membrane damage & Inflammation, Swelling, pathological cell death induced by noxae and physical damage such as heat or O2 deficiency Nekrosis

Degeneracy

Metastases-formation, 3. mutations: Breakthrough through basement membrane: numerous new mutations, Malignant cell proliferation Scattering to neighboring tissue =malignant tumor, 2. mutations: Damaged DNArepair, benign cell proliferation basement membrane intact =benign tumor, 1. mutation Accelerated Cell division, healthy cell in the cell association at Basement membrane

Reasons for mutations: Hereditary predisposition; Nutrition; Toxic Substances; Radiation / Sunlight; Infections; Physical inactivity

Aminosäuren

Alanine, Cysteine, Aspartate, Glutamate, Phenylalanine, Tyrosine, Tryptophane, Methionine, Proline, Glycine, Serine, Threonine, Asparagine, Glutamine, Arginine, Lysine, Histidine, Isoleucine, Leucine, Valine, Asparagine, Aspartate, Glutamate, Arginine, Lysine, Histidine

Sugar

Glucose, Haworth-Projection, Sessel Projection, Fischer Projection, Sum-formula, Mannose, Fructose, Galactose, Sucrose, Lactose, Maltose, Cellulose

Nucleoside/Nucleotide

Nucleoside, Base, Ribose, Phosphate residues, Monophosphate, Diphosphate, Triphosphate, Nucleotide

Fatty acids

Palmacitic acid 16:0, Stearic acid 18:0, Oleic acid 18:1 Δ⁹, Linoleic acid 18:2 Δ⁹,¹², Linolenic acid 18:3 Δ⁹,¹²,¹⁵, Arachidonic acid 20:4 Δ⁵,⁸,¹¹,¹⁴, most important reaction product of fatty acid synthase, Occurrence in almost all animal and vegetable fats, most common fatty acid in human fat cells, essential, = Omega-3 fatty acid essential, Basis for Eicosanoids

Isoprene derivative

Steroids - Cholesterol - D vitamins - Steroid hormones - Bile acids; Terpens - Vitamin A - Vitamin E - Vitamin K (Phylochinone) - Dolichol

Storage lipids

Triacylglycerols, Fats, oils, Glycerin, Fatty acid

Membrane lipids

Phospholipids: Glycerophospholipids, Alcohol— PO_4, Glycerin, Fatty acid, Fatty acid; Sphingophospholipids, Choline— PO_4, Sphingosine, Fatty acid

Glycolipids: Sphingoglycollipids, Mono- or Oligosaccharide, Sphingosine, Fatty acid

Cholesterol

Constants

Dalton: 1,661 x 10^{-24}g

Avogadro number: 6,022 x 10^{23}/mol

Gas constant: 8,315J/molºK

Conversion factors

Lengths	1m = 10^2cm = 10^3mm = 10^6 µm = 10^9nm =10^{10}A
Mass	1kg = 10^3g =10^6mg = 10^9 µg = 10^{12}ng
Temperature	K = °C + 273 °C= 5/9(°F-32)
Energy	1J = 0,239 cal 1cal = 4,184J
Pressure	1mmHg = 1,333 x 10^2Pa = 1,32 x 10^{-3}atm

Chemical groups

Hydroxyl R–OH; Carbonyl (Aldehyde) R–C(=O)–H; Carbonyl (ketone) R–C(=O)–R; Carboxyl R–C(=O)–OH; Amino R–NH_2; Thiol (sulfhydryl) R–SH

Enzymes, Key enzymes*: building up, degrading, remodeling, Transportation, Intermediate steps

MeCell the human cell