# Appendix 16

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## 16.1 List of Species

**Table 16.1** Species

| Scientific name | Vernacular name | Superior taxon | Class/phylum |
|---|---|---|---|
| *Acheta domesticus* | House cricket | Gryllidae | Insecta |
| *Achlya ambisexualis* | | Peronosporomycetes | Fungi |
| *Acyrthosiphon pisum* | Pea aphid | Aphidoidea | Insecta |
| *Aedes aegyptii* | Yellow fever mosquito | Culicidae | Insecta |
| *Aeshna cyanea* | Blue-eyed darner | Odonata | Insecta |
| *Agelenopsis aperta* | Desert grass spider | Agelenidae | Arachnida |
| *Agrotis ipsilon* | Dark sword-grass | Noctuidae | Insecta |
| *Anopheles gambiae* | | Culicidae | Insecta |
| *Apis melifera* | Honeybee | Apidae | Insecta |

(continued)



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**Table 16.1** (continued)

| Scientific name | Vernacular name | Superior taxon | Class/phylum |
|---|---|---|---|
| *Aplysia californica* | California sea hare | Anaspidea | Mollusca |
| *Aplysia kurodai* | Kuroda's sea hare | Anaspidea | Mollusca |
| *Armadillidium vulgare* | Common pill bug | Isopoda | Crustacea |
| *Bombyx mori* | Silk moth | Lepidoptera | Insecta |
| *Brugia malayi* | | Filarioidea | Nematoda |
| *Busycon contrarium* | Lightning whelk | Neogastropoda | Mollusca |
| *Caenorhabditis elegans* | | Rhabditida | Nematoda |
| *Callinectes sapidus* | Atlantic blue crab | Brachyura | Malacostraca |
| *Cancer magister* | Dungeness crab | Brachyura | Malacostraca |
| *Carausius morosus* | Indian stick insect | Neoptera | Insecta |
| *Carcinus maenas* | European shore crab | Brachyura | Malacostraca |
| *Ciona intestinalis* | Vase tunicate | Cionidae | Urochordata |
| *Dipetalogaster maxima* | (Blood sucking bug) | Heteroptera | Insecta |
| *Drosophila melanogaster* | Fruit fly | Neoptera | Insecta |
| *Eisenia fetida* | Redworm | Lumbricidae | Annelida |
| *Euphyllia anchora* | Anchor coral | Scleractinia | Cnidaria |
| *Helicoverpa armigera* | Cotton bollworm | Noctuidae | Insecta |
| *Helicoverpa assulta* | Oriental tobacco budworm | Noctuidae | Insecta |
| *Helicoverpa zea* | Cotton earworm | Noctuidae | Insecta |
| *Helix aspersa* | Garden snail | Pulmonata | Gastropoda |
| *Helix pomatia* | Burgundy snail | Pulmonata | Gastropoda |
| *Homarus americanus* | American lobster | Astacidea | Malacostraca |
| *Leucophaea maderae* | Madeira cockroach | Blattodea | Insecta |
| *Locusta migratoria* | Migratory locust | Cealifera | Insecta |
| *Lumbricus terrestris* | Common earthworm | Lumbricidae | Annelida |
| *Lymnea stagnalis* | Great pond snail | Pulmonata | Gastropoda |
| *Macrobrachium rosenbergii* | Giant river prawn | Caridea | Malacostraca |
| *Macrocallista nimbosa* | Sunray Venus clam | Veneroida | Bivalvia |
| *Manduca sexta* | Tobacco hornworm | Lepidoptera | Insecta |
| *Mytilus edulis* | Blue mussel | Mytiloida | Bivalvia |
| *Neobellieria bullata* | Grey flesh fly | Neoptera | Insecta |
| *Oncopeltus fasciatus* | Mildweed bug | Hemiptera | Insecta |
| *Orconectes immunis* | Calico crayfish | Astacidea | Malacostraca |
| *Orconectes limosus* | Spiny-cheek crayfish | Astacidea | Malacostraca |
| *Pagurus bernhardus* | Common hermit crab | Pleocyemata | Malacostraca |
| *Pandalus borealis* | Great northern prawn | Caridea | Malacostraca |
| *Pandalus jordani* | Pacific/ocean shrimp | Caridea | Malacostraca |
| *Pacifastacus leniusculus* | Signal crayfish | Astacidea | Malacostraca |
| *Penaeus aztecus* | Brown shrimp | Penaeidae | Malacostraca |
| *Penaeus japonicus* | Kuruma prawn | Penaeidae | Malacostraca |
| *Penaeus vannamei* | Pacific white shrimp | Penaeidae | Malacostraca |
| *Phormia regina* | Black blow fly | Neoptera | Insecta |

(continued)

**Table 16.1** (continued)

| Scientific name | Vernacular name | Superior taxon | Class/phylum |
|---|---|---|---|
| *Procambarus clarkii* | Red swamp crayfish | Astacidea | Malacostraca |
| *Psacothea hilaris* | Yellow spotted longicorn beetle | Neoptera | Insecta |
| *Rhodnius prolixus* | (Triatomid bug) | Heteroptera | Insecta |
| *Romalea microptera* | Eastern lubber grasshopper | Caelifera | Insecta |
| *Schistocerca gregaria* | Desert locust | Caelifera | Insecta |
| *Schistocerca nitens* | Gray bird grasshopper | Caelifera | Insecta |
| *Strongylocentrotus purpuratus* | Purple sea urchin | Echinoida | Echinodermata |
| *Tenebrio molitor* | Mealworm | Coeleoptera | Insecta |
| *Tribolium castaneum* | Red flour beetle | Coeleoptera | Insecta |
| *Trichoplax adhaerens* | | – | Placozoa |
| *Uca puligator* | Sand fiddler crab | Brachyura | Malacostraca |

## 16.2 Glossary

### 16.2.1 Cell Components

**ATP:** Adenosine triphosphate (ATP) is a molecule generated during intracellular oxidation of glucose and which stores energy. By enzymatic transfer of phosphate, the energy is also transferred.

**Cyclic AMP:** Cyclic adenosine monophosphate (cAMP) is generated from ATP by adenylate cyclase. Adenylate cyclase is, for example, stimulated by the hormone glucagon. Within the cell, cAMP has function a hormone has in the organism: it is a messenger. With hormones seen as primary messengers, cAMP is the prototype of second messengers. Other second messengers are cyclic guanosine monophosphate, diacyl glycerol, inositol trisphosphate, and nitrogen monoxide.

**Enzymes:** Enzymes are protein molecules performing chemical reactions.

**Molecules:** A cell consists of amino acids, proteins, glycerol derivatives, fatty acids, lipids, large and small sugar molecules, deoxyribonucleic acid (DNA), ribonucleic acid (RNA), and a multitude of other substances, such as vitamins, salts, trace elements, and other organic compounds. To obtain information about all these substances, please consult a biochemistry textbook.

**Nucleic acids:** Nucleic acids are built with a chain where a sugar and a phosphate alternate. To each sugar a so-called base is linked, the sequence of the base determining genetic information. Two different sugars are used differing from each other by a single oxygen atom. Genetic information in all living cells from bacteria to plants to animals consists of DNA using deoxyribose with four bases—adenine, cytidine, guanine, and thymine. Within the cell, information from the cellular nucleus is transcribed into RNAs built with a ribose phosphate backbone and where together with adenine, cytidine and guanine, uracil is used

instead of thymine. There are functionally different RNAs: messenger RNA (mRNA), ribosomal RNA, and transfer RNA (tRNA).

In viruses, genetic information consists of DNA or RNA.

**Proteins:** Proteins are described in detail in Chap. 4.

**Ribonucleic acid (RNA):** See nucleic acids.

**Ribosomes:** A ribosome consists of two ribosomal RNA strands and a multitude of proteins. It has two different subunits. Ribosomes serve to translate genetic information from the mRNA in a polypeptide sequence. The amino acids are transferred by tRNAs to the ribosomes.

**RNA cap:** To the 5′ end of mRNA, a guanosine phosphate is linked to form a guanosine 5′-phosphate 5′-RNA cap. In addition, the guanine at the 7-position is methylated. The RNA cap is a signal for export from the cellular nucleus and enhances RNA stability by providing degradation protection.

**Transfer RNA:** Transfer RNAs (tRNAs) are loaded by enzymes with amino acids which will then be brought to the ribosome by these aminoacyl-tRNAs. For any of the 20 amino acids, there is at least one tRNA; for selenocysteine (used in deiodinase, which converts thyroxine into triiodothyronine in the thyroid gland), another tRNA is necessary.

### 16.2.2 Cell Structure

**Cell membrane:** The animal cell is enclosed by a cell membrane separating the interior from the environment and keeping the cell contents together. Cell membranes have distinguishable inner and outer faces. They are built from lipids, proteins, and sugar-modified lipids.

**Cell nucleus:** In eukaryotic cells, genetic information is enclosed by a membrane forming the cellular nucleus. The membrane is called a nuclear membrane. The cellular nucleus consists of DNA strands, protein such as histones which pack DNA closely, and enzymes replicating or transcribing DNA. By the binding of further proteins to gene segments, the activity of transcribing enzymes for the respective segment can be controlled. Thus, these DNA-binding proteins regulate the activity of genes—that is, a DNA stretch with genetic information for a certain protein.

**Cellular interior, the cytosol or cytoplasm:** The cytosol is the intracellular space filled with protein, salts, and small and large membrane-enclosed droplets within the cellular membrane. Signals from the cellular membrane to the cellular nucleus have to be mediated in the cytosol. This cytosol is by no means only a thick solution; a dense fiber network called the cytoskeleton links different components into functional units.

**Cytoskeleton:** The cytoskeleton consists of protein fibers. It fixes the position of the cellular nucleus within the cell, as well as the other intracellular, membrane-enclosed compartments; that is, mitochondria or vesicles such as the Golgi apparatus, the endoplasmic reticulum (ER), and secretory granules (with, e.g., hormones to be released on triggering) are maintained in place by the cytoskeleton. Even cell-to-cell connections are stabilized by the cytoskeleton.

**Endoplasmic reticulum:** The endoplasmic reticulum (ER) is a special intracellular compartment enclosed by an individual membrane. Its outer face is related to the inner face of the cell membrane, and its inner face is related to the outer side of the cell membrane. The ER is the place where those metabolic steps happen which determine whether a freshly made protein is targeted to the cell membrane or even further for secretion. In addition to the smooth ER, there is the rough ER.

**Golgi apparatus:** The Golgi apparatus looks like a pile of folded pizza getting larger with greater distance from the cellular nucleus. In the Golgi apparatus, proteins are modified with sugar residues. Such sugars serve as target signals and are used to sort the proteins into the different compartments. These compartments form by invagination of the Golgi apparatus and separation from it and are transported with the help of the cytoskeleton and helper proteins.

**Mitochondria:** In mitochondria glucose is used for ATP formation. This ATP is used in almost all metabolic steps. For this ATP formation, glucose, oxygen, and a set of enzymes are required, the latter located at the inner mitochondrial membrane.

**Nucleolus:** With use of electron microscopy, round structures in the cellular nucleus are visible, and represent ribosome-forming sites. The ribosomal RNAs are transcribed from the chromosome and loaded with the different proteins imported into the cellular nucleus.

**Rough endoplasmic reticulum:** The rough ER is the place of protein formation. The growing proteins in the rough ER are, however, transferred further into the rough ER through a pore. The many ribosomes on the outer (cytosolic) surface of the rough ER have a rough appearance when viewed by electron microscopy.

**Secretory granules:** These intracellular structures are hormone stores. Almost all peptide hormones, catecholamines, and melatonin are stored in vesicles. These arise by invagination of the Golgi apparatus or the ER. By intracellular transport, these granules are stored close to the cell membrane.

### 16.2.3 Intracellular Vesicles and Their Transport

**Endocytosis and exocytosis:** Endocytosis is a mechanism where particles, bacteria, or other solid material outside the cell become enclosed by the cellular membrane to become a membrane-enclosed vesicle within the cell. Most important in the process are clathrin molecules organizing a frame around the vesicle together with the cytoskeleton and which are visible under the electron microscope (coated pits).

The process in the opposite direction, from the cell to the exterior, is called exocytosis. By means of exocytosis, peptides, proteins, and other amino acid derived hormones are released. Most significant is the act of vesicle membrane fusion to the plasma membrane facilitated by soluble *N*-ethylmaleimide sensitive factor attachment receptors (SNAREs) and induced by calcium ions.

**Lysosome:** A lysosome is one of the Golgi apparatus derived vesicles packed with enzymes to digest proteins and lipids from, for example, bacteria. Such

a lysosome fuses to a phagosome, by which process the enzymes can reach the phagosomal content and digest it. Such a process happens in the thyroid gland, where thyroglobulin is stored in the follicular lumen and phagocytosed on demand, and thyroxine is generated by digestion of thyroglobulin within phagolysosomes (see Chap. 7). Bacteria are often phagocytosed and digested in phagolysosomes.

**Phagosome:** A phagosome is an intracellular vesicle formed by particle endocytosis. Such particles might be a bacterium, a virus, a crystal, or another foreign particle.

**Pinocytosis:** Liquid droplets can also be taken up by cells and enclosed within a membrane. Such a process is called pinocytosis; the intracellular vesicle is also called a phagosome.

### 16.2.4 Additional Definitions

**14-3-3 proteins:** 14-3-3-proteins are ubiquitous in eukaryotic cells. They preferentially bind to phosphorylated serines and thus control protein functions in many cells

**Acidophilic/basophilic:** Cells or the cellular compartment that are stained by the acidic eosin are called acidophilic. Cells that are stained by a basic dye are named basophilic.

**Affinity:** Reversible chemical reactions at equilibrium are characterized by reaction constants indicating whether the reactions occur autonomously or, for example, only because of catalysis. Antibody–antigen reactions are equally reversible reactions under the law of mass action, with the equilibrium the more on the side of the antibody–antigen complex the higher the antibody affinity for a given antigen. Affinity is thus the attracting force of the antibody for the antigen.

**Avidity:** In an immunoreaction where many different, even structurally diverse antibodies participate with individual affinities, the force of the reaction cannot be measured. When compared with other immunoreactions with the same antibody but a different antigen, the reactions can be compared and given a scale. Avidity is the term by which these different reactions are compared.

**Crossing over:** During meiosis, sister chromosomes associate lengthwise. Thereafter, genetic exchange happens, with entire chromosomal sections exchanged.

**C-terminus, N-terminus:** Amino acids have an amino group and a carboxy group. For a peptide bond, the carboxy group of one amino acid reacts with the amino group of the next. One amino group and one carboxy group are retained. These are called the N-terminal group (for $NH_2$, i.e., amino) and the C-terminal group (for COOH, i.e., carboxy).

**Genetic code:** The bases of trinucleotides form the code of amino acids. The four bases are uracil (U), cytidine (C), adenine (A), and guanine (G). The following table shows the translation code, the *genetic code*, from RNA to amino acid occurring in the ribosomes. The trinucleotide ACA would be translated to threonine (Thr), and GAA would be translated to glutamine (Gln). Some trinucleotides cause strand termination, such as UAA and UAG.

| 1st position | 2nd position | | | | 3rd position |
|---|---|---|---|---|---|
| | U | C | A | G | |
| U | Phe | Ser | Tyr | Cys | U |
| | Phe | Ser | Tyr | Cys | C |
| | Leu | Ser | Stop | Stop | A |
| | Leu | Ser | Stop | Trp | G |
| C | Leu | Pro | His | Arg | U |
| | Leu | Pro | His | Arg | C |
| | Leu | Pro | Gln | Arg | A |
| | Leu | Pro | Gln | Arg | G |
| A | Ile | Thr | Asn | Ser | U |
| | Ile | Thr | Asn | Ser | C |
| | Ile | Thr | Lys | Arg | A |
| | Met | Thr | Lys | Arg | G |
| G | Val | Ala | Asp | Gly | U |
| | Val | Ala | Asp | Gly | C |
| | Val | Ala | Glu | Gly | A |
| | Val | Ala | Glu | Gly | G |

**HLA:** HLA molecules are protein products of the major histocompatibility complex gene locus. HLA proteins have pockets for peptide fragments derived by digestion of cellular peptides in the proteasome. Such HLA–peptide complexes on the surface of a cell signal to T lymphocytes that such a cell belongs to the respective individual. Virus-infected cells incorporate viral peptides into the HLA–peptide pockets. Since T lymphocytes have not learned of these virus—HLA complexes when primed for their host, such complexes are recognized as foreign and the cells are attacked and destroyed by T lymphocytes.

**Imprinting** Imprinting denotes the fact that certain alleles are inactivated because of their paternal or maternal origin. In about 50 human genes, genes on one allele cannot be activated since they are strongly inactivated by DNA methylation and association with inactivator proteins. Since this inactivation has already occurred in the fertilized egg, it must be of paternal or maternal origin. The inactivation is maintained in the progeny after cell division. If imprinting is defective—for example, in inactivator protein or DNA methyltransferase mutants—severe developmental complications arise. *IGF2* is an example of an imprinted gene.

**Karyotype:** A karyotype is the description of the number and the appearance of chromosomes in the cell analyzed. Diploid karyotype means that with the exception of the sex chromosomes all chromosomes appear as pairs (in normal cells). In a haploid karyotype, chromosomes appear once, and the sex chromosomes are X *or* Y (in the egg or sperm). In chromosomal aberrations, individual chromosomes are lacking or exist in triplicate. Sometimes chromosomes exist in four copies (tetraploid). In plants, there are eightfold and further multiplied karyotypes.

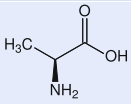
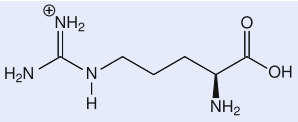
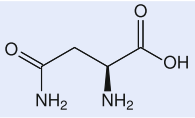
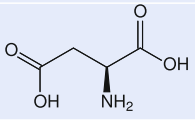
**Signal peptide:** Membrane and secretory proteins are translated not in the cytosol, but on the surface of the ER and are stored therein. Their synthesis is directed to the ER by the so-called signal peptide. When peptide synthesis starts, the first 20–35 amino acids, the signal peptide, are translated. Signal recognition particles bind to these and target the complex of RNA and ribosome plus nascent chain to the ER membrane. There a pore is formed through which the growing chain is directly transfered into the ER. In the ER the signal peptide is cleaved by the signal peptidase. Protein folding does not happen until the chain has reached the ER.

**Synapse:** Two neurons form a synapse with their axons at the contact site, where neurotransmitters are secreted, and diffuse through the narrow cleft to postsynaptic receptors.

**Tumor:** A tumor is a space-demanding proliferation of cells, synonymous with neoplasia. There are benign and malignant tumors. Depending on the kind of tumor and the type of the tissue pushed away, pathological conditions up to death may occur. Malignant tumors are those where secondary tumors (metastases) due to tumor cell dissemination are formed.

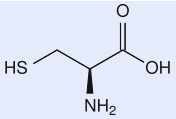
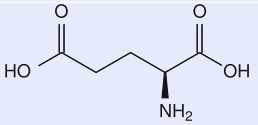
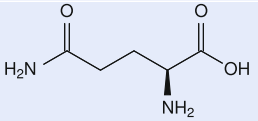
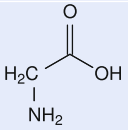
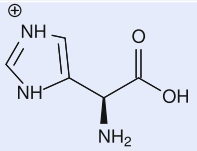
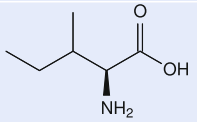
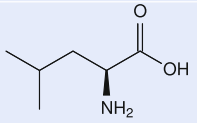
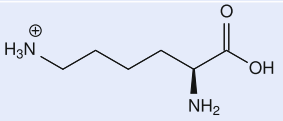
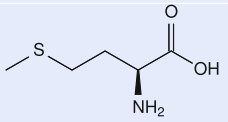
### 16.2.5 Amino Acids

**Table 16.2** Amino acids, three-letter and one-letter codes, and structures

| Amino acid | 3-letter code | 1-letter code | Structure |
|---|---|---|---|
| Alanine | Ala | A |  |
| Arginine | Arg | R |  |
| Asparagine | Asn | N |  |
| Aspartic acid | Asp | D |  |

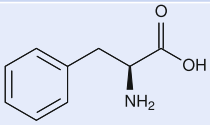
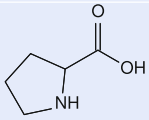
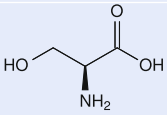
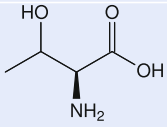
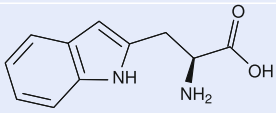
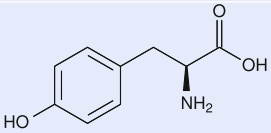
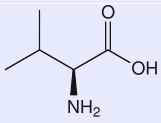
(continued)

**Table 16.2** (continued)

| Amino acid | 3-letter code | 1-letter code | Structure |
|---|---|---|---|
| Cysteine | Cys | C |  |
| Glutamic acid | Glu | E |  |
| Glutamine | Gln | Q |  |
| Glycine | Gly | G |  |
| Histidine | His | H |  |
| Isoleucine | Ile | I |  |
| Leucine | Leu | L |  |
| Lysine | Lys | K |  |
| Methionine | Met | M |  |

(continued)

**Table 16.2** (continued)

| Amino acid | 3-letter code | 1-letter code | Structure |
|---|---|---|---|
| Phenylalanine | Phe | F |  |
| Proline | Pro | P |  |
| Serine | Ser | S |  |
| Threonine | Thr | T |  |
| Tryptophan | Try | W |  |
| Tyrosine | Tyr | Y |  |
| Valine | Val | V |  |

## 16.3 PyMOL Scripts

### 16.3.1 Glycoprotein Hormone α Chain

```
    #load ~/Science/pymol/TSHalpha.pml

load ~/Science/strukturen/gonadotropin/1HRP.pdb
cmd.hide("everything","1HRP")
select alphachain, chain a
select betachain, chain b
select helices, ss h
select helicesalpha, alphachain and helices
```

```
select betas, ss s
select betasA, betas and alphachain
select schwefel, name SG
select schwalpha, schwefel and alphachain
select cysteins, resn cys
select cysalpha, cysteins and alphachains
select cysalpha, cysteins and alphachain
select mychainalpha1, (resi 28–32) and alphachain
select mychainalpha2, (resi 82–84) and alphachain
select myringalpha, mychainalpha1 or mychainalpha2
select mypierce, (resi 10+60) and alphachain
select piercesulfur, (name SG) and mypierce
cmd.hide("everything","schwefel")
set sphere_scale, 0.4, cysteins
set sphere_scale, 0.4, mypierce
set sphere_scale, 0.3, myringalpha
set sphere_scale, 0.5, piercesulfur
cmd.color(13,"piercesulfur")
set_view (\\
    −0.721869946,   −0.651766121,    0.232594654,\\
    −0.195120096,   −0.130773291,   −0.972020864,\\
     0.663950145,   −0.747057140,   −0.032772087,\\
     0.000103876,    0.000121470, −174.335067749,\\
    15.360612869,   34.682048798,    3.615572453,\\
   135.404708862,  213.288848877,  −20.000000000 )

cmd.color("grey70" ,"alphachain")
cmd.show("cartoon" ,"alphachain")
util.cba(6,"myringalpha",_self=cmd)
cmd.show("sticks"    ,"mypierce")
cmd.show("sticks"    ,"myringalpha")
cmd.color(13,"schwalpha")
cmd.show("cartoon"   ,"betasA")
cmd.show("spheres"   ,"cysteins")
util.cba(154,"mypierce",_self=cmd)
cmd.show("sticks"    ,"cysalpha")
cmd.show("spheres"   ,"schwalpha")
cmd.hide("everything","betachain")

set sphere_scale, 0.5, piercesulfur
cmd.color(13,"piercesulfur")

stereo swap
stereo crosseye
ray 1000,1000
png ~/Science/pymol/TSHalpha.png
save TSHalpha.png
```

### 16.3.2 Growth Hormone/Prolactin Using PyMOL

```
 load ~/Science/strukturen/Prolaktin/1N9D_Prolaktin.pdb
cmd.hide("everything","1N9D_Prolaktin")
cmd.show("cartoon"   ,"1N9D_Prolaktin")
```

```
cmd.spectrum("count",selection="(1N9D_Prolaktin)&*/ca")
set_view (\
     0.080638364,    −0.958228469,    −0.274401009,\
     0.513196349,     0.275917083,    −0.812711596,\
     0.854475081,    −0.075285666,     0.514008284,\
     0.000000000,     0.000000000, −196.476440430,\
    −0.272903442,     0.056584358,     0.227214813,\
   154.903518677,   238.049346924,   −20.000000000 )
stereo crosseye
stereo swap
ray 1000,1000
png ~/Science/pymol/PRL.png
```

(The growth hormone drawing using 1HGU.pdb was done with an almost identical script.)

### 16.3.3 CYP51

```
stereo off
load ~/Science/strukturen/CYP/CYP51/1EA1.pdb
hide everything
sele chainA, chain a
cmd.color(5278,"chainA")
sele haem, resi 460
sele helices, (ss h) and chainA
sele sheets, (ss s) and chainA
show cartoon, chainA
util.cba(13,"haem",_self=cmd)
set sphere_scale, 0.7, haem
show spheres, haem
sele hemcys, resi 394
cmd.color(5259,"hemcys")
cmd.show("spheres"   ,"hemcys")
sele CysS, hemcys and name "SG"
cmd.color(13,"CysS")
cmd.show("sticks", "hemcys")
set sphere_scale, 0.4, hemcys
set sphere_scale, 0.7, CysS
cmd.spectrum("count",selection="helices",byres=1)
cmd.color(8,"sheets")
util.cba(144,"haem",_self=cmd)
util.cba(6,"hemcys",_self=cmd)
set\_view (\
     0.368408203,    −0.457030654,    −0.809582591,\
    −0.865943551,     0.148186371,    −0.477703989,\
     0.338291317,     0.877034962,    −0.341159761,\
    −0.000179388,     0.000013747, −398.444000244,\
   −16.277500153,    −4.500016689,    64.140602112,\
   368.594787598,   428.240142822,   −20.000000000 )

ray 1000,1000
png ~/Science/strukturen/CYP/CYP51/CYP51_mono.png
stereo swap
```

```
stereo crosseye
stereo on
ray 1100,1000

png ~/Science/strukturen/CYP/CYP51/CYP51_stereo.png
stereo off
```

### 16.3.4 CYP19

```
load ~/Science/strukturen/CYP/CYP19/3EQM.pdb
cmd.hide("everything","3EQM")
#select the heme residue
select heme, resi 600
# sphere diameter
set sphere_scale, 0.4, heme
#color scheme for heme:
util.cba(5,"heme",_self=cmd)
#show sticks with larger spheres
cmd.show("spheres"   ,"heme")
cmd.show("sticks"    ,"heme")

# select androstendion
select androst, resi 601
set sphere_scale, 0.6, androst
util.cba(144,"androst",_self=cmd)
cmd.show("sticks"    ,"androst")
cmd.show("spheres"   ,"androst")

select mysheets, ss s
color white, mysheets
show cartoon, mysheets

select myhelices, ss h
cmd.spectrum("count",selection="myhelices",byres=1)
set cartoon_oval_length, 0.5, myhelices
set cartoon_oval_width, 0.13, myhelices
set cartoon_fancy_helices,1

show cartoon, myhelices

select cpychain, resi 45-496
select loops, ss l+"" and cpychain
cmd.color(6,"loops")
show cartoon, loops

select cnineteen, name C19
select ceighteen, name C18


select ringone, name C1+C2+C3+C4+C5+C10
cmd.color(34,"ringone")

cmd.color(8,"cnineteen")
```

```
cmd.color(11,"ceighteen")

_ set_view (\
_     0.314305723,    0.076195419,   -0.946257472,\
_     0.248245627,    0.955489814,    0.159396768,\
_     0.916289091,   -0.285004675,    0.281401485,\
_     0.000000000,    0.000000000, -208.213180542,\
_    83.395401001,   50.151500702,   46.364837646,\
_   112.259994507,  304.166656494,  -20.000000000 )


ray 1000, 1000
png ~/Science/pymol/CYP19.png
```