Biological Systems

Elements of Biophysics
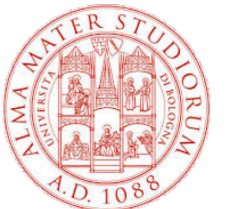
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Biomolecules Folding and Disease

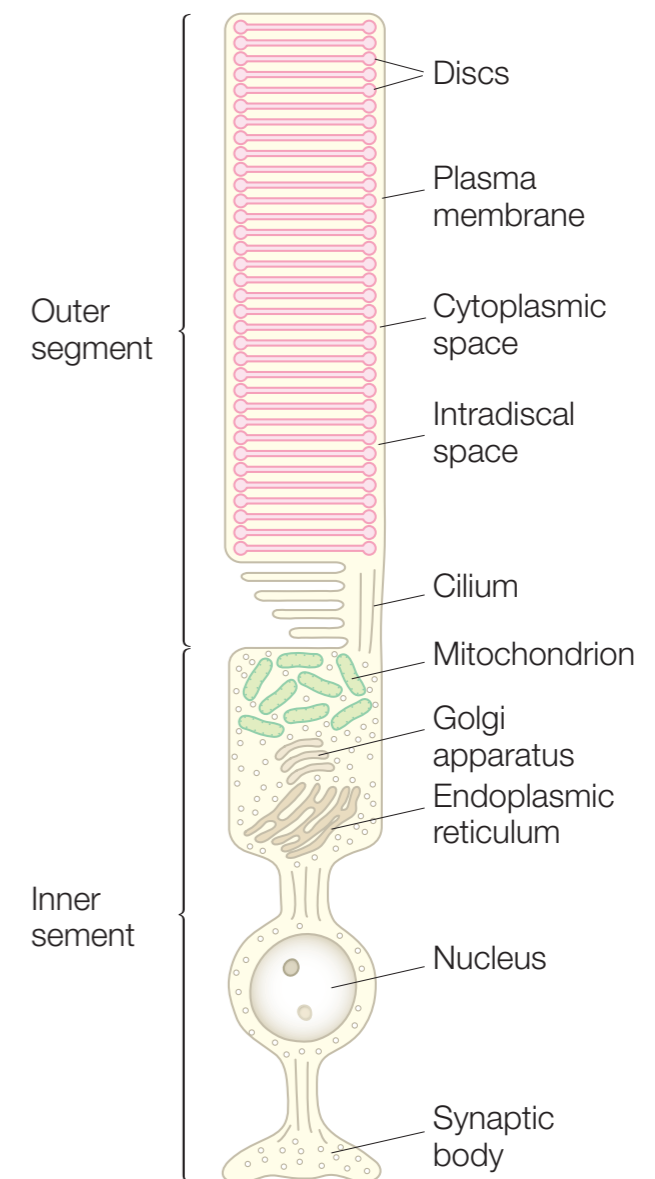# Signal Transduction

In signal transduction, an external signal (light, or odor, or taste) is converted into a neurological signal that can be interpreted by the brain.

Transduction processes occur in certain cellular membranes and involve protein complexes that are able to transform the signal with great sensitivity and specificity.

The detection of light in vision, the retina contains millions of neurons inner and outer compartments.

- The outer compartment of a retinal rod cell contains stacks of discs, which are densely packed with the receptor for light, rhodopsin.

- The inner compartment generates ATP to power the transduction process and also synthesizes the necessary proteins.

Outer segment

Inner sement

Discs

Plasma membrane

Cytoplasmic space

Intradiscal space

Cilium

Mitochondrion

Golgi apparatus

Endoplasmic reticulum

Nucleus

Synaptic body

Biological Pathway

The visual process can be decided in four steps: recognition, conversion, amplification, and processing.

- Recognition: absorption of light by a pigment buried inside of a protein called rhodopsin

- Conversion: structural change of the protein and an associated molecule in response to light absorption.

- Amplification and processing: the signal is amplified to be processed into a change in membrane potential and consequently a signal to the brain.

Molecular mechanism

The excitation of Rhodopsin leads to a conformational change which facilitates binding of the protein transducin.

Upon binding, transducin undergoes to a modification that results in the exchange of transducin-bound GDP for GTP.

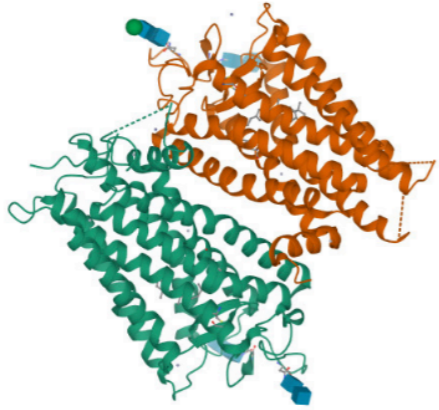The α subunit of transducin bound with GTP activating an enzymatic conversion from GTP to GMP.

Finally the rhodopsin returns to the original state with the incorporation of retinal after the regeneration of cis-retinal by a retinal isomerase
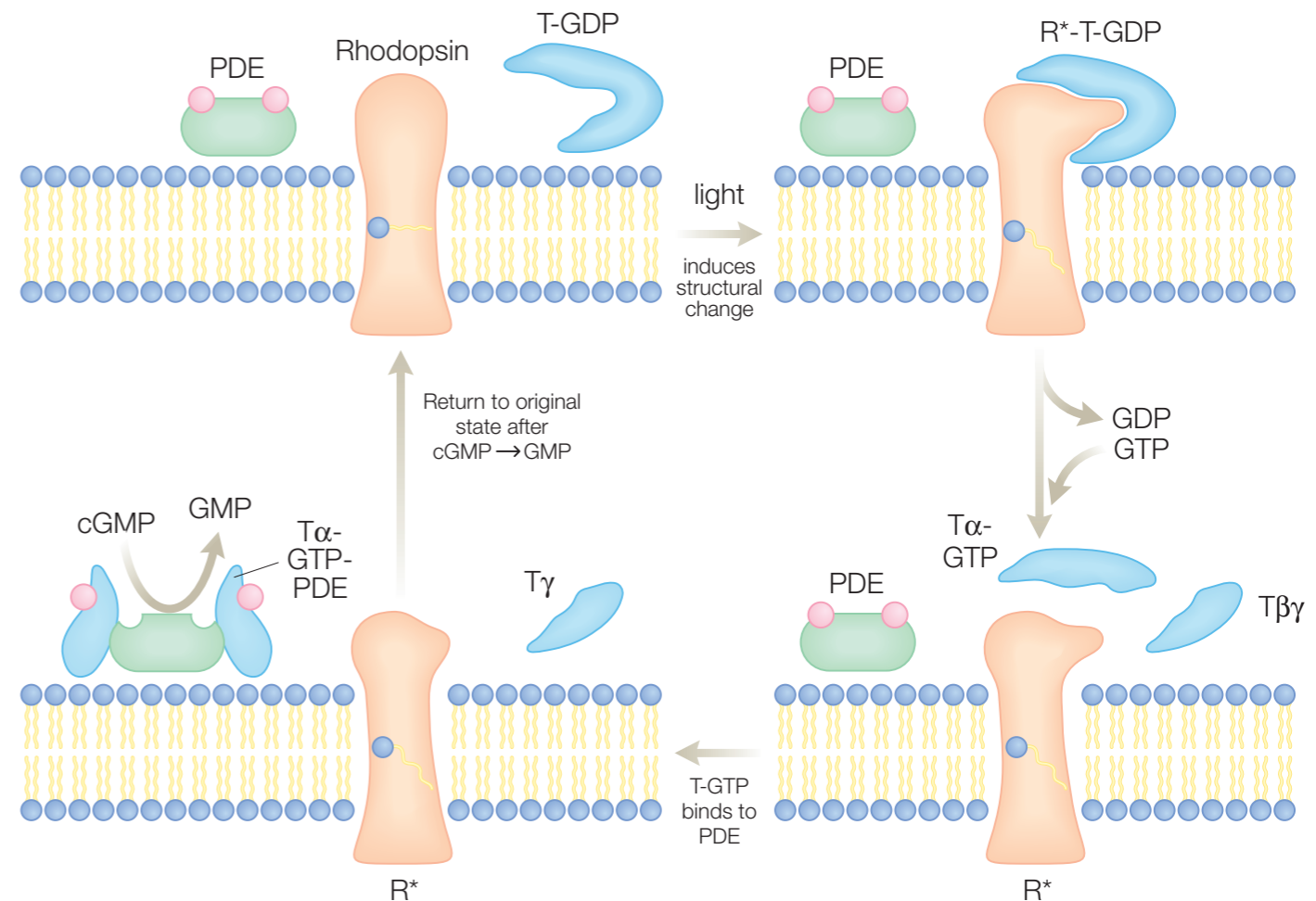
The Bovine Rhodopsin

The Bovine Rhodopsin structure (1F88) was crystallized at 2.8 Å.

Rhodopsin structure

The structure is a dimer each monomer with 7 helices in the transmembrane region.

Structural information

This sequence shows the presence of seven long stretches of hydrophobic amino acid residues connected by short segments of hydrophilic residues. The hydrophobic regions form the transmembrane helices.
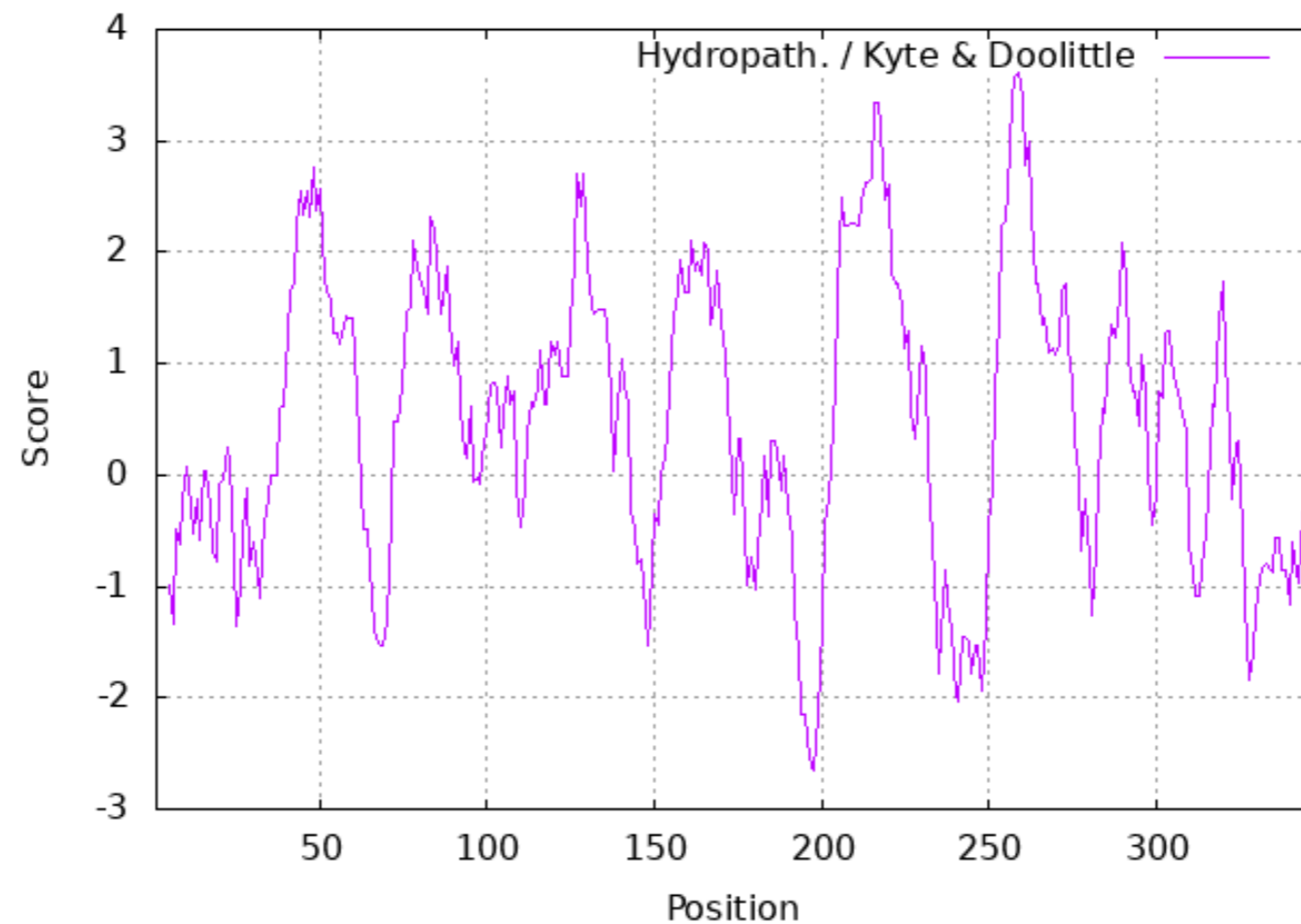
Important residues

Retinal is bound to rhodopsin through a protonated Schiff-base linkage, which is formed when the aldehyde group of retinal binds with the amino group of Lys296 in a hydrolysis reaction.
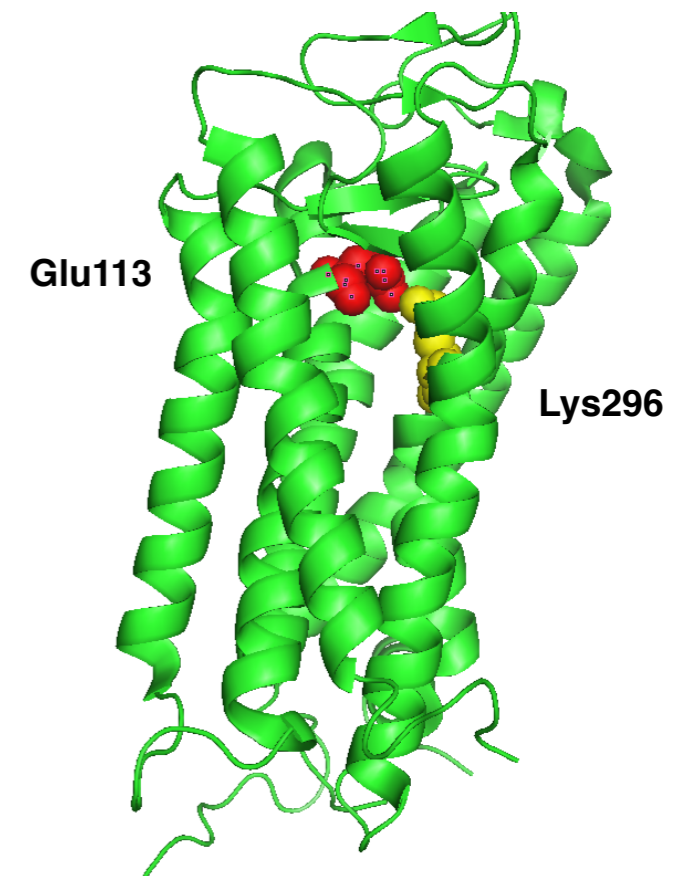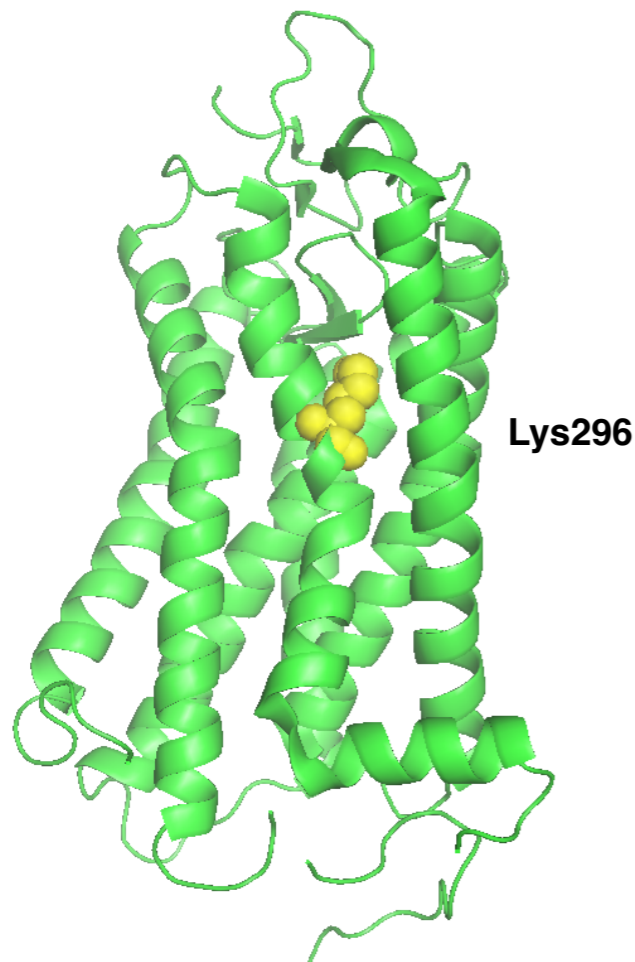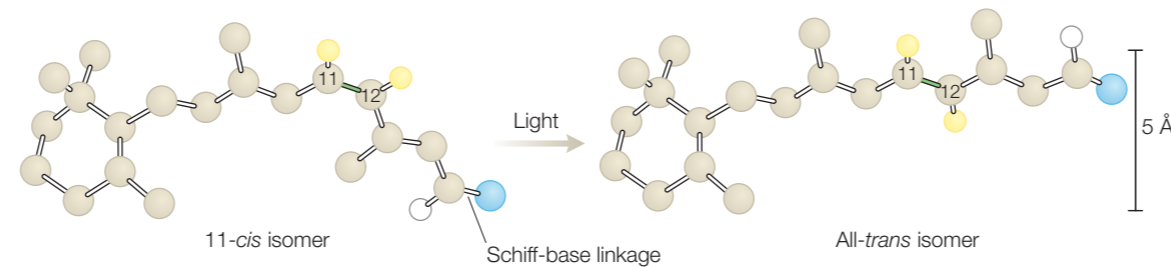
Comparison of Rhodopsins

Members of the rhodopsin family are found in all three domains of life, the Archaea, Eubacteria, and Eukaryota.

Rhodopsin and bacteriorhodopsin is consistent with the concept that all opsins have similar folds with seven transmembrane helices.

Despite the structural homology, the different opsins have significantly different functions. Rhodopsin serves as a G-coupled protein whereas bacteriorhodopsin serves as ion transporter.

The Bacterial Rhodopsin

The structure of a Bacterial Rhodopsin (1FBB) was obtained by Electron Microscopy at 3.2 Å resolution.

Biological Assembly 1

3D View: Structure | 1D-3D View |
Validation Report | Ligand Interaction |
Predict Membrane

Global Symmetry: Cyclic - C3 (3D View)
Global Stoichiometry: Homo 3-mer - A3

Find Similar Assemblies

Biological assembly 1 assigned by authors and

1FBB

CRYSTAL STRUCTURE OF NATIVE CONFORMATION OF BACTERIORHODOPSIN

PDB DOI: 10.2210/pdb1FBB/pdb

Classification: PROTON TRANSPORT
Organism(s): Halobacterium salinarum
Mutation(s): No
Membrane Protein: Yes   PDBTM   MemProtMD

Deposited: 2000-07-15 **Released:** 2000-08-09
Deposition Author(s): Subramaniam, S., Henderson, R.

Experimental Data Snapshot

Method: ELECTRON CRYSTALLOGRAPHY
Resolution: 3.20 Å
R-Value Free: 0.310
R-Value Work: 0.239

wwPDB Validation   3D Report   Full Report

Metric	Percentile Ranks	Value
Clashscore		47
Ramachandran outliers		10.4%
Sidechain outliers		7.8%

Worse   Better
■ Percentile relative to all structures
▯ Percentile relative to all EM structures
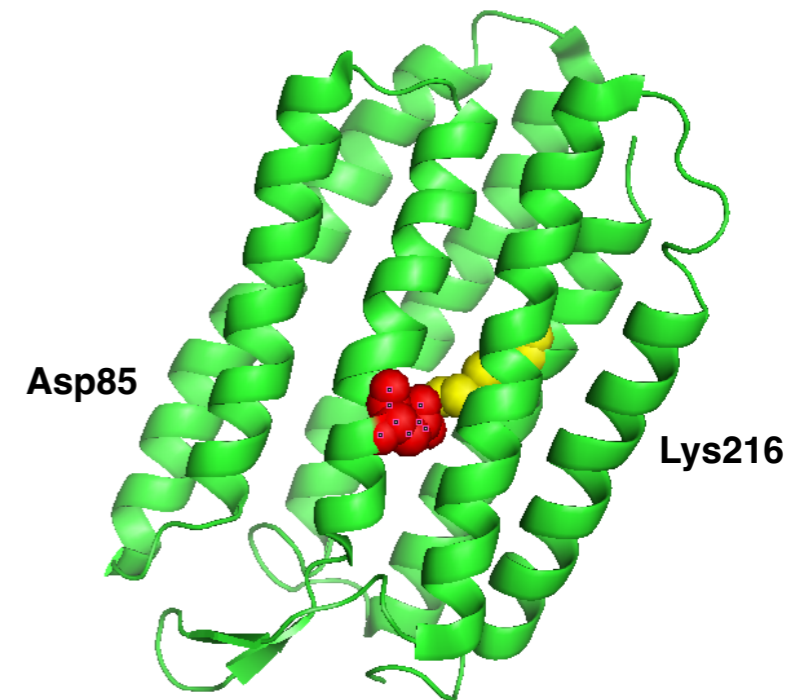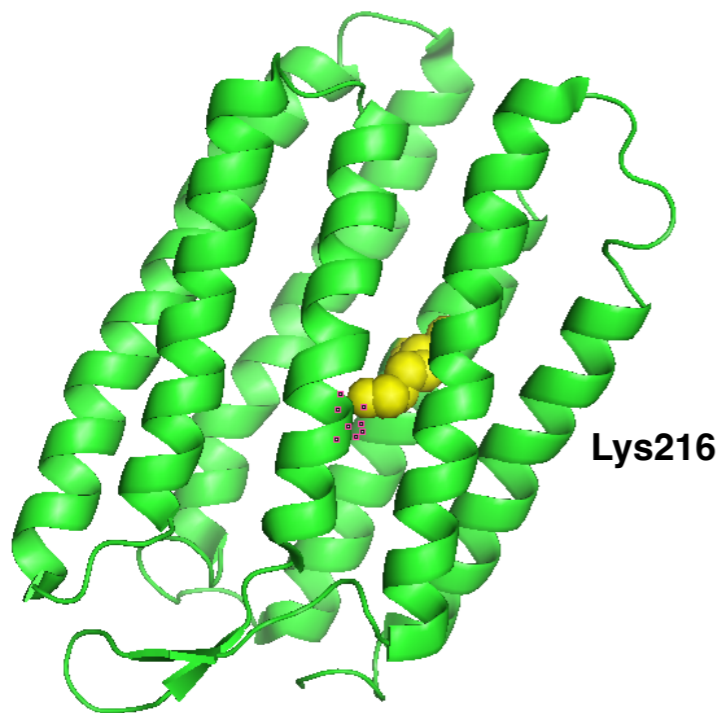
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Literature   Download Primary Citation

Important residues

The deprotonation process which involves the displacement of the Schiff-base can be explained by the conformational changes of Lys216 and Asp85.

Lys216

Asp85

Lys216

Sequence Alignment

The sequences of the Bacterial and Bovine Rhodopsin align with a percentage of identity of 22.9%.

Structure Alignment

The structures of the Bacterial and Bovine Rhodopsin align structurally with a RMSD of 3.97 Å.
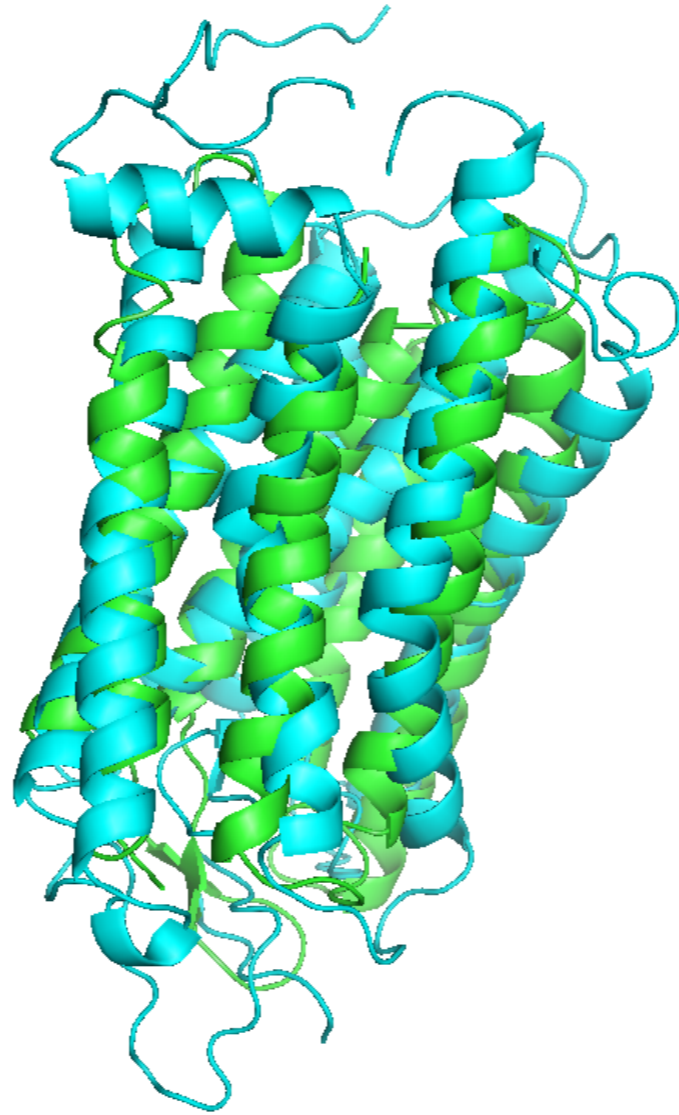
Functional Genomics

Functional genomics is a field of molecular biology that attempts to describe gene and protein functions and interactions.

Focusing on proteins, how can we assign the function to a new protein? Experimental techniques are expensive and time consuming.

In silico strategies for the comparison between new proteins and proteins with known functions are needed.

What should we compare?

- Sequences: Amino acid composition of proteins
- Structures: when available secondary or tertiary structures of the proteins