

# ASSIGNMENT (CLASS - 03.04.2020)

## BIOMOLECULAR STRUCTURES

SHREEYA PAHUNE - 2018113011

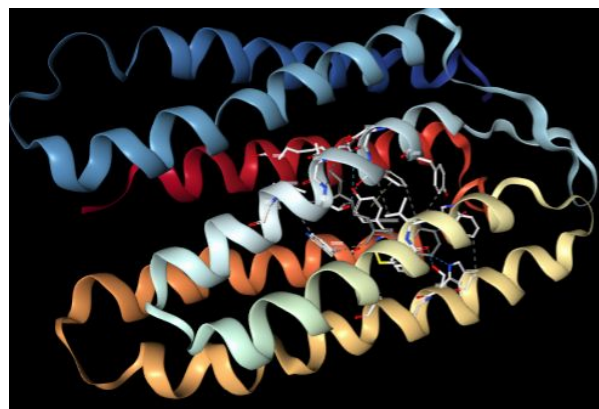
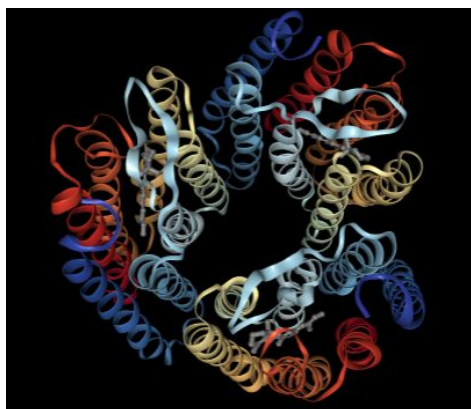
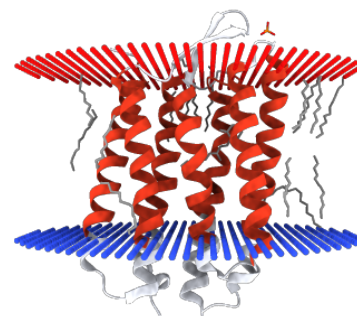
### Structure of Bacteriorhodopsin



Bacteriorhodopsin (bR) is a membrane protein present in the cell membrane of an halophilic organism called *Halobacterium salinarum*. It is a light driven pump which transports protons across the cell membrane and has a relative molecular mass of 27,000.

The overall structure of the protein includes both alpha helices (green) and beta sheets (red). Its conformation is essential to its function.

bR aggregates to form two-dimensional crystalline patches in the plasma membrane. This differentiated area of membrane, which is called purple membrane



Each bR molecule is composed of 7 alpha helices and, in the purple membrane, bR trimers align to form a hexagonal lattice. The polypeptide chain of bR consists of 248 amino acids and the retinal is bound to the e-amino group of Lys-216. The polypeptide chain is composed of seven extremely hydrophobic segments 22-25 residues long, which form alpha helices in the nonpolar environment of the membrane and each of these chains consisting of the seven transmembrane alpha helices contains one molecule of retinal within the helices.

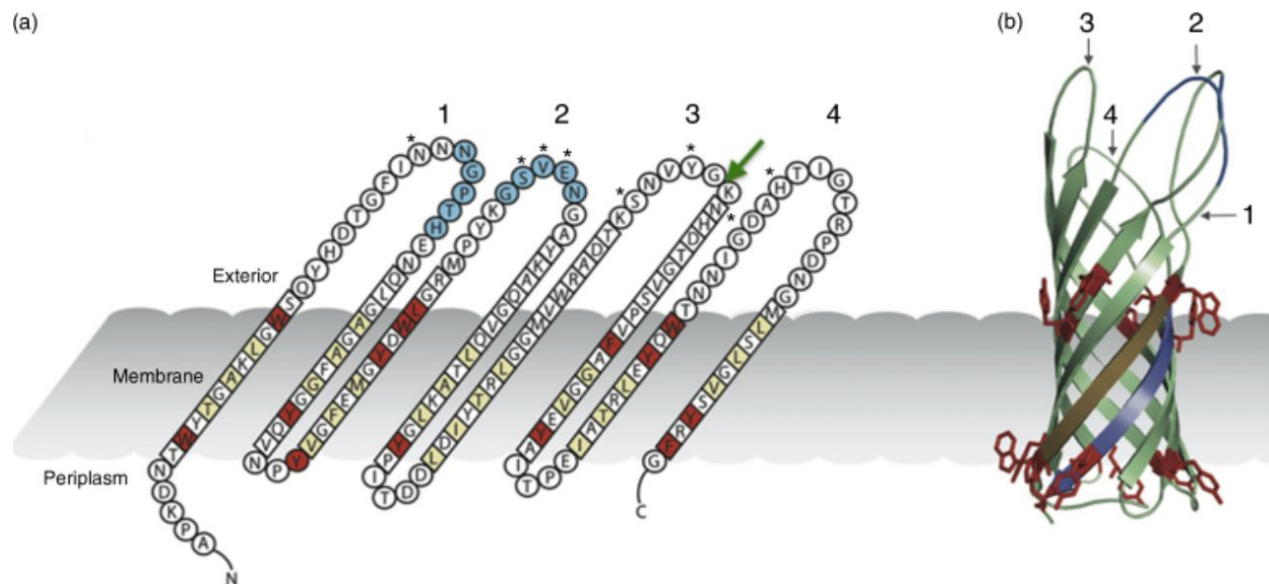
bR exists in two interconvertible forms, one containing all-trans and the other 13-ds retinal isomer, which exists in equilibrium with first in the dark.

\*(Retinal is one of the forms of vitamin A - shown by lines molecular representation in figure on right)

\*( $\epsilon$ -amino group: An essential amino acid, has a positively charged  $\epsilon$ -amino group (a primary amine. Eg: Lysine)

## Structure of Outer membrane protein A (OmpA)

The outer membrane protein A from Escherichia coli (OmpA) is a  $\beta$ -barrel type of membrane protein. It is very abundant in E.coli and one of its functions include stabilizing the outer membrane.

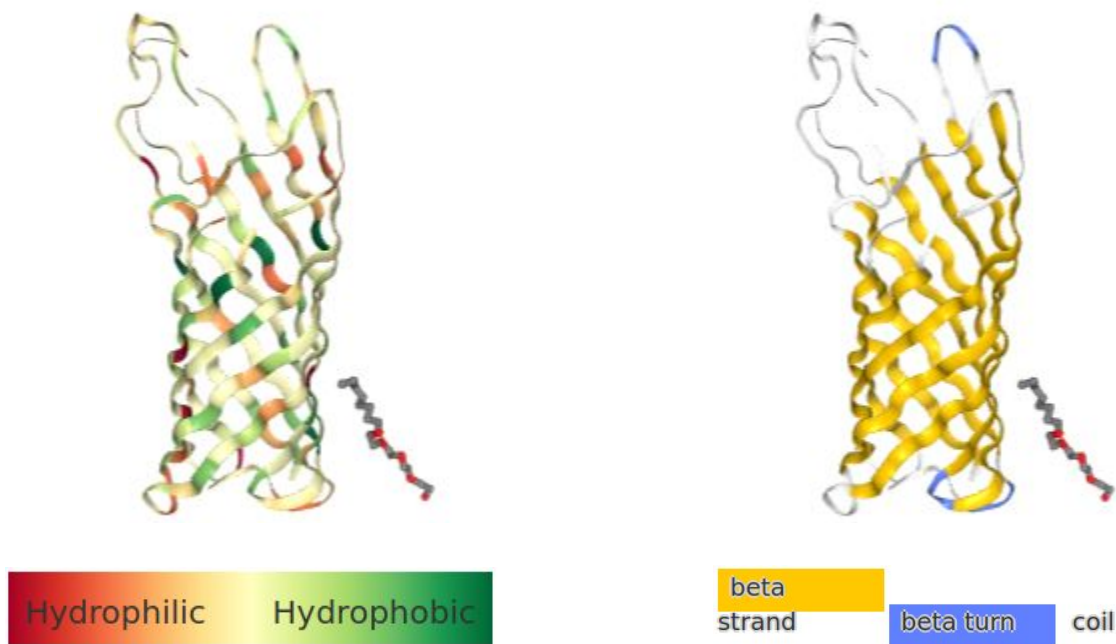


(a)Topological view: Blue residues are highly mobile

(b)The protein approximates a cylinder with a diameter of 26 Å and a length of 57 Å. The barrel is exceptionally long with an average strand length of 13 residues: its conformation is very regular.

It has a two domain structure:

- **Exterior:** The N-terminal domain (NTD) resides within the outer membrane. It is an eight-stranded  $\beta$ -barrel domain consisting of antiparallel  $\beta$ -strands connected by four long loops at the outer surface of the membrane and three short turns at the periplasmic face. that.
- **Membrane:** A15-amino-acid linker region connects the barrel to the soluble C-terminal domain (CTD).
- **Periplasm:** The CTD is located in the periplasm, a gel-like region that separates the OM from the inner cytoplasmic membrane.



The barrel is believed to like an inverted micelle with a hydrophobic surface and a largely polar core stabilized by extensive hydrogen bonding, and a nonpolar external since its located in the membrane. The barrel interior contains an intricate hydrogen bonding network (polar), including several salt bridges and several large water-filled cavities, but there is no passage for water or ions. The external loops are stabilized by dimerization and interaction with LPS molecules.

\*(LPS molecules: Large molecules consisting of a lipid and a polysaccharide, outer core and inner core joined by a covalent bond; they are found in the outer membrane of Gram-negative bacteria)