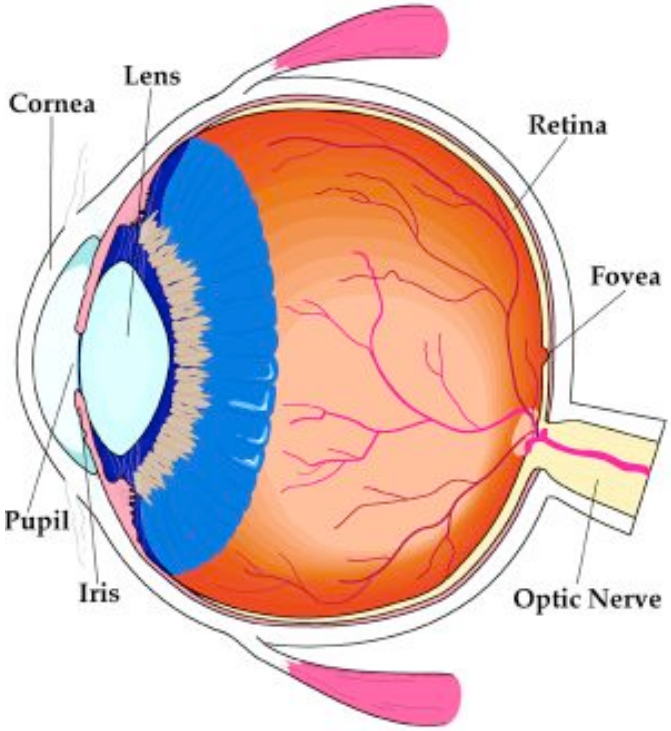
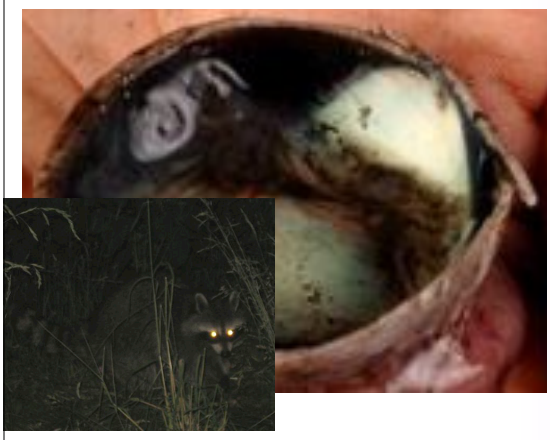
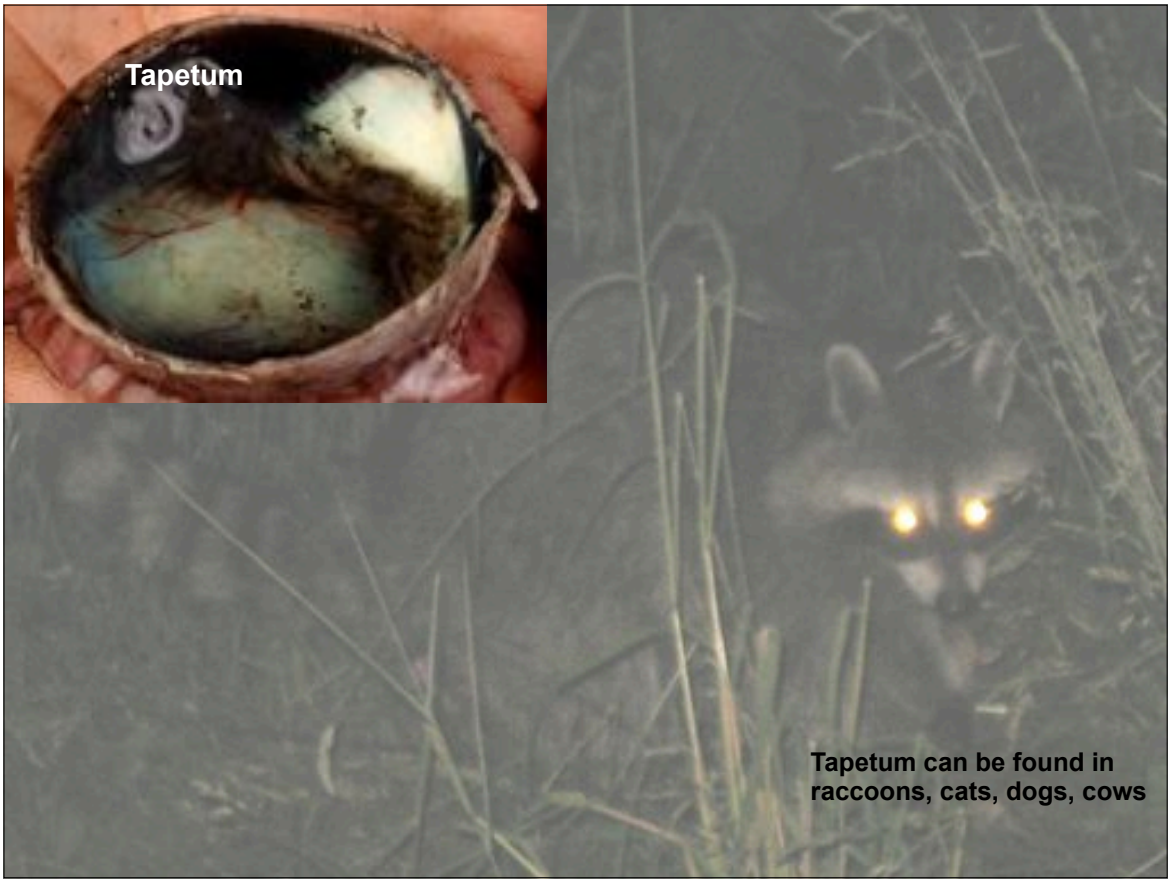
The architecture of the eye

Whose eye is this?

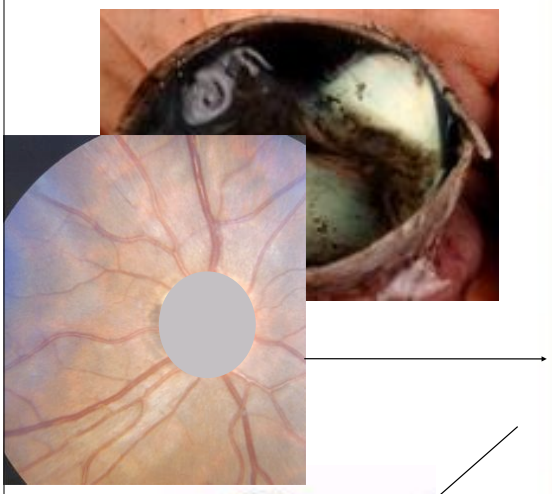


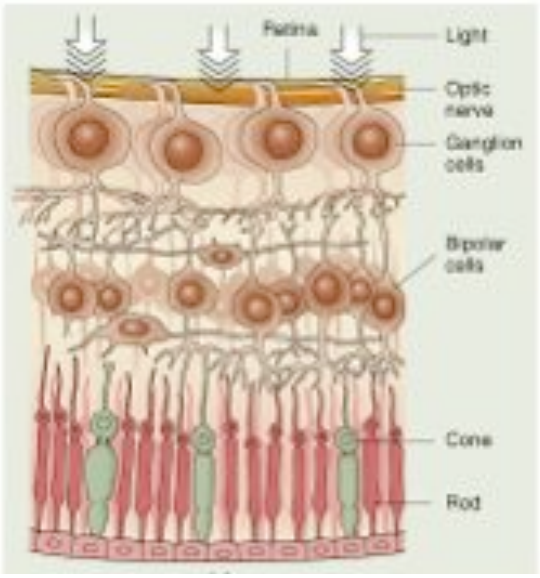
The Tapetum of the Eye

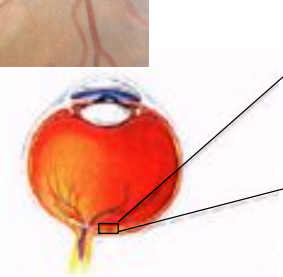




Retina -- it's a layer of light-sensitive cells



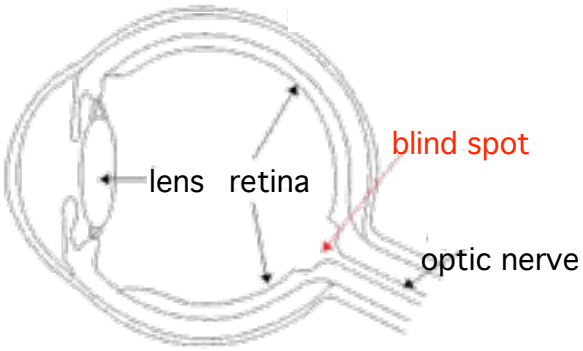




* Rod cells sense brightness
* Cone cells sense color

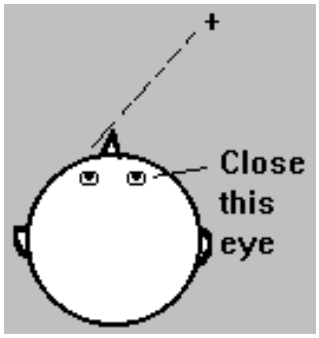
More rod and cone cells than citizens in the US!

Retina -- only attached to the eye in one spot



* All the nerves from the retina join to form optic nerve at the blind spot
* There are no light-sensitive cells at the blind spot
* Cannot see anything that lands on blind spot

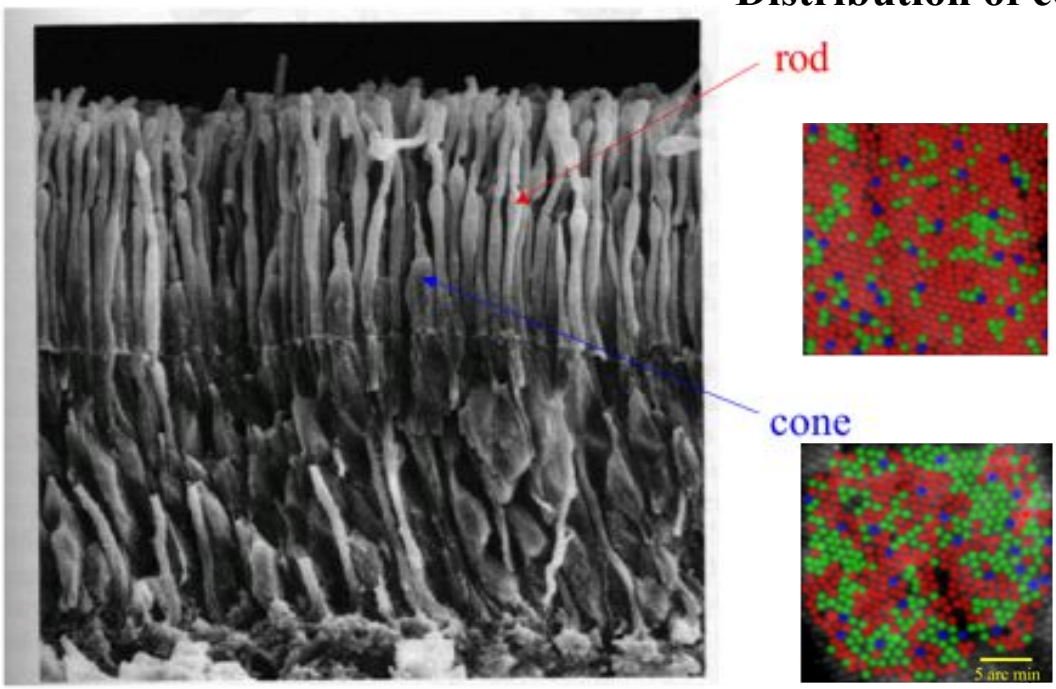
Blind Spot Test



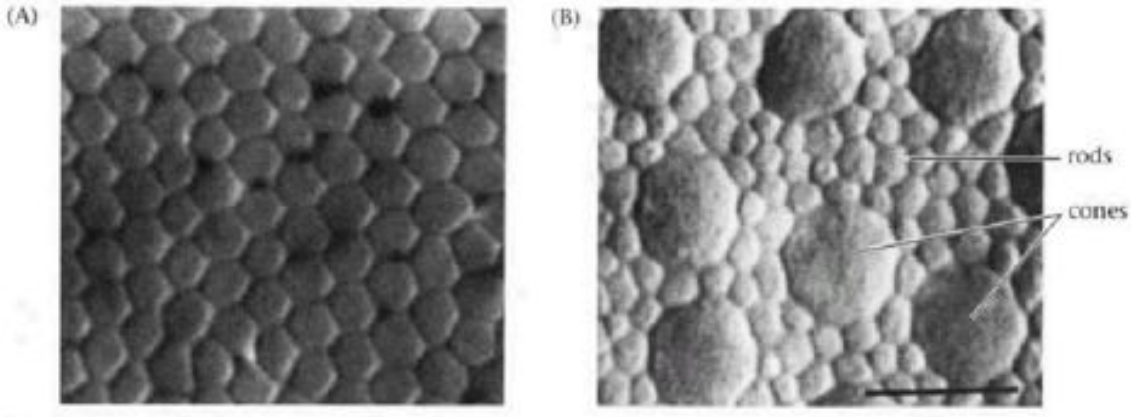
1. Hold the blind spot test paper at arm's length
2. Close your right eye
3. Look at the "+" symbol with your left eye
4. Slowly move the paper closer and closer, until the "•" symbol disappears.

Rods and Cones

Distribution of cones



Distribution of Rods and Cones

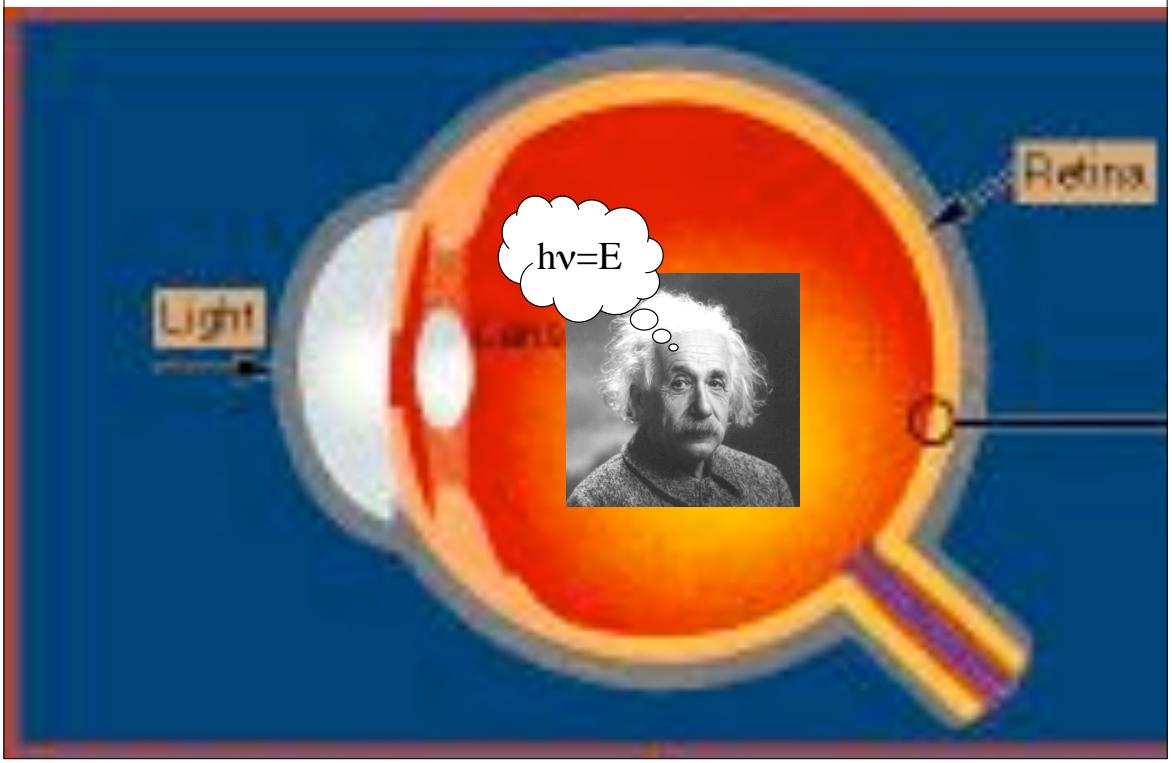


Cones in Fovea. Note complete absence of rods.

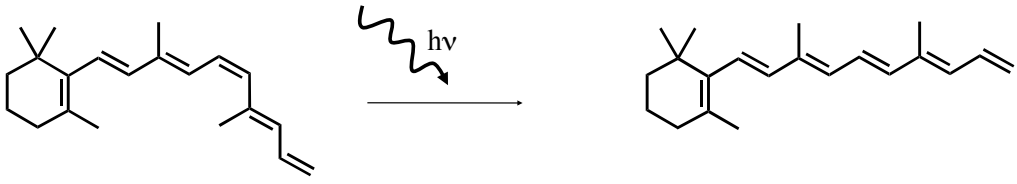
Cones and Rods in periphery.

Why do humans have color vision? What's the evolutionary advantage?

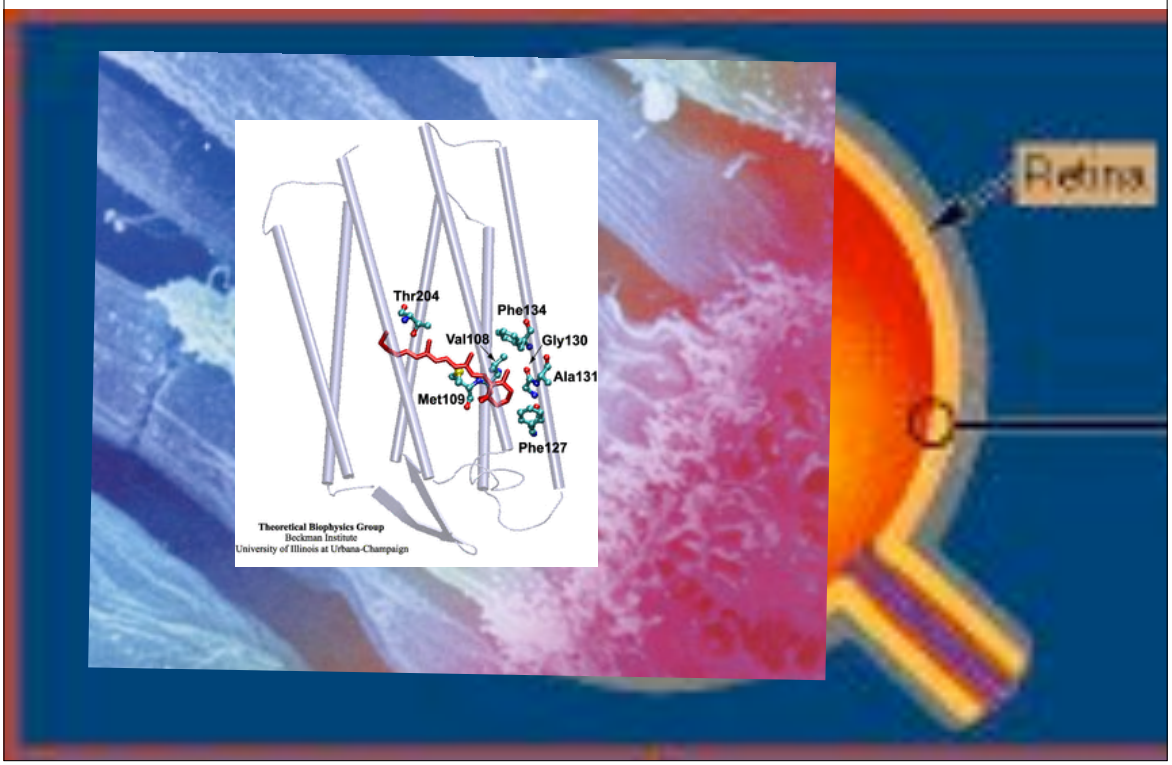
The Eye is a Photonreceptor



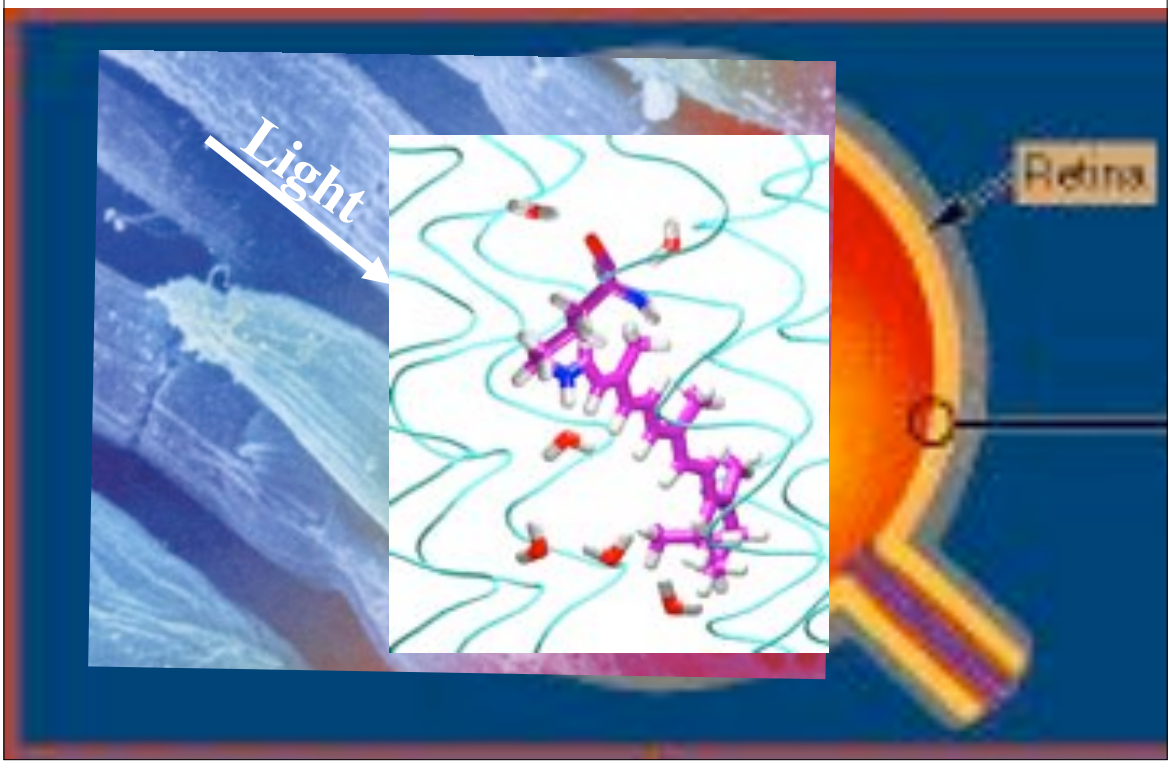
Photophysics of Vision



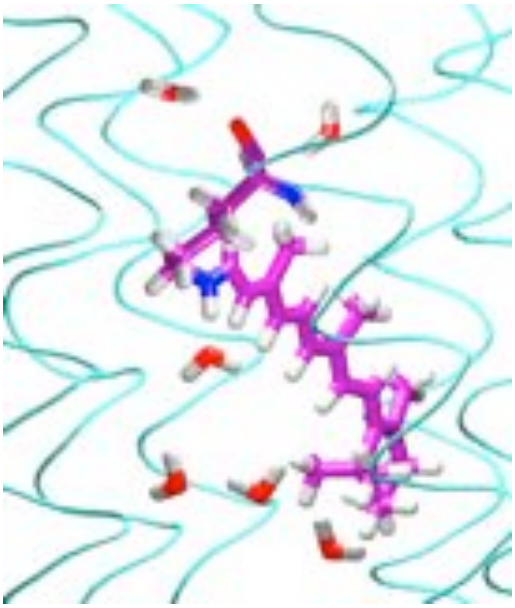
Retina → Rod cell → Rhodopsin

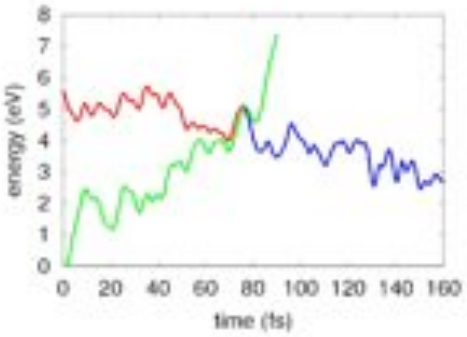


Retina → Rod cell → Rhodopsin

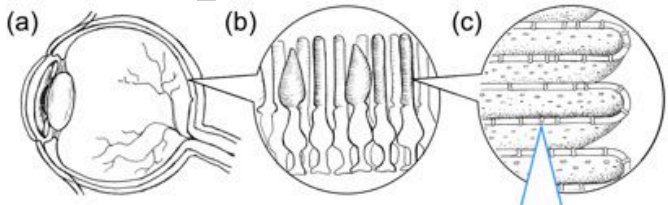


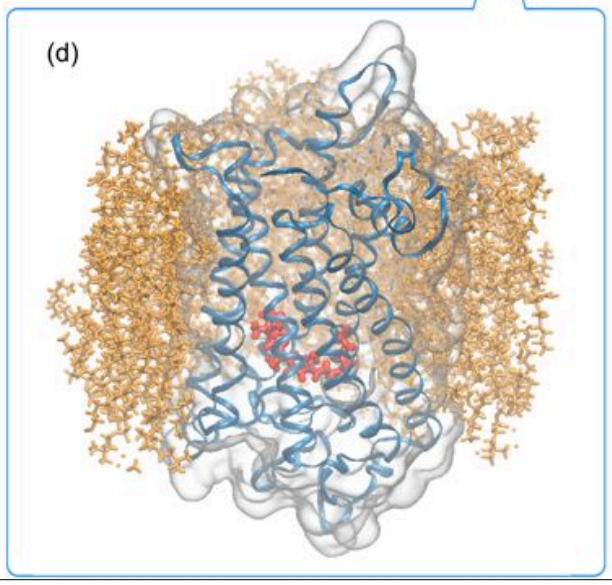
Photoisomerization of Retinal



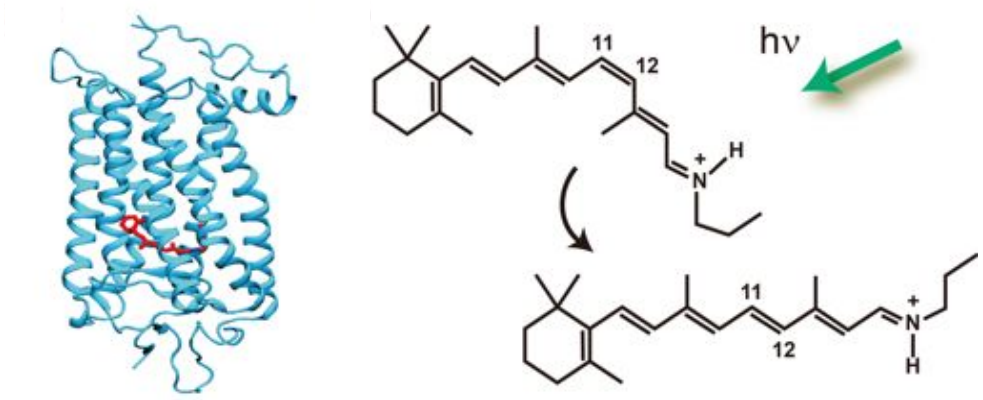


Visual Receptor Protein Rhodopsin

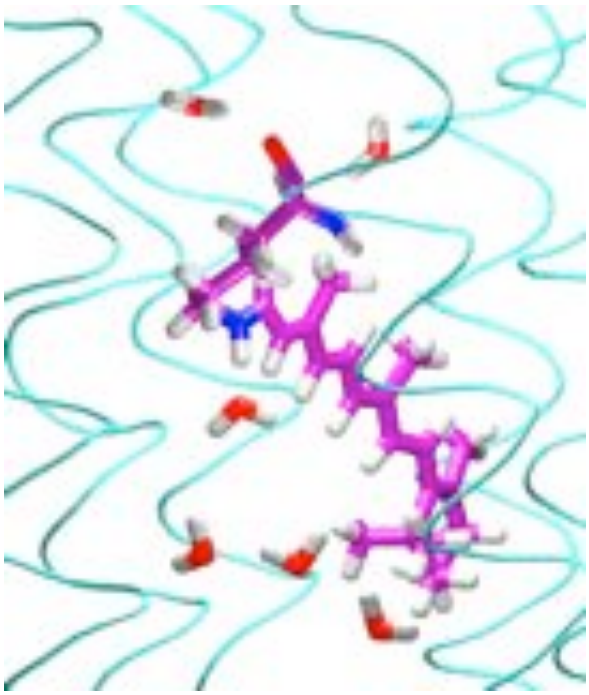


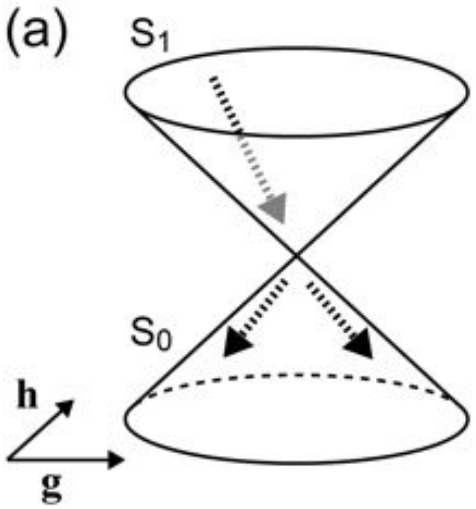


Photophysical Process in Rhodopsin



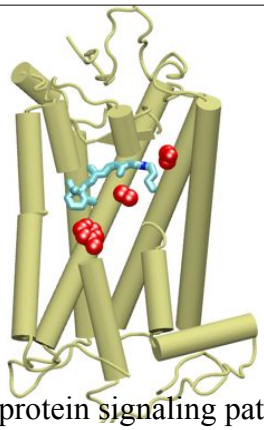
Excited State - Ground State Transition in Rhodopsin



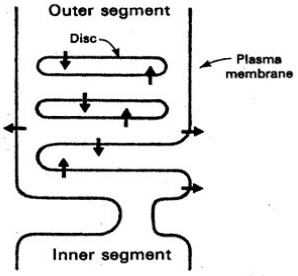


Visual signaling

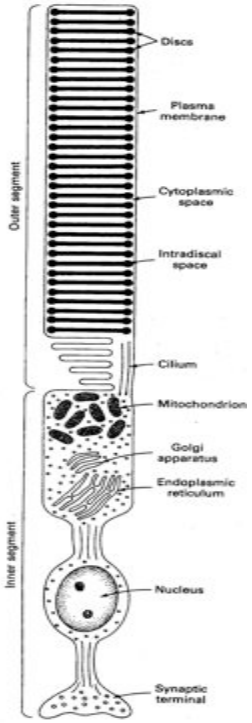
Light

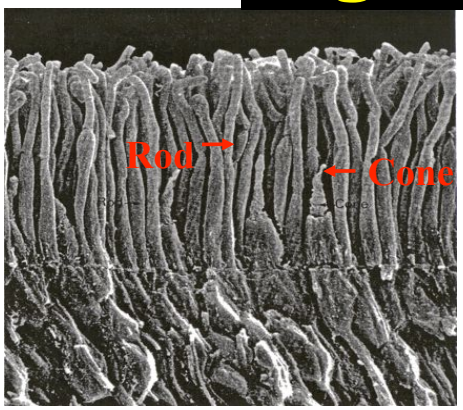


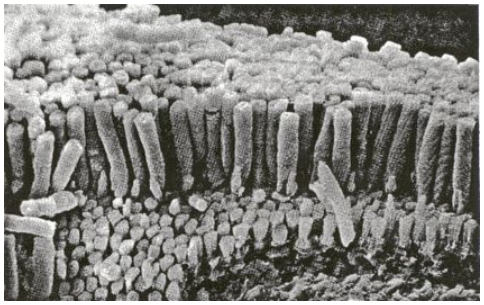
G-protein signaling pathway



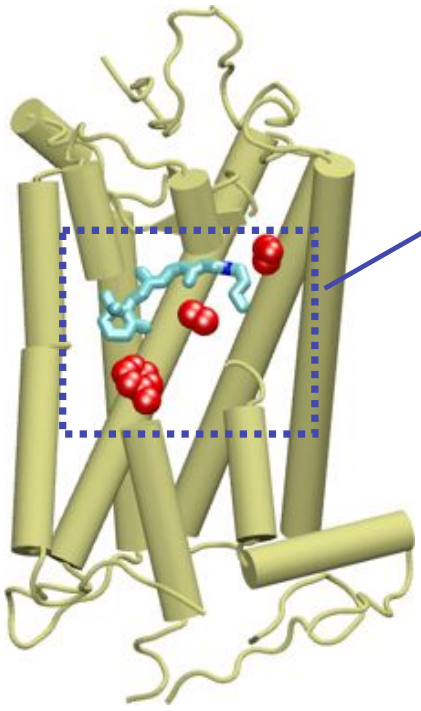
Rhodopsin

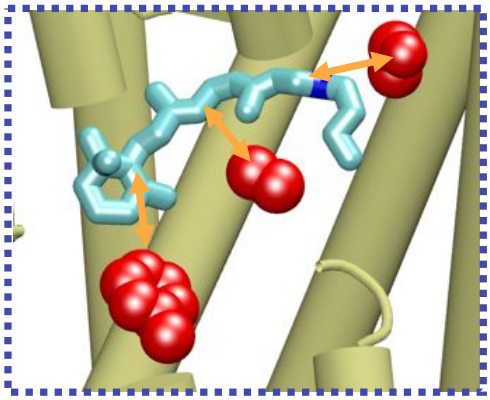




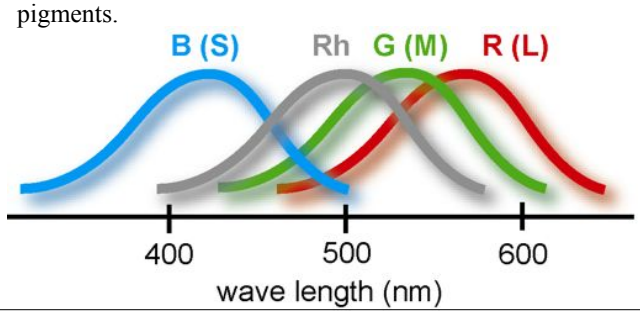


Physics of Color Vision





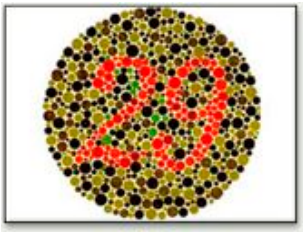
Interaction between the chromophore and side groups of amino acids determines color sensitivity of the visual pigments.



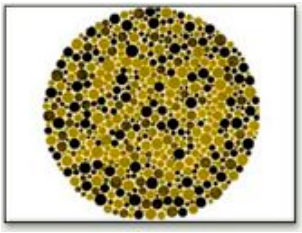
Deficiency

(Example: mutant in the side group **Ala**164**S** (Phe261Y, Ala269T) leads to weakness in sensitivity to green; deuternopia)

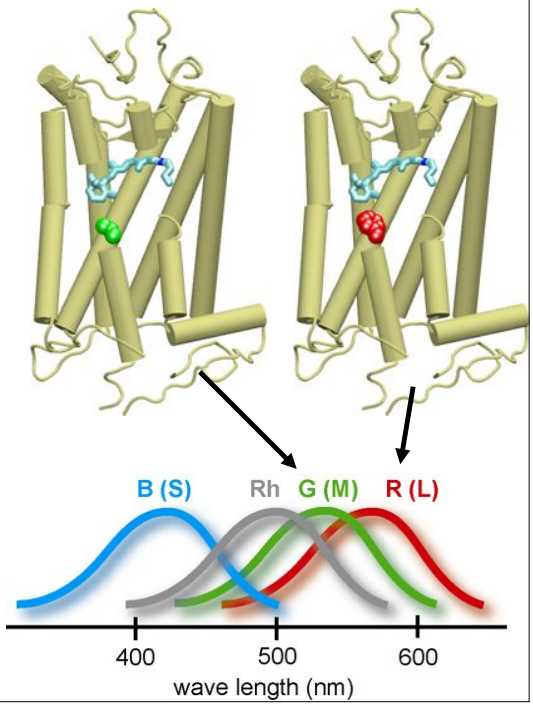
Normal



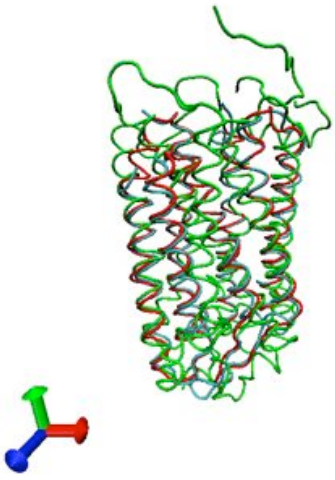
Deutan (M-cone)



Boys are afflicted more often than girls! Why?



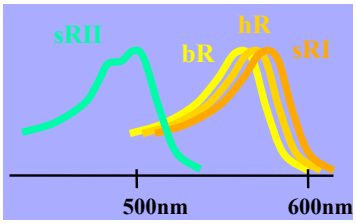
Alignment of Rh, bR, and sRII

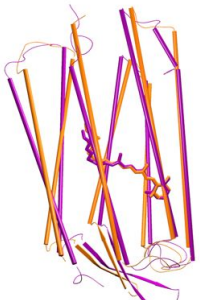


Spectral Tuning in Archaeal Retinal Proteins

Hayashi et al. Structural determinants of spectral tuning in retinal proteins – bacteriorhodopsin vs sensory rhodopsin II. *J. Phys. Chem.* B, 105:10124–10131, 2001.

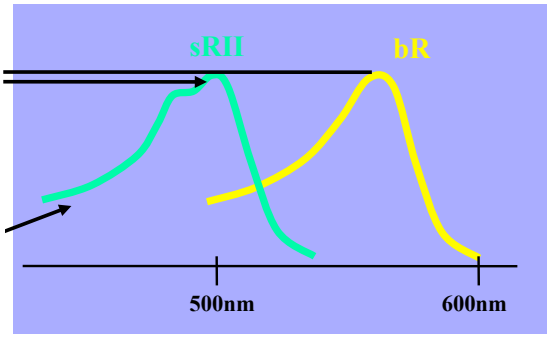
Sensory rhodopsin I (sRI):
attractant (repellent) to orange (near UV) light
Sensory rhodopsin II (sRII):
repellent to blue-green light
phototaxis





orange: sRII, purple: bR

- **Absorption maximum of sRII (vs. bR) is blue-shifted (70 nm) despite close homology**
- **sRII spectrum exhibits a prominent sub-band.**



Sequences of bR and sRII

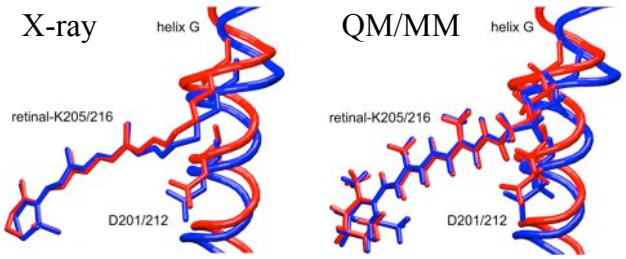
```
                    |   A   |         |         |   50|   B   |
BACR_HALHA    1 QAQITGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSM  60
BACT_NATPH    1 -----MVGLTTLFWLGAIGMLVGTLAFAMAGRDAGSGE-RRYYVTLVGISGIAAVAYVVM  54
                                                      |   50|

                    |         |   C   |  100|         |   D   |
BACR_HALHA   61 LLGYGLTMVPFGGEQNPIYWARYADWLFTTPLLLLDLALLVDADQGTILALVGADGIMIG 120
BACT_NATPH   55 ALGVGWVPV----AERTVPAPRYIDWILTTPLIVYFLGLLAGLDSREFGIVITLNTVVML 110
                          |         |         |  100|         |   |

                    |         |   E   |  150|         |   F   |
BACR_HALHA  121 TGLVGALTKVYSYRFVWWAISTAAMLYILYVLFFGFTSKAESMRPEVASTFKVLRNVTVV 180
BACT_NATPH  111 AGFAGAMVPGIE-RYALFGMGAVAFLGLVYYLVGPMTESASQRSSGIKSLYVRLRNLTVI 169
                          |         |         |  150|         |

                    |         |  200|         |   G   |         |
BACR_HALHA  181 LWSAYPVVWLIGSEGAGIVPLNIETLLFMVLDVSAKVGFGLILLRSRAIFGEAEAPEPSA 240
BACT_NATPH  170 LWAIYPFIWLLGPPGVALLTPTVDVALIVYLDLVTKVGFGFIALDAAATLR-AEHGESLA 228
                          |         |  200|         |         |

BACR_HALHA  241 G-D-GAAATSD                                                  249
BACT_NATPH  229 GVDTDAPAVAD                                                  239
```

BACR_HALHA: bR, *Halobacterium halobium*
BACT_NATPH: sR-II, *Natronobacterium pharaonis*
Helical region
Identical residues
Binding pocket

X-ray Structures of bR and sRII

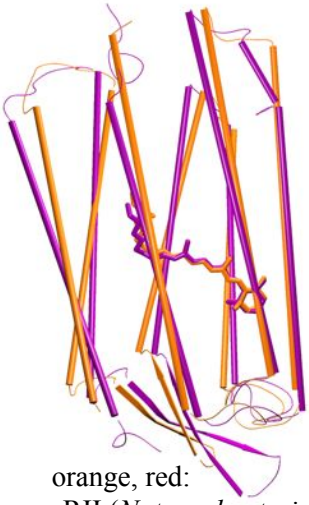
- X-ray crystallography shows structures are homologous.

[structure: Royant, A.; Nollert, P.; Edman, K.; Neutze, R.; Landau, E. M.; Pebay-Peyroula, E.; Navarro, J. *Proc. Natl. Acad. Sci. U.S.A.* **200**1]



Note helix shift!

Homology: computational errors cancel when comparing spectra



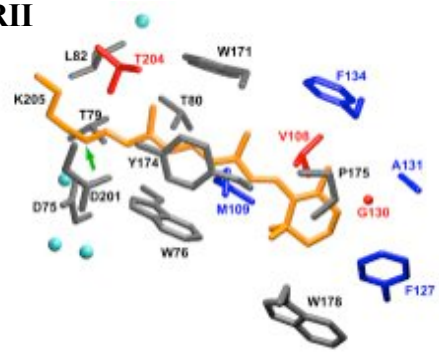
But there is also a significant difference in overall structure!

orange, red:
sRII (*Natronobacterium pharanois*)

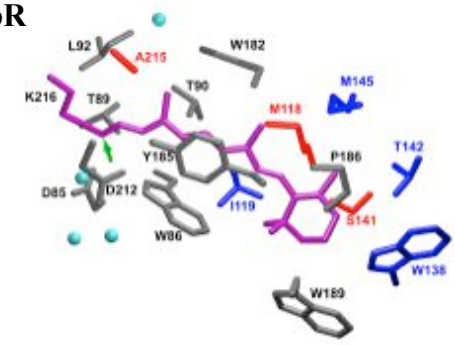
purple, blue:
bR (*Halobacterium salinarum*)

Binding Sites of bR and sRII

sRII



bR



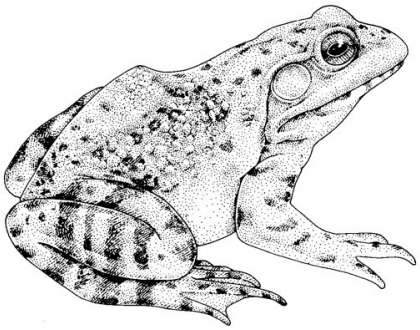
Similar structure

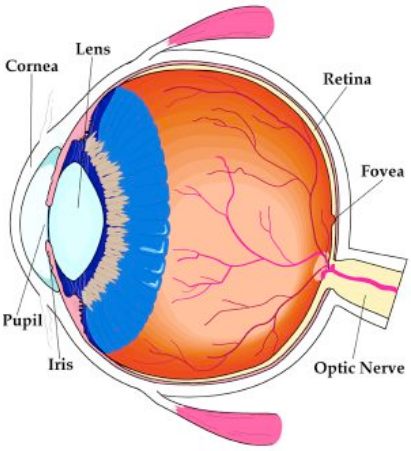
- **Aromatic residues.**
- **Hydrogen-bond network. (counter-ion aspartates, internal water molecules)**

Mutagenic substitutions
(Shimono, Kamo *et al.)*

T204A/V108M/G130S of sRII produces only 20 nm (30%) spectral shift.

What is missing? What are the main determinants of spectral tuning: side groups or protein structure? Both!





Retinal I

Retinal II