Universitat
Pompeu Fabra
Barcelona

Photosynthetic reaction center from ***Rhodopseudomonas viridis***

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4° Human Biology
Structural Biology

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INTRODUCTION

PURPLE BACTERIA

Purple bacteria are **gram-negative phototrophic** bacteria, pigmented with bacteriochlorophyll *a* or *b*, together with various carotenoids, which give them colours ranging between purple, red, brown, and orange.

Rhodopseudomonas viridis

Green sulfur bacteria

Green nonsulfur bacteria

Purple sulfur bacteria

Purple nonsulfur bacteria

Heliobacteria

- Most diverse group
- S^0 deposited outside the cell

TAXONOMY

Genus
Blastochoris

Family
Blastochloridaceae

Order Hyphomicrobacteria

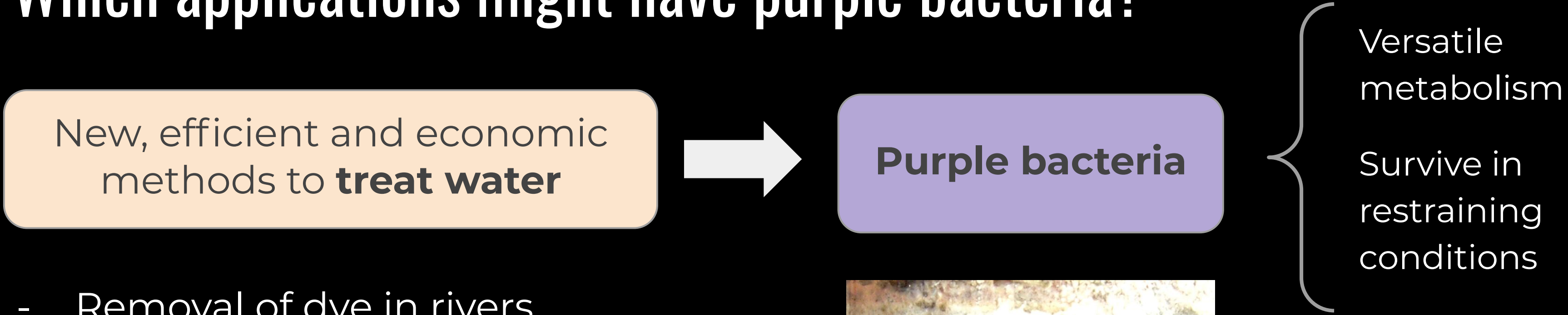
Class Alphaproteobacteria

Phylum Proteobacteria

Species

Blastochloris viridis
=
Rhodopseudomonas viridis

Which applications might have purple bacteria?



New, efficient and economic methods to **treat water**

Purple bacteria

Versatile metabolism

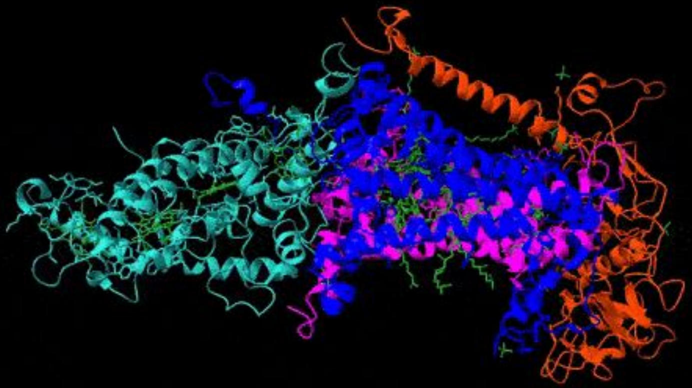
Survive in restraining conditions

- Removal of dye in rivers
- Removal of macro-pollutants
- Removal of heavy metals

Photo from:
https://cutt.ly/bzcacQY
Public Domain

STRUCTURAL ORGANISATION

Photosynthetic reaction center



L M H C

Core

Resolution: **2,9Å**

Co-factors

Heme molecules (x4)

Bacteriochlorophyll b (x4)

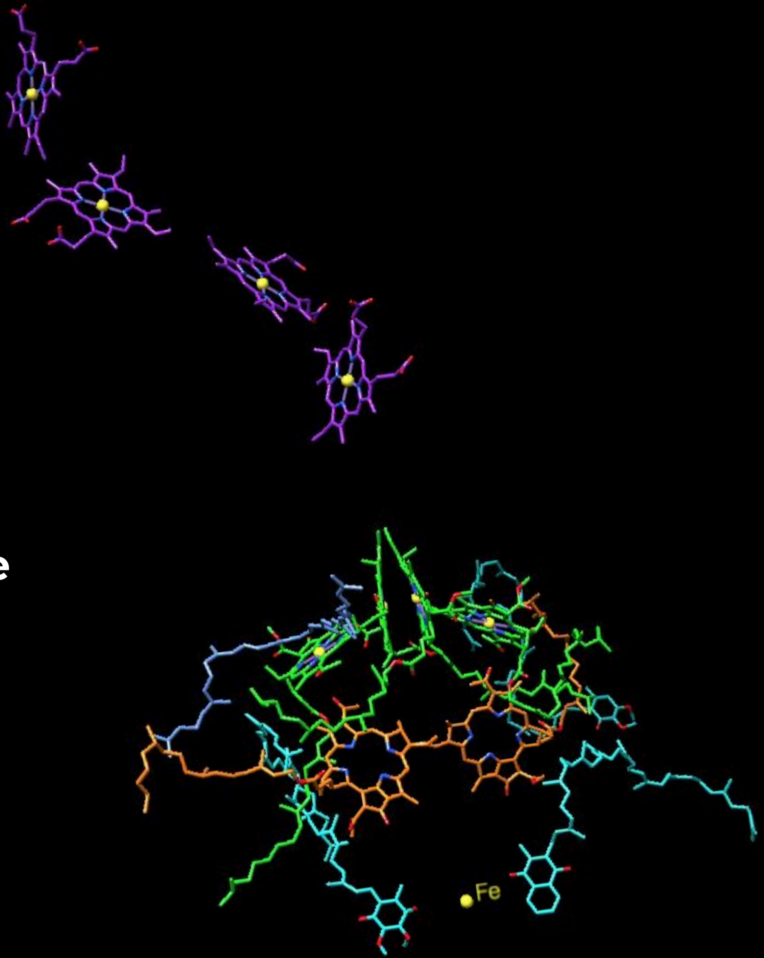
Bacteriopheophytin b (x2)

Carotenoid (x1)

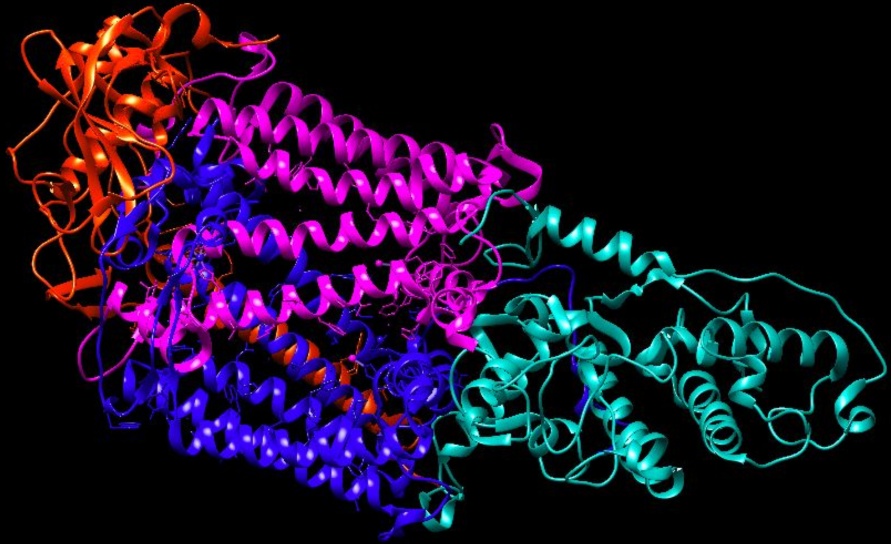
Non-heme iron (x1)

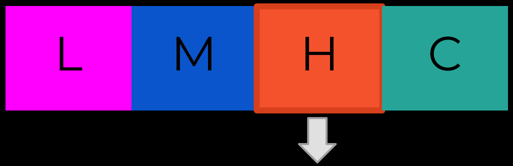
Quinones (x3)

Core



H subunit



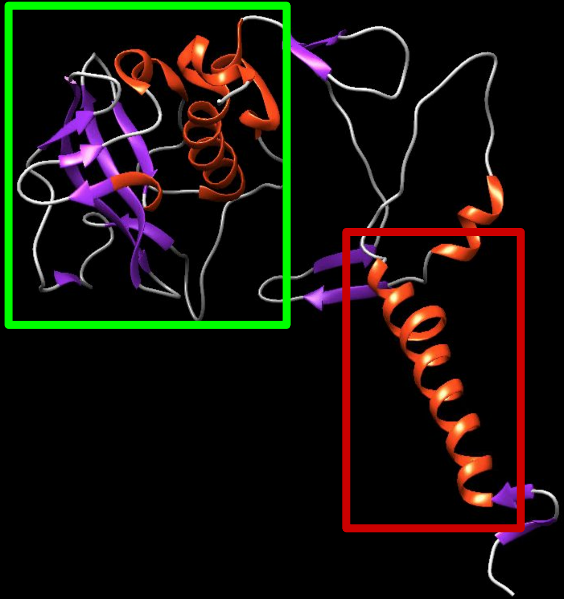


258 residues

H subunit

Structural regions

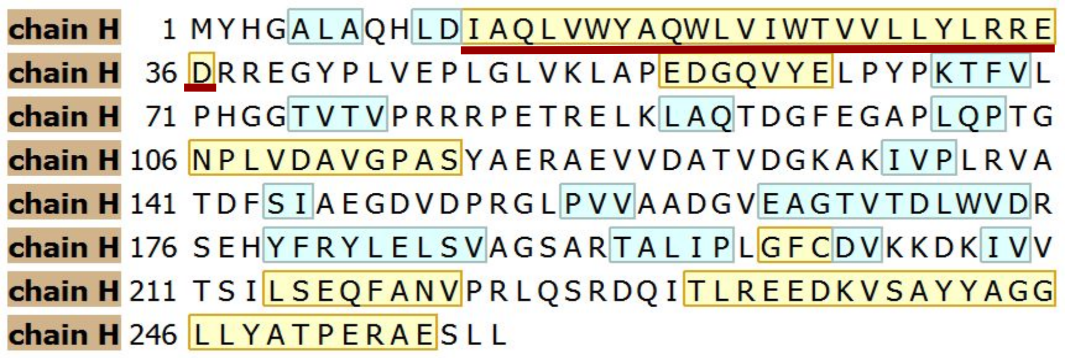
- **N-terminal segment contains** a transmembrane helix
- **Globular domain** contains antiparallel β sheets



Secondary structure

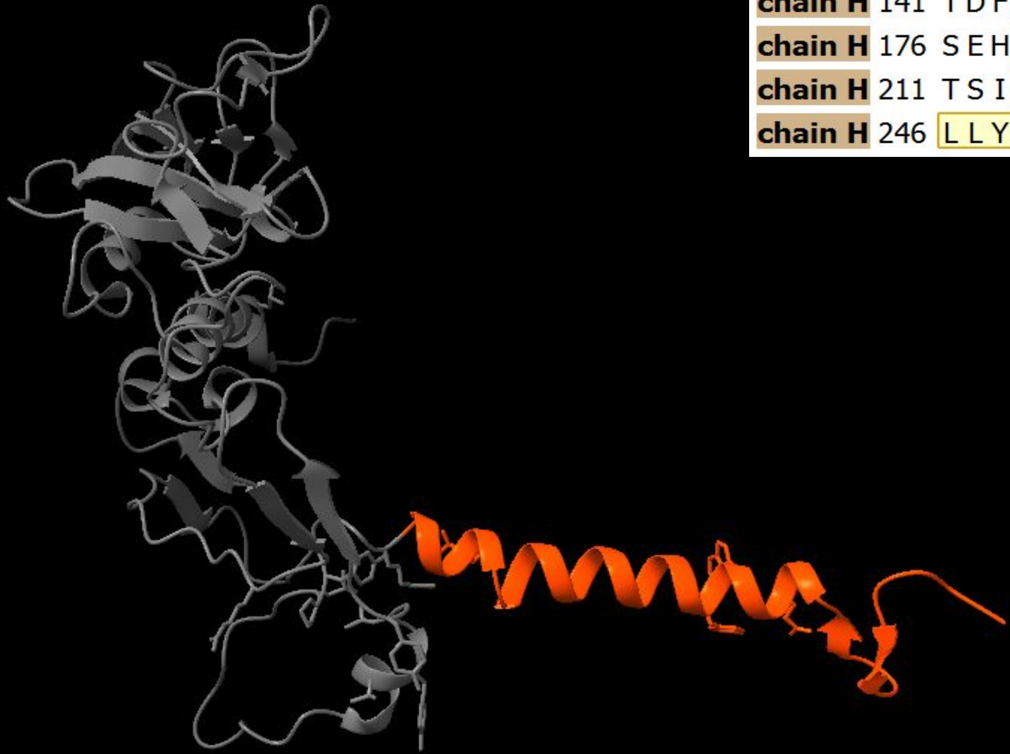
H subunit

N-terminal segment



chain H 1 MYHGALAQHLDIAQLVWYAQWLVIWTVVLLYLRRE
chain H 36 DRREGYPLVEPLGLVKLAPEDGQVYELPYPKTFVL
chain H 71 PHGGTVTVPRRRPETRELKLAQTDGFEGAPLQPTG
chain H 106 NPLVDAVGPASYAERAEVVDATVDGKAKIVPLRVA
chain H 141 TDFSIAEGDVDPRGLPVVAADGVEAGTVTDLWVDR
chain H 176 SEHYFRYLELSVAGSARTALIPLGFCDVKKDKIVV
chain H 211 TSILSEQFANVPRLQSRDQITLREEDKVSAYYAGG
chain H 246 LLYATPERAESLL

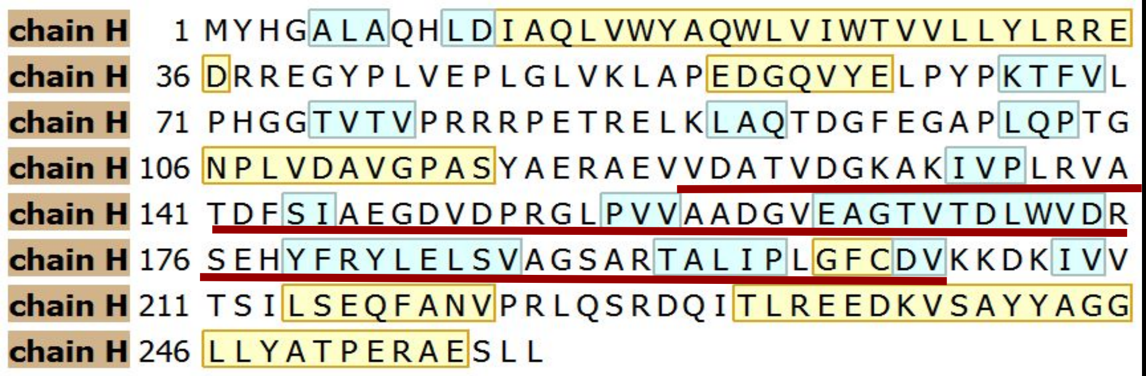
Helix
β-sheet



N-terminal segment.
Transmembrane helix.
IleH12 - AspH36

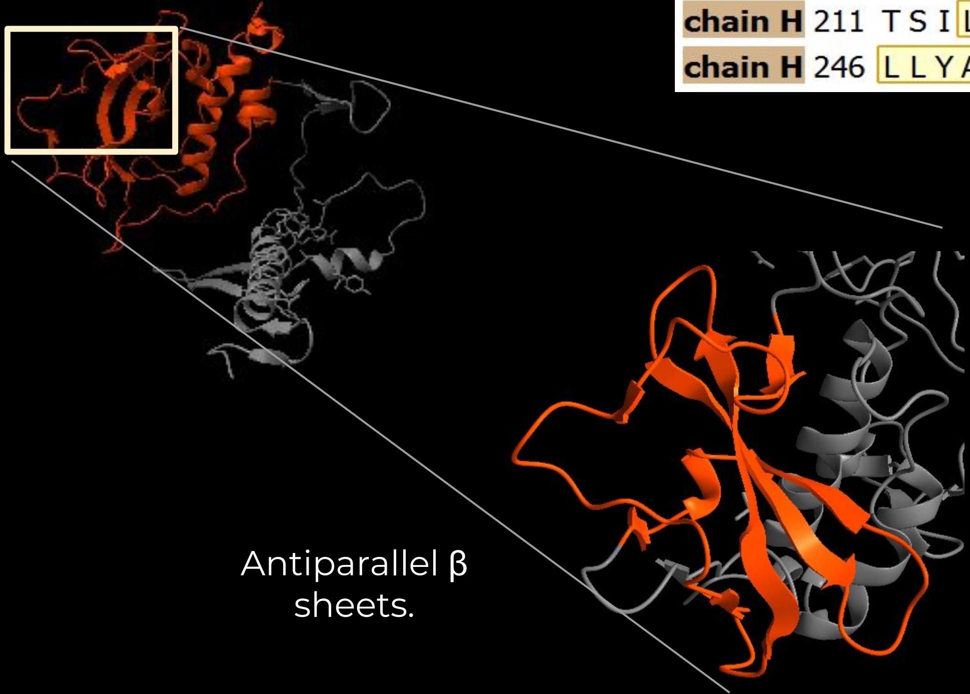
H subunit

Globular domain



chain H 1 MYHGALAQHLDIAQLVWYAQWLVIWTVVLLYLRRE
chain H 36 DRREGYPLVEPLGLVKLAPEDGQVYELPYPKTFVL
chain H 71 PHGGTVTVPRRRPETRELKLAQTDGFEGAPLQPTG
chain H 106 NPLVDAVGPASYAERAEVVDATVDGKAKIVPLRVA
chain H 141 TDFSIAEGDVDPRGLPVVAADGVEAGTVTDLWVDR
chain H 176 SEHYFRYLELSVAGSARTALIPLGFCDVKKDKIVV
chain H 211 TSILSEQFANVPRLQSRDQITLREEDKVSAYYAGG
chain H 246 LLYATPERAESLL

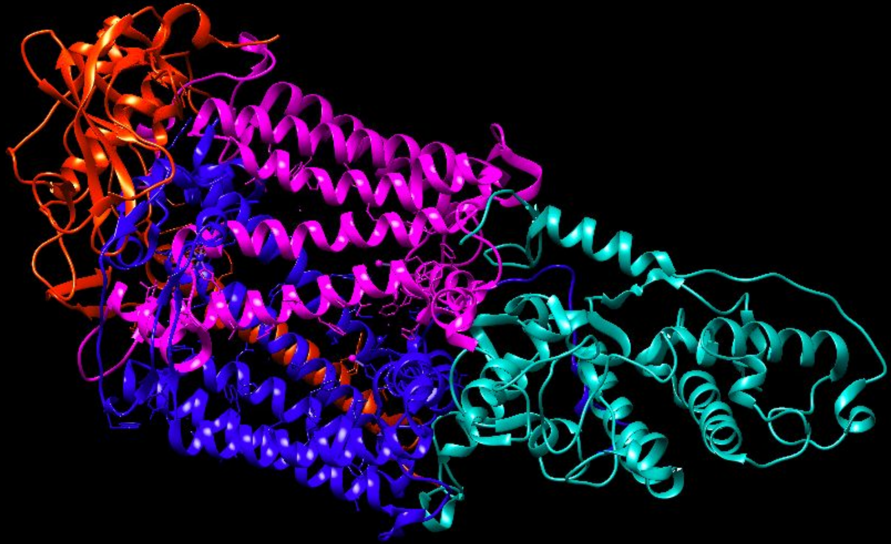
Helix
β-sheet

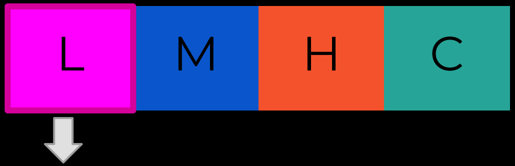


Antiparallel β sheets.

Globular domain.
Antiparallel β sheets.
ValH124 - ValH203

L subunit





L M H C

274 residues

L subunit

Co-factors

Bacteriochlorophyll-b

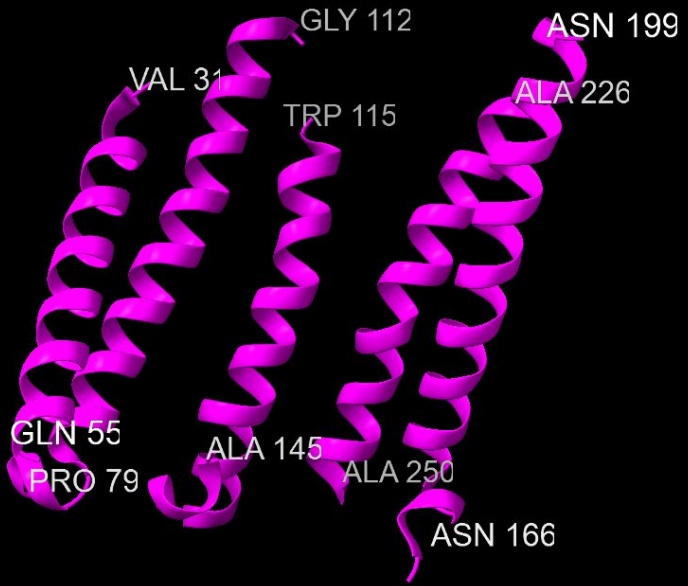
Bacteriopheophytin-b

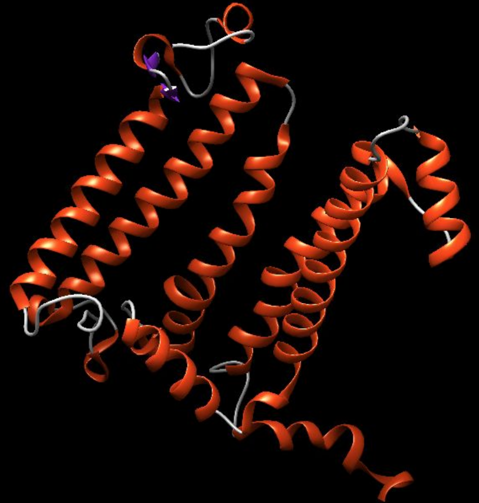
Quinone

L subunit

5 transmembrane helices

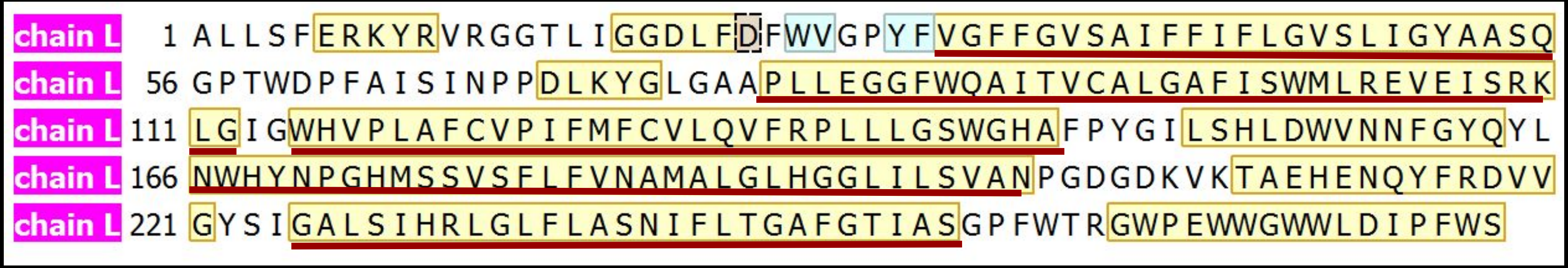
1) ValL31 - GlnL55
2) ProL79 - GlyL112
3) TrpL115 - AlaL145
4) AsnL166 - AsnL199
5) AlaL226 - AlaL250





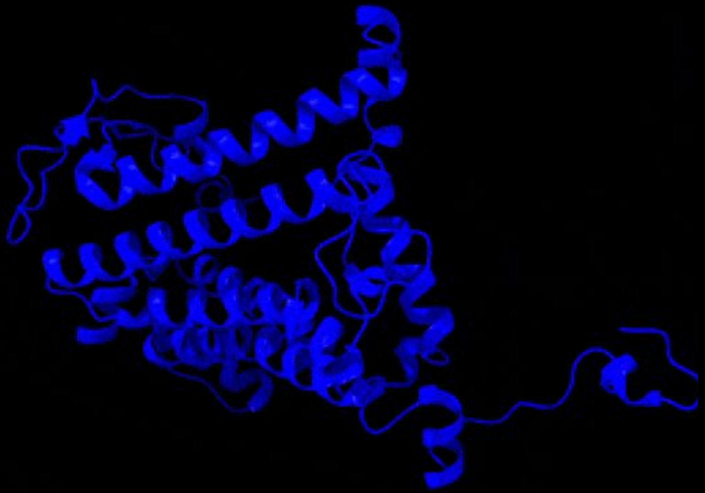
Secondary structure

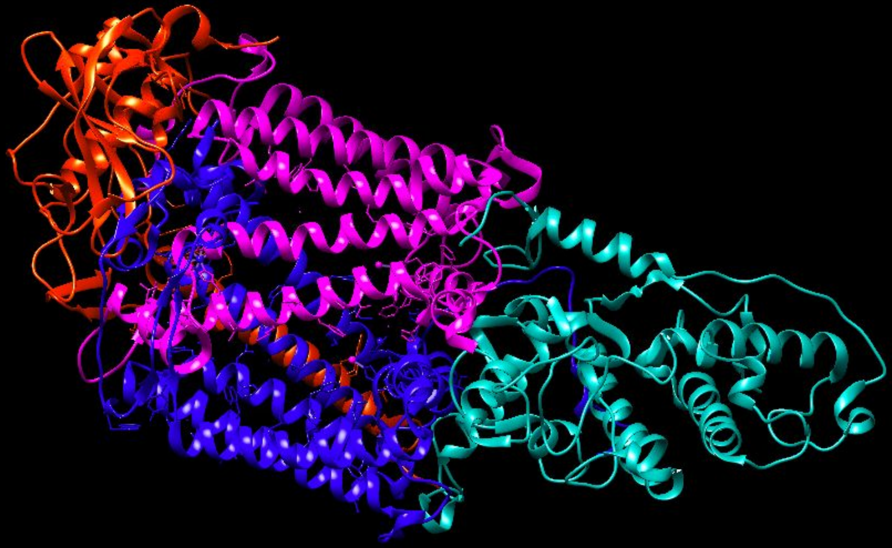
Helix
β-sheet

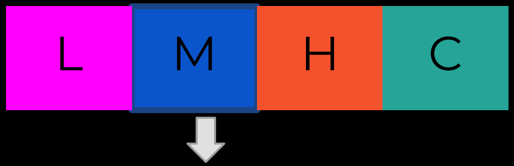


chain L 1 ALLSFERKYRVRGGTLIGGDLFDFWVGPYFVGFFGVSAIFFIFLGVSLIGYAASQ
chain L 56 GPTWDPFAISINPPDLKYGLGAAPLLEGGFWQAITVCALGAFISWMLREVEISRK
chain L 111 LGIGWHVPLAFCVPIFMFCVLQVFRPLLLGSWGHAFPYGILSHLDWVNNFGYQYL
chain L 166 NWHYNPGHMSSVSFLFVNAMALGLHGGLILSVANPGDGDKVKTAEHENQYFRDVV
chain L 221 GYSIGALSIHRLGLFLASNIFLTGAFGTIASGPFWTRGWPEWWGWWLDIPFWS

M subunit







324 residues

M subunit

Co-factors

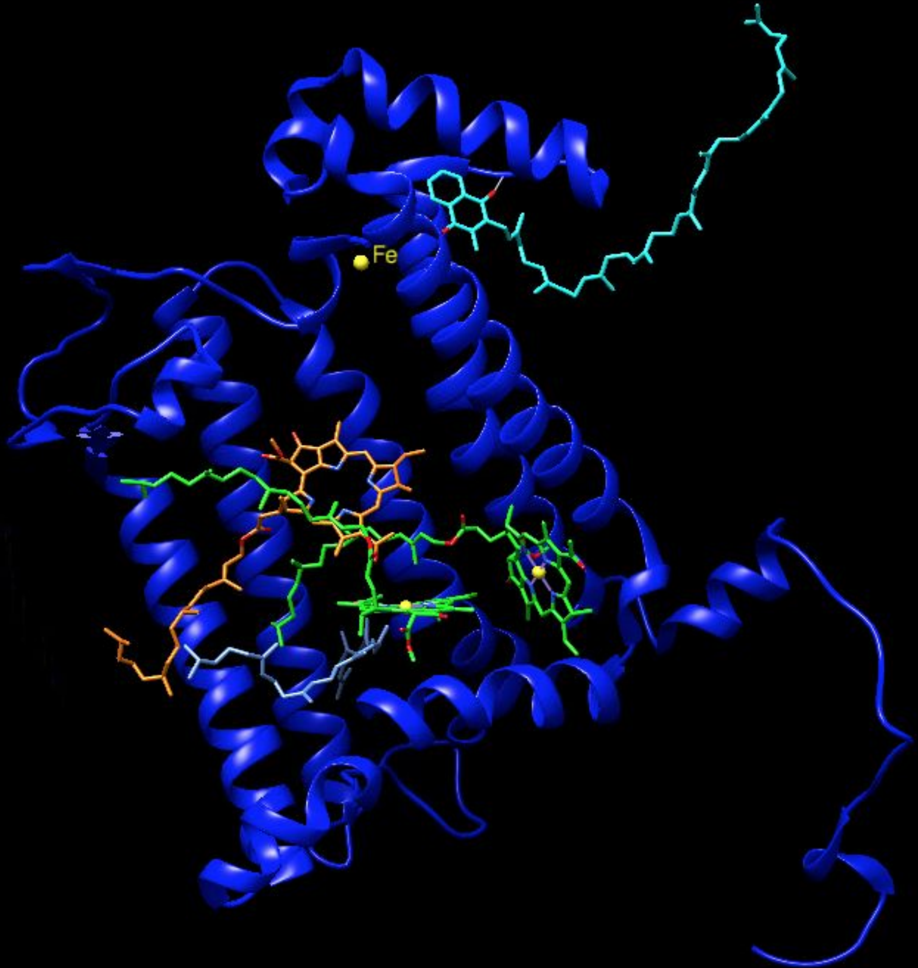
Bacteriochlorophyll-b

Bacteriopheophytin-b

Quinone

Non - heme iron

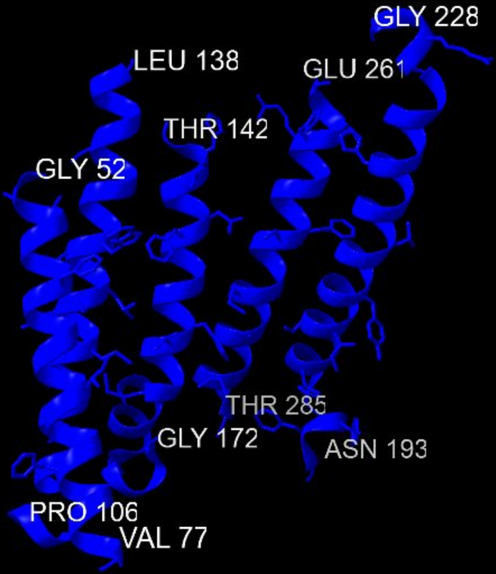
Carotenoid

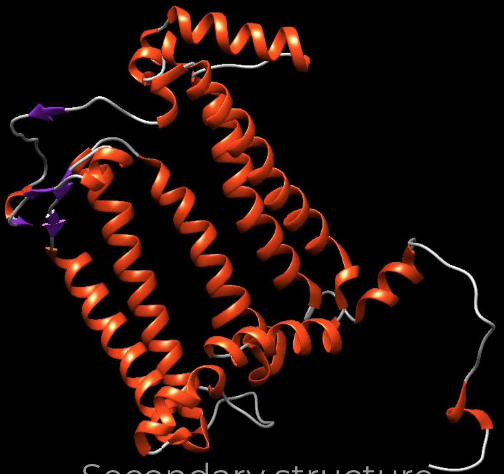


M subunit

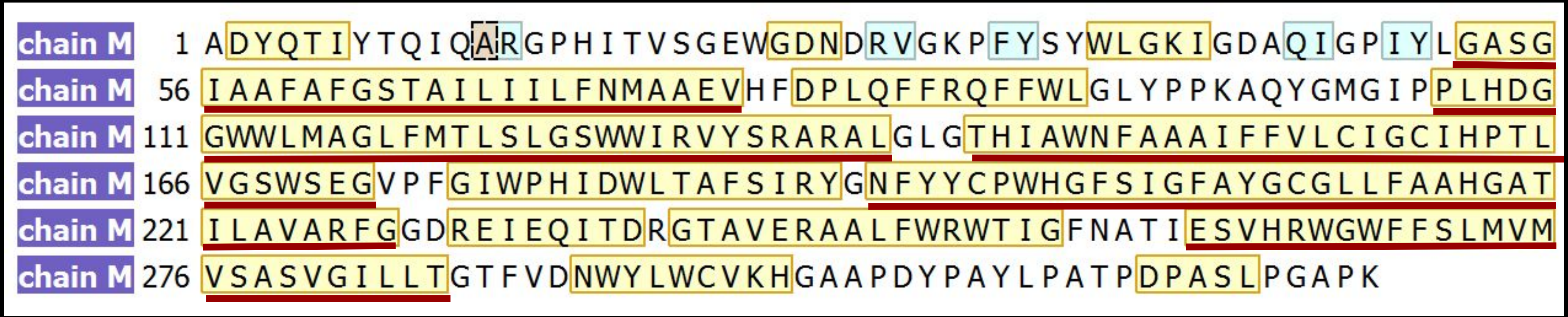
5 transmembrane helices.

1) GlyM52 - ValM77
2) ProM106 - LeuM138
3) ThrM142- GlyM172
4) AsnM193 - GlyM228
5) GluM261 - ThrM285

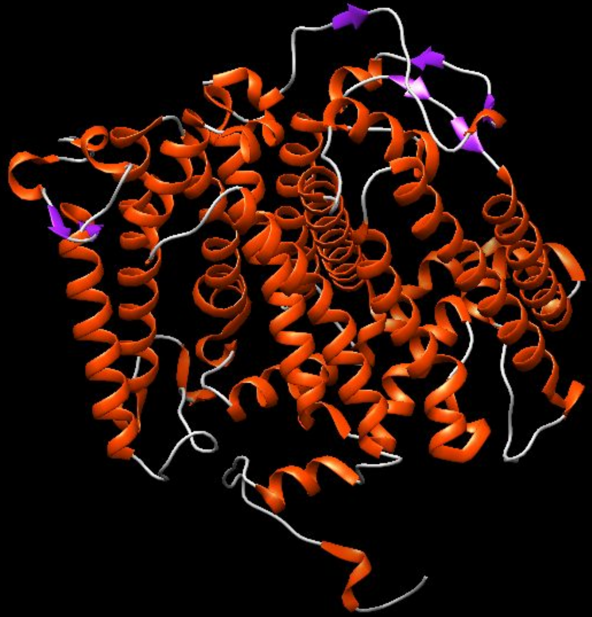



Secondary structure

Helix
β-sheet

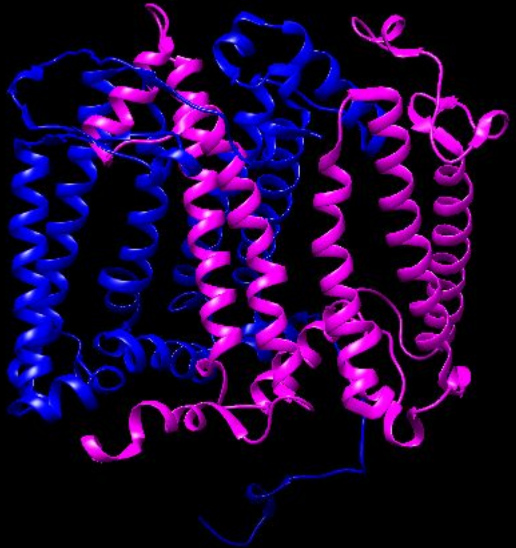

chain M 1 ADYQTIYTQIQARGPHITVSGEWGDNDRVGKPFYSYWLGKIGDAQIGPIYLGASG
chain M 56 IAAFAFGSTAILIILFNMAAEVHFDPLQFFRQFFWLGLYPPKAQYGMGIPPLHDG
chain M 111 GWWLMAGLFMTLSLGSWWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTL
chain M 166 VGSWSEGVPFGIWPHIDWLTAFSIRYGNFYYCPWHGFSIGFAYGCGLLFAAHGAT
chain M 221 ILAVARFGGDREIEQITDRGTAVERAALFWRWTIGFNATIESVHRWGWFFSLMVM
chain M 276 VSASVGILLTGTFVDNWYLWCVKHGAAPDYPAYLPATPDPASLPGAPK

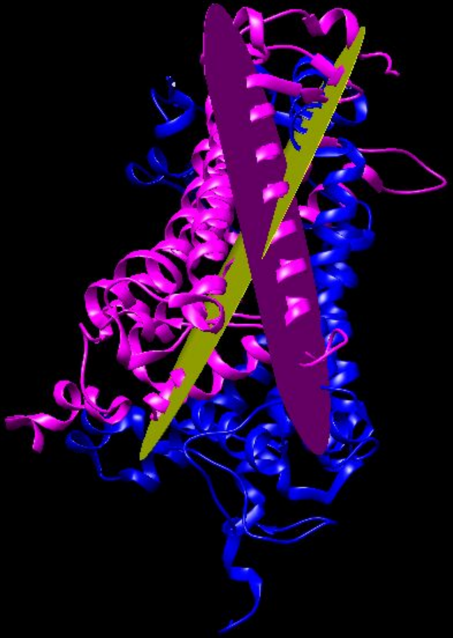
Subunits L-M: Core complex



Secondary structure

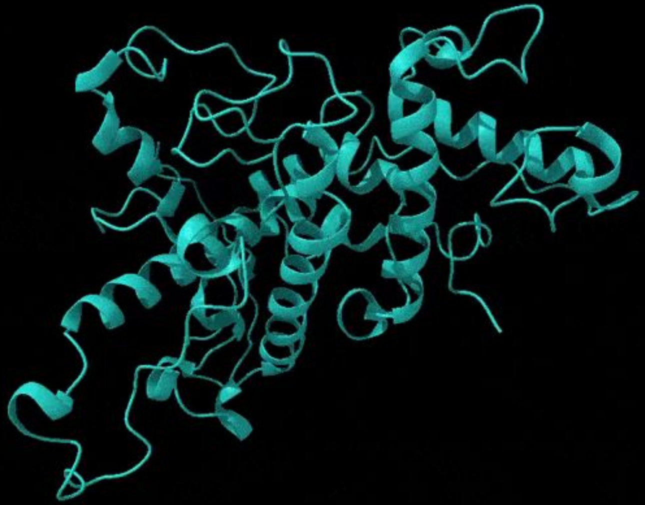
10 membrane-spanning alpha helices

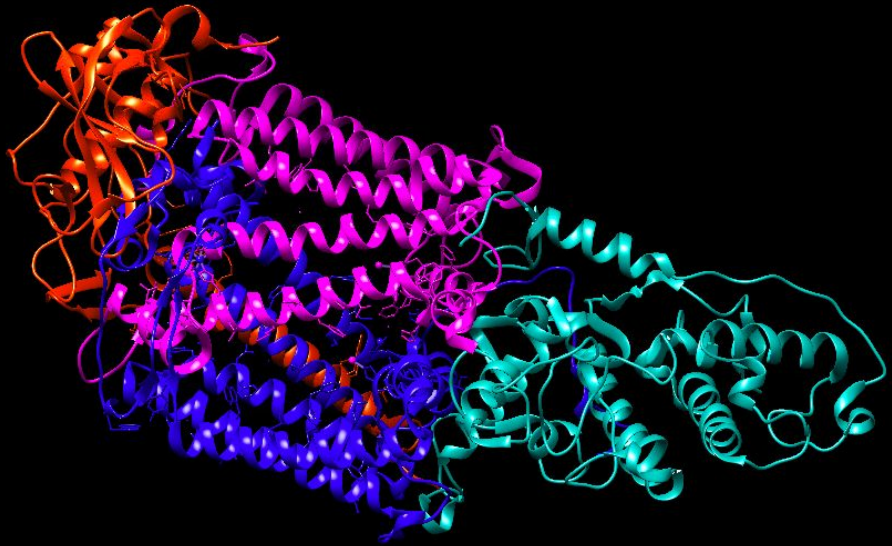


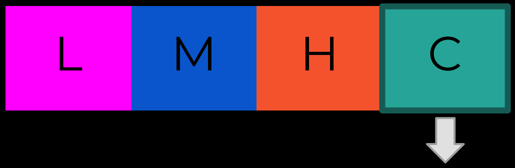


Helices cross each other in an X shape

C subunit: Cytochrome







336 residues

C subunit: Cytochrome

Co-factors

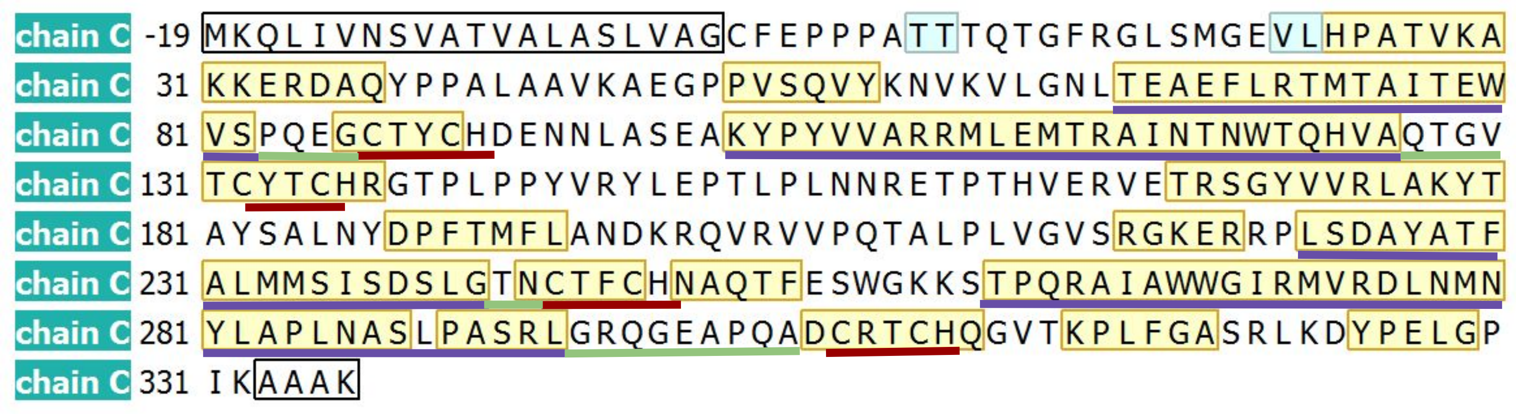
4 Heme groups

C subunit: Cytochrome

Secondary structure

4 Heme group binding segments:

17-20-residue helix → turn → Cys-X-Y-Cys-His

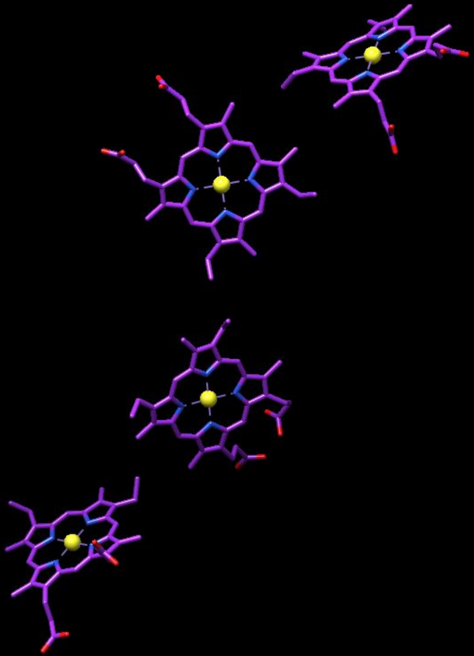


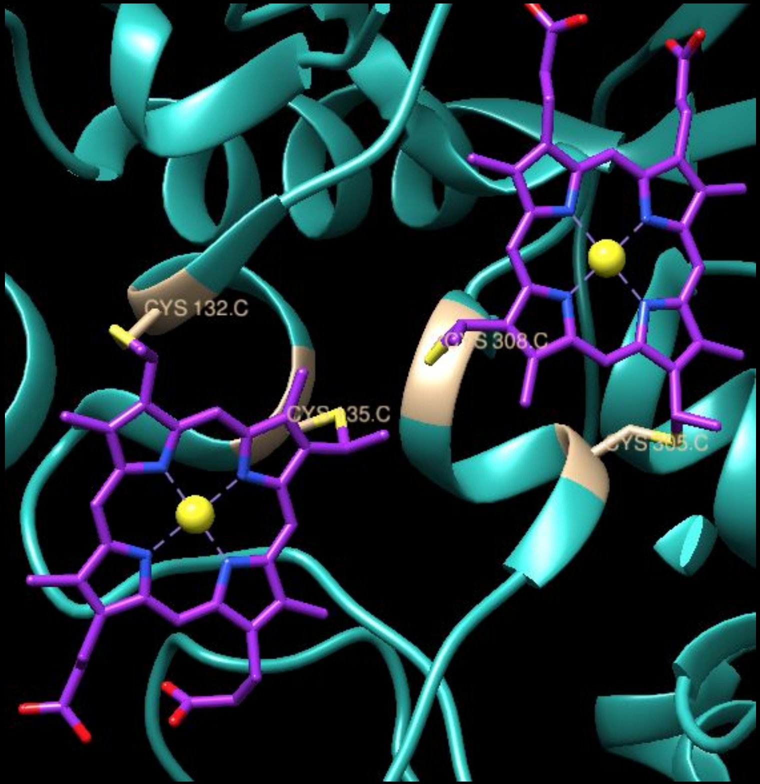
```
chain C  -19 MKQLIVNSVATVALASLVAGCFEPPPATTTQTGFRGLSMGEVLHPATVKA
chain C   31 KKERDAQYPPALAAVKAEGPPVSQVYKNVKVLGNLTEAEFLRTMTAITEW
chain C   81 VSPQEGCTYCHDENNLASEAKYPYVVARRMLEMTRAINTNWTQHVAQTGV
chain C  131 TCYTCHRGTPLPPYVRYLEPTLPLNNRETPTHVERVETRSGYVVRLAKYT
chain C  181 AYSALNYDPFTMFLANDKRQVRVVPQTALPLVGVSRGKERRPLSDAYATF
chain C  231 ALMMSISDSLGTNCTFCHNAQTFESWGKKSTPQRAIAWWGIRMVRDLNMN
chain C  281 YLAPLNASLPASRLGRQGEAPQADCRTCHQGVTKPLFGASRLKDYPELGP
chain C  331 IKAAAK
```

Helix
β-sheet

C subunit: Cytochrome

Cys-X-Y-Cys-His

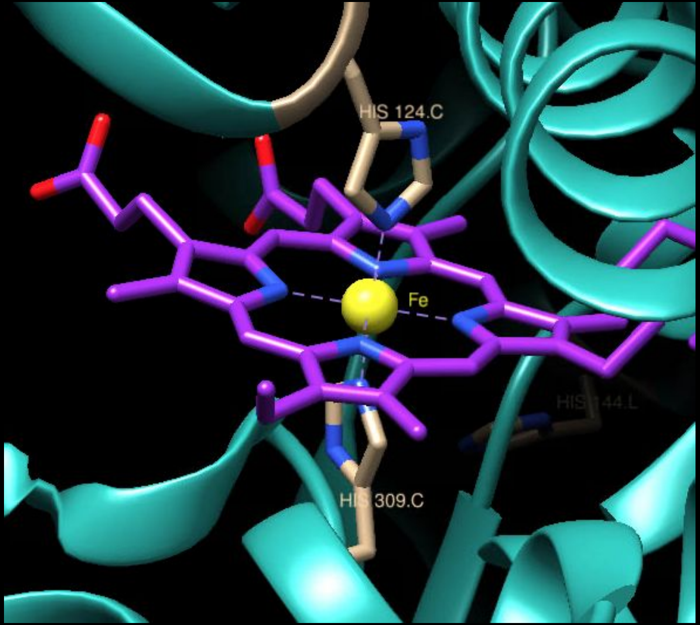


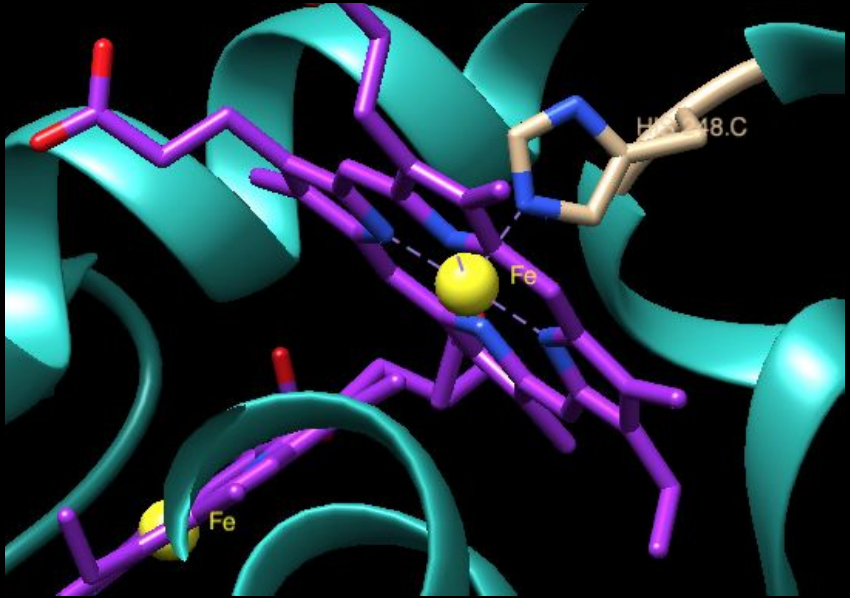


Heme groups are connected to cytochrome cysteines with thioether bonds

CYS: 244, 247, 305, 308, 135, 132, 90, 87

C subunit: Cytochrome



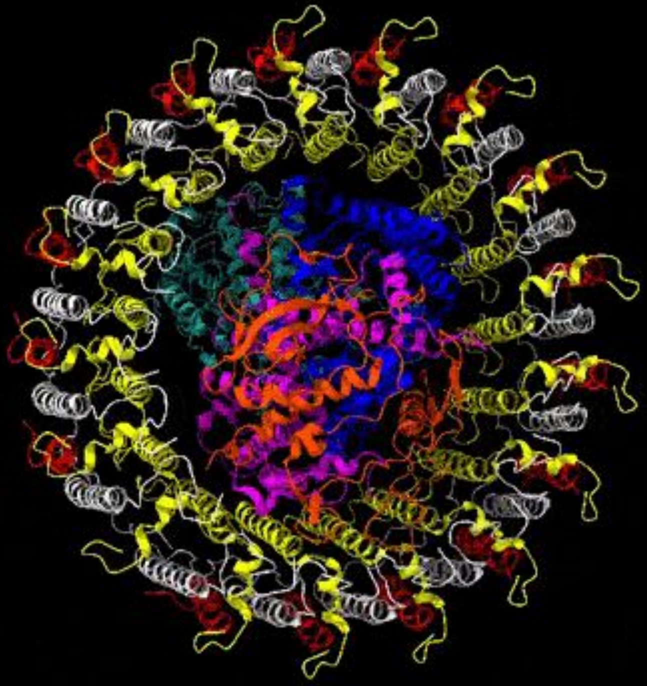


Fe helps to **stabilize the union** between subunit C and heme groups interacting with Histidines.

HIS: 91, 124, 136, 248, 309

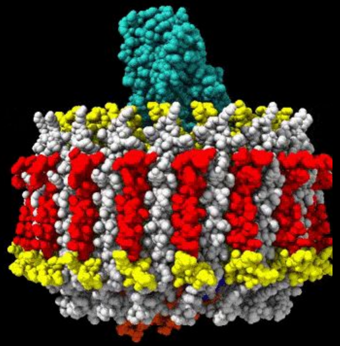
Light harvesting complex

Light harvesting complex
17 alpha-polypeptides
17 beta-polypeptides
16 gamma-polypeptides



Light harvesting complex

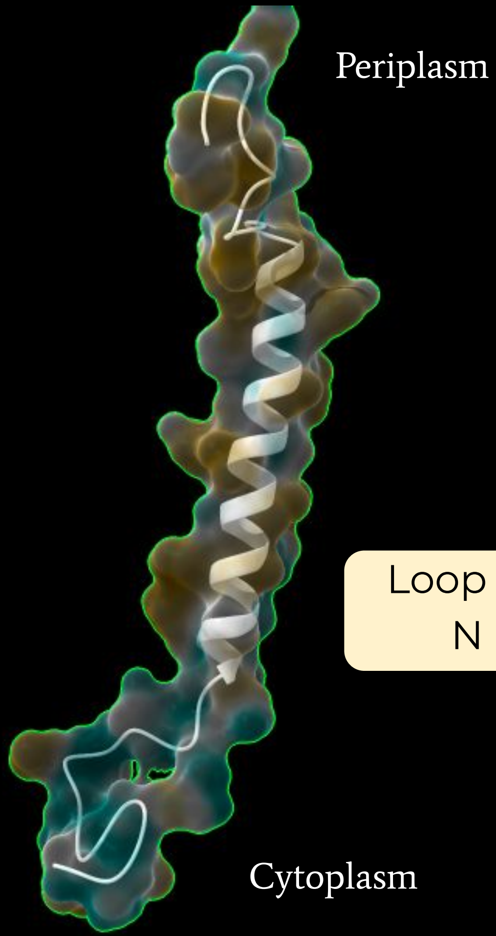
Light harvesting complex
17 alpha-polypeptides
17 beta-polypeptides
16 gamma-polypeptides

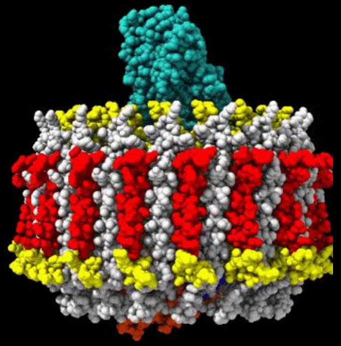


Short N-terminal helix

Light harvesting complex

Light harvesting complex
17 alpha-polypeptides
17 beta-polypeptides
16 gamma-polypeptides

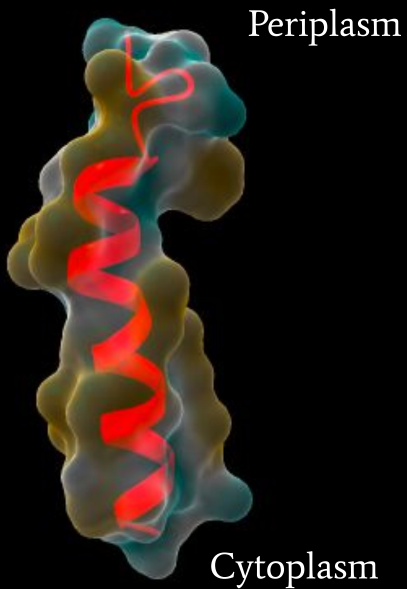


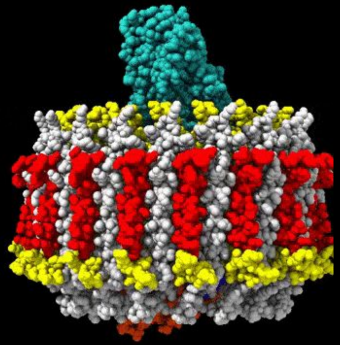


Loop structures in both N and C terminal

Light harvesting complex

Light harvesting complex
17 alpha-polypeptides
17 beta-polypeptides
16 gamma-polypeptides

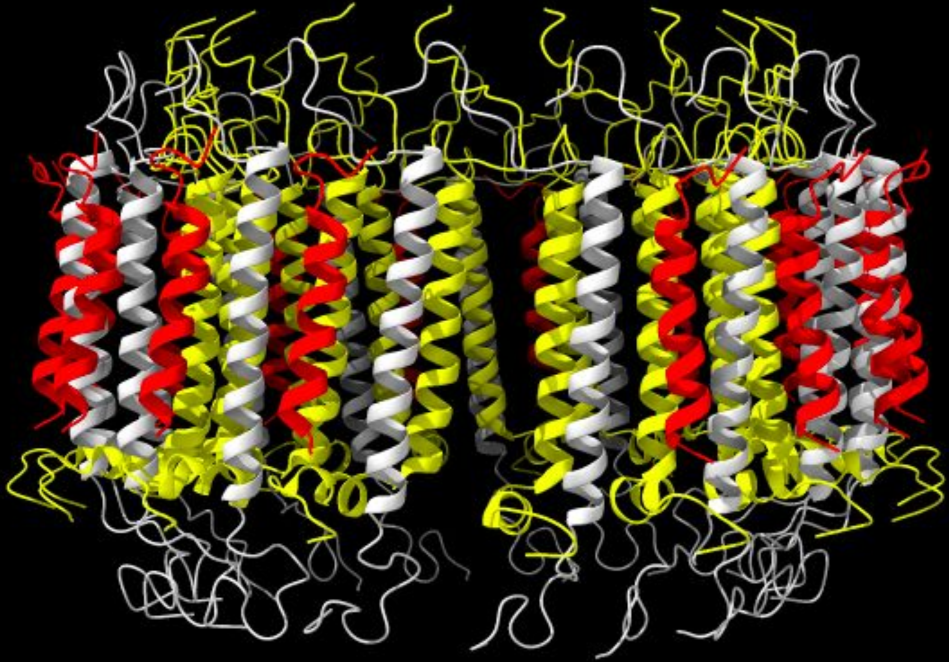




N-terminus on periplasm

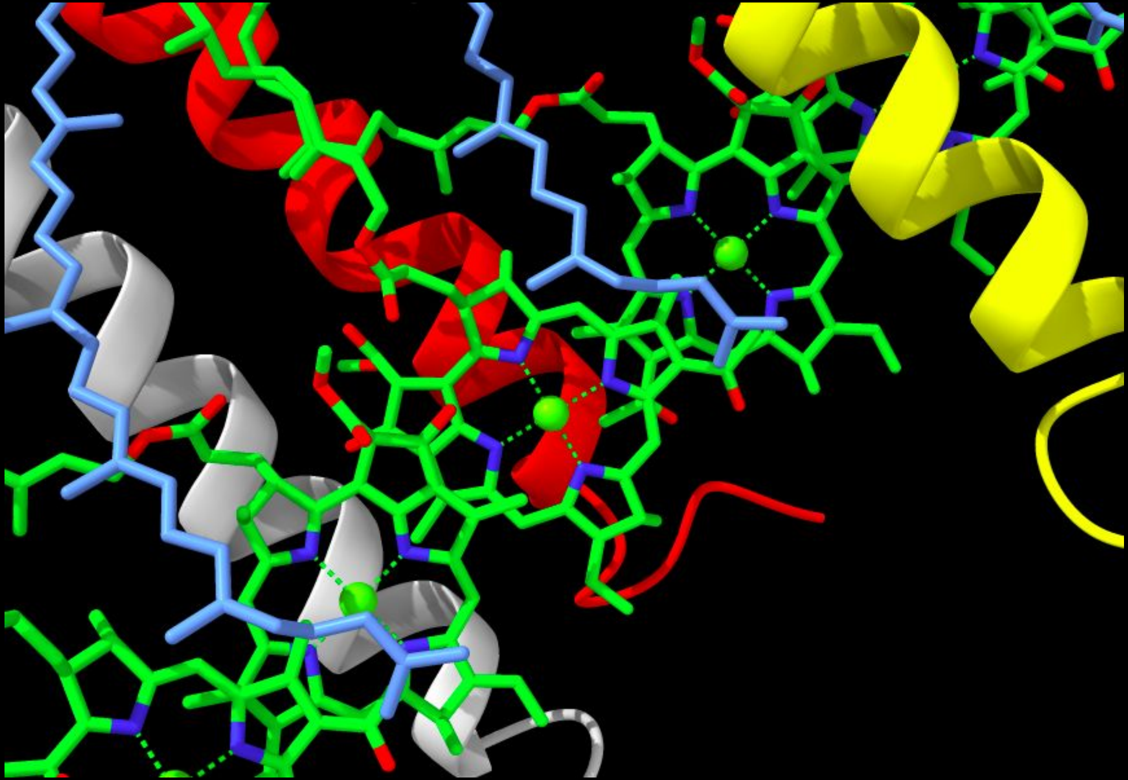
Light harvesting complex

Gamma-polypeptide gap for quinol exchange



Light harvesting complex

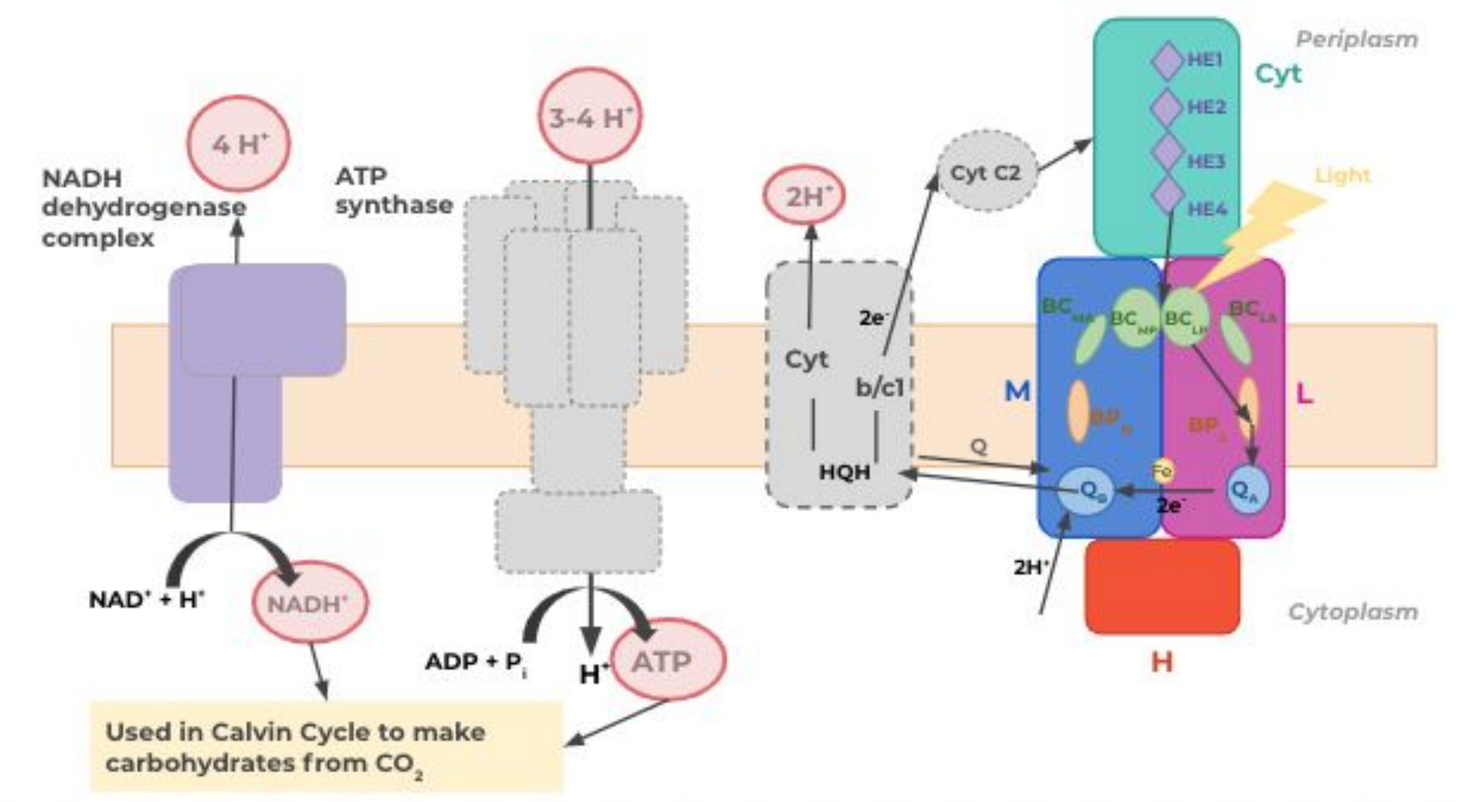
Two BCB and one carotenoid bound between each alpha-beta heterodimer



FUNCTIONAL OVERVIEW

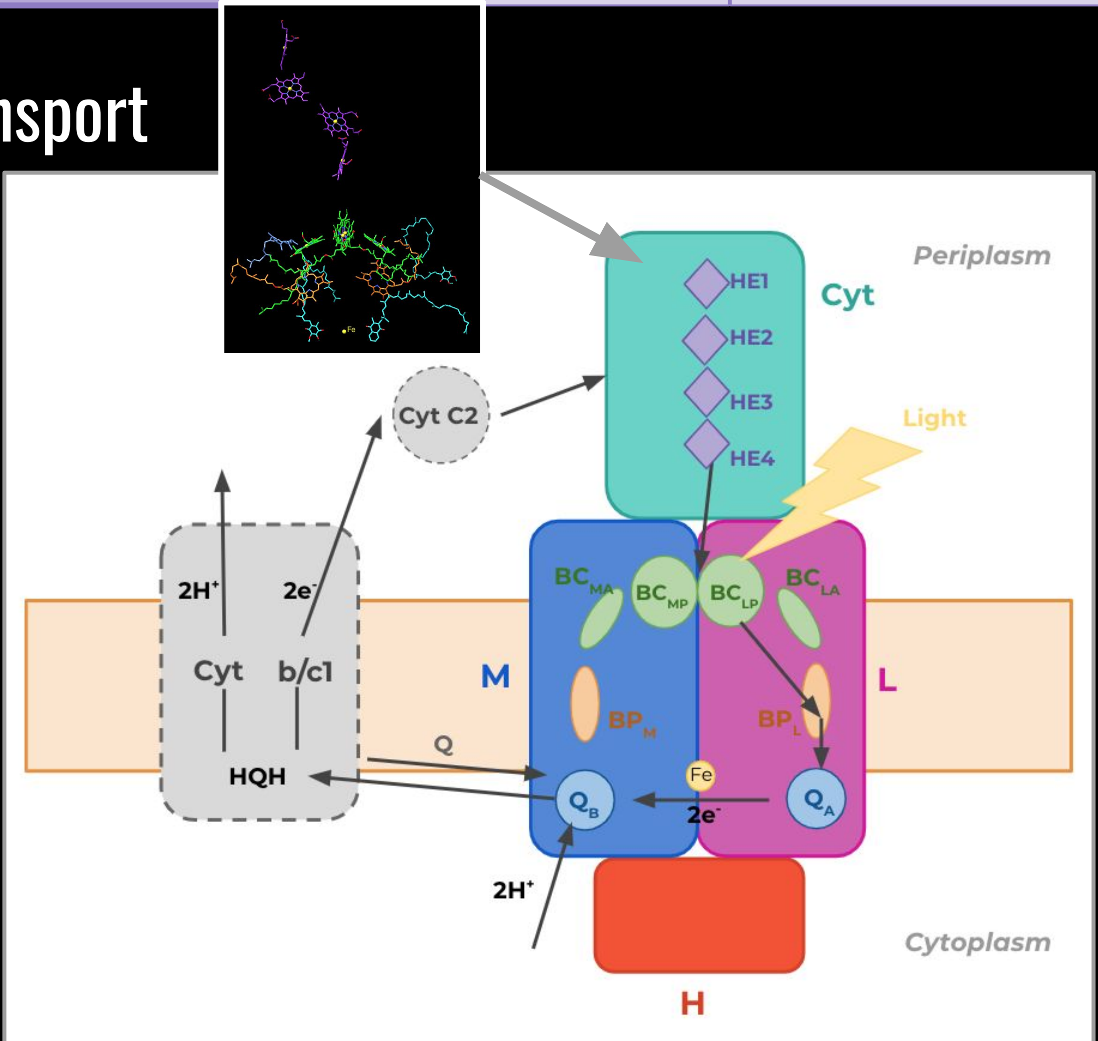
- Which is the function of the Photosynthetic Reaction Center?
- Which are the chemical processes behind the function?

Photosynthetic electron transport

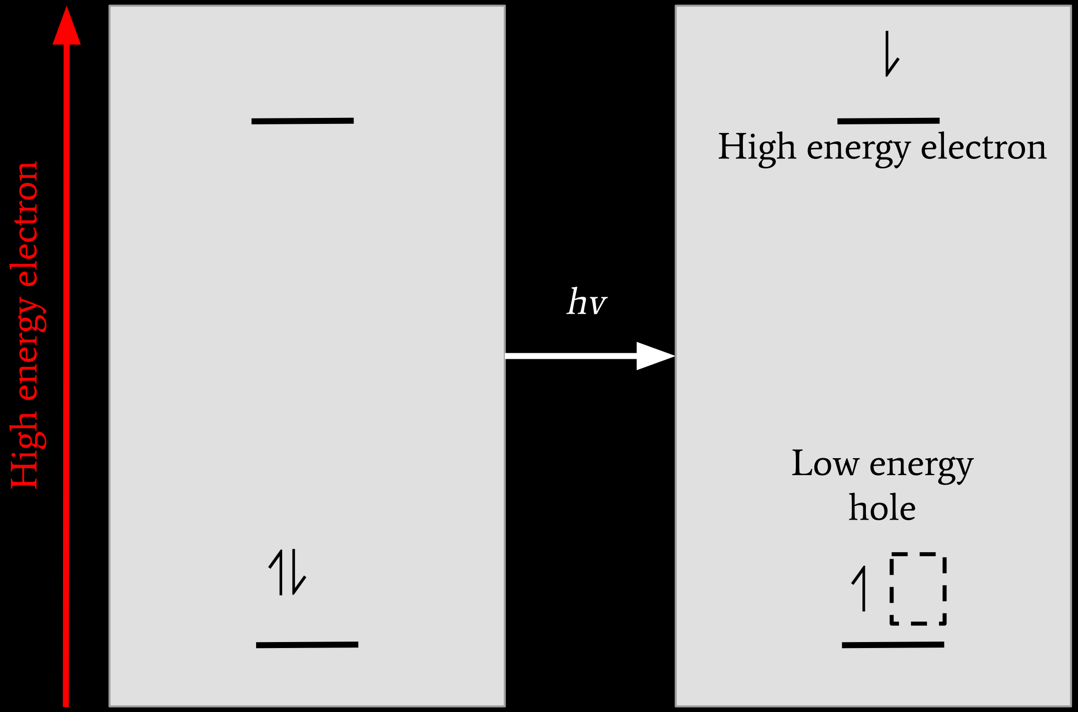


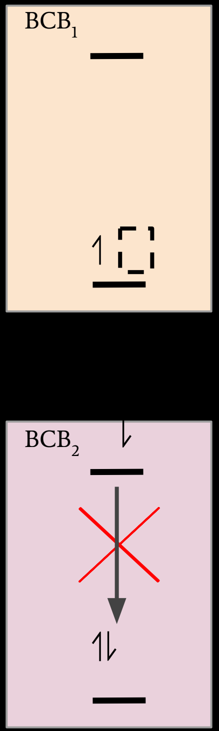
Photosynthetic electron transport

1. A photon excites an electron of BC_{LP}
2. The excited electron moves to BP_L
3. The excited electron moves to menaquinone-9
4. Two electrons reach the ubiquinone-9 and it becomes protonated
5. QBH_2 dissociates and moves to the Cytochrome b/c1 protein
6. There the electrons and protons are transferred outside the membrane to generate a proton gradient and synthesize ATP



Photoexcitation





NON-RADIOACTIVE
DECAY

The excited electron passes from BCB1 to BCB2 so it can not return to the ground state because in BCB2 there is no low energy hole.

INTERACTIONS

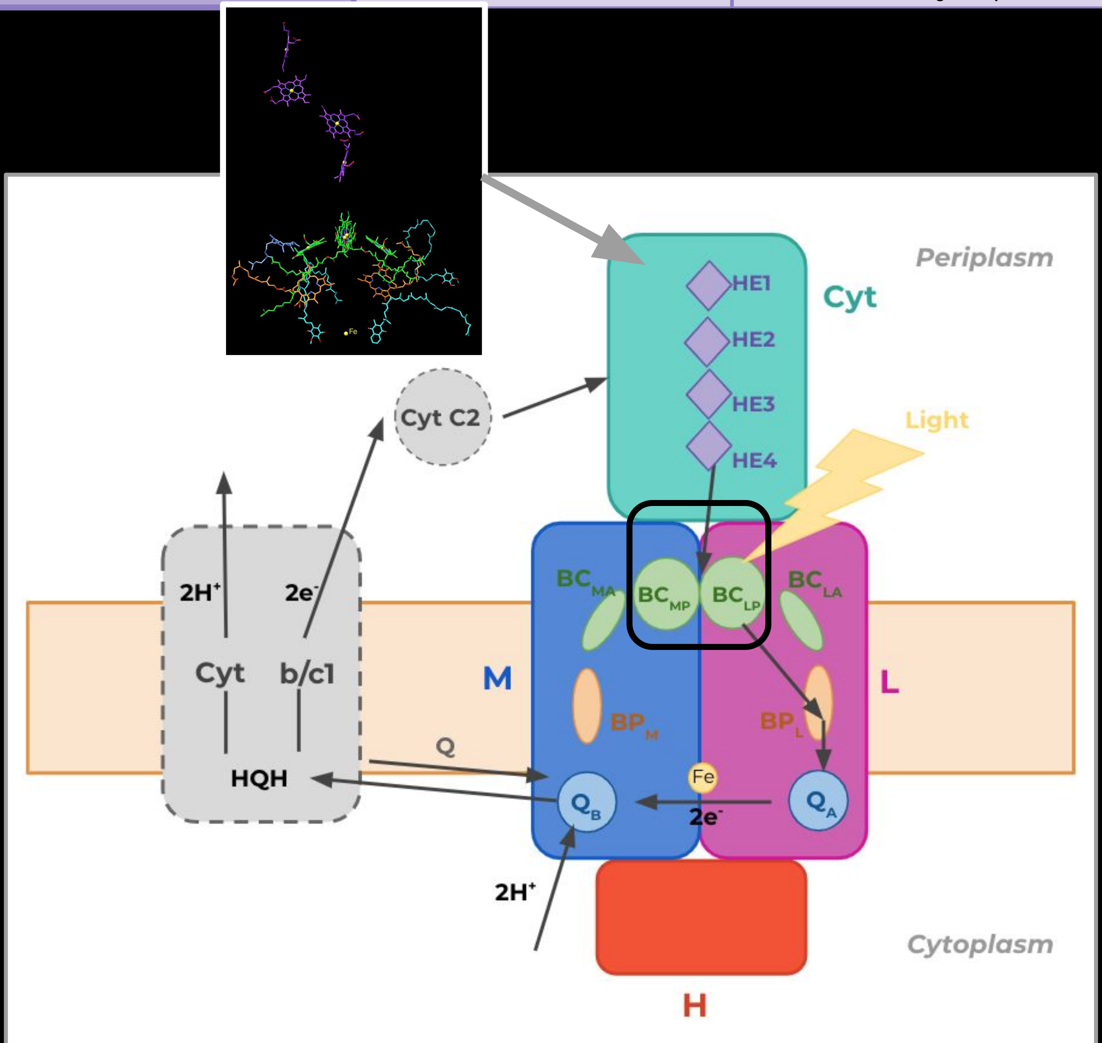
- Which interactions take place between cofactors and the core complex subunit in order to develop their function?

- Which are the fundamental interactions that cause unidirectional transport?

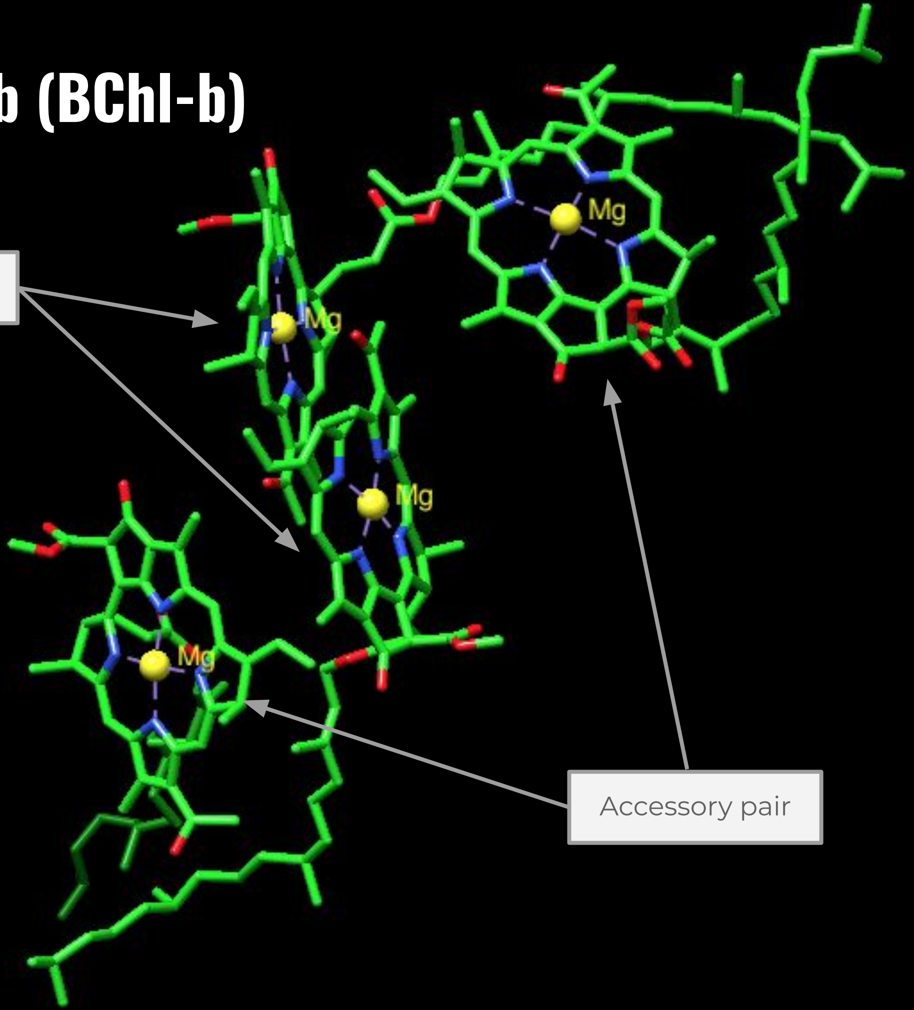
- Which interactions allow the transport of the excited electrons?

BCB excitation

1. **A photon excites an electron of BC_{LP}**
2. The excited electron moves to BP_L
3. The excited electron moves to menaquinone-9
4. Two electrons reach the ubiquinone-9
5. Quinone B is twicely protonated
6. QBH_2 dissociates and moves to the Cytochrome b/c1 protein
7. There the electrons and protons are transferred outside the membrane to generate a proton gradient and synthesize ATP



Bacteriochlorophyll-b (BChl-b)



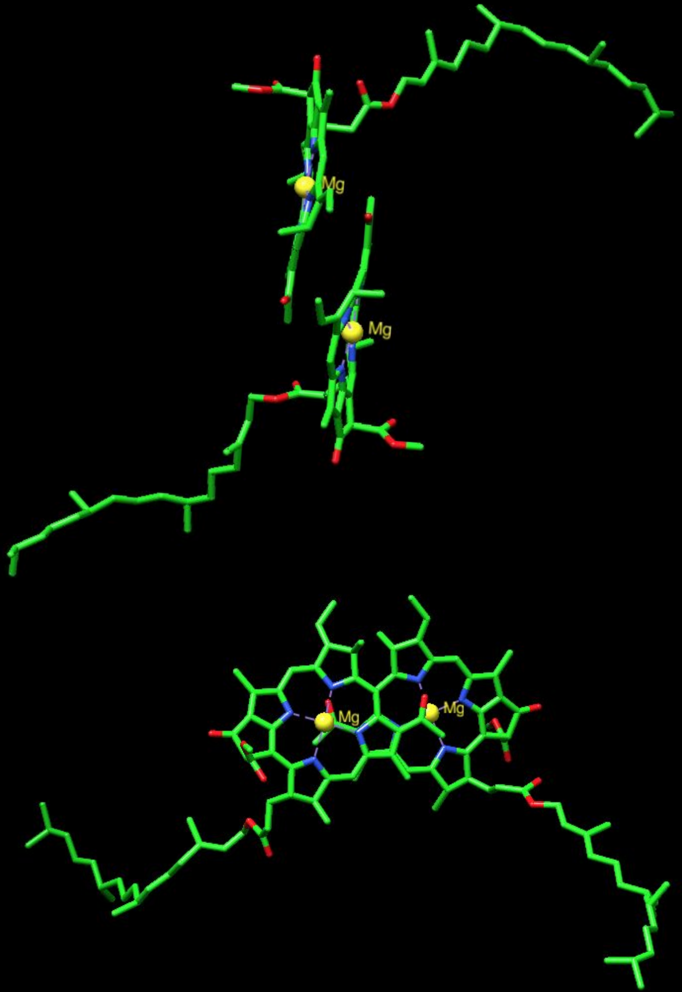
Special pair

Accessory pair

Bacteriochlorophyll-b (BChl-b)

Special pair

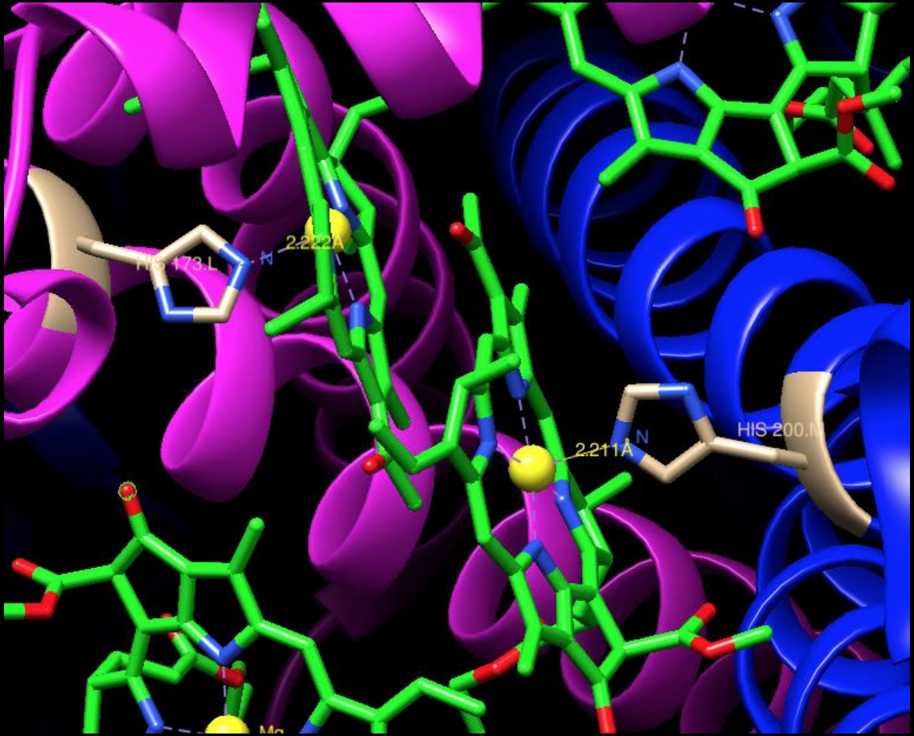
- Overlap of the pyrrole rings
- Two-fold symmetry
- Paralel pyrrole rings



Bacteriochlorophyll-b (BChl-b)

Symmetry

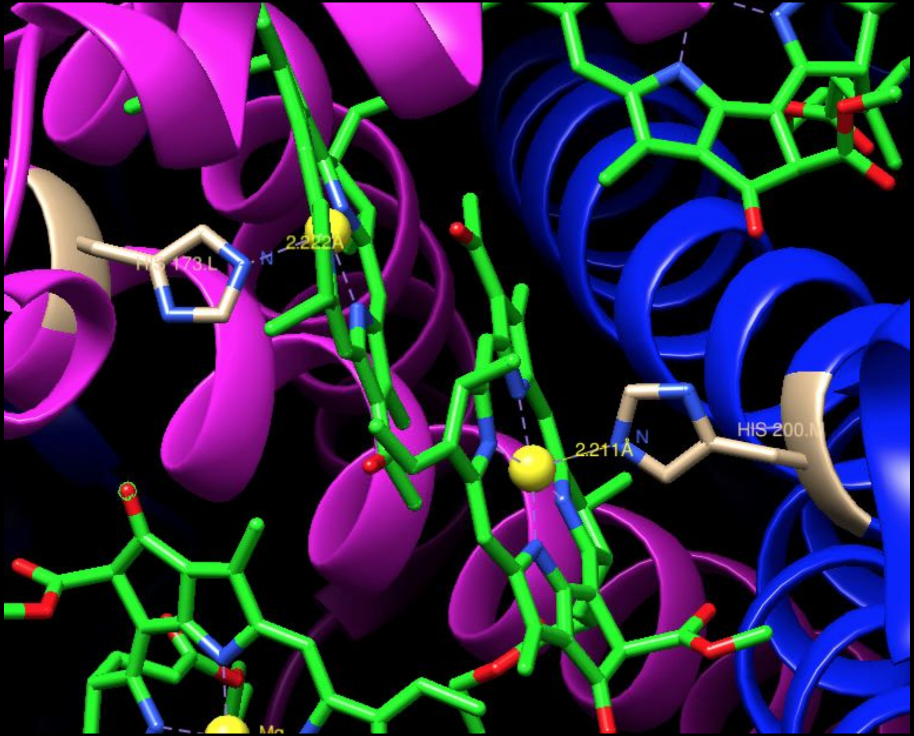
Obey the symmetry	**Break the symmetry**
HIS **L173**, **M200**	$\mathbf{BC_{MA}}$ contacting carotenoid molecule
Accessory BChl-bs rings	Side chains of accessory BChl-bs
H_2O molecules h-bonded to HIS and accessory BChl-bs	Subunit **H** transmembrane helix
Subunits **L** and **M** transmembrane helices	



Bacteriochlorophyll-b (BChl-b)

Symmetry

Obey the symmetry	Break the symmetry
HIS **L173**, **M200**	**BC**$_{\mathrm{MA}}$ contacting carotenoid molecule
Accessory BChl-bs rings	Side chains of accessory BChl-bs
H_2O molecules h-bonded to HIS and accessory BChl-bs	Subunit **H** transmembrane helix
Subunits **L** and **M** transmembrane helices	



Bacteriochlorophyll-b (BChl-b)

Symmetry

Obey the symmetry	**Break the symmetry**
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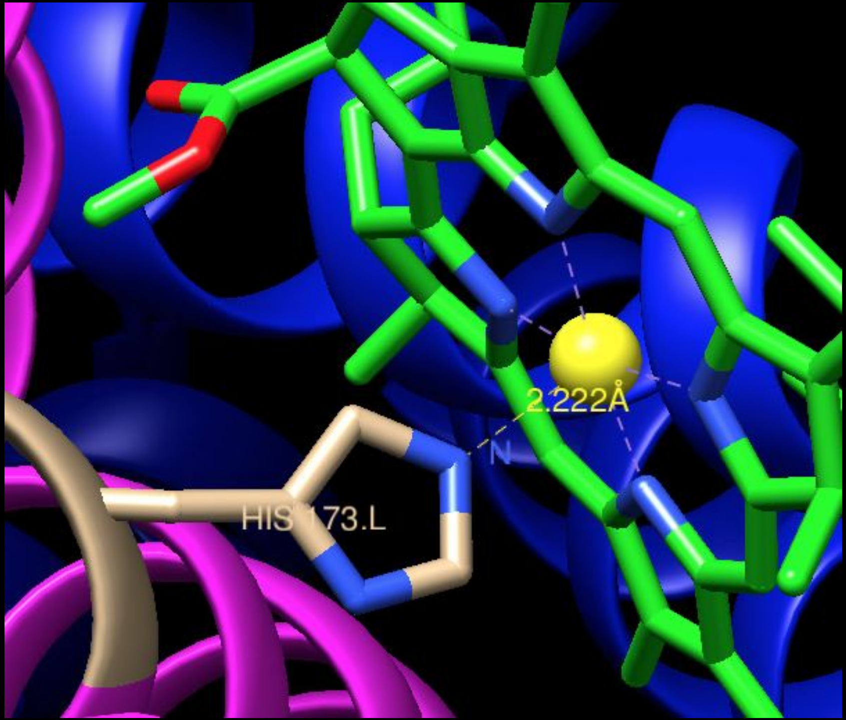
HIS L173



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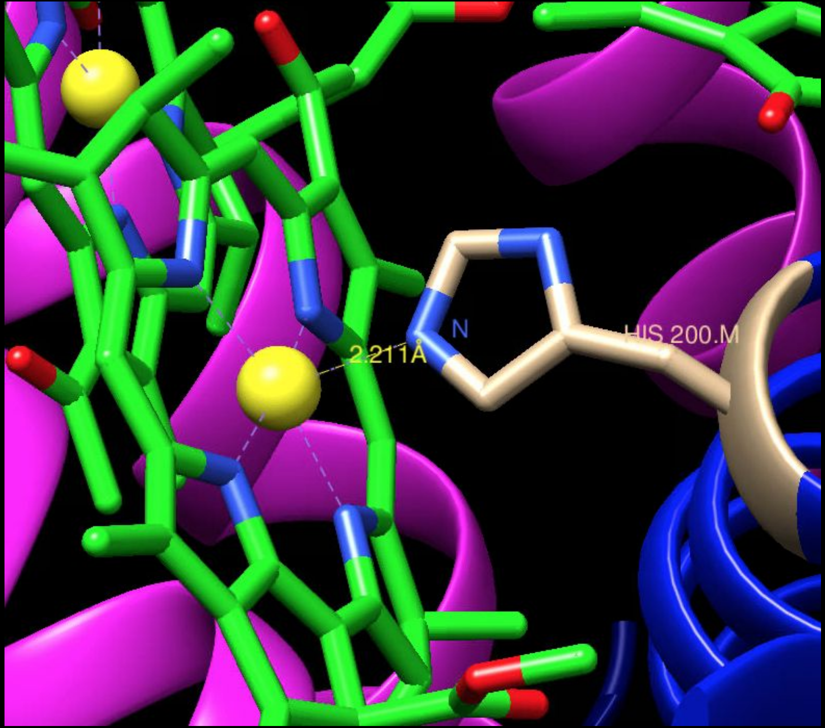
HIS M200



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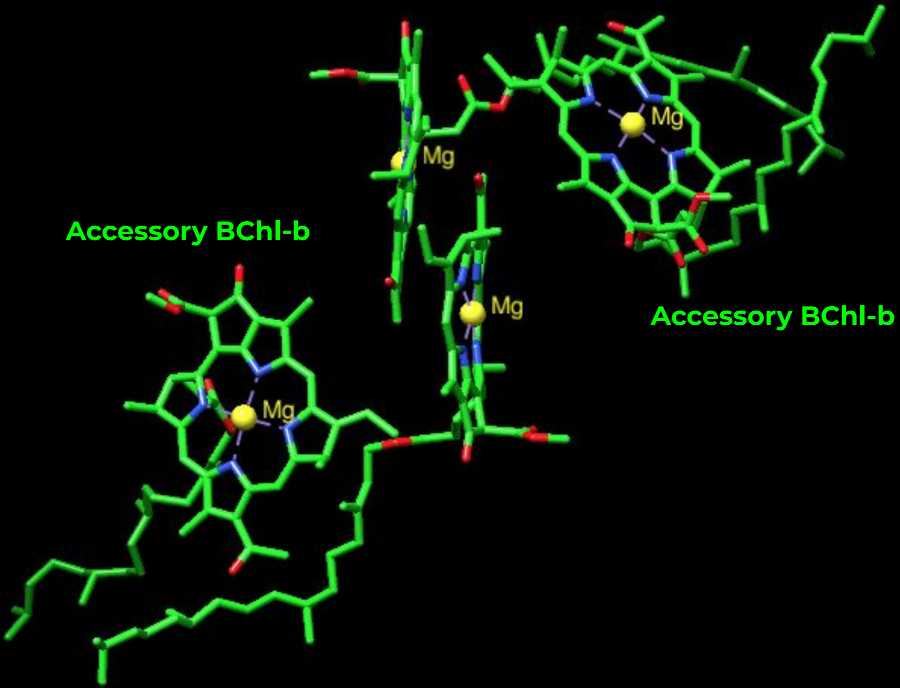

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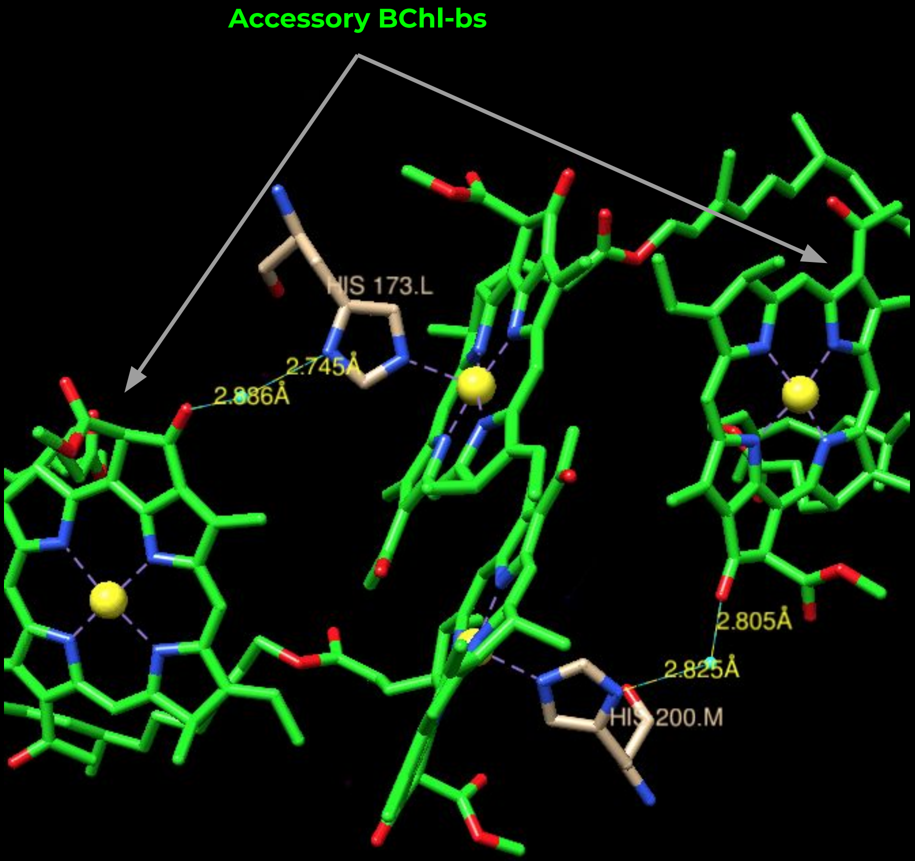

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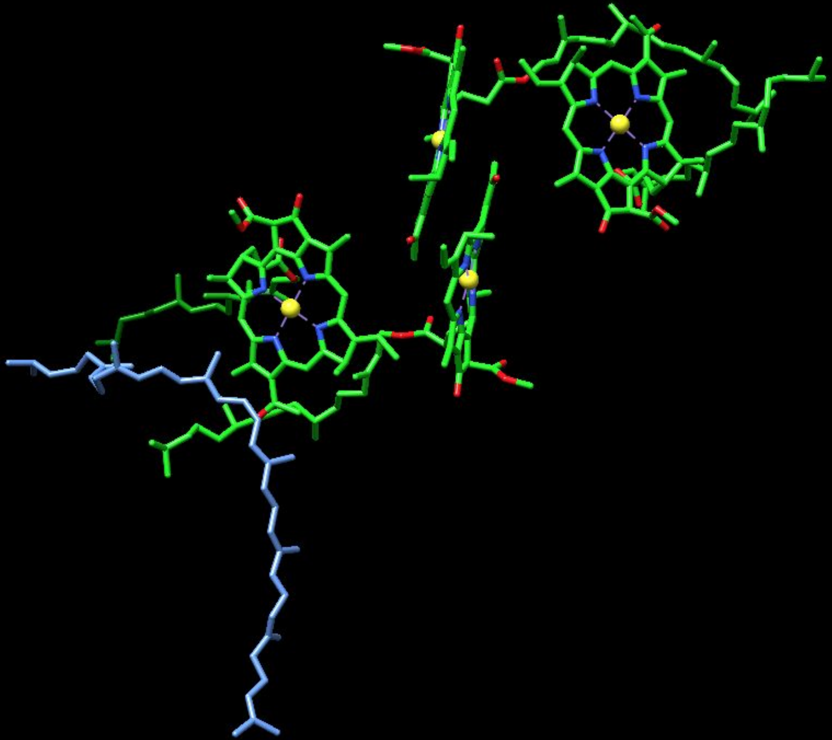

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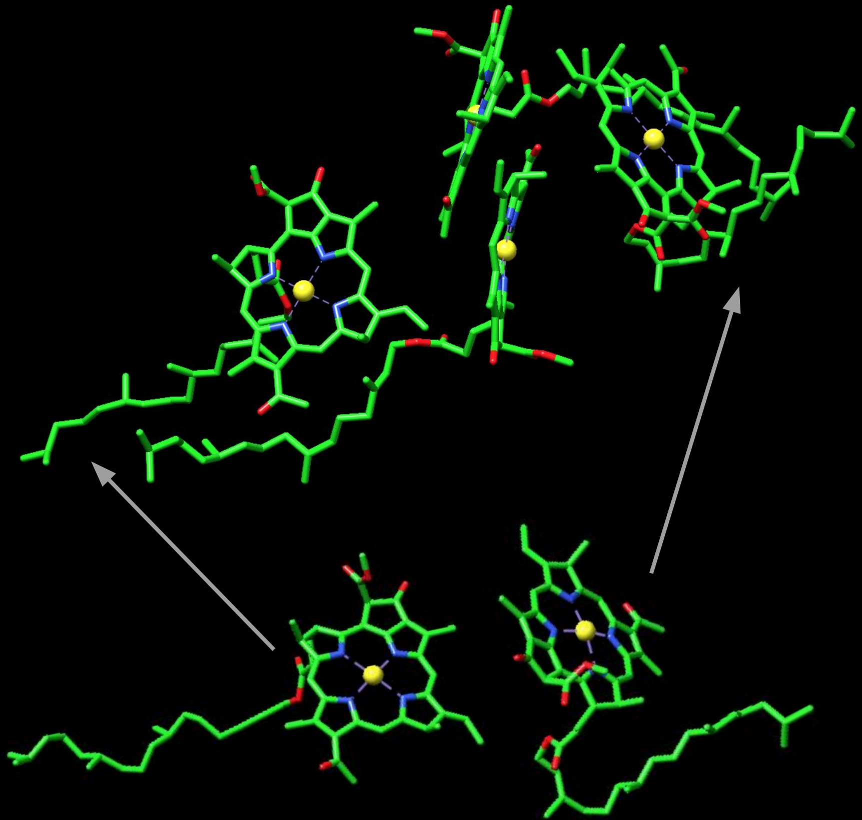

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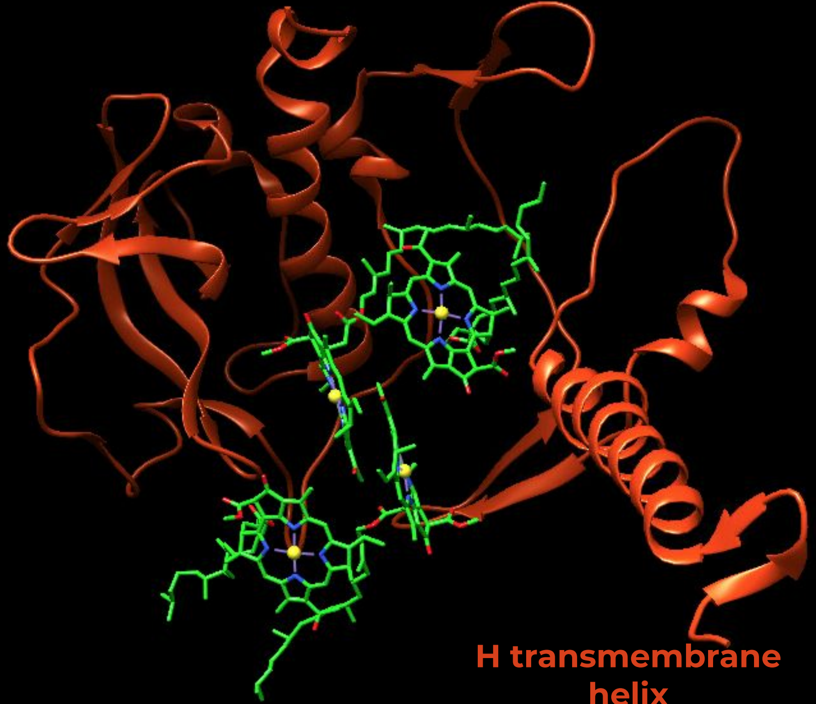
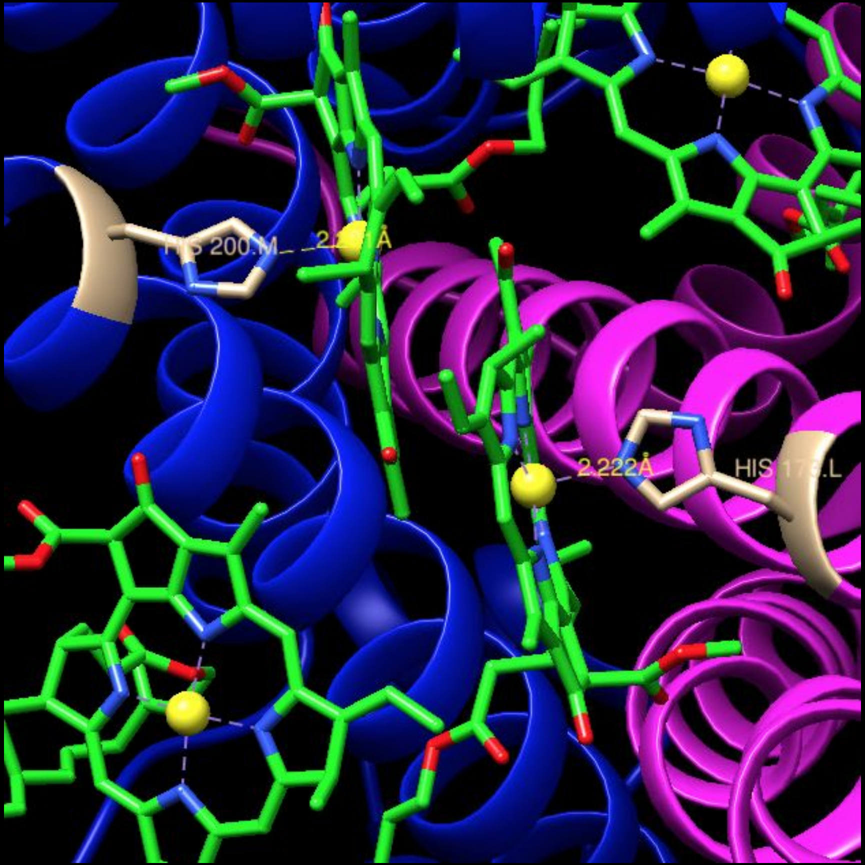


H transmembrane helix

Bacteriochlorophyll-b (BChl-b)

Protein-pigment interactions

Interactions between:
Nitrogen of histidine L173 with Mg^{2+} of BC_{LP} and Nitrogen of histidine M200 with Mg^{2+} of BC_{MP}
BC_{LP} acetyl group to histidine L168
BC_{MP} acetyl group to tyrosine M195
Ring V keto carbonyl oxygen and threonine L248, just in L chain



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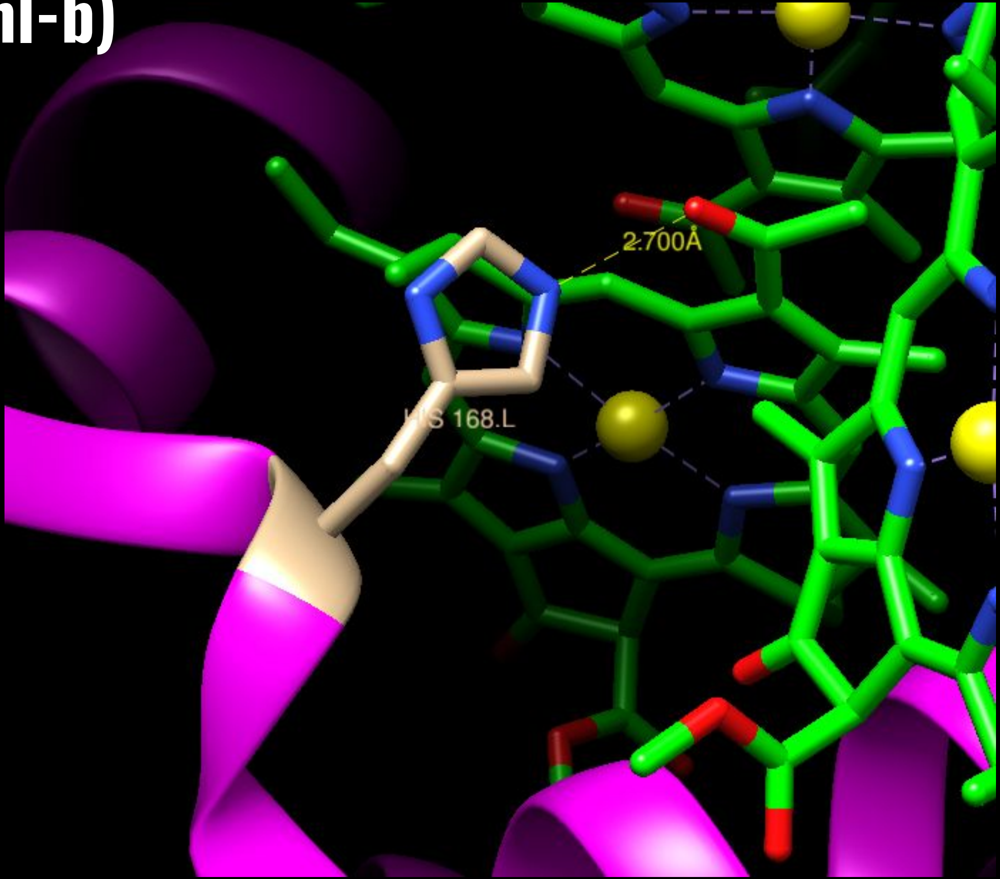

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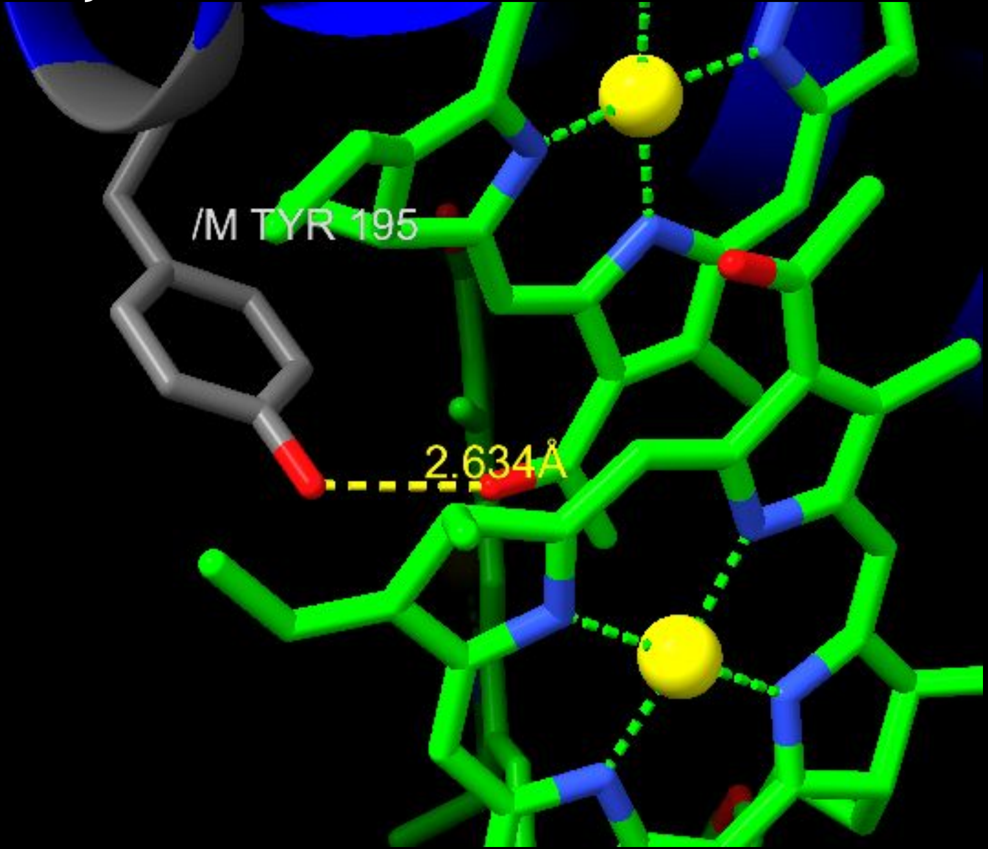

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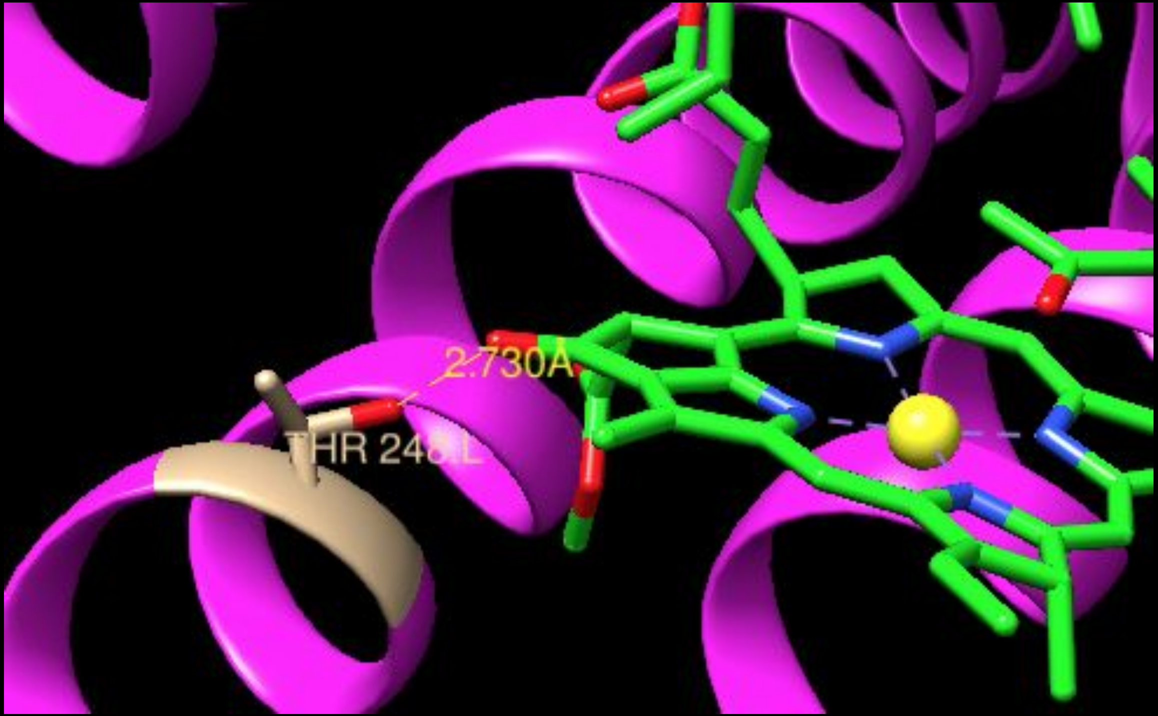

Bacteriochlorophyll-b (BChl-b)

Protein-pigment interactions

Special pair environment of aromatic residues in direct contact of with its tetrapyrrole rings

Tyrosine L162 located between the special pair and the closest heme group (HE3) of the cytochrome

Bacteriochlorophyll-b (BChl-b)

Protein-pigment interactions

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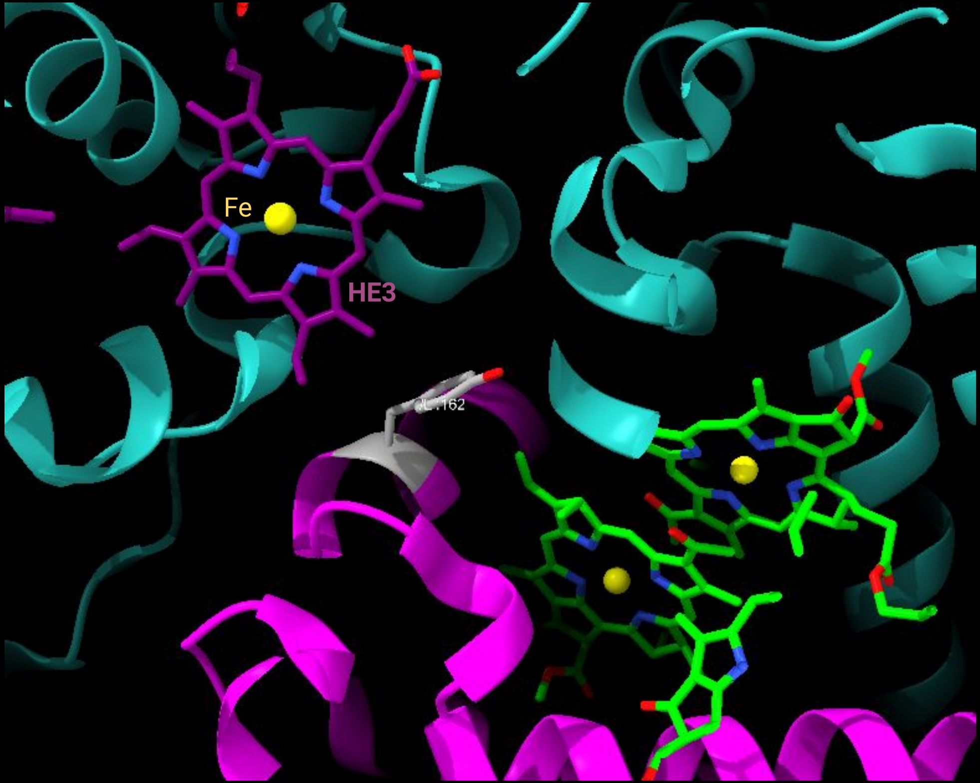

Electron transfer from BCB to BPB

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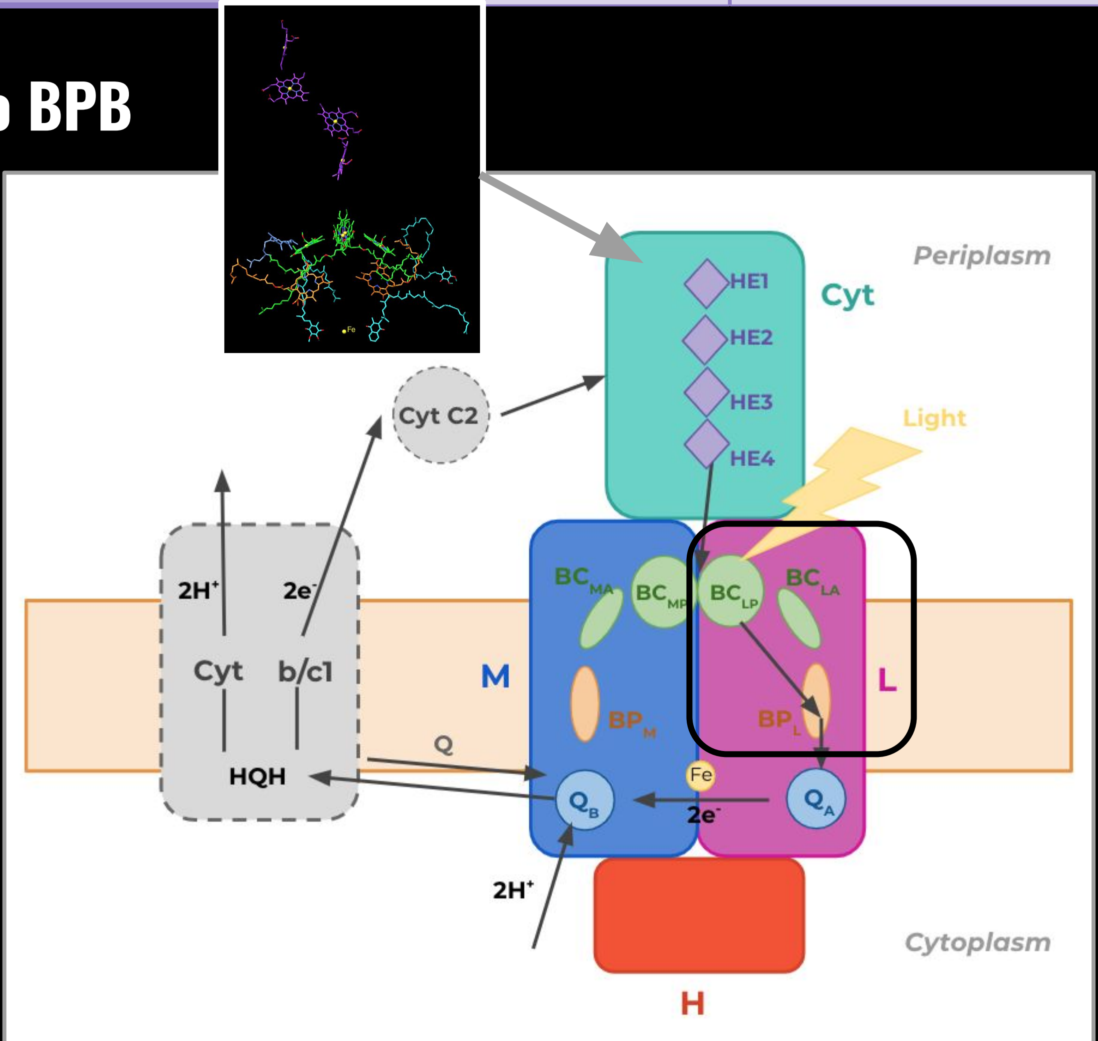
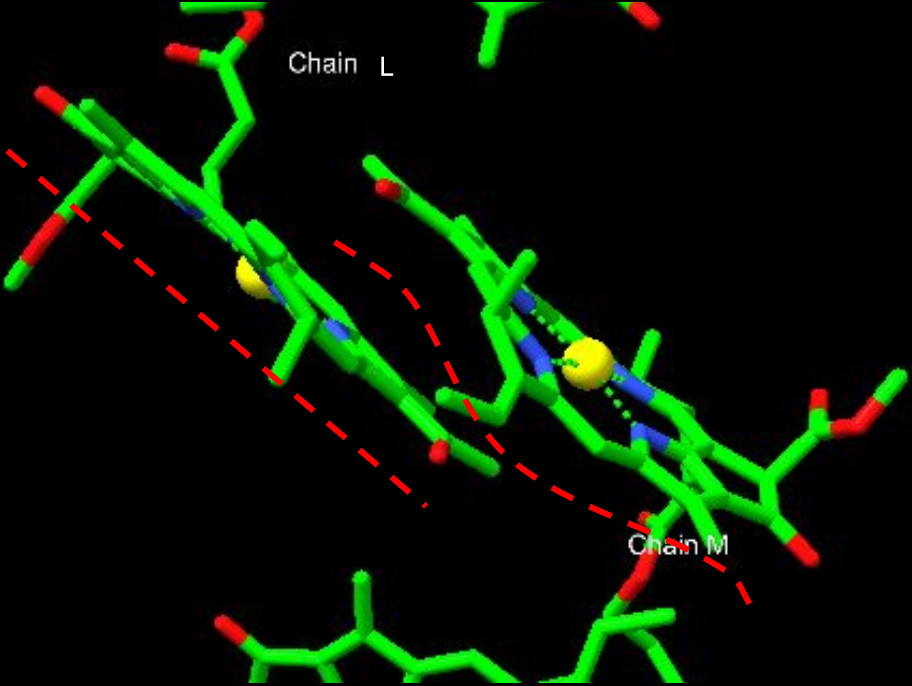


Electron transfer from BCB to BPB

Unidirectional transport

Electrons are transferred from the special pair only to the cofactors of the L chain in an **unidirectional way**

Structural differences of BCB rings:
Deviation from symmetry: M ring more deformed than L ring.
BP_L is 0.5A closer to the special pair than BP_M is.



Electron transfer from BCB to BPB

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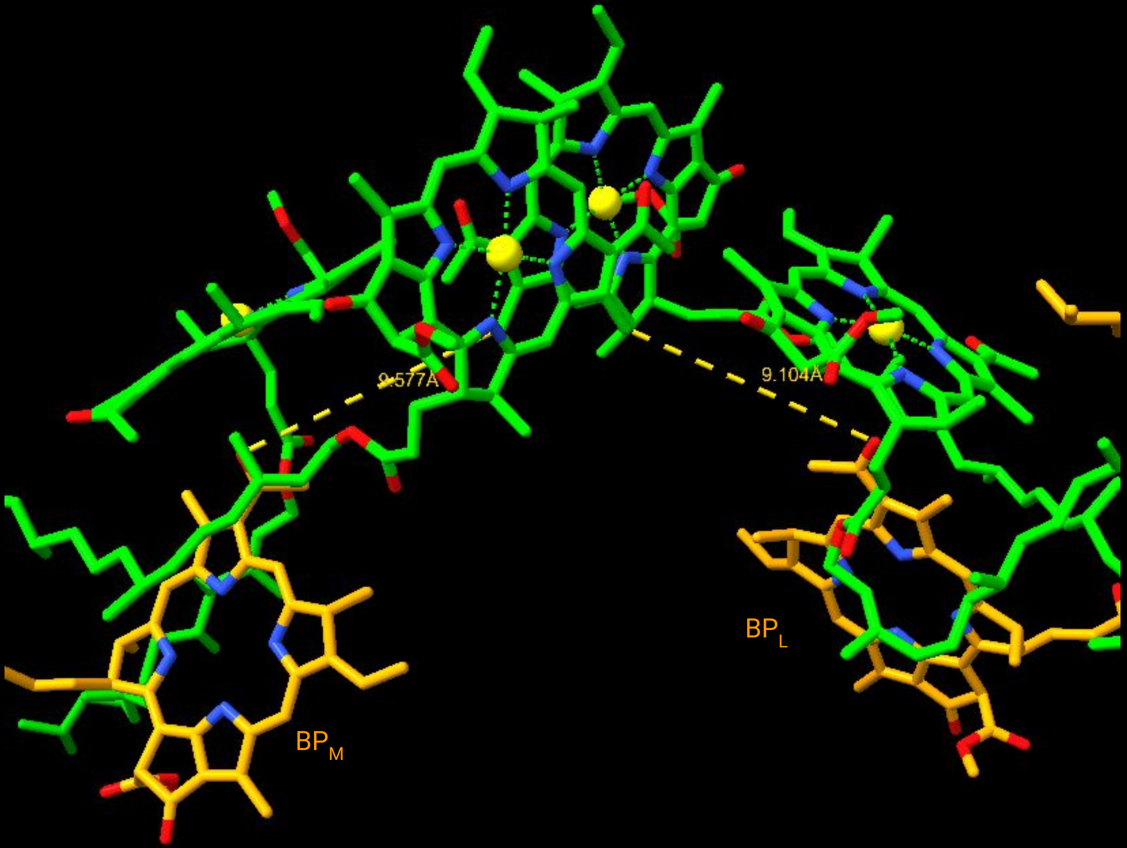
⬇

Differences in overlap of electron orbitals



Electron transfer from BCB to BPB

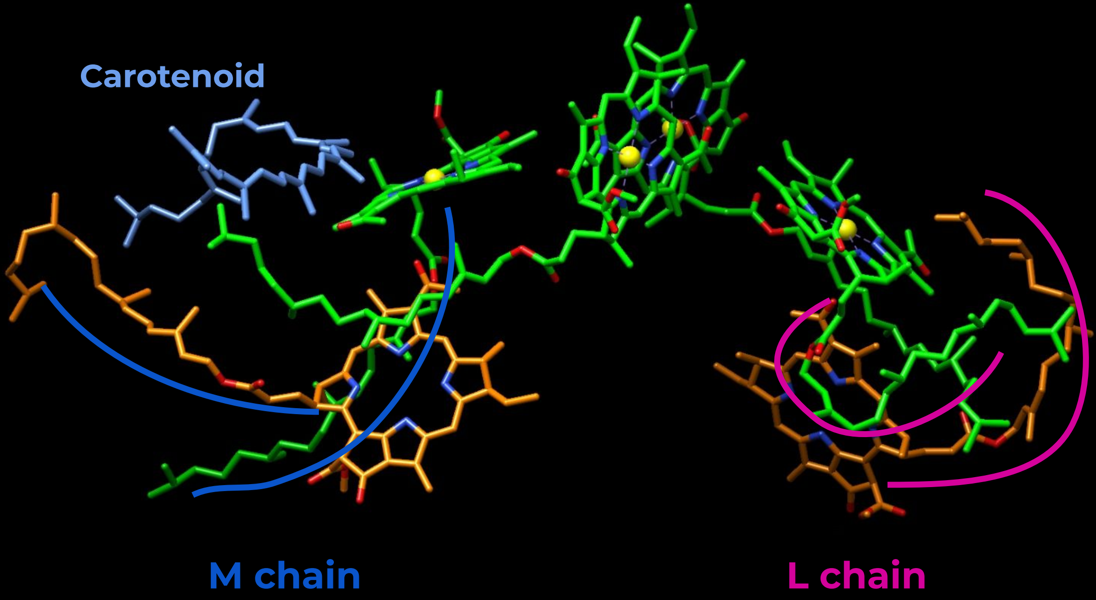
Unidirectional transport

Differences in structural order between L and M branches

Phytyl side chains of **BC_{MA}** and **BP_{M}** are partially disordered at their ends

Carotenoid in M chain also contributes to structural differences.

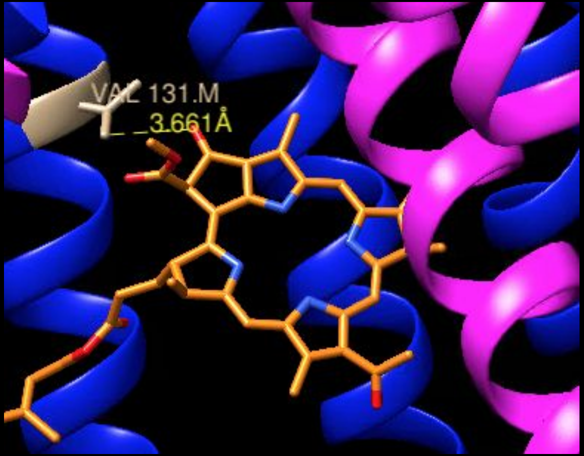
M-branch is more disordered than the L-branch.

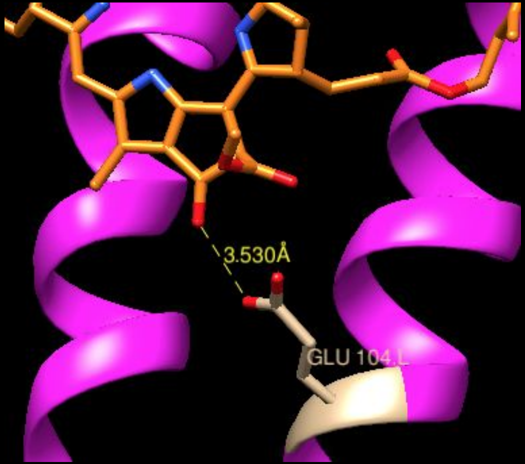


Electron transfer from BCB to BPB

Unidirectional transport

Differences between BP_L and BP_M
BP_M interacts with valine M131, while BP_L interacts with glutamic acid L104, through H-bonds.
Tryptofan **M250** is bound to BP_L and facilitates the electron transmission to QA. The equivalent in chain L is phenylalanine **L216**, with a smaller side chain, so it cannot perform a similar bridging.





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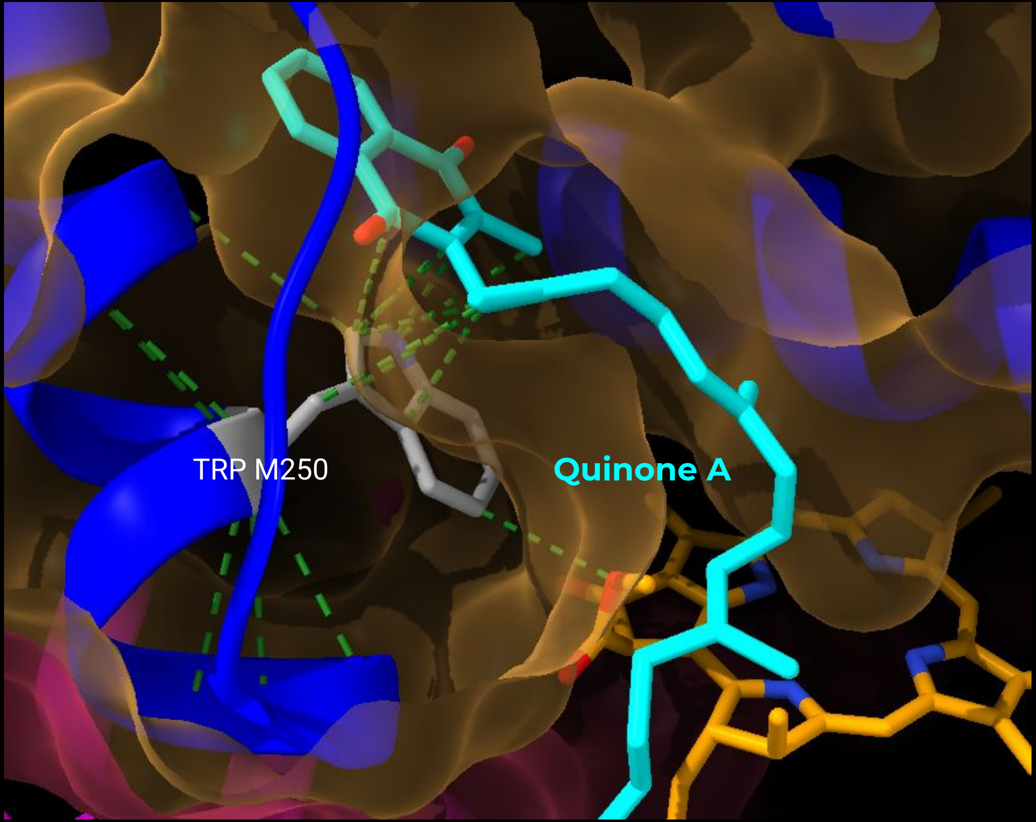

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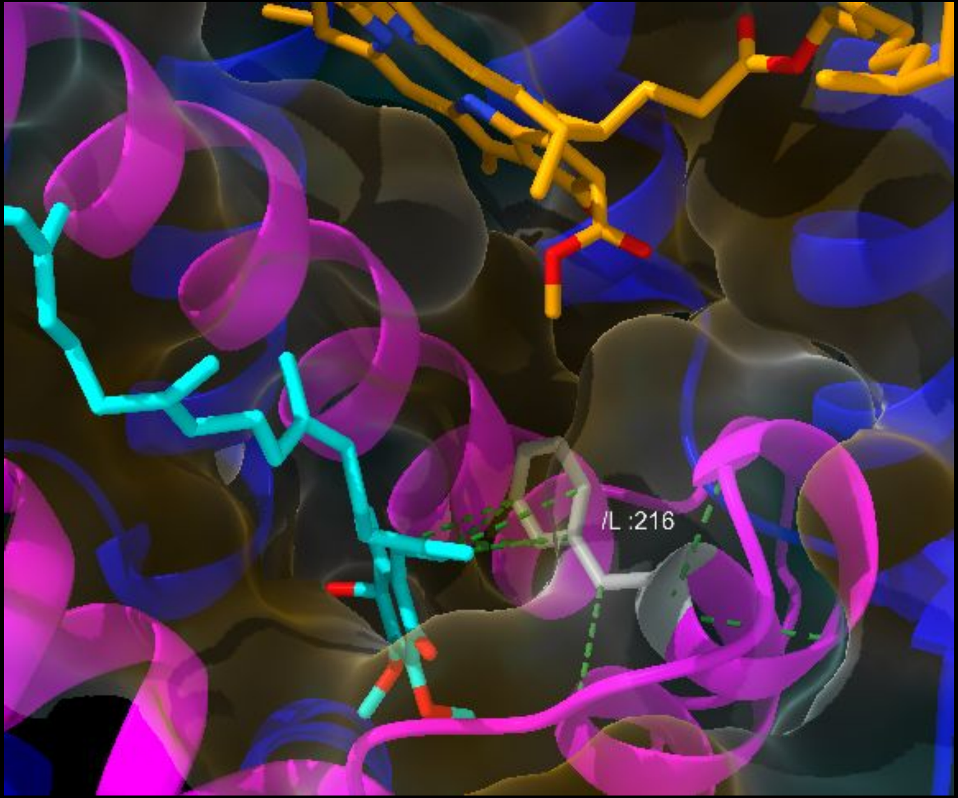
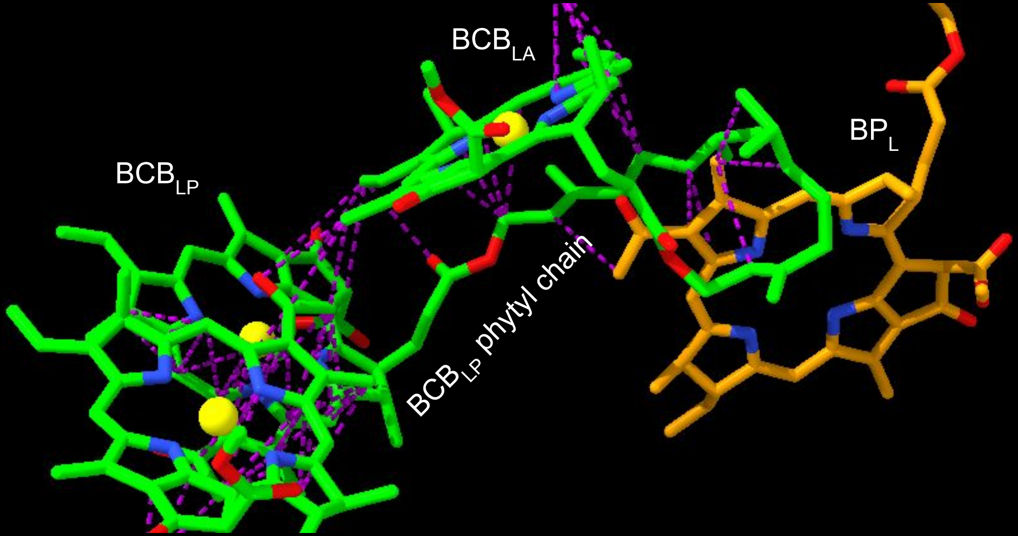


Electron transfer from BCB to BP_L

Protein environment of the pigments: BCB

BCB_{LP}	The phytyl chain is in Van der Waals contact to tetrapyrrole rings of BCB_{LA} and BP_L
	Distance between the special pair and BP_L is close to 10A
BCB_{LA}	Van der Waals contacts with both the special pair and BP
	It is in the middle of the special pair and BP_L, but BP_L is directly reduced.



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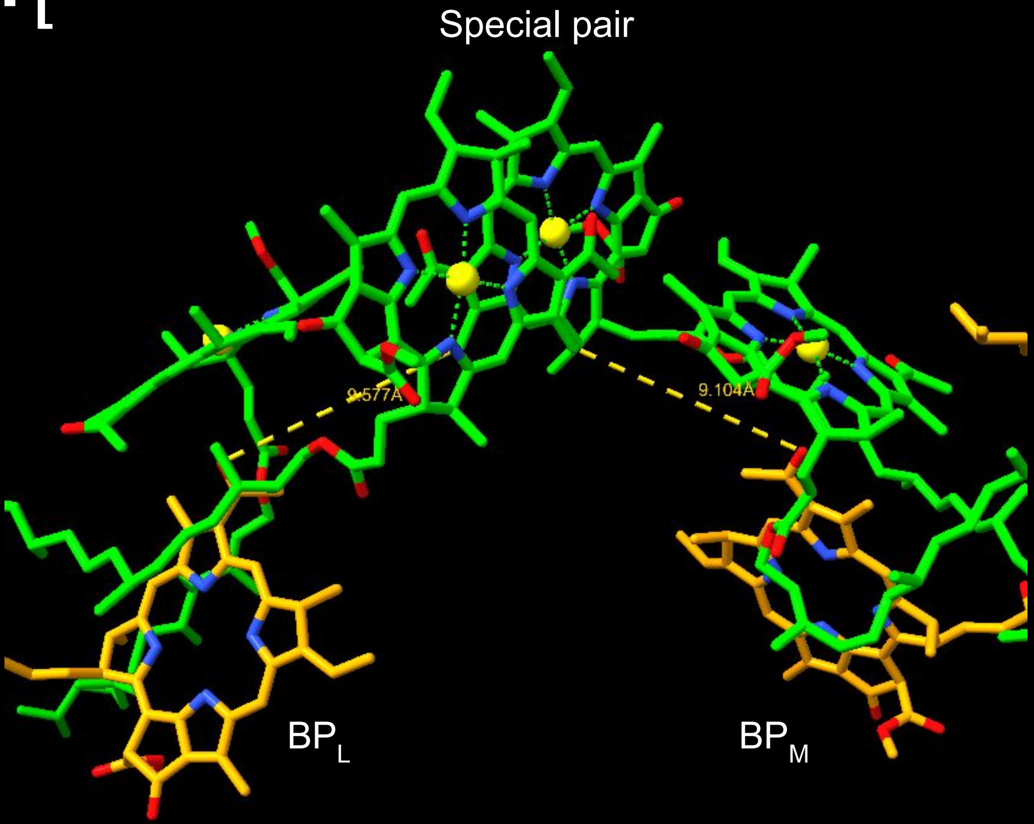

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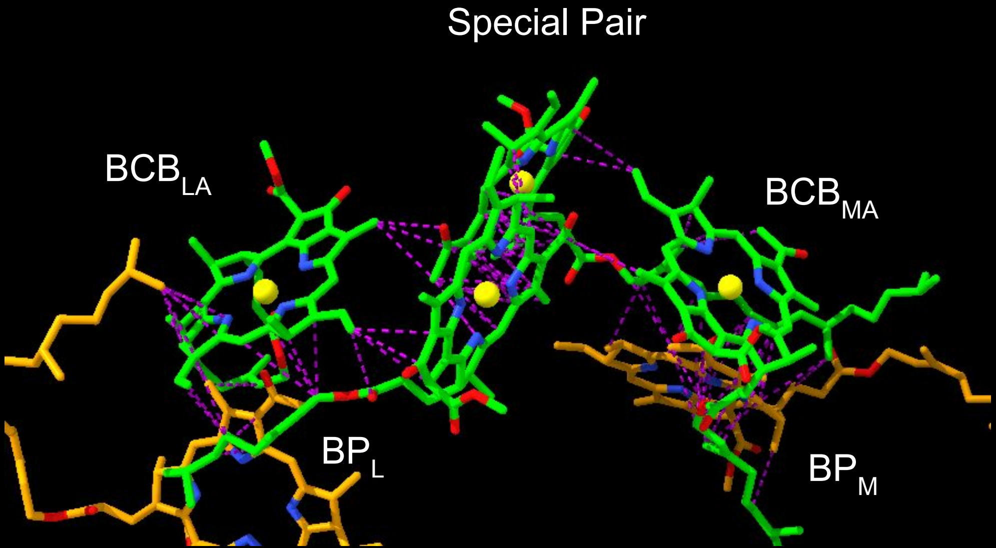

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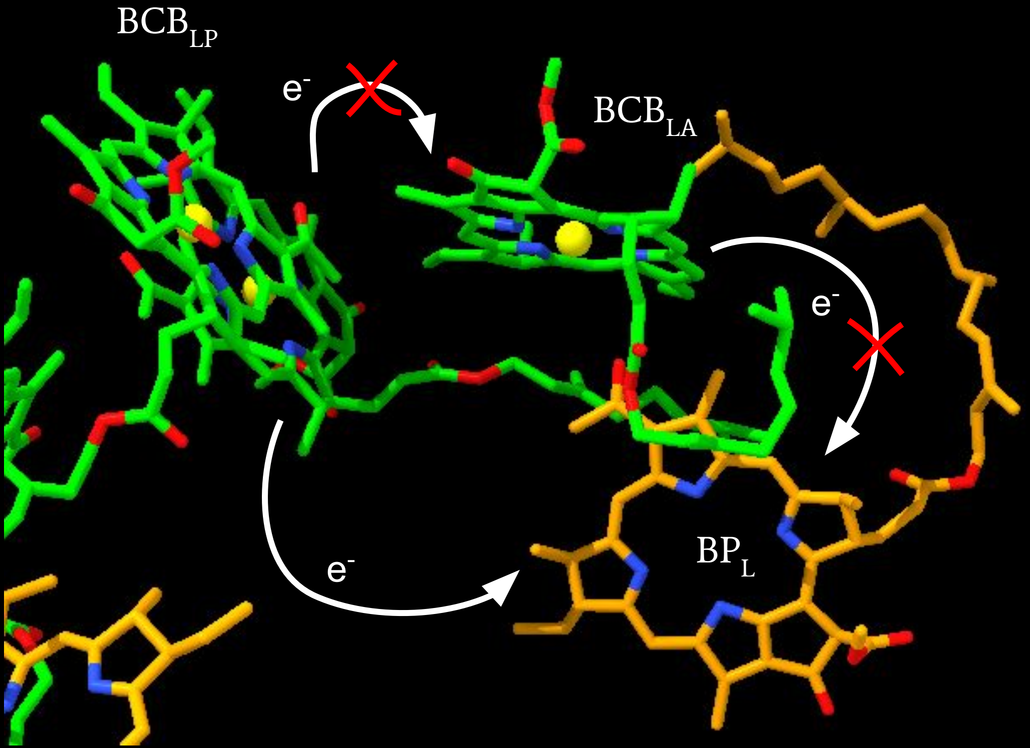


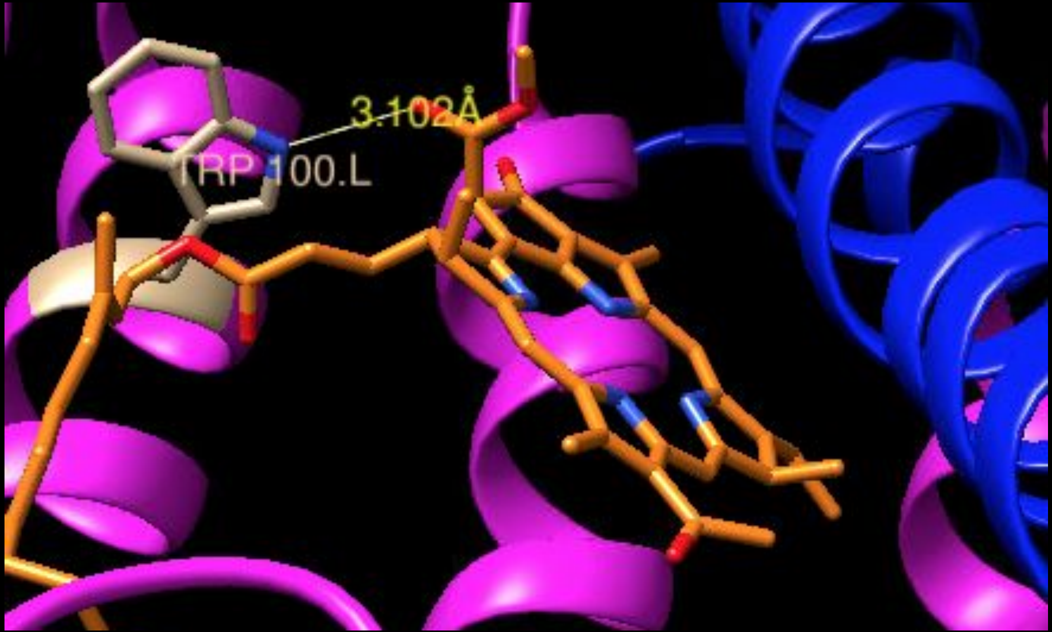
Electron transfer from BCB to BP_L

Protein environment of the pigments: BPB

BP_L Hydrogen bonds

Ring V ester carbonyl group and tryptophan L100.

Ring V keto carbonyl oxygen and glutamic acid L104. Unique for the L-branch.



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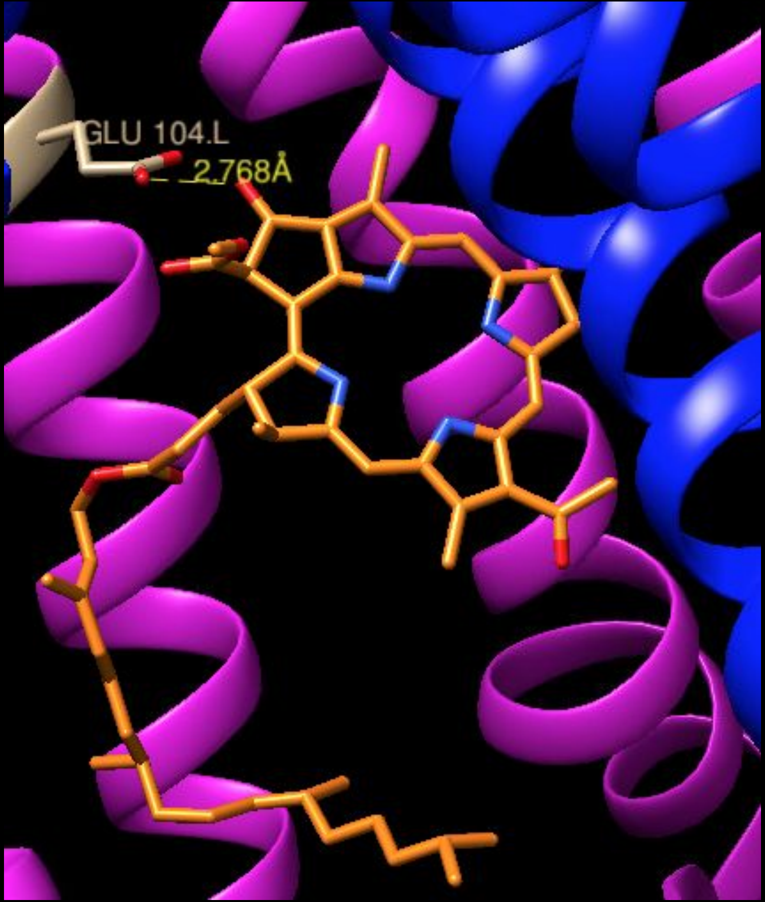


Electron transfer from BCB to BP_L

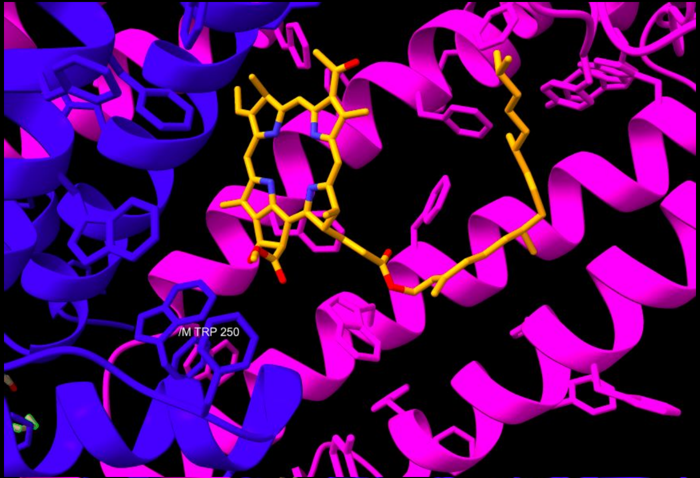
Protein environment of the pigments: Special pair

Aromatic residues

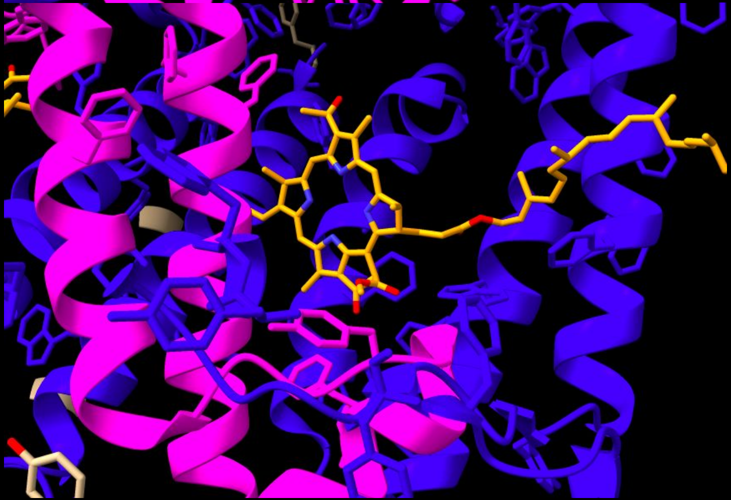
Neighborhood of BP_L is richer in aromatic residues than that of BP_M

<u>Tryptophan M250.</u> Bridge between BP_L and Q_A

BP_M

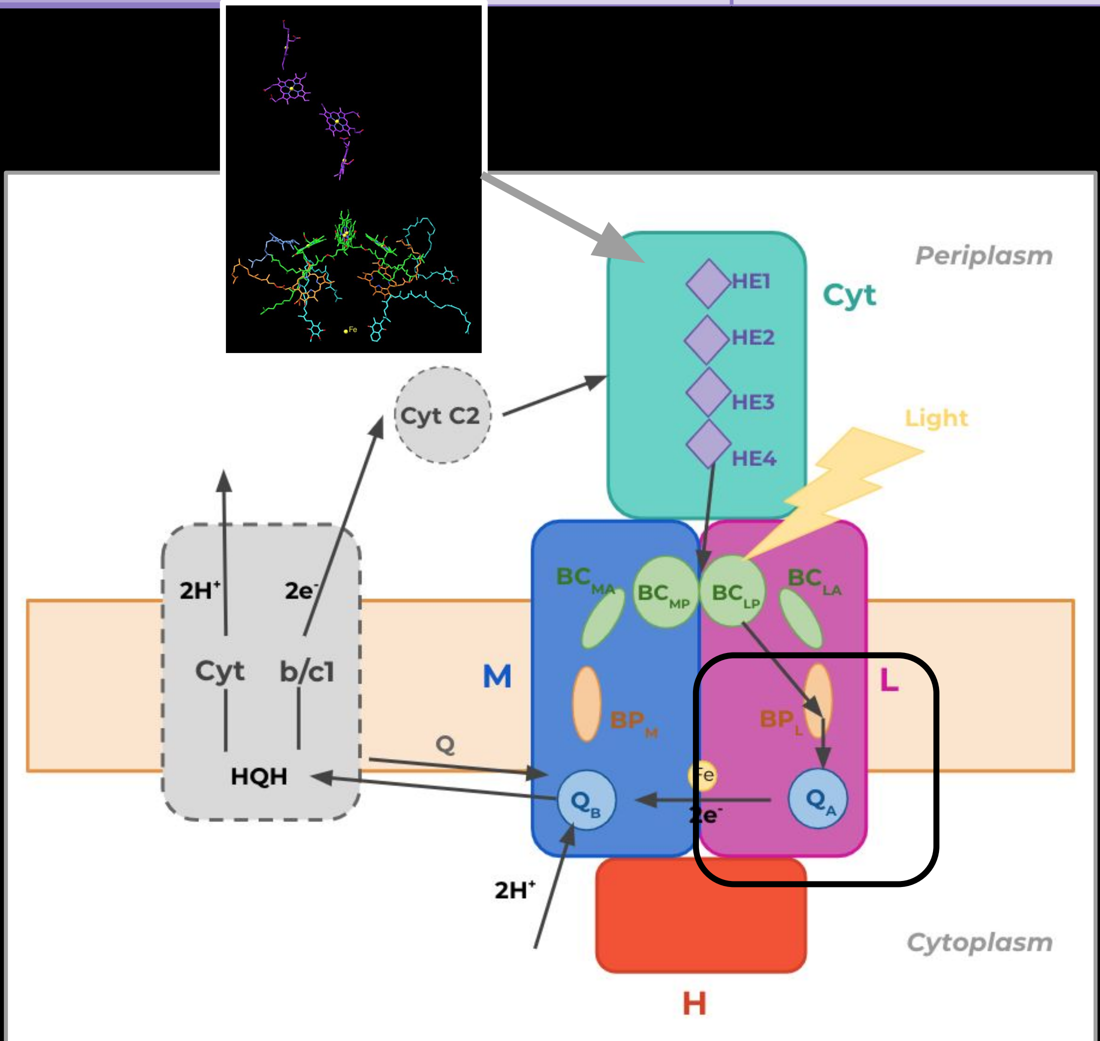


BP_L



From BP_L to QA

1. A photon excites an electron of BC_{LP}
2. The excited electron moves to BP_L
3. **The excited electron moves to menaquinone-9 (QA)**
4. Two electrons reach the ubiquinone-9.
5. Quinone B is twicely protonated
6. QBH_2 dissociates and moves to the Cytochrome b/c1 protein
7. There the electrons and protons are transferred outside the membrane to generate a proton gradient and synthesize ATP

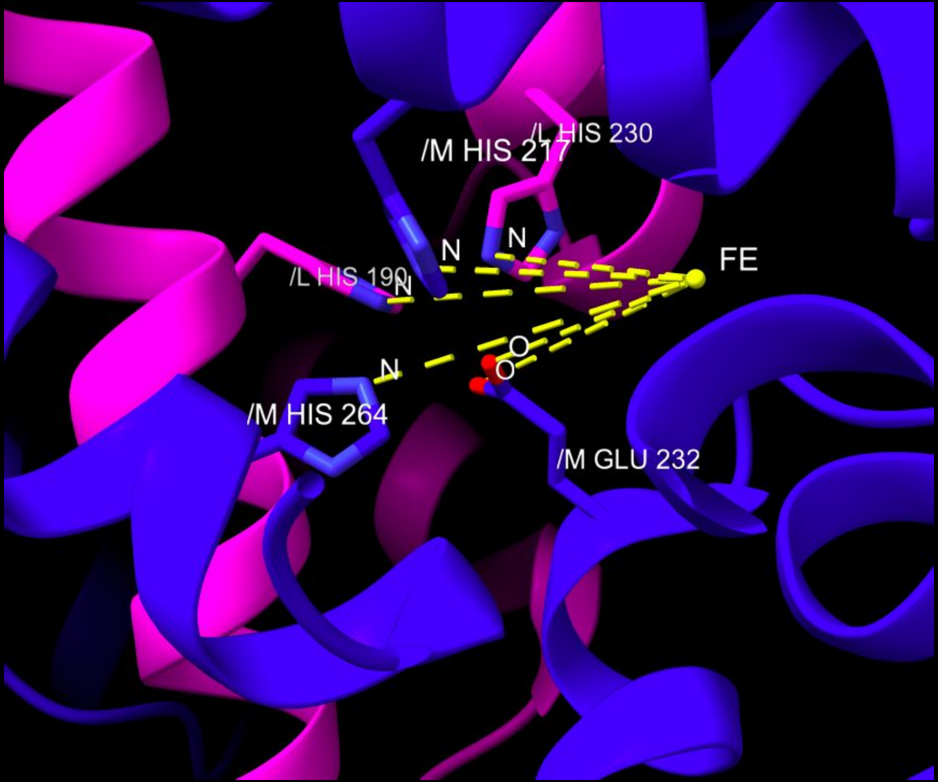


From BP_L to QA (MNQ-9)

Quinones. Near the non-heme iron.

Non-heme iron. Bound by five protein side chains:

Two histidines from L chain
Two histidines from M chain
One glutamic acid from M chain



From BP_L to QA (MNQ-9)

Non-heme iron. Octahedral environment.

Axial ligands

His L230

His M264

Equatorial ligands

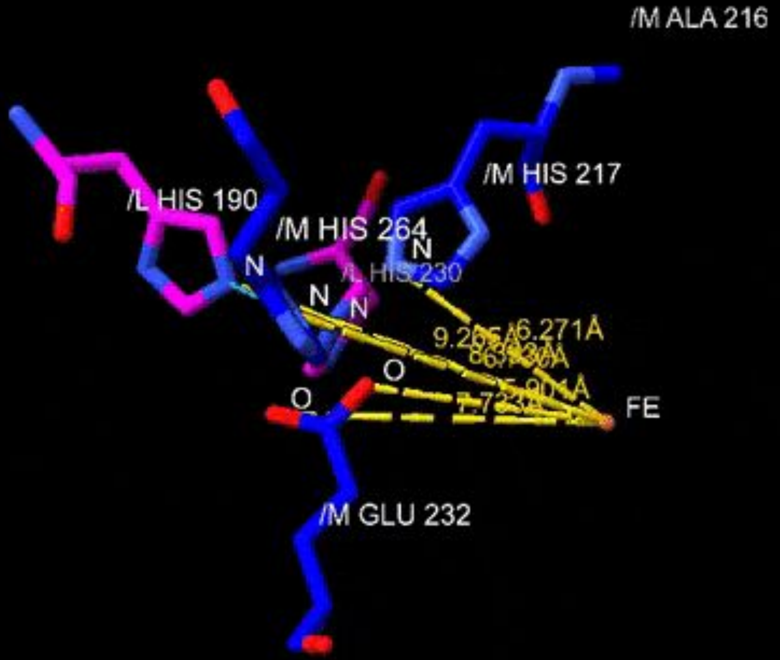
His L190

His M217

Glu M232

His L190: binding of Q_B

His M217: binding of Q_A



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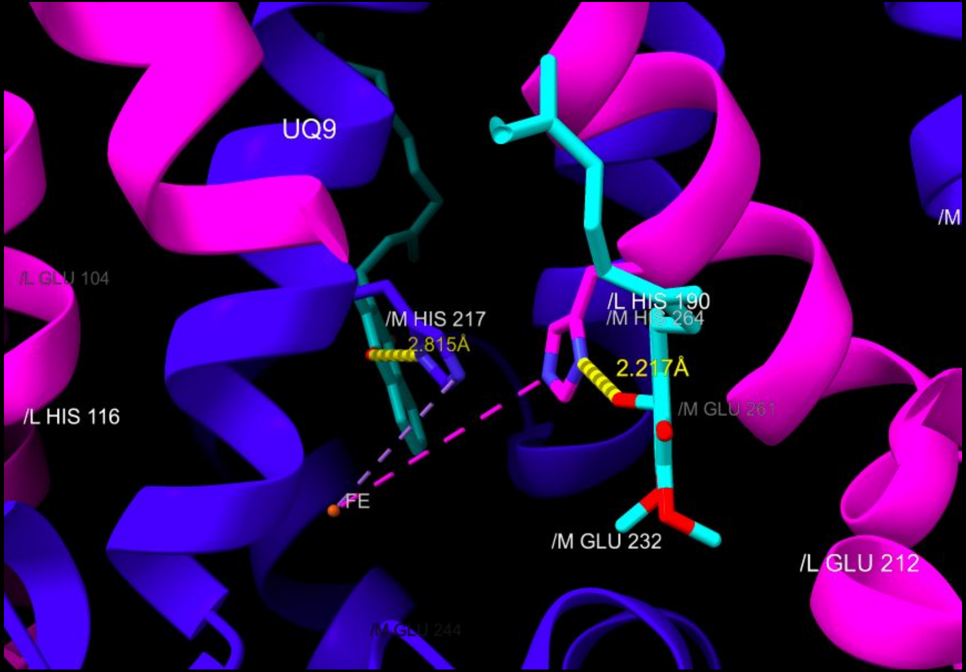
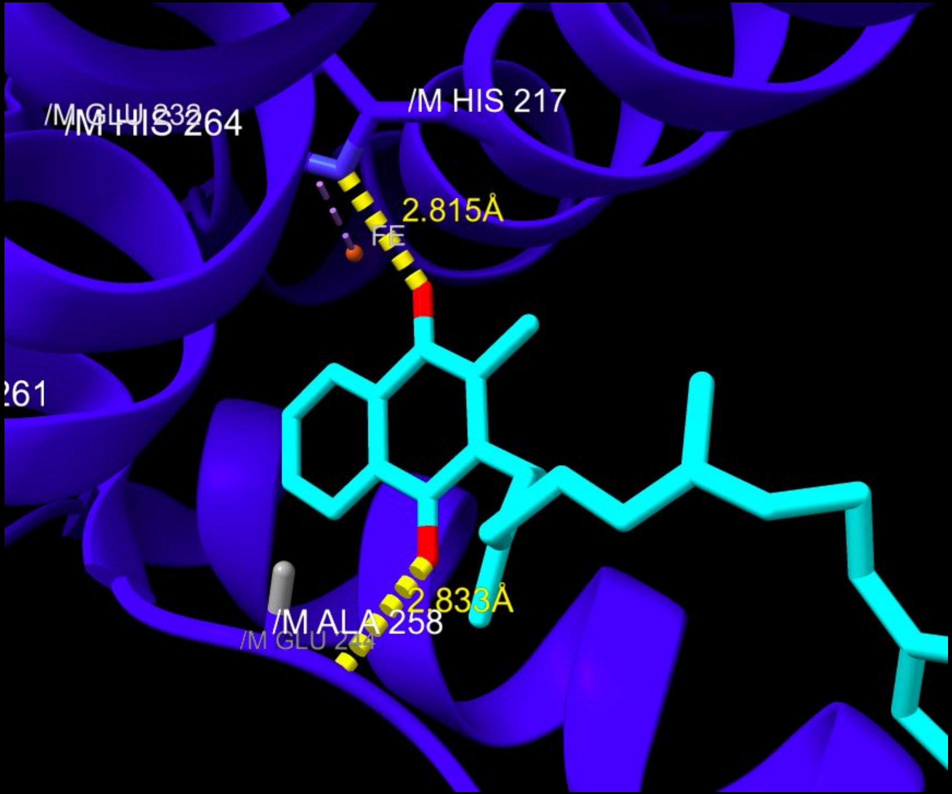


From BP_L to QA (MNQ-9)

Quinone A (MNQ-9)

Head group bound in a hydrophobic pocket.

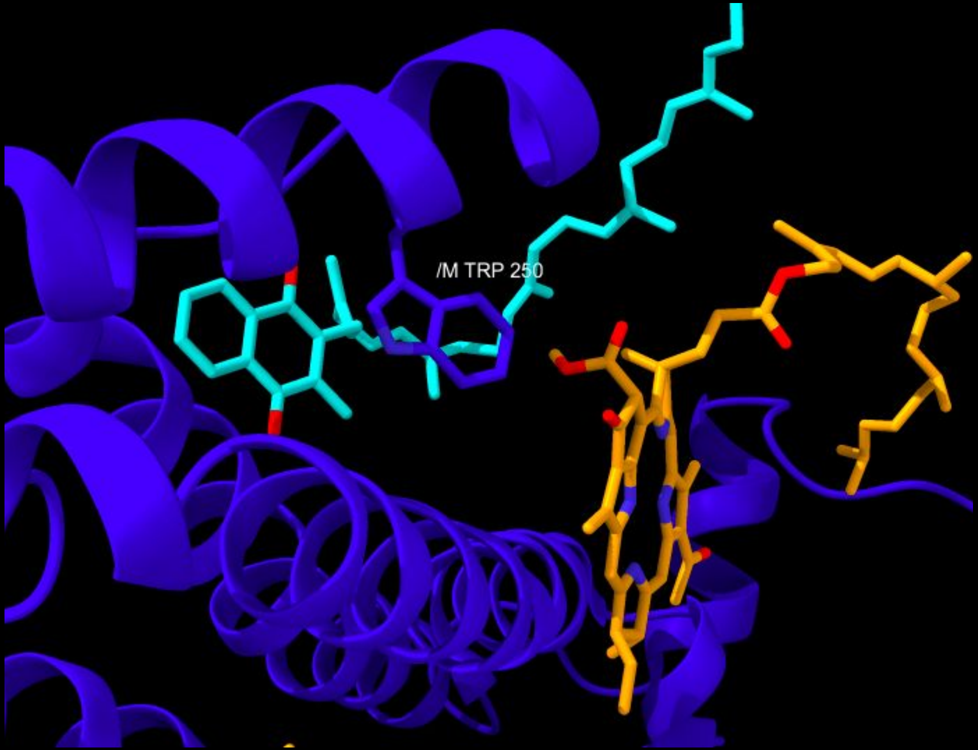
Carbonyl oxygens bound to -NH of Ala M258 and N6 of His M217



From BP_L to QA (MNQ-9)

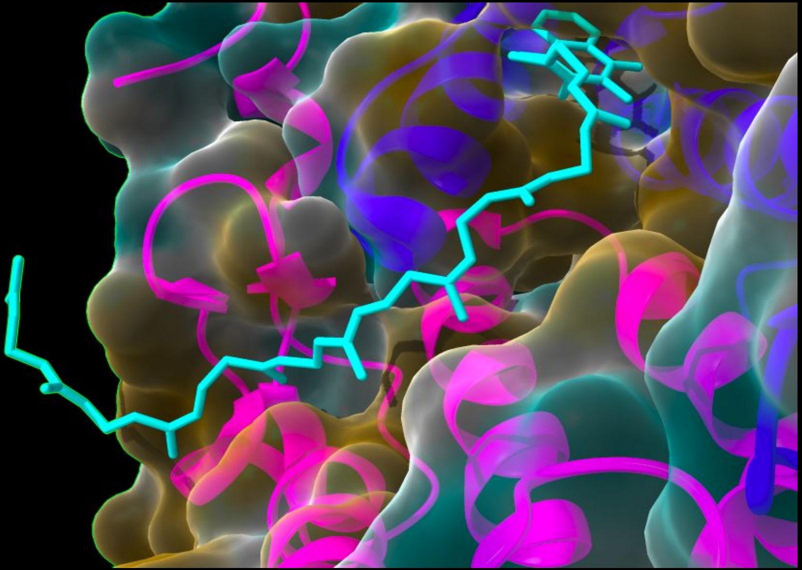
Quinone A (MNQ-9)

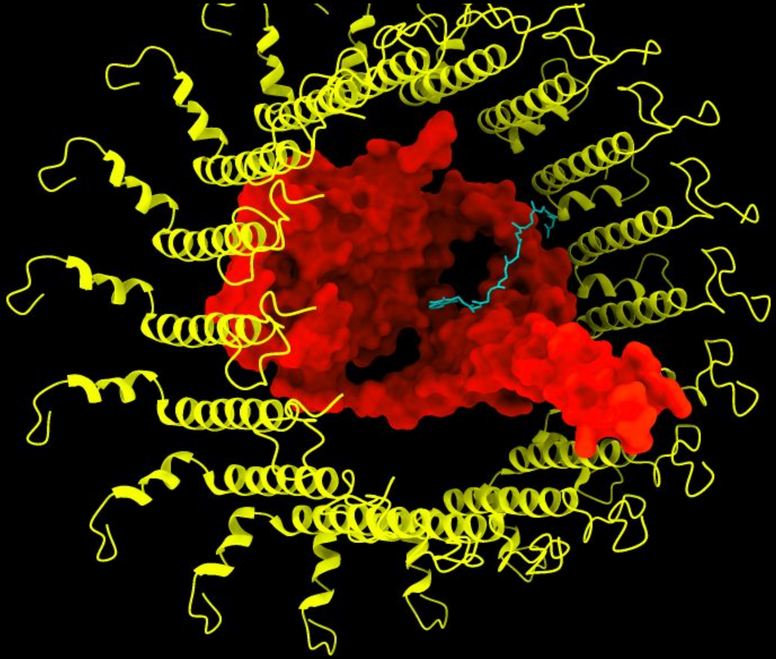
Trp M250 is part of the QA'S binding pocket and participates in the electron transfer



From BP_L to QA (MNQ-9)

QA binding pocket is well shielded from the cytoplasm by the globular domain of the H-subunit





Isoprenoid side chain of QA is folded along the surface of the L-M complex

From QA to QB

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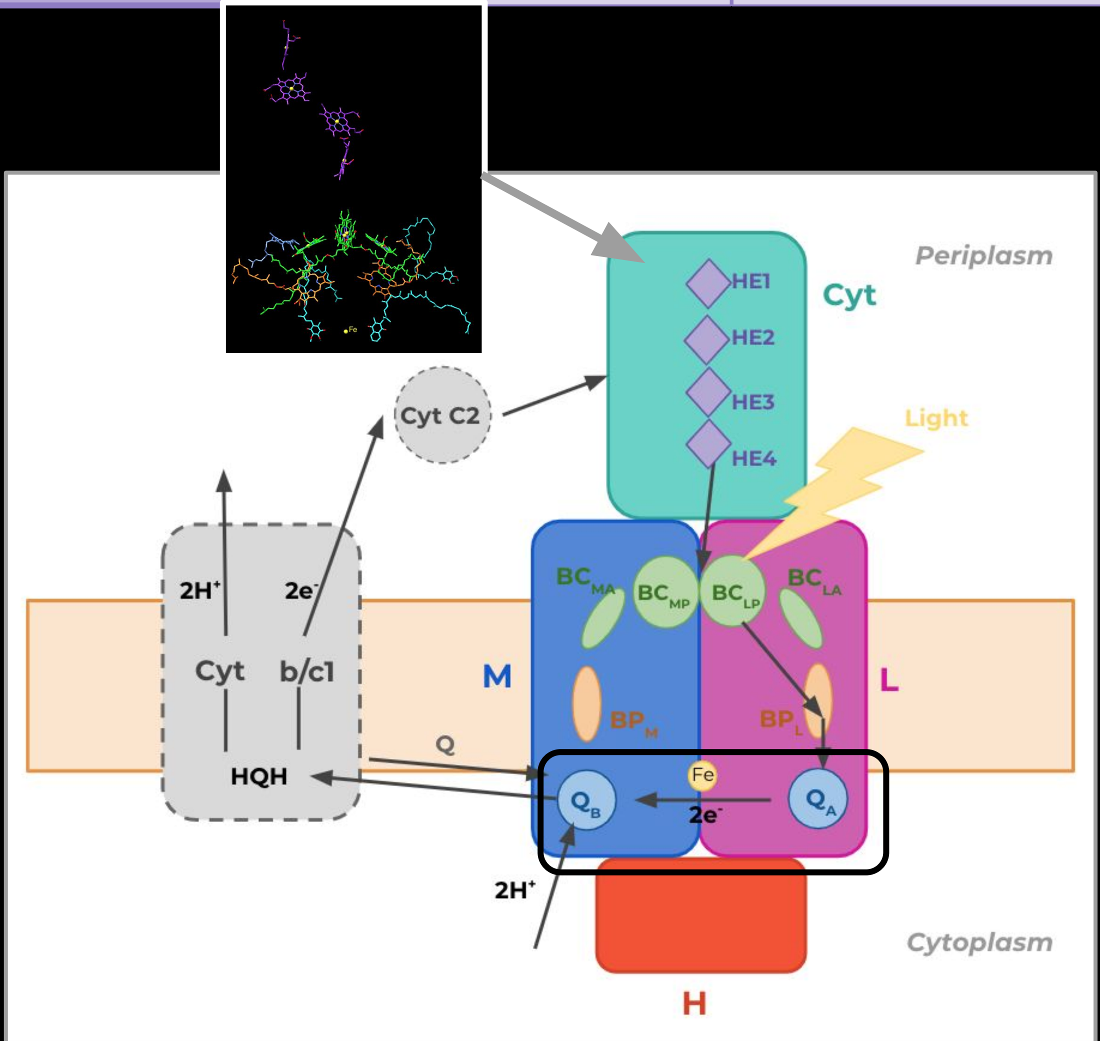
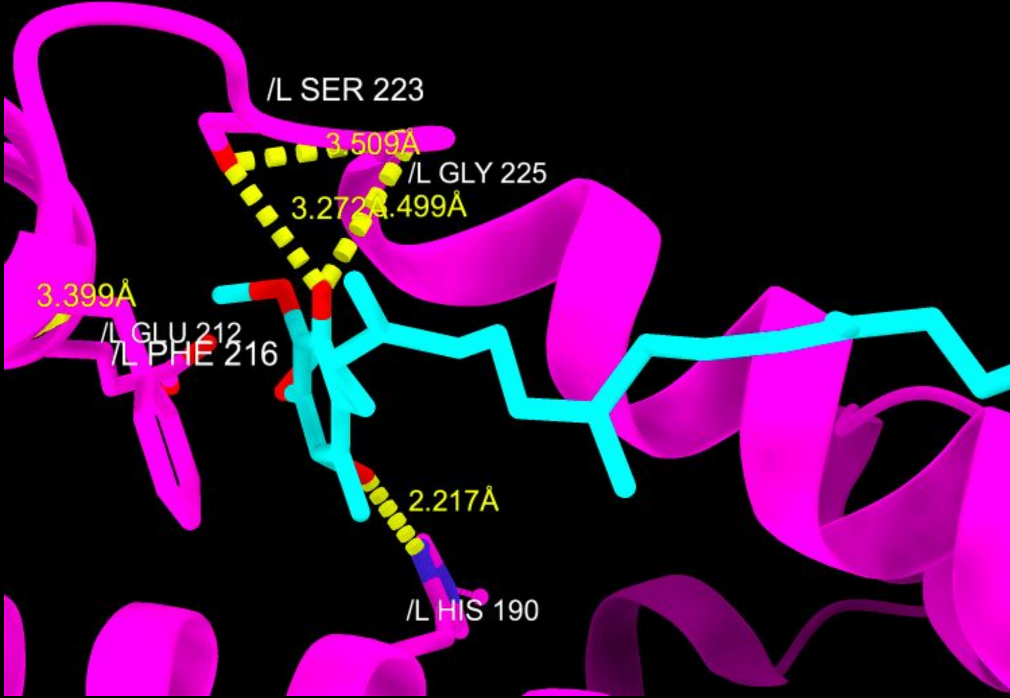


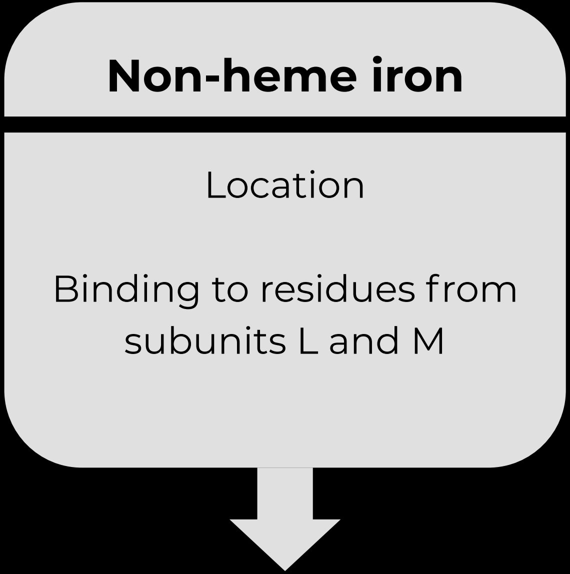
From QA to QB

Hydrogen bonds to Histidine L190, Serine L223 and glycine L225

Phe L216 forms a significant part of the QB binding pocket



From Q_A to Q_B

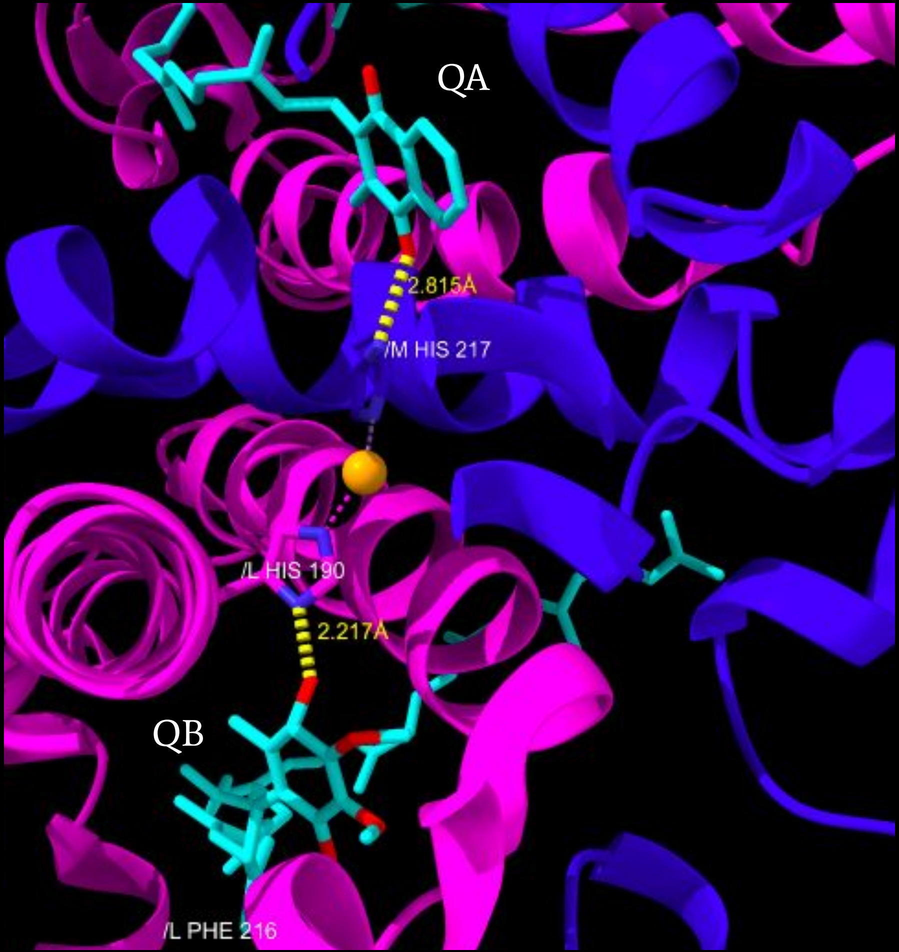


Non-heme iron

Location

Binding to residues from subunits L and M

Increases the structural stability of the reaction centre



From QB^{--} to QBH_2

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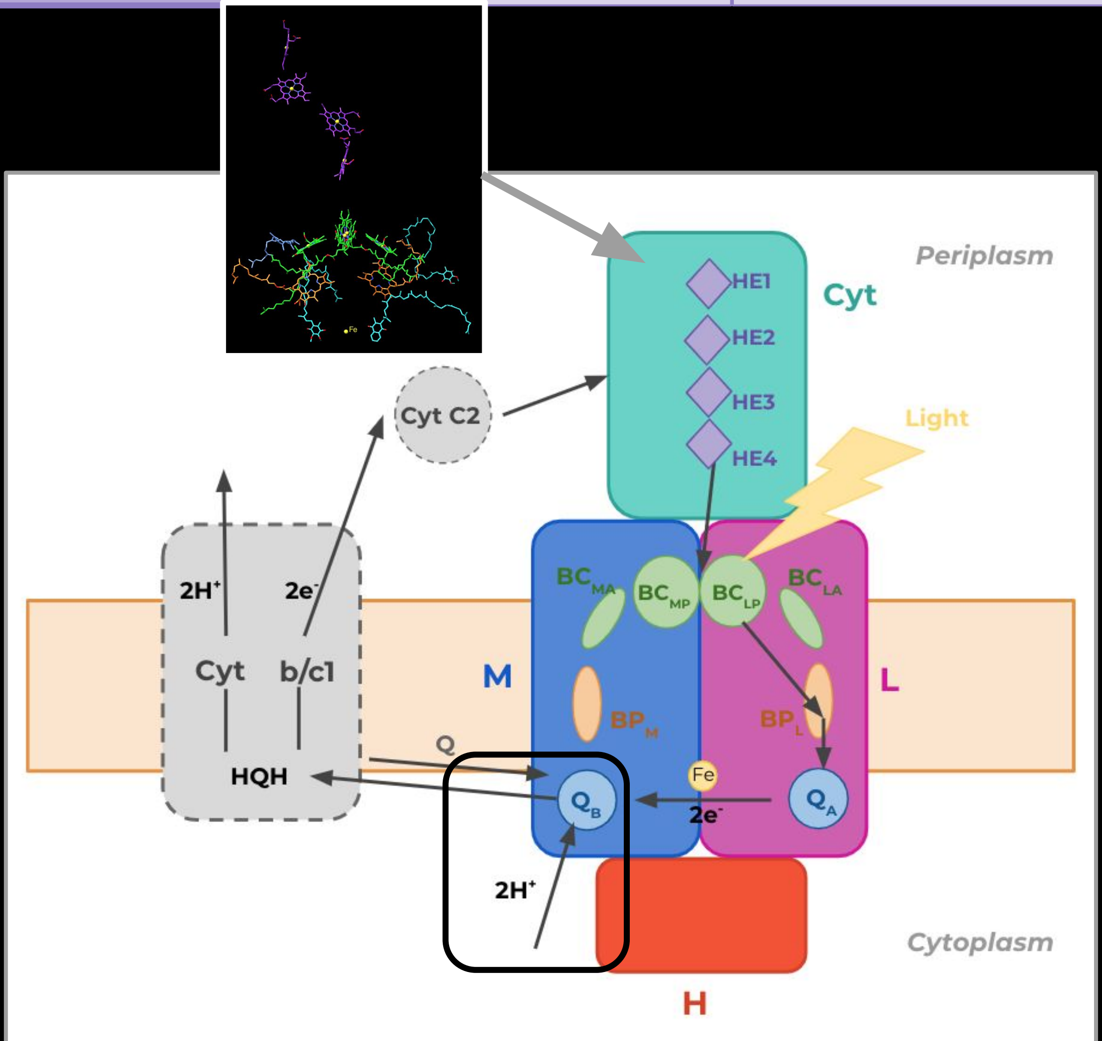
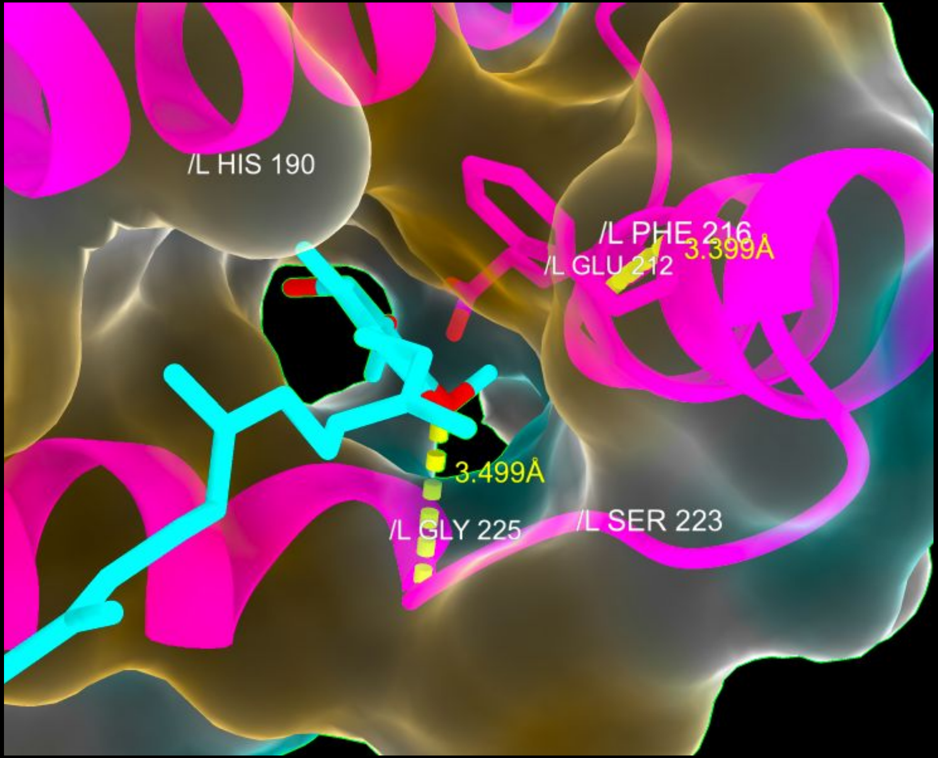
2. The excited electron moves to BP_L
3. The excited electron moves to menaquinone-9
4. Two electrons reach the ubiquinone-9.
5. **Quinone B is twicely protonated**
6. QBH_2 dissociates and moves to the Cytochrome b/c1 protein
7. There the electrons and protons are transferred outside the membrane to generate a proton gradient and synthesize ATP



From QB^{--} to QBH$_2$



QB is twicely protonated and transferred to cytochrome bc1.

QB site: polar nature
Bottom is formed to a large part by the side chain of **Glu L212.**

Protons’ path:
Cytoplasm → Glu L212 → QB

From QB^{--} to QBH$_2$

Rhodobacter sphaeroides

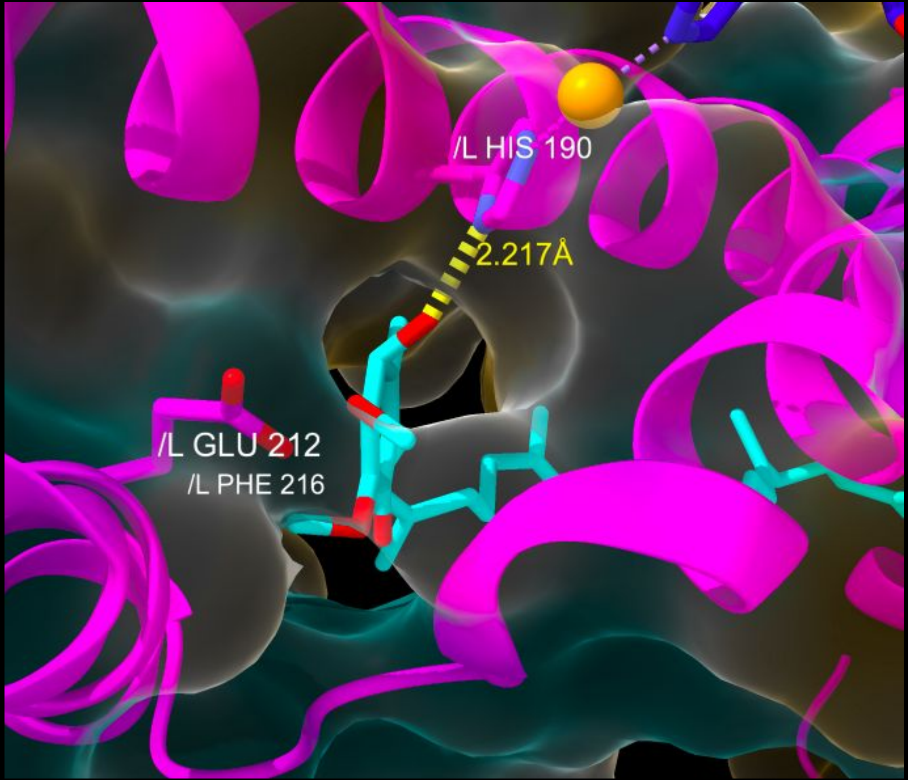
First proton transfer:

Asp H124 → His H126 → His H128

Asp L210 → Asp L213 → Ser L223

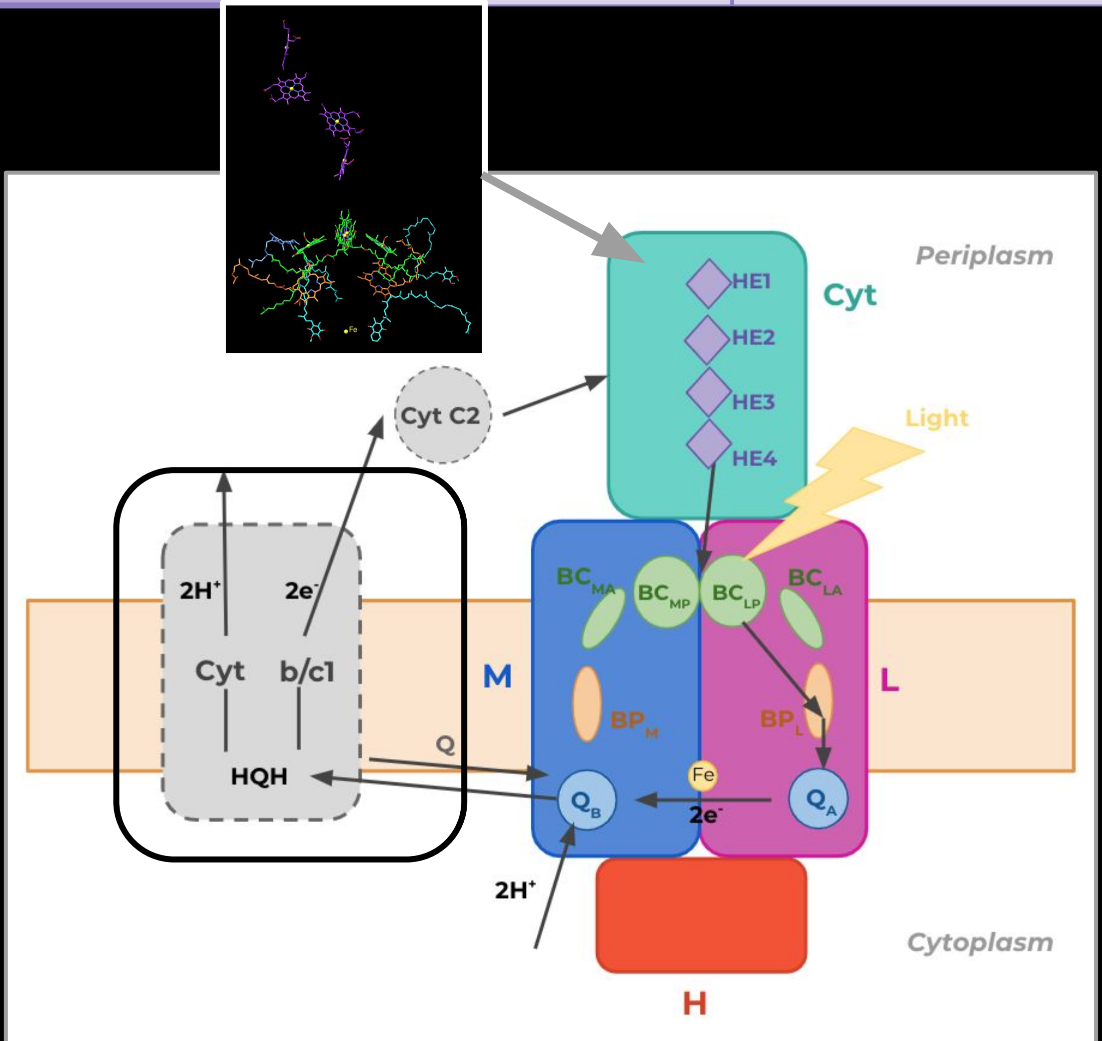
Second proton transfer:

Involves glutamic L212



From QB^{--} to QBH_2

1. A photon excites an electron of BC_{LP}
2. The excited electron moves to BP_L
3. The excited electron moves to menaquinone-9
4. Two electrons reach the ubiquinone-9.
5. Quinone B is twicely protonated
6. **QBH_2 dissociates and moves to the Cytochrome b/c1 protein**
7. **There the electrons and protons are transferred outside the membrane to generate a proton gradient and synthesize ATP**



EVOLUTIONARY ASPECTS

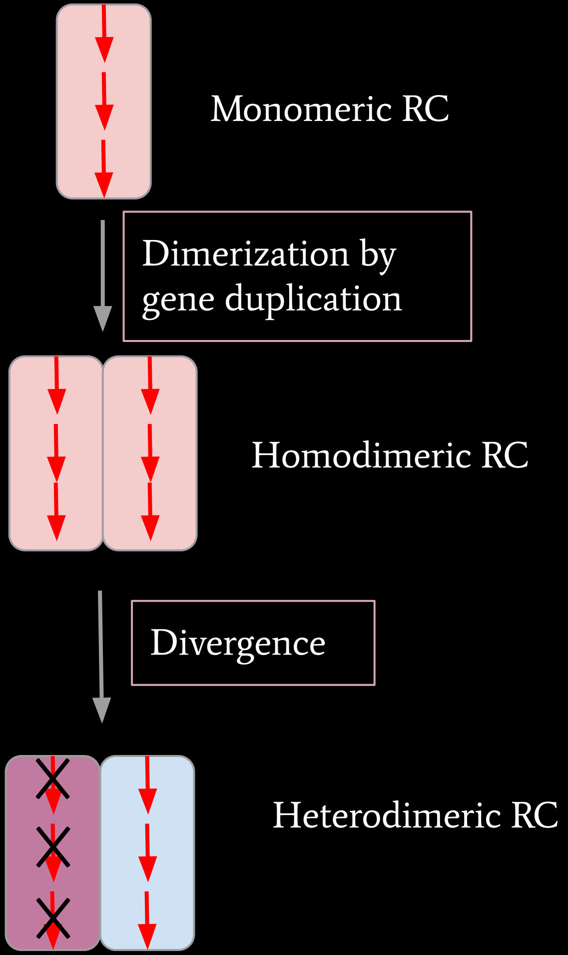
- How are chains M and L related?
- Is the Reaction Center of *Rhodopseudomonas viridis* related to the reaction center of Plants photosystem II?
- Are the Reaction Center of *Rhodopseudomonas viridis* sequences conserved among Purple Bacteria and other Photosynthetic bacteria?

Evolutionary theory of heterodimeric RC

Photosynthetic reaction centers have a **heterodimeric arrangement** with two subunits.

1. Monomeric ancestor
2. Gene duplication and dimerization
3. Divergence
4. Heterodimeric complex

Two potential electron transfer pathways



Monomeric RC

Dimerization by gene duplication

Homodimeric RC

Divergence

Heterodimeric RC

Subunits L-M: Core complex

Sequence alignment

```
CLUSTAL 2.1 multiple sequence alignment


1prcL           -ALLSFERKYRVRG-----------GTLIGGDLFDFWVG--------PYFVGFFGVSAIF
1prcM           ADYQTIYTQIQARGPHITVSGEWGDNDRVGKPFYSYWLGKIGDAQIGPIYLGASGIAAFA
                    ::  : :.**           .  :*  ::.:*:*        * ::*  *::*:

1prcL           FIFLGVSLIGYAASQGPTWDP-------FAISINPPDLKYGLGAAPLLEGGFWQAITVCA
1prcM           FGSTAILIILFNMAAEVHFDPLQFFRQFFWLGLYPPKAQYGMGIPPLHDGGWWLMAGLFM
                *   .: :* :  :    :**       * :.: **. :**:* .** :**:*    :

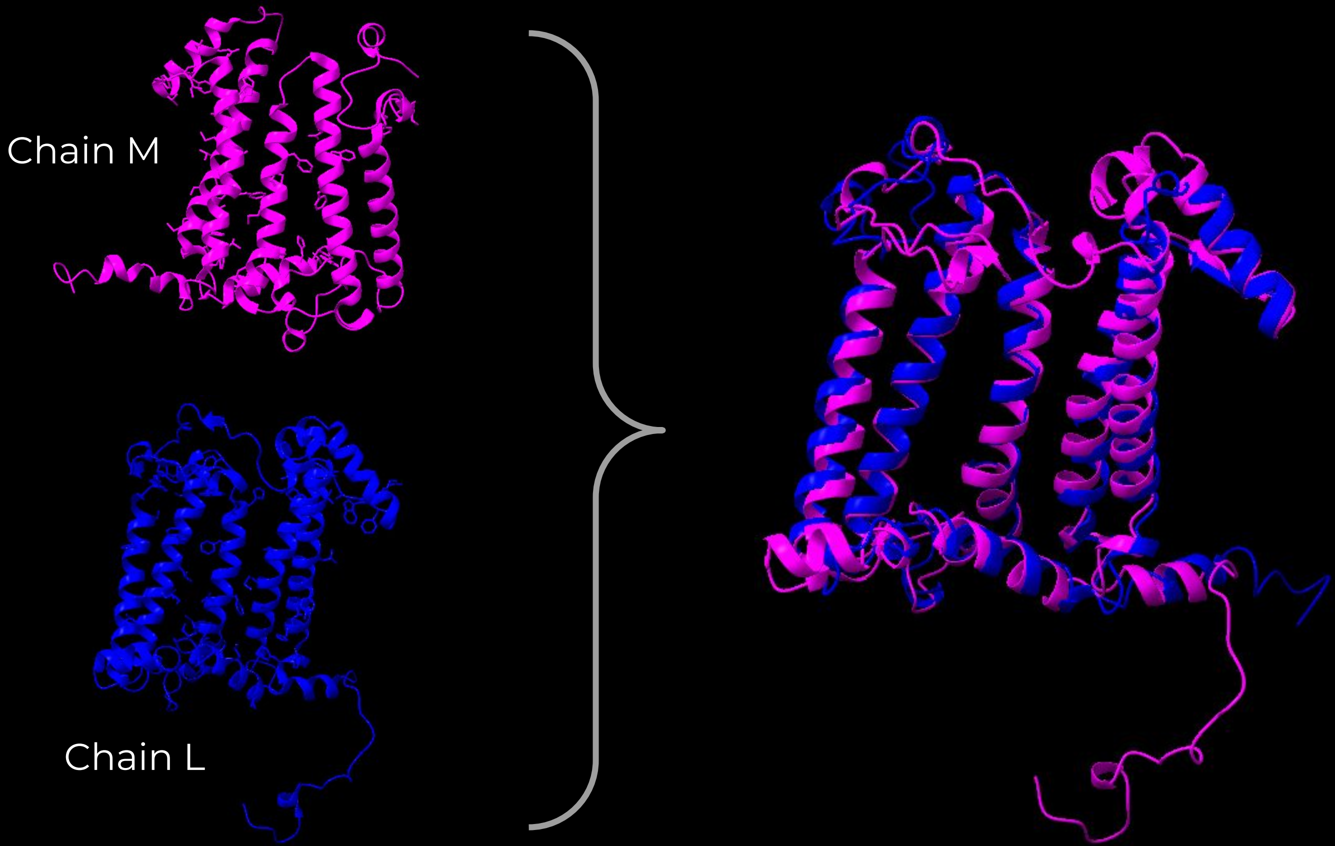
1prcL           LGAFISWMLREVEISRKLGIGWHVPLAFCVPIFMFCVLQVFRPLLLGSWGHAFPYGILSH
1prcM           TLSLGSWWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVPFGIWPH
                  :: ** :*  . :* **:* *:.  *...**:.  :  ::* *:***....*:** .*

1prcL           LDWVNNFGYQYLNWHYNPGHMSSVSFLFVNAMALGLHGGLILSVANPGDG-------DKV
1prcM           IDWLTAFSIRYGNFYYCPWHGFSIGFAYGCGLLFAAHGATILAVARFGGDREIEQITDRG
                :**:. *. :* *::* * *  *:.* :  .: :. **. **:**. *..       *:

1prcL           KTAEHENQYFRDVVGYSIGALSIHRLGLFLASNIFLTGAFGTIASGPFWTRGWPEWWGWW
1prcM           TAVERAALFWRWTIGFNATIESVHRWGWFFSLMVMVSASVGILLTGTFVDN-WYLWCVKH
                .:.*:   ::* .:*:.    *:** * *::  ::::.:.* : :*.*  . *  *

1prcL           LDIPFWS-----------------
1prcM           GAAPDYPAYLPATPDPASLPGAPK
                   * :.
```

Core complex: L - M superimposition



RMSD: 1.28

Nfit: 225

I% 29.22

1PRC
Deisenhofer, J., et al

Photosystem reaction center origin

- Photosystem II of plants contains two homologous proteins D1 and D2
- Photosynthetic reaction center of purple bacteria contains two homologous proteins L and M

Sequence analysis

↓

Different ancestor
Convergent evolution

VS

Functional data

↓

Common ancestor
Divergent evolution

L and D1 alignment

Amino acids important for the function:

- **histidine173:** ligand to the Mg2+ of the special pair
- L: **Phe216** **i** D1: **Phe255** binding to Q_B

Amino acids properties are more conserved than the sequence, which may lead to convergent evolution.

```
1prcL  --ALLSFERKYRVRG-----GTLIGGDLFDFWVGPYFVG--FFGVSAIFFIFLGVSLIGY
D1     MTAILERRESTSLWGRFCNWITSTENRLYIGWFGVLMIPTLLTATSVFIIAFIAAPPVDI
         *:*. ...  : *      *   . *:  *.*  ::   : ..*.::: *:... :.

1prcL  AASQGPTWDPFAIS-------INPPDLKYGLGAAP----------LLEGGFWQAITVCAL
D1     DGIREPVSGSLLYGNNIISGAIIPTSAAIGLHFYPIWEAASVDEWLYNGGPYELIVLHFL
        . : *. ..:  .       * *..   **   *          * :** :: *.:  *

1prcL  GAFISWMLREVEISRKLGIGWHVPLAFCVPIFMFCVLQVFRPLLLGSWGHAFPYGILSHL
D1     LGVACYMGREWELSFRLGMRPWIAVAYSAPVAAATAVFLIYPIGQGSFSDGMPLGISGTF
        .. .:* ** *:* :**:   :.:*:..*:    .: :: *:  **:...:* ** . :

1prcL  DWVNNFGYQYLNWHYNPGHMSSVSFLFVNAMALGLHGGLILS----------VANP----
D1     NFMIVFQAEHN-ILMHPFHMLGVAGVFGGSLFSAMHGSLVTSSLIRETTENESANEGYRF
       :::  *  ::     :* ** .*: :* .::  .:**.*: *           **

1prcL  GDGDKVKTAEHENQYFRDVVGYSIGALSIHRLGLFLASN-----IFLTGAFGTIAS---G
D1     GQEEETYNIVAAHGYFGRLIFQYASFNNSRSLHFFLAAWPVVGIWFTALGISTMAFNLNG
       *: ::. .    : **  ::    .  . : * :***:       * : .:.*:*    *

1prcL  PFWTRGWPEWWG----WWLDIPFWS-----------------------------
D1     FNFNQSVVDSQGRVINTWADIINRANLGMEVMHERNAHNFPLDLAAVEVPSTNG
         :.:.  :  *     * **   :
```

M and D2 alignment

Amino acids important for the function:

- **histidine200**: ligand to the Mg2+ of the special pair
- M: **Trp 250** i D2: **Trp254** binding to Q_A

Amino acids properties are more conserved than the sequence, which may lead to convergent evolution.

```
1prcM  ADYQTIYTQIQARGPHITVSGEWGDNDRVGKP-FYSYWLGKIGDAQIGPIYLGASGIA-A
D2     -MTIAIGKFAKEENDLFDIMDDWLRRDRFVFVGWSGLLLFPCAYFALGGWFTGTTFVTSW
           :* .  : ..  : : .:*  .**.    : .  *   .   :*  : *:: ::

1prcM  FAFGSTAILIILFNMAAEVHFDPLQFFRQFFWLGLYPPKAQYGMGIPPLHDGGWLMAGL
D2     YTHGLASSYLEGCNFLTAAVSTPANSLAHSLLL-LWGPEAQGDFTR-WCQLGGLWTFVAL
       ::.* ::  :   *: : .   * : : : : * *: *:** .:     : ** * :..*

1prcM  FMTLSLGSWWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVPFGIW
D2     HGAFGLIGFMLRQFELARSVQLRPYNAIAFSGPIAVFVSVFLIYPLGQSGWFFAPSFGVA
       . ::.* .: :* :. **:: * .: *  *:..* ..:.:  *:*   ..*  . .**:

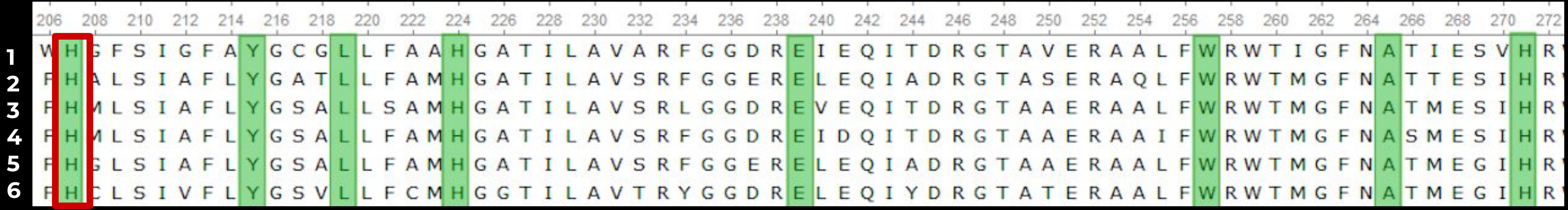
1prcM  PHIDWLTAFSIRYGNFYYCPWHGFSIGFAYGCGLLFAAHGATILAVARFGGDRE------
D2     AIFRFILFFQG-FHNWTLNPFHMMGVAGVLGAALLCAIHGATVENTLFEDGDGANTFRAF
       . : ::  *.  : *:   *:* :.:. . *..** * ****:  .   .**

1prcM  IEQITDRGTAVERAALFWRWTIGFNATIESVHRWGWFFSLMVMVS----ASVGILLTGTF
D2     NPTQAEETYSMVTANRFWSQIFGVAFSNK---RWLHFFMLFVPVTGLWMSALGVVGLALN
           ::.  ::  *  **   :*.  : :   **  ** *:* *:    :::*::  .

1prcM  VDNWYLWCVKHGAAPD----------------YPAYLPATPDPAS--------LPGAPK-
D2     LRAYDFVSQEIRAAEDPEFETFYTKNILLNEGIRAWMAAQDQPHENLIFPEEVLPRGNAL
       :  : : . :  ** *                  *::.*  :* .        ** .
```

Homology M

1 **Rhodopseudomonas viridis**
2 Rubrivivax_gelatinosus
3 Rhodospirillum_rubrum
4 Allochromatium_vinosum
5 Rhodobacter_sphaeroides
6 Roseobacter_dentrificans



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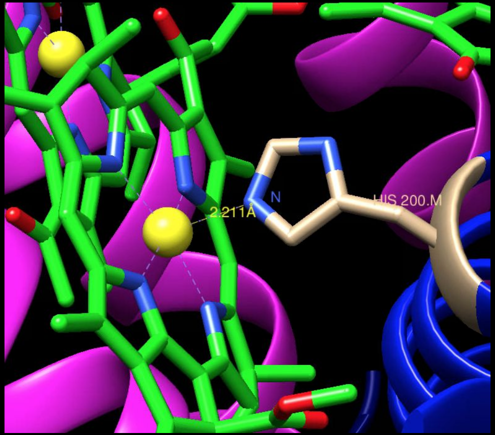
2   F H A L S I A F L Y G A T L L F A M H G A T I L A V S R F G G E R E L E Q I A D R G T A S E R A Q L F W R W T M G F N A T T E S I H R
3   F H M L S I A F L Y G S A L L S A M H G A T I L A V S R L G G D R E V E Q I T D R G T A A E R A A L F W R W T M G F N A T M E S I H R
4   F H M L S I A F L Y G S A L L F A M H G A T I L A V S R F G G D R E I D Q I T D R G T A A E R A A I F W R W T M G F N A S M E S I H R
5   F H G L S I A F L Y G S A L L F A M H G A T I L A V S R F G G E R E L E Q I A D R G T A A E R A A L F W R W T M G F N A T M E G I H R
6   F H C L S I V F L Y G S V L L F C M H G G T I L A V T R Y G G D R E L E Q I Y D R G T A T E R A A L F W R W T M G F N A T M E G I H R
```

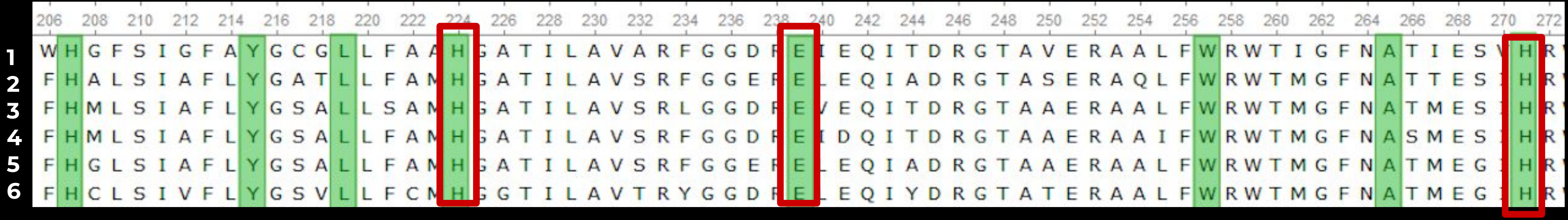
Histidine M200
Histidine M217
Glutamic acid M232

Tryptophan M250
Alanine M258
Histidine M264



Homology M

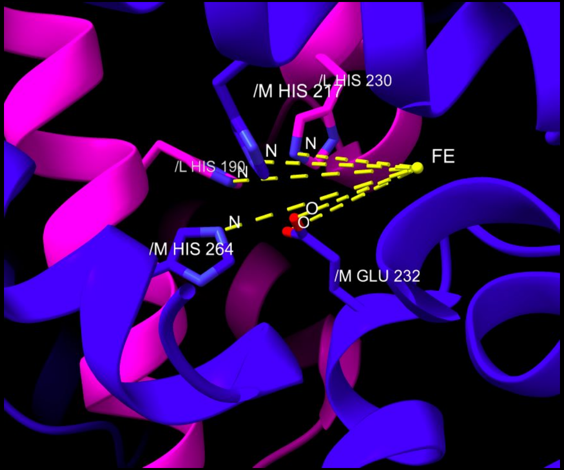
1 **Rhodopseudomonas viridis**
2 Rubrivivax_gelatinosus
3 Rhodospirillum_rubrum
4 Allochromatium_vinosum
5 Rhodobacter_sphaeroides
6 Roseobacter_dentrificans



	206 ... 272
1	W H G F S I G F A Y G C G L L F A A H G A T I L A V A R F G G D F E I E Q I T D R G T A V E R A A L F W R W T I G F N A T I E S V H R
2	F H A L S I A F L Y G A T L L F A M H G A T I L A V S R F G G E F E L E Q I A D R G T A S E R A Q L F W R W T M G F N A T T E S I H R
3	F H M L S I A F L Y G S A L L S A M H G A T I L A V S R L G G D F E V E Q I T D R G T A A E R A A L F W R W T M G F N A T M E S I H R
4	F H M L S I A F L Y G S A L L F A M H G A T I L A V S R F G G D F E I D Q I T D R G T A A E R A A I F W R W T M G F N A S M E S I H R
5	F H G L S I A F L Y G S A L L F A M H G A T I L A V S R F G G E F E L E Q I A D R G T A A E R A A L F W R W T M G F N A T M E G I H R
6	F H C L S I V F L Y G S V L L F C M H G G T I L A V T R Y G G D F E L E Q I Y D R G T A T E R A A L F W R W T M G F N A T M E G I H R

Histidine M200
Histidine M217
Glutamic acid M232

Tryptophan M250
Alanine M258
Histidine M264



Homology M

1 **Rhodopseudomonas viridis**
2 Rubrivivax_gelatinosus
3 Rhodospirillum_rubrum
4 Allochromatium_vinosum
5 Rhodobacter_sphaeroides
6 Roseobacter_dentrificans

```
  206 208 210 212 214 216 218 220 222 224 226 228 230 232 234 236 238 240 242 244 246 248 250 252 254 256 258 260 262 264 266 268 270 272
1 W H G F S I G F A Y G C G L L F A A H G A T I L A V A R F G G D R E I E Q I T D R G T A V E R A A L   W R W T I G F   A T I E S V H R
2 F H A L S I A F L Y G A T L L F A M H G A T I L A V S R F G G E R E L E Q I A D R G T A S E R A Q L   W R W T M G F   A T T E S I H R
3 F H M L S I A F L Y G S A L L S A M H G A T I L A V S R L G G D R E V E Q I T D R G T A A E R A A L   W R W T M G F   A T M E S I H R
4 F H M L S I A F L Y G S A L L F A M H G A T I L A V S R F G G D R E I D Q I T D R G T A A E R A A I   W R W T M G F   A S M E S I H R
5 F H G L S I A F L Y G S A L L F A M H G A T I L A V S R F G G E R E L E Q I A D R G T A A E R A A L   W R W T M G F   A T M E G I H R
6 F H C L S I V F L Y G S V L L F C M H G G T I L A V T R Y G G D R E L E Q I Y D R G T A T E R A A L   W R W T M G F   A T M E G I H R
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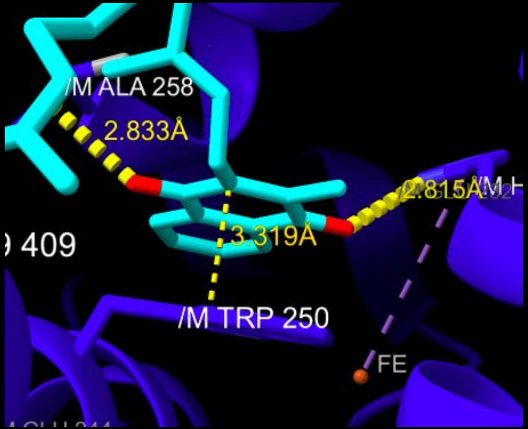
Histidine M200
Histidine M217
Glutamic acid M232

Tryptophan M250
Alanine M258
Histidine M264



Homology L

1 **Rhodopseudomonas viridis**
2 Allochromatium vinosum
3 Rubrivivax gelatinosus
4 Rhodopseudomonas palustris
5 Rhodobacter spheroides
6 Roseobacter dentrificans

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  110   112   114   116   118   120   122   124   126   128   130   132   134   136   138   140   142   144   146   148   150   152   154   156   158   160   162   164   166   168   170   172   174   176   178   180   182
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2 L R E Y E I C R K L G I G F H I P F A F A F A I G A Y L V L V V V R P I L M G A W G H G F P Y G I L S H L D W V S N V G Y Q F L H F H Y N P A H M
3 L R E Y E I C R K L G M Q Y H V P I A F S F A I L A Y V T L V V I R P I L M G A W G H G F P Y G I F S H L D W V S N V G Y Q Y L H F H Y N P A H M
4 L R E Y E I C R K L G I G F H V P F A F S F A I F A Y V T L V V I R P V L M G S W S Y G F P Y G I F T H L D W V S N T G Y S Y G Q F H Y N P A H M
5 L R E Y E I C R K L G I G Y H I P F A F A F A I L A Y L T L V L F R P V M M G A W G Y A F P Y G I W T H L D W V S N T G Y T Y G N F H Y N P A H M
6 L R E Y E I C R K L G M G Y H V P F G F A A A I I A Y M T L V I F R P L L M G A W G H G F P Y G I F S H L D W V S N V G Y A Y L H F H Y N P A H M
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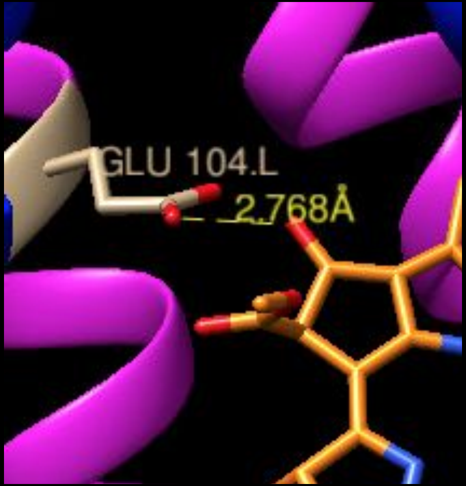
Glutamic L104
Tyrosine L162
Histidine L168
Histidine L173
Histidine L190
Asparatic L210

Glutamic L212
Aspartic L213
Phenylalanine L216
Serine L223
Glycine L225
Histidine L230



Homology L

1 **Rhodopseudomonas viridis**
2 Allochromatium vinosum
3 Rubrivivax gelatinosus
4 Rhodopseudomonas palustris
5 Rhodobacter spheroides
6 Roseobacter dentrificans

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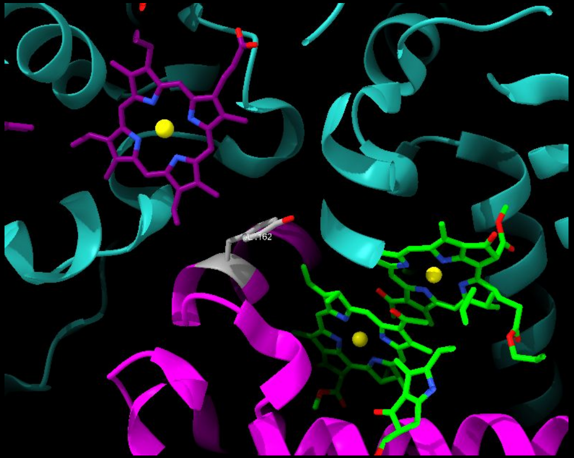
2 L R E V E I C R K L G I G F H I P F A F A F A I G A Y L V L V V V R P I L M G A W G H G F P Y G I L S H L D W V S N V G Y Q F L H F H Y N P A H M
3 L R E V E I C R K L G M Q Y H V P I A F S F A I L A Y V T L V V I R P I L M G A W G H G F P Y G I F S H L D W V S N V G Y Q Y L H F H Y N P A H M
4 L R E V E I C R K L G I G F H V P F A F S F A I F A Y V T L V V I R P V L M G S W S Y G F P Y G I F T H L D W V S N T G Y S Y G Q F H Y N P A H M
5 L R E V E I C R K L G I G Y H I P F A F A F A I L A Y L T L V L F R P V M M G A W G Y A F P Y G I W T H L D W V S N T G Y T Y G N F H Y N P A H M
6 L R E V E I C R K L G M G Y H V P F G F A A A I I A Y M T L V I F R P L L M G A W G H G F P Y G I F S H L D W V S N V G Y A Y L H F H Y N P A H M
```

Glutamic L104
Tyrosine L162
Histidine L168
Histidine L173
Histidine L190
Asparatic L210

Glutamic L212
Aspartic L213
Phenylalanine L216
Serine L223
Glycine L225
Histidine L230



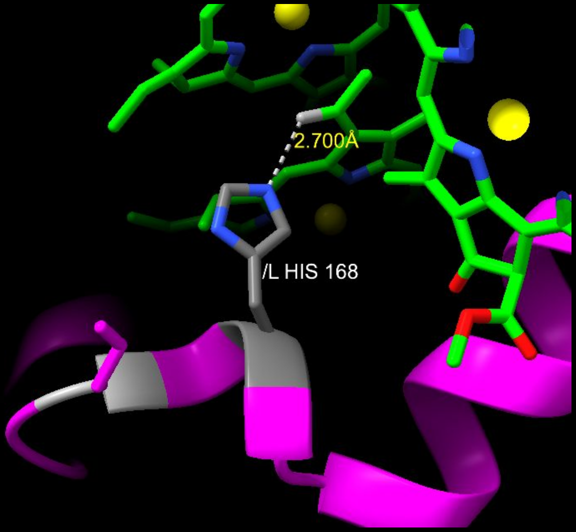
Homology L

1 **Rhodopseudomonas viridis**
2 Allochromatium vinosum
3 Rubrivivax gelatinosus
4 Rhodopseudomonas palustris
5 Rhodobacter spheroides
6 Roseobacter dentrificans

```
1 LREVEISRKLGIGWHVPLAFCVPIFMFCVLQVFRPLLLGSWGHAFPYGILSHLDWVNNFGYQYLNWHYNPGHM
2 LREVEICRKLGIGFHIPFAFAFAIGAYLVLVVVRPILMGAWGHGFPYGILSHLDWVSNVGYQFLHFHYNPAHM
3 LREVEICRKLGMQYHVPIAFSFAILAYVTLVVIRPILMGAWGHGFPYGIFSHLDWVSNVGYQYLHFHYNPAHM
4 LREVEICRKLGIGFHVPFAFSFAIFAYVTLVVIRPVLMGSWSYGFPYGIFTHLDWVSNTGYSYGQFHYNPAHM
5 LREVEICRKLGIGYHIPFAFAFAILAYLTLVLFRPVMMGAWGYAFPYGIWTHLDWVSNTGYTYGNFHYNPAHM
6 LREVEICRKLGMGYHVPFGFAAAIIAYMTLVIFRPLLMGAWGHGFPYGIFSHLDWVSNVGYAYLHFHYNPAHM
```

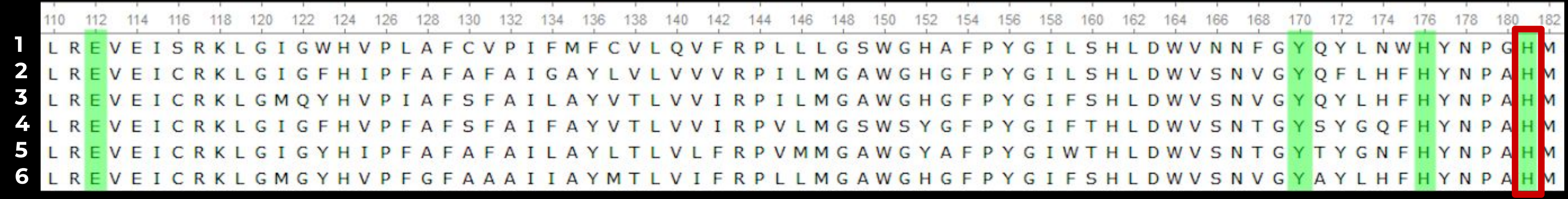
Glutamic L104
Tyrosine L162
Histidine L168
Histidine L173
Histidine L190
Asparatic L210

Glutamic L212
Aspartic L213
Phenylalanine L216
Serine L223
Glycine L225
Histidine L230



Homology L

1 **Rhodopseudomonas viridis**
2 Allochromatium vinosum
3 Rubrivivax gelatinosus
4 Rhodopseudomonas palustris
5 Rhodobacter spheroides
6 Roseobacter dentrificans



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2 L R E V E I C R K L G I G F H I P F A F A F A I G A Y L V L V V V R P I L M G A W G H G F P Y G I L S H L D W V S N V G Y Q F L H F H Y N P A H M
3 L R E V E I C R K L G M Q Y H V P I A F S F A I L A Y V T L V V I R P I L M G A W G H G F P Y G I F S H L D W V S N V G Y Q Y L H F H Y N P A H M
4 L R E V E I C R K L G I G F H V P F A F S F A I F A Y V T L V V I R P V L M G S W S Y G F P Y G I F T H L D W V S N T G Y S Y G Q F H Y N P A H M
5 L R E V E I C R K L G I G Y H I P F A F A F A I L A Y L T L V L F R P V M M G A W G Y A F P Y G I W T H L D W V S N T G Y T Y G N F H Y N P A H M
6 L R E V E I C R K L G M G Y H V P F G F A A A I I A Y M T L V I F R P L L M G A W G H G F P Y G I F S H L D W V S N V G Y A Y L H F H Y N P A H M
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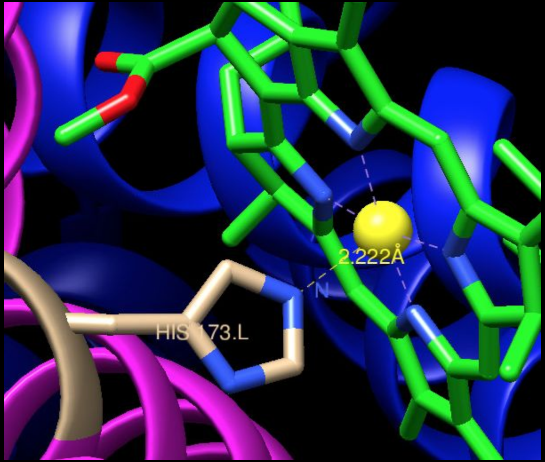
Glutamic L104	Glutamic L212
Tyrosine L162	Aspartic L213
Histidine L168	Phenylalanine L216
Histidine L173	Serine L223
Histidine L190	Glycine L225
Asparatic L210	Histidine L230

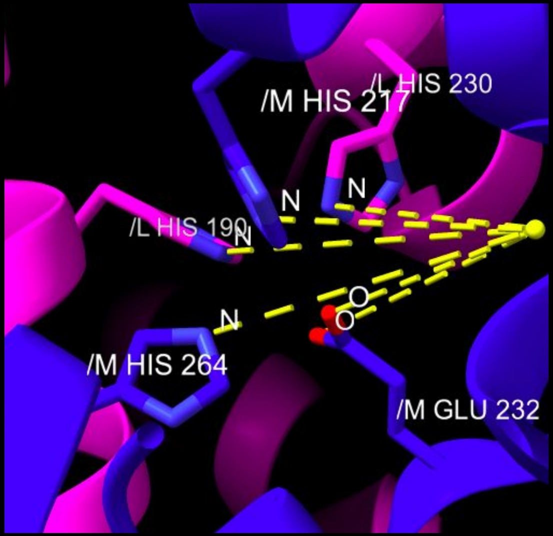


Homology L

1 **Rhodopseudomonas viridis**
2 Allochromatium vinosum
3 Rubrivivax gelatinosus
4 Rhodopseudomonas palustris
5 Rhodobacter spheroides
6 Roseobacter dentrificans

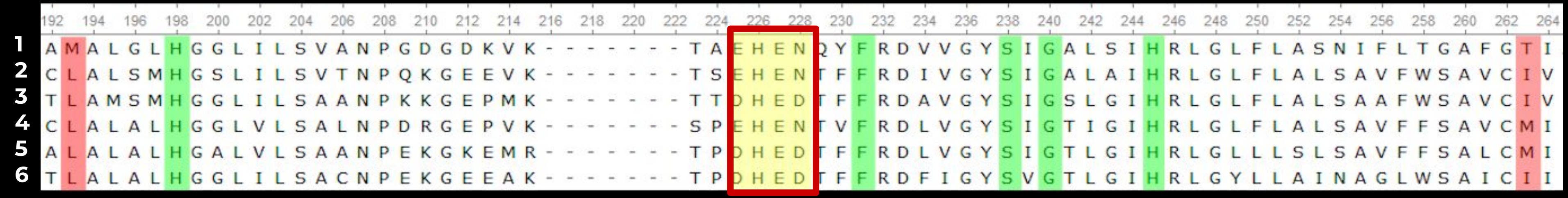
```
  192 194 196 198 200 202 204 206 208 210 212 214 216 218 220 222 224 226 228 230 232 234 236 238 240 242 244 246 248 250 252 254 256 258 260 262 264
1 A M A L G L H G G L I L S V A N P G D G D K V K - - - - - - - - T A E H E N Q Y F R D V V G Y S I G A L S I H R L G L F L A S N I F L T G A F G T I
2 C L A L S M H G S L I L S V T N P Q K G E E V K - - - - - - - - T S E H E N T F F R D I V G Y S I G A L A I H R L G L F L A L S A V F W S A V C I V
3 T L A M S M H G G L I L S A A N P K K G E P M K - - - - - - - - T T D H E D T F F R D A V G Y S I G S L G I H R L G L F L A L S A A F W S A V C I V
4 C L A L A L H G G L V L S A L N P D R G E P V K - - - - - - - - S P E H E N T V F R D L V G Y S I G T I G I H R L G L F L A L S A V F F S A V C M I
5 A L A L A L H G A L V L S A A N P E K G K E M R - - - - - - - - T P D H E D T F F R D L V G Y S I G T L G I H R L G L L L S L S A V F F S A L C M I
6 T L A L A L H G G L I L S A C N P E K G E E A K - - - - - - - - T P D H E D T F F R D F I G Y S V G T L G I H R L G Y L L A I N A G L W S A I C I I
```

Glutamic L104	Glutamic L212
Tyrosine L162	Aspartic L213
Histidine L168	Phenylalanine L216
Histidine L173	Serine L223
Histidine L190	Glycine L225
Asparatic L210	**Histidine L230**



Homology L

1 **Rhodopseudomonas viridis**
2 Allochromatium vinosum
3 Rubrivivax gelatinosus
4 Rhodopseudomonas palustris
5 Rhodobacter spheroides
6 Roseobacter dentrificans



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2 CLALSMHGSLILSVTNPQKGEEVK-------TSEHENTFFRDIVGYSIGALAIHRLGLFLALSAVFWSAVCIV
3 TLAMSMHGGLILSAANPKKGEPMK-------TTDHEDTFFRDAVGYSIGSLGIHRLGLFLALSAAFWSAVCIV
4 CLALALHGGLVLSALNPDRGEPVK-------SPEHENTVFRDLVGYSIGTIGIHRLGLFLALSAVFFSAVCMI
5 ALALALHGALVLSAANPEKGKEMR-------TPDHEDTFFRDLVGYSIGTLGIHRLGLLLSLSAVFFSALCMI
6 TLALALHGGLILSACNPEKGEEAK-------TPDHEDTFFRDFIGYSVGTLGIHRLGYLLAINAGLWSAICII
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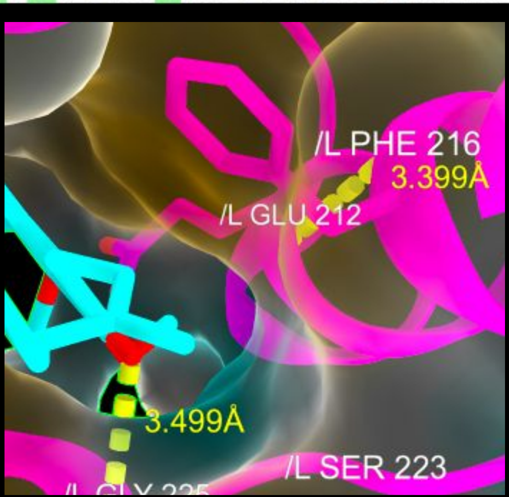
Glutamic L104
Tyrosine L162
Histidine L168
Histidine L173
Histidine L190
Asparatic L210

Glutamic L212
Aspartic L213
Phenylalanine L216
Serine L223
Glycine L225
Histidine L230



Homology L

1 **Rhodopseudomonas viridis**
2 Allochromatium vinosum
3 Rubrivivax gelatinosus
4 Rhodopseudomonas palustris
5 Rhodobacter spheroides
6 Roseobacter dentrificans

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  192 194 196 198 200 202 204 206 208 210 212 214 216 218 220 222 224 226 228 230 232 234 236 238 240 242 244 246 248 250 252 254 256 258 260 262 264
1 A M A L G L H G G L I L S V A N P G D G D K V K - - - - - - - T A E H E N Q Y F R D V V G Y S I G A L S I H R L G L F L A S N I F L T G A F G T I
2 C L A L S M H G S L I L S V T N P Q K G E E V K - - - - - - - T S E H E N T F F R D I V G Y S I G A L A I H R L G L F L A L S A V F W S A V C I V
3 T L A M S M H G G L I L S A A N P K K G E P M K - - - - - - - T T D H E D T F F R D A V G Y S I G S L G I H R L G L F L A L S A A F W S A V C I V
4 C L A L A L H G G L V L S A L N P D R G E P V K - - - - - - - S P E H E N T V F R D L V G Y S I G T I G I H R L G L F L A L S A V F F S A V C M I
5 A L A L A L H G A L V L S A A N P E K G K E M R - - - - - - - T P D H E D T F F R D L V G Y S I G T L G I H R L G L L L S L S A V F F S A L C M I
6 T L A L A L H G G L I L S A C N P E K G E E A K - - - - - - - T P D H E D T F F R D F I G Y S V G T L G I H R L G Y L L A I N A G L W S A I C I I
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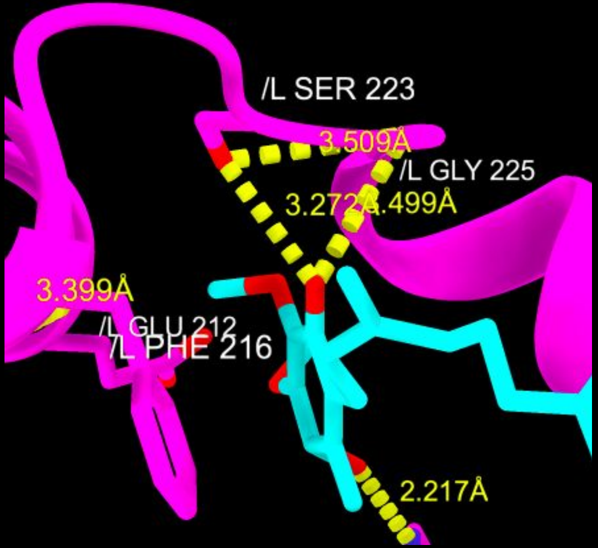
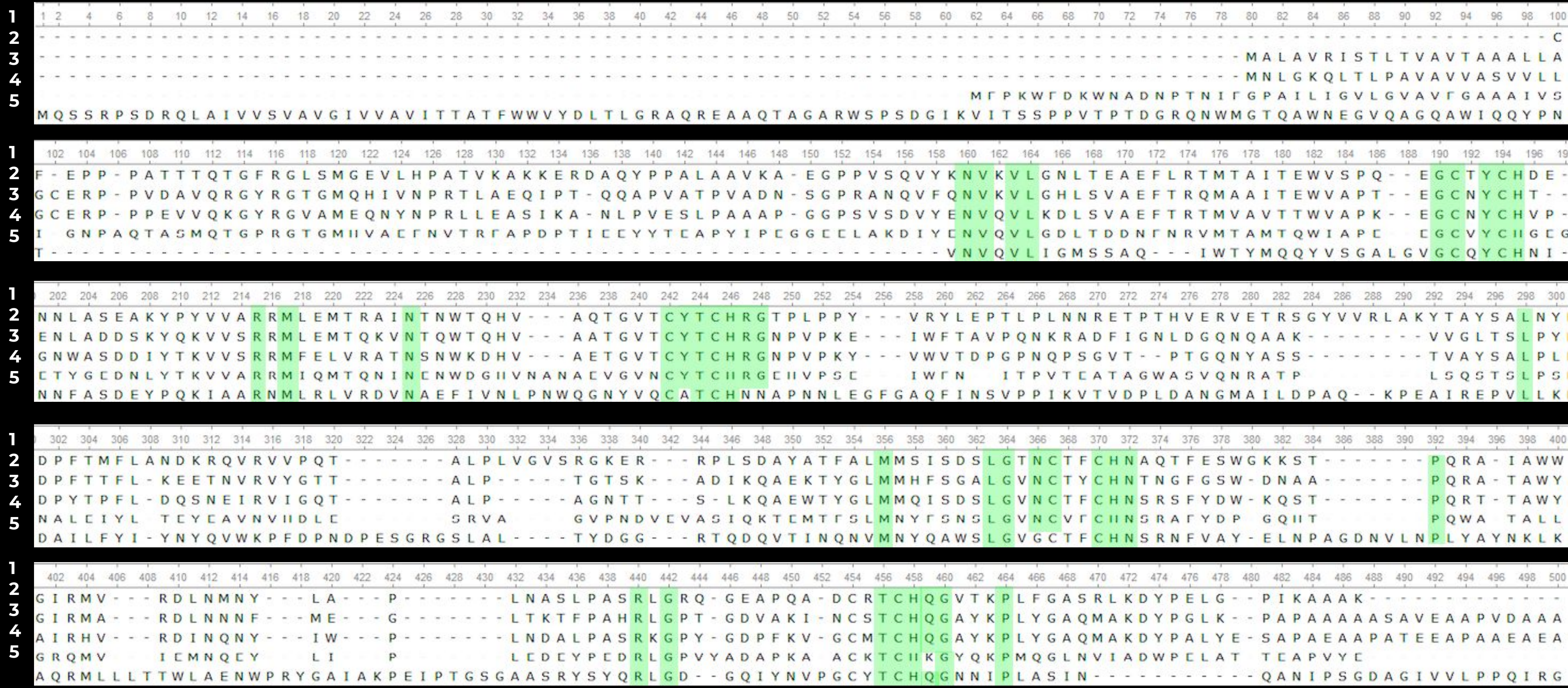
Glutamic L104	Glutamic L212
Tyrosine L162	Aspartic L213
Histidine L168	**Phenylalanine L216**
Histidine L173	**Serine L223**
Histidine L190	**Glycine L225**
Asparatic L210	Histidine L230



Homology C

1 Chain_C
2 Rubrivivax gelatinosus
3 Allochromatium vinosum
4 Roseobacter denitrificans
5 Chloroflexus aurantiacus



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1  1 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78 80 82 84 86 88 90 92 94 96 98 100
2  ---------------------------------------------------------------------------------------------------C
3  -------------------------------------------------------------------------------MALAVRISTLTVAVTAAALLA
4  -------------------------------------------------------------------------------MNLGKQLTLPAVAVVASVVLL
5                                                               MFPKWFDKWNADNPTNIFGPAILIGVLGVAVFGAAAIVS
   MQSSRPSDRQLAIVVSVAVGIVVAVITTATFWWVYDLTLGRAQREAAQTAGARWSPSDGIKVITSSPPVTPTDGRQNWMGTQAWNEGVQAGQAWIQQYPN

1  102 104 106 108 110 112 114 116 118 120 122 124 126 128 130 132 134 136 138 140 142 144 146 148 150 152 154 156 158 160 162 164 166 168 170 172 174 176 178 180 182 184 186 188 190 192 194 196 19
2  F-EPP-PATTTQTGFRGLSMGEVLHPATVKAKKERDAQYPPALAAVKA-EGPPVSQVYKNVKVLGNLTEAEFLRTMTAITEWVSPQ--EGCTYCHDE-
3  GCERP-PVDAVQRGYRGTGMQHIVNPRTLAEQIPT-QQAPVATPVADN-SGPRANQVFQNVKVLGHLSVAEFTRQMAAITEWVAPT--EGCNYCHT--
4  GCERP-PPEVVQKGYRGVAMEQNYNPRLLEASIKA-NLPVESLPAAAP-GGPSVSDVYENVQVLKDLSVAEFTRTMVAVTTWVAPK--EGCNYCHVP-
5  I GNPAQTASMQTGPRGTGMHVAEFNVTRFAPDPTIEEYYTEAPYIPEGGEELAKDIYENVQVLGDLTDDNFNRVMTAMTQWIAPE  EGCVYCHGEG
   T----------------------------------------------------------VNVQVLIGMSSAQ---IWTYMQQYVSGALGVGCQYCHNI-

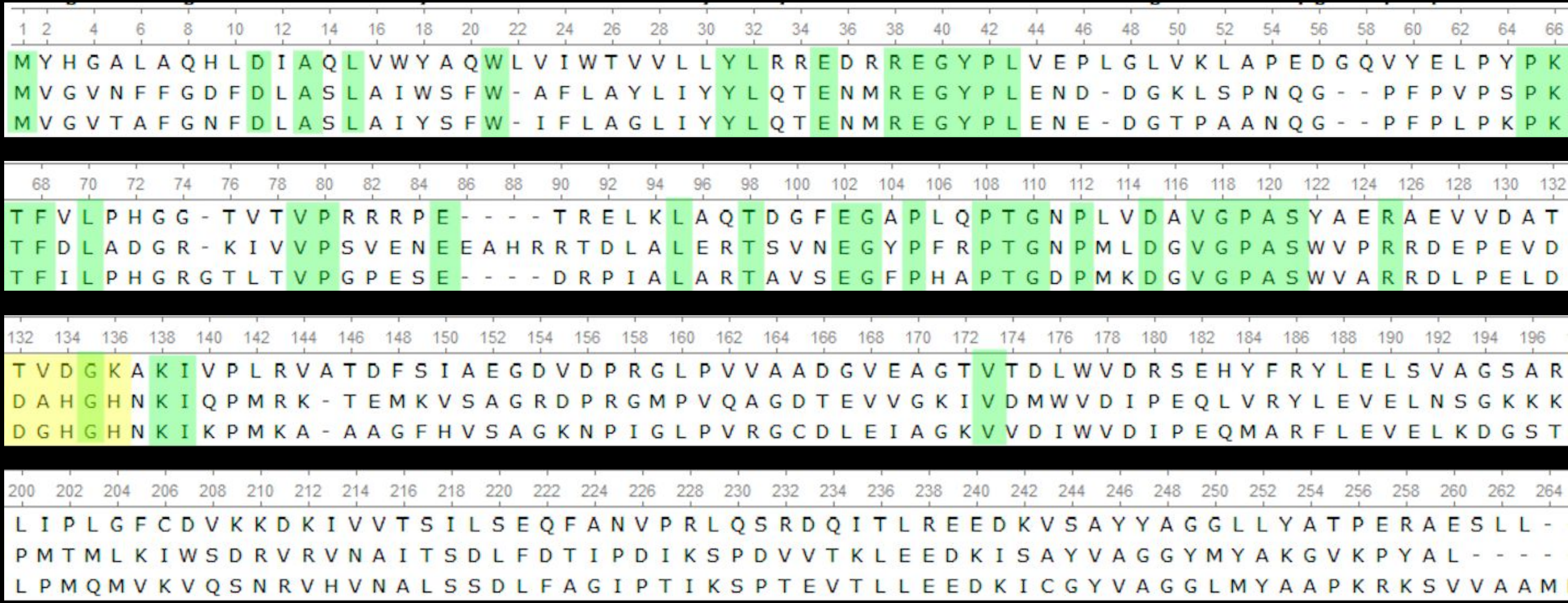
1  202 204 206 208 210 212 214 216 218 220 222 224 226 228 230 232 234 236 238 240 242 244 246 248 250 252 254 256 258 260 262 264 266 268 270 272 274 276 278 280 282 284 286 288 290 292 294 296 298 300
2  NNLASEAKYPYVVARRMLEMTRAINTNWTQHV---AQTGVTCYTCHRGTPLPPY---VRYLEPTLPLNNRETPTHVERVETRSGYVVRLAKYTAYSALNY
3  ENLADDSKYQKVVSRRMLEMTQKVNTQWTQHV---AATGVTCYTCHRGNPVPKE---IWFTAVPQNKRADFIGNLDGQNQAAK--------VVGLTSLPY
4  GNWASDDIYTKVVSRRMFELVRATNSNWKDHV---AETGVTCYTCHRGNPVPKY---VWVTDPGPNQPSGVT--PTGQNYASS--------TVAYSALPL
5  ETYGEDNLYTKVVARRMIQMTQNINENWDGHVNANAEVGVNCYTCHRGEHVPSE   IWFN  ITPVTEATAGWASVQNRATP        LSQSTSLPS
   NNFASDEYPQKIAARNMLRLVRDVNAEFIVNLPNWQGNYVQCATCHNNAPNNLEGFGAQFINSVPPIKVTVDPLDANGMAILDPAQ--KPEAIREPVLLK

1  302 304 306 308 310 312 314 316 318 320 322 324 326 328 330 332 334 336 338 340 342 344 346 348 350 352 354 356 358 360 362 364 366 368 370 372 374 376 378 380 382 384 386 388 390 392 394 396 398 400
2  DPFTMFLANDKRQVRVVPQT--------ALPLVGVSRGKER---RPLSDAYATFALMMSISDSLGTNCTFCHNAQTFESWGKKST--------PQRA-IAWW
3  DPFTTFL-KEETNVRVYGTT--------ALP-----TGTSK---ADIKQAEKTYGLMMHFSGALGVNCTYCHNTNGFGSW-DNAA--------PQRA-TAWY
4  DPYTPFL-DQSNEIRVIGQT--------ALP-----AGNTT---S-LKQAEWTYGLMMQISDSLGVNCTFCHNSRSFYDW-KQST--------PQRT-TAWY
5  NALEIYL TEYEAVNVHDLE        SRVA     GVPNDVEVASIQKTEMTFSLMNYFSNSLGVNCVFCHNSRAFYDP GQHT        PQWA TALL
   DAILFYI-YNYQVWKPFDPNDPESGRGSLAL----TYDGG---RTQDQVTINQNVMNYQAWSLGVGCTFCHNSRNFVAY-ELNPAGDNVLNPLYAYNKLK

1  402 404 406 408 410 412 414 416 418 420 422 424 426 428 430 432 434 436 438 440 442 444 446 448 450 452 454 456 458 460 462 464 466 468 470 472 474 476 478 480 482 484 486 488 490 492 494 496 498 500
2  GIRMV---RDLNMNY---LA---P--------LNASLPASRLGRQ-GEAPQA-DCRTCHQGVTKPLFGASRLKDYPELG--PIKAAAK-------------
3  GIRMA---RDLNNNF---ME---G--------LTKTFPAHRLGPT-GDVAKI-NCSTCHQGAYKPLYGAQMAKDYPGLK--PAPAAAAASAVEAAPVDAAA
4  AIRHV---RDINQNY---IW---P--------LNDALPASRKGPY-GDPFKV-GCMTCHQGAYKPLYGAQMAKDYPALYE-SAPAEAAPATEEAPAAEAEA
5  GRQMV   IEMNQEY   LI   P        LEDEYPEDRLGPVYADAPKA ACKTCHKGYQKPMQGLNVIADWPELAT TEAPVYE
   AQRMLLLTTWLAENWPRYGAIAKPEIPTGSGAASRYSYQRLGD--GQIYNVPGCYTCHQGNNIPLASIN-----------QANIPSGDAGIVVLPPQIRG
```

Homology H

1 Chain_H
2 Rhodobacter capsulatus
3 Rhodobacter sphaeroides



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3 MVGVTAFGNFDLASLAIYSFW-IFLAGLIYYLQTENMREGYPLENE-DGTPAANQG--PFPLPKPK

1 TFVLPHGG-TVTVPRRRPE----TRELKLAQTDGFEGAPLQPTGNPLVDAVGPASYAERAEVVDAT
2 TFDLADGR-KIVVPSVENEEAHRRTDLALERTSVNEGYPFRPTGNPMLDGVGPASWVPRRDEPEVD
3 TFILPHGRGTLTVPGPESE----DRPIALARTAVSEGFPHAPTGDPMKDGVGPASWVARRDLPELD

1 TVDGKAKIVPLRVATDFSIAEGDVDPRGLPVVAADGVEAGTVTDLWVDRSEHYFRYLELSVAGSAR
2 DAHGHNKIQPMRK-TEMKVSAGRDPRGMPVQAGDTEVVGKIVDMWVDIPEQLVRYLEVELNSGKKK
3 DGHGHNKIKPMKA-AAGFHVSAGKNPIGLPVRGCDLEIAGKVVDIWVDIPEQMARFLEVELKDGST

1 LIPLGFCDVKKDKIVVTSILSEQFANVPRLQSRDQITLREEDKVSAYYAGGLLYATPERAESLL-
2 PMTMLKIWSDRVRVNAITSDLFDTIPDIKSPDVVTKLEEDKISAYVAGGYMYAKGVKPYAL----
3 LPMQMVKVQSNRVHVNALSSDLFAGIPTIKSPTEVTLLEEDKICGYVAGGLMYAAPKRKSVVAAM
```

CONCLUSIONS

Purple bacteria are important because they can be used in **processes of water decontamination**

Each subunit has a **specific structure** that allows it to perform its **function**

Interactions between subunits and cofactors allow the **electron transport** and **define its path**

The photoreaction center from *Rhodopseudomona viridis* and Photosystem II might have a **common ancestor**

The **L and M** subunits are **more conserved among different species** than C and H subunits

THANK YOU FOR YOUR ATTENTION!

Do you have any questions?

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BIBLIOGRAPHY

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PEM QUESTIONS

QUESTIONS

1. Select the **CORRECT** option:

- a) *Blastochloridis viridis* also known as *Rhodopseudomonas viridis* is a purple sulfur bacteria which deposits S^0 inside the cell.
- b) The core subunit of the photosynthetic reaction center is formed by 11 spanning helices, 6 in the M chain and 5 in the L chain.
- c) The photosynthetic reaction center has fifteen co-factors, one of which is a non-heme iron.
- d) Chains L and C have a lot of non-polar residues because they are transmembrane.
- e) The H subunit has a globular domain and does not have any transmembrane helix.

2. Which of the following statements about the *Rhodopseudomonas viridis* photosynthetic reaction center **cofactors** are **TRUE**?

1. The four heme groups are connected to cytochrome cysteines through thioether bonds.
2. The carotenoid is in contact with the accessory bacteriochlorophyll b of chain M.
3. The bacteriochlorophyll b is formed by four pyrrole rings: a special pair and an accessory chain.
4. The quinones are very far from the non-heme iron.

- **a) 1, 2, 3**
- b) 1, 3
- c) 2, 4
- d) 1, 2, 3, 4
- e) 4

QUESTIONS

3. Which statement about the **bacteriochlorophyll b special pair** is **FALSE**:

a) The special pair are arranged with a nearly perfect twofold symmetry.
b) Transmembrane helices of subunits L and M contribute to maintain the twofold symmetry.
c) a and b are correct
d) Histidines L173 and M200 act as a ligand to the special pair Mg^{2+} ions.
e) All options are correct

4. Select the **CORRECT** option about the **light-harvesting complex** of the *Rhodopseudomonas viridis* photosynthetic reaction center:

1. The light harvesting complex is not involved in the energy transfer to the reaction center.
2. Has an absorption maximum at 680 nm.
3. It consists of α- and β- apoproteins bound to bacteriochlorophyll and carotenoid covalenlty.
4. The light harvesting complex is associated with the reaction center forming a polymeric ring-like structure around it.

a) 1,2,3
b) 1,3
c) 2,4
d) 4
e) 1,2,3,4

QUESTIONS

5. Which of the following statements is **TRUE**?

a) Glutamic acid L104 is conserved in all currently known sequences of reaction centre L-subunits from purple bacteria
b) The photosynthetic reaction center from *Blastochloris viridis* is related to the photosystem II from plants.
c) a and b are true.
d) The core complex subunits L and M have 60% structural homology.
e) All are true.

6. Which of the following statements regarding **photoexcitation** is/are **TRUE**?

a) The photosynthetic reaction in *Rhodopseudomonas viridis* is a cyclic electron transport.
b) The electron follows an unidirectional pathway in the photosynthetic reaction center.
c) Both a and b are correct.
d) The photosynthetic reaction starts at chain H.
e) All the statements are correcT

7. Which of these statements about **quinones** redox processes is **TRUE**?

a) Quinone A reduces Quinone B to QB- and then quinone B is protonated to QBH.
b) Quinone A does not participate in the reduction of quinone B.
c) Quinone B is transported to the cytochrome and then is protonated.
d) Quinone A reduces quinone B two times to a fully reduced QB-- and then it is twicely protonated to QBH_2.
e) Quinone A is in direct contact with the cytoplasm to be easily protonated.

QUESTIONS

8. Which of these statements about **important residues** in photosynthetic function are **TRUE**?

a) Tyrosine 162 is located between the special pair and the closest heme group (HE3) of the cytochrome, and may play a role during reduction of P+ by the cytochrome.
b) Glutamic acid L104 is conserved in all currently known sequences of reaction centre L-subunits from purple bacteria and is involved in the protonation of QB.
c) Both a and b are correct
d) Tryptophan M250 is an especially noteworthy aromatic residue, whose side chain forms a bridge between BPL and the next electron acceptor, QA- .
e) All the statements are correct.

9. Select the correct answer about the **evolutionary theory** of the photosynthetic reaction center of *Rhodopseudomonas viridis*:

a) It is thought that the ancestor of photosynthetic reaction centers from plants and bacteria was already heterodimeric.
b) Photosystem II from plants and Photosynthetic reaction center of purple bacteria do not share a similar pattern in their core complex.
c) L and M subunits from the photosynthetic reaction center of *Rhodopseudomonas viridis* are homologous to D1 and D2 subunits from the photosystem II of plants.
d) The histidine residues that coordinate the special pair of bacteriochlorophyll II molecules are found in a different relative position with respect to photosystem II from plants.
e) Bacteria and plants photosynthetic reaction center do not share a common ancestor.

QUESTIONS

10. Select the **FALSE** option:
    1. The subunit H has a transmembrane helix in its N-terminal segment which corresponds to the eleventh transmembrane helix from the core complex.
    2. The 4 heme groups are placed in the H subunit
    3. Histidines 173L and 200M are bound to a H_2O molecule which in turn is bound to the accessory bacteriochlorophyll b through hydrogen bonds.
    4. The side chains of the accessory bacteriochlorophyll b help to maintain the symmetry.

a) 1,2,3
b) 1,3
c) 2,4
d) 4
e) 1,2,3,4