

REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: P02945

User: siqipian2008@outlook.com

Designing code: QTY

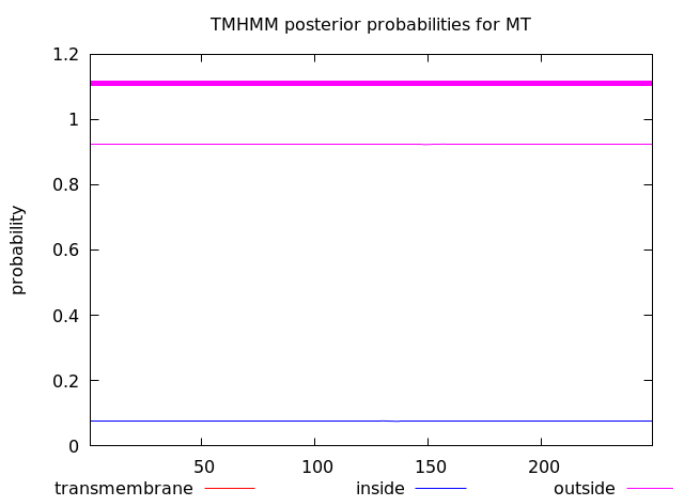
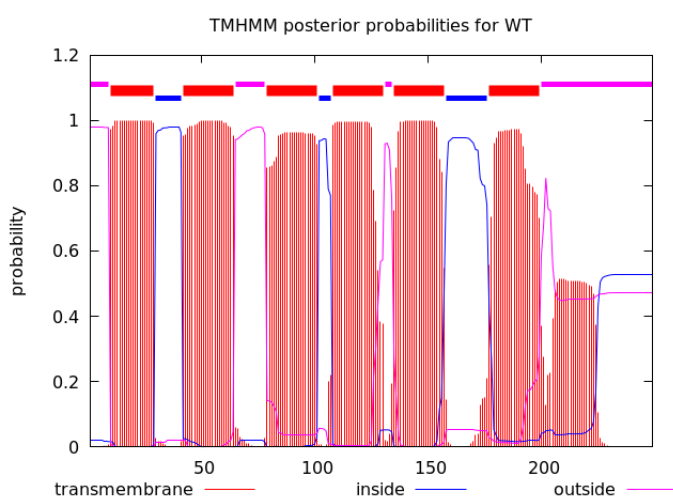
Length of protein sequence: 249

Number of modified TM regions: 7

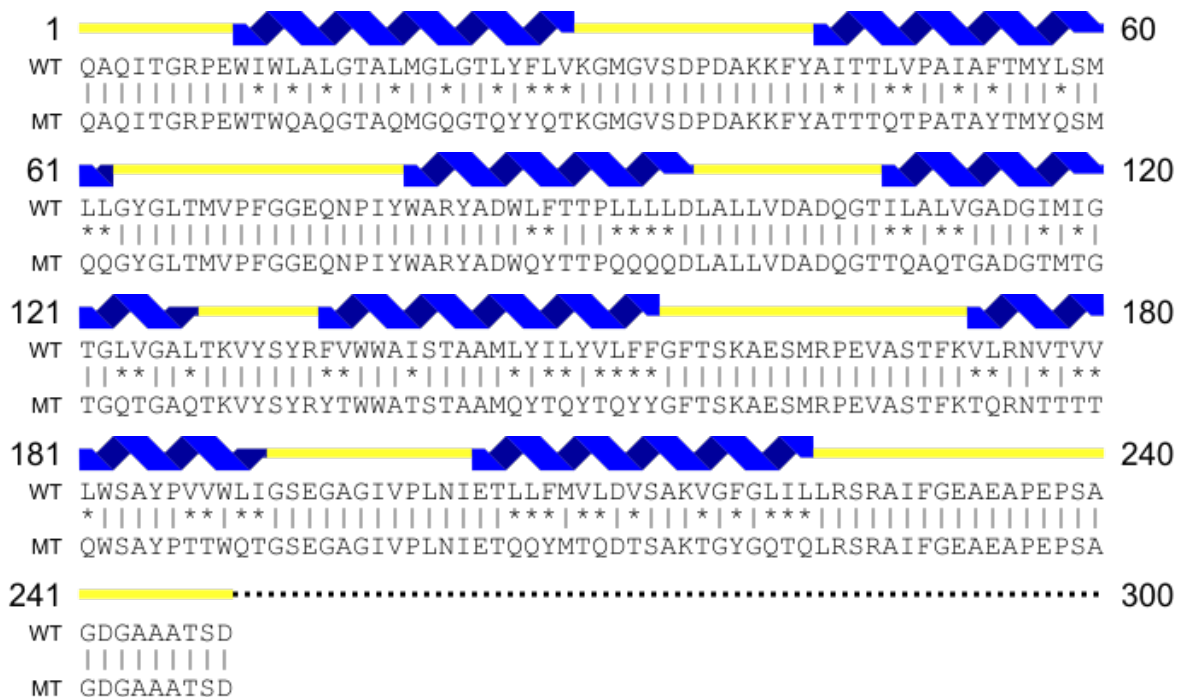
2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	4.75	26.9157	0.7080	/	/
MT	4.75	27.4018	-0.8071	46.67	25.30

3. Comparison of TM prediction:



4. Comparison of sequences:



5. Detailed comparison of TM regions:

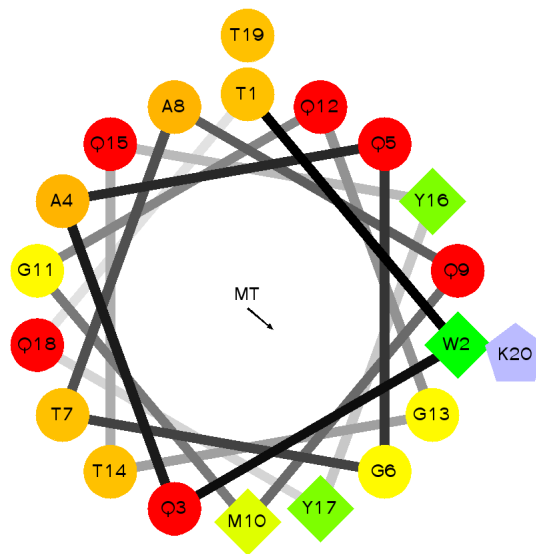
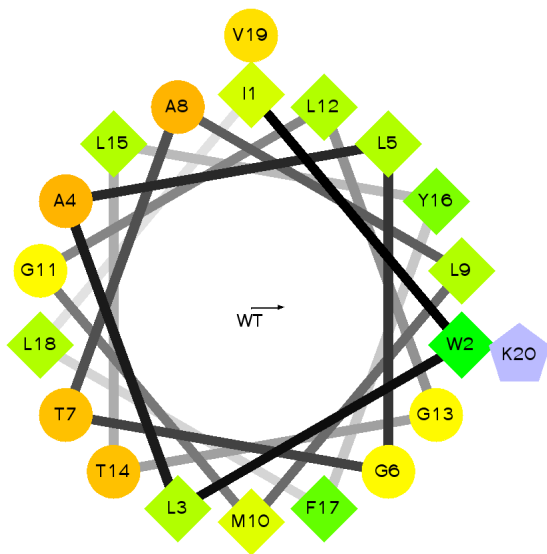
TM1

AA sequence comparison:

TM1-wt: IWLALGTALMGLGTLYFLVK
* | * | * | | * | | * | | * | * * * |
TM1-mt: TWOAOGTAOMGOGTOYYOTK

Alpha-helix prediction comparison:

TM1-wt: HHHHHHHHHHHHHHHHHHHHHHHHHH
| | | | | | | | | * * * * *
TM1-mt: HHHHHHHHHHHHHHHHHHEEEEEEE



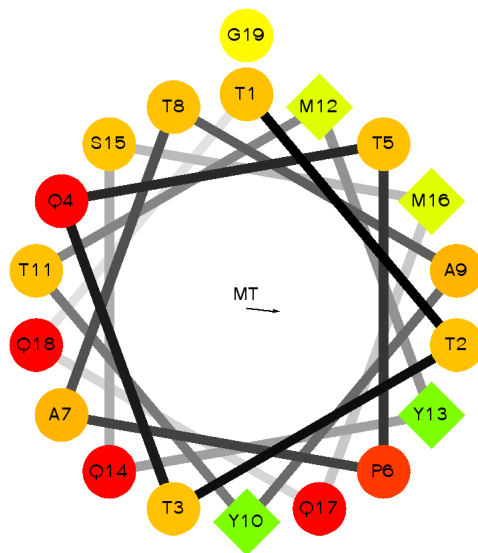
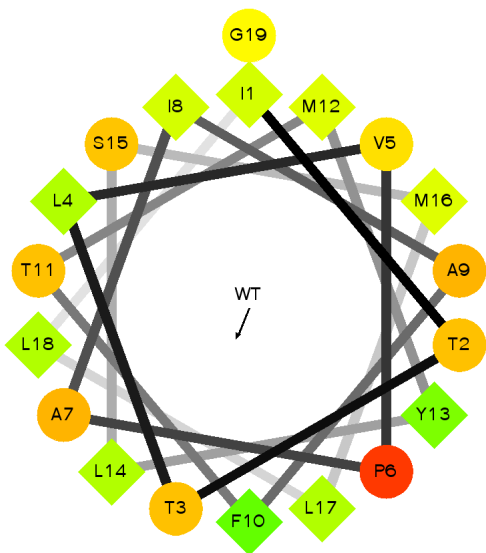
TM2

AA sequence comparison:

TM2-wt: ITTLVPAIAFTMYLSMLLG
* || ** | | * | * | | | * | | ** |
TM2-mt: TTTQTPATAYTMYQSMQQG

Alpha-helix prediction comparison:

TM2-wt: EEECCHHHHHHHHHHHHHHHC
 TM2-mt: EEECCHHHHHHHHHHHHHHHC



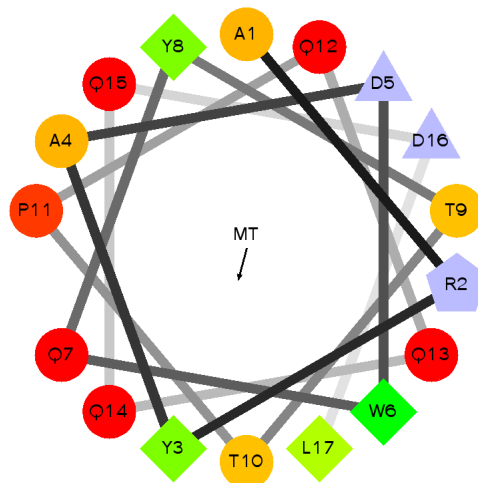
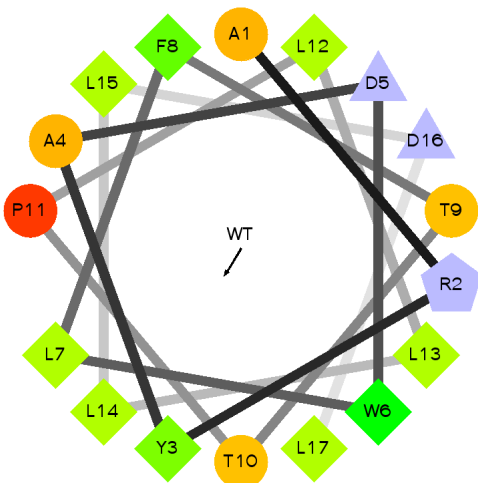
TM3

AA sequence comparison:

TM3-wt: ARYADWLF^{TT}PLLLLLDL
 ||| ||| ** ||| **** |||
TM3-mt: ARYADWQY^{TT}PQQQQDL

Alpha-helix prediction comparison:

TM3-wt: HHHHHHEECCHHHHHH
* || *** | | | | |
TM3-mt: EHHCCCEECCHHHHHH



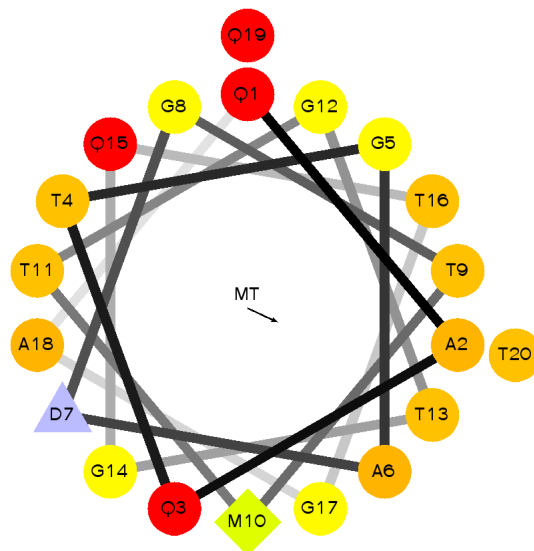
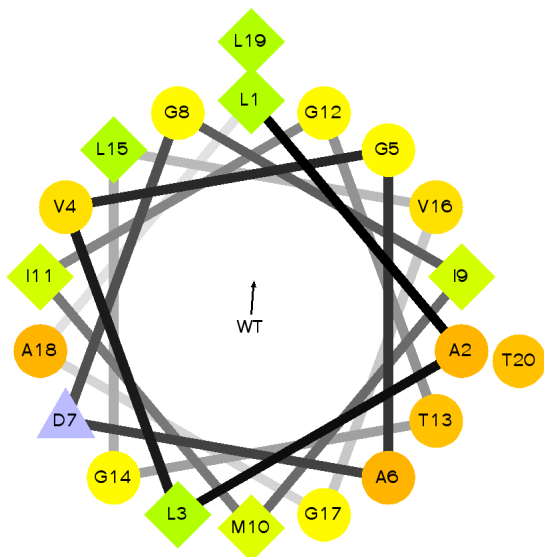
TM4

AA sequence comparison:

TM4-wt: LALVGADGIMIGTGLVGALT
 *|**|||*|*||**|*|
 TM4-mt: QAQTGADGTMTGTGQTGAQT

Alpha-helix prediction comparison:

TM4-wt: HHHHHHHHHHHHHHHHHHHHHHH
 |||||
 TM4-mt: HHHHHHHHHHHHHHHHHHHHHH



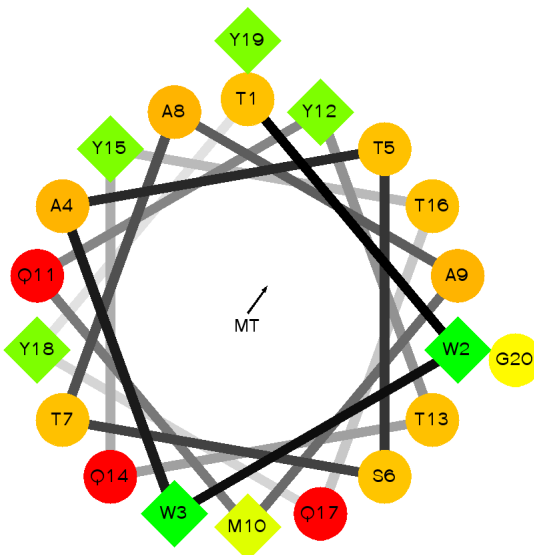
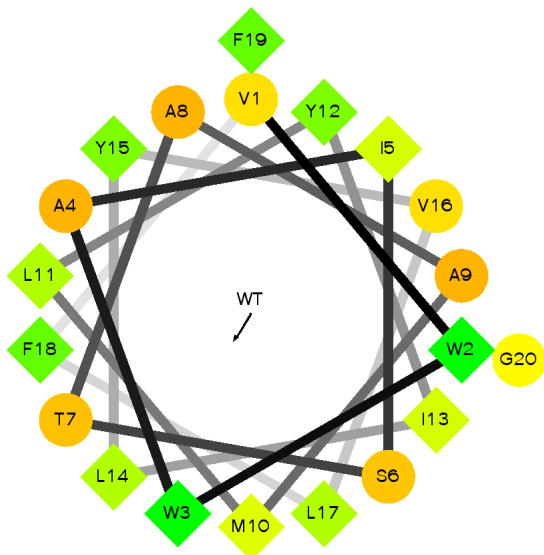
TM5

AA sequence comparison:

TM5-wt: VWWAISTAAMLYILYVLFFG
 ||||||*||**||**||
 TM5-mt: TWWATSTAAMQYTQYTQYYG

Alpha-helix prediction comparison:

TM5-wt: HHHHHHHHHHHHHHHHHHHHHHH
 |||||
 TM5-mt: HHHHHHHHHHHHHHHHHHHHHH



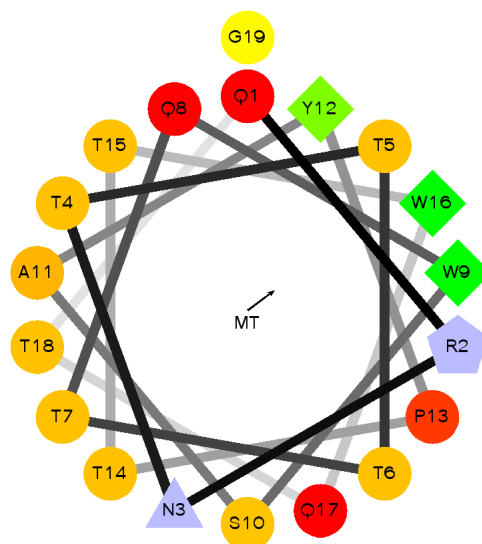
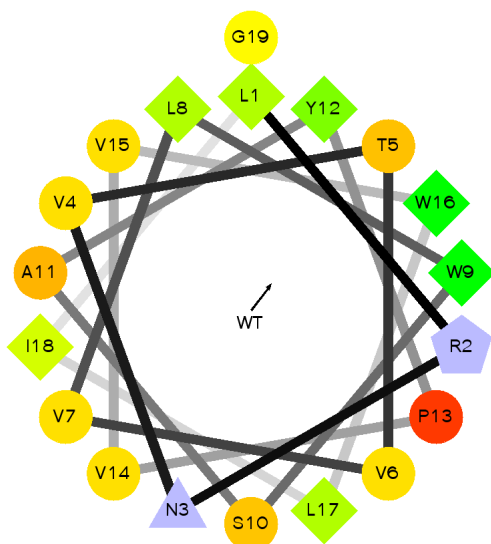
TM6

AA sequence comparison:

TM6-wt: LRNVTVVLWSAYPVVWLIG
| ||***| | | |**|**|
TM6-mt: QRNTTTTQWSAYPTTWQTG

Alpha-helix prediction comparison:

TM6-wt: HHHHHHHHHHHHCCHEEEEC
 |||||
 TM6-mt: HHHHHHHHHHHHCCCEEEEC

**TM7**

AA sequence comparison:

TM7-wt: TLLFMVLDVSAKVGFLILL
 |***|**|*||*|*|***|
 TM7-mt: TQQYMTQDTSAKTGYGQTQL

Alpha-helix prediction comparison:

TM7-wt: HHHHHHHHHHCCCEEEEE
 |||||*
 TM7-mt: HHHHHHHHHHCCCEEEEE

