

REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: P08100

User: siqipian2008@outlook.com

Designing code: QTY

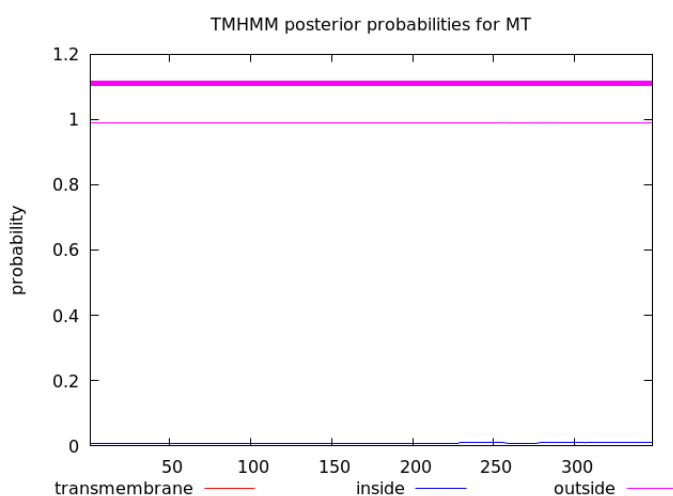
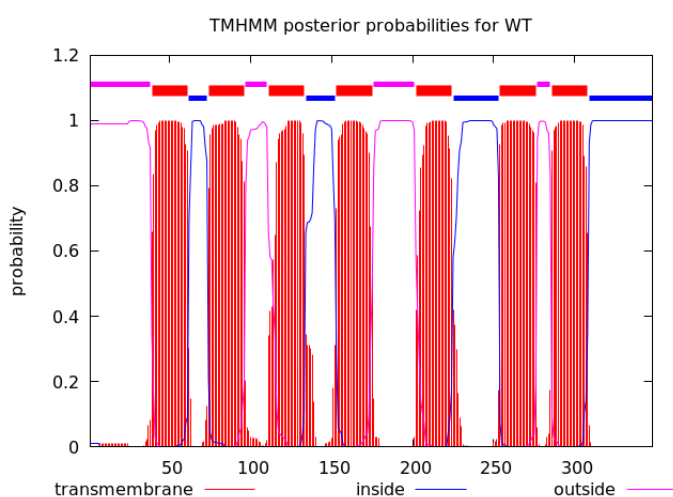
Length of protein sequence: 348

Number of modified TM regions: 7

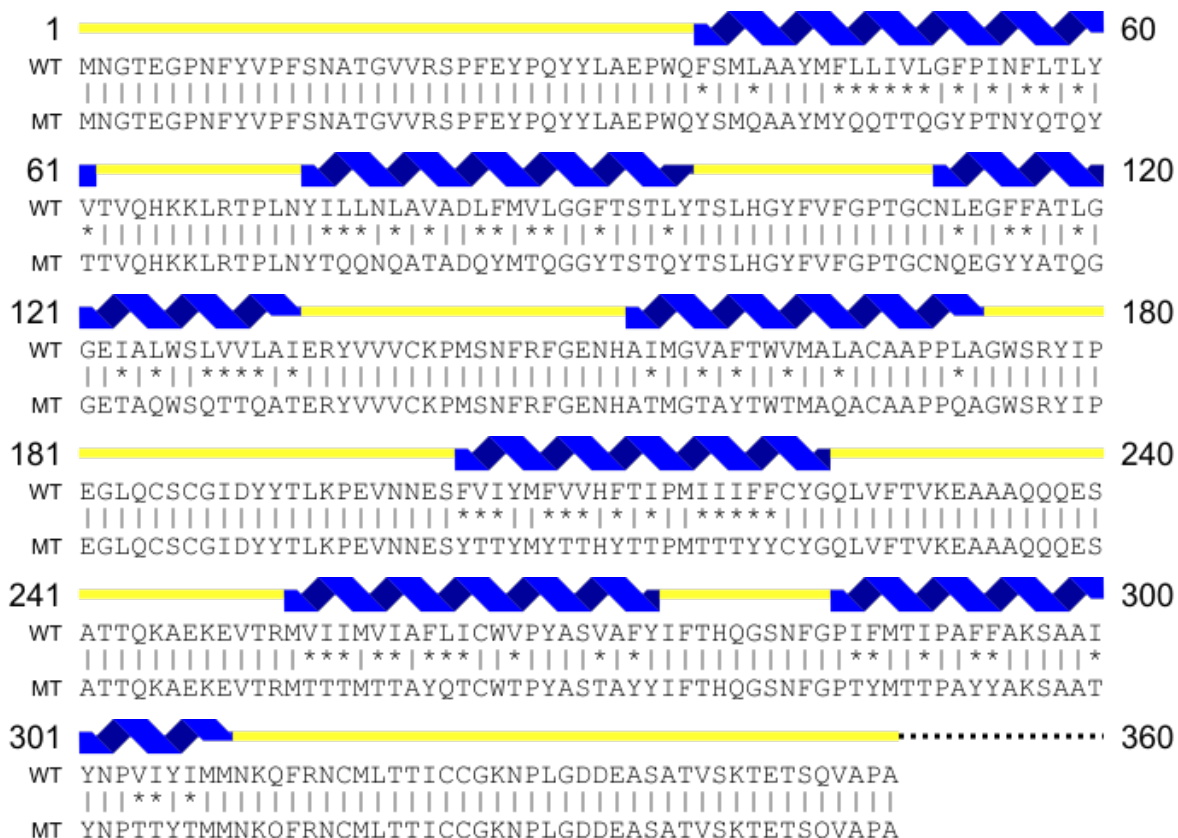
2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	6.20	38.8926	0.5187	/	/
MT	6.20	39.2865	-0.6488	46.58	21.55

3. Comparison of TM prediction:



4. Comparison of sequences:



5. Detailed comparison of TM regions:

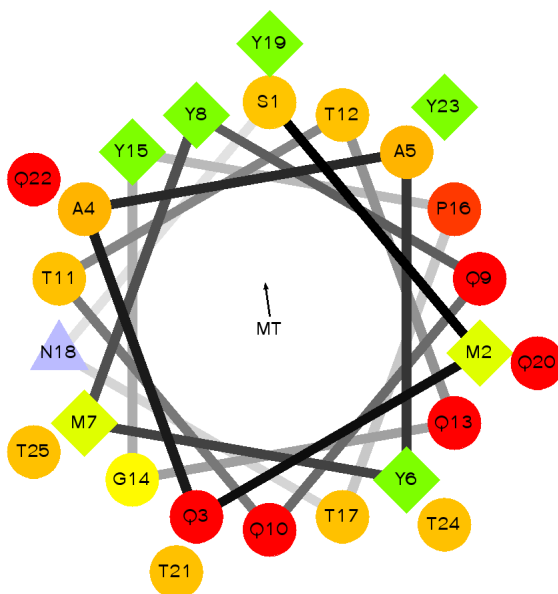
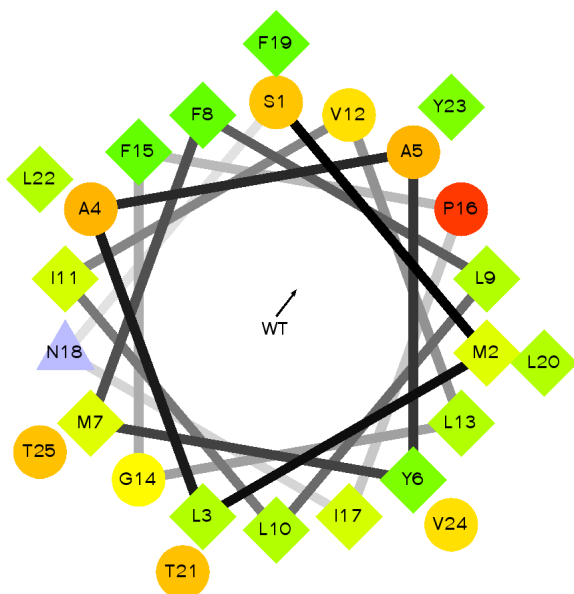
TM1

AA sequence comparison:

TM1-wt: SMLAAYMFLLIVLGFPINFLTLVYT
 |||*|||*****|*|*||*|*|
 TM1-mt: SMOAAYMYOOTTOGYPTNYOTOYTT

Alpha-helix prediction comparison:

TM1-wt : HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
| | | | |
TM1-mt : HHHHHHHHHHHHHHHHHHHHHHHHHHHHHH



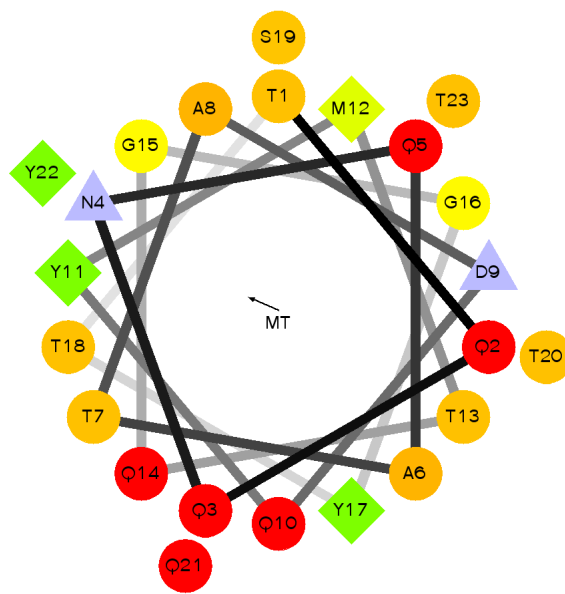
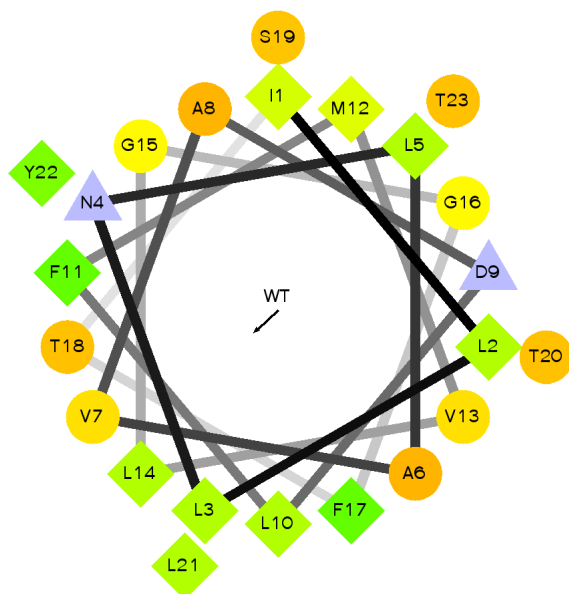
TM2

AA sequence comparison:

TM2-wt: ILLNLAVADLFMVLGGFTSTLYT
 ***|*|*|**|**|*|*|
 TM2-mt: TQONQATADQYMTQGGYTSTQYT

Alpha-helix prediction comparison:

TM2-wt: HHHHHHHHHHHHHHHHHHCCHHHHHH
 |||||*|||*
 TM2-mt: HHHHHHHHHHHHHHHHHCCCCHHHHHH



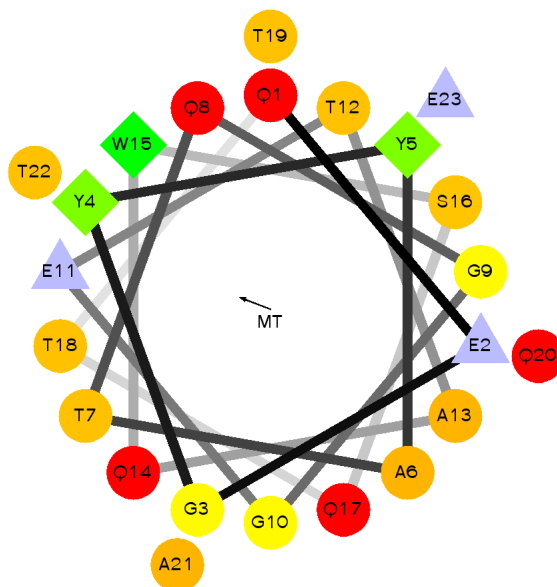
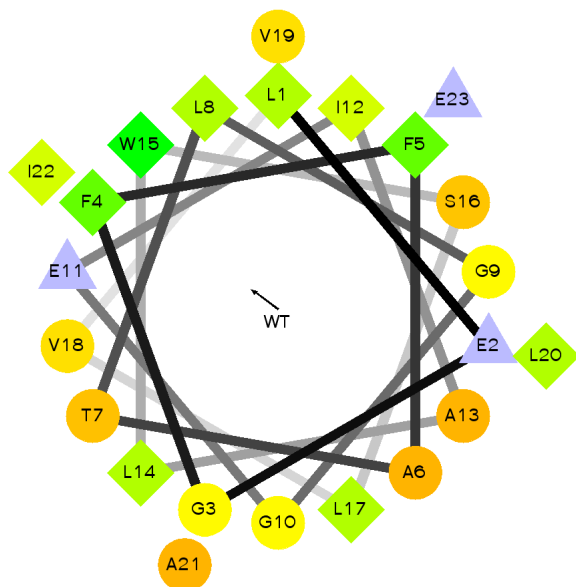
TM3

AA sequence comparison:

TM3-wt : L E G F F A T L G G E I A L W S L V V L A I E
 * | * * * | * * | * * * * * |
TM3-mt : Q E G Y Y A T O G G E T A O W S O T T O A T E

Alpha-helix prediction comparison:

TM3-wt : HHHHHHHHHHHHHHHHHHHHHHHHHHHH
* * * |||||
TM3-mt : EEEHHHHHHHHHHHHHHHHHHHHHHHHH



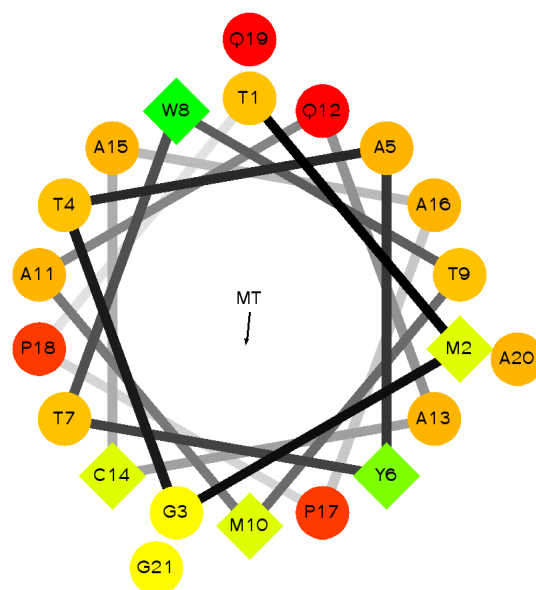
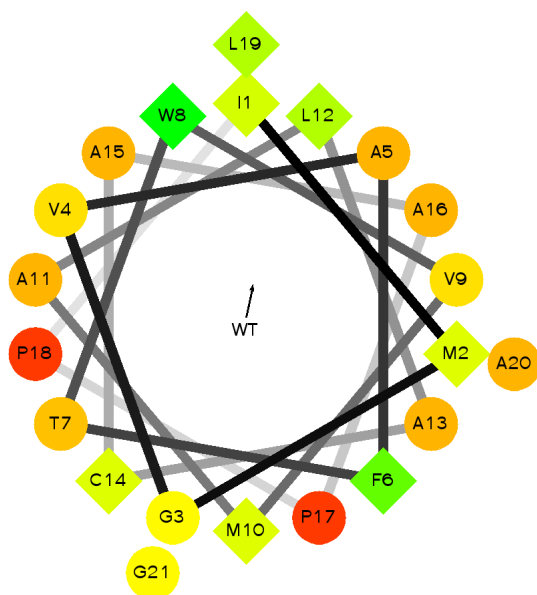
TM4

AA sequence comparison:

TM4-wt: IMGVAF'TWVMALACAAPPLAG
* | * | * | * | * | | | | * |
TM4-mt: TMGTAYTWTMAQACAAPPQAG

Alpha-helix prediction comparison:

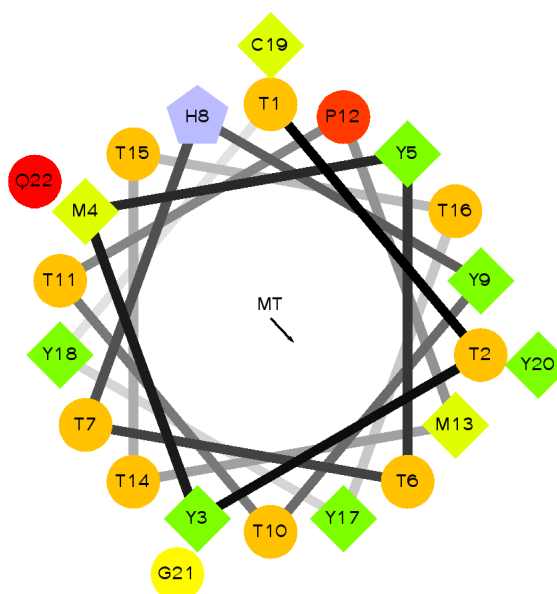
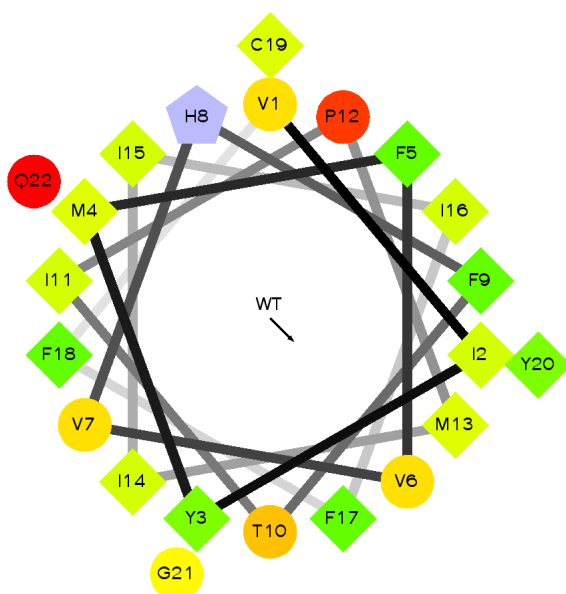
TM4-wt: HHHHHHHHHHHHHHHHHHCCCEEE
 |||||
 TM4-mt: HHHHHHHHHHHHHHHHHHCCCHEE

**TM5**

AA sequence comparison:

TM5-wt: VIYMFVVHFTIPMIIIFFCYGO
 ||*|*|*||*****|||
 TM5-mt: TTYMYTTHYTTTPMTTTYCYGO

Alpha-helix prediction comparison:

[illegible]

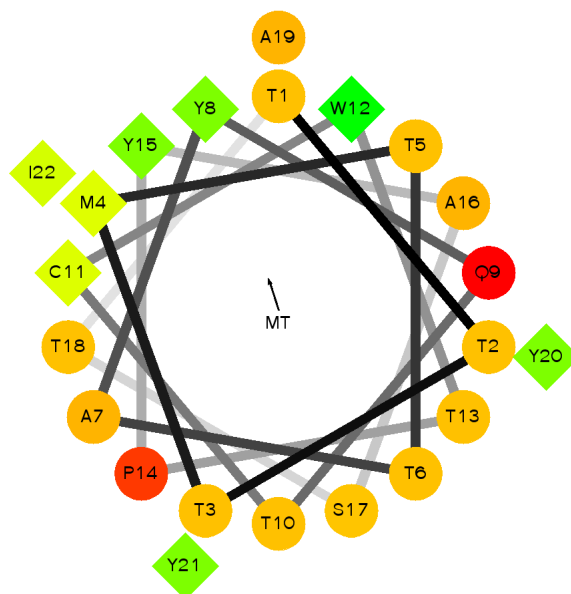
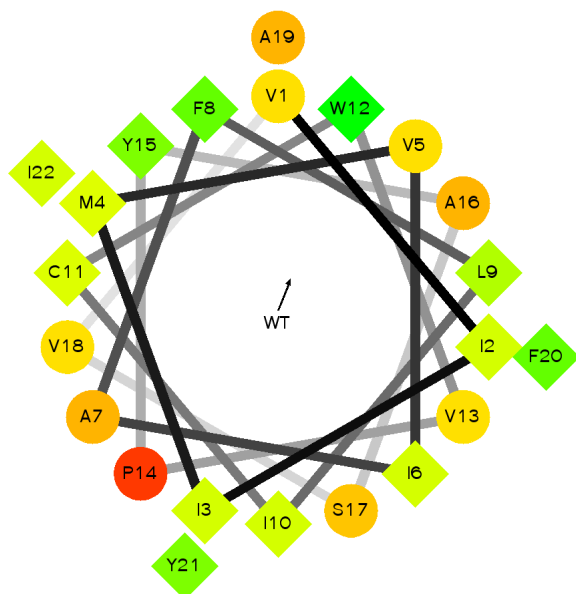
TM6

AA sequence comparison:

TM6-wt: VIIMVIAFLICWVPYASVAFYI
 |**|||*|||*|*||
 TM6-mt: TTTMTTAYQTCWTPYASTAYYI

Alpha-helix prediction comparison:

TM6-wt: HHHHHHHHHHHHCCHHHHHHHHHH
 |||||
 TM6-mt: HHHHHHHHHHHHCCHHHHHHHHHH



TM7

AA sequence comparison:

TM7-wt: IFMTIPAFFAKSAAIYNPVIYIMMN
 |*||||*||**|*|||
 TM7-mt: TYMTTPAYYAKSAATYNPTTYTMMN

Alpha-helix prediction comparison:

TM7-wt: HHHHHHHHHHHHHHHHHHHHCHHHHHHHHC
| | | | | | | | | | * * * * | | | |
TM7-mt: HHHHHHHHHHHHHHHHHCCCCCHHHHHCC

