

REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: P03999

User: siqipian2008@outlook.com

Designing code: QTY

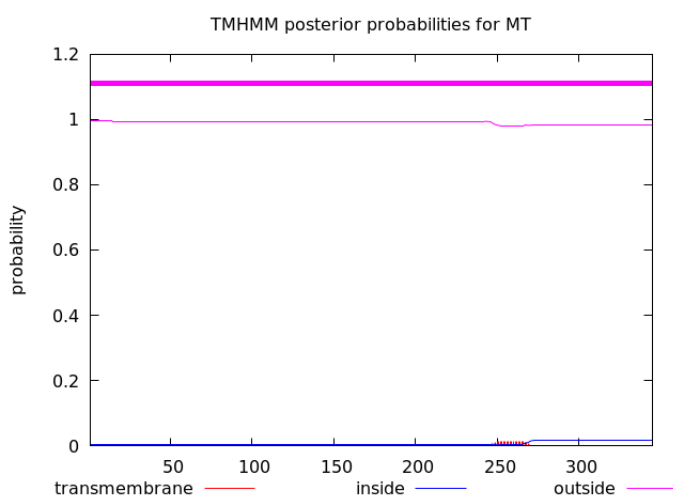
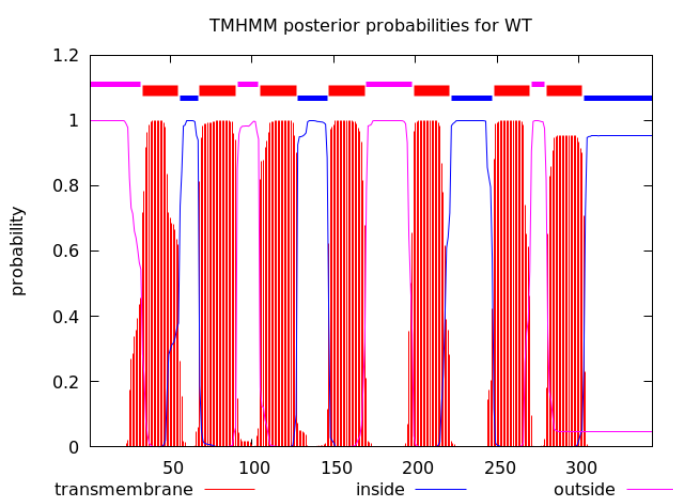
Length of protein sequence: 345

Number of modified TM regions: 7

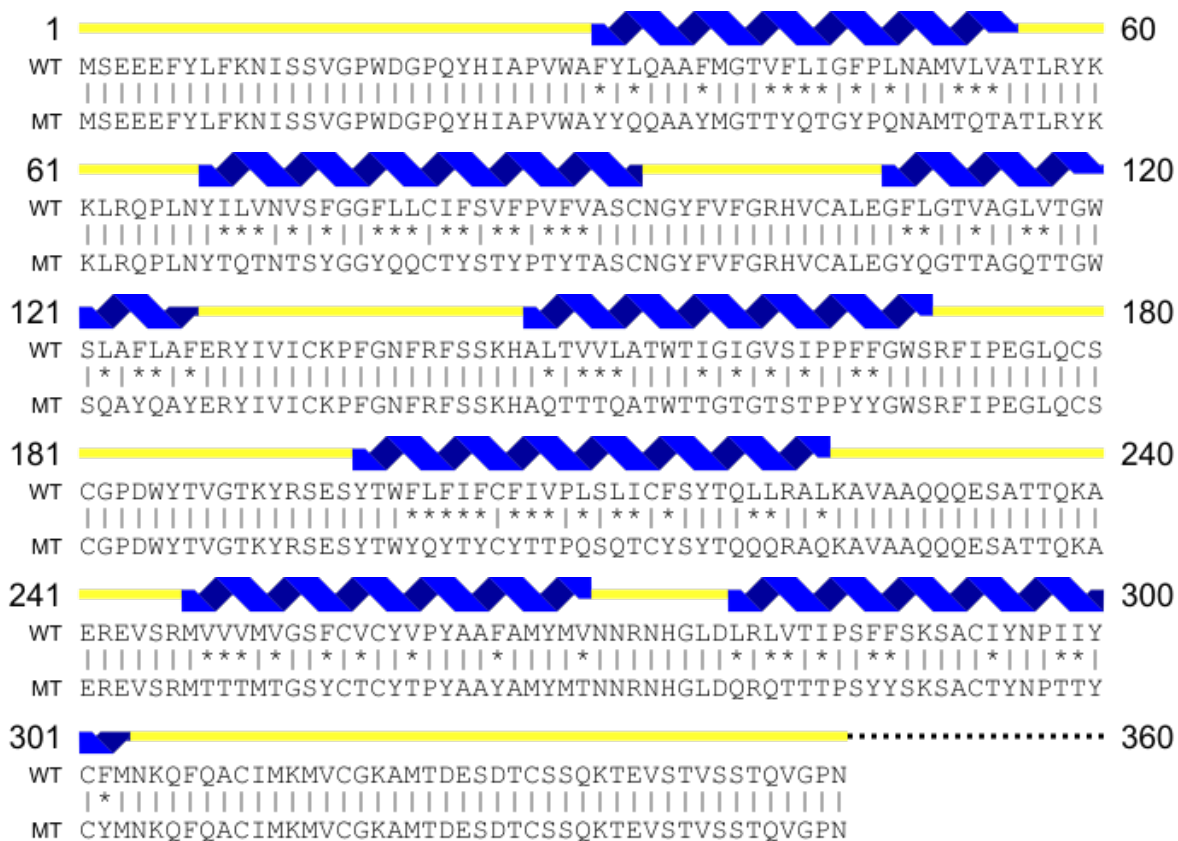
2. Comparison of general characteristics:

| Type | pI | MW (kDa) | Hydrophobicity | Mutation rate (TM, %) | Mutation rate (%) |
|------|------|----------|----------------|-----------------------|-------------------|
| WT | 8.75 | 38.7194 | 0.4881 | / | / |
| MT | 8.66 | 39.3045 | -0.7498 | 46.51 | 23.19 |

3. Comparison of TM prediction:



4. Comparison of sequences:



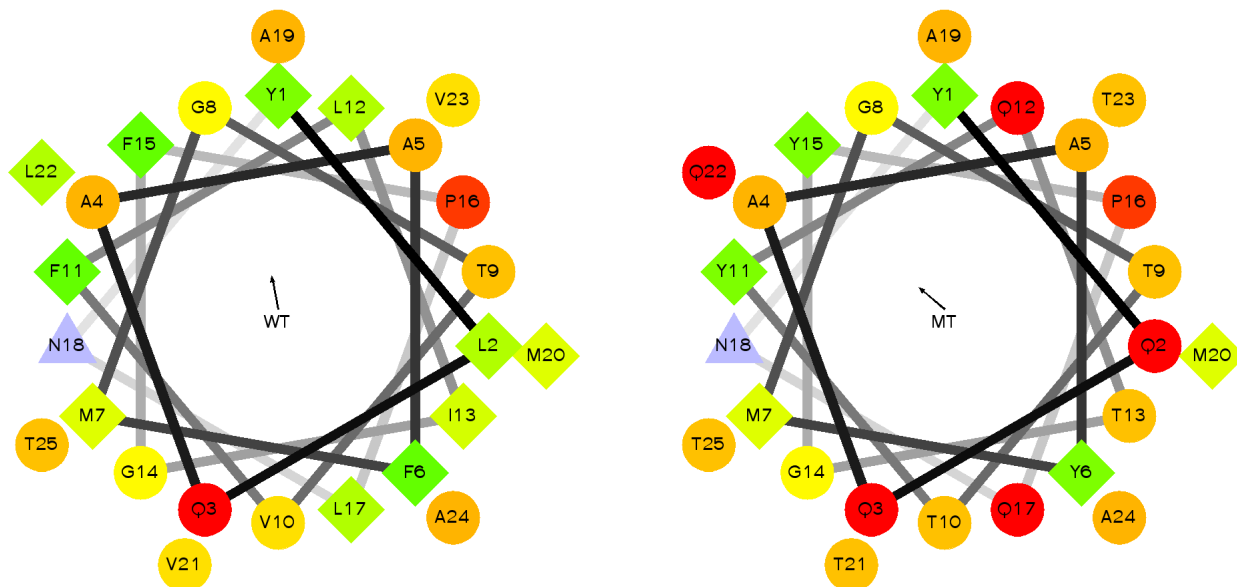
5. Detailed comparison of TM regions:

TM1

AA sequence comparison:

TM1-wt: YLQAAFMGTVFLIGFPLNAMVLVAT
 TM1-mt: YOOAA YMGT TYOTGYPONAMTOTAT

Alpha-helix prediction comparison:

[illegible]

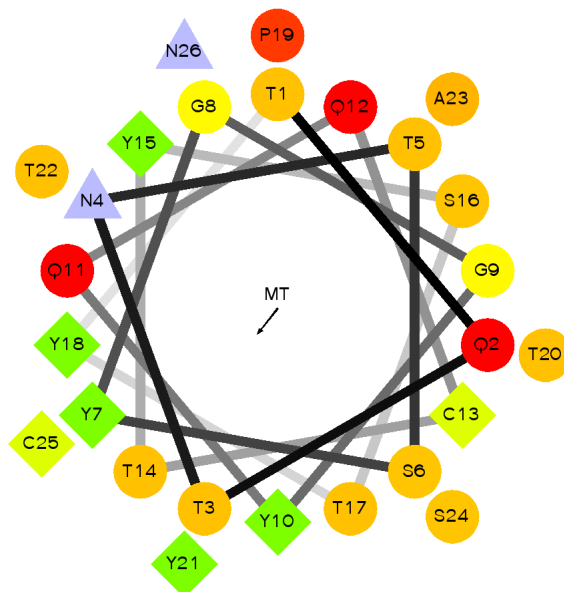
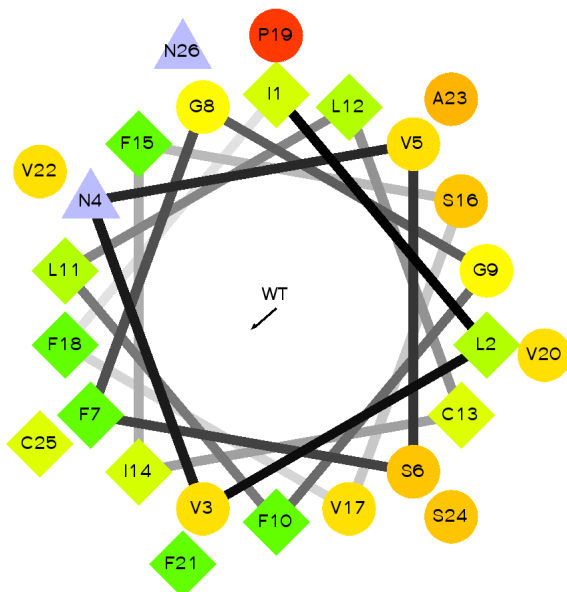
TM2

AA sequence comparison:

TM2-wt: ILVNVSFGGFLLCIFSVFPVFVASCN
 |*|*||**|**|***|
 TM2-mt: TQTNTSYGGYQOCTYSTYPTYTASCN

Alpha-helix prediction comparison:

TM2-wt: HHHHHHHHHHHHHHHHHHCCHHHHHHHCC
 |||||
 TM2-mt: HHHHHHHHHHHHHHHHHCCHCCCHHEEHCC



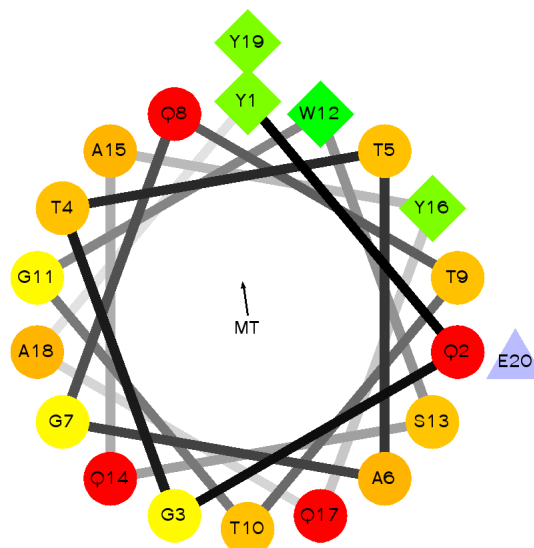
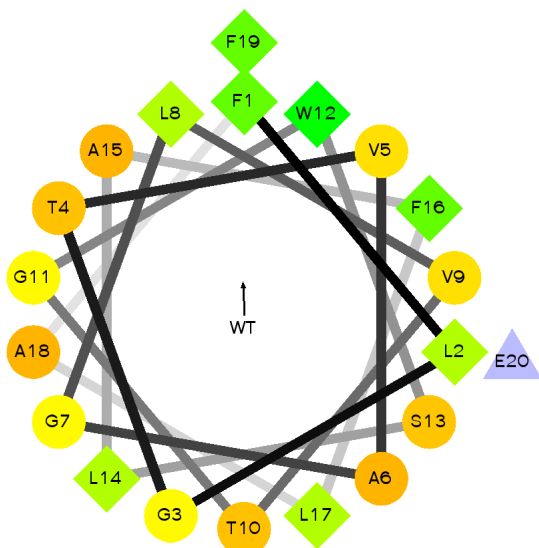
TM3

AA sequence comparison:

TM3-wt: FLGTVAGLVTGWSLAFLAFE
 ||*|||||*||**|*|
 TM3-mt: YQGTTAGQTTGWSQAYQAYE

Alpha-helix prediction comparison:

TM3-wt: C H H H H H H H H H H H H H H H H H H
* | | | | | | | | | | | | |
TM3-mt: H H H H H H H H H H H H H H H H H H



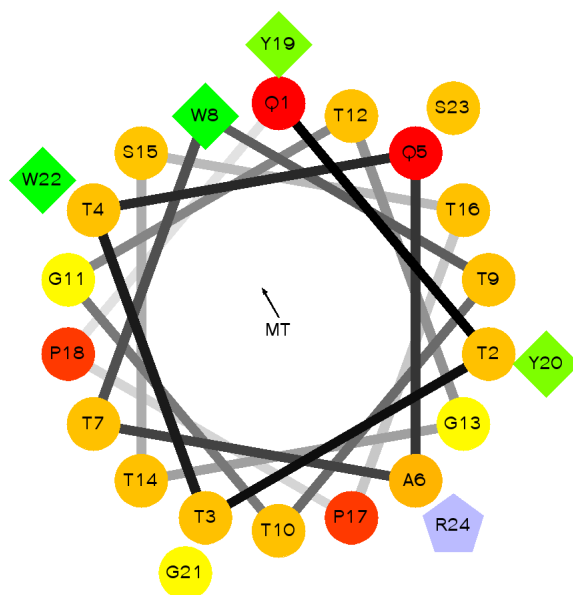
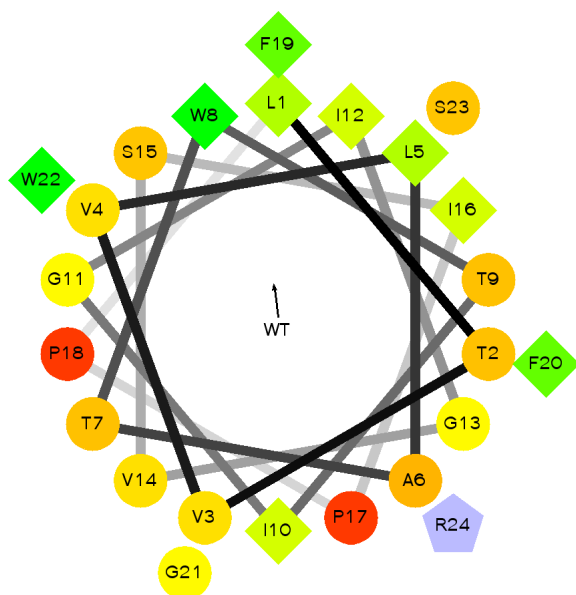
TM4

AA sequence comparison:

TM4-wt : LTVVLATWTIGIGVSIPPFFGWSR
* | * * * | * | * | * | * * |
TM4-mt : OTTTOATWTTGTGTSTPPYYGWSR

Alpha-helix prediction comparison:

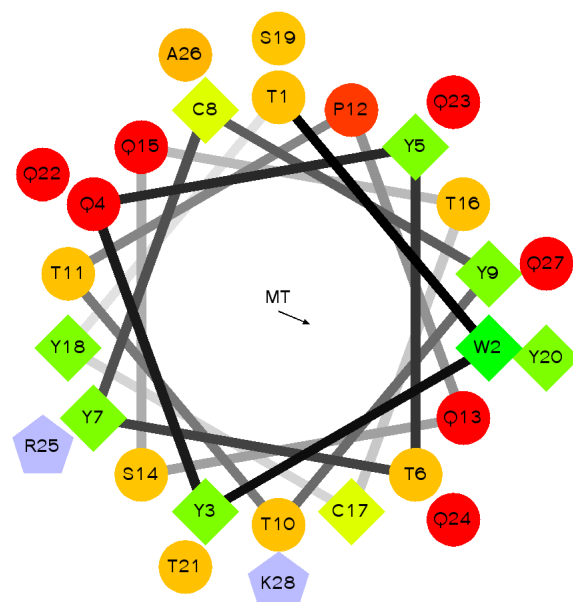
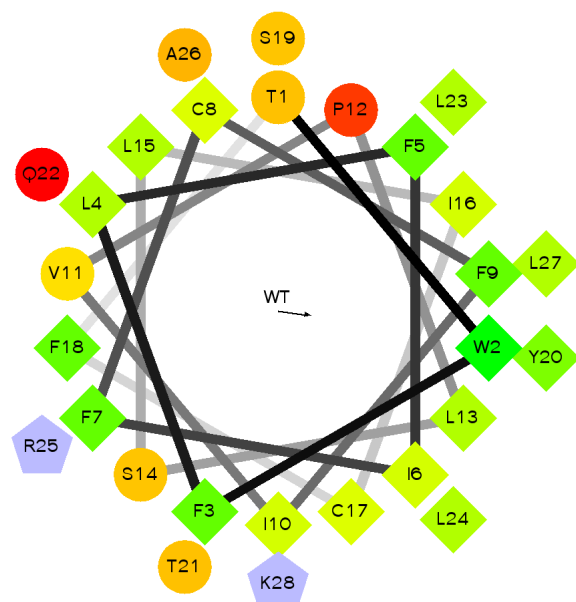
TM4-wt: HHHHHHHHHHHHHHHHHHCCCCEEEEEE
 |||||
 TM4-mt: HHHHHHHHHHHHHHHHHHCCCCEEEECE

**TM5**

AA sequence comparison:

TM5-wt : TWFLFIFCFIVPLSLICFSYTO¹LLRALK
| | * * * * * | * * * | * | * * | * | | * * | * |
TM5-mt : TWYQYTYCYTTPO¹SQTCSYTQQRAOK

Alpha-helix prediction comparison:

[illegible]

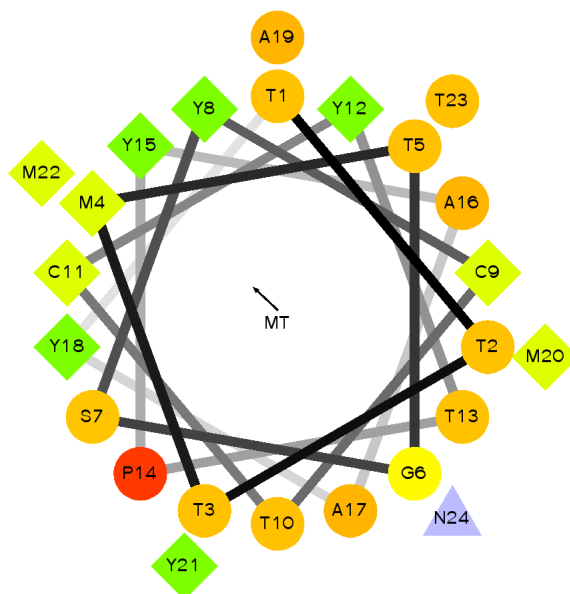
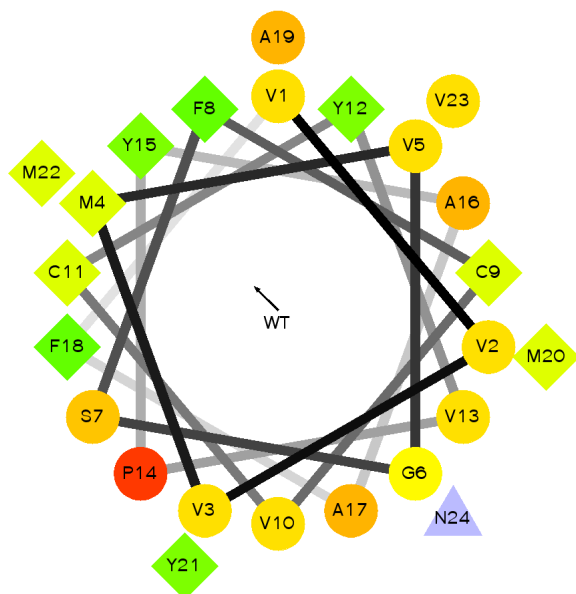
TM6

AA sequence comparison:

TM6-wt : VVV MVG SFCVCYVPYA AFAM YMVN
***|*||*|*|*||*||*||
TM6-mt : TTTMTGSYCTCYTPYA AYAMYTN

Alpha-helix prediction comparison:

TM6-wt: HHHHHHHHHHHHHHCCHHHHHHHHHHHHH
 |||||
 TM6-mt: HHHHHHHHHHHHHHCCHHHHHHHHHHHHH

**TM7**

AA sequence comparison:

TM7-wt: RLVTIPSFFSKSACIYNPIIYCFMN
 ** * ** *
 TM7-mt: ROTTTPSYYSKSACTYNPTTYCYMN

Alpha-helix prediction comparison:

TM7-wt: HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHC
| | | | | | | | | | | | | | | | * * * * | | | | *
TM7-mt: HHHHHHHHHHHHHHHHHHHCCCCHHHHHHHCC

