

REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: B0R2U4

User: siqipian2008@outlook.com

Designing code: QTY

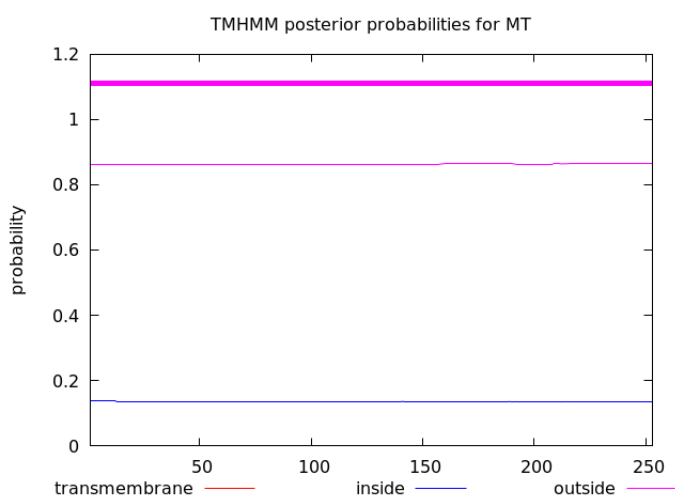
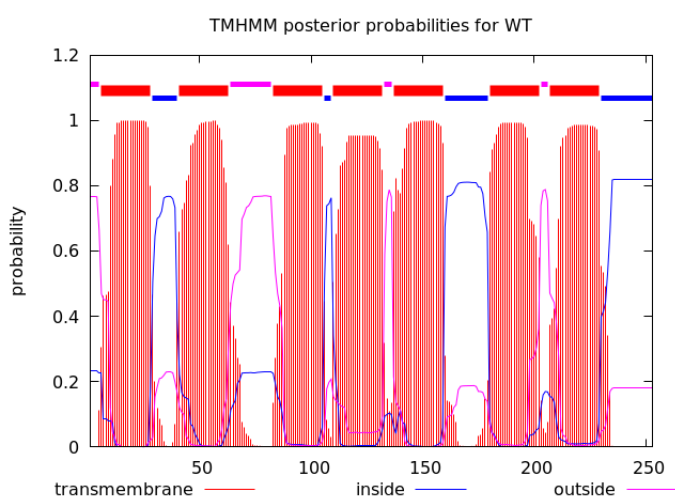
Length of protein sequence: 253

Number of modified TM regions: 7

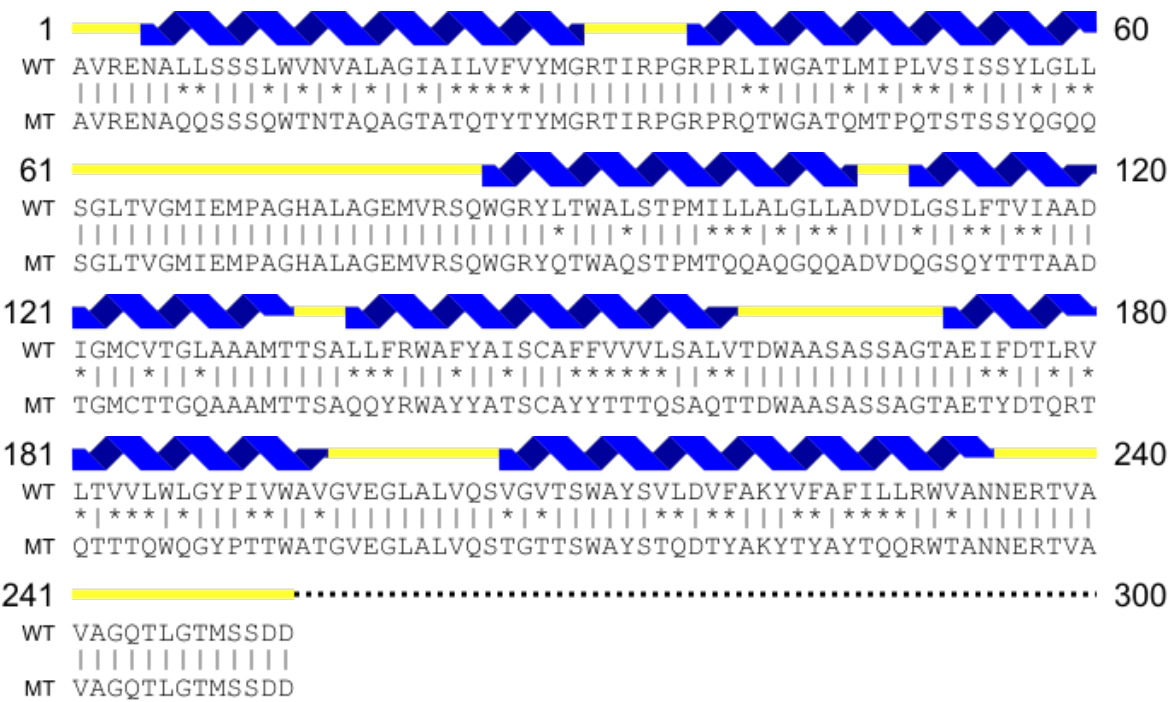
2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	5.34	26.9618	0.9794	/	/
MT	5.34	27.4996	-0.7786	44.19	30.04

3. Comparison of TM prediction:



4. Comparison of sequences:



5. Detailed comparison of TM regions:

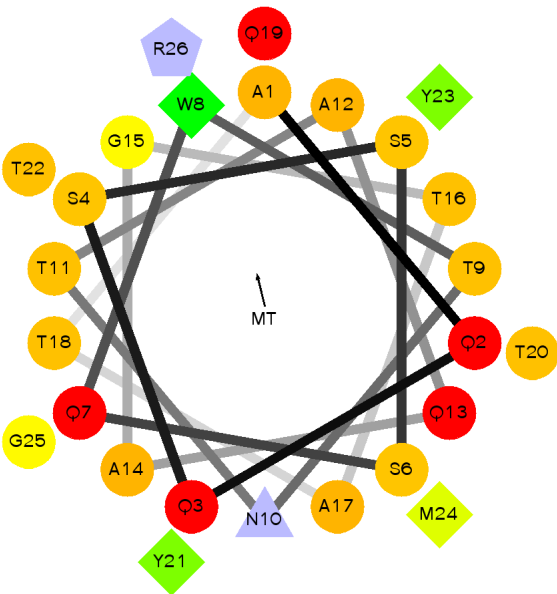
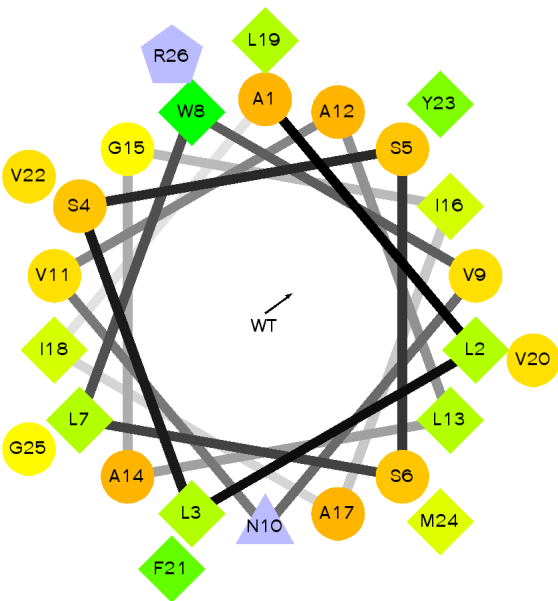
TM1

AA sequence comparison:

TM1-wt: ALLSSSLWVNVALAGIAILVFVYMGR
TM1-mt: AQQSSSQWTNTAQAGTATQTYTYMGR

Alpha-helix prediction comparison:

TM1-wt: CCCCHHHHHHHHHHHHHHHHHHHHHHCC
TM1-mt: CCHHHHHHHHHHHHHHHHHHHHHHHHCC



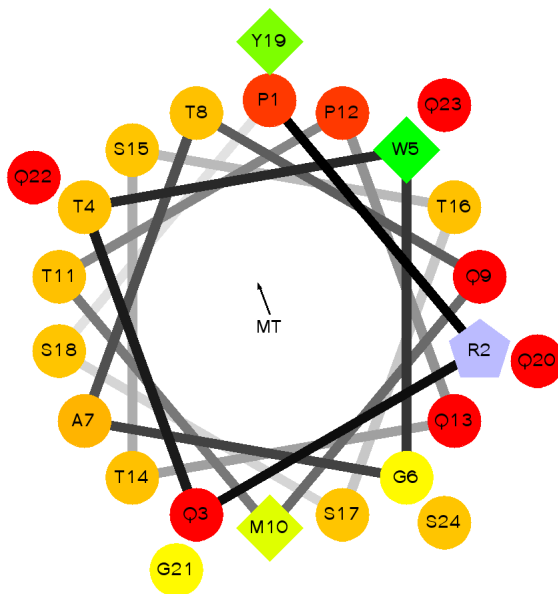
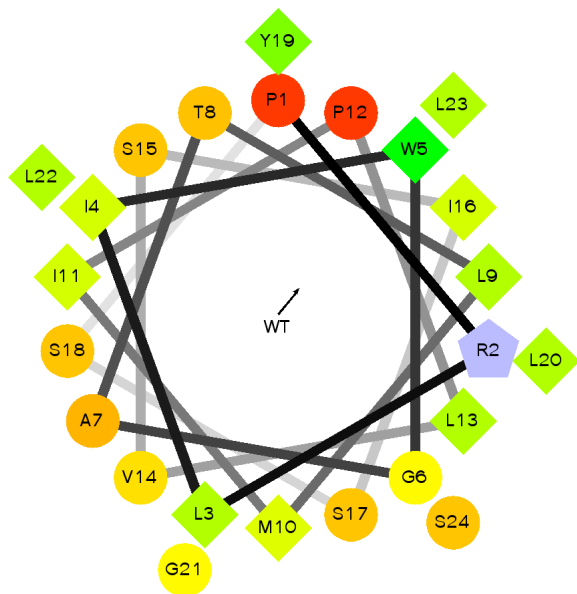
TM2

AA sequence comparison:

TM2-wt: PRLIWGATLMIPLVSISSYLGLLS
 | * * | | * * | * * | * | * | * * |
 TM2-mt: PRQTWGATQMTPQTSTSSYQGQQS

Alpha-helix prediction comparison:

TM2-wt: CEEEEEEECCHHHHHHHHHHHHHHHH*
TM2-mt: CEEEEEEECCHHHHHHHHHHHHHHHC



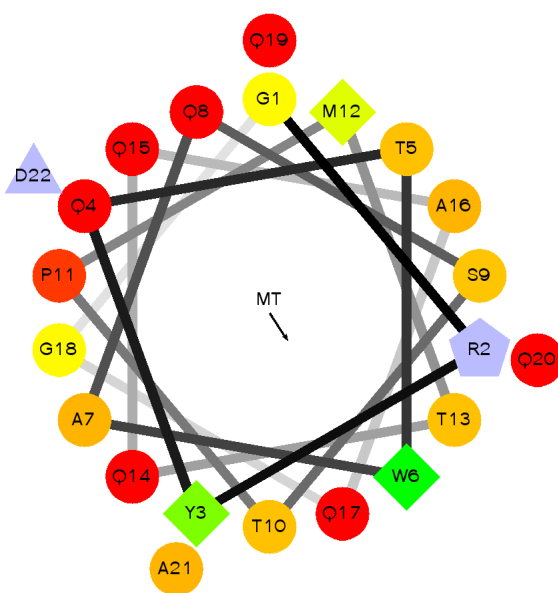
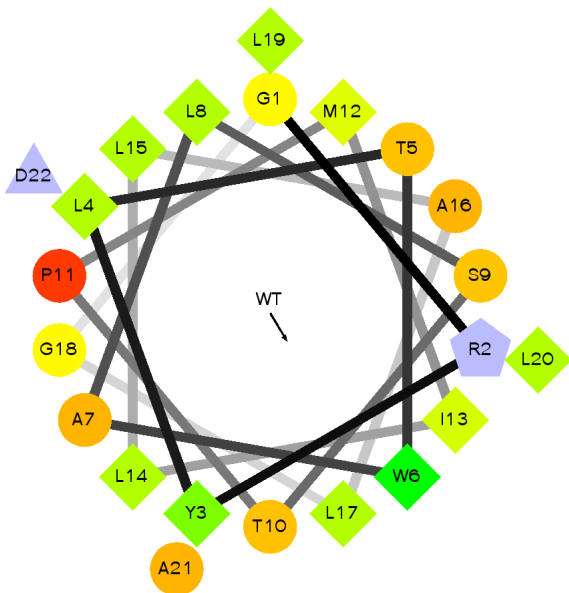
TM3

AA sequence comparison:

TM3-wt: GRYLTWALSTPMILLALGLLAD
 |||*|||*|||***|**||
 TM3-mt: GRYQTWAQSTPMTQQAQGQQAD

Alpha-helix prediction comparison:

TM3-wt: EEEEEEEECCHHHHHHHHHHCC
 |||||
 TM3-mt: EEEEEEEECCHHHHHHHHHHCC

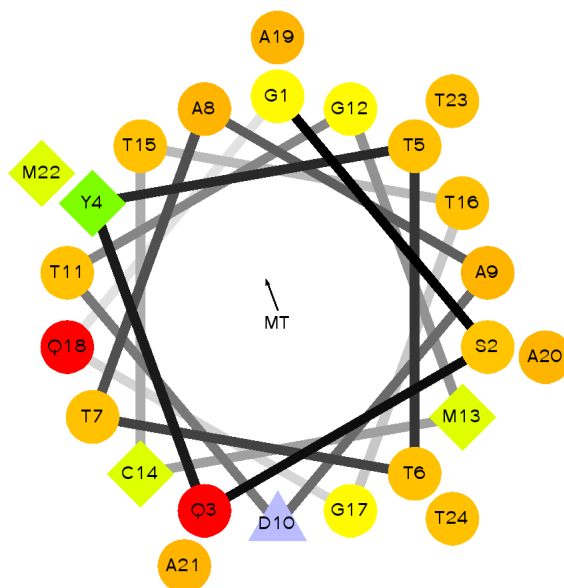
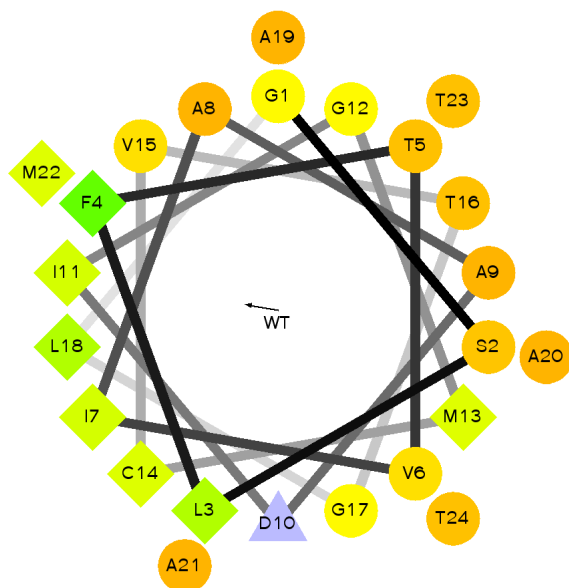


TM4

AA sequence comparison:

TM4-wt: G S L F T V I A A D I G M C V T G L A A A M T T
 | * * | * | * | * |
TM4-mt: G S Q Y T T T A A D T G M C T T G Q A A A M T T

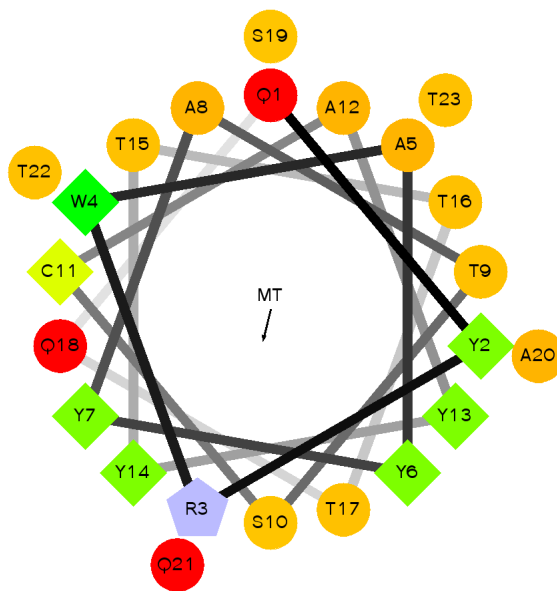
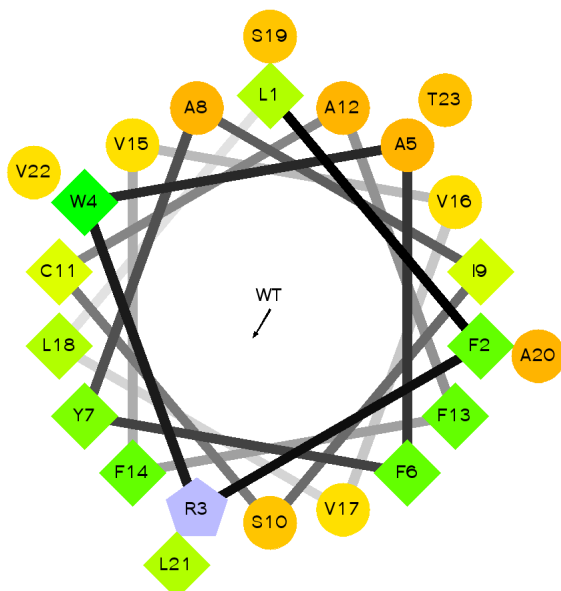
Alpha-helix prediction comparison:

[illegible]**TM5**

AA sequence comparison:

TM5-wt: LFRWAFYAISCAFFVVVLSALVT
 |||*||*|||***||**||
 TM5-mt: QYRWAYYATSCAYTTTTSQAQTT

Alpha-helix prediction comparison:

[illegible]

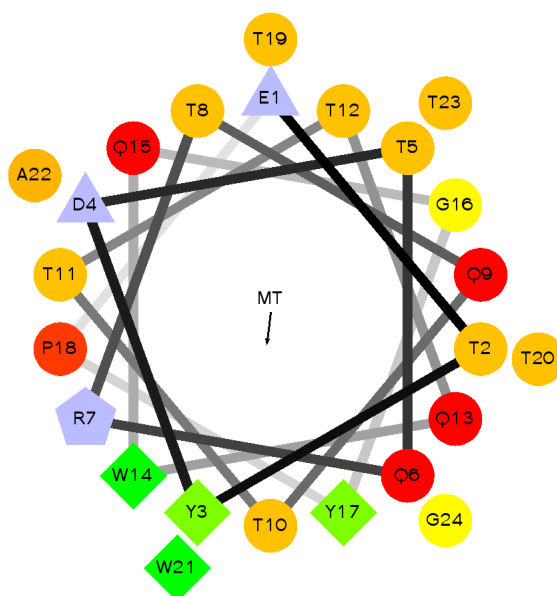
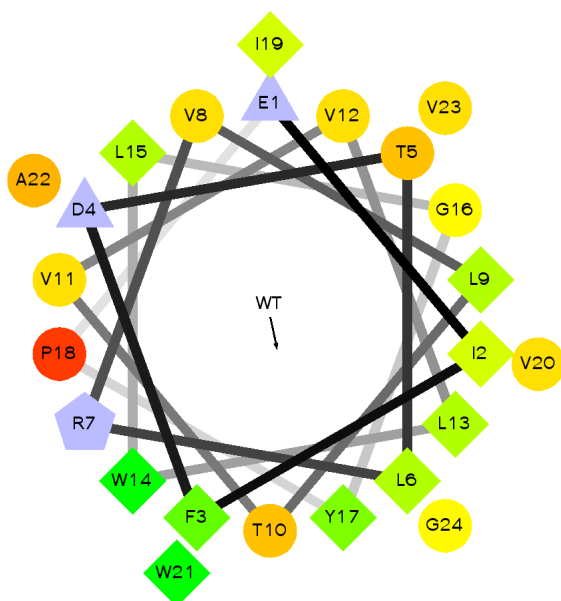
TM6

AA sequence comparison:

TM6-wt: EIFDTRLVLTVVWLGYPIVWAVG
 |*||***|*|**|*
 TM6-mt: ETYDTORTOTTTQWQGYPTTWATG

Alpha-helix prediction comparison:

TM6-wt: HHHHHHHHHHHHHHHHHHHHCHHHHHHC
| | | | | | | | | | | | | | | * * * * *
TM6-mt: HHHHHHHHHHHHHHHHHHHHCCCHEEEEC

**TM7**

AA sequence comparison:

TM7-wt: GVTSWAYSVLDFVFAKYVF¹AFILLRWVANN
 |*| | | |**|**| |**|*****|*| | |
 TM7-mt: GTTSWAYSTQDTYAKYTYAYTQQRWTANN

Alpha-helix prediction comparison:

TM7-wt : HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCC
 * | | | | | | | | | | | | | | | | | | | *
TM7-mt : CHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCC

