

REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: P47804

User: siqipian2008@outlook.com

Designing code: QTY

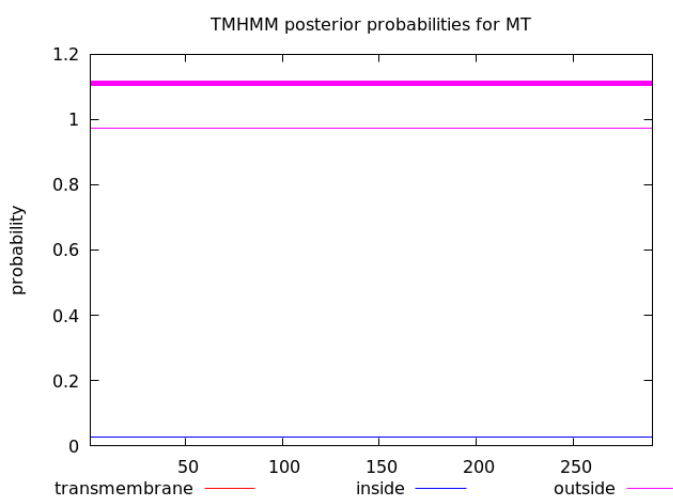
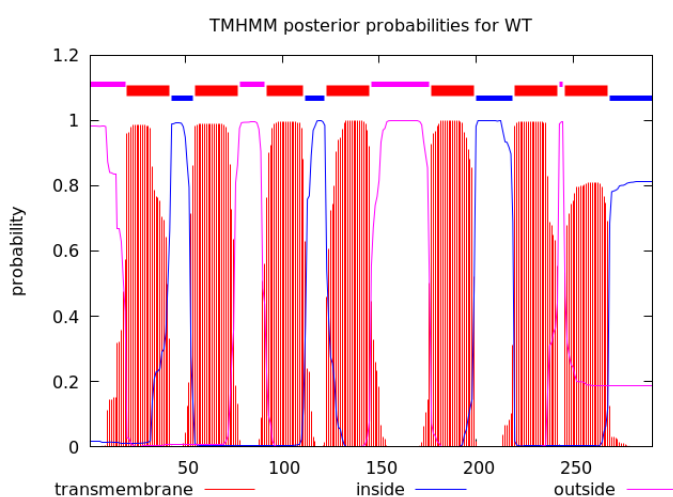
Length of protein sequence: 291

Number of modified TM regions: 7

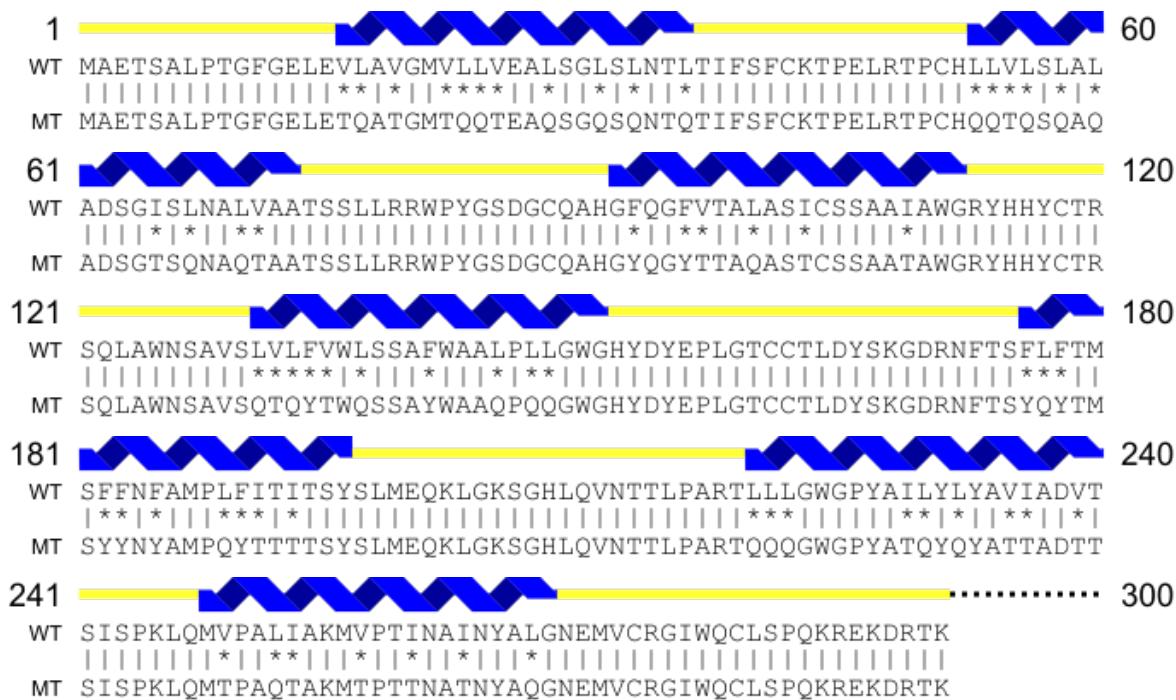
2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	8.34	31.8742	0.4144	/	/
MT	8.29	32.3884	-0.8765	42.86	21.65

3. Comparison of TM prediction:



4. Comparison of sequences:



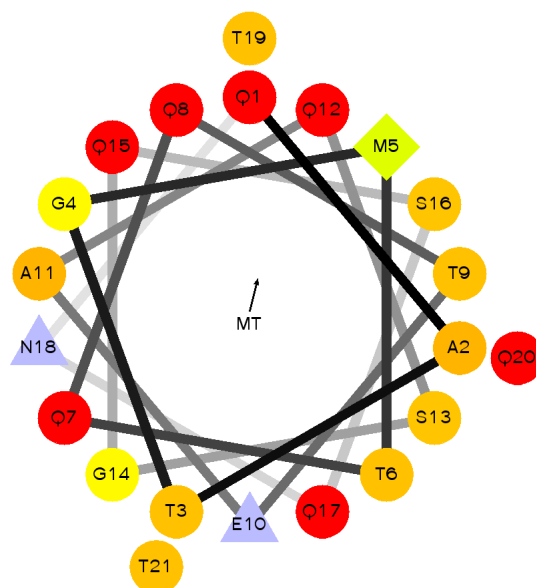
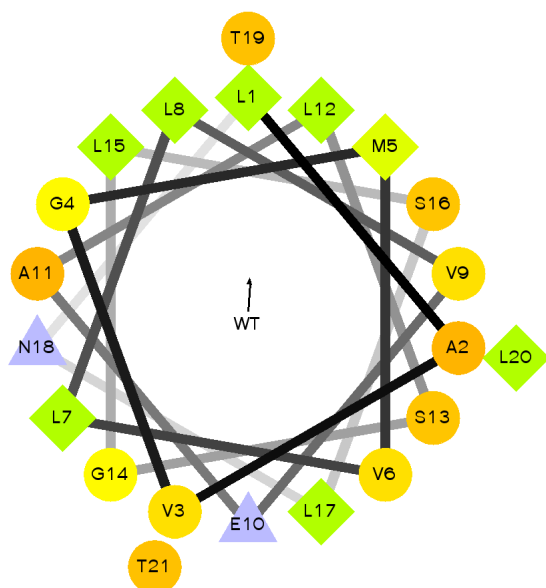
5. Detailed comparison of TM regions:

TM1

AA sequence comparison:

TM1-wt: LAVGMVLLVEALSGLSLNTLT
|||****||*||*||*||*|
TM1-mt: QATGMTQOTEASGOSONTOT

Alpha-helix prediction comparison:

[illegible]

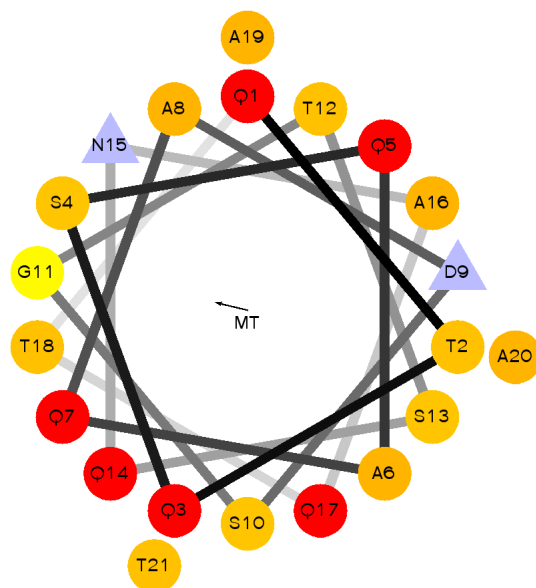
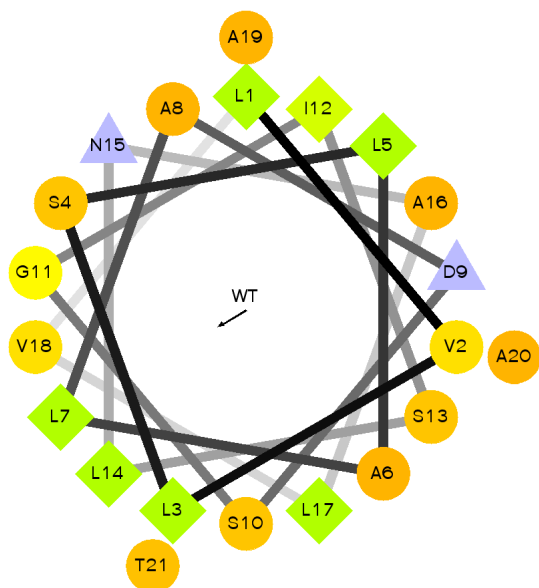
TM2

AA sequence comparison:

TM2-wt : LVL^{***}SLALADSGISL^{***}NALVAAT
 TM2-mt : QTQSQAQADSGTSQNAQTAAT

Alpha-helix prediction comparison:

TM2-wt : HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
 TM2-mt : HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH



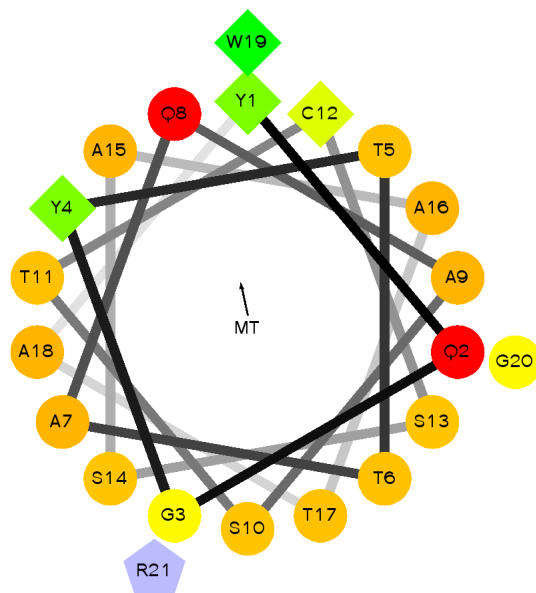
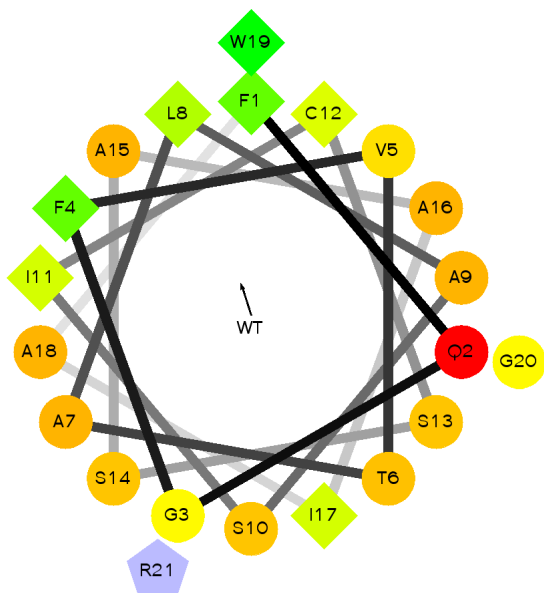
TM3

AA sequence comparison:

TM3-wt : FQGFV^{*}TALASICSSAAIAWGR
 TM3-mt : YQGYTTAQASTC^{*}SSAATAWGR

Alpha-helix prediction comparison:

TM3-wt : CHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
 TM3-mt : HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH



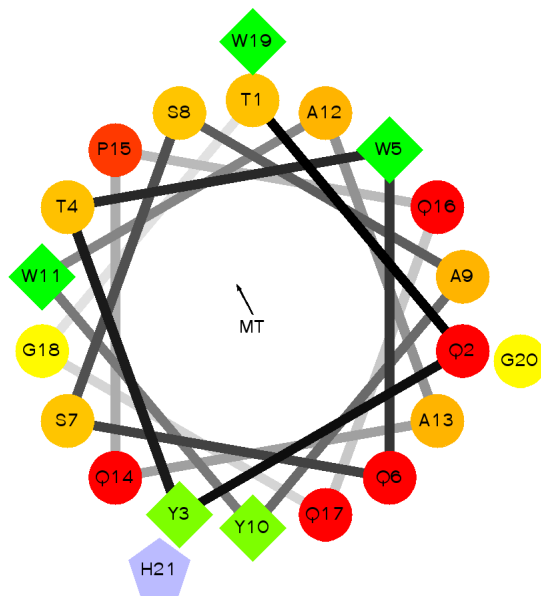
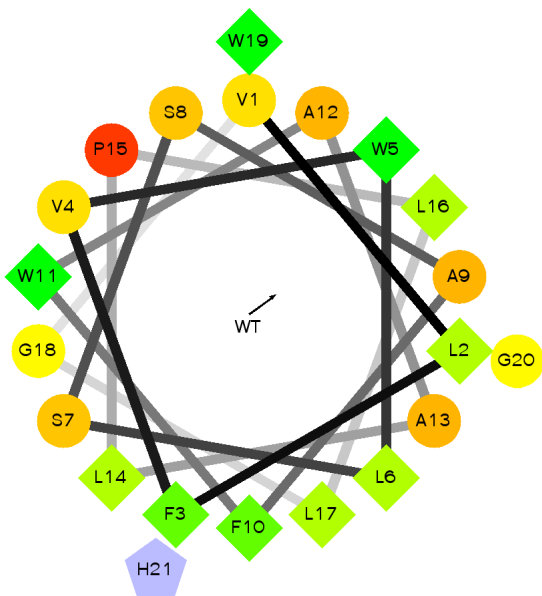
TM4

AA sequence comparison:

TM4-wt: VLFVWLSSAFWAALPLLGWGH
 *****|*|||*|||*||**|||
 TM4-mt: TQYTWQSSAYWAAQPQQGWGH

Alpha-helix prediction comparison:

TM4-wt : HHHHHHHHHHHHHHHHHHCCCC
| | | | | | | | | * * * * |
TM4-mt : HHHHHHHHHHHHHHCCCHECCCC

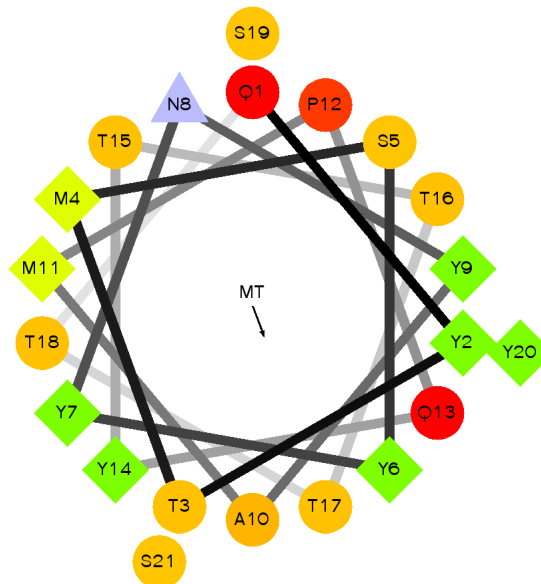
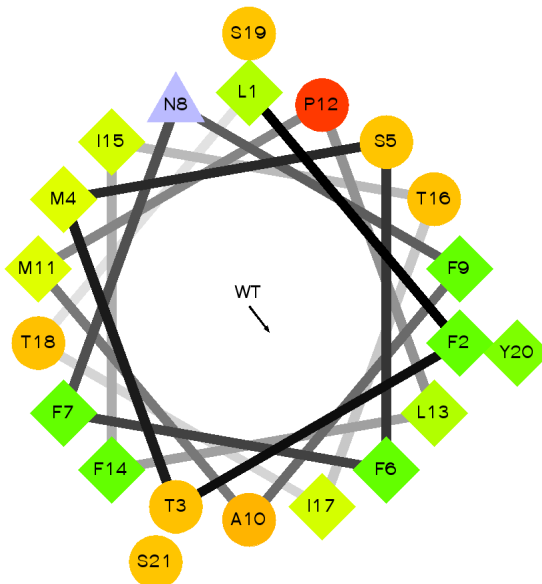
**TM5**

AA sequence comparison:

TM5-wt: LFTMSFFNFAMPLFITITSYS
 ||||*|||***|*|||
 TM5-mt: QYTMSYYNYAMPQYTTTTSYS

Alpha-helix prediction comparison:

TM5-wt: HHHHHHHHHHHHHHHHHHHHHHHHHHHHH
 |||
 TM5-mt: HHHHHHHHHHHHHHHHHHHHHHHHHHHHH



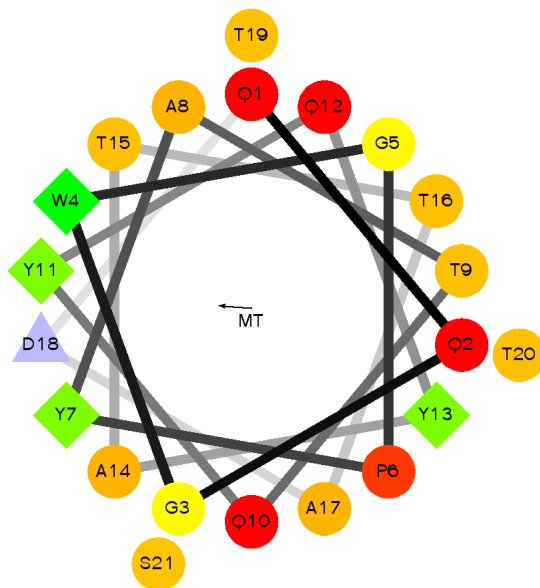
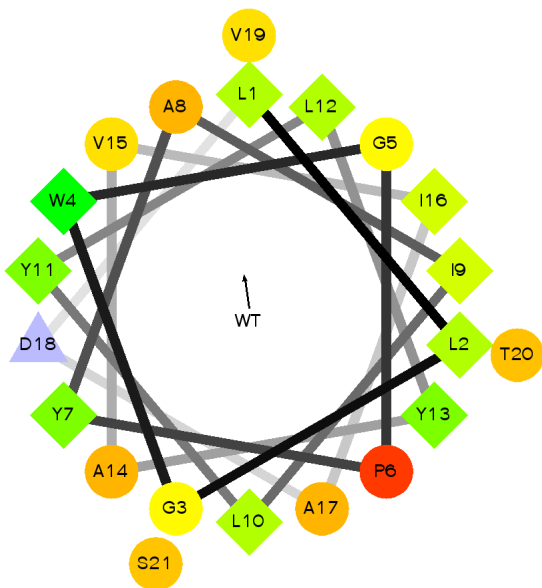
TM6

AA sequence comparison:

TM6-wt: LLGWGPYAILYLYAVIADVTS
 ||||*||**|*||
 TM6-mt: QQGWGPYATQYQYATTADTTS

Alpha-helix prediction comparison:

TM6-wt: HHCCCHHHHHHHHHHHCCCC
 |||*|||
 TM6-mt: HHCCCHHHHHHHHHHHCCCC

**TM7**

AA sequence comparison:

TM7-wt: VPALIAKMVPTINAINYALGN
*| |**|||*| |*| |*| |*| |
TM7-mt: TPAQTAKMTPTTNATNYAQGN

Alpha-helix prediction comparison:

TM7-wt: HHHHHHHHCHHHHHHHHHHCC
 ||||| * * |||||
 TM7-mt: HHHHHHHHCCCHHHHHHHHCC

