

REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: Q6U736

User: siqipian2008@outlook.com

Designing code: QTY

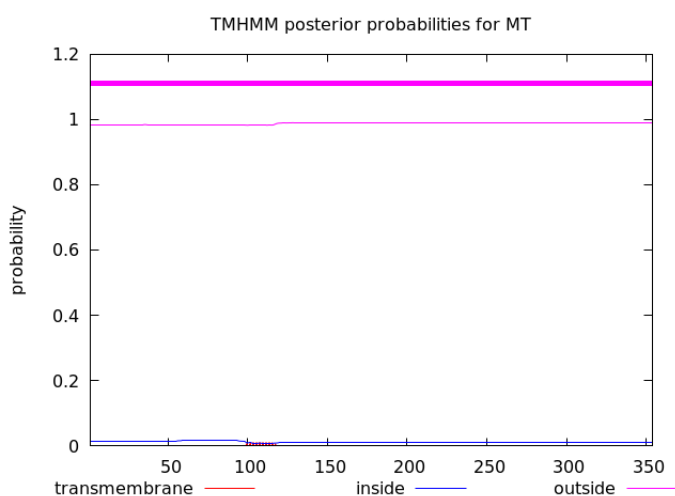
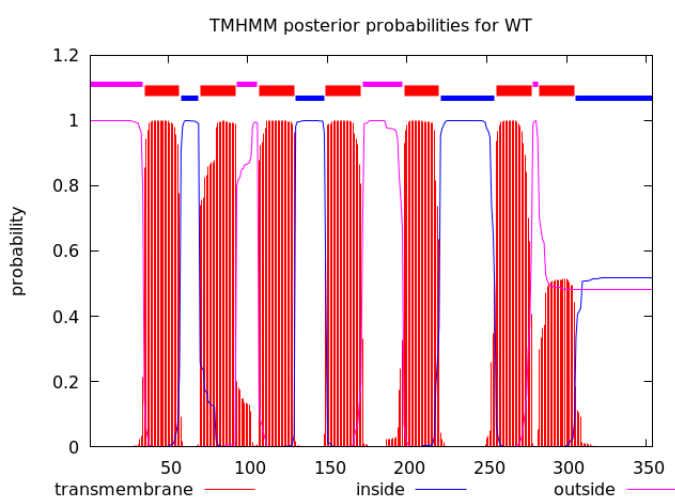
Length of protein sequence: 354

Number of modified TM regions: 7

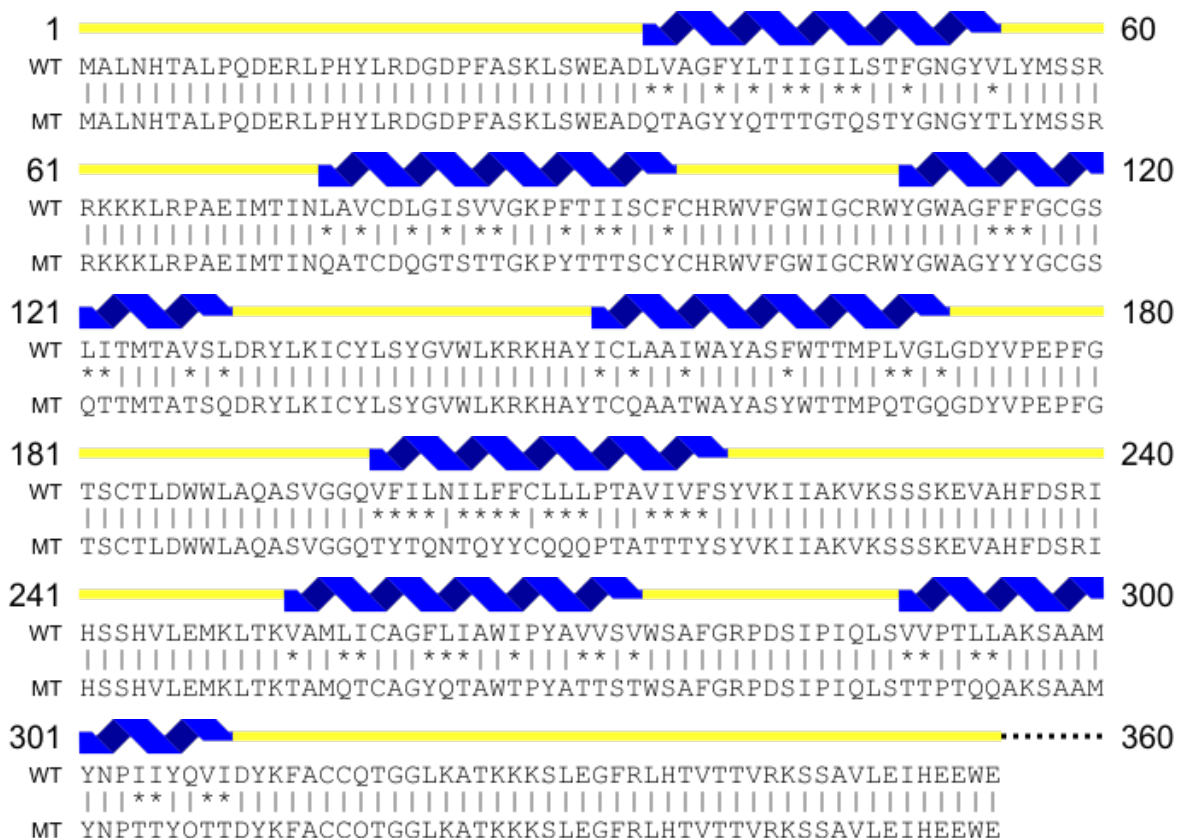
2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	9.11	39.7269	0.4472	/	/
MT	9.02	40.0359	-0.5948	45.58	18.93

3. Comparison of TM prediction:



4. Comparison of sequences:



5. Detailed comparison of TM regions:

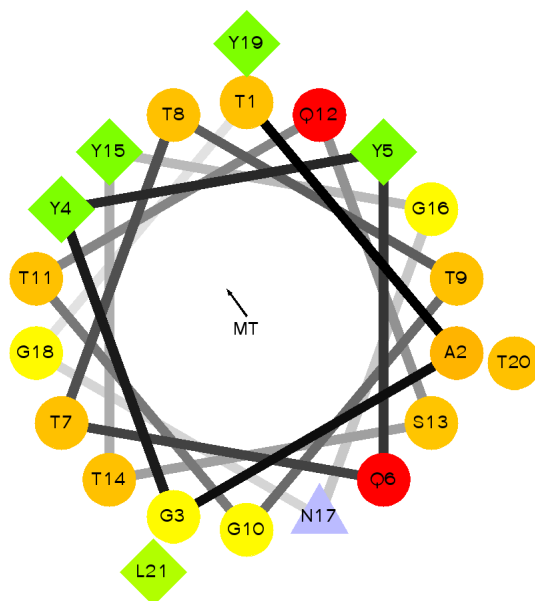
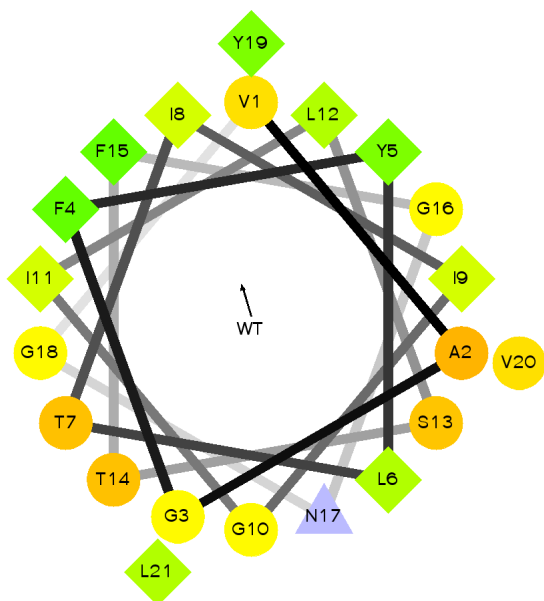
TM1

AA sequence comparison:

TM1-wt: VAGFYLTIIIGILSTFGNGYVL
* | * | * | * | * | * | * | * | * |
TM1-mt: TAGYYOTTTGTOSTYGNGYTL

Alpha-helix prediction comparison:

TM1-wt: HHHHHHHHHHHHHHHHHHHHHHHHHHHHH
 |||||
 TM1-mt: HHHHHHHHHHHHHHHHHHHHHHHHHHHHH



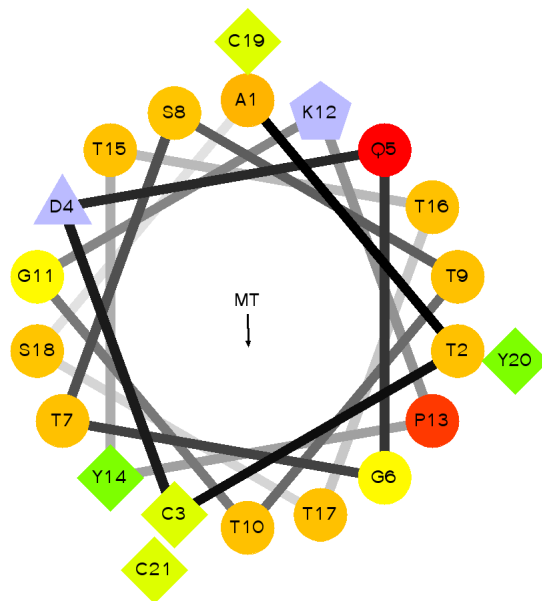
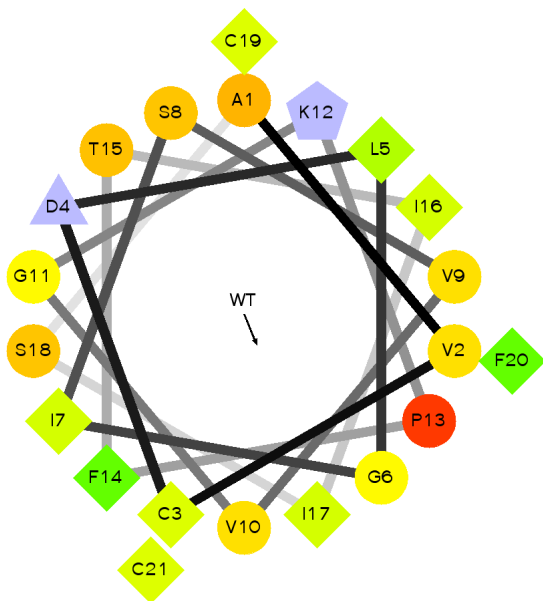
TM2

AA sequence comparison:

TM2-wt : AVCDLGISVVGKPF^{|||||}TIISCFC
 TM2-mt : ATCDQGTSTTGKPY^{|||||}TTTSCYC

Alpha-helix prediction comparison:

TM2-wt : HHHHHHHHHH^{|||||}CHHHHHHHHH
 TM2-mt : HHHHHHHHHH^{|||||}CCCCHHHHHHCC



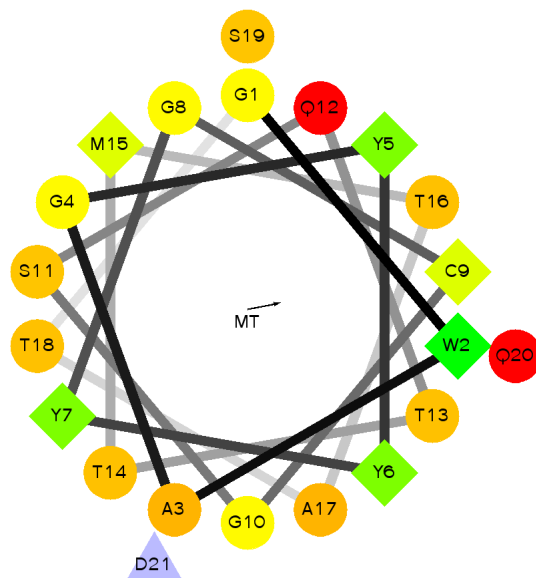
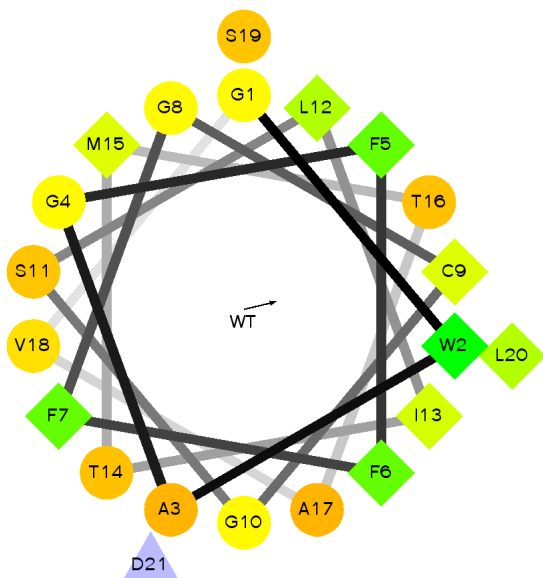
TM3

AA sequence comparison:

TM3-wt : GWAGFFFGCGSLITMTAVSLD
 TM3-mt : GWAGYYYGCGSQTTMTATSQD

Alpha-helix prediction comparison:

TM3-wt : C^{|||||}HHHHHHHHHHHHHHHHHHHHHH
 TM3-mt : C^{|||||}HHHHHHHHHHHHHHHHHHHHHH



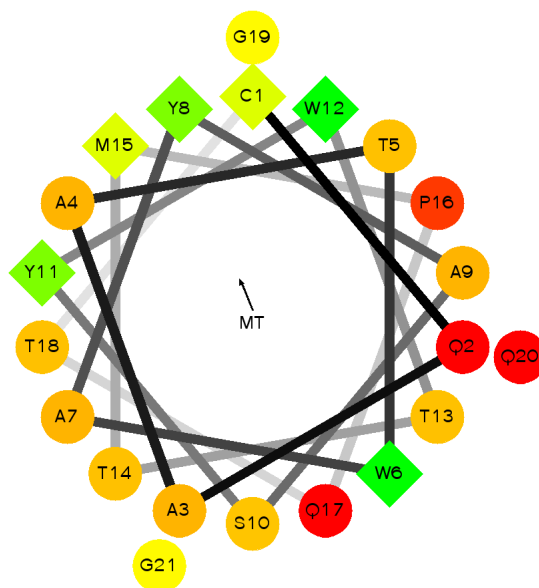
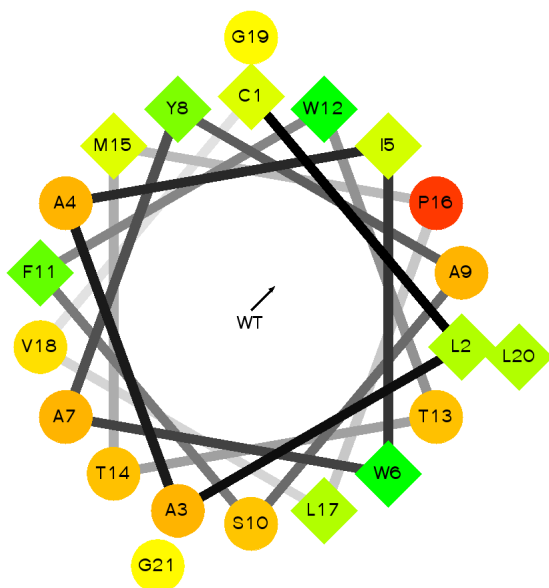
TM4

AA sequence comparison:

TM4-wt: CLAAIWAYASF^{*}WT^{*}TMPLVGLG
 TM4-mt: CQAATWAYASYWTTMPQTGQG

Alpha-helix prediction comparison:

TM4-wt: HHHHHHHHHHHHHHCCCEEEEC
 |||||
 TM4-mt: HHHHHHHHHHHHHHCCCHEEECC

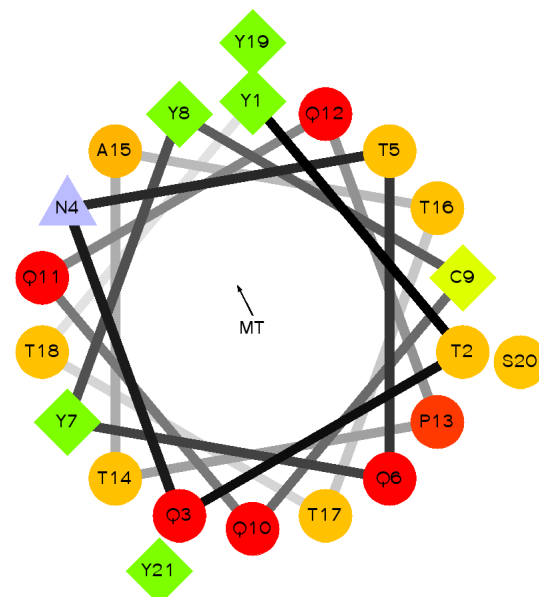
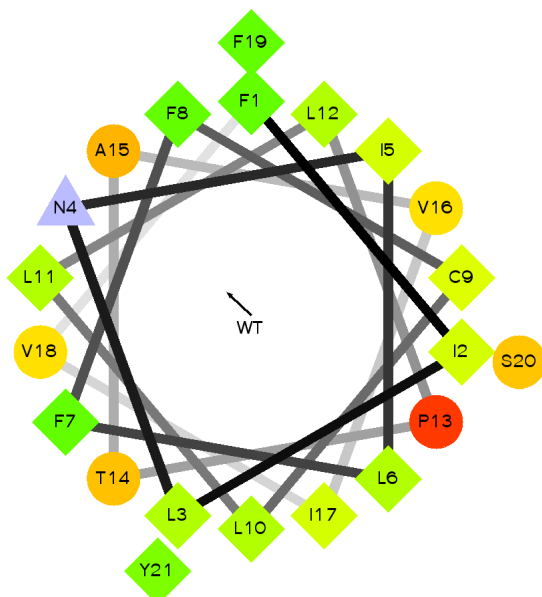
**TM5**

AA sequence comparison:

TM5-wt: FILNILFFCLLLPTAVIVFSY
 |**|***|||*****||
 TM5-mt: YTQNTQYYCQQOPTATTTYSY

Alpha-helix prediction comparison:

TM5-wt: HHHHHHHHHHHHHHHHHHHHHHHHHHHH
 |||
 TM5-mt: HHHHHHHHHHHHHHHHHHHHHHHHHHHH



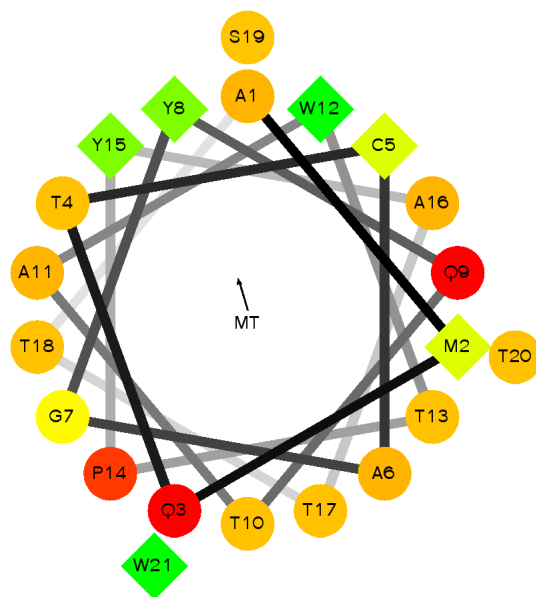
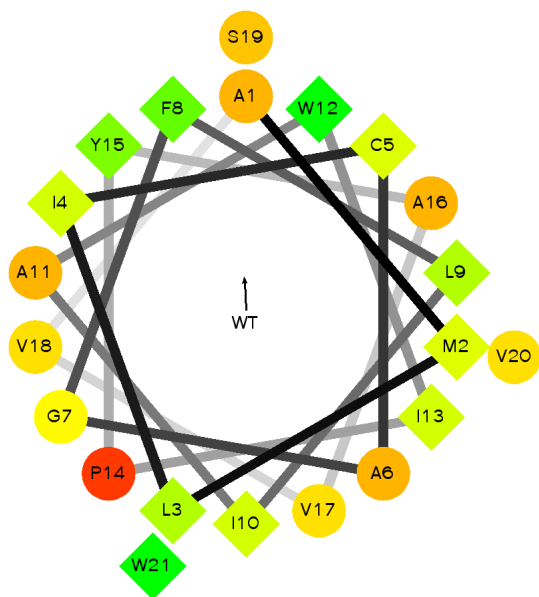
TM6

AA sequence comparison:

TM6-wt: AMLICAGFLIAWIPYAVVSVW
 ||**|||***|*|||**|*|
 TM6-mt: AMQTCAGYQTAWTPYATTSTW

Alpha-helix prediction comparison:

TM6-wt: HHHHHHHHHHHHCCHHHHHHHH
 |||||
 TM6-mt: HHHHHHHHHHHHCCHHHHHHHH



TM7

AA sequence comparison:

TM7-wt: VPTLLAKSAAMYNPPIIYOVID
 *||**|||**||**||
 TM7-mt: TPTQQAKSAAMYNPTTYQTTD

Alpha-helix prediction comparison:

TM7-wt: HHHHHHHHHHHCHCHHHHHHCC
 |||||
 TM7-mt: HHHHHHHHHHHCCCHHHHHCC

