

REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: O14718

User: siqipian2008@outlook.com

Designing code: QTY

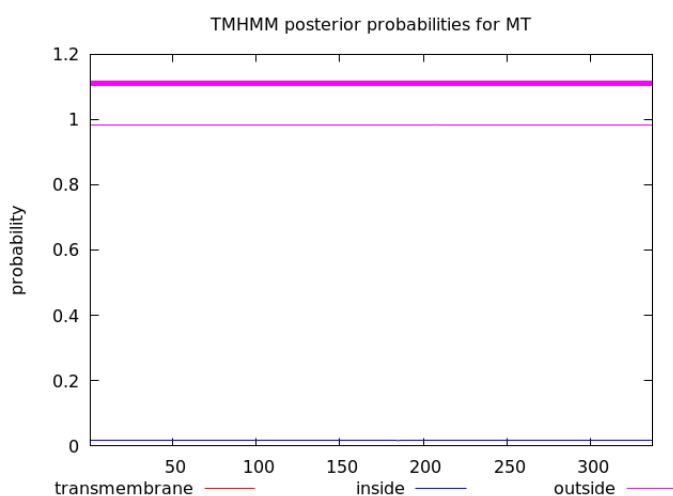
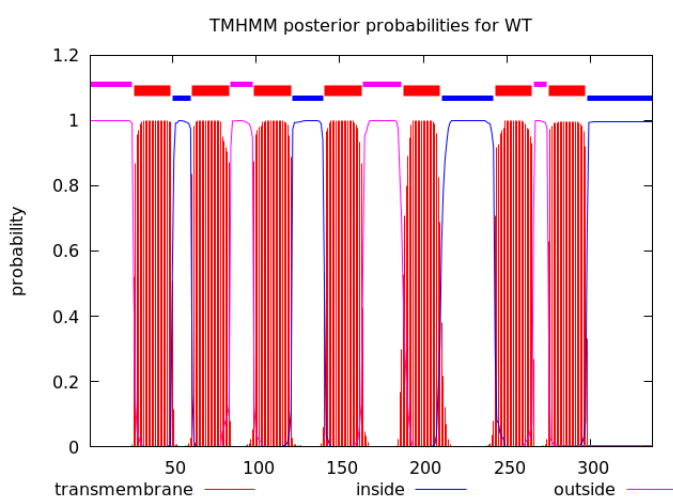
Length of protein sequence: 337

Number of modified TM regions: 7

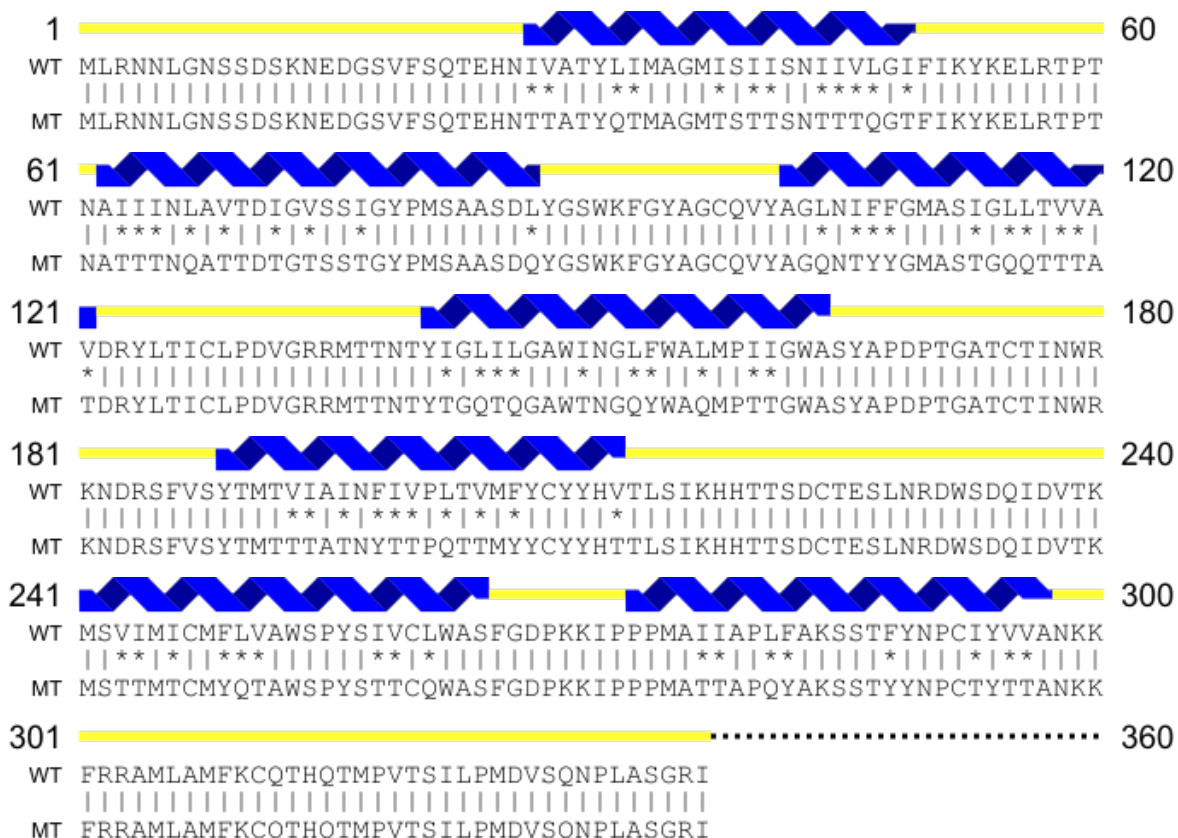
2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	8.77	37.4229	0.3941	/	/
MT	8.72	37.4575	-0.7082	40.96	20.18

3. Comparison of TM prediction:



4. Comparison of sequences:



5. Detailed comparison of TM regions:

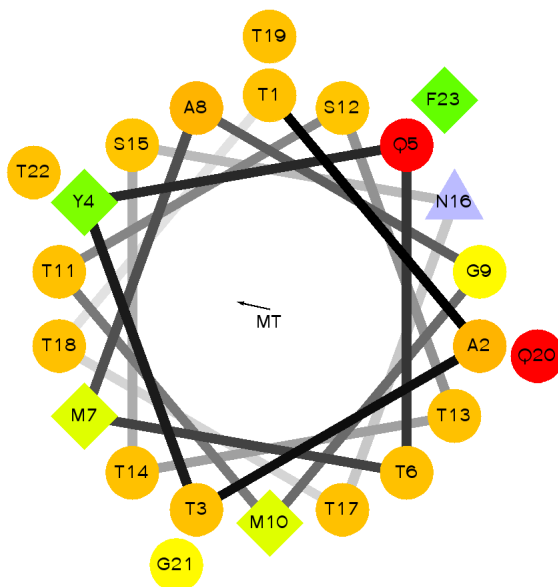
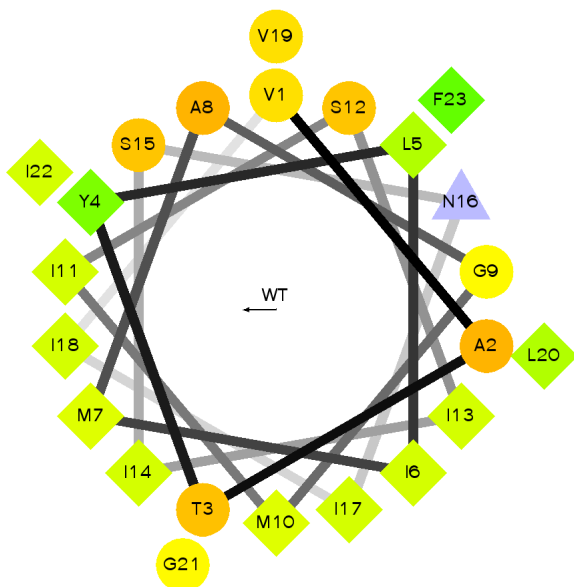
TM1

AA sequence comparison:

TM1-wt: VATYLI MAGMISII SNII VLGI F
*| | | *| | | *| | | *| | | *|
TM1-mt: TATYOT MAGMTSTTSNTTTTGTF

Alpha-helix prediction comparison:

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



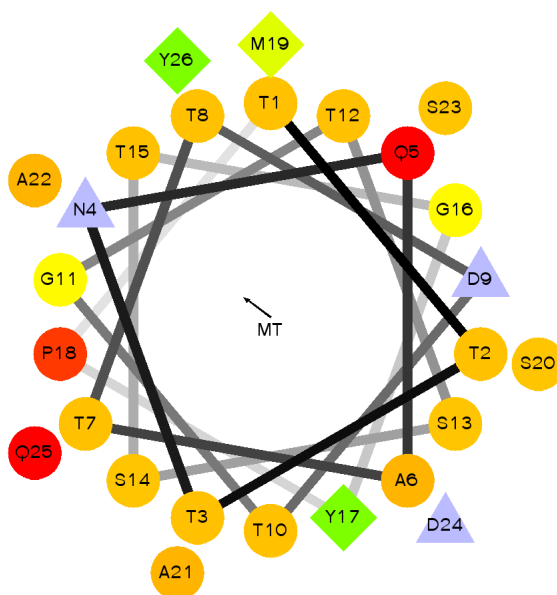
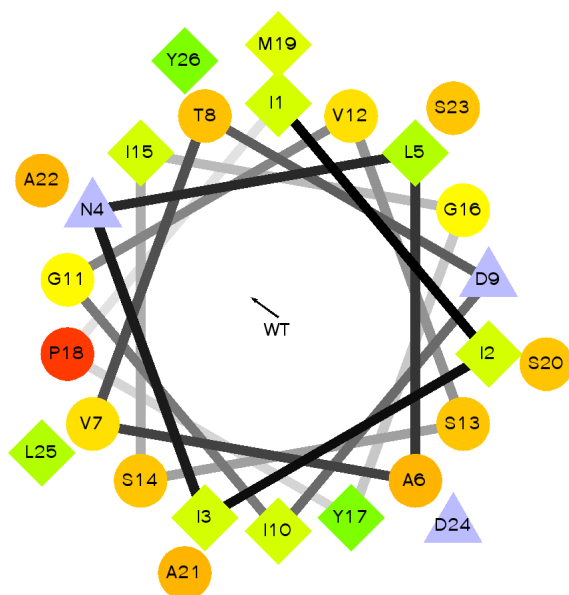
TM2

AA sequence comparison:

TM2-wt : I I I N L A V T D I G V S S I G Y P M S A A S D L Y
 * * * | * | * | * | * | * | * | * |
 TM2-mt : T T T N Q A T T D T G T S S T G Y P M S A A S D Q Y

Alpha-helix prediction comparison:

TM2-wt: HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
| | | | | | | | | | | | * * | | | | | | | |
TM2-mt: HHHHHHHHHHHHHHHHHHCCHHHHHHHHHHH



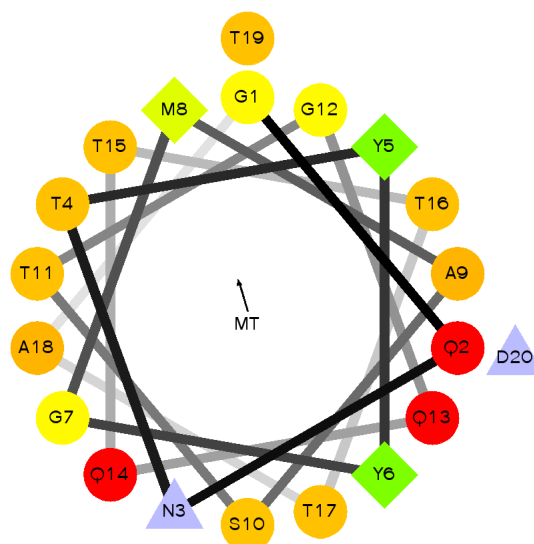
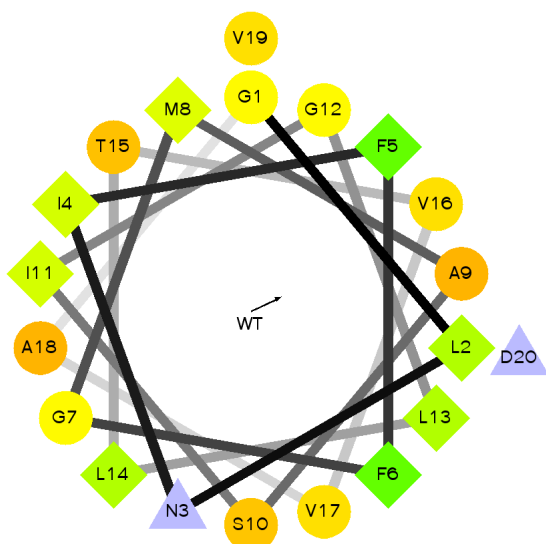
TM3

AA sequence comparison:

TM3-wt: GLNIFFGMASIGLLTVVAVD
 |*|***|||*|**|**|*|
 TM3-mt: GONTYYGMASSTGOQTTTATD

Alpha-helix prediction comparison:

TM3-wt: CHHHHHHHHHHHHHHHHHHHHHH
| | | | | | | | | | | | |
TM3-mt: CHHHHHHHHHHHHHHHHHHHHHH



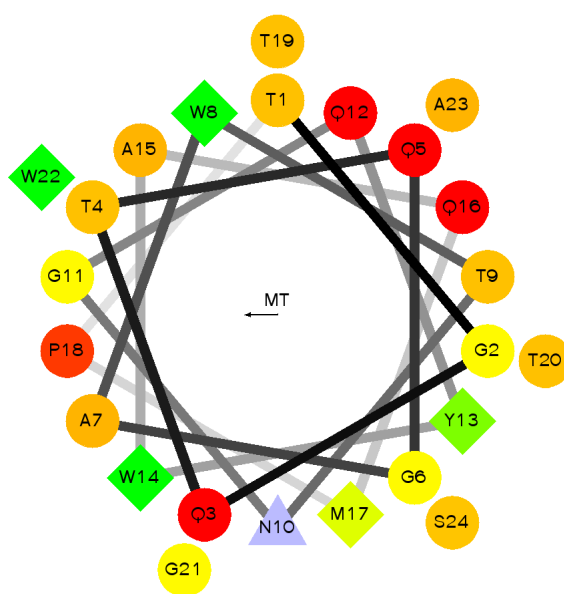
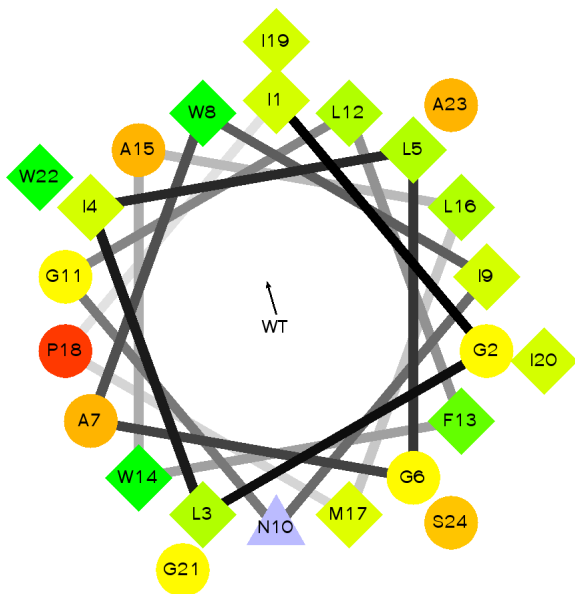
TM4

AA sequence comparison:

TM4-wt : IGLILGAWINGLFWALMPIIGWAS
* | * * * | | * | | * * | | * | * *
TM4-mt : TGQTQGAWTNGQYWAQMPTTGWAS

Alpha-helix prediction comparison:

TM4-wt: HHHHHHHHHHHHHHHHHHHHCCEEEEEEC*
 TM4-mt: HHHHHHHHHHHHHHHHHHHHCCEEEEEE

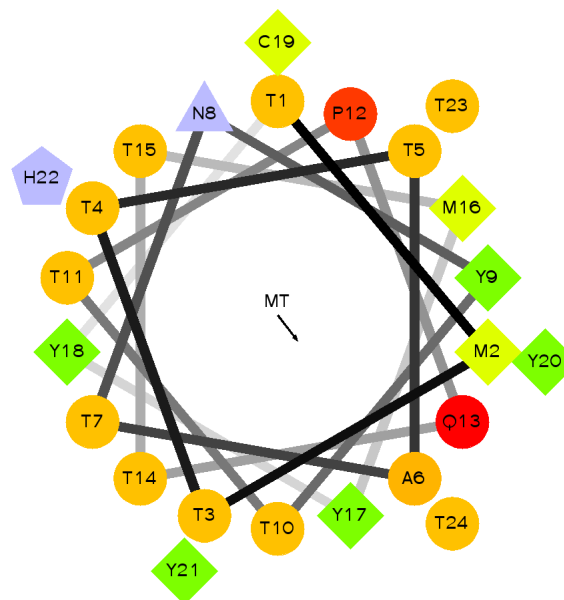
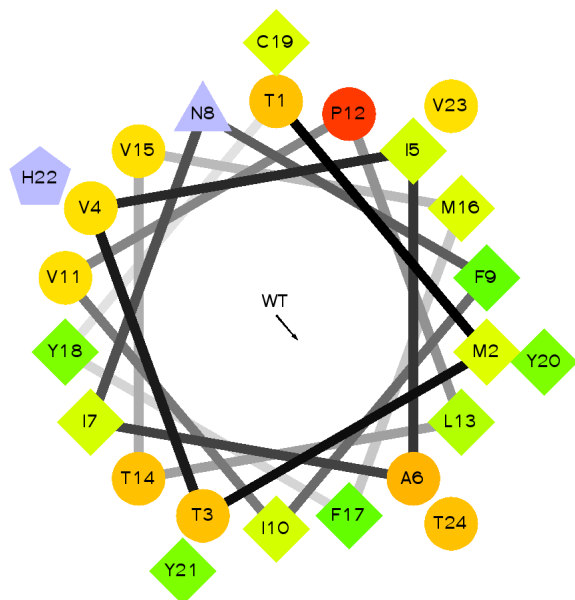
**TM5**

AA sequence comparison:

TM5-wt: TMTVIAINFIVPLTVMFYCYHHVT
 TM5-mt: TMTTTATNYTTPQTMMYYCYHHT

Alpha-helix prediction comparison:

TM5-wt : HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
| | | | |
TM5-mt : HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH



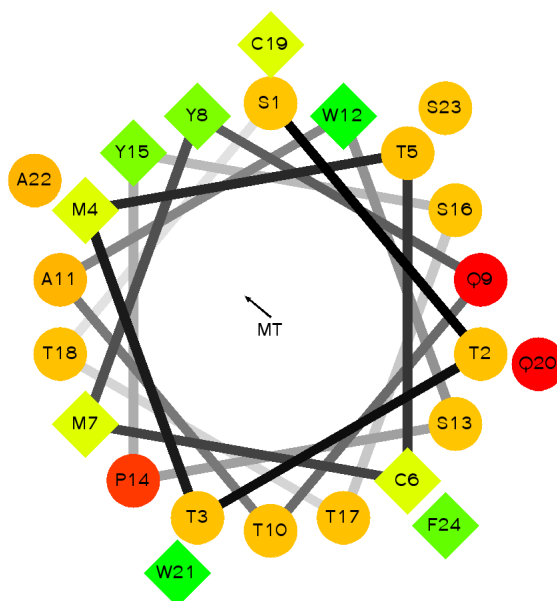
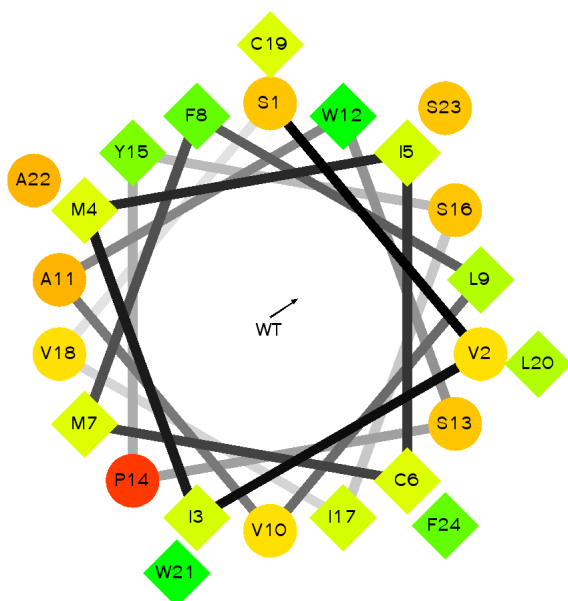
TM6

AA sequence comparison:

TM6-wt: SVIMICMFLVAWSPYSIVCLWASF
 |*|*| |**|*|
 TM6-mt: STTMTCMYQTAWSPYSTTCQWASF

Alpha-helix prediction comparison:

TM6-wt: HHHHHHHHHHHHHHCCHHHHHHHHHHHH
 |||||
 TM6-mt: HHHHHHHHHHHHHHCCHHHHHHHHHHHH

**TM7**

AA sequence comparison:

TM7-wt: PMAIIAPLFAKSSTFYNPCIYVVAN
 |||**||**||*|||*||**||
 TM7-mt: PMATTAPQYAKSSTYYNPCTYTTAN

Alpha-helix prediction comparison:

TM7-wt : HHHHHHHHHHHHHHCCCCCHHHHHHHC
| | | | | | | | | | * * *
TM7-mt : HHHHHHHHHHHHHHCCCCCHEHHHCC

