

REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: B4Y105

User: siqipian2008@outlook.com

Designing code: QTY

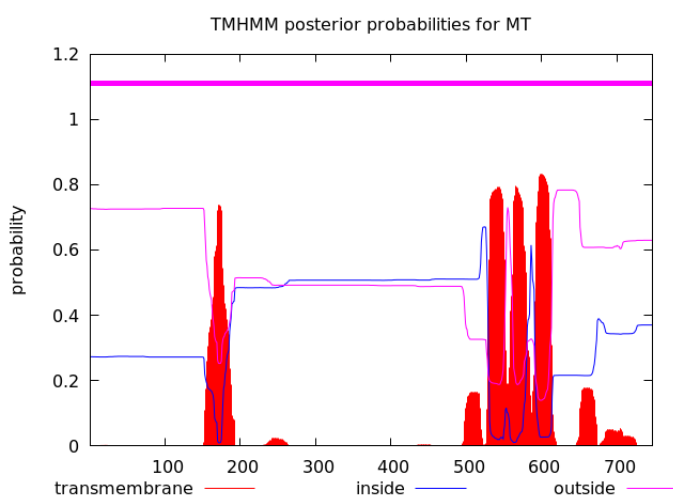
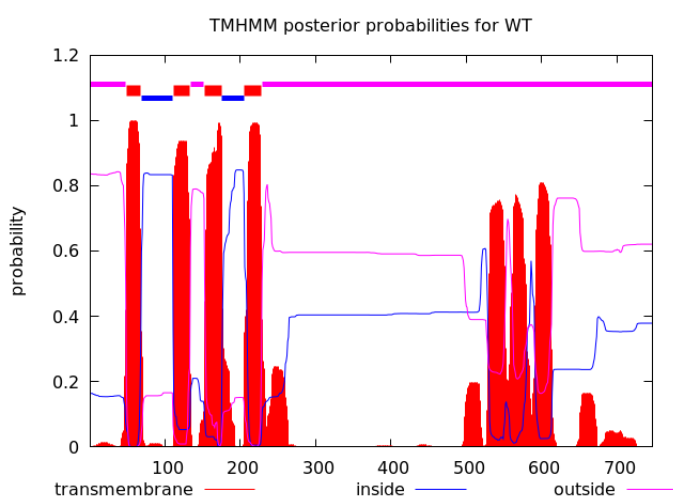
Length of protein sequence: 747

Number of modified TM regions: 4

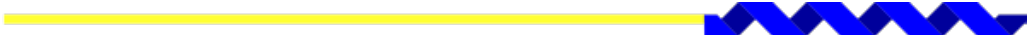
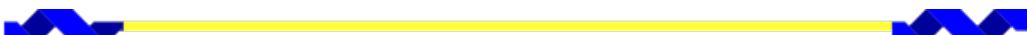


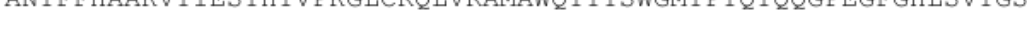

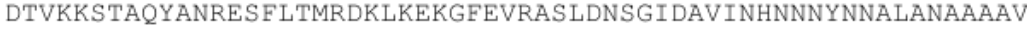
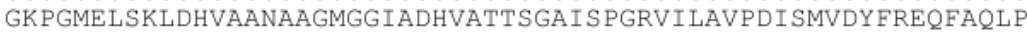
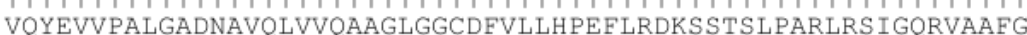




2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	6.73	77.8289	0.2386	/	/
MT	6.73	78.0919	-0.0394	40.23	4.69

3. Comparison of TM prediction:



4. Comparison of sequences:

1		60
WT	MDHPVARSLIGSSYTNLNNGSIVIPSDACFCMKWLKSKGSPVALKMANALQWAAFALSVI	
MT	MDHPVARSLIGSSYTNLNNGSIVIPSDACFCMKWLKSKGSPTAQKMANAQWAAAYAQSTT	
61		120
WT	ILIYYAYATWRITTCGWEEVYVCCVELTKVVIEFFHEFDEPGMLYLANGNRVLWLRYGEWL	
MT	TQTYAYATWRITTCGWEEVYVCCVELTKVVIEFFHEFDEPGMLYLANGNRVLWQRYGEWQ	
121		180
WT	LTCPVILIHLSNLTGLKDDYNKRTMRLLVSDVGTIVWGATAAMSTGYIKVIFLLGCMYG	
MT	QTCPTTQTHQSNQTGLKDDYNKRTMRQQTSDTGTITWGATAAMSTGYIKVIFLLGCMYG	
181		240
WT	ANTFFHAAKVYIESYHTVPKGLCRQLVRAMAWLFFVSWGMPVLFLLGPEGFGHLSVYGS	
MT	ANTFFHAAKVYIESYHTVPKGLCRQLVRAMAWQYYTSWGMYPYQYQQGPEGFGHLSVYGS	
241		300
WT	TIGHTIIDLLSKNCWGLLGHFRLRLKIHILLYGDIRKVQKIRVAGEELEVETLMTEEAP	
MT	TIGHTIIDLLSKNCWGLLGHFRLRLKIHILLYGDIRKVQKIRVAGEELEVETLMTEEAP	
301		360
WT	DTVKKSTAQYANRESFLTMRDKLKEKGFEVRASLDNSGIDAVINHNNNNYNALANAAAAV	
MT	DTVKKSTAQYANRESFLTMRDKLKEKGFEVRASLDNSGIDAVINHNNNNYNALANAAAAV	
361		420
WT	GKPGMELSKLDHVAANAAGMGGIADHVATTSGAISPGRVILAVPDISMVDYFREQFAQLP	
MT	GKPGMELSKLDHVAANAAGMGGIADHVATTSGAISPGRVILAVPDISMVDYFREQFAQLP	
421		480
WT	VQYEVVPALGADNAVQLVVQAAGLGGCDFVLLHPEFLRDKSSTSLPARLRSIGQRVAAFQ	
MT	VQYEVVPALGADNAVQLVVQAAGLGGCDFVLLHPEFLRDKSSTSLPARLRSIGQRVAAFQ	
481		540
WT	WSPVGPVRDLIESAGLDGWLEGPSFGLGISLPNLASLVLRMQHARKMAAMLGGMGMLGS	
MT	WSPVGPVRDLIESAGLDGWLEGPSFGLGISLPNLASLVLRMQHARKMAAMLGGMGMLGS	
541		600
WT	NLMSGSGGVGLMGAGSPGGGGGAMGVGMTGMGMVGTNAMGRGAVGNSVANASMGGGSAGM	
MT	NLMSGSGGVGLMGAGSPGGGGGAMGVGMTGMGMVGTNAMGRGAVGNSVANASMGGGSAGM	
601		660
WT	GMGMMGMVGAGVGGQQQMGANGMGPTSFQLGSNPLYNTAPSPLSSQPGGDASAAAAAAA	
MT	GMGMMGMVGAGVGGQQQMGANGMGPTSFQLGSNPLYNTAPSPLSSQPGGDASAAAAAAA	
661		720
WT	AAATGAASNSMNAMQAGGSVRNSGILAGGLGSMMGPPGAPAAAPTAAATAAPAVTMGAPGG	
MT	AAATGAASNSMNAMQAGGSVRNSGILAGGLGSMMGPPGAPAAAPTAAATAAPAVTMGAPGG	
721		780
WT	GGAAASEAEMLQQLMAEINRLKSELGE	
MT	GGAAASEAEMLQQLMAEINRLKSELGE	

5. Detailed comparison of TM regions:

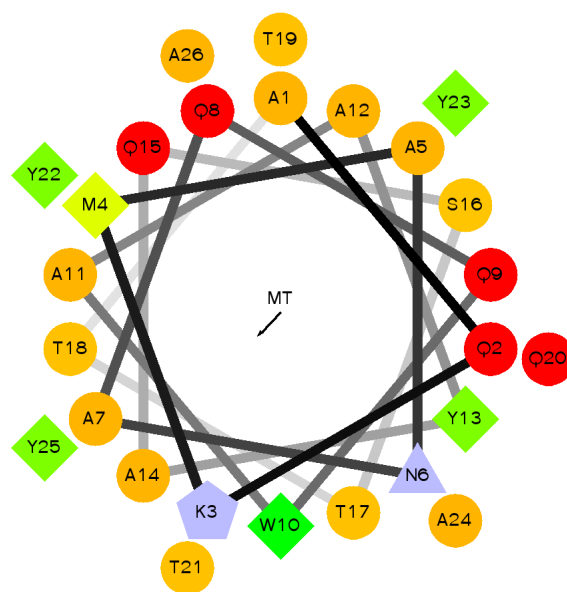
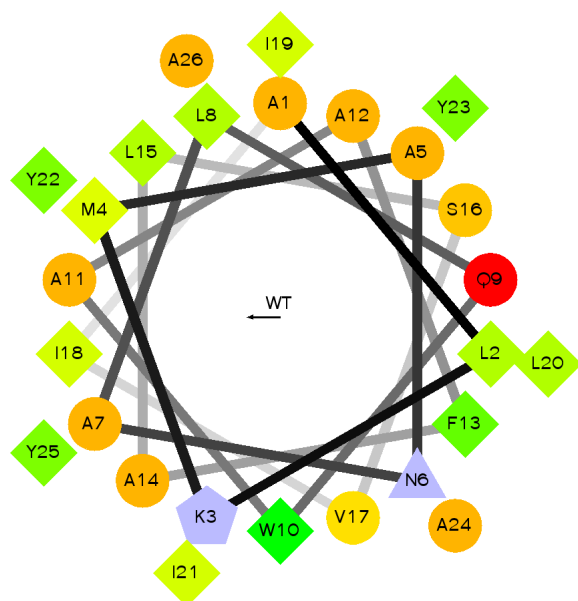
TM1

AA sequence comparison:

TM1-wt: ALKMANALQWAAFALSVIILIYYAYA
 | * | | | * | | | * | * | * * * * | | | |
 TM1-mt: AOKMANAQOWAAYAOSTTTTQTYAYA

Alpha-helix prediction comparison:

TM1-wt: HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
| | | | | | | | | | * * * | | | | |
TM1-mt: HHHHHHHHHHHHHHHHHHHCCCCHHHHHHHE

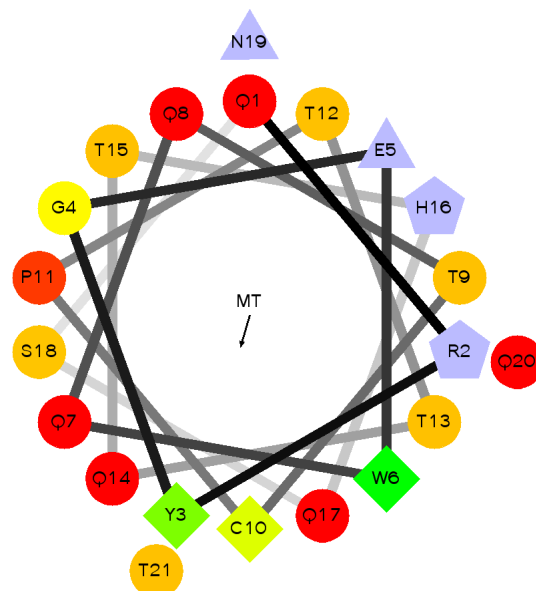
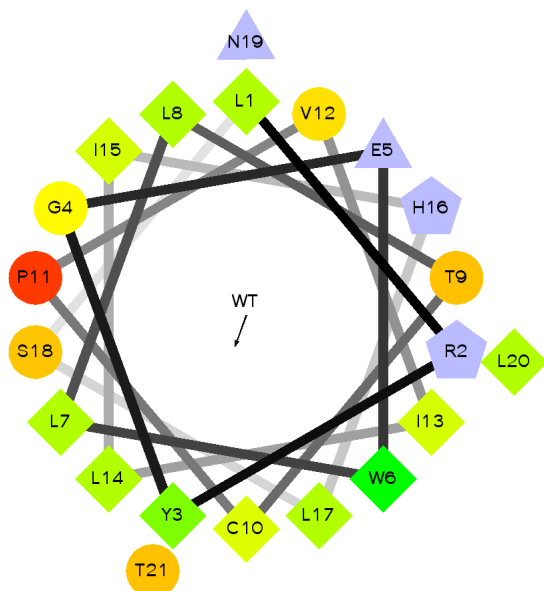
**TM2**

AA sequence comparison:

TM2-wt: LRYGEWLLTCPVILIHLSNLT
*| ||| **| ||| ****|*| |*|
TM2-mt: QRYGEWQOTCPTTQTHOSNOT

Alpha-helix prediction comparison:

TM2-wt: EEECEEEECCHHHHHHHHHHC
| | * | * * * * | * * * * * * * * *
TM2-mt: EECCCCCCCCCCCCCCCCCCC



TM3

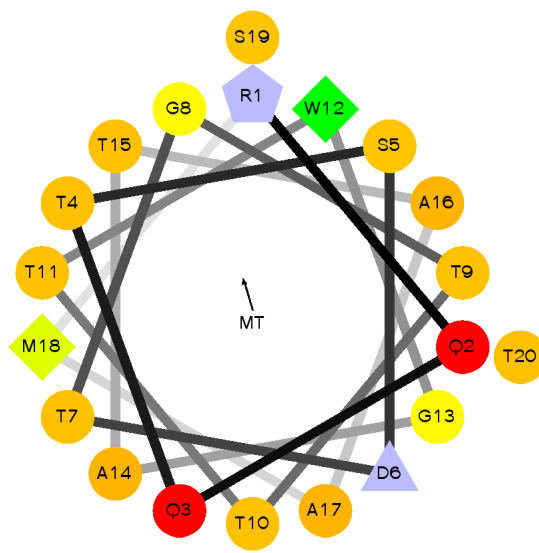
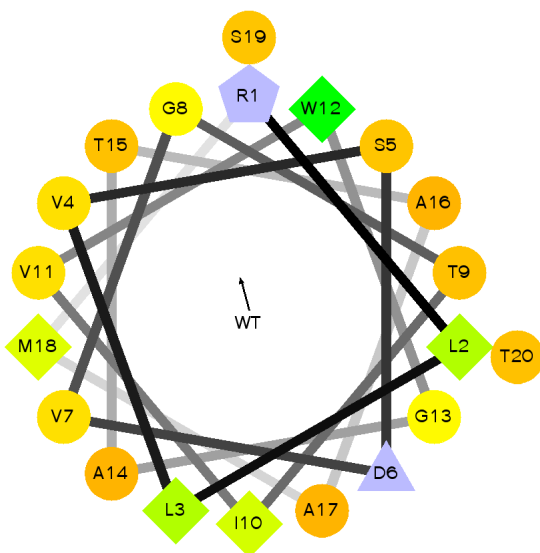
AA sequence comparison:

TM3-wt: RLLVSDVGTIVWGATAAMST
 |***|*|**|||
 TM3-mt: RQQTSDTGTTTWGATAAMST

Alpha-helix prediction comparison:

TM3-wt: HHHHHHHHHHHHHHHHHHHHHHHHHH
 ***** ||||*

TM3-mt: ECCCCCCCCCCCCCHHHHHHCH



TM4

AA sequence comparison:

TM4-wt: MAWLFFVSWGMFPVLFLLGP
 |||****|||*|*****||
 TM4-mt: MAWQYYTSWGMYPYQYQGP

Alpha-helix prediction comparison:

TM4-wt: HHHHHHHHHHCHHEEEEC
 ||||| ||| *** |||
 TM4-mt: HHHHHHHHCCCCCECCCC

