REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: P04000
User: siqipan2008@outlook.com
Designing code: QTY
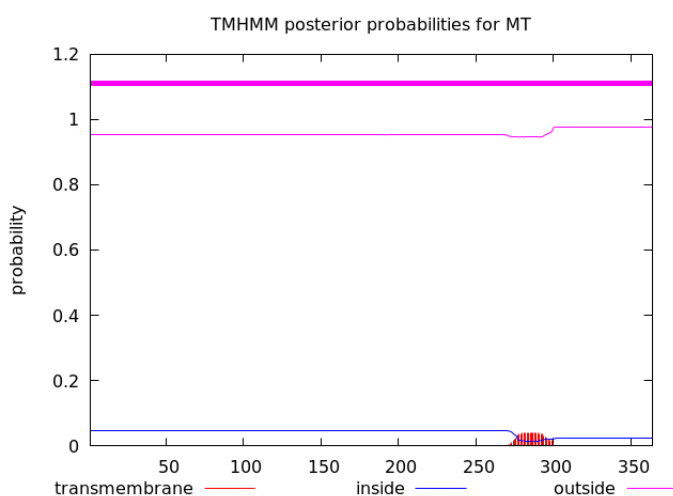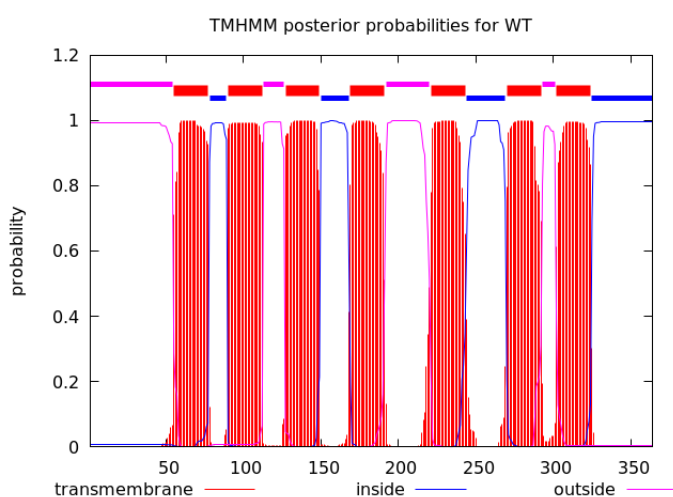Length of protein sequence: 364
Number of modified TM regions: 7

2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	8.89	40.5744	0.3753	/	/
MT	8.83	40.7642	-0.6543	40.12	18.96

3. Comparison of TM prediction:

4. Comparison of sequences:

```
  1 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━◆◆◆◆◆◆  60
 WT MAQQWSLQRLAGRHPQDSYEDSTQSSIFTYTNSNSTRGPFEGPNYHIAPRWVYHLTSVWM
    ||||||||||||||||||||||||||||||||||||||||||||||||||||*||*||
 MT MAQQWSLQRLAGRHPQDSYEDSTQSSIFTYTNSNSTRGPFEGPNYHIAPRWVYHQTSTWM

 61 ◆◆◆◆◆◆◆◆◆◆━━━━━━━━━━━━◆◆◆◆◆◆◆◆◆◆◆◆◆◆◆━━━ 120
 WT IFVVTASVFTNGLVLAATMKFKKLRHPLNWILVNLAVADLAETVIASTISIVNQVSGYFV
    ****|||**|||***||||||||||||||||||***|*|*||*|||**|||*|**||*|||||
 MT TYTTTASTYTNGQTQAATMKFKKLRHPLNWTQTNQATADQAETTTASTTSTTNQTSGYFV

121 ━━━━━━━━◆◆◆◆◆◆◆◆◆━━━━━━━━━━━━━━◆◆◆◆◆ 180
 WT LGHPMCVLEGYTVSLCGITGLWSLAIISWERWMVVCKPFGNVRFDAKLAIVGIAFSWIWA
    |||||||||||*|*||*||*||*|**|||||||||||||||||||||**|*|*||*||
 MT LGHPMCVLEGYTTSQCGTTGQWSQATTSWERWMVVCKPFGNVRFDAKLATTGTAYSWTWA

181 ◆◆◆◆◆◆◆━━━━━━━━━━━━━◆◆◆◆◆◆◆◆◆◆◆◆◆◆ 240
 WT AVWTAPPIFGWSRYWPHGLKTSCGPDVFSGSSYPGVQSYMIVLMVTCCIIPLAIIMLCYL
    |*||||||**|||||||||||||||||||||||||***|*|||**|*|**|*||*
 MT ATWTAPPTYGWSRYWPHGLKTSCGPDVFSGSSYPGVQSYMTTQMTTCCTTPQATTMQCYQ

241 ◆◆◆◆━━━━━━━━━━━◆◆◆◆◆◆◆◆◆◆◆━━━━━ 300
 WT QVWLAIRAVAKQQKESESTQKAEKEVTRMVVVMIFAYCVCWGPYTFFACFAAANPGYAFH
    |*|*|*|||||||||||||||||||||||||***|**|||*||||||**||*||||||||
 MT QTWQATRAVAKQQKESESTQKAEKEVTRMTTTMTYAYCTCWGPYTYYACYAAANPGYAFH

301 ◆◆◆◆◆◆◆◆◆◆━━━━━━━━━━━━━━━━━━━━━━━━━━━ 360
 WT PLMAALPAYFAKSATIYNPVIYVFMNRQFRNCILQLFGKKVDDGSELSSASKTEVSSVSS
    |*|||*|||*|||||*|||**|**||||||||||||||||||||||||||||||||
 MT PQMAAQPAYYAKSATTYNPTTYTYMNRQFRNCILQLFGKKVDDGSELSSASKTEVSSVSS

361 ━━━·········································································· 420
 WT VSPA
    ||||
 MT VSPA
```

5. Detailed comparison of TM regions:

TM1

AA sequence comparison:

```
TM1-wt:  HLTSVWMIFVVTASVFTNGLVLAAT
         |*||*||****|||**|||***|||
TM1-mt:  HQTSTWMTYTTTASTYTNGQTQAAT
```

Alpha-helix prediction comparison:

```
TM1-wt:  HHHHHHHHHHHHHHHHHHHHHHHHH
         |||||||||||||||||||||||||
TM1-mt:  HHHHHHHHHHHHHHHHHHHHHHHHH
```
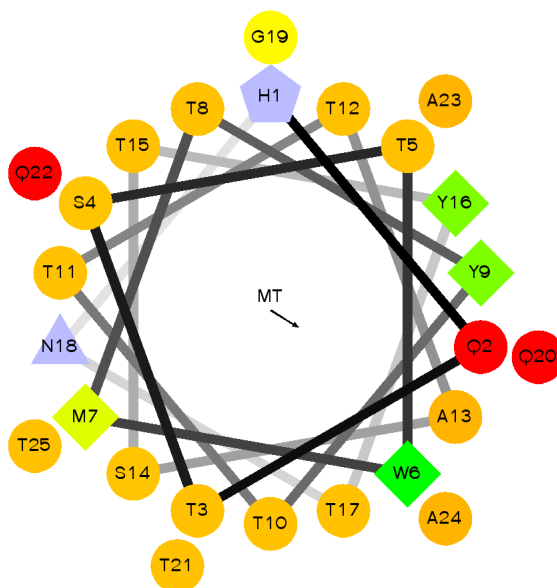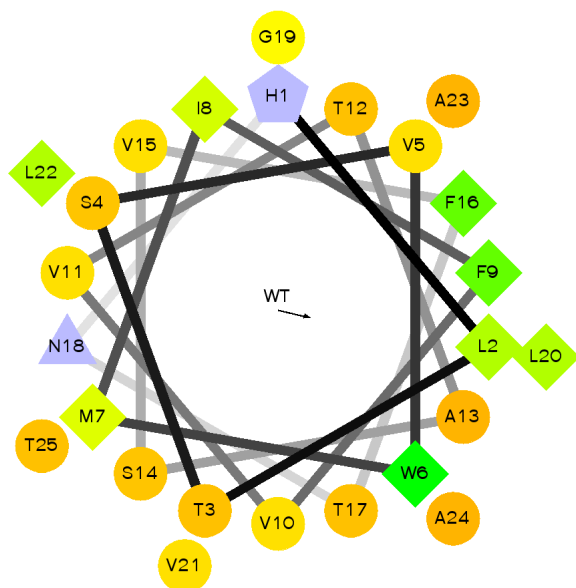

TM2

AA sequence comparison:

```
TM2-wt:  ILVNLAVADLAETVIASTISIVNQVS
         ***|*|*||*|||**|||*|**||*|
TM2-mt:  TQTNQATADQAETTTASTTSTTNQTS
```

Alpha-helix prediction comparison:

```
TM2-wt:  HHHHHHHHHHHHHHHHHHHHHHHHHC
         ||||||||||||||||||**|||||||*|
TM2-mt:  HHHHHHHHHHHHHHHCCHHHHHHHCC
```
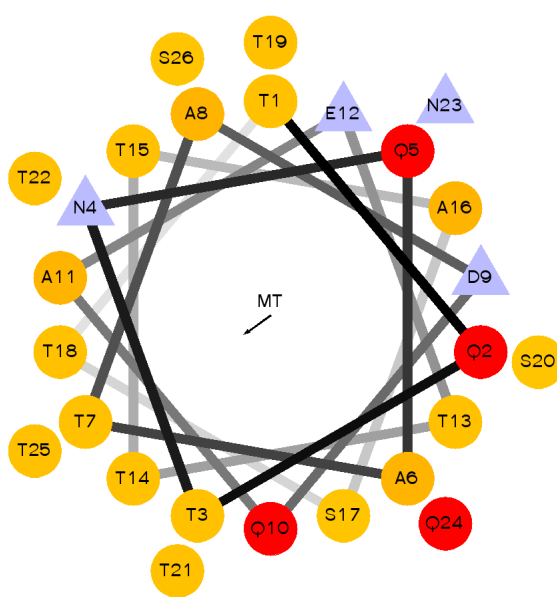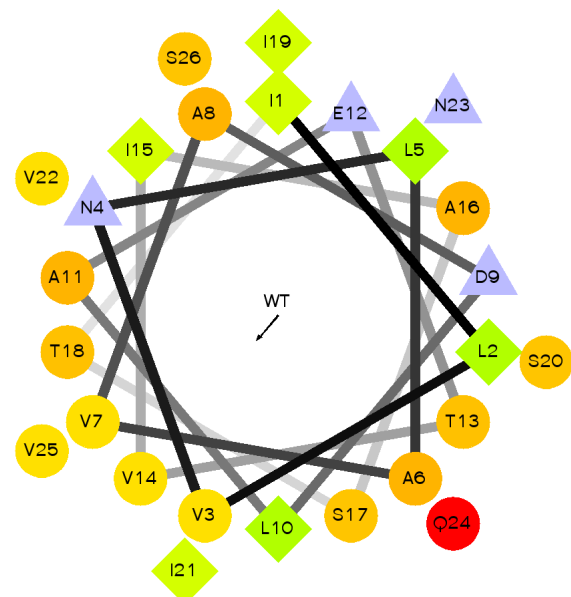
TM3

AA sequence comparison:

```
TM3-wt:  YTVSLCGITGLWSLAIISWE
         ||*|*||*||*||*|**|||
TM3-mt:  YTTSQCGTTGQWSQATTSWE
```

Alpha-helix prediction comparison:

```
TM3-wt:  HHHHHHHHHHHHHHHHHHHH
         *|||||||||||||||||||
TM3-mt:  CHHHHHHHHHHHHHHHHHHH
```
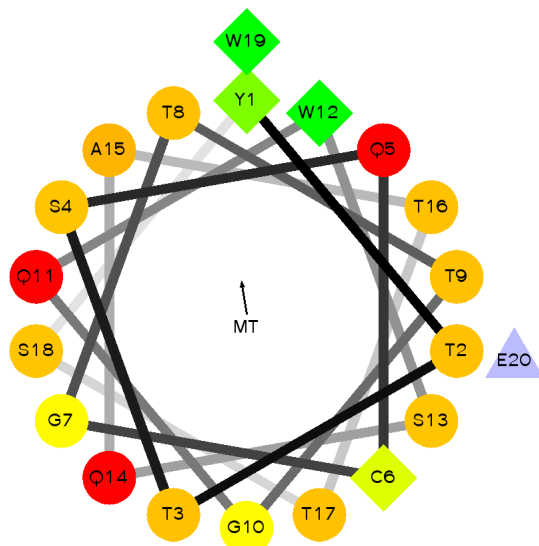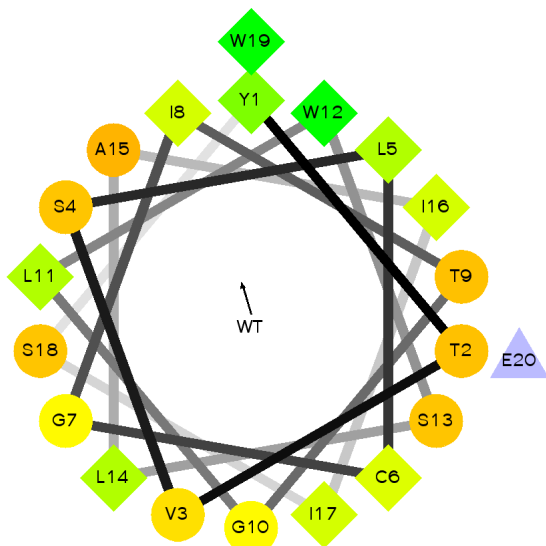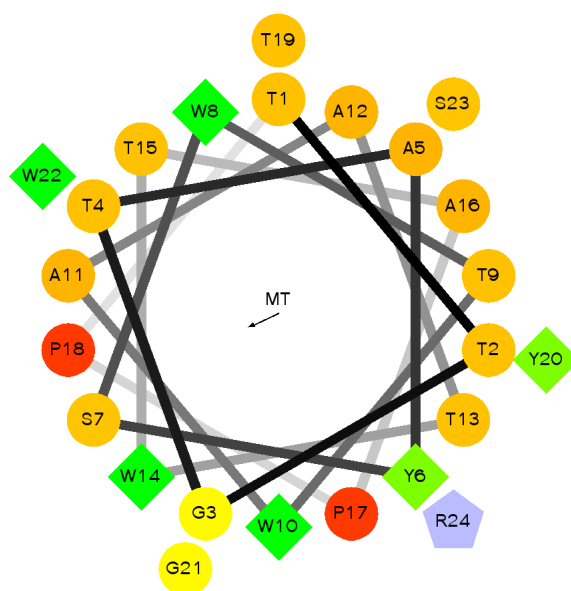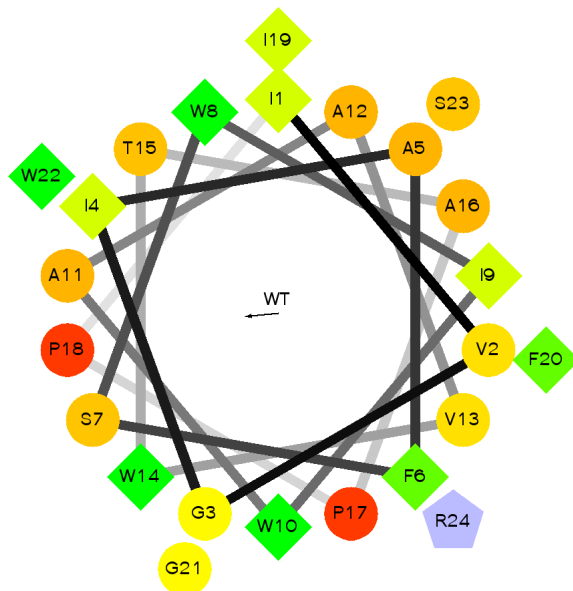

TM4

AA sequence comparison:

```
TM4-wt:  IVGIAFSWIWAAVWTAPPIFGWSR
         **|*|*||*|||*||||||**||||
TM4-mt:  TTGTAYSWTWAATWTAPPTYGWSR
```

Alpha-helix prediction comparison:

```
TM4-wt:  HHHHHHHHHHHHHHHHCCCEEEEEE
         ||||||||||||||||||||||**
TM4-mt:  HHHHHHHHHHHHHHHHCCCEEEECC
```

AA sequence comparison:

```
TM5-wt:  MIVLMVTCCIIPLAIIMLCYLQVWLAIR
         |***|*|||**|*|**|*||*|*|*|*|
TM5-mt:  MTTQMTTCCTTPQATTMQCYQQTWQATR
```

Alpha-helix prediction comparison:

```
TM5-wt:  HHHHHHHHHHHHHHHHHHHHHHHHHHHH
         ||||||||||||||||||||||||||||
TM5-mt:  HHHHHHHHHHHHHHHHHHHHHHHHHHHH
```
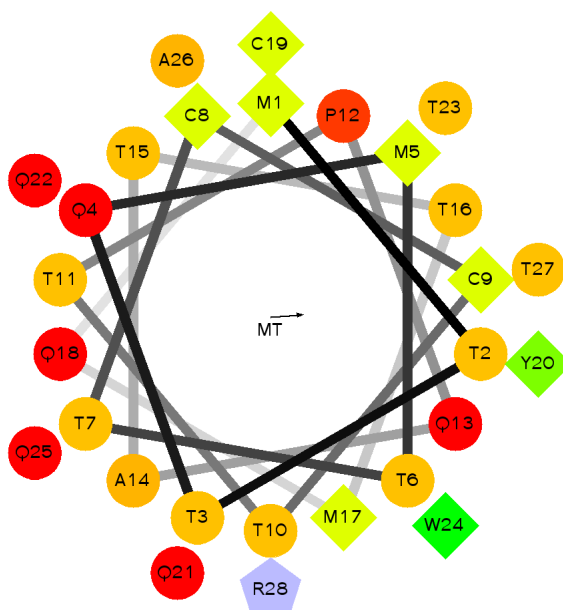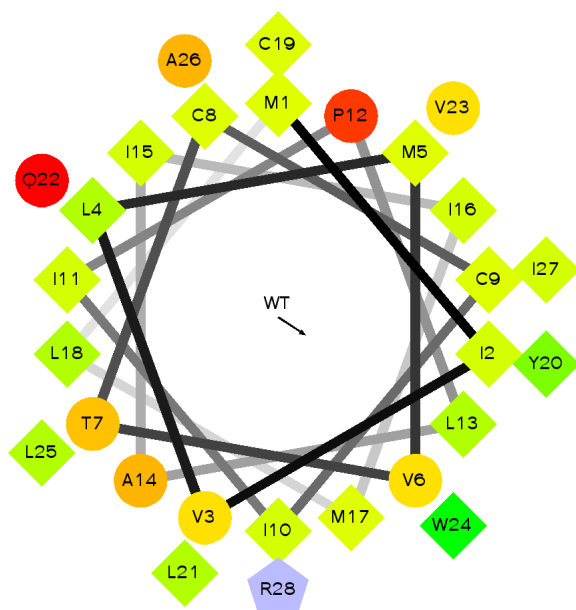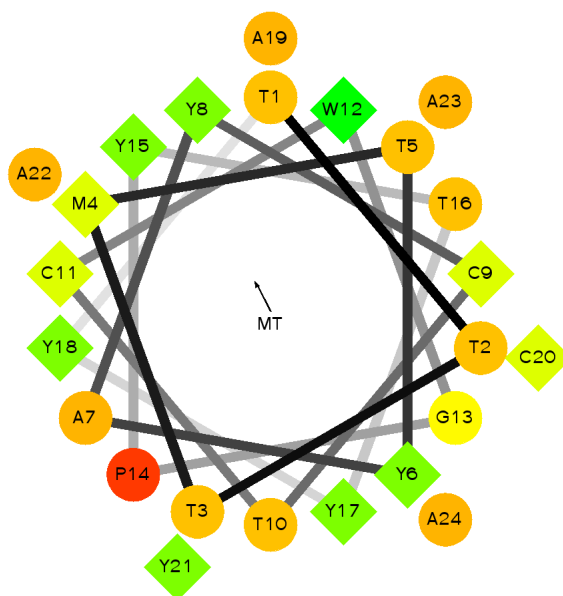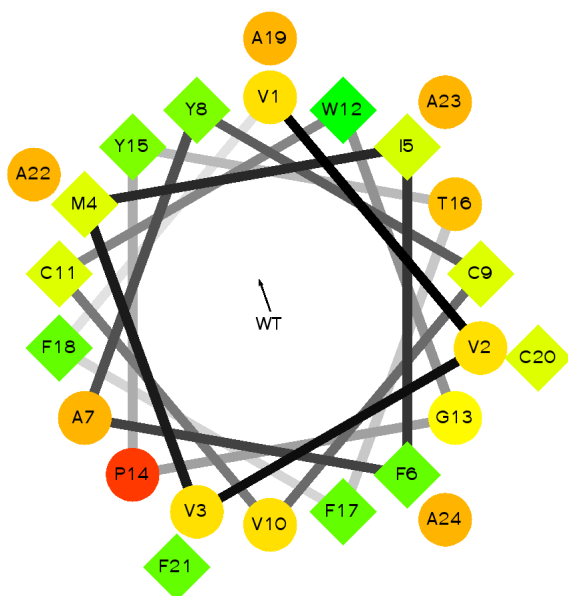
AA sequence comparison:

```
TM6-wt:  VVVMIFAYCVCWGPYTFFACFAAA
         ***|**|||*||||||**||*|||
TM6-mt:  TTTMTYAYCTCWGPYTYYACYAAA
```

Alpha-helix prediction comparison:

```
TM6-wt:  HHHHHHHHHHHCCHHHHHHHHHHHH
         ||||||||||||||||||||||||
TM6-mt:  HHHHHHHHHHHCCHHHHHHHHHHHH
```

TM7

AA sequence comparison:

```
TM7-wt:  LMAALPAYFAKSATIYNPVIYVFMN
         *|||*|||*|||||*|||**|**||
TM7-mt:  QMAAQPAYYAKSATTYNPTTYTYMN
```

Alpha-helix prediction comparison:

```
TM7-wt:  HHHHHHHHHHHHHCCHCHHHHHHHC
         |||||||||||||||*|||||||||
TM7-mt:  HHHHHHHHHHHHHCCCCHHHHHHHC
```