REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: P04001
User: siqipan2008@outlook.com
Designing code: QTY
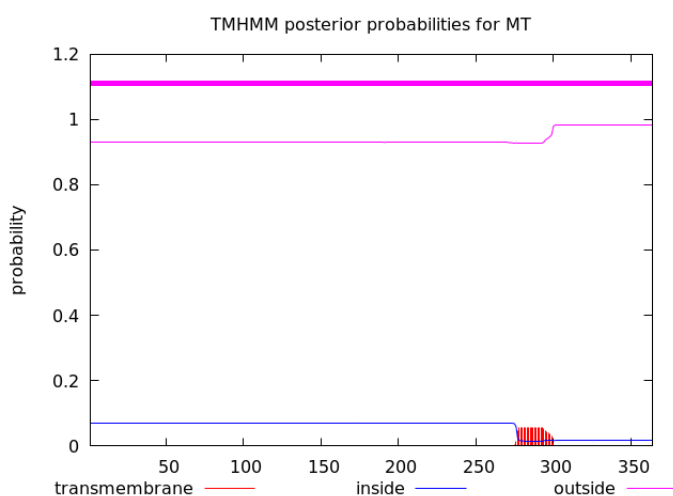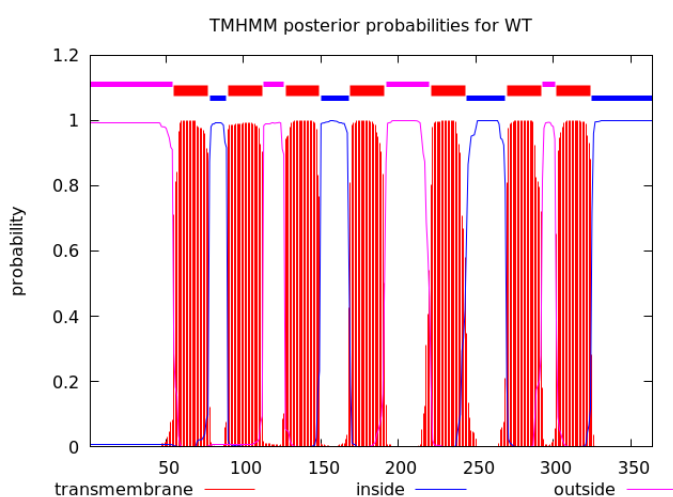Length of protein sequence: 364
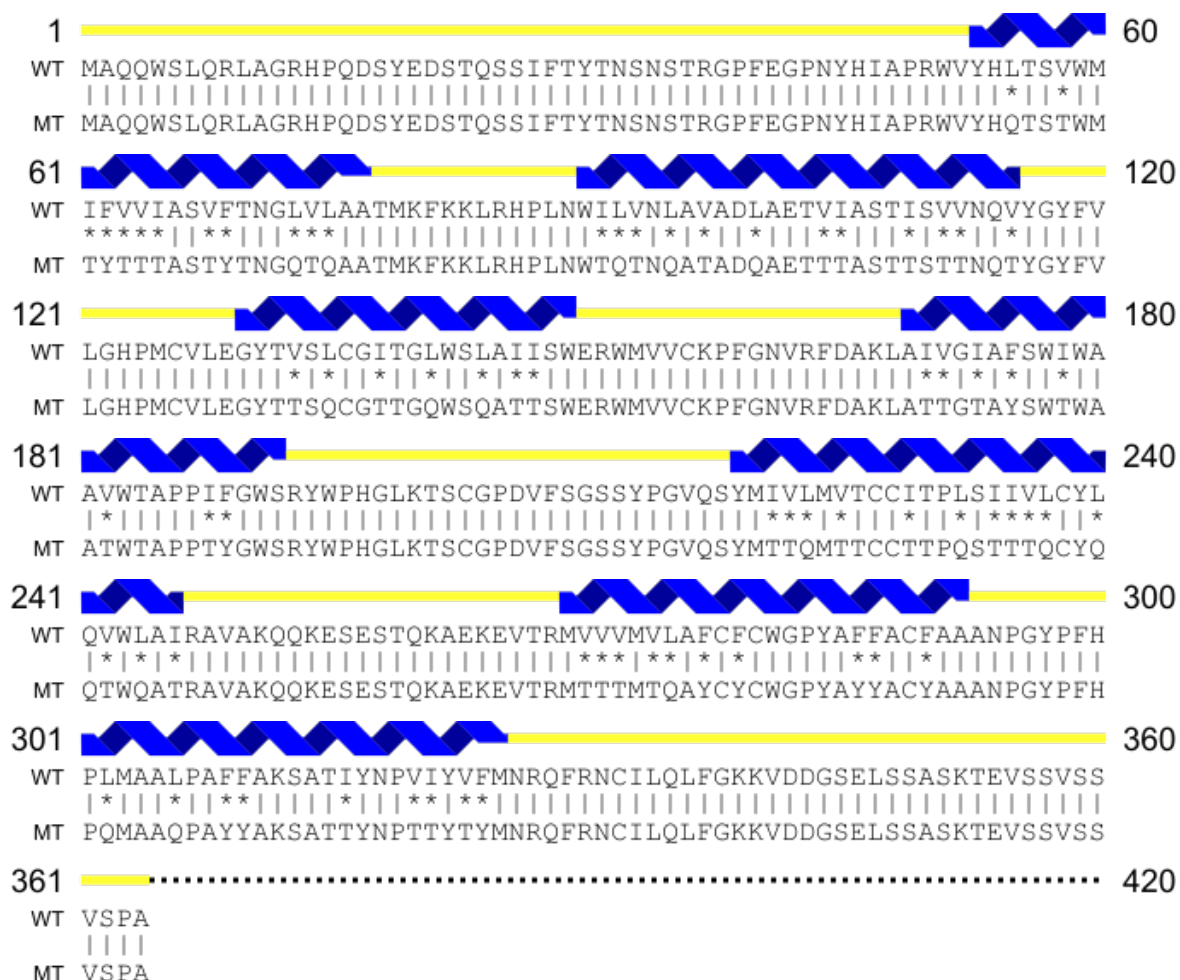Number of modified TM regions: 7

2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	8.90	40.5844	0.3904	/	/
MT	8.82	40.8492	-0.6801	41.86	19.78

3. Comparison of TM prediction:

4. Comparison of sequences:

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

 61                                                           120
WT  IFVVIASVFTNGLVLAATMKFKKLRHPLNWILVNLAVADLAETVIASTISVVNQVYGYFV
    *****||**|||***|||||||||||||||||***|*|*||*|||**|||*|**||*|||||
MT  TYTTTASTYTNGQTQAATMKFKKLRHPLNWTQTNQATADQAETTTASTTSTTNQTYGYFV

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

181                                                          240
WT  AVWTAPPIFGWSRYWPHGLKTSCGPDVFSGSSYPGVQSYMIVLMVTCCITPLSIIVLCYL
    |*||||||**||||||||||||||||||||||||||||||***|*|||*||*|****||*
MT  ATWTAPPTYGWSRYWPHGLKTSCGPDVFSGSSYPGVQSYMTTQMTTCCTTPQSTTTQCYQ

241                                                          300
WT  QVWLAIRAVAKQQKESESTQKAEKEVTRMVVVMVLAFCFCWGPYAFFACFAAANPGYPFH
    |*|*|*|||||||||||||||||||||||||***|**|*|*|||||**||*|||||||||
MT  QTWQATRAVAKQQKESESTQKAEKEVTRMTTTMTQAYCYCWGPYAYYACYAAANPGYPFH

301                                                          360
WT  PLMAALPAFFAKSATIYNPVIYVFMNRQFRNCILQLFGKKVDDGSELSSASKTEVSSVSS
    |*|||*||**||||||*|||**|**|||||||||||||||||||||||||||||||||
MT  PQMAAQPAYYAKSATTYNPTTYTYMNRQFRNCILQLFGKKVDDGSELSSASKTEVSSVSS

361                                                          420
WT  VSPA
    ||||
MT  VSPA
```

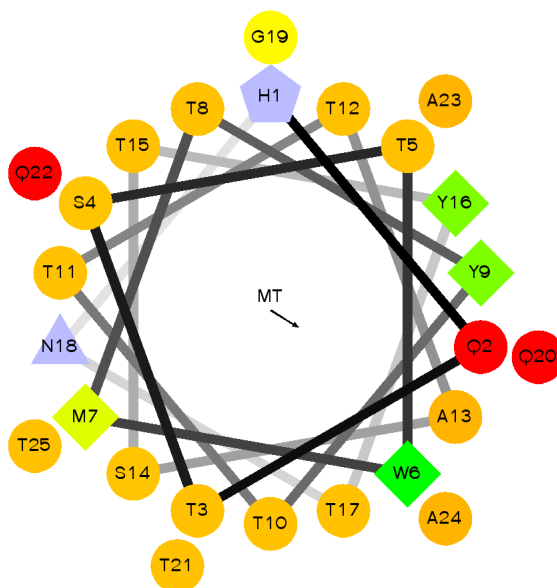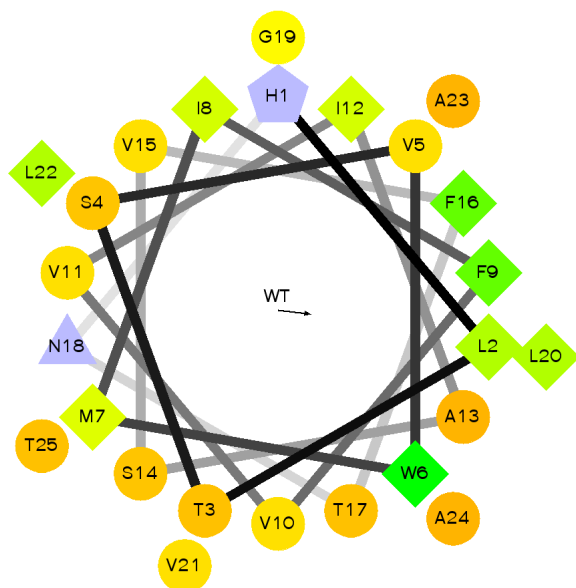## 5. Detailed comparison of TM regions:

TM1

AA sequence comparison:

```
TM1-wt:  HLTSVWMIFVVIASVFTNGLVLAAT
         |*||*||*****||**|||***|||
TM1-mt:  HQTSTWMTYTTTASTYTNGQTQAAT
```
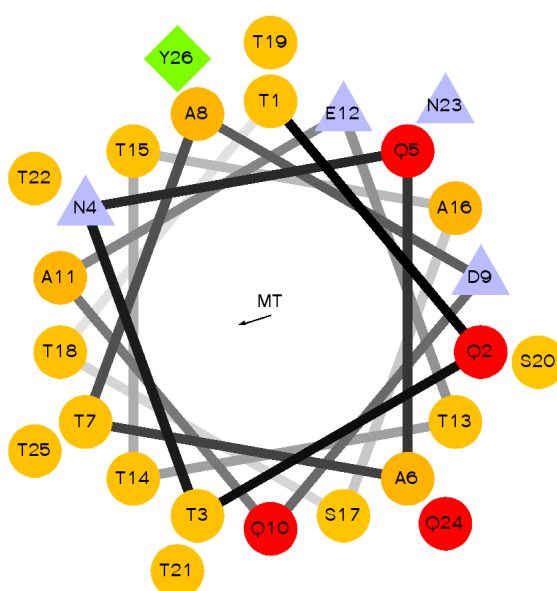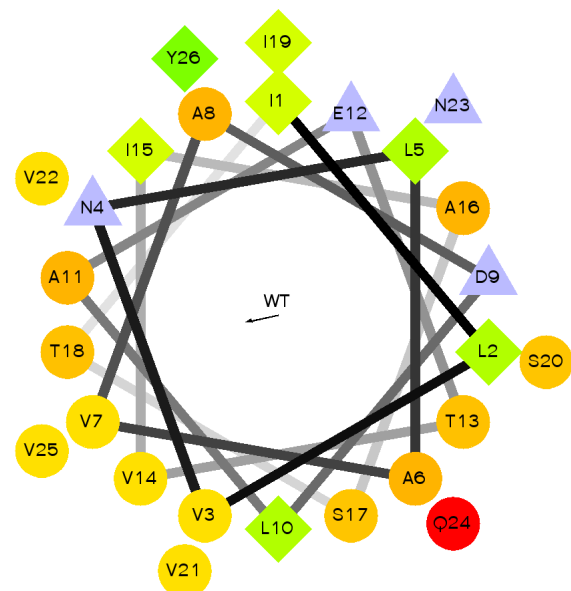
Alpha-helix prediction comparison:

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


TM2

AA sequence comparison:

```
TM2-wt:  ILVNLAVADLAETVIASTISVVNQVY
         ***|*|*||*|||**|||*|**||*|
TM2-mt:  TQTNQATADQAETTTASTTSTTNQTY
```

Alpha-helix prediction comparison:

```
TM2-wt:  HHHHHHHHHHHHHHHHHHHHHHHHHH
         ||||||||||||||||||*|||||||**
TM2-mt:  HHHHHHHHHHHHHHHHCHHHHHHHCC
```

TM3

AA sequence comparison:

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

Alpha-helix prediction comparison:

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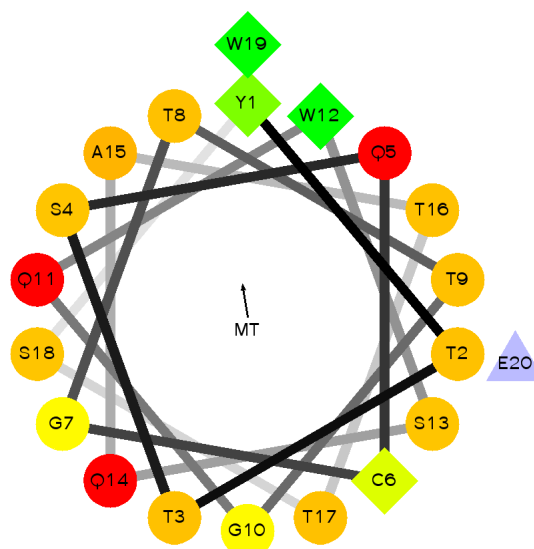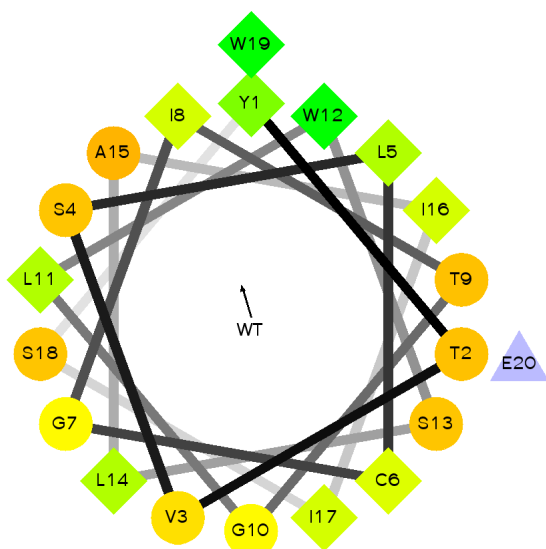

TM4

AA sequence comparison:

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

Alpha-helix prediction comparison:

```
TM4-wt:  HHHHHHHHHHHHHHHCCCEEEEEE
         ||||||||||||||||||||||***
TM4-mt:  HHHHHHHHHHHHHHHCCCEEECCC
```
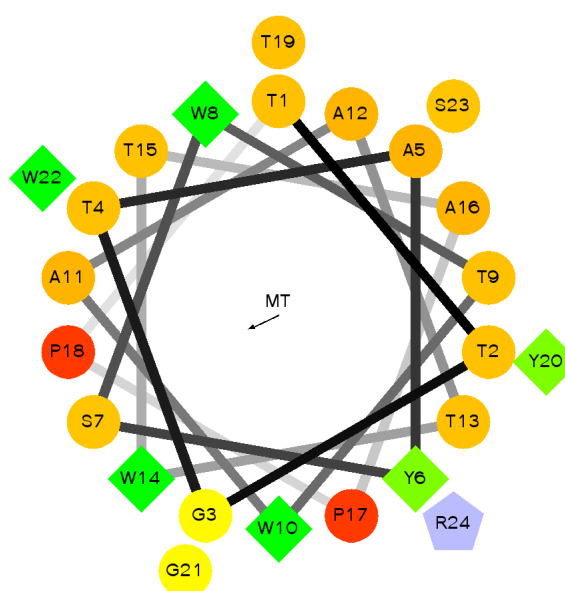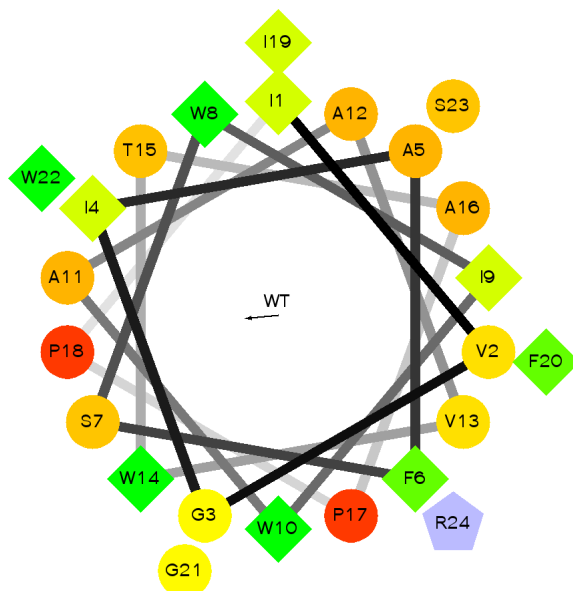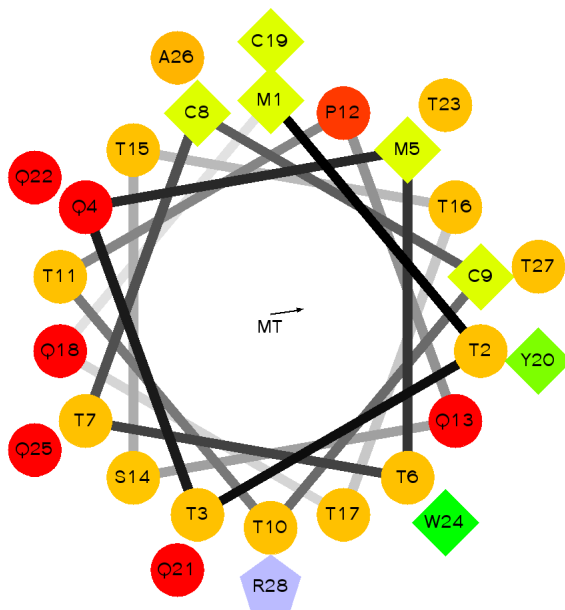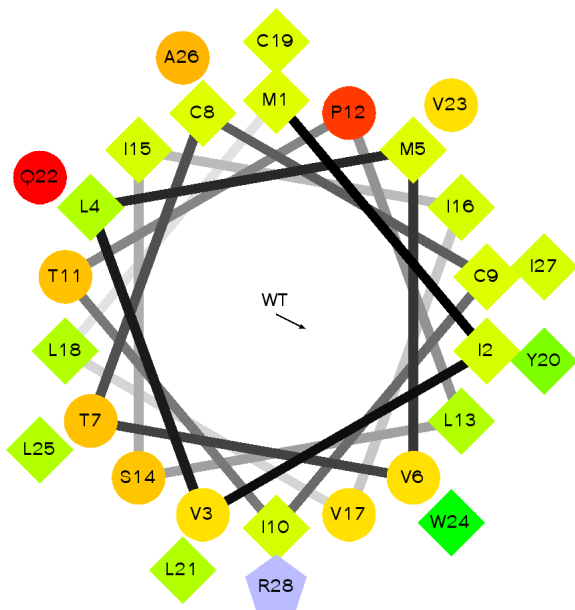
TM5

AA sequence comparison:

```
TM5-wt:  MIVLMVTCCITPLSIIVLCYLQVWLAIR
         |*** *||| *|| *|****|| *|*|*|
TM5-mt:  MTTQMTTCCTTPQSTTTQCYQQTWQATR
```

Alpha-helix prediction comparison:

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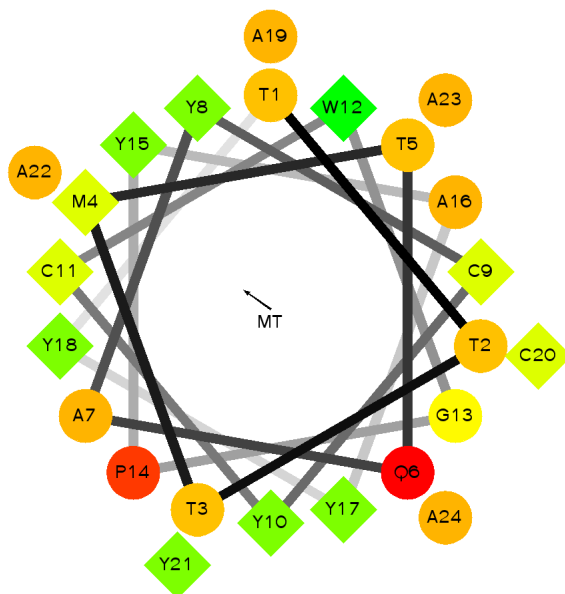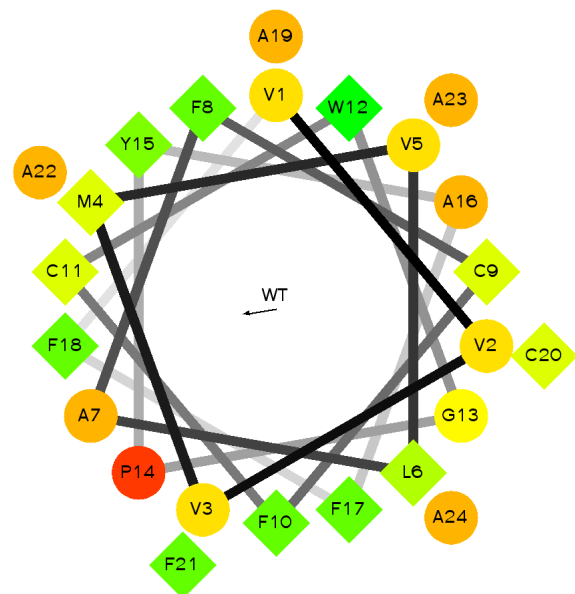

TM6

AA sequence comparison:

```
TM6-wt:  VVVMVLAFCFCWGPYAFFACFAAA
         ***|**|*|*||||||**||*|||
TM6-mt:  TTTMTQAYCYCWGPYAYYACYAAA
```

Alpha-helix prediction comparison:

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

TM7

AA sequence comparison:

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

Alpha-helix prediction comparison:

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