REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: RhodopsinQTY
User: siqipan2008@outlook.com
Designing code: QTY
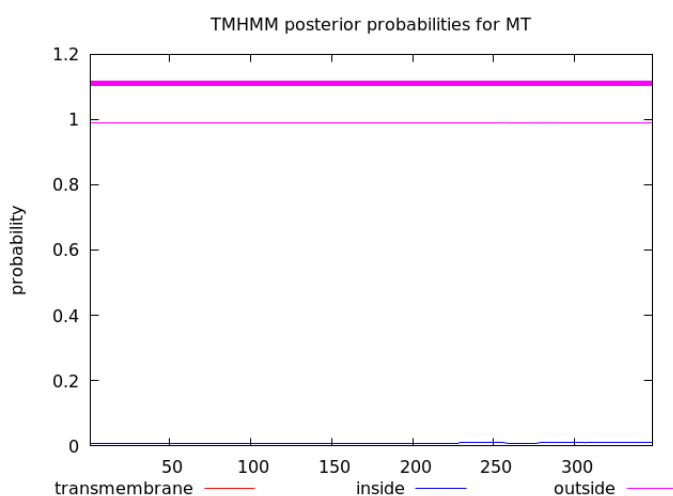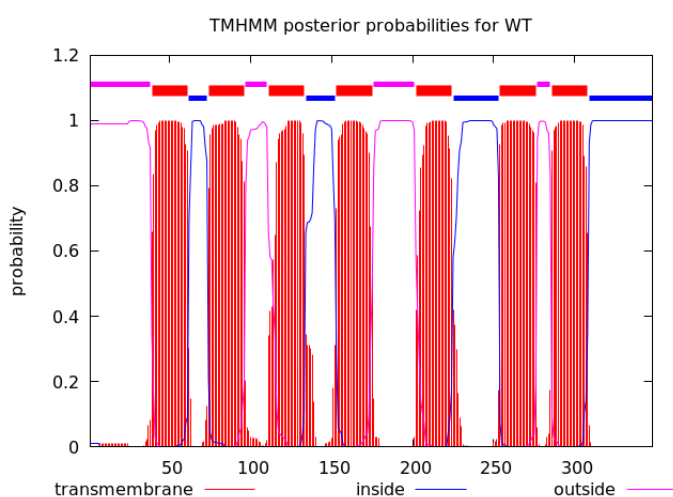Length of protein sequence: 348
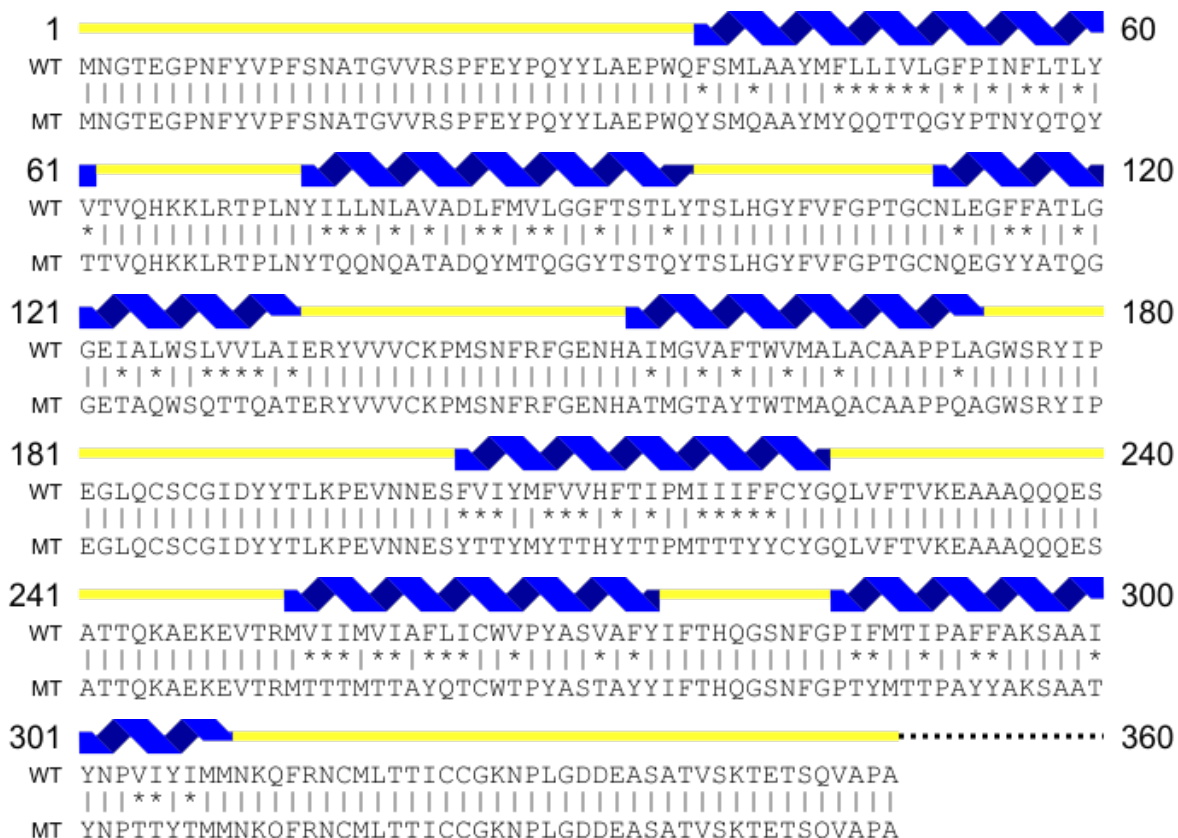Number of modified TM regions: 7

2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	6.20	38.8926	0.5187	/	/
MT	6.20	39.2865	-0.6488	46.58	21.55

3. Comparison of TM prediction:

4. Comparison of sequences:

```
 1 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━〜〜〜〜〜〜〜〜〜〜〜〜〜 60
WT MNGTEGPNFYVPFSNATGVVRSPFEYPQYYLAEPWQFSMLAAYMFLLIVLGFPINFLTLY
   |||||||||||||||||||||||||||||||||*||*||||******|*|*|**|*|
MT MNGTEGPNFYVPFSNATGVVRSPFEYPQYYLAEPWQYSMQAAYMYQQTTQGYPTNYQTQY

 61 〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜 120
WT VTVQHKKLRTPLNYILLNLAVADLFMVLGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLG
   *||||||||||||||  ***|*|*||**|**||*|||*|||||||||||||*||**||*|
MT TTVQHKKLRTPLNYTQQNQATADQYMTQGGYTSTQYTSLHGYFVFGPTGCNQEGYYATQG

121 〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜 180
WT GEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLAGWSRYIP
   ||*|*||****|*|||||||||||||||||||||*||*|*||*||*|||||*|||||||
MT GETAQWSQTTQATERYVVVCKPMSNFRFGENHATMGTAYTWTMAQACAAPPQAGWSRYIP

181 〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜 240
WT EGLQCSCGIDYYTLKPEVNNESFVIYMFVVHFTIPMIIIFFCYGQLVFTVKEAAAQQQES
   |||||||||||||||||||||||***||***|*|*||*****|||||||||||||||||
MT EGLQCSCGIDYYTLKPEVNNESYTTYMYTTHYTTPMTTTYYCYGQLVFTVKEAAAQQQES

241 〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜〜 300
WT ATTQKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMTIPAFFAKSAAI
   ||||||||||||||***|**|***||*||||*|*|||||||||||**||*||**||||*
MT ATTQKAEKEVTRMTTTMTTAYQTCWTPYASTAYYIFTHQGSNFGPTYMTTPAYYAKSAAT

301 〜〜〜〜〜〜〜━━━━━━━━━━━━━━━━━━━━━━━━━━━━·············· 360
WT YNPVIYIMMNKQFRNCMLTTICCGKNPLGDDEASATVSKTETSQVAPA
   |||**|*|||||||||||||||||||||||||||||||||||||||||
MT YNPTTYTMMNKQFRNCMLTTICCGKNPLGDDEASATVSKTETSQVAPA
```
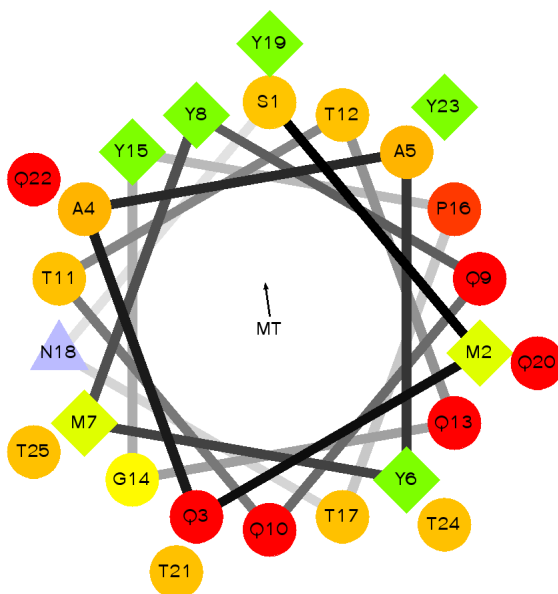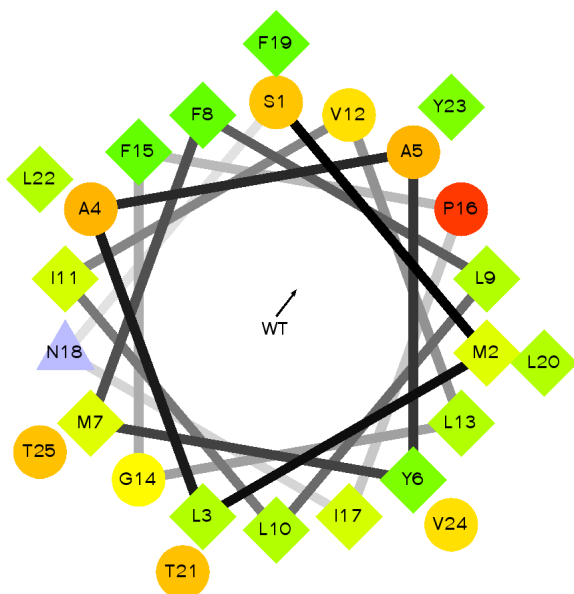
5. Detailed comparison of TM regions:

TM1

AA sequence comparison:

```
TM1-wt:  SMLAAYMFLLIVLGFPINFLTLYVT
         ||*|||||******|*|*|**|*|*
TM1-mt:  SMQAAYMYQQTTQGYPTNYQTQYTT
```

Alpha-helix prediction comparison:

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

TM2

AA sequence comparison:

```
TM2-wt:  ILLNLAVADLFMVLGGFTSTLYT
         *** | * | * | | ** | ** | | * | | | * | |
TM2-mt:  TQQNQATADQYMTQGGYTSTQYT
```

Alpha-helix prediction comparison:

```
TM2-wt:  HHHHHHHHHHHHHHHHCCHHHHHH
         | | | | | | | | | | | | | | | | * | | * | | | | |
TM2-mt:  HHHHHHHHHHHHHHHCCCCHHHHH
```
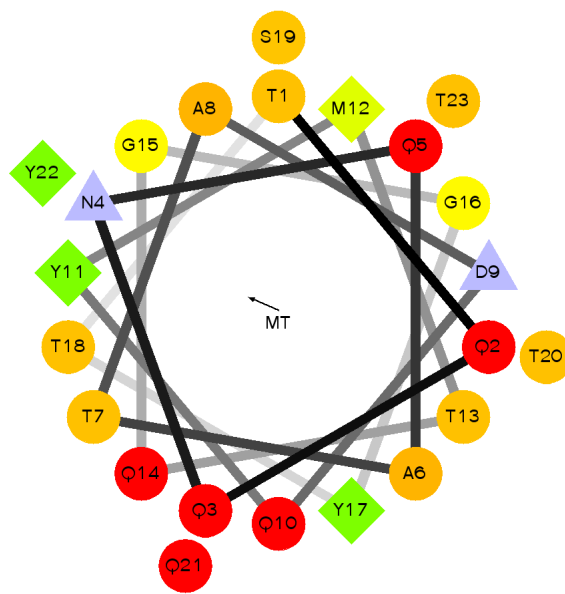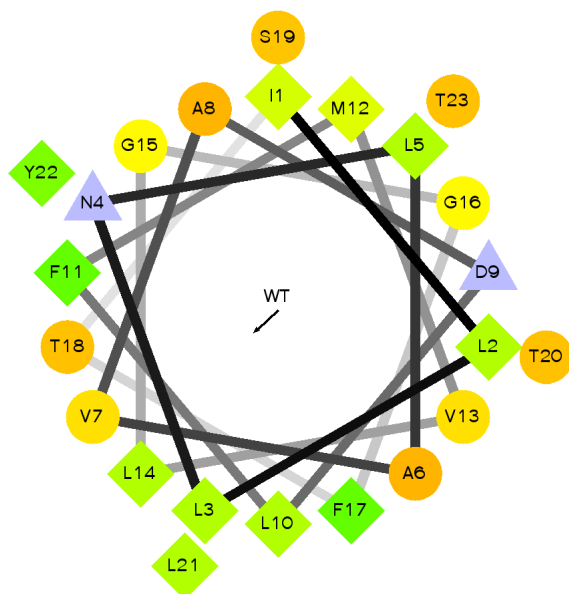

TM3

AA sequence comparison:

```
TM3-wt:  LEGFFATLGGEIALWSLVVLAIE
         * | | ** | | * | | | * | * | | **** | * |
TM3-mt:  QEGYYATQGGETAQWSQTTQATE
```

Alpha-helix prediction comparison:

```
TM3-wt:  HHHHHHHHHHHHHHHHHHHHHHHH
         *** | | | | | | | | | | | | | | | | | | | | |
TM3-mt:  EEEHHHHHHHHHHHHHHHHHHHHH
```
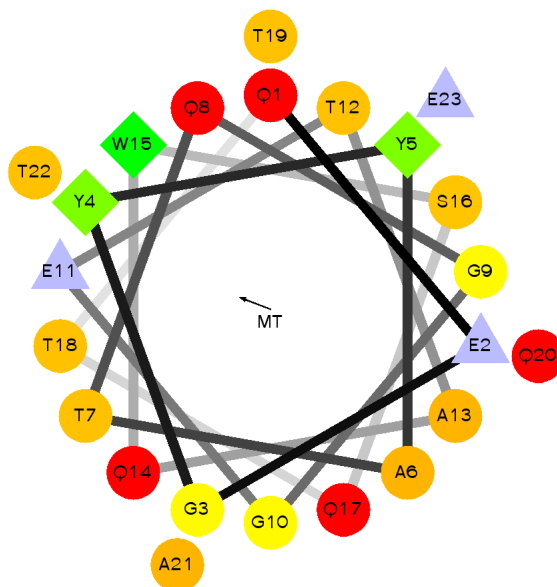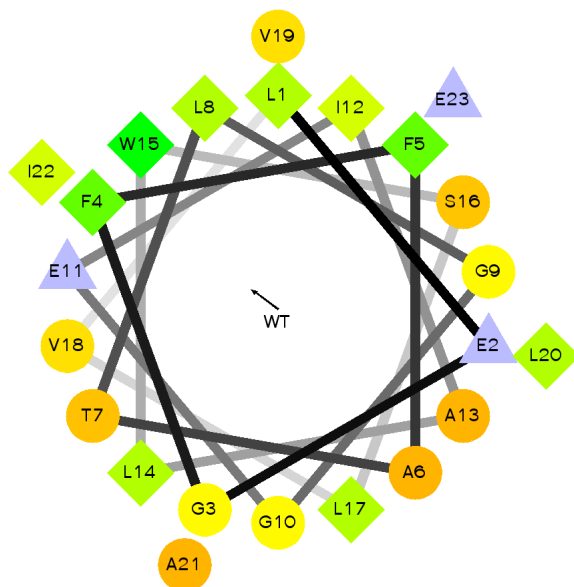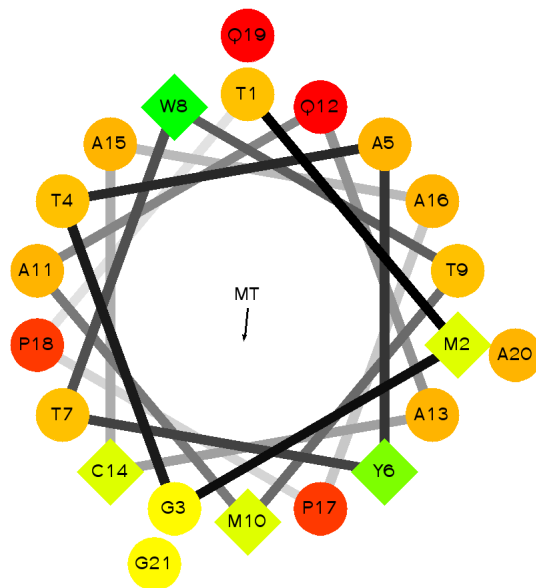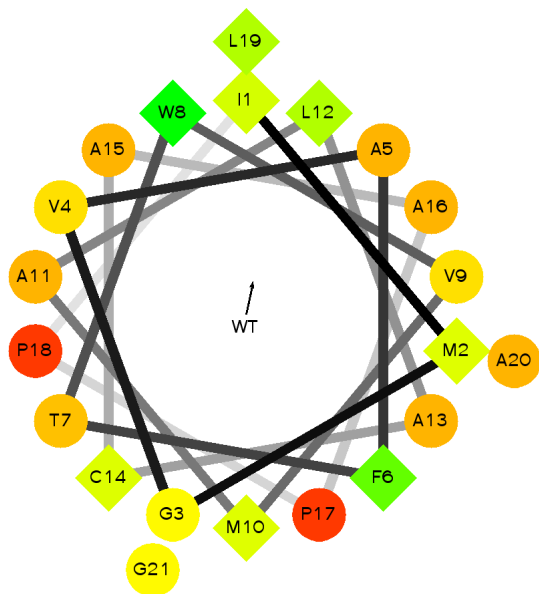
TM4

AA sequence comparison:

```
TM4-wt:  IMGVAFTWVMALACAAPPLAG
         *||*|*||*||*||||||*||
TM4-mt:  TMGTAYTWTMAQACAAPPQAG
```

Alpha-helix prediction comparison:

```
TM4-wt:  HHHHHHHHHHHHHHHHCCCEEE
         ||||||||||||||||||||*||
TM4-mt:  HHHHHHHHHHHHHHHHCCCHEE
```


TM5

AA sequence comparison:

```
TM5-wt:  VIYMFVVHFTIPMIIIFFCYGQ
         **||***|*|*||*****||||
TM5-mt:  TTYMYTTHYTTPMTTTYYCYGQ
```

Alpha-helix prediction comparison:

```
TM5-wt:  HHHHHHHHHHHHHHHHHHHHHH
         ||||||||||||||||||||||
TM5-mt:  HHHHHHHHHHHHHHHHHHHHHH
```
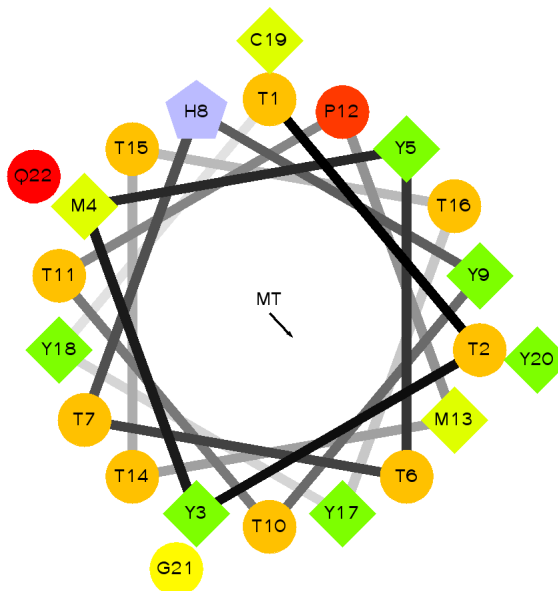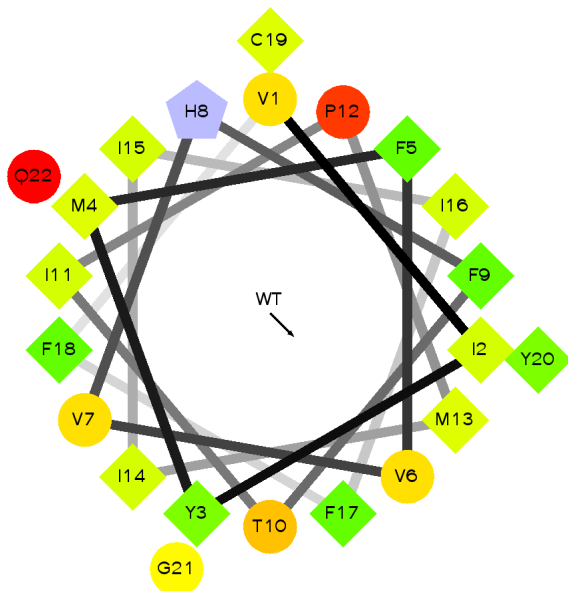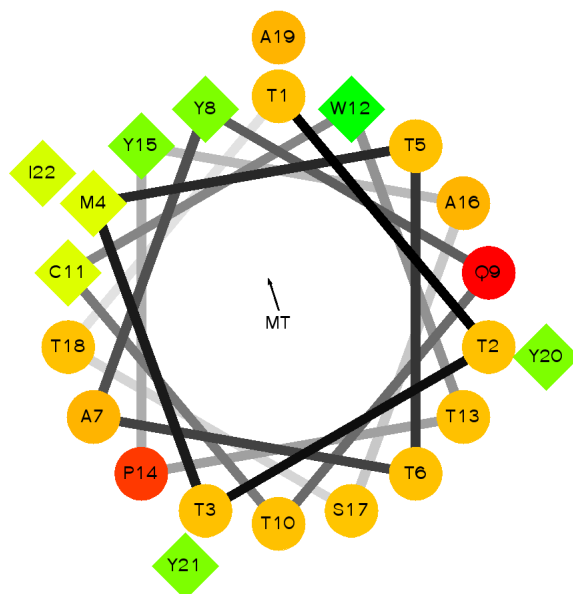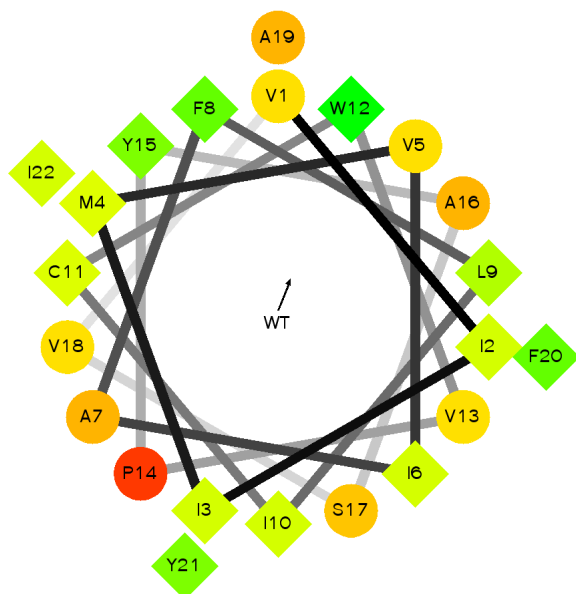
TM6

AA sequence comparison:

```
TM6-wt:  VIIMVIAFLICWVPYASVAFYI
         ***|**|***||*||||*|*||
TM6-mt:  TTTMTTAYQTCWTPYASTAYYI
```

Alpha-helix prediction comparison:

```
TM6-wt:  HHHHHHHHHHHCCHHHHHHHHH
         ||||||||||||||||||||||
TM6-mt:  HHHHHHHHHHHCCHHHHHHHHH
```


TM7

AA sequence comparison:

```
TM7-wt:  IFMTIPAFFAKSAAIYNPVIYIMMN
         **||*||**|||||*|||**|*|||
TM7-mt:  TYMTTPAYYAKSAATYNPTTYTMMN
```

Alpha-helix prediction comparison:

```
TM7-wt:  HHHHHHHHHHHHHHHHHCHHHHHHHC
         |||||||||||||||||***|*|||||*|
TM7-mt:  HHHHHHHHHHHHHHCCCCCHHHHHCC
```