REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: Q9H1Y3
User: siqipan2008@outlook.com
Designing code: QTY
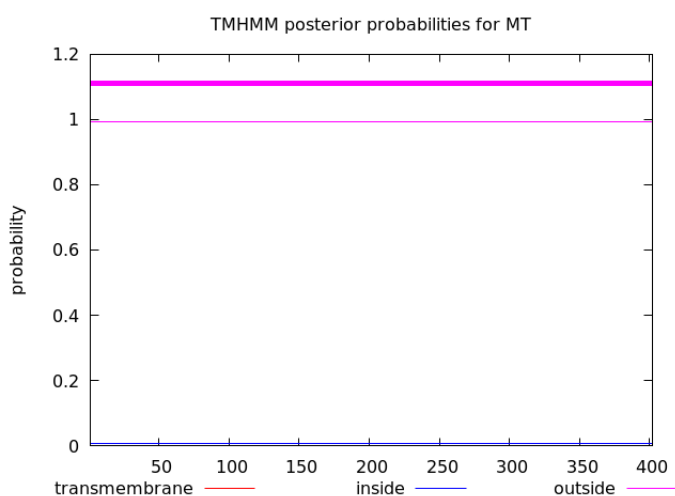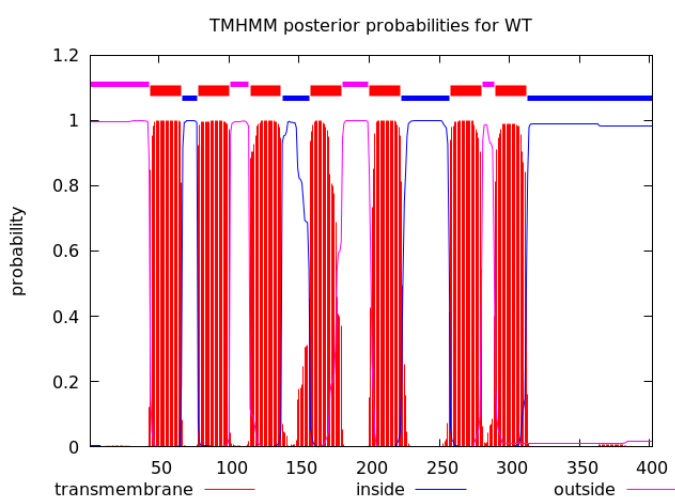Length of protein sequence: 402
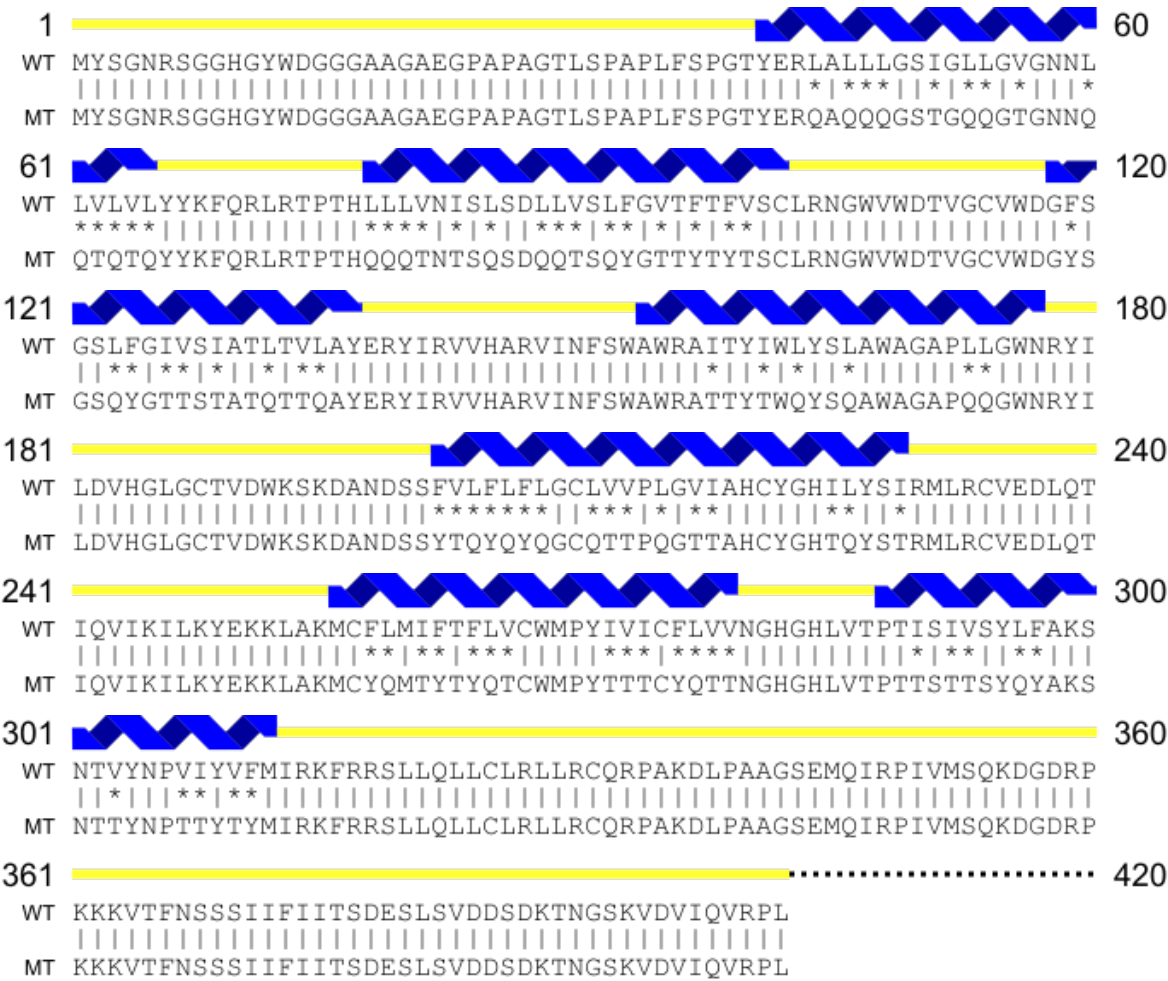Number of modified TM regions: 7

2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	9.29	44.8729	0.4572	/	/
MT	9.18	45.4666	-0.7529	49.12	20.90

3. Comparison of TM prediction:

4. Comparison of sequences:

```
  1  ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━▰▰▰▰▰▰▰▰▰▰▰▰▰▰▰▰  60
 WT  MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNL
     |||||||||||||||||||||||||||||||||||||||||*|***||*|**|*|||*
 MT  MYSGNRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERQAQQQGSTGQQGTGNNQ

 61  ▰▰▰━━━━━━━━━━━━━▰▰▰▰▰▰▰▰▰▰▰▰━━━━━━━━━━━━━━━━━▰▰ 120
 WT  LVLVLYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFS
     *****|||||||||||||****|*|*||***|**|*|*|**|||||||||||||||||*|
 MT  QTQTQYYKFQRLRTPTHQQQTNTSQSDQQTSQYGTTYTYTSCLRNGWVWDTVGCVWDGYS

121  ▰▰▰▰▰▰▰▰▰━━━━━━━━━━━━━━━━━▰▰▰▰▰▰▰▰▰▰▰▰▰▰▰▰━━━━ 180
 WT  GSLFGIVSIATLTVLAYERYIRVVHARVINFSWAWRAITYIWLYSLAWAGAPLLGWNRYI
     ||**|**|*||*|**|||||||||||||||||||||*||*|*||*|||||**|||||
 MT  GSQYGTTSTATQTTQAYERYIRVVHARVINFSWAWRATTYTWQYSQAWAGAPQQGWNRYI

181  ━━━━━━━━━━━━━━━━━━━━━━▰▰▰▰▰▰▰▰▰▰▰▰▰▰▰▰▰━━━━━━━ 240
 WT  LDVHGLGCTVDWKSKDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDLQT
     ||||||||||||||||||||||*******||***|*|**||||||**||*|||||||||
 MT  LDVHGLGCTVDWKSKDANDSSYTQYQYQGCQTTPQGTTAHCYGHTQYSTRMLRCVEDLQT

241  ━━━━━━━━━━━━━━━▰▰▰▰▰▰▰▰▰▰▰▰━━━━━━━▰▰▰▰▰▰▰━━━━━ 300
 WT  IQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFAKS
     |||||||||||||||**|**|***||||***|****|||||||||*|**||**|||
 MT  IQVIKILKYEKKLAKMCYQMTYTYQTCWMPYTTTCYQTTNGHGHLVTPTTSTTSYQYAKS

301  ▰▰▰▰▰━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 360
 WT  NTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP
     ||*|||**|**||||||||||||||||||||||||||||||||||||||||||||||||
 MT  NTTYNPTTYTYMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGDRP

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

5. Detailed comparison of TM regions:

AA sequence comparison:

```
TM1-wt:  ERLALLLGSIGLLGVGNNLLVLVLY
         ||*|***||*|**|*|||******|
TM1-mt:  ERQAQQQGSTGQQGTGNNQQTQTQY
```

Alpha-helix prediction comparison:

```
TM1-wt:  HHHHHHHHHHHHHHHHHHHHHHHHH
         |||||||||||||||||||||||||
TM1-mt:  HHHHHHHHHHHHHHHHHHHHHHHHH
```
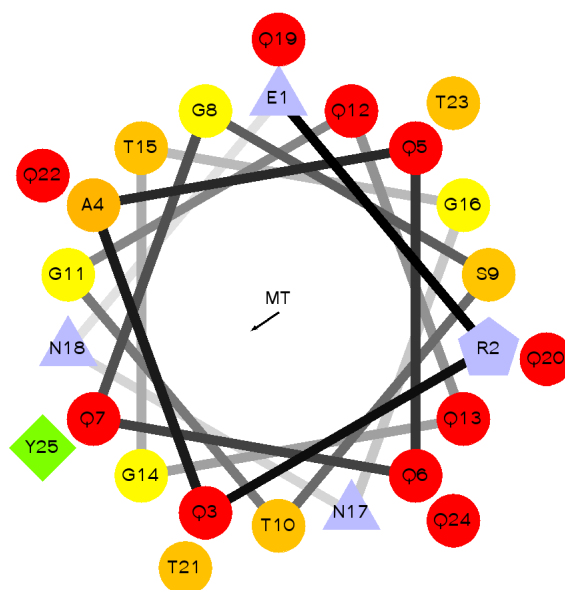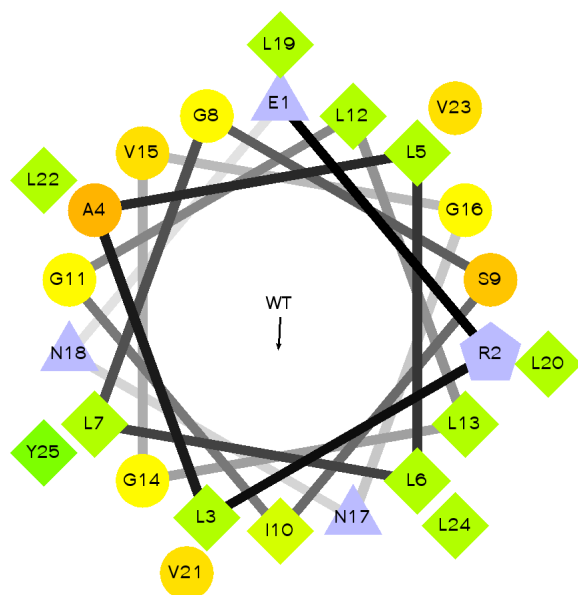
AA sequence comparison:

```
TM2-wt:  LLVNISLSDLLVSLFGVTFTFVSCL
         ***|*|*||***|**|*|*|**|||
TM2-mt:  QQTNTSQSDQQTSQYGTTYTYTSCL
```

Alpha-helix prediction comparison:

```
TM2-wt:  HHHHHHHHHHHHHHHHHHHHHHHHH
         |||||||||||||||||||||||||
TM2-mt:  HHHHHHHHHHHHHHHHHHHHHHHHH
```
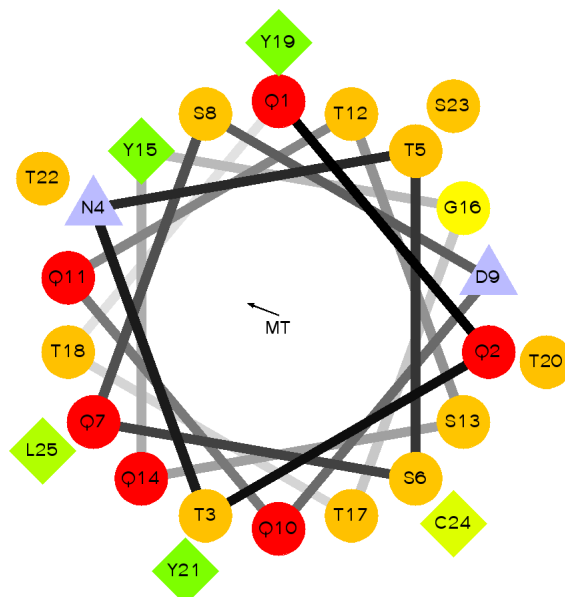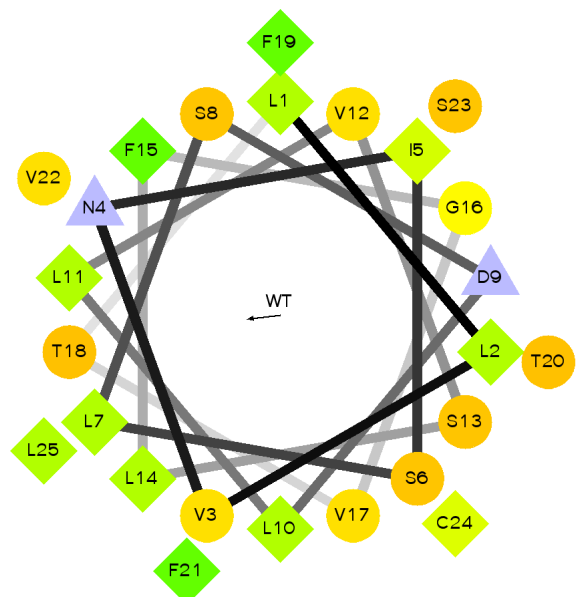
AA sequence comparison:

```
TM3-wt:  FSGSLFGIVSIATLTVLAYE
         *|||**|**|*|*|**|||
TM3-mt:  YSGSQYGTTSTATQTTQAYE
```

Alpha-helix prediction comparison:

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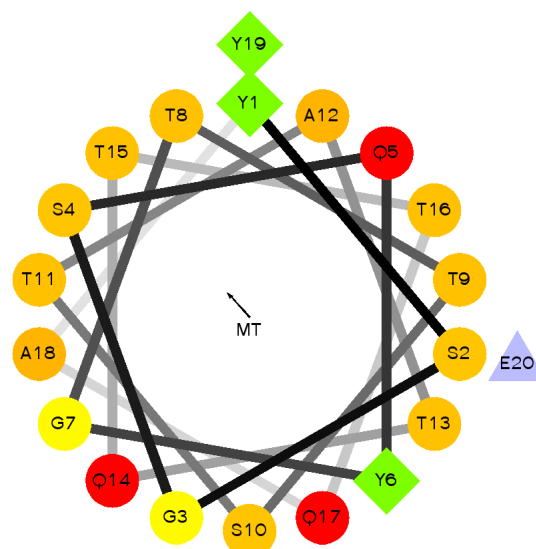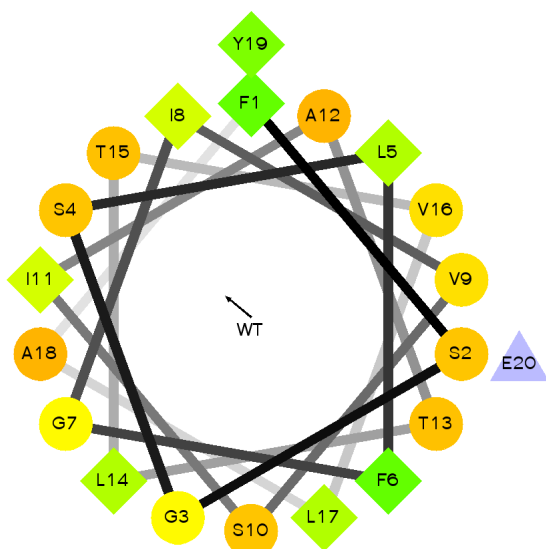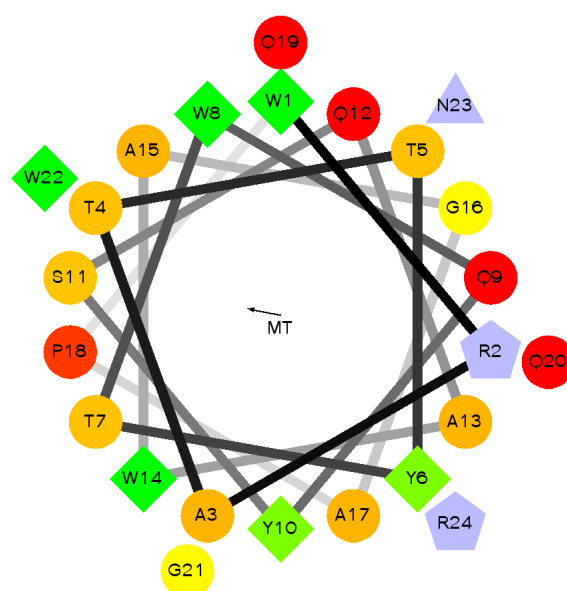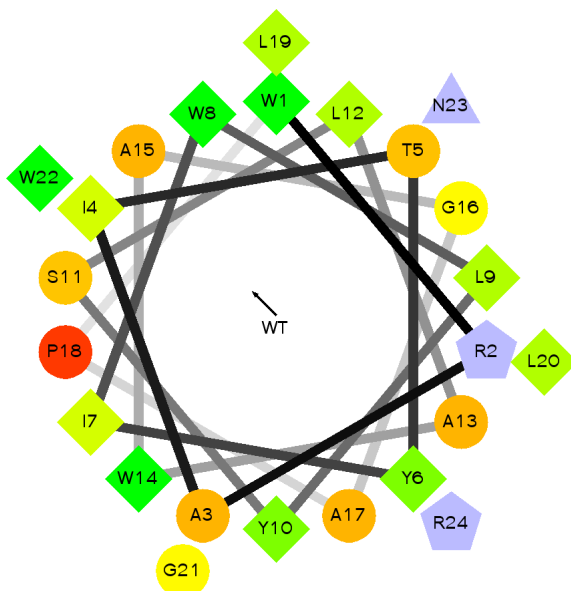

TM4

AA sequence comparison:

```
TM4-wt:  WRAITYIWLYSLAWAGAPLLGWNR
         |||*||*|*||*|||||||**|||
TM4-mt:  WRATTYTWQYSQAWAGAPQQGWNR
```

Alpha-helix prediction comparison:

```
TM4-wt:  HHHHHHHHHHHHHHHHCCCEEEEEE
         |||||||||||||||||||||||||
TM4-mt:  HHHHHHHHHHHHHHHHCCCEEEEEE
```
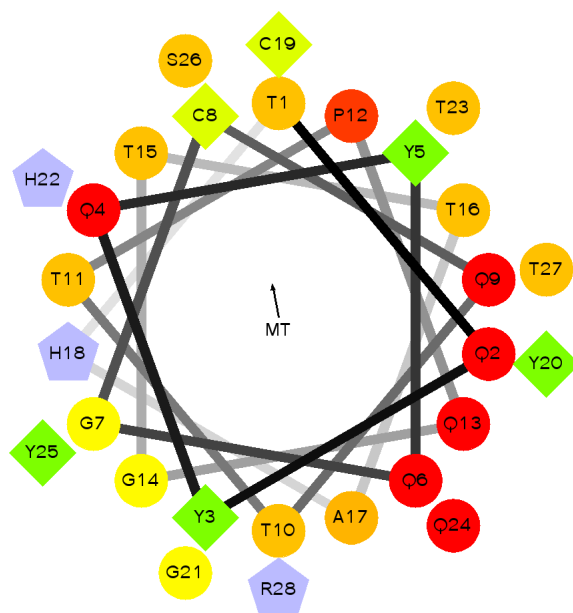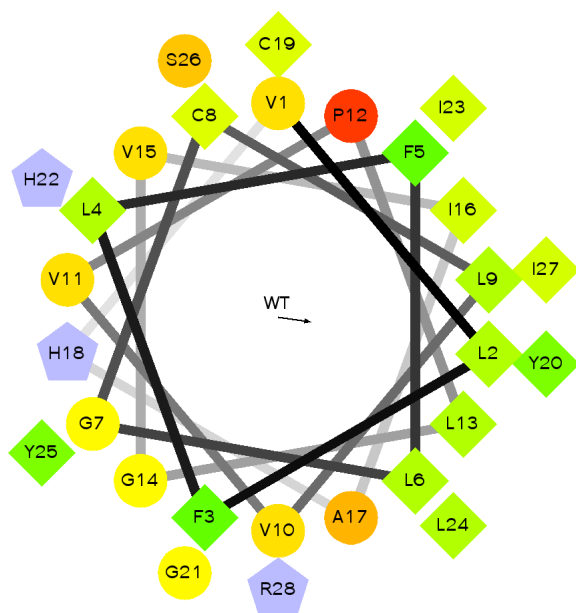
TM5

AA sequence comparison:

```
TM5-wt:  VLFLFLGCLVVPLGVIAHCYGHILYSIR
         ******||***|*|**|||||**|||*|
TM5-mt:  TQYQYQGCQTTPQGTTAHCYGHTQYSTR
```

Alpha-helix prediction comparison:

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


TM6

AA sequence comparison:

```
TM6-wt:  CFLMIFTFLVCWMPYIVICFLVVN
         |**|**|***|||||***|****|
TM6-mt:  CYQMTYTYQTCWMPYTTTCYQTTN
```

Alpha-helix prediction comparison:

```
TM6-wt:  HHHHHHHHHHHCCHHHHHHHHHHHH
         ||||||||||||||||||||||||
TM6-mt:  HHHHHHHHHHHCCHHHHHHHHHHHH
```
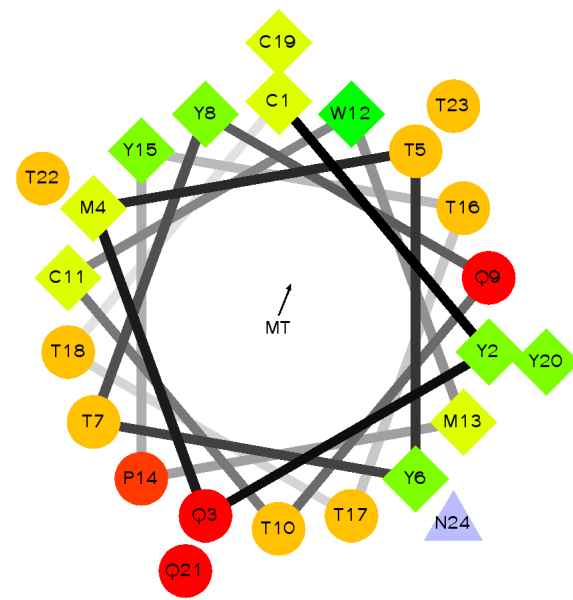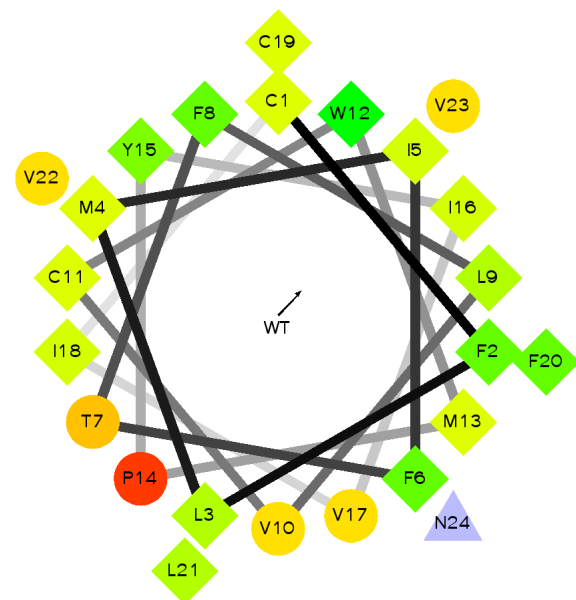
TM7

AA sequence comparison:

```
TM7-wt:  TISIVSYLFAKSNTVYNPVIYVFMI
         |*|**||**|||||*|||**|**||
TM7-mt:  TTSTTSYQYAKSNTTYNPTTYTYMI
```

Alpha-helix prediction comparison:

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