REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: Q9UHM6
User: siqipan2008@outlook.com
Designing code: QTY
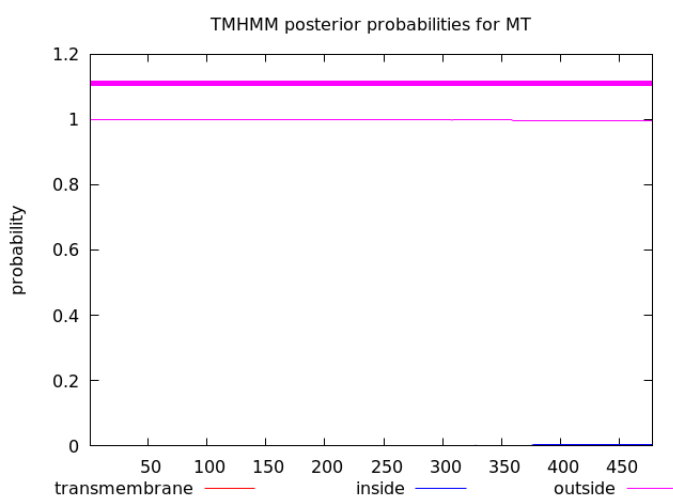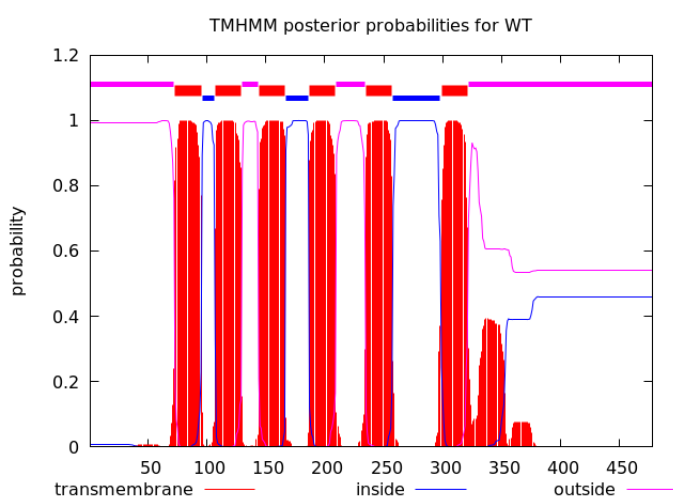Length of protein sequence: 478
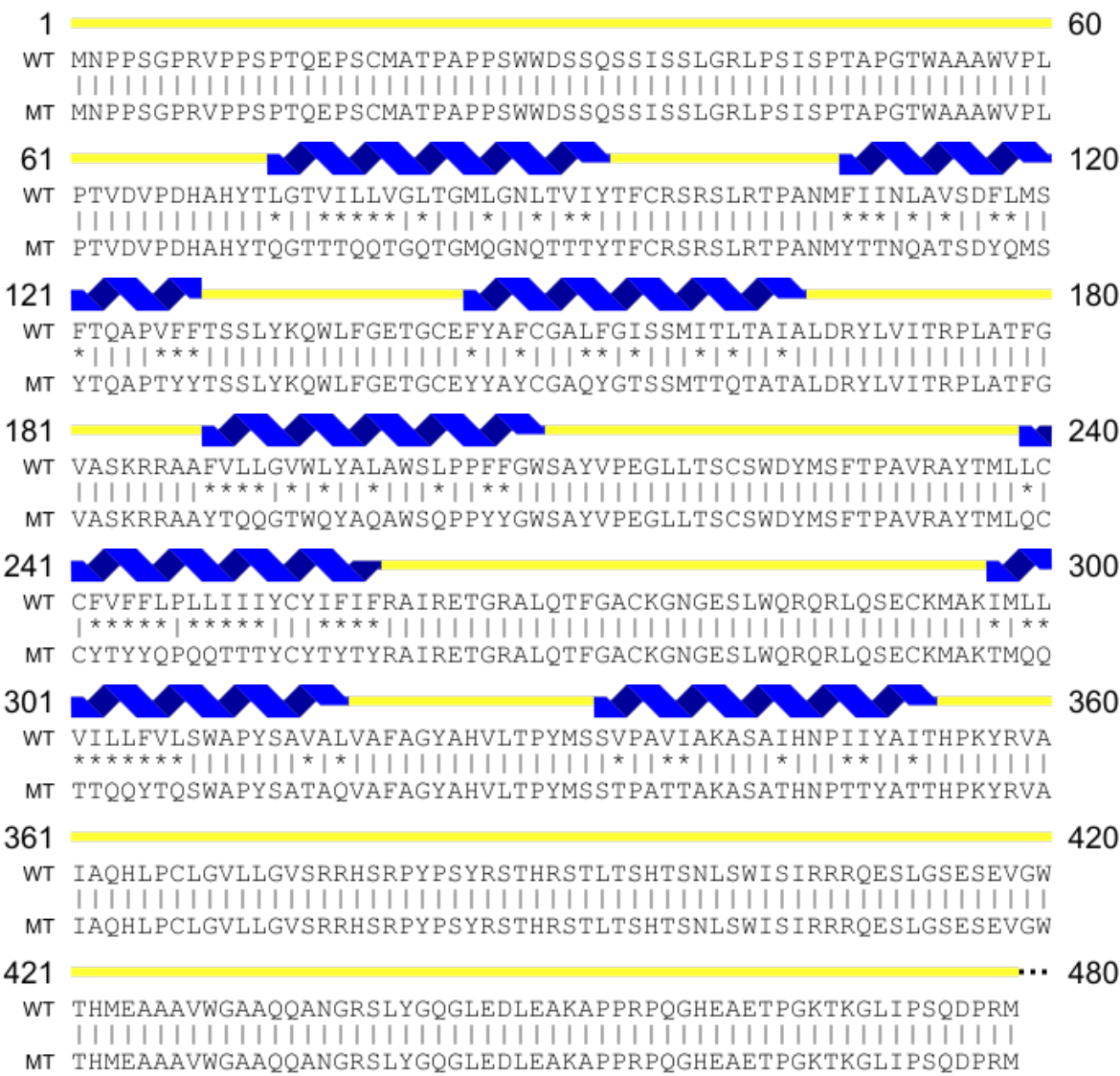Number of modified TM regions: 7

2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	9.35	52.6353	0.2391	/	/
MT	9.19	53.0782	-0.6284	50.34	15.48

3. Comparison of TM prediction:

4. Comparison of sequences:

```
   1 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━  60
WT MNPPSGPRVPPSPTQEPSCMATPAPPSWWDSSQSSISSLGRLPSISPTAPGTWAAAWVPL
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MT MNPPSGPRVPPSPTQEPSCMATPAPPSWWDSSQSSISSLGRLPSISPTAPGTWAAAWVPL

  61 ━━━━━━━━━━━━━━━━━━━∿∿∿∿∿∿∿∿∿━━━━━━━━━━∿∿∿∿∿∿  120
WT PTVDVPDHAHYTLGTVILLVGLTGMLGNLTVIYTFCRSRSLRTPANMFIINLAVSDFLMS
   |||||||||||*|*|*****|*|||*||*|**|||||||||||||||***|*|*||**||
MT PTVDVPDHAHYTQGTTTQQTGQTGMQGNQTTTYTFCRSRSLRTPANMYTTNQATSDYQMS

 121 ∿∿∿∿━━━━━━━━∿∿∿∿∿∿∿∿∿━━━━━  180
WT FTQAPVFFTSSLYKQWLFGETGCEFYAFCGALFGISSMITLTAIALDRYLVITRPLATFG
   *||||***|||||||||||||||||*||*|||**|*|||*|*||*|||||||||||||||
MT YTQAPTYYTSSLYKQWLFGETGCEYYAYCGAQYGTSSMTTQTATALDRYLVITRPLATFG

 181 ━━━━━━∿∿∿∿∿∿∿∿∿━━━━━━━━━━━━━━━━━━∿∿  240
WT VASKRRAAFVLLGVWLYALAWSLPPFFGWSAYVPEGLLTSCSWDYMSFTPAVRAYTMLLC
   ||||||||****|*|*||*|||*||**||||||||||||||||||||||||||||||||*|
MT VASKRRAAYTQQGTWQYAQAWSQPPYYGWSAYVPEGLLTSCSWDYMSFTPAVRAYTMLQC

 241 ∿∿∿∿∿∿∿∿∿━━━━━━━━━━━━━━━━━━━━━━∿∿  300
WT CFVFFLPLLIIIYCYIFIFRAIRETGRALQTFGACKGNGESLWQRQRLQSECKMAKIMLL
   |*****|*****|||****||||||||||||||||||||||||||||||||||||*|**
MT CYTYYQPQQTTTYCYTYTYRAIRETGRALQTFGACKGNGESLWQRQRLQSECKMAKTMQQ

 301 ∿∿∿∿∿∿∿∿∿━━━━━━━━━━∿∿∿∿∿∿∿∿∿━━━  360
WT VILLFVLSWAPYSAVALVAFAGYAHVLTPYMSSVPAVIAKASAIHNPIIYAITHPKYRVA
   *******||||||*|*||||||||||||||||||*||**|||||*|||**||*||||||||
MT TTQQYTQSWAPYSATAQVAFAGYAHVLTPYMSSTPATTAKASATHNPTTYATTHPKYRVA

 361 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━  420
WT IAQHLPCLGVLLGVSRRHSRPYPSYRSTHRSTLTSHTSNLSWISIRRRQESLGSESEVGW
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MT IAQHLPCLGVLLGVSRRHSRPYPSYRSTHRSTLTSHTSNLSWISIRRRQESLGSESEVGW

 421 ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ ···  480
WT THMEAAAVWGAAQQANGRSLYGQGLEDLEAKAPPRPQGHEAETPGKTKGLIPSQDPRM
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MT THMEAAAVWGAAQQANGRSLYGQGLEDLEAKAPPRPQGHEAETPGKTKGLIPSQDPRM
```

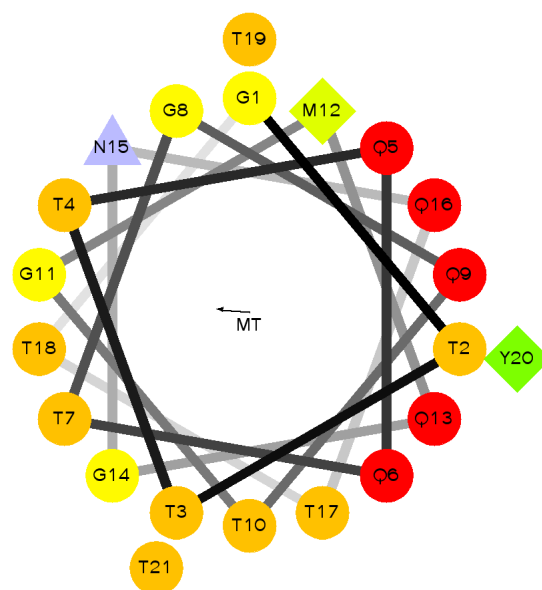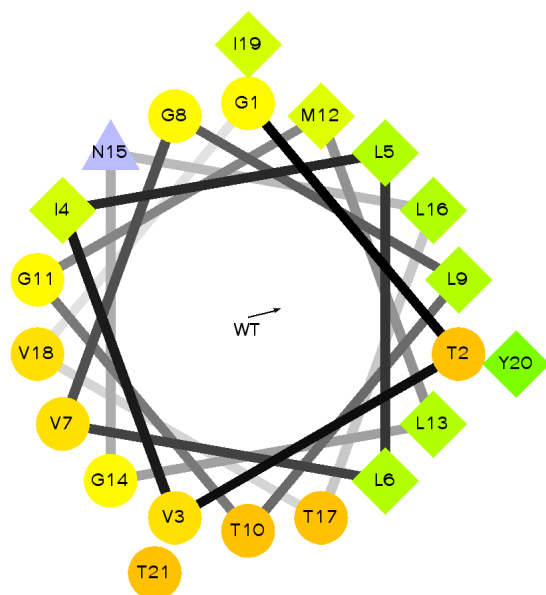## 5. Detailed comparison of TM regions:

TM1

AA sequence comparison:

```
TM1-wt:  GTVILLVGLTGMLGNLTVIYT
         ||*****|*|||*||*|**||
TM1-mt:  GTTTQQTGQTGMQGNQTTTYT
```

Alpha-helix prediction comparison:

```
TM1-wt:  HHHHHHHHHHHHHHHHHHHHH
         |||||||||||||||||||||
TM1-mt:  HHHHHHHHHHHHHHHHHHHHH
```
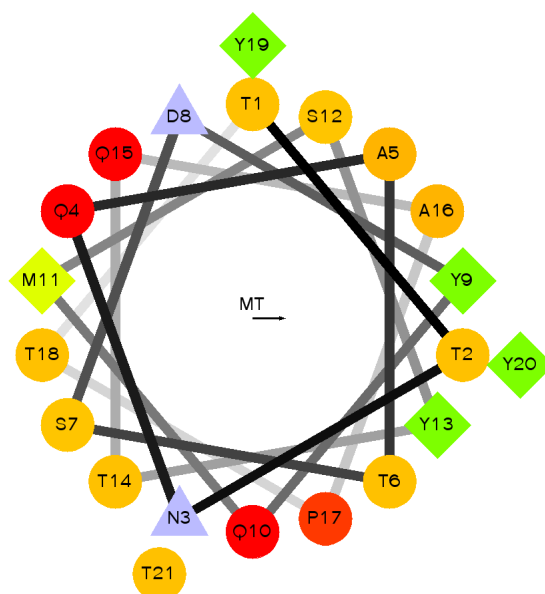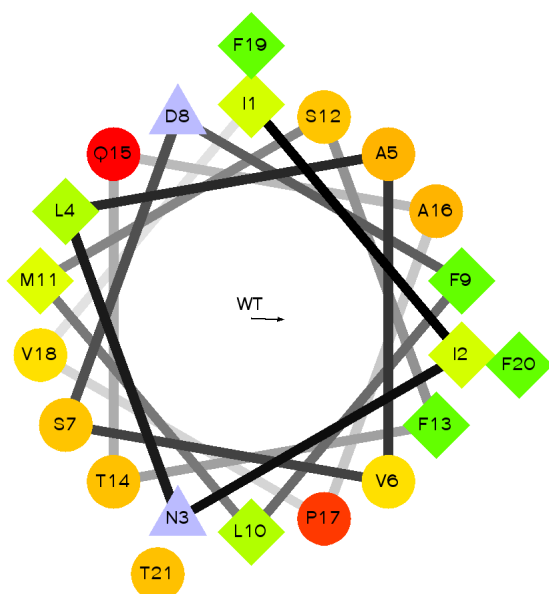

TM2

AA sequence comparison:

```
TM2-wt:  IINLAVSDFLMSFTQAPVFFT
         **|*|*||**||*|||***|
TM2-mt:  TTNQATSDYQMSYTQAPTYYT
```

Alpha-helix prediction comparison:

```
TM2-wt:  HHHHHHHHHHHHHHHCCHHHHH
         ||||||||||||||||||||||
TM2-mt:  HHHHHHHHHHHHHHHCCHHHHH
```

TM3

AA sequence comparison:

```
TM3-wt:  YAFCGALFGISSMITLTAIAL
         ||*|||**|*|||*|*||*||
TM3-mt:  YAYCGAQYGTSSMTTQTATAL
```

Alpha-helix prediction comparison:

```
TM3-wt:  HHHHHHHHHHHHHHHHHHHHH
         *||||||||||||||||||||
TM3-mt:  EHHHHHHHHHHHHHHHHHHHH
```
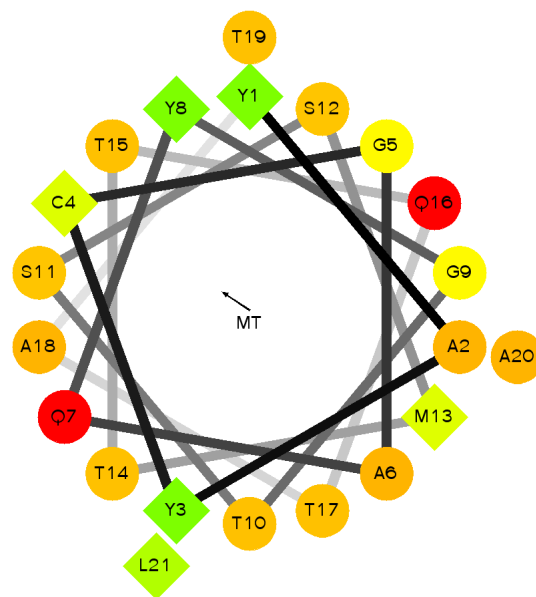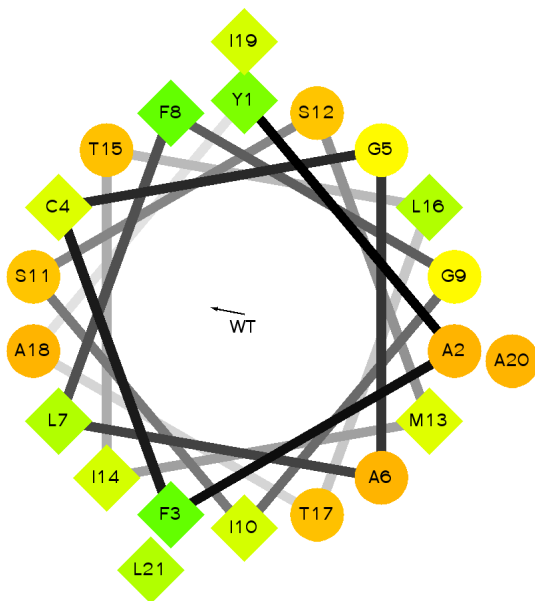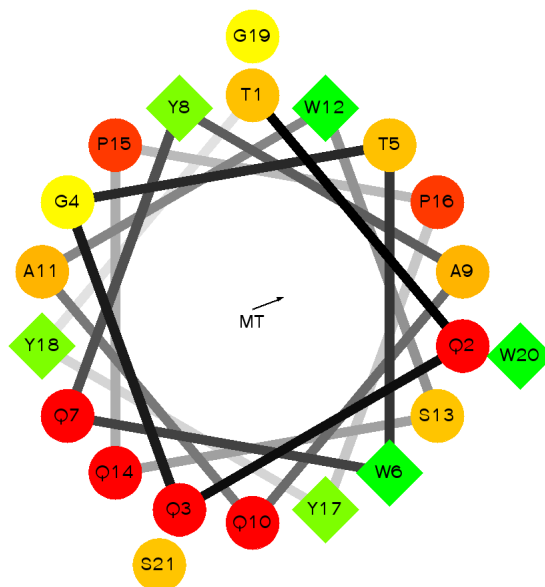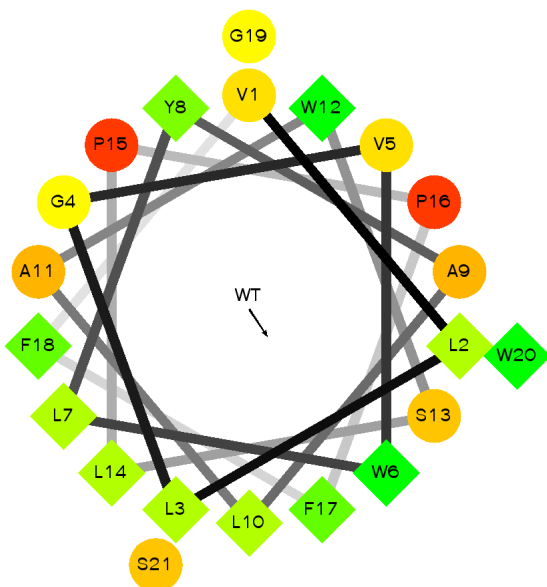

TM4

AA sequence comparison:

```
TM4-wt:  VLLGVWLYALAWSLPPFFGWS
         ***|*|*||*|||*|**|||
TM4-mt:  TQQGTWQYAQAWSQPPYYGWS
```

Alpha-helix prediction comparison:

```
TM4-wt:  HHHHHHHHHHHHHCCCCEEECC
         |||||||||||||||||||||**
TM4-mt:  HHHHHHHHHHHHHCCCCEEEEE
```
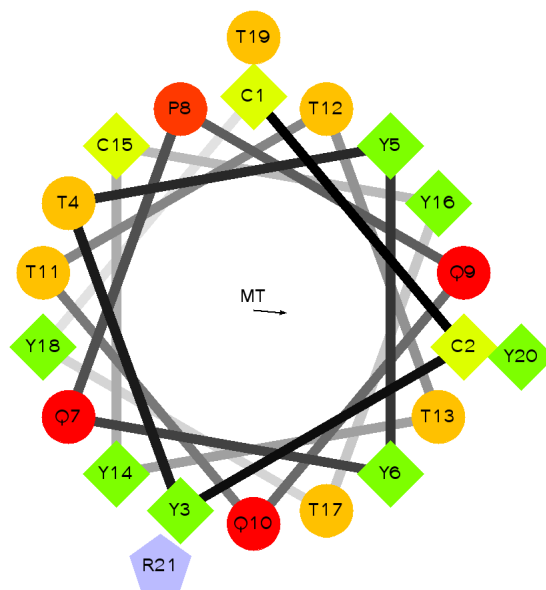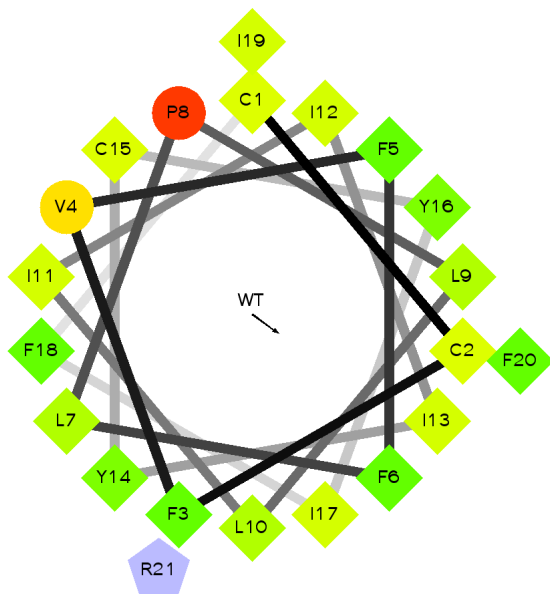
TM5

AA sequence comparison:

```
TM5-wt:  CCFVFFLPLLIIIYCYIFIFR
         ||*****|*****|||****|
TM5-mt:  CCYTYYQPQQTTTYCYTYTYR
```

Alpha-helix prediction comparison:

```
TM5-wt:  HHHHHHHHHHHHHHHHHHHHH
         |||||||||||||||||||||
TM5-mt:  HHHHHHHHHHHHHHHHHHHHH
```
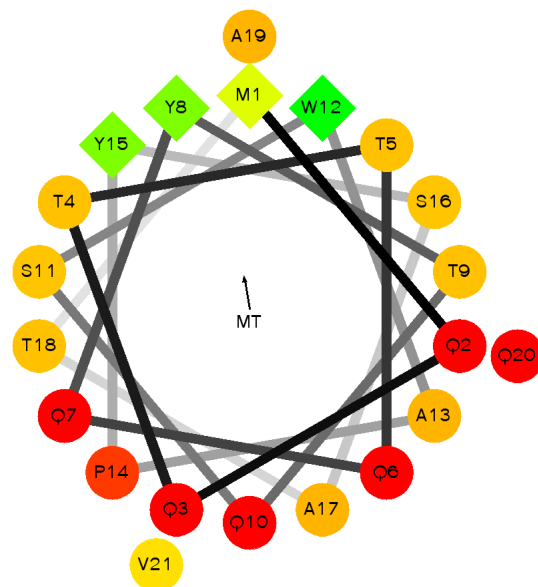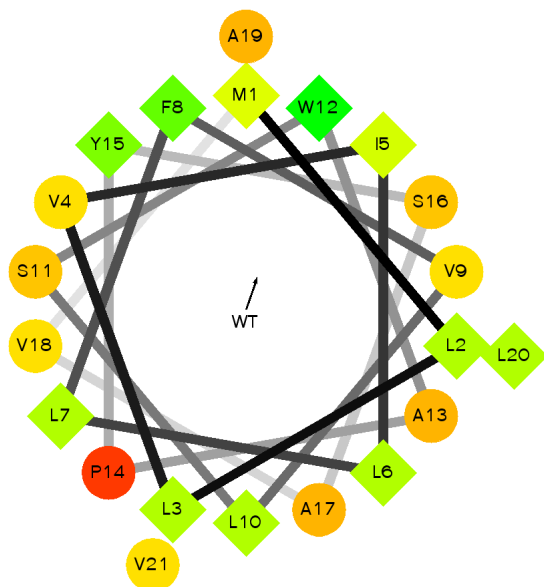

TM6

AA sequence comparison:

```
TM6-wt:  MLLVILLFVLSWAPYSAVALV
         |*******|||||||*|*|
TM6-mt:  MQQTTQQYTQSWAPYSATAQV
```

Alpha-helix prediction comparison:

```
TM6-wt:  HHHHHHHHHHHCCHHHHHHHH
         |||||||||||||||||||||
TM6-mt:  HHHHHHHHHHHCCHHHHHHHH
```

TM7

AA sequence comparison:

```
TM7-wt:  VPAVIAKASAIHNPIIYAITH
         *||**|||||*|||**||*||
TM7-mt:  TPATTAKASATHNPTTYATTH
```

Alpha-helix prediction comparison:

```
TM7-wt:  HHHHHHHHHHCCCCHHHHHCC
         ||||||||||*||||*****||
TM7-mt:  HHHHHHHHHCCCCCEEEEECC
```