REPORT OF QTY/NTY DESIGN

1. Job information:

Job/Protein Name: Q8RUT8_QTY_EXP
User: siqipan2008@outlook.com
Designing code: QTY
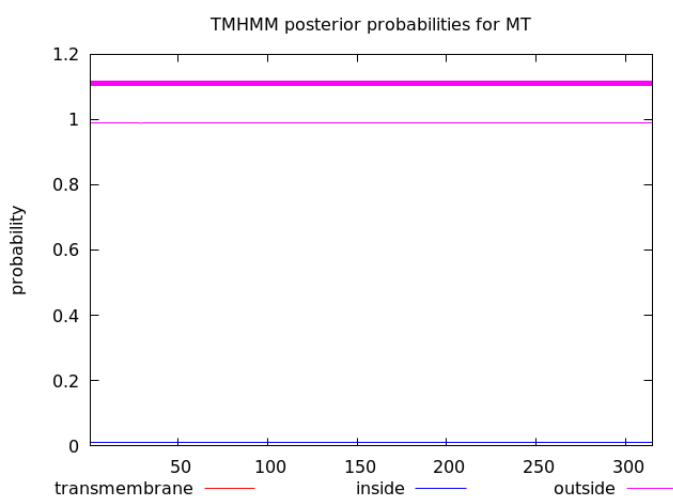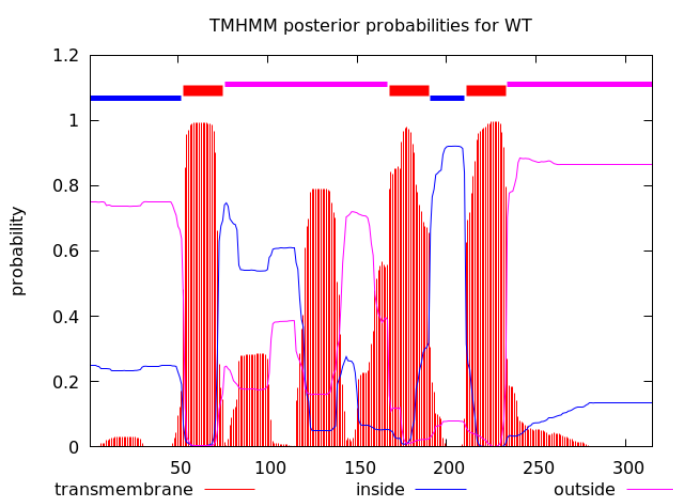Length of protein sequence: 315
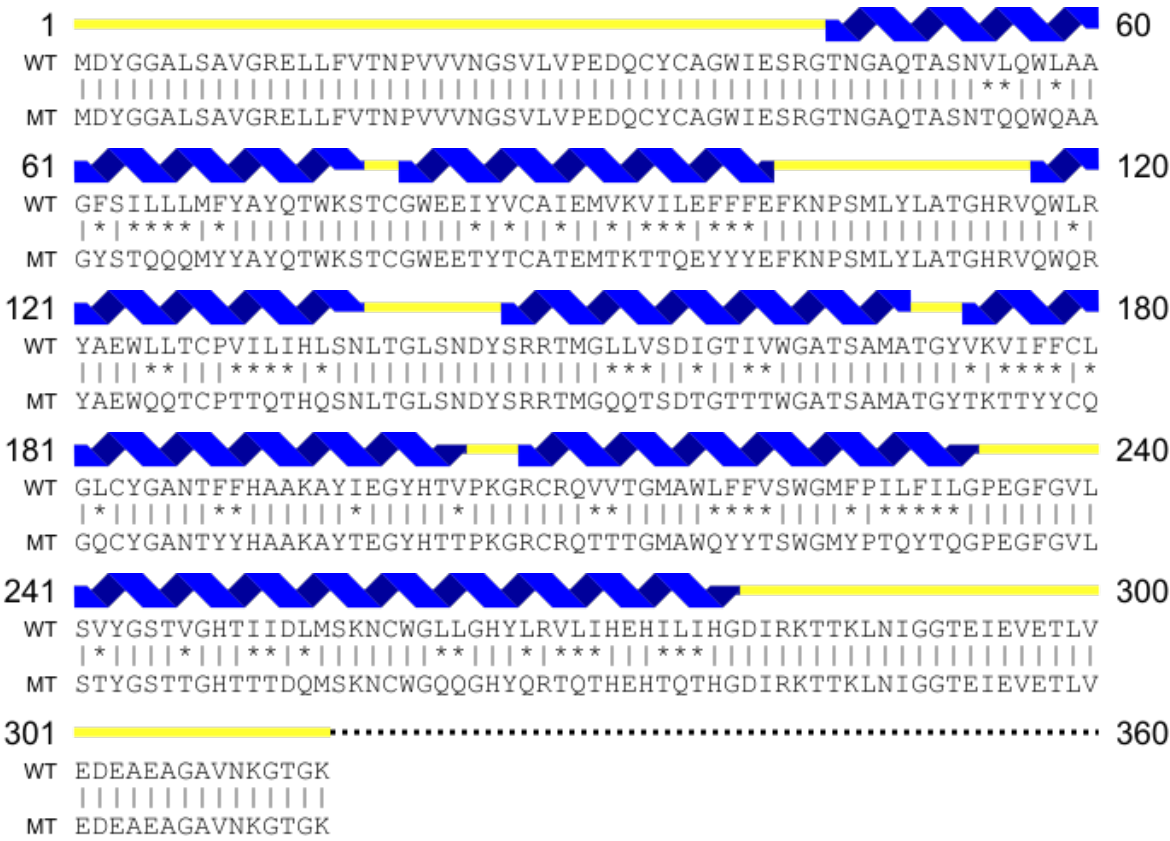Number of modified TM regions: 7

2. Comparison of general characteristics:

Type	pI	MW (kDa)	Hydrophobicity	Mutation rate (TM, %)	Mutation rate (%)
WT	6.13	34.9016	0.3975	/	/
MT	6.13	35.2956	-0.8574	35.53	22.22

3. Comparison of TM prediction:

4. Comparison of sequences:

```
  1 ─────────────────────────────────────────────────────〰〰〰〰〰 60
WT  MDYGGALSAVGRELLFVTNPVVNGSVLVPEDQCYCAGWIESRGTNGAQTASNVLQWLAA
    ||||||||||||||||||||||||||||||||||||||||||||||||||**||*||
MT  MDYGGALSAVGRELLFVTNPVVNGSVLVPEDQCYCAGWIESRGTNGAQTASNTQQWQAA

 61 〰〰〰〰〰〰〰〰〰〰〰─〰〰〰〰〰〰〰〰〰───────〰〰 120
WT  GFSILLLMFYAYQTWKSTCGWEEIYVCAIEMVKVILEFFFEFKNPSMLYLATGHRVQWLR
    |*|****|*||||||||||||||||*|*||*||*|***|***||||||||||||||||*|
MT  GYSTQQQMYYAYQTWKSTCGWEETYTCATEMTKTTQEYYYEFKNPSMLYLATGHRVQWQR

121 〰〰〰〰〰〰─〰〰〰〰〰〰〰〰〰〰〰───〰〰〰〰〰〰 180
WT  YAEWLLTCPVILIHLSNLTGLSNDYSRRTMGLLVSDIGTIVWGATSAMATGYVKVIFFCL
    ||||**|||****|*|||||||||||||||***||*||**|||||||||||*|****|*
MT  YAEWQQTCPTTQTHQSNLTGLSNDYSRRTMGQQTSDTGTTTWGATSAMATGYTKTTYYCQ

181 〰〰〰〰〰〰〰〰〰─〰〰〰〰〰〰〰〰〰〰〰〰─────── 240
WT  GLCYGANTFFHAAKAYIEGYHTVPKGRCRQVVTGMAWLFFVSWGMFPILFILGPEGFGVL
    |*||||||**|||||*||||*|||||||**|||**||****||||*|*****||||||||
MT  GQCYGANTYYHAAKAYTEGYHTTPKGRCRQTTTGMAWQYYTSWGMYPTQYTQGPEGFGVL

241 〰〰〰〰〰〰〰〰〰〰〰〰〰〰─────────────── 300
WT  SVYGSTVGHTIIDLMSKNCWGLLGHYLRVLIHEHILIHGDIRKTTKLNIGGTEIEVETLV
    |*||||*|||**|*|||||||**|||*|***|||***|||||||||||||||||||||||
MT  STYGSTTGHTTTDQMSKNCWGQQGHYQRTQTHEHTQTHGDIRKTTKLNIGGTEIEVETLV

301 ─────────┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄┄ 360
WT  EDEAEAGAVNKGTGK
    |||||||||||||||
MT  EDEAEAGAVNKGTGK
```

5. Detailed comparison of TM regions:

TM1

AA sequence comparison:

```
TM1-wt:  NGAQTASNVLQWLAAGFSILLLMFYAYQTWKST
         |||||||||**||*|||*|****|*|||||||||
TM1-mt:  NGAQTASNTQQWQAAGYSTQQQMYYAYQTWKST
```

Alpha-helix prediction comparison:

```
TM1-wt:  CCCCCHHHHHHHHHHHHHHHHHHHHHHHHHCCCCC
         ||||||***||||||||****|||||||||||****|
TM1-mt:  CCCCCCCCHHHHHHCCCCHHHHHHHHHHHHHHHHC
```
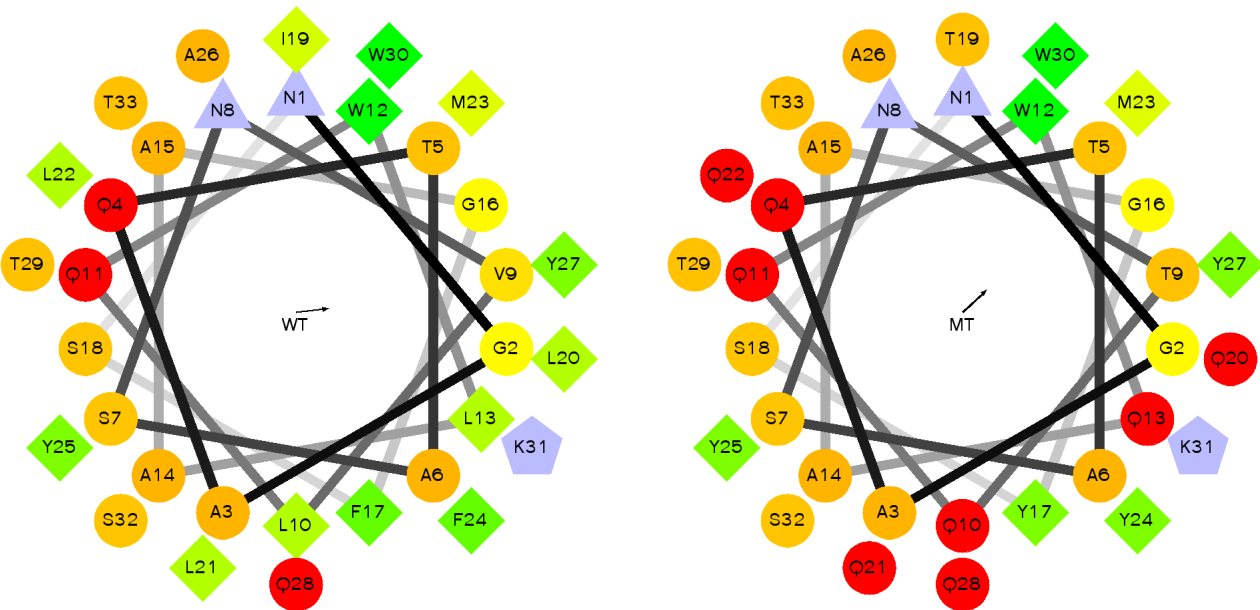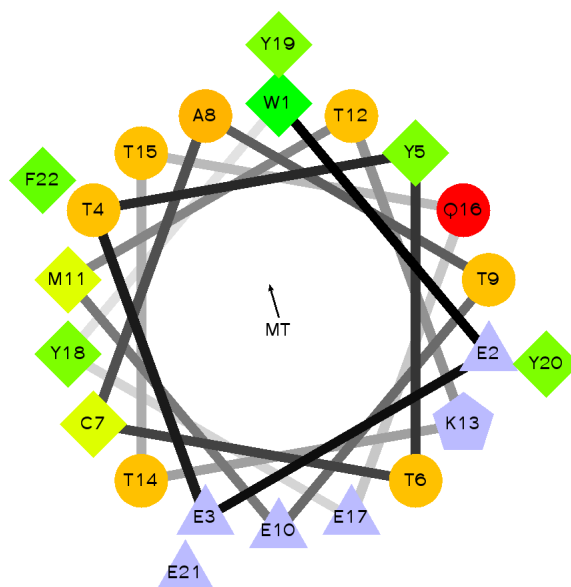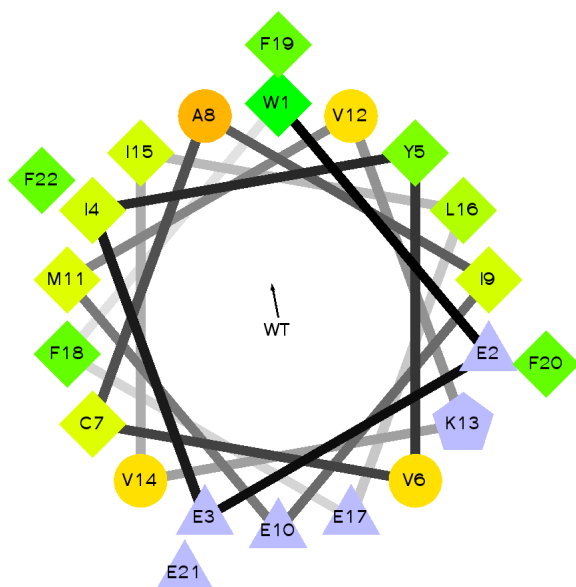
TM2

AA sequence comparison:

```
TM2-wt:  WEEIYVCAIEMVKVILEFFFEF
         |||*|*||*||*|***|***||
TM2-mt:  WEETYTCATEMTKTTQEYYYEF
```

Alpha-helix prediction comparison:

```
TM2-wt:  CEEEEEEEEHHHHHHHHHHHHC
         |*|||||***|****||||||||
TM2-mt:  CCEEEECCCHCCCCHHHHHHHC
```
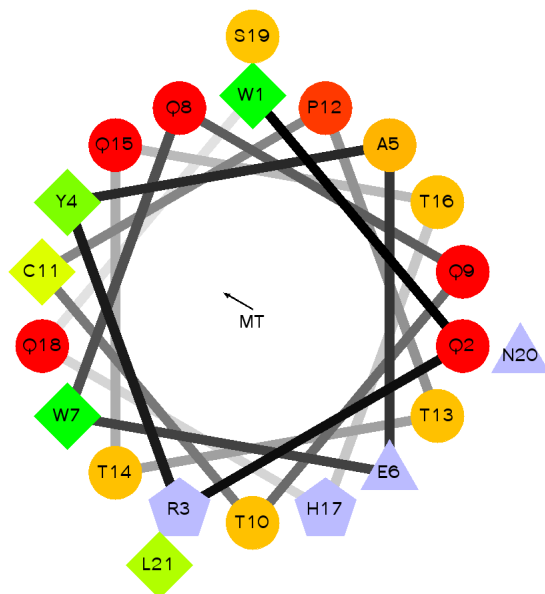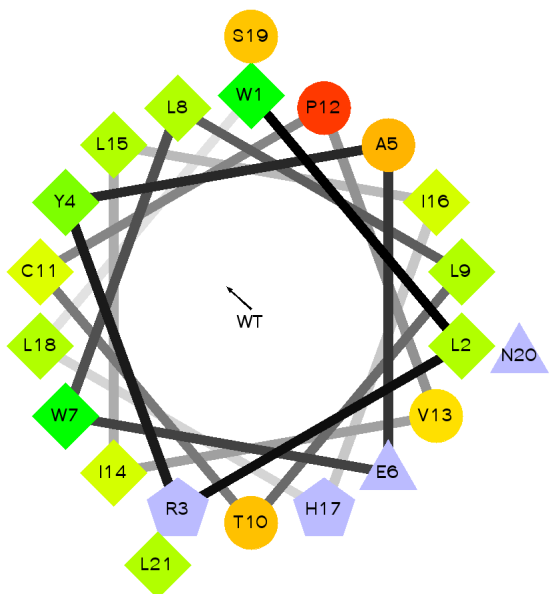

TM3

AA sequence comparison:

```
TM3-wt:  WLRYAEWLLTCPVILIHLSNL
         |*|||||**|||****|*|||
TM3-mt:  WQRYAEWQQTCPTTQTHQSNL
```

Alpha-helix prediction comparison:

```
TM3-wt:  HHHHHHHEECCHHHHHHHHHHH
         *****|||*||*********
TM3-mt:  EEEEEHHECCCCCCCCCCCCC
```
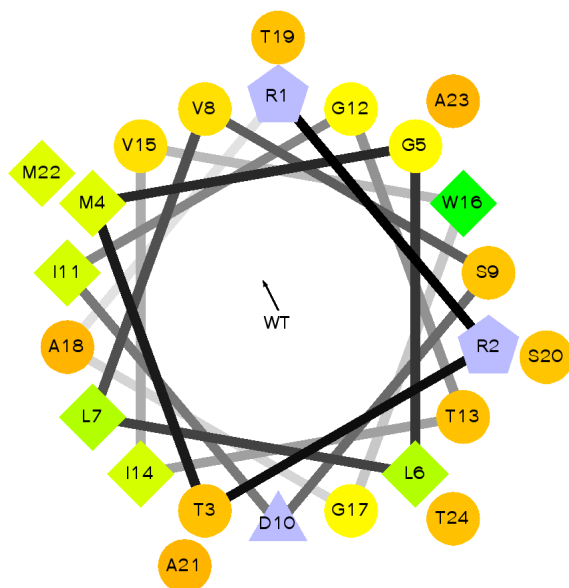
AA sequence comparison:

```
TM4-wt:   RRTMGLLVSDIGTIVWGATSAMAT
          |||||***||*||**||||||||
TM4-mt:   RRTMGQQTSDTGTTTWGATSAMAT
```

Alpha-helix prediction comparison:

```
TM4-wt:   HHHHHHHHHHHHHHHHHHHHHHHH
          ******************|||*
TM4-mt:   CCCCCCCCCCCCCEECCCCCHHHC
```
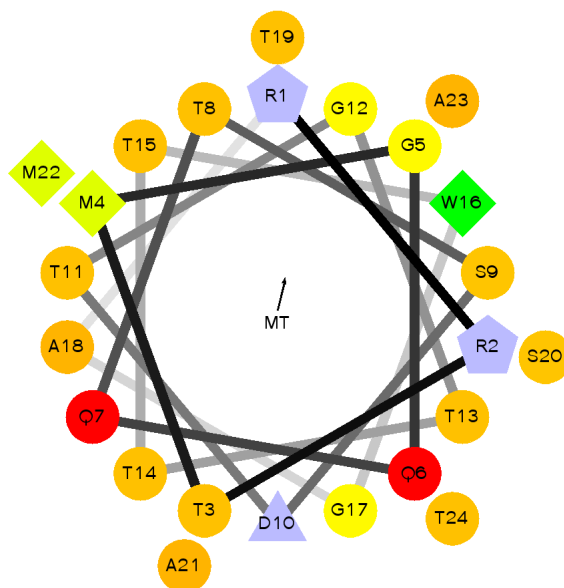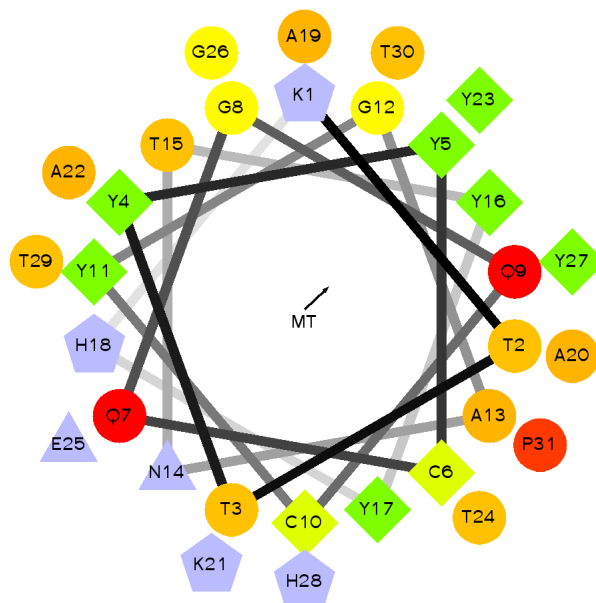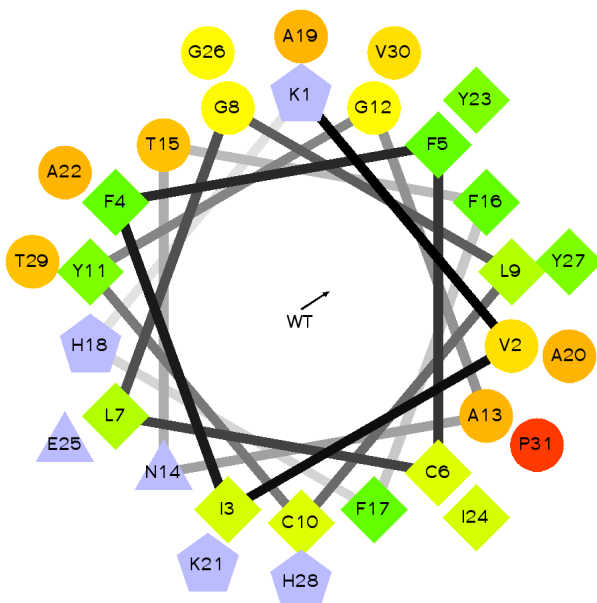

TM5

AA sequence comparison:

```
TM5-wt:   KVIFFCLGLCYGANTFFHAAKAYIEGYHTVP
          |****|*|*||||||**||||||*||||||*
TM5-mt:   KTTYYCQGQCYGANTYYHAAKAYTEGYHTTP
```

Alpha-helix prediction comparison:

```
TM5-wt:   HHHHHHHHHHHHHHHHHHHHHHHHCCCCCC
          **************||||||||*||||||
TM5-mt:   CEEEEECCEECCCCCHHHHHHHHHCCCCCCC
```

TM6

AA sequence comparison:

```
TM6-wt:  CRQVVTGMAWLFFVSWGMFPILFILGP
         ||| ** |||| **** ||| * **** **
TM6-mt:  CRQTTTGMAWQYYTSWGMYPTQYTQGP
```

Alpha-helix prediction comparison:

```
TM6-wt:  HHHHHHHHHHHHHHHHHHCCEEEEECC
         ******* ||||||| **** || *****||
TM6-mt:  CCCCCCCHHHHHHCCCCCCCCCCCCC
```
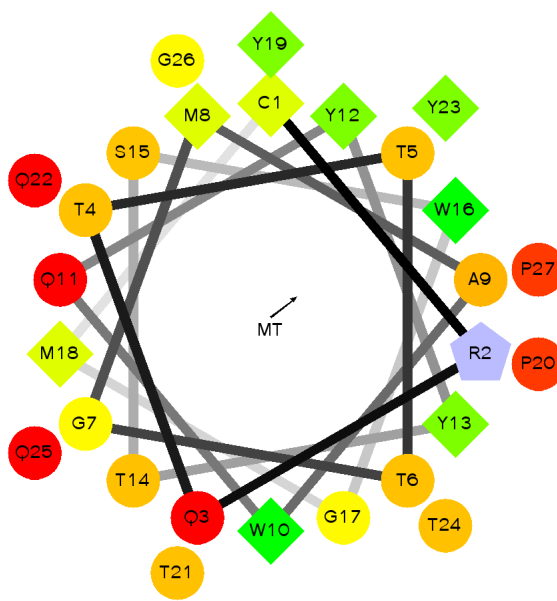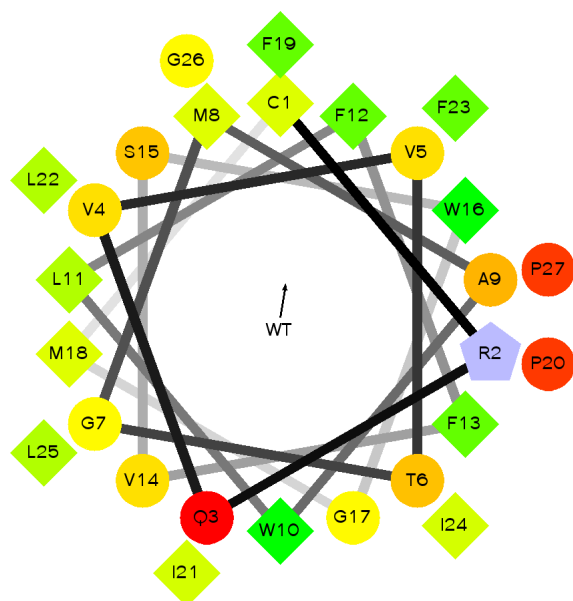

TM7

AA sequence comparison:

```
TM7-wt:  VYGSTVGHTIIDLMSKNCWGLLGHYLRVLIHEHILIHGD
         * ||||| * ||| ** | ||||||||| ** ||| * *** ||| *** |||
TM7-mt:  TYGSTTGHTTTDQMSKNCWGQQGHYQRTQTHEHTQTHGD
```

Alpha-helix prediction comparison:

```
TM7-wt:  HHHHHHHHHHHHHHHHCCCEEEEEEEEEEEEEEEEEEECCC
         ********* ||||||| **************** |||
TM7-mt:  CCCCCCCCCHHHHHCCCCCCCCCCCCCCCCCCCCCCCCC
```