Supplementary file 4: Correlation of conformational parameters for TM helices

The differences amino acid compositions of TM and non-TM in Figure 5 of our manuscript can be regarded as conformational parameters for TM regions. Similarly, Gromiha also developed a set of conformational parameters for TM helices ¹. Interestingly, measures by Gromiha and ours are consistent, with a Pearson's correlation coefficient 0.932. The values obtained by two methods are presented in Table S2. In Table S2, the measure developed by Gromiha is shown in G-measure column while ours is given in Y-measure column.

| Method | G-measure ^a | Y-measure |
|--------|------------------------|-----------|
| А | 1.334 | 0.018 |
| С | 1.062 | 0.003 |
| D | 0.171 | -0.029 |
| E | 0.168 | -0.042 |
| F | 1.707 | 0.053 |
| G | 0.998 | -0.005 |
| Н | 0.530 | -0.019 |
| Ι | 1.803 | 0.063 |
| K | 0.115 | -0.054 |
| L | 1.623 | 0.088 |
| М | 1.413 | 0.014 |
| Ν | 0.494 | -0.018 |
| Р | 0.563 | -0.018 |
| Q | 0.343 | -0.035 |
| R | 0.169 | -0.070 |
| S | 0.817 | -0.022 |
| Т | 0.838 | -0.010 |
| V | 1.599 | 0.064 |
| W | 1.274 | 0.007 |
| Y | 1.146 | 0.012 |

Table S2. Conformational parameters for TM helices by Gromiha and ours.

^a The data of G-measure is cited from ¹.

References

1. M. M. Gromiha, *Protein engineering*, 1999, **12**, 557-561.