```
                β1      TT        α1                  β2      β3      β4      TT      β5          β6
1GQ8:A          →                                     →       →       →               →           →
                1         10        20        30        40        50        60
1GQ8:A          NVVVAADGSGDYKTVSEAVAAAPEDSKT.RYVIRIKAGVYRENVDVPKKKKNIMFLGDGRTSTIITASKN
3g05620cat      NTVVAIDGKGKYRTINEAINEAPNH.STKRYVIYVKKGVYKENIDLKKKKTNIMLVGDGIGQTIITGDRN
3g43270cat      DAVVAADGTGNFTTISDAVLAAPDY.STKRYVIHVKRGVYVENVEIKKKKWNIMMVGDGIDATVITGNRS
4g33220cat      DVSVALDGTGNFTKIMDAIKKAPDY.SSTRFVIYIKKGLYLENVEIKKKKWNIVMLGDGIDVTVISGNRS

                    η1      β7      TT      β8          η2      β9      TT      β10         TT      β11     β12
1GQ8:A              ~~~     →               →           ~~~     →               →           →       →       —
                70        80        90        ★100      110       120       130
1GQ8:A          VQDGSTTFNSATVAAVGAGFLARDITFQNTAGAAKHQAVALRVGSDLSAFYRCDILAYQDSLYVHSNRQF
3g05620cat      FMQGLTTFRTATVAVSGRGFIAKDITFRNTAGPQNRQAVALRVDSDQSAFYRCSVEGYQDTLYAHSLRQF
3g43270cat      FIDGWTTFRSATFAVSGRGFIARDITFQNTAGPEKHQAVAIRSDTDLGVFYRCAMRGYQDTLYAHSMRQF
4g33220cat      FIDGWTTFRSATFAVSGRGFLARDITFQNTAGPEKHQAVALRSDSDLSVFFRCAMRGYQDTLYTHTMRQF

                    β13     β14     β15     β16         TT      β17         TT      β18     β19     η3
1GQ8:A              →       →       →       →                   →               →       →       ~~~
                140 ★     150       160       ★170      180       190       200
1GQ8:A          FINCFIAGTVDFIFGNAAVVLQDCDIHARR.PGSGQKNMVTAQGRTDPNQNTGIVIQKSRIGATSDLQPV
3g05620cat      YRDCEIYGTIDFIFGNGAAVLQNCKIYTR.VPLPLQKVTITAQGRKSPNQNTGFVIQNSYVLATQ.....
3g43270cat      FRECIITGTVDFIFGDATAVFQSCQIKAK.QGLPNQKNSITAQGRKDPNEPTGFTIQFSNIAADTDLL..
4g33220cat      YRECTITGTVDFIFGDGTVVFQNCQILAK.RGLPNQKNTITAQGRKDVNQPSGFSIQFSNISADADLV..

                    β20         β21     β22     TT      TT                  β23     η4      TT
1GQ8:A              →           →       →               →                   →       ~~~     →
                210       220       230       240       250       260       270
1GQ8:A          QSSF....PTYLGRPWKEYSRTVVMQSSITNVINPAGWFPWDGNFALDTLYYGEYQNTGAGAATSGRVTW
3g05620cat      ........PTYLGRPWKLYSRTVYMNTYMSQLVQPRGWLEWFGNFALDTLWYGEYNNIGPGWRSSGRVKW
3g43270cat      ..LNLNTTATYLGRPWKLYSRTVFMQNYMSDAINPVGWLEWNGNFALDTLYYGEYMNSGPGASLDRRVKW
4g33220cat      ..PYLNTTRTYLGRPWKLYSRTVFIRNNMSDVVRPEGWLEWNADFALDTLFYGEFMNYGPGSGLSSRVKW

                β24     α2      α3      η5      η6
1GQ8:A          TT→     ~~~     ~~~     ~~~     ~~~
                    280       290       300 ★     310
1GQ8:A          KGFKVITSSTEAQGFTPGSFIAGGSWLKATTFPFSLGL
3g05620cat      PGYHIM.DKRTALSFTVGSFIDG................
3g43270cat      PGYHVLNTSAEANNFTVSQLIQG................
4g33220cat      PGYHVFNNSDQANNFTVSQFIKG................
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