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      : : ** ** : * . ** : : : . : : : ** : : * ** : * * : : : * : * : * * * *
gi | 194672460 | ref | XP_873514.3 | DYG---SYIRLNSKGLIYSVGLLLASVFVTVFGVHLNKWQLDRKLGCGCLFLYGVFLCFSIMTEFNVFTFVNLPPCGDH 800
gi | 23956242 | ref | NP_444425.1 | DYG---SYIRLNSRGLIYSVGLLLASVFVTVFGVHLNKWQLDKKLGCGCLFLYGVFLCFSIMTEFNVFTFVNLPPCGD- 595
gi | 31563526 | ref | NP_065740.2 | DYG---SYIRLNSRGLIYSVGLLLASVFVTVFGVHLNKWQLDKKLGCGCLLYGVFLCFSIMTEFNVFTFVNLPPCGDH 644
gi | 109468912 | ref | XP_342534.3 | DYG---SYIRLNSRGLIYSVGLLLASVFVTVFGVHLNKWQLDKKLGCGCLFLYGVFLCFSIMTEFNVFTFVNLPPCGD- 562
gi | 73991392 | ref | XP_849585.1 | DYG---SYIRLNSRGLIYSVGLLLASVFVTVFGVHLNKWQLDKKLGCGCLFLYGVFLCFSIMTEFNVFTFVNLPPCGDH 699
gi | 118087566 | ref | XP_419316.2 | NYG---SYIRLNSRGLIYSVGLLLASVFVTVFGVHMNKWQLDKKLGCVCLSLYGFVFLCFSIMTEFNVFTFVNLPPCRDH 627
gi | 292620225 | ref | XP_685302.3 | NYG---STIHLNSKGLIFS VGLLLASVFLTVLGVHLNWKLDKRLGFACLLMYAVFLCFSILLIEFNIFTFVNLPPCREE 559
gi | 281366820 | ref | NP_001015260.3 | FTQPCGNYVAINSAGLEYSAITLLSNLFLLYLTFETKFKLDKKVGLACLVMYLVFMVFASLIELNVFFRVNLPPCGRS 535
gi | 158287819 | ref | XP_001688244.1 | PAVPGERWVALNSGGLIYSSAISLLSLCGLYLAFWCKRFKLDKVGLTCLSMYIGFLTVSSLIELNVFFVNLPPCPH- 563
      .....760.....770.....780.....790.....800.....810.....820.....

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