

* — diagnostic positions

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1
GQ871484_RAG1 ATGTACCGCACCCTCAAGGCCACCACTGGACGCCAGATCTTCCAGCCTTTGCACACTTTACGCGCTGCAGAGAAGGAGCTCCTCCC
GQ871481_RAG1 .....

87
GQ871484_RAG1 AGGCTACCACCCCTTTGAGTGGCAGCCGGCCCTCAAGAGTGTGTCCACATCCTGCCATGTGGGGATCATTAAACGGGCTATCAGGGT
GQ871481_RAG1 .....

173
GQ871484_RAG1 GGGTCGCTTCGGTGGACGACTCCCCAGCAGATACAGTCACGCGTCGGTTTCGCTACGACGTGGCCCTGGTGTCTGGCCCTGAAGGAC
GQ871481_RAG1 .....

259
GQ871484_RAG1 CTGGAGGAGGACATCATGGAGGGGCTGAGAGAGCGAGGCCCTGGAGGACAGTGCTTGCACTCAGGCTTCAGCGTTATGATCAAGGA
GQ871481_RAG1 .....A.....G.....
                                     *

345
GQ871484_RAG1 GTCTGCGATGGCATGGGGGACGTCACTGAGAAGCATGGCCGGAGGGCCGGCCGTCCCGGAAAAGGCTGTGCGTTTCTCCTTCACCA
GQ871481_RAG1 .....

431
GQ871484_RAG1 TCATGTCCGTCTCTATTCAAGCTGAGGGAGAAGATGAGGCGATCACCATTTCCTGGGAGCCCAAGCCCAACTCAGAGATGTCTCTGC
GQ871481_RAG1 .....

517
GQ871484_RAG1 AAGCCGCTCTGCTGATGTTTGTGGACGAGTCGGACCAAGAGACTCTCACAGGTGTCTTGGGGCTGTGGTGGCCGAAAGGAACGC
GQ871481_RAG1 .....

603
GQ871484_RAG1 TATGAAGCACAGCCGTCTCATCCTGTCTGTGGGCGGCCTTTCTCGCTCCTTCCGCTTCCACTTCCGGGGCACGGGCTATGATGAGA
GQ871481_RAG1 .....

689
GQ871484_RAG1 AGATGGTGGAGAGATGGAGGGTTTGGAGGCCCTCTGGCTCCGCTTACATCTGCACACTGTGTGACTCCACTCGGGCAGAGGCCCTCC
GQ871481_RAG1 .....

775
GQ871484_RAG1 CAAAAATGACTCTCCACTCTGTCAACCCGAGCCACGACGAGAACCTGGAGCGCTACGAACTTTGGAGGACCAACCCCTCATTCTGA
GQ871481_RAG1 .....

861
GQ871484_RAG1 GTCAGCTGAAGAGCTGCGAGACCGAGTCAAAGGCGTCTCTGCCAAGCCCTTCATGGAGAAGCCAGCCCACTGGACGCCCTGCACT
GQ871481_RAG1 .....A.....

947
GQ871484_RAG1 GTGATATCGGCAATGCCACTGAGTTCTACAAGATCTTCCAGGATGAGATAGGGGAGGTCTATCACAAGGCAAAACCCAGCCGGGAG
GQ871481_RAG1 .....

1033
GQ871484_RAG1 CAGCGTCGGAGCTGGCGGGCCGCCCTGGACAAGCAGCTGAGGAAGAAGATGAAGCTGAAGCCTGTGATGAGGATGAATGGGAACTA
GQ871481_RAG1 .....A.....
                                     *

1119
GQ871484_RAG1 TGCACGGAAGCTGATGACCCGGGAGGCAGTGGAGGCAGTGTGTGAGCTGGTGCGCTCAGAGGAGCGTCAGGAAGCCCTGAGGGAGC
GQ871481_RAG1 .....

1205
GQ871484_RAG1 TGATGGGGCTCTACATCCAGATGAAGCCTGTGTGGCGCTCCACCTGCCCGGCGAAGGAGTGCCCGAGCCAGCTCTGCGCGGTATAGC
GQ871481_RAG1 .....

1291
GQ871484_RAG1 TTCAACTCCCAACGCTTCGCGAGAGCTGCTCTCCACCGTCTTCAAGTACAGGTATGACGGAAAGATCACCACCTACCTGCACAAGAC
GQ871481_RAG1 .....

1377
GQ871484_RAG1 CTTGGCCCATGTGCCAGAGATTGTGGAGAGGGATGGCTCCATCGGGCCCTGGGCGAGCGAGGGGAATGAGTCTGGGAACAAGCTGT
GQ871481_RAG1 .....

1463
GQ871484_RAG1 TCAGACGGTTCAGGAAGATGAATGCCCCCAGTCCAAGACCTTTGAGCTGGAGGACGTGCTG
GQ871481_RAG1 .....
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