The Sequence Manipulation Suite: Show Translation

Results for 8673 residue sequence "hg18_refGene_NM_004048 range=chr15:42789977-42798649 5'pad=0 3'pad=0 strand=+ repeatMasking=none" starting "gatgcagtcc".

1 gatgcagtccaaactctcactaaaattgccgagccctttgtcttccagtgtctaaaatat 61 taatgtcaatggaatcaggccagagtttgaattctagtctcttagcctttgtttcccctg 181 cattcattcatccattcqttcattcqqtttactqaqtacctactatqtqccaqccc 241 ctgttctagggtggaaactaagagaatgatgtacctagagggcgctggaagctctaaagc 361 aatcaacagaacaaagaaaattacctaaacagcaaggacatagggaggaacttcttggca 421 cagaactttccaaacactttttcctgaagggatacaagaagcaagaaaggtactctttca 481 ctaggaccttctctgagctgtcctcaggatgctttttgggactatttttcttacccagaga 541 atggagaaaccctgcagggaattcccaagctgtagttataaacagaagttctccttctgc 601 taggtagcattcaaagatcttaatcttctgggtttccgttttctcgaatgaaaaatgcag 661 gtccgagcagttaactggctggggcaccattagcaagtcacttagcatctctggggccag $721 \ {\tt tctgcaaagcgaggggcagccttaatgtgcctccagcctgaagtcctagaatgagcgcc}$ 841 ctcacccaqtctaqtqcatqccttcttaaacatcacqaqactctaaqaaaaqqaaactqa 901 aaacgggaaagtccctctctctaacctggcactgcgtcgctggcttggagacaggtgacg 1 N I S G G V A 961 gtccctgcgggccttgtcctgattggctgggcacgcgtttAATATAAGTGGAGGCGTCGC 8 L A G I P E A D S I R A E M S R S V A L 1021 GCTGGCGGGCATTCCTGAAGCTGACAGCATTCGGGCCGAGATGTCTCGCTCCGTGGCCTT 28 A V L A L L S L S G L E A I Q R 1081 AGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAGGCTATCCAGCgtgagtctctcct 1141 acceteccgetetggtcettecteteccgetetgcaccetetgtggccetegetgtgete 1201 tctcgctccgtgacttcccttctccaagttctccttggtggcccgccgtggggctagtcc 1261 agggctggatctcggggaagcggcggggtggcctgggagtggggaagggggtgcgcaccc 1321 gggacgcgctacttgcccctttcggcgggagcaggggagaccttttggcctacggcga 1381 cgggagggtcgggacaaagtttagggcgtcgataagcgtcagagcgccgaggttgggga $1441 \ {\tt gggtttctcttccgctctttcgcggggcctctggctcccccagcgcagctggagtggggg}$ 1501 acqqqtaqqctcqtcccaaaqqcqcqqcqtqaqqtttqtqaacqcqtqqaqqqqcqctt 1561 ggggtctgggggggggtcgcccgggtaagcctgtctgctgcggctctgcttcccttaga 1621 ctggagagctgtggacttcgtctaggcgcccgctaagttcgcatgtcctagcacctctgg 1681 gtctatgtggggccacaccgtggggaggaaacagcacgcgacgtttgtagaatgcttggc 1741 tgtgatacaaagcggtttcgaataattaacttatttgttcccatcacatgtcacttttaa 1801 aaaattataaqaactacccqttattqacatctttctqtqtqccaaqqactttatqtqctt 1861 tgcgtcatttaattttgaaaacagttatcttccgccatagataactactatggttatctt 1921 ctgcctctcacagatgaagaaactaaggcaccgagattttaagaaacttaattacacagg 1981 ggataaatggcagcaatcgagattgaagtcaagcctaaccagggcttttgcgggagcgca 2101 attctccagagcaaactgggcggcatgggcctgtggtcttttcgtacagagggcttcct 2161 ctttggctctttgcctggttgtttccaagatgtactgtgcctcttactttcggttttgaa 2221 aacatgaggggttgggcgtggtagcttacgcctgtaatcccagcacttagggaggccga 2281 ggcgggaggatggcttgaggtccgtagttgagaccagcctggccaacatggtgaagcctg 2341 gtctctacaaaaataataacaaaaattagccgggtgtggtggctcgtgcctgtggtccc 2401 agctgctccggtggctgaggcgggaggatctctttgagcttaggcttttgagctatcatgg 2461 cgccagtgcactccagcgtgggcaacagagcgagaccctgtctctcaaaaaaagaaaaaa 2581 tgtaaaaccattaataaagataatccaagatggttaccaagactgttgaggacgccagag 2641 atcttgagcactttctaagtacctggcaatacactaagcgcgctcaccttttcctctggc 2701 aaaacatgatcgaaagcagaatgttttgatcatgagaaaattgcatttaatttgaataca

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 58 G K S N F L N C Y V S G F H P S D I E V
78 D L L K N G E R I E K V E H S D L S F S
5041 GACTTACTGAAGAATGGAGAGAATTGAAAAAGTGGAGCATTCAGACTTGTCTTTCAGC
 98 K D W S F Y L L Y Y T E F T P T E K D E
5101 AAGGACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAG
118 Y A C R V N H V T L S Q P K I V K W D
5161 TATGCCTGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAGATAGTTAAGTGGGGqtaaq
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7201 ACACTTTATGCACAAAATGTAGGGTTATAATAATGTTAACATGGACATGATCTTCTTTAT
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7261 AATTCTACTTTGAGTGCTGTCTCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTA
     S R R A G N L E V G S R E F
                                           S Y P T
7321 GCTCTAGGAGGGCTGGCAACTTAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAA
     S W S D L N S S I S C T Q S L L R * L S
7381 CATCTTGGTCAGATTTGAACTCTTCAATCTCTTGCACTCAAAGCTTGTTAAGATAGTTAA
    V H K L T S N L H T L L R I W G K I * K
7441 GCGTGCATAAGTTAACTTCCAATTTACATACTCTGCTTAGAATTTGGGGGAAAATTTAGA
     YN * Q D Y W K F V I M N E T F C H I R
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7561 GATTCATATTTACTTCTTATACATTTGATAAAGTAAGGCATGGTTGTGGTTAATCTGGTT
      F L F H K L N K S * N L M C Y L L
7621 TATTTTTGTTCCACAAGTTAAATAAATCATAAAACTTGATGTGTTATCTCTTAtatctca
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