The Sequence Manipulation Suite: Show Translation

Results for 4116 residue sequence "hg18_knownGene_uc010bdx.1 range=chr15:42791037-42795152 5'pad=0 3'pad=0 strand=+ repeatMasking=none" starting "ATGTCTCGCT".

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   1 M  S  R  S  V  A  L  A  V  L  A  L  L  S  L  S  G  L  E  A
   1 ATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAGGCT
  21 I  Q  R
  61 ATCCAGCgtgagtctctcctaccctcccgctctggtccttcctctcccgctctgcaccct
 121 ctgtggccctcgctgtgctctctcgctccgtgacttcccttctccaagttctccttggtg
 181 gcccgccgtggggctagtccagggctggatctcggggaagcggcggggtggcctgggagt
 241 ggggaagggggtgcgcacccgggacgcgcgctacttgcccctttcggcggggagcagggg
 301 agacctttggcctacggcgacgggagggtcgggacaaagtttagggcgtcgataagcgtc
 361 agagcgccgaggttgggggagggtttctcttccgctctttcgcggggcctctggctcccc
 421 cagcgcagctggagtgggggacgggtaggctcgtcccaaaggcgcggcgctgaggtttgt
 481 gaacgcgtggaggggcgcttgggtctggggaggcgtcgcccgggtaagcctgtctgct
 541 gcggctctgcttcccttagactggagagctgtggacttcgtctaggcgcccgctaagttc
 601 gcatgtcctagcacctctgggtctatgtggggccacaccgtggggaggaaacagcacgcg
 661 acgtttgtagaatgcttggctgtgatacaaagcggtttcgaataattaacttatttgttc
 721 ccatcacatgtcacttttaaaaaattataagaactacccgttattgacatctttctgtgt
 781 gccaaggactttatgtgctttgcgtcatttaattttgaaacagttatcttccgccatag
 841 ataactactatggttatcttctgcctctcacagatgaagaaactaaggcaccgagatttt
 901 aagaaacttaattacacaggggataaatggcagcaatcgagattgaagtcaagcctaacc
 961 agggcttttgcgggagcgcatgcctttggctgtaattcgtgcattttttttttaagaaaa
1021 acgcctgccttctgcgtgagattctccagagcaaactgggcggcatgggccctgtggtct
1081 tttcgtacagagggcttcctctttggctctttgcctggttgtttccaagatgtactgtgc
1141 ctcttactttcggttttgaaaacatgagggggttgggcgtggtagcttacgcctgtaatc
1201 ccagcacttagggaggccgaggcgggaggatggcttgaggtccgtagttgagaccagcct
1261 ggccaacatggtgaagcctggtctctacaaaaaataataacaaaaattagccgggtgtgg
1321 tggctcgtgcctgtggtcccagctgctccggtggctgaggcgggaggatctcttgagctt
1381 aggcttttgagctatcatggcgccagtgcactccagcgtgggcaacagagcgagaccctg
1441 tctctcaaaaagaaaaaaaaaaaaaagaaagagaaaagaaaagaaagaaagaagtgaa
1501 ggtttgtcagtcaggggagctgtaaaaccattaataaagataatccaagatggttaccaa
1561 gactgttgaggacgccagagatcttgagcactttctaagtacctggcaatacactaagcg
1621 cgctcacctttcctctggcaaaacatgatcgaaagcagaatgtttttgatcatgagaaaa
1681 ttgcatttaatttgaatacaatttatttacaacataaaggataatgtatatatcaccacc
1741 attactggtatttgctggttatgttagatgtcattttaaaaaataacaatctgatattta
1801 aaaaaaatcttattttgaaaatttccaaagtaatacatgccatgcatagaccatttctg
1861 gaagataccacaagaaacatgtaatgatgattgcctctgaaggtctattttcctcctctg
1921 acctgtgtgtgggttttgttttttgttttactgtgggcataaattaattttttcagttaagt
1981 tttggaagcttaaataactctccaaaagtcataaagccagtaactggttgagcccaaatt
2041 caaacccagcctgtctgatacttgtcctcttcttagaaaagattacagtgatgctctcac
2101 aaaatcttgccgccttccctcaaacagagagttccaggcaggatgaatctgtgctctgat
2161 ccctgaggcatttaatatgttcttattattagaagctcagatgcaaagagctctcttagc
2221 ttttaatgttatgaaaaaatcaggtcttcattagattccccaatccacctcttgatggg
2281 gctagtagcctttccttaatgatagggtgtttctagagagatatatctggtcaaggtggc
2341 ctggtactcctccttctccccacagcctcccagacaaggaggagtagctgccttttagtg
2401 atcatgtaccctgaatataagtgtatttaaaagaatttttatacacatatatttagtgtca
2461 atctgtatatttagtagcactaacacttctcttcattttcaatgaaaaatatagagttta
2521 taatattttcttcccacttccccatggatggtctagtcatgcctctcattttggaaagta
2581 ctgtttctgaaacattaggcaatatattcccaacctggctagtttacagcaatcacctgt
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2701 aaagtatgttctgtcccatttgccatagtcctcacctatccctgttgtattttatcgggt
2761 ccaactcaaccatttaaggtatttgccagctcttgtatgcatttaggttttgtttctttg
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2821 ttttttagctcatgaaattaggtacaaagtcagagaggggtctggcatataaaacctcag
2881 cagaaataaagaggttttgttgtttggtaagaacataccttgggttggttgggcacggtg
2941 gctcgtgcctgtaatcccaacactttgggaggccaaggcaggctgatcacttgaagttgg
3001 gagttcaagaccagcctggccaacatggtgaaatcccgtctctactgaaaatacaaaaat
3061 taaccaggcatggtggtgtgtgcctgtagtcccaggaatcacttgaacccaggaggcgga
3121 ggttgcagtgagctgagatctcaccactgcacactgcactccagcctgggcaatggaatg
3181 agattccatcccaaaaaataaaaaaataaaaaaataaagaacataccttgggttgatcca
3241 cttaggaacctcagataataacatctgccacgtatagagcaattgctatgtcccaggcac
3301 tctactagacacttcatacagtttagaaaatcagatgggtgtagatcaaggcaggagcag
3361 gaaccaaaaagaaaggcataaacataagaaaaaaaatggaaggggtggaaacagagtaca
3421 ataacatgagtaatttgatgggggctattatgaactgagaaatgaactttgaaaagtatc
3481 ttggggccaaatcatgtagactcttgagtgatgtgttaaggaatgctatgagtgctgaga
3541 gggcatcagaagtccttgagagcctccagagaaaggctcttaaaaatgcagcgcaatctc
3601 cagtgacagaagatactgctagaaatctgctagaaaaaaaacaaaaaaggcatgtataga
3661 ggaattatgagggaaagataccaagtcacggtttattcttcaaaatggaggtggcttgtt
3721 gggaaggtggaagctcatttggccagagtggaaatggaattgggagaaatcgatgaccaa
3781 atgtaaacacttggtgcctgatatagcttgacaccaagttagccccaagtgaaataccct
  24                                                T  P  K  I  Q  V  Y  S
3841 ggcaatattaatgtgtcttttcccgatattcctcagGTACTCCAAAGATTCAGGTTTACT
  32   R  H  P  A  E  N  G  K  S  N  F  L  N  C  Y  V  S  G  F  H
3901 CACGTCATCCAGCAGAGAATGGAAAGTCAAATTTCCTGAATTGCTATGTGTCTGGGTTTC
  52   P  S  D  I  E  V  D  L  L  K  N  G  E  R  I  E  K
3961 ATCCATCCGACATTGAAGTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAgtggagc
4021 attcagacttgtctttcagcaaggactggtctttctatctcttgtactacactgaattca
  69                M  S  M  P  A  V  *
4081 cccccactgaaaaagATGAGTATGCCTGCCGTGTGA
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