

HeLaTM7SF2.xdna x NCBI\_transcript1.xdna [163 to 1419] => DNA Parallel

DNA sequence 1401 bp GTCTGCGTTCGG ... TACATCTACTGA linear
DNA sequence 1614 bp GGGACGAGAGCG ... AAAAAAAAAAAAA linear

Method: Blocks (Martinez)
Layout: Standard
Mismatch penalty: Smaller (1)
Gap penalty: Medium (2)
Translation: Bottom only

1 GTCTGCGTTCGGTTCAGGCAGGTGCAGGCGCCGCGGGGCGCGGATCCTCCGCGCGGCCGAGTCCATCTCTGGGAAATG 80
====
81 GGGCGGACAGTGTTCCTTGACTGACTATGTGAGCGCCCTCTCTCTCCGGCGGAGCGGAGACCATGGCCCCACTCAGG 160
163 =====ATGGCCCCACTCAGG 178
M A P T Q G
161 GCCCCGGGGCCCCGCTGGAATTCGGAGGGGCCCTGGGCGCGCGGCTCTGCTACTGCTGCTGCCCGCCACCATGTTCCAC 240
179 GCCCCGGGGCCCCGCTGGAATTCGGAGGGGCCCTGGGCGCGCGGCTCTGCTACTGCTGCTGCCCGCCACCATGTTCCAC 258
P R A P L E F G G P L G A A A L L L L L P A T M F H
180
241 CTGCTCCTGGCGGGCCGTTTCGGGCCCCGCGCGCTGCTGGGTCCACCCGCTCCCTGCCCGGGCTGGAGGTGCTGTGGAG 320
259 CTGCTCCTGGCGGGCCGTTTCGGGCCCCGCGCGCTGCTGGGTCCACCCGCTCCCTGCCCGGGCTGGAGGTGCTGTGGAG 338
L L L A A R S G P A R L L G P P A S L P G L E V L W S
260
321 CCCACGGGGCGCTGCTGCTGTTGCTGCGCTGGCTCGGCTGCAGGCGGCGCTCTACCTACTGCCGGCGCGCAAGGTGGCCG 400
339 CCCACGGGGCGCTGCTGCTGTTGCTGCGCTGGCTCGGCTGCAGGCGGCGCTCTACCTACTGCCGGCGCGCAAGGTGGCCG 418
P R A L L L W L A W L G L Q A A L Y L L P A R K V A E
340
401 AGGGGCAGGAATTGAAGGACAAGAGTCGCTGCGCTATCTTATTAACGGCTTCCAGGCCCTGGTGTGACAGCCCTGTTG 480
419 AGGGGCAGGAATTGAAGGACAAGAGTCGCTGCGCTATCTTATTAACGGCTTCCAGGCCCTGGTGTGACAGCCCTGTTG 498
G Q E L K D K S R L R Y P I N G F Q A L V L T A L L
420
481 GTGGGGCTGGGGATGTCAGCGGGGCTGCCTCTGGGGGCGTCCCGGAAATGCTCCTGCCCTTGGCGTTTGTCCGCCACCT 560
499 GTGGGGCTGGGGATGTCAGCGGGGCTGCCTCTGGGGGCGTCCCGGAAATGCTCCTGCCCTTGGCGTTTGTCCGCCACCT 578
V G L G M S A G L P L G A L P E M L L P L A F V A T L
500
561 CACCGCTTTCATCTTCAGCCTCTTCTCTACATGAAGGCGCAGGTAGCCCCAGTTTCGGCCCTGGCACCTGGGGGGAAC 640
579 CACCGCTTTCATCTTCAGCCTCTTCTCTACATGAAGGCGCAGGTAGCCCCAGTTTCGGCCCTGGCACCTGGGGGGAAC 658
T A F I F S L F L Y M K A Q V A P V S A L A P G G N S
580
641 CAGGCAATCCGATTTACGACTTTTTTCTGGGACGAGAGCTCAACCCCTCGTATCTGTTTCTTCGACTTCAAATATTTCTGT 720
659 CAGGCAATCCGATTTACGACTTTTTTCTGGGACGAGAGCTCAACCCCTCGTATCTGTTTCTTCGACTTCAAATATTTCTGT 738
G N P I Y D F F L G R E L N P R I C F F D F K Y F C
660
721 GAACTGCGACCCCGCTCATCGGCTGGGTCTCATCAACCTGGCCCTGTGATGAAGGAGGCAGAGCTTCGAGGCAGTCC 800
739 GAACTGCGACCCCGCTCATCGGCTGGGTCTCATCAACCTGGCCCTGTGATGAAGGAGGCAGAGCTTCGAGGCAGTCC 818
E L R P G L I G W V L I N L A L L M K E A E L R G S P
740
801 CTCACTGGCCATGTGGCTGGTCAATGGCTTCCAGTTGCTCTACGTGGGTGATGCCCTCTGGCACGAGGAGGCCCTCCTCA 880
819 CTCACTGGCCATGTGGCTGGTCAATGGCTTCCAGTTGCTCTACGTGGGTGATGCCCTCTGGCACGAGGAGGCCCTCCTCA 898
S L A M W L V N G F Q L L Y V G D A L W H E E A V L T
820
840 860 880

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      .           900           .           920           .           940           .           960
881 CCACCATGGATATCACACATGACGGGTTTGGCTTCATGCTGGCGTTTGGGGACATGGCCTGGGTGCCCTTCACCTACAGC 960
      |||
899 CCACCATGGATATCACACATGACGGGTTTGGCTTCATGCTGGCGTTTGGGGACATGGCCTGGGTGCCCTTCACCTACAGC 978
      T M D I T H D G F G F M L A F G D M A W V P F T Y S
      900           .           920           .           940           .           960           .           1040
961 CTGCAGGCCAGTTCTCTGCTGCACCACCCGAGCCCTGGGGTTGCCCATGGCCTCTGTGCATCTGCCTCATCAATGCTAC 1040
      |||
979 CTGCAGGCCAGTTCTCTGCTGCACCACCCGAGCCCTGGGGTTGCCCATGGCCTCTGTGCATCTGCCTCATCAATGCTAC 1058
      L Q A Q F L L H H P Q P L G L P M A S V I C L I N A T
      980           .           1000           .           1020           .           1040           .           1120
1041 TGGTACTACATCTCCGTTGGGGCGAATTCACAGAAAAACACTTCCGAAAGAATCCTTCTGACCCAGAGTGGGTGGGC 1120
      |||
1059 TGGTACTACATCTCCGTTGGGGCGAATTCACAGAAAAACACTTCCGAAAGAATCCTTCTGACCCAGAGTGGGTGGGC 1138
      G Y Y I F R G A N S Q K N T F R K N P S D P R V A G L
      1060           .           1080           .           1100           .           1120           .           1200
1121 TTGAGACCATCTCTACAGCCACAGGGCGGAAACTGCTGGTGTCTGGGTGGGTATGGTCCGCCATCCCAACTATCTT 1200
      |||
1139 TTGAGACCATCTCTACAGCCACAGGGCGGAAACTGCTGGTGTCTGGGTGGGTATGGTCCGCCATCCCAACTATCTT 1218
      E T I S T A T G R K L L V S G W W G M V R H P N Y L
      1140           .           1160           .           1180           .           1200           .           1280
1201 GGAGACCTCATCATGGCTCTGGCTTGGTCCTTGCCCTGCGGGGTGTCACACCTGCTGCCCTACTTCTACCTCCTTACTT 1280
      |||
1219 GGAGACCTCATCATGGCTCTGGCTTGGTCCTTGCCCTGCGGGGTGTCACACCTGCTGCCCTACTTCTACCTCCTTACTT 1298
      G D L I M A L A W S L P C G V S H L L P Y F Y L L Y F
      1220           .           1240           .           1260           .           1280           .           1360
1281 CACCGCGCTGCTGGTGCACCGTGAGGCCCGGGATGAGCGGCAGTGCCTGCAGAAGTACGGCCTGGCCTGGCAGGAGTACT 1360
      |||
1299 CACCGCGCTGCTGGTGCACCGTGAGGCCCGGGATGAGCGGCAGTGCCTGCAGAAGTACGGCCTGGCCTGGCAGGAGTACT 1378
      T A L L V H R E A R D E R Q C L Q K Y G L A W Q E Y C
      1300           .           1320           .           1340           .           1360           .           1400
1361 GCCGGCGTGTGCCTTACCGCATCATGCCCTACATCTACTGA 1401
      |||
1379 GCCGGCGTGTGCCTTACCGCATCATGCCCTACATCTACTGA 1419
      R R V P Y R I M P Y I Y *
      1380           .           1400           .

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% Identity = 89.7 (1257/1401)

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