

BLASTN 2.9.0+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 9AC73PMW114

Query= atp1

Length=864

Sequences producing significant alignments:	Score (Bits)	E Value	Max ident
Query_75155 atpA	343	4e-98	69%

ALIGNMENTS

>Query_75155 atpA
Length=1533

Score = 343 bits (380), Expect = 4e-98
Identities = 578/832 (69%), Gaps = 26/832 (3%)
Strand=Plus/Plus

Query 40	GCCCCGGGATTATTGCTCGCCGTTCTGTACACGAGCCGATGCAAACCTGGAATTAAGCT	99
Sbjct 403	GCACCTGGTATTATTGCACGACAATCTGTTTTGAACCATTACAACAGGGCTGTAGCT	462
Query 100	GTGGATAGTCTGGTCCCATCGGCCGTGGTCAACGGGAATTAATTATTGGGGATCGTCAA	159
Sbjct 463	ATCGATTCTATGATTCTATAGGTAGAGGGCAACGAGAATTAATTATTGGTGATAGACAA	522
Query 160	ACCGGTAAAACAGCAATCGCTTTGGATACTATTTTGAATCAAAAACACAACACTGGAGAG	219
Sbjct 523	ACAGGAAAACATCAATCGCTGTTGATACTATTTTGAATCAAAAAGGTAATCTG-----	577
Query 220	GCTCAGCTCTATTGTGTCTATGTGGCCATTGGTCAAAAACGGTCAACCGTGGCCCA-GTT	278
Sbjct 578	-----TTTATTGCAATTTATGTAGCTATTGGACAAAAGCTTCTCTATTGCTCAAGTT	630
Query 279	GGTAAAAATTTTATCTGACGCTCAGGCAATGGAGTATACCACTGTAGTGGCTGCCACGGC	338
Sbjct 631	GTTTCGACTTTAAAGAAACAAGG-GGCTATGGAATATACTATTATTGTTGCTGCACCAGC	689
Query 339	CTCAGAT---CCCGCGCCTTTACAGTTTTTAGCACCTTATACTGGATGTGCTATATCTGA	395
Sbjct 690	---AGATTCTCCAGCTACTTTACAATATTTAGCTCCTTATACTGGTGCTACTTTGGCAGA	746
Query 396	ATTTTTCCGGGATAATGGTATGCATGCGCTCATTATTTTCGATGATCTCAGCAAAACAAAG	455
Sbjct 747	ATATTTTCATGTATAAAGGAGGTACATACCTTGTGATTTATGATGATTTATCTAAACAAGC	806
Query 456	TGTGGCCTATAGGCAATGTCACTATTGTTGCGTCGACCTCCCGGTAGAGAGGCGTTTCC	515
Sbjct 807	TCAAGCTTATAGAGAAATGTCTTTACTTTTAAGACGACCACCTGGTCGTGAAGCTTTTCC	866
Query 516	AGGAGATGTATTTTATCTTCATAGTCGACTACTTGAACGGGCTGCGAAACTAAGTGATAC	575
Sbjct 867	TGGGGATGTTTTTATCTTCATTCAAGACTTTTAGAACGGGCAGCAAACTGAATAAACA	926
Query 576	ACTAGGAGCAGGCAGTATGACCGCCTTACCTATCATTGAAACACAATCGGGGGATGTGTC	635
Sbjct 927	AATGGGTGGAGGTAGTATGACAGCTCTTCTATTGTTGAAACACAAGAAGGAGATGTATC	986
Query 636	GGCTTATATTCTACCAATGTGATTTGATTACTGATGGACAAAATTCCTGGAAACATC	695
Sbjct 987	TGCTTATATTCCAACAAATGTAATTTCTATTACTGATGGACAGATTTTTTT---ATCAGC	1043
Query 696	A-CTATTTT---ATAAAGGTATTCGTCAGCAATTAATGTGGGAATTTCTGTGAGTCGTGT	752
Sbjct 1044	AGATATTTTTAATAGTGAATTCTGCCAGCTATTAATGTTGGTATTTCTGTTTCTCGTGT	1103

