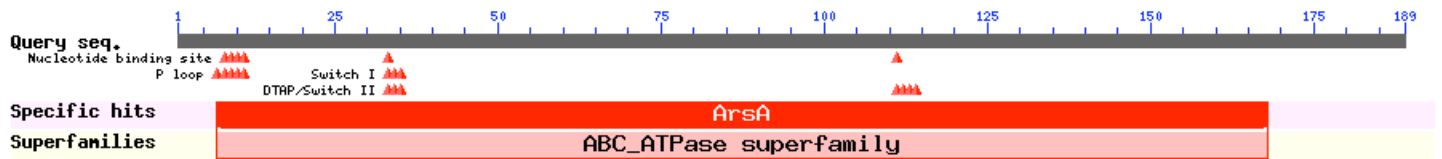


BLAST Basic Local Alignment Search Tool

Job Title: lcl|P76387|WZC_ECOLI No comment found

Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



- Your search is limited to records matching entrez query: G-K-[ST]-X(7,27)-[ILVFM](3)-D-X-D-X-R-X(60,80)[ILVFM](3)-D-X(2)-P-X(30,150)-Y-X(0,5)-Y..

[Please, try our new design!](#)

Informational Message: No sequences corresponding to the entrez query G-K-[ST]-X(7,27)-[ILVFM](3)-D-X-D-X-R-X(60,80)[ILVFM](3)-D-X(2)-P-X(30,150)-Y-X(0,5)-Y. were found in the swissprot database

Informational Message: Query 'lcl|26850' (# 1): Warning: GI or TI list filtering resulted in an empty database.

BLASTP 2.2.18+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, 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. **Reference for compositional score matrix adjustment:** Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109. RID: 8DYWTEB7011 **Database:** Non-redundant SwissProt sequences 343,377 sequences; 128,612,170 total letters

Results of PSI-Blast iteration 1

Taxonomy reports

Query= lcl|P76387|WZC_ECOLI No comment found Length=189

No significant similarity found. For reasons why, [click here](#).

Database: Non-redundant SwissProt sequences
Posted date: Jul 22, 2008 4:57 AM
Number of letters in database: 0
Number of sequences in database: 0

Lambda K H
0.317 0.134 0.383

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 0

Number of Hits to DB: 0

Number of extensions: 0

Number of successful extensions: 0

Number of sequences better than 100: 0

Number of HSP's better than 100 without gapping: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Length of query: 189

Length of database: 0

Length adjustment: 13

Effective length of query: 176

Effective length of database: 0

Effective search space: 11968

Effective search space used: 11968

T: 11

A: 40

X1: 6 (2.7 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 6 (6.9 bits)

S2: 6 (6.9 bits)