BLAST ® » blastn suite-2sequences » RID-8RX748E0114

BLAST Results

Questions/comments

Blast 2 sequences

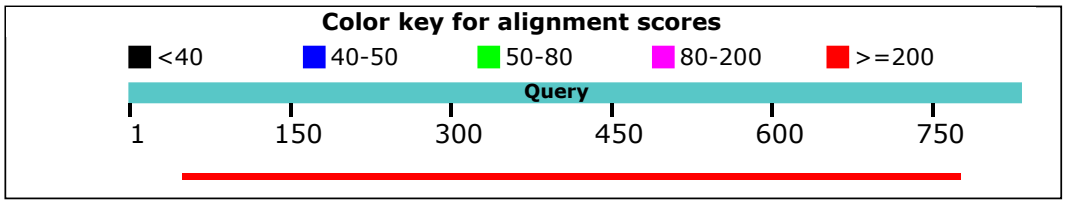
Job title: 901E-F

RID	8RX748E0114 (Expires on 03-17 02:54 am)

Query ID	lcl|Query_160581	**Subject ID**	4799 subjects
Description	901E-F	**Description**	See details
Molecule type	nucleic acid	**Molecule type**	nucleic acid
Query Length	813	**Subject Length**	4343931
		Program	BLASTN 2.9.0+

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKLPCM_04537 Toxin coregulated pilus biosynthesis protein T	1116	1116	88%	0.0	94.26%	Query_165119

Alignments

MHIKLPCM_04537 Toxin coregulated pilus biosynthesis protein T

Sequence ID: Query_165119 Length: 1566 Number of Matches: 1

Range 1: 729 to 1448

Score	Expect	Identities	Gaps	Strand	Frame
1116 bits(604)	0.0()	690/732(94%)	23/732(3%)	Plus/Minus	

Features:

```
Query  52    GCCATTGTTATcccccccAAGCTATTCACCCAKYTGGTCAACAGCTTCTTTACGTTTAGC  111
Sbjct  1448  GCCATTGTTATCCCCCCCAAGCTATTCACCCA-GTGGTCAACAGCTTCTTTACGTTTAGC  1390

Query  112   AGCACAAACAAGTYCTAAAAATGTTGTATCTGGTTCAACTATCTCTGCAATAACTGTACG  171
Sbjct  1389  AGCACAAACAAGTTCTAAAAATGTTGTATCTGGTTCAACTATCTCTGCAATAACTGTACG  1330

Query  172   TCCTGTATATCCAGCATAACAACAATCACATCCACTTTCATTGGCAAAACGTATAGAATC  231
Sbjct  1329  TCCTGTATATCCAGCATAACAACAATCACATCCACTTTCATTGGCAAAACGTATAGAATC  1270

Query  232   TTCATATCCTTCAATTATGTTTCGTTCCAGAACATCCAGATTTTTATGTTTAGCTATATA  291
Sbjct  1269  TTCATATCCTTCAATTATGTTTCGTTCCAGAACATCCAGATTTTTATGTTTAGCTATATA  1210

Query  292   TTTATCTAACGTAACACAACATTTATTACATAATTTTTTAACTAATCTTTGTGCTATCAA  351
Sbjct  1209  TTTATCTAACGTAACACAACATTTATTACATAATTTTTTAACTAATCTTTGTGCTATCAA  1150

Query  352   ACCTGTTACTAAATCAGGATCCGTAAGCTTAAAATCATCAACTCCCTGATCCTTTAGACG  411
Sbjct  1149  ACCTGTTACTAAATCAGGATCCGTAAGCTTAAAATCATCAACTCCCTGATCCTTTAGACG  1090

Query  412   GTCAAATATAGATAATGCGCTGTTTGCATGTAATGAAGTCCATAWGTGATGGCCGGTCAT  471
Sbjct  1089  GTCAAATATAGATAATGCGCTGTTTGCATGTAATGAAGTCCATACCTGATGGCCGGTCAT  1030

Query  472   TGCAGCAGTAAACACTAGACTAATAACTTCAGCATCTCGTGCTTCACCGGGCATTATAAT  531
Sbjct  1029  TGCAGCAGTAAACACTAGACTAATAACTTCAGCATCTCGTGCTTCACCGGGCATTATAAT  970

Query  532   ATCAGGGATCTGAACGTAGKGCAGCAATAATAGCCTTTCTGTATTCCCCTCCCTCGTTCT  591
Sbjct  969   ATCAGG-ATCTGAACGTAGTGCAGCAATAATAGCCTTTCTGTATTCCC-TCCCTCGTTCT  912

Query  592   TCCTCTGTTTCAACGTTGGTTAWARGGTAATTGTGCGGTTCCCTMA-TT-CATAWTTCAG  649
Sbjct  911   TCCTCTGTTTCAACGTTGGTTATA-GGTAATTGTGCGGTTCCCTCAATTTCATA-TTCAG  854

Query  650   GAGGG-CTTCAW-ACTGATTATWTAAACTTTCC-tttttttCTTCAKAAAGRAAGGTTT  706
Sbjct  853   GAGGGTCTTCAATACTGATTATATTAACTTTCCCTTTTTTTCTTCATAAAG-AAG-TTC  796

Query  707   YTAGGCAWATTCCTTTAGK-TCGKAGATT-AC-GGA-CCTKGTGGGTCCAGA-ATWTATT  761
Sbjct  795   -TAG-CATATTC-TTTAGTGTCGTAGATTTACCGGAGCCT-GTTGGTCCAGAGAT-TATA  741

Query  762   TGAAC-CCTTAA  772
Sbjct  740   TTAACACCTAAA  729
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