

[BLAST®](#) » [blastn suite-2sequences](#) » RID-6BKJA42D11R

BLAST Results

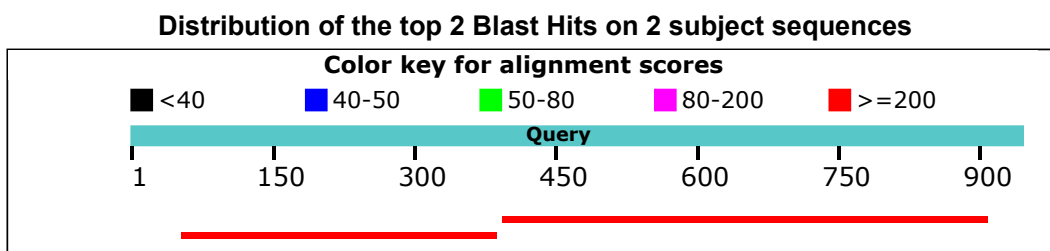
[Questions/comments](#)

Blast 2 sequences

Job title: 43,700-1F

RID	6BKJA42D11R (Expires on 02-16 03:23 am)	Subject ID	4799 subjects
Query ID	lcl Query_27289	Description	See details
Description	43,700-1F	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	917	Program	BLASTN 2.8.1+

[Graphic Summary](#)



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKPCM_04539 Putative type II secretion system protein E	904	904	55%	0.0	99.01%	Query_31829
MHIKPCM_04538 Toxin coregulated pilus biosynthesis protein E	571	571	35%	3e-163	97.87%	Query_31828

Alignments

MHIKPCM_04539 Putative type II secretion system protein E
 Sequence ID: Query_31829 Length: 978 Number of Matches: 1
 Range 1: 1 to 502

Score	Expect	Identities	Gaps	Strand	Frame
904 bits(489)	0.0()	501/506(99%)	4/506(0%)	Plus/Plus	

Features:

Query	391	ATGAAGTGTCTAAGAGAAATA	+++++CAGATCTACTTATCAGTGACAATGGATACTTT	450
Sbjct	1	ATGAAGTGTCTAAGAGAAATA	+++++CAGATCTACTTATCAGTGACAATGGATACTTT	60
Query	451	TTGCGCTATTTAGAAGGGGAGTCAGAGCCAGTTATTAAGCTACCTATGGCTTATATGGAT		510
Sbjct	61	TTGCGCTATTTAGAAGGGGAGTCAGAGCCAGTTATTAAGCTACCTATGGCTTATATGGAT		120
Query	511	GACGCGTTGGCGTTAAGGAGTGATTTAGAGAAAAAATAAAGAGGAGGGGAAAAAAGAA		570
Sbjct	121	GACGCGTTGGCGTTAAGGAGTGATTTAGAGAAAAAATAAAGAGGAGGGGAAAAAAGAA		180
Query	571	TTCTTTTATTTCATATATGGACATACCATATCGAGCAGCGGTAGTTACAACCTATTGATGGA		630
Sbjct	181	TTCTTTTATTTCATATATGGACATACCATATCGAGCAGCGGTAGTTACAACCTATTGATGGA		240
Query	631	GAAGGATATTTCTTAAGAAGATTAACAACCTCCAGTGCCATAATTAATACACTAGGGTTT		690
Sbjct	241	GAAGGATATTTCTTAAGAAGATTAACAACCTCCAGTGCCATAATTAATACACTAGGGTTT		300
Query	691	CCAGATGCTACCCTTGCAACTCTTAAATCTCTTGGTAAATCTAGAGGCGGGCTATTTTA		750
Sbjct	301	CCAGATGCTACCCTTGCAACTCTTAAATCTCTTGGTAAATCTAGAGGCGGGCTATTTTA		360
Query	751	ATTTTCAGGTGCAACTGGTAGTGGTAAGTCTACGTCTATATATTCATTACTAACAGAGTAT		810
Sbjct	361	ATTTTCAGGTGCAACTGGTAGTGGTAAGTCTACGTCTATATATTCATTACTAACAGAGTAT		420
Query	811	GTATCAGTTTATGGGGGATGTAGTTATTTCCATTGAAGATCCTCCTGAATTTGCCCTGT		870
Sbjct	421	GTATCAGTTTATGGGGGATGTAGTTATTTCCATTGAAGATCCTCCTGAATTTGCCCTGT		476
Query	871	TCAGGGTAGCTATAATTACAGAGGGA	896	
Sbjct	477	TCAGGGTAGCTATAATTACAGAGGGA	502	

MHIKPCM_04538 Toxin coregulated pilus biosynthesis protein E
 Sequence ID: Query_31828 Length: 996 Number of Matches: 1
 Range 1: 669 to 996

Score	Expect	Identities	Gaps	Strand	Frame
571 bits(309)	3e-163()	322/329(98%)	1/329(0%)	Plus/Plus	

Features:

Query	54	ATGTGTATAAGAGACAGCTCTTATCCMCCGTTTGTGCTACTAAACGGGGCTAAAAATC	113
Sbjct	669	ATG-GTATAAGGAACGCCCTTATCCACCCGTTTGTGCTACTAAACGGGGCTAAAAATC	727
Query	114	TTGGTGAMGCTTTACATTTATCTGGATATGTTTTCCGTCTAAGGCGTTAGTTATGGATA	173
Sbjct	728	TTGGTGAAAGCTTTACATTTATCTGGATATGTTTTCCGTCTAAGGCGTTAGTTATGGATA	787

```

Query 174 TTAGATCTTATGCTGCACTGGATGGTTTTGAAATGATGCTTGGAAAACCTGCTCGTCAGT 233
Sbjct 788 TTAGATCTTATGCTGCACTGGATGGTTTTGAAATGATGCTTGGAAAACCTGCTCGTCAGT 847
Query 234 GGCAGGATGAGAGTATTCAAGTCATATCAAAGCAGATGGATTTTTTCAGAAACGCAGCAA 293
Sbjct 848 GGCAGGATGAGAGTATTCAAGTCATATCAAAGCAGATGGATTTTTTCAGAAACGCAGCAA 907
Query 294 TAATTATGATGGGACTTATCTTCATGTGGATAGTTTCTGGTATGTTTCGCGTTACAACAAC 353
Sbjct 908 TAATTATGATGGGACTTATCTTCATGTGGATAGTTTCTGGTATGTTTCGCGTTACAACAAC 967
Query 354 AAATAAGTCAAGCTGCTCAATTTTCGTGA 382
Sbjct 968 AAATAAGTCAAGCTGCTCAATTTTCGTGA 996

```

BLAST is a registered trademark of the National Library of Medicine



[Support center Mailing list](#)

[YouTube](#)



- [National Library Of Medicine](#)



- [National Institutes Of Health](#)



- [U.S. Department of Health & Human Services](#)



- [USA.gov](#)

NCBI

[National Center for Biotechnology Information](#), [U.S. National Library of Medicine](#) 8600 Rockville Pike, Bethesda MD, 20894 USA
[Policies and Guidelines](#) | [Contact](#)