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BLAST Results

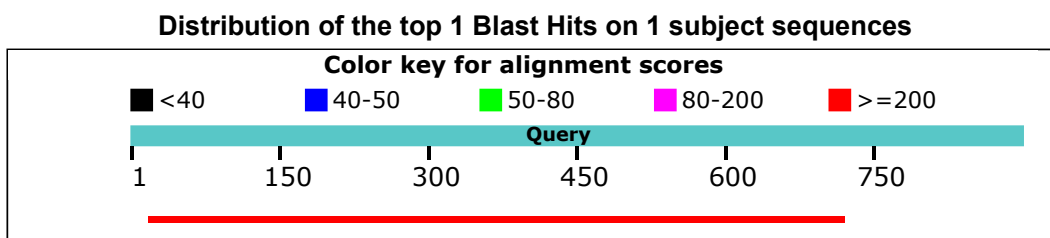
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Blast 2 sequences

Job title: 44,700-1R

RID	6BKJR7YB11R (Expires on 02-16 03:23 am)	Subject ID	4799 subjects
Query ID	lcl Query_78803	Description	See details
Description	44,700-1R	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	873	Program	BLASTN 2.8.1+

[Graphic Summary.](#)



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKLPCM_04538 Toxin coregulated pilus biosynthesis protein E	1238	1238	79%	0.0	98.70%	Query_83342

Alignments

MHIKLPCM_04538 Toxin coregulated pilus biosynthesis protein E

Sequence ID: Query_83342 Length: 996 Number of Matches: 1

Range 1: 1 to 691

Score	Expect	Identities	Gaps	Strand	Frame
1238 bits(670)	0.0()	685/694(99%)	3/694(0%)	Plus/Minus	

Features:

Query	18	ATAAGAGGCGTTCCTTATACCATGGGCGCCAKYTGTTCTTGAAATAATCCTGAGTGCTTC	77
Sbjct	691	ATAAGAGGCGTTCCTTATACCATGGG-G-TAGCTGTTCCTTGAAATAATCCTGAGTGCTTC	634
Query	78	AGGAGCAGGAWTCCCTGCCTCAATTAATGAAGATAAAGACAGCAGAAAACACAGCCCAC	137
Sbjct	633	AGGAGCAGGAATCCCTGCCTCAATTAATGAAGATAAAGACAGCAGAAAACACAGCCCAC	574
Query	138	GACTGTTTTATAAATGTCCATGGCGGAAACTTATCAAAAAACATCCTTACCTTACCTAC	197
Sbjct	573	GACTGTTTTATAAATGTCCATGGCGGAAACTTATCAAAAAACATCCTTACCTTACCTAC	514
Query	198	CCACAGCCCTAATGTCACAATAATGCATATAAAAAATCATAAAAAACAATAACCATCGTCAA	257
Sbjct	513	CCACAGCCCTAATGTCACAATAATGCATATAAAAAATCATAAAAAACAATAACCATCGTCAA	454
Query	258	CAAAAGATAATTTTGCACAAACAATGCAAGATGGTACATTAGTCGTCCGGCCCCCTTGCCA	317
Sbjct	453	CAAAAGATAATTTTGCACAAACAATGCAAGATGGTACATTAGTCGTCCGGCCCCCTTGCCA	394
Query	318	CTCTTCTACAGGTAAAACCTGAGAAAATGCAGGCACAACCCGATTTCCAAAGATATATAA	377
Sbjct	393	CTCTTCTACAGGTAAAACCTGAGAAAATGCAGGCACAACCCGATTTCCAAAGATATATAA	334
Query	378	ATATAAACAGGTGGTTAAGACAAGCACTAACGGATAAACAATACCAAAATAGAGCTGATTT	437
Sbjct	333	ATATAAACAGGTGGTTAAGACAAGCACTAACGGATAAACAATACCAAAATAGAGCTGATTT	274
Query	438	TAttttttttCCTGGTCTGATTGATGTGTATGATAATTATCAATAGATTCATAAAGTTTTCC	497
Sbjct	273	TATTTTTTCTTGGTCTGATTGATGTGTATGATAATTATCAATAGATTCATAAAGTTTTCC	214
Query	498	TGAATACTCCCAGCTGAAAGAAATGAAATCTCATCAGCAGGAACCCAGAATTTCAAGGC	557
Sbjct	213	TGAATACTCCCAGCTGAAAGAAATGAAATCTCATCAGCAGGAACCCAGAATTTCAAGGC	154
Query	558	ATCAGAGAAGCTCTGCCCGTTCCTGACTGAACGCAAGACATCACGAATAACAATTGAAGA	617
Sbjct	153	ATCAGAGAAGCTCTGCCCGTTCCTGACTGAACGCAAGACATCACGAATAACAATTGAAGA	94
Query	618	TGTTGTTTTCTTTCTTTCTGAATCGGTAGTAAACTGATAAAGTTCATTCAATGCATARAS	677
Sbjct	93	TGTTGTTTCTTTCTTTCTGAATCGGTAGTAAACTGATAAAGTTCATTCAATGCATA-AG	35
Query	678	ATAACGGAACKCCATTAACAAGGTAACGAGACAT 711	
Sbjct	34	ATAACGGAACGCCATTAACAAGGTAACGAGACAT 1	

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