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BLAST Results

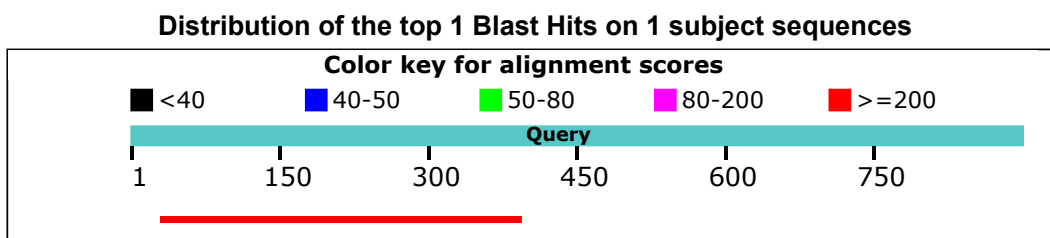
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Blast 2 sequences

Job title: 19,781-1F

RID	77W7ECMZ11R (Expires on 02-26 20:43 pm)	Subject ID	4799 subjects
Query ID	lcl Query_11015	Description	See details
Description	19,781-1F	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	877	Program	BLASTN 2.8.1+

[Graphic Summary.](#)



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKPCM_04534 Outer membrane lipoprotein BfpB	632	632	41%	0.0	98.34%	Query_15550

Alignments

MHIKPCM_04534 Outer membrane lipoprotein BfpB

Sequence ID: Query_15550 Length: 1662 Number of Matches: 1

Range 1: 1042 to 1399

Score	Expect	Identities	Gaps	Strand	Frame
632 bits(342)	0.0()	355/361(98%)	3/361(0%)	Plus/Plus	

Features:

Query	30	GTTACAGGCCATTATGMGCACGACTGCCGGGAGTACCTTTGCCGGATACTGCYAATGGG	89
Sbjct	1042	GTTACAGG-CGATTATG-GCACGACTGCCGGGAGTACCTTTGCCGGATACTG-GAATGGG	1098
Query	90	AATGGTAGTAGTATGAAAACCGAGTTCCTATTTTCGGCGTTAGAAGAAAATGGTAATGTTAGT	149
Sbjct	1099	AATGGTAGTAGTATGAAAACCGAGTTCCTATTTTCGGCGTTAGAAGAAAATGGTAATGTTAGT	1158
Query	150	AACGTCACATCYGCAGTAGTTACAACGATGTCAGGGGTCCTGTACCGGTTCTGGTAGGT	209
Sbjct	1159	AACGTCACATCTGCAGTAGTTACAACGATGTCAGGGGTCCTGTACCGGTTCTGGTAGGT	1218
Query	210	AGTGAAAGTACCTATGTATCCGAACGAGGAAACATCATTTAATGATAACGTAGCAACAACA	269
Sbjct	1219	AGTGAAAGTACCTATGTATCCGAACGAGGAAACATCATTTAATGATAACGTAGCAACAACA	1278
Query	270	ACTGCAAGAACAGAAACTATAACATCAGGTTTTTTGATGAATTTATTGCCTCGGGTTATG	329
Sbjct	1279	ACTGCAAGAACAGAAACTATAACATCAGGTTTTTTGATGAATTTATTGCCTCGGGTTATG	1338
Query	330	GATAATGGAAATATATTACTTCAATATGGTGAAAATTTATCTACTTTAGTCGGTGCATAT	389
Sbjct	1339	GATAATGGAAATATATTACTTCAATATGGTGAAAATTTATCTACTTTAGTCGGTGCATAT	1398
Query	390	G 390	
Sbjct	1399	G 1399	

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