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BLAST Results

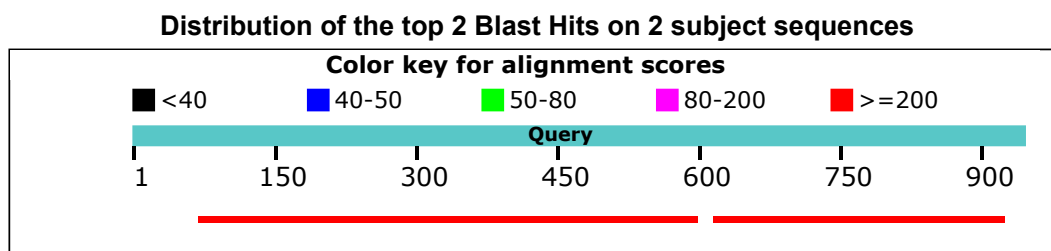
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Blast 2 sequences

Job title: 39,661-1F

RID	6BJVKUNM114 (Expires on 02-16 03:11 am)	Subject ID	4799 subjects
Query ID	lcl Query_127973	Description	See details
Description	39,661-1F	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	923	Program	BLASTN 2.8.1+

[Graphic Summary](#)



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKLPCM_04534 Outer membrane lipoprotein BfpB	955	955	56%	0.0	99.43%	Query_132508
MHIKLPCM_04533 hypothetical protein	488	488	33%	3e-138	96.08%	Query_132507

Alignments

MHIKLPCM_04534 Outer membrane lipoprotein BfpB

Sequence ID: Query_132508 Length: 1662 Number of Matches: 1

Range 1: 1 to 524

Score	Expect	Identities	Gaps	Strand	Frame
955 bits(517)	0.0()	521/524(99%)	0/524(0%)	Plus/Minus	

Features:

Query	72	GGACCAGASYAYTCGACAGCCATATAATCAGTGCTGGCTTTAAGGTCGAGTAAACTTTGA	131
Sbjct	524	GGACCAGAGTAATCGACAGCCATATAATCAGTGCTGGCTTTAAGGTCGAGTAAACTTTGA	465
Query	132	AGTGATGAAGTGAAGCAGCACTTTTTTCACTATTTTCAACCAATTACTTTTGATAATTCT	191
Sbjct	464	AGTGATGAAGTGAAGCAGCACTTTTTTCACTATTTTCAACCAATTACTTTTGATAATTCT	405
Query	192	TCTGATACCTTAGTTACTTCTGCAGTCCCTGTTGCAtttttttGGGTATTGTATAACA	251
Sbjct	404	TCTGATACCTTAGTTACTTCTGCAGTCCCTGTTGCATTTTTTGGGTATTGTATAACA	345
Query	252	TAATCtttttttATAATTGGTATAATTGGTATTTCTTCAAGCATTTTTACAACGCCATCC	311
Sbjct	344	TAATCTTTTTTATAAATTGGTATAATTGGTATTTCTTCAAGCATTTTTACAACGCCATCC	285
Query	312	AGTTTAAAGAGGCAATCCTGAATTCATCGATATCCAGTTTTACCTCAAACGAATAGGT	371
Sbjct	284	AGTTTAAAGAGGCAATCCTGAATTCATCGATATCCAGTTTTACCTCAAACGAATAGGT	225
Query	372	AACGGATCGCCATGCGTACTGACTGAACTTTTGTGCCAAGATAAACACTGTCTGAGACT	431
Sbjct	224	AACGGATCGCCATGCGTACTGACTGAACTTTTGTGCCAAGATAAACACTGTCTGAGACT	165
Query	432	TGCACCGGTGTACattttttgtaagattatcatttttggaaattataagataattttct	491
Sbjct	164	TGCACCGGTGTACATTTTTTGTAAAGATTATCATTTTTGGAAATATAAGATATTTTCT	105
Query	492	gcaatatttttttCTGCGTCATGACTATTTTGTAGTTCTTTTATAGACATCTGTAGAGCAT	551
Sbjct	104	GCAATATTTTTTCTGCGTCATGACTATTTTGTAGTTCTTTTATAGACATCTGTAGAGCAT	45
Query	552	GACACAATTAACGGAAAAGCCAGCATAAAGCTTTAATCGACGCAT	595
Sbjct	44	GACACAATTAACGGAAAAGCCAGCATAAAGCTTTAATCGACGCAT	1

MHIKLPCM_04533 hypothetical protein

Sequence ID: Query_132507 Length: 423 Number of Matches: 1

Range 1: 129 to 423

Score	Expect	Identities	Gaps	Strand	Frame
488 bits(264)	3e-138()	294/306(96%)	12/306(3%)	Plus/Minus	

Features:

Query	612	TTAGAATTGTGGAGTAGATGAAATAAGAATAACTTTTATTACCTTTATACAGGGTAACGTA	671
Sbjct	423	TTAGAATTGTGGAGTAGATGAAATAAGAATAACTTTTATTACCTTTATACAGGGTAACGTA	364
Query	672	TAGCTTGGGATTGGTCTCACCAATTGCTTCAATAAATTTCCGACAGCCTGTTCAAAAAGT	731
Sbjct	363	TAGCTTGGGATTGGTCTCACCAATTGCTTCAATAAATTTCCGACAGCCTGTTCAAAAAGT	304

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Query 732 TTTGTTACTGAATGAAGCGCCGGCCAGCATTTTTATATGAAAGGTTTCGACCGCCATACTA 791
Sbjct 303 TTTGTTACTGAATGAAGCGCCGGCCAGCATTTT-ATATGAAAGGTTTCGACCGCCATACTA 245
Query 792 A-TCCCATCCGGCAGTATATGACCATTGAGACAAAACATTAACAGGTCCCTGACCTTTA 850
Sbjct 244 AATCCCATCCGGCAGTATATGACCATTGAGACAAAACATTAACAGGTCC-TGACCTTTA 186
Query 851 ATTACAGTCCAGTCCGGGGTTAGAAGGGAGGTAAAACGGAAACCCGGAAGTTTCKTGAAT 910
Sbjct 185 ATTACAGTCCAGTCCGGG-TTAGA-GGGAGGTAAAA-GGAA-CCCGGA-GTT-C-TGA-T 134
Query 911 TTATTA 916
Sbjct 133 T-ATTA 129

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