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BLAST Results

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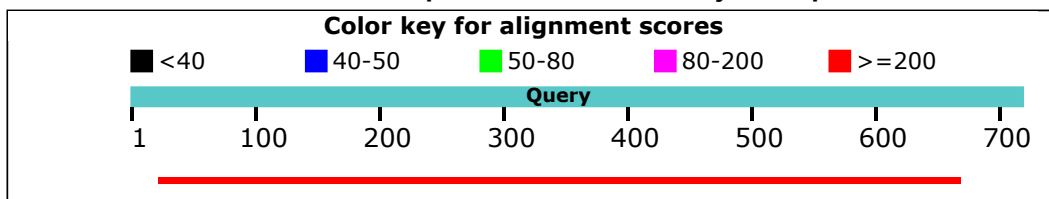
Blast 2 sequences

Job title: 20,780-1R

RID	77WG3MB111R (Expires on 02-26 20:47 pm)	Subject ID	4799 subjects
Query ID	lcl Query_54045	Description	See details
Description	20,780-1R	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	701	Program	BLASTN 2.8.1+

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_04534 Outer membrane lipoprotein BfpB	992	992	91%	0.0	94.40%	Query_58580

Alignments

MHIKLPCM_04534 Outer membrane lipoprotein BfpB

Sequence ID: Query_58580 Length: 1662 Number of Matches: 1
Range 1: 273 to 896

Score	Expect	Identities	Gaps	Strand	Frame
992 bits(537)	0.0()	607/643(94%)	21/643(3%)	Plus/Minus	

Features:

Query	24	GAAACTTTTTTTCATTACTGATGGTGATGTTCTCACGAGTATAGATGAAGTGCTTTGTGAT	83
Sbjct	896	GAAACTTTTTTTCATTACTGATGGTGATGTTCTCACGAGTATAGATGAAGTGCTTTGTGAT	837
Query	84	ATGCTGTATGCACCGATGTCTCCAAGCAAACCTTCAATTCAGAATCA-CATCTTCCAA	142
Sbjct	836	ATGCTGTATGCACCGATGTCTCCAAGCAAACCTTCAATTCAGAATCAACATCTTCCAA	777
Query	143	AAATCTAATGAAACTTCCATATCTAAGGTTTGTCTGATGTACCGCTACTTGAGCTGTTT	202
Sbjct	776	AAATCTAATGAAACTTCCATATCTAAGGTTTGTCTGATGTACCGCTACTTGAGCTGTTT	717
Query	203	GAACCACCGGTACCCCTCCACCCTACTGCCACTACTTCTACTACCTATACTACTTGTA	262
Sbjct	716	GAACCACCGGTACCCCTCCACCCTACTGCCACTACTTCTACTACCTATACTACTTGTA	657
Query	263	GATTCKATTTTGTGGTAATGAGCTTATAGAAAATTTCTGACCTCSTCTGTCSATATT	322
Sbjct	656	GATTCGATTTTGTGGTAATGAGCTTATAGAAAATTTCTGACCTCGTCTGTCGATATT	597
Query	323	AATAATTGACCATCAWCATATTGCCATGCMAGGTCAAATGTGACRAGAATTTATCAAGA	382
Sbjct	596	AATAATTGACCATCAACATATTGCCATGCAAGGTCAAATGTGACGAGAATTTATCAAGA	537
Query	383	AACACTGATAWTGKACCAGAGTAATCSACAGCCATATAATCAGTGCCTGGCTTTAAGGTCG	442
Sbjct	536	AACACTGATAATGGACCAGAGTAATCGACAGCCATATAATCAGTGCCTGGCTTTAAGGTCG	477
Query	443	AGTAAAACCTTTGAAAGTGATGAARTGGAAGCAGCACTTTTTCACTATTTTACCCATTA	502
Sbjct	476	AGTAAA-CTTTG-AAGTGATGAAGTGGAAGCAGCACTTTTTCACTATTTTACCCATTA	419
Query	503	CTTTTGATAAATCTTCTGATACCTTASTTACTTCTGCAGTCCCTGTWGCA+tttttttG	562
Sbjct	418	CTTTTGATAAATCTT-CTGATACCTTAGTT-ACTTCTGCAGTCCCTGTTGCA+TTTTTTG	361
Query	563	SGGTATTGTATACAACATAAACTTTTTWTTTTMTAATTGGRTATATTGGGTTATT-CTT	621
Sbjct	360	-GGTATTGTATACAACATAA-TC-TTTT-TTTA-TAATTGG-TATATTGG-TTATTCTT	308
Query	622	CARGCA+tttttttAMCAACCGCCATCMCAGGATTAGAGAGGC	664
Sbjct	307	CAAGCA-TTTTT--A-CAAC-GCCATC-CAGT-TTA-AGAGGC	273

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