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BLAST Results

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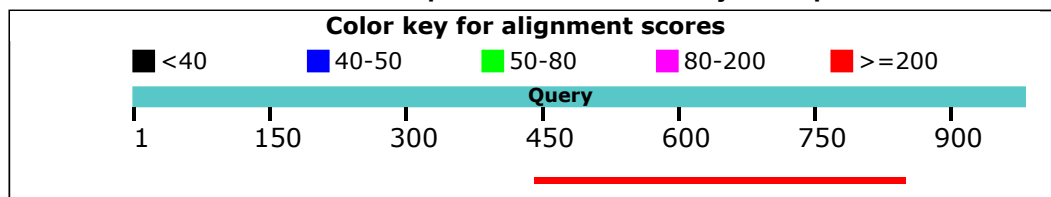
Blast 2 sequences

Job title: 47,780-2F

RID	6BM8UJAT114 (Expires on 02-16 03:35 am)	Subject ID	4799 subjects
Query ID	lcl Query_130913	Description	See details
Description	47,780-2F	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	957	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_01023 RutC family protein YjgH	649	649	42%	0.0	95.56%	Query_131937

Alignments

MHIKLPCM_01023 RutC family protein YjgH

Sequence ID: Query_131937 Length: 396 Number of Matches: 1

Range 1: 3 to 396

Score	Expect	Identities	Gaps	Strand	Frame
649 bits(351)	0.0()	387/405(96%)	12/405(2%)	Plus/Minus	

Features:

Query	442	TTACAGCTCAGGGATGCGCGCTATCACTTTAATTTCAAATCAAAGCCTGCCAGCCAGGT	501
Sbjct	396	TTACAGCTCAGGGATGCGCGCTATCACTTTAATTTCAAATCAAAGCCTGCCAGCCAGGT	337
Query	502	AACGCCACCGCCGTCAGTTTGGATAAAGGAGGGGCGCTAAATATTTCATTTTTGACCGT	561
Sbjct	336	AACGCCACCGCCGTCAGTTTGGATAAAGGAGGGGCGCTAAATATTTCATTTTTGACCGT	277
Query	562	CATGATGTCCTCAAATTTGTTTTCCGGATCGGTATGAAAGCTCGTAACATCAATGATATC	621
Sbjct	276	CATGATGTCCTCAAATTTGTTTTCCGGATCGGTATGAAAGCTCGTAACATCAATGATATC	217
Query	622	GTCAAAGTGATCCCGCAGCAGCCAGGGTTCGCATGCAAATATCAAATGCCAGTCTGAC	681
Sbjct	216	GTCAAAGTGATCCCGCAGCAGCCAGGGTTCGCATGCAAATATCAAATGCCAGTCTGAC	157
Query	682	TTGTTGCTTGAAAATCGGGTCTGGTGTCCGTCCTCTTCGACTTCTACTTTGCCCGGA	741
Sbjct	156	TTGTTGCT-GAAAATCGGGTCTGGTGTCCGTCCTCT-CGACTTCTACTT-GCCCGG-	101
Query	742	AAACAAACAGCAAATCGCCCGGAACGAAATAGCCCGCWGAATAACGATGCTYCASCATAC	801
Sbjct	100	AAACAAACAGCAAATCGCC-GGAACGAA-TAG-CCGCAGAAATAACGATGCT-CAGCATAC	45
Query	802	AGTGAATGTCCGGCCASKCAGGGAAA-CAGSGGKTYCTTTCTWCC	845
Sbjct	44	AGTGAATGTC-GGCCAG-CAGGGAAAACAGCGGTT-CTTCTACC	3

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