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## BLAST Results

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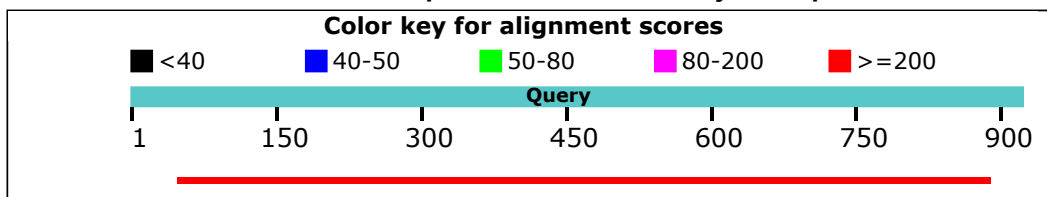
### Blast 2 sequences

Job title: 901M-F

<b>RID</b>	<a href="#">8RXWOWN1114</a> (Expires on 03-17 03:05 am)	<b>Subject ID</b>	4799 subjects
<b>Query ID</b>	lcl Query_173335	<b>Description</b>	<a href="#">See details</a>
<b>Description</b>	901M-F	<b>Molecule type</b>	nucleic acid
<b>Molecule type</b>	nucleic acid	<b>Subject Length</b>	4343931
<b>Query Length</b>	901	<b>Program</b>	BLASTN 2.9.0+

## [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_01514 hypothetical protein	1502	1502	92%	0.0	99.16%	Query_174850

## Alignments

MHIKLPCM\_01514 hypothetical protein

Sequence ID: Query\_174850 Length: 1218 Number of Matches: 1

Range 1: 125 to 955

Score	Expect	Identities	Gaps	Strand	Frame
1502 bits(813)	0.0()	829/836(99%)	5/836(0%)	Plus/Plus	

Features:

Query	49	TATCTATACTAATGATTATTACGGTAATCTATCAAGTTTCTCGTGCTCCGGGAACATTTA	108
Sbjct	125	TATCTATACTAATGATTATTACGGTAATCTATCAAGTTTCTCGTGCTCCGGGAACATTTA	184
Query	109	AAGTACTCTATWAAAATAATCTTTTTTATAGTGTCTGGCACTATCACTCATTCTTTTAT	168
Sbjct	185	AAGTACTCTATAAAAAATAATCTTTTTTATAGTGTCTGGCACTATCACTCATTCTTTTAT	244
Query	169	ATGCTACTTTTTATATCACCTGATCTGAAAAATCAGTTTTAAAGAAATCAGTAATACGGTAC	228
Sbjct	245	ATGCTACTTTTTATATCACCTGATCTGAAAAATCAGTTTTAAAGAAATCAGTAATACGGTAC	304
Query	229	TTAAAGGATTTTTGGCCTATAGTTTACTTATACCTGCATTATTTAAAGATGAAGATAATG	288
Sbjct	305	TTAAAGGATTTTTGGCCTATAGTTTACTTATACCTGCATTATTTAAAGATGAAGATAATG	364
Query	289	AAAGCATTGGTAAAAATGTACTATACTCATTAGTTACCGGACTTGGCTTACGTTGTCTTG	348
Sbjct	365	AAAGCATTGGTAAAAATGTACTATACTCATTAGTTACCGGACTTGGCTTACGTTGTCTTG	424
Query	349	TTGAACTTATTTCTTTATATTAGGATATAATAAAGGAATAATGCCATTTTCCACCTATG	408
Sbjct	425	TTGAACTTATTTCTTTATATTAGGATATAATAAAGGAATAATGCCATTTTCCACCTATG	484
Query	409	AACACCGTAGTATTTCCGATTCAATGGTGTCTGTTTCCAGCATTATTAACCTTTGGC	468
Sbjct	485	AACACCGTAGTATTTCCGATTCAATGGTGTCTGTTTCCAGCATTATTAACCTTTGGC	544
Query	469	TTATCAAGAAAACCTCTTATAAAAATAGCATTTCGTAATTTTTAGTGCAGTTTCTTATTTT	528
Sbjct	545	TTATCAAGAAAACCTCTTATAAAAATAGCATTTCGTAATTTTTAGTGCAGTTTCTTATTTT	604
Query	529	TGCTATTAGGAACGCTGTCTCGTGGTGCATGGCTGGCAGTATTCATAGTGACTCTGCTAT	588
Sbjct	605	TGCTATTAGGAACGCTGTCTCGTGGTGCATGGCTGGCAGTATTCATAGTGACTCTGCTAT	664
Query	589	GGTTAATCTTAAATCGTCAGTGGAAATTTGATGCTGACTTCCATCGTTATTTCTGTTG	648
Sbjct	665	GGTTAATCTTAAATCGTCAGTGGAAATTTGATGCTGACTTCCATCGTTATTTCTGTTG	724
Query	649	CCGCAGTGGGTGATTTTACCTATAAAGGTGATCATGCTGGTAAAGACAGGCTTATTTATA	708
Sbjct	725	CCGCAGTGGGTGATTTTACCTATAAAGGTGATCATGCTGGTAAAGACAGGCTTATTTATA	784
Query	709	AACTTCAACAGACCGACAGTTCTTATCGCTATACCAATGGTACTCAAGGTACGGCGTGCA	768
Sbjct	785	AACTTCAACAGACCGACAGTTCTTATCGCTATACCAATGGTACTCAAGGTACGGCGTGGA	844
Query	769	CATTAATTATGGAAAAATCCTCTTAAAGGGATATGGCTACGGCGATGATATTTACCATGCA	828
Sbjct	845	CATTAATTATGGAAAAATCCTCTTAAAGGGATATGGCTACGGCGATGATA-TTTACCATGCA	903
Query	829	ATATATAATAAGCGTGTGTAGATTTTCCGTCATGGAAAAGCTTACGGGCAATCCA	884
Sbjct	904	ATATATAATAAGCGTGTGTAGATTTTCCGTCATGGAA--G-TTCAGG-CAATCCA	955



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