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## BLAST Results

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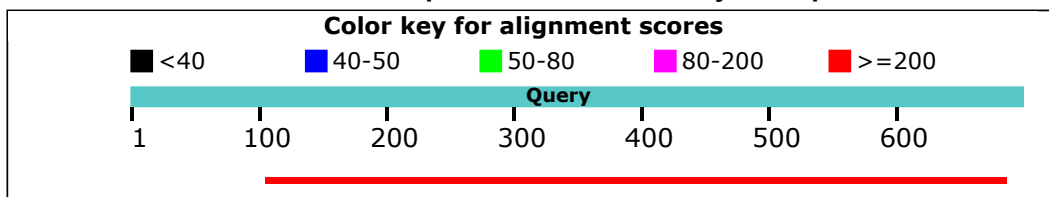
### Blast 2 sequences

Job title: 48,780-2R

<b>RID</b>	<a href="#">6BM96ZY0114</a> (Expires on 02-16 03:35 am)	<b>Subject ID</b>	4799 subjects
<b>Query ID</b>	lcl Query_219193	<b>Description</b>	<a href="#">See details</a>
<b>Description</b>	48,780-2R	<b>Molecule type</b>	nucleic acid
<b>Molecule type</b>	nucleic acid	<b>Subject Length</b>	4343931
<b>Query Length</b>	676	<b>Program</b>	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_01024 Aspartate carbamoyltransferase catalytic subunit	1002	1002	84%	0.0	98.08%	Query_220218

## Alignments

MHIKLPCM\_01024 Aspartate carbamoyltransferase catalytic subunit

Sequence ID: Query\_220218 Length: 936 Number of Matches: 1

Range 1: 1 to 568

Score	Expect	Identities	Gaps	Strand	Frame
1002 bits(542)	0.0()	562/573(98%)	6/573(1%)	Plus/Plus	

Features:

Query	105	ATGGCTAATCCGCTATWTCAGAAACATATCATTTCCATAAACGACCTTAGTCGCGATGAC	164
Sbjct	1	ATGGCTAATCCGCTATATCAGAAACATATCATTTCCATAAACGACCTTAGTCGCGATGAC	60
Query	165	CTTAATCTGGTGCTGGCGACAGCGGCGAAACTGAAAGCAAACCCGCAACCAGAGCTGTTG	224
Sbjct	61	CTTAATCTGGTGCTGGCGACAGCGGCGAAACTGAAAGCAAACCCGCAACCAGAGCTGTTG	120
Query	225	AAGCACAAAGTCATTGCCAGCTGTTTCTTCGAAGCCTCTACCCGTACCCGCCTCTCTTTC	284
Sbjct	121	AAGCACAAAGTCATTGCCAGCTGTTTCTTCGAAGCCTCTACCCGTACCCGCCTCTCTTTC	180
Query	285	GAAACATCTATGCACCGCCTGGGTGCCAGCGTGGTGGGCTTCTCCGACAGCGCAATACA	344
Sbjct	181	GAAACATCTATGCACCGCCTGGGTGCCAGCGTGGTGGGCTTCTCCGACAGCGCAATACA	240
Query	345	TCWCTGGGTAAAAAGGGCGAAACGCTGGCCGATACCATTTTCGGTTATCAGCACTTACRTC	404
Sbjct	241	TCACTGGGTAAAAAGGGCGAAACGCTGGCCGATACCATTTTCGGTTATCAGCACTTACGTC	300
Query	405	GATGCGATAGTGATGCGTCATCCGCAGGAAGGTGCGGCGCGCCTGGCCACCGAGTTTTCC	464
Sbjct	301	GATGCGATAGTGATGCGTCATCCGCAGGAAGGTGCGGCGCGCCTGGCCACCGAGTTTTCC	360
Query	465	GGCAATGTACCGGTACTGAATGCCGGTGATGGCTCCAACCAACATCCGACGCAAACCTTG	524
Sbjct	361	GGCAATGTACCGGTACTGAATGCCGGTGATGGCTCCAACCAACATCCGACGCAAACCTTG	420
Query	525	CTGGACTTATTCACTATTTCAGGAAACCCAGGGGCGTCTGGACAATCTCCACGTCGMAATG	584
Sbjct	421	CTGGACTTATTCACTATTTCAGGAAACCCAGGGGCGTCTGGACAATCTCCACGTCGCAATG	480
Query	585	GTTGGTGACCTGAAATATGGCCGCACCGYTCCTCCCTGACTCAGGCGTTAGCGAAGTT	644
Sbjct	481	GTTGGTGACCTGAAATATGGCCGCACCGTTCCTCCCTGACTCAGGCG-TTAGCGAAGTT	539
Query	645	CGATGGCAACCCGYTTTTTTAACTTCATC-CGC	676
Sbjct	540	CGATGGCAACC-G-TTTTT-A-CTTCATCGCGC	568

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