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### BLAST Results

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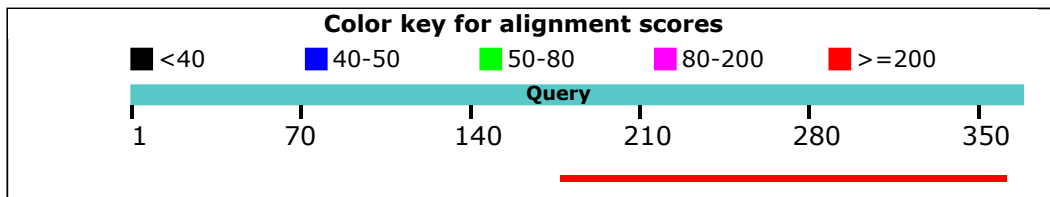
#### Blast 2 sequences

Job title: 63,976-1F

<b>RID</b>	<a href="#">7801XP92114</a> (Expires on 02-26 21:48 pm)	<b>Subject ID</b>	4799 subjects
<b>Query ID</b>	lcl Query_139993	<b>Description</b>	<a href="#">See details</a>
<b>Description</b>	63,976-1F	<b>Molecule type</b>	nucleic acid
<b>Molecule type</b>	nucleic acid	<b>Subject Length</b>	4343931
<b>Query Length</b>	358	<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_02563 ATP-dependent 6-phosphofructokinase isozyme 1	303	303	50%	4e-83	95.60%	Query_142557

## Alignments

MHIKLPCM\_02563 ATP-dependent 6-phosphofructokinase isozyme 1

Sequence ID: Query\_142557 Length: 963 Number of Matches: 1

Range 1: 585 to 766

Score	Expect	Identities	Gaps	Strand	Frame
303 bits(164)	4e-83()	174/182(96%)	0/182(0%)	Plus/Plus	

Features:

Query	177	TGAATT	CAGCCGTGAMGACCTGGTAAACGAAATCAAAGCGGGTATCGCGAAAGG	waaaaa	236
Sbjct	585	TGAATT	CAGCCGTGAAGACCTGGTAAACGAAATCAAAGCGGGTATCGCGAAAGG	AAAAA	644
Query	237	aCACGCGATCGTGGCGATTACCGAACATATGTGTGATGTTGACRAACTGGCGYKTTTCAT			296
Sbjct	645	ACACGCGATCGTGGCGATTACCGAACATATGTGTGATGTTGACGAACCTGGCGCATTTTCAT			704
Query	297	CGAGAAAGAAACYGGTCGTGAAASCCGCGCATCTGTGCTGGGCCACATCCAGCGCGGTGG			356
Sbjct	705	CGAGAAAGAAACCGGTCGTGAAACCCGCGCAACTGTGCTGGGCCACATCCAGCGCGGTGG			764
Query	357	TT			358
Sbjct	765	TT			766

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