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BLAST Results

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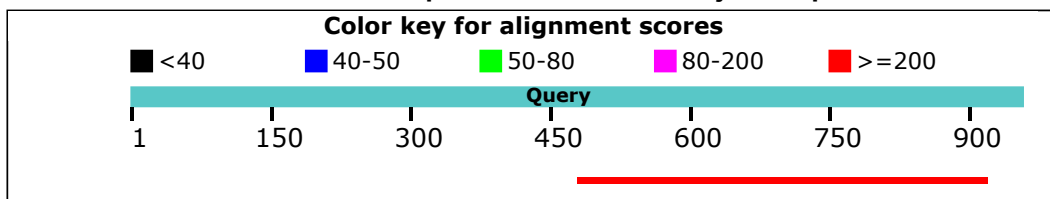
Blast 2 sequences

Job title: 27,310-1

RID	6B9UUXHZ114 (Expires on 02-16 00:37 am)	Subject ID	4799 subjects
Query ID	lcl Query_140611	Description	See details
Description	27,310-1	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	928	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_01203 N-isopropylammelide isopropyl amidohydrolase	739	739	46%	0.0	97.92%	Query_141815

Alignments

MHIKLPCM_01203 N-isopropylammelide isopropyl amidohydrolase

Sequence ID: Query_141815 Length: 1383 Number of Matches: 1

Range 1: 961 to 1383

Score	Expect	Identities	Gaps	Strand	Frame
739 bits(400)	0.0()	423/432(98%)	9/432(2%)	Plus/Minus	

Features:

Query	476	TCAACCTGCCACACTCCCCACACCAGTTGCCCTTTATGGAACGTTGCGGTTCTCGGCGA	535
Sbjct	1383	TCAACCTGCCACACTCCCCACACCAGTTGCCCTTTATGGAACGTTGCGGTTCTCGGCGA	1324
Query	536	GATACGCGCCACCGCCTCGGCGGAACAGGAGGCGTCCACCAGCACAAAGCTGGCGTCATC	595
Sbjct	1323	GATACGCGCCACCGCCTCGGCGGAACAGGAGGCGTCCACCAGCACAAAGCTGGCGTCATC	1264
Query	596	CTGCGCTTTTGGCCATACACGCTCGCCTTTTTTCATTCAGCGGCAATACATTGCCAGTGGC	655
Sbjct	1263	CTGCGCTTTTGGCCATACACGCTCGCCTTTTTTCATTCAGCGGCAATACATTGCCAGTGGC	1204
Query	656	TAAAAACAGCGAGCGGGAGAGGTTCTGTTCTGTTAGGACGAATATAGAGCTGCGCGTACAG	715
Sbjct	1203	TAAAAACAGCGAGCGGGAGAGGTTCTGTTCTGTTAGGACGAATATAGAGCTGCGCGTACAG	1144
Query	716	ATTGGCTTTTTCCAGCATGTCGCCAGACCATAAGGCGACCAGTGGTCGATAAACGCTGTC	775
Sbjct	1143	ATTGGCTTTTTCCAGCATGTCGCCAGACCATAAGGCGACCAGTGGTCGATAAACGCTGTC	1084
Query	776	AGTGCCAGTCATCACTTTTACGCCTTTGTGCTGCAACTGTTTGTGAGCGGGCATATGCAGCG	835
Sbjct	1083	AGTGCCAGTCATCACTTTTACGCCTTTGTGCTGCAACTGTTTGTGAGCGG-CATATGCAGCG	1025
Query	836	TGGCCAATCGGCACCCGTCGAAGGCGAWTAGAAAAATTTTGTGACCACCATCCGGTTCCG	895
Sbjct	1024	TG-CCAATCGGCACC-GTCGA-GGCGA-TAGAAA--TTTGTGACCACCATCCGGTTCCG	971
Query	896	CCAGCTTTCATC	907
Sbjct	970	CCAG-TT-CATC	961

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