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BLAST Results

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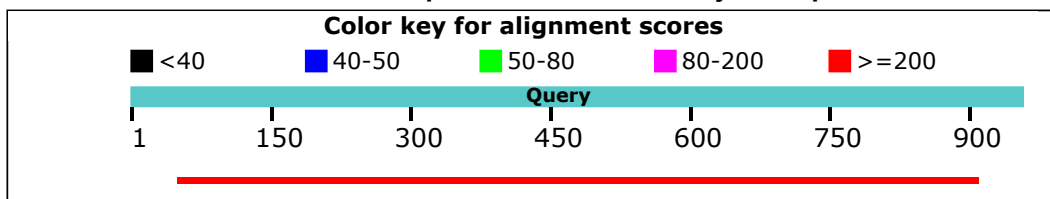
Blast 2 sequences

Job title: 28,310-1R

RID	6B9WHPFN114 (Expires on 02-16 00:38 am)	Subject ID	4799 subjects
Query ID	lcl Query_135015	Description	See details
Description	28,310-1R	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	927	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_01204 Aldehyde reductase YahK	1507	1507	91%	0.0	98.70%	Query_136220

Alignments

MHIKLPCM_01204 Aldehyde reductase YahK

Sequence ID: Query_136220 Length: 1050 Number of Matches: 1

Range 1: 19 to 861

Score	Expect	Identities	Gaps	Strand	Frame
1507 bits(816)	0.0()	838/849(99%)	7/849(0%)	Plus/Plus	

Features:

Query	51	GGTGCATATTCCGCTAAACAACCACTTGMYYGATGGATATCACCCGGCGTGAACCGGGA	110
Sbjct	19	GGTGCATATTCCGCTAAACAACCACTTGAACCGATGGATATCACCCGGCGTGAACCGGGA	78
Query	111	CCGAATGATGTCAAAATCGAAATCGCTTACTGTGGCGTTTGCCATTCGGATCTCCACCAG	170
Sbjct	79	CCGAATGATGTCAAAATCGAAATCGCTTACTGTGGCGTTTGCCATTCGGATCTCCACCAG	138
Query	171	GTCCGTTCAGAGTGGGCGGGGACGGTTTACCCCTGCGTGCCGGGTGATGAAATTTGGGG	230
Sbjct	139	GTCCGTTCAGAGTGGGCGGGGACGGTTTACCCCTGCGTGCCGGGTGATGAAATTTGGGG	198
Query	231	CGTGTGGTAGCCGTTGGTGATCAGGTAGAAAAATATGCGCCGGGCGATCTGGTCGGTGTC	290
Sbjct	199	CGTGTGGTAGCCGTTGGTGATCAGGTAGAAAAATATGCGCCGGGCGATCTGGTCGGTGTC	258
Query	291	GGCTGCATTGTCGACAGTTGTAACATTGCGAAGAGTGTGAAGACGGGTGGAAAACTAC	350
Sbjct	259	GGCTGCATTGTCGACAGTTGTAACATTGCGAAGAGTGTGAAGACGGGTGGAAAACTAC	318
Query	351	TGTGATCACATGACCGGCACCTATAACTCGCCGACGCCGGACGAACCGGGCCATACTCTG	410
Sbjct	319	TGTGATCACATGACCGGCACCTATAACTCGCCGACGCCGGACGAACCGGGCCATACTCTG	378
Query	411	GGCGGCTACTCACAACAGATCGTCGTTTCATGAGCGATATGTTCTGCGTATTCGTACCCG	470
Sbjct	379	GGCGGCTACTCACAACAGATCGTCGTTTCATGAGCGATATGTTCTGCGTATTCGTACCCG	438
Query	471	CAAGAGCAGCTGGCGGCGGTGGCTCCTTTGTTGTGTGCAGGGATCACACGTAATCGCCG	530
Sbjct	439	CAAGAGCAGCTGGCGGCGGTGGCTCCTTTGTTGTGTGCAGGGATCACACGTAATCGCCG	498
Query	531	CTACGTCACCTGGCAGGCCGGCCGGGTAAAAAAGTGGGCGTGGTCGGCATCGGCGGTCTG	590
Sbjct	499	CTACGTCACCTGGCAGGCCGGCCGGGTAAAAAAGTGGGCGTGGTCGGCATCGGCGGTCTG	558
Query	591	GGACATATGGGGATTAAAGCTGGCCACGCGATGGGGGCACATGTGGTGGCATTACCACT	650
Sbjct	559	GGACATATGGGGATTAAAGCTGGCCACGCGATGGGGGCACATGTGGTGGCATTACCACT	618
Query	651	TCTGAGGCAAAACGCGAAAGCGGCAAAAGCCCTGGGGGCGGATGAAGTTGTTAACTCACG	710
Sbjct	619	TCTGAGGCAAAACGCG-AAAGCGGCAAAAGCCCTGGGGGCGGATGAAGTTGTTAACTCACG	677
Query	711	CAATGCCGATGAGATGGCGGCTCATCTGAAGAGTTTCGATTTCAATTTGAATACAGTAGC	770
Sbjct	678	CAATGCCGATGAGATGGCGGCTCATCTGAAGAGTTTCGATTTCAATTTGAATACAGTAGC	737
Query	771	TGCGCCACATAATCTCGACGATTTTACCACCTTGCTGAAGCGTGATGGCACCATGACGCT	830
Sbjct	738	TGCGCCACATAATCTCGACGATTTTACCACCTTGCTGAAGCGTGATGGCACCATGACGCT	797
Query	831	GGGTTGGTGCCTCGGACACCGCATAAATCGCCGGAAGTTTTTCAACCTGGATCATGA	890
Sbjct	798	GG-TTGGTGC-CCTGCGACACCGCATAAATCGCCGGAAGTTTTT-CAACCTG-ATCATGA	853
Query	891	A-CGTCCGT 898	
Sbjct	854	AACG-CCGT 861	

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