

[BLAST®](#) » [blastp suite-2sequences](#) » RID-8NAY7KFC114

BLAST Results

Blast 2 sequences

Job title: eyeless protein for the fruit fly v protein for the mouse

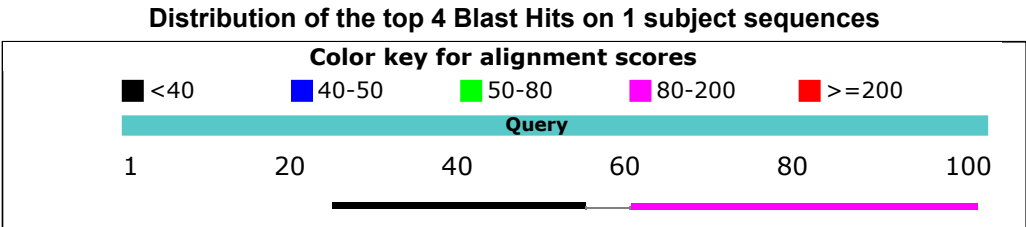
RID [8NAY7KFC114](#) (Expires on 02-20 17:49 pm)

Query ID Icd|Query_71891
Description tr|O96791|O96791_DROME Eyeless protein (Fragment) OS=Drosophila melanogaster GN=ey PE=4 SV=1
Molecule type amino acid
Query Length 101

Subject ID Icd|Query_71893
Description sp|P63015|PAX6_MOUSE Paired box protein Pax-6 OS=Mus musculus GN=Pax6 PE=1 SV=1
[See details](#)
Molecule type amino acid
Subject Length 422
Program BLASTP 2.8.0+

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Graphic Summary

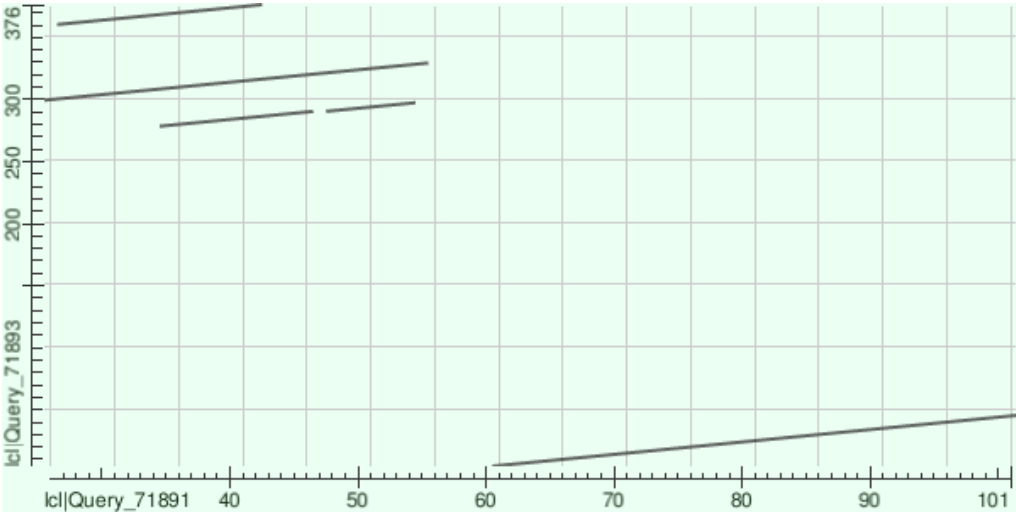


Dot Matrix View



Plot of Icl|Query_71891 vs Icl|Query_71893

[?]



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
sp P63015 PAX6_MOUSE Paired box protein Pax-6 OS=Mus musculus GN=Pax6 PE=1 SV=1	88.2	127	70%	2e-26	98%	Query_71893

Alignments

sp|P63015|PAX6_MOUSE Paired box protein Pax-6 OS=Mus musculus GN=Pax6 PE=1 SV=1
Sequence ID: Query_71893 Length: 422 Number of Matches: 4
Range 1: 5 to 45

Score	Expect	Method	Identities	Positives	Gaps	Frame
88.2 bits(217)	2e-26()	Compositional matrix adjust.	40/41(98%)	40/41(97%)	0/41(0%)	

Features:

Query	61	HSGVNQLGGVFVGRPLPDSTROKIVELAHSGARPCDISRI	101
Sbjct	5	HSGVNQLGGVFVGRPLPDSTROKIVELAHSGARPCDISRI	45

Range 2: 279 to 297

Score	Expect	Method	Identities	Positives	Gaps	Frame
13.9 bits(24)	2.1()	Compositional matrix adjust.	8/20(40%)	13/20(65%)	1/20(5%)	

Features:

Query	35	ASTASHPHSTSSYFATYYH	54
Sbjct	279	SNTPSHIPISSS-FSTSVYQ	297

Range 3: 300 to 329

Score	Expect	Method	Identities	Positives	Gaps	Frame
13.1 bits(22)	3.8()	Compositional matrix adjust.	8/30(27%)	11/30(36%)	0/30(0%)	

Features:

Query26PSPTMEAVEASTASHPSTSSYFATTYYHL55

PPT++ST+TYL

Sbjct300PQPTTPVSSFTSGSMLGRDTDALTNTYSAL329

Range 4: 361 to 376

Score	Expect	Method	Identities	Positives	Gaps	Frame
12.7 bits(21)	5.0()	Compositional matrix adjust.	5/16(31%)	8/16(50%)	0/16(0%)	

Features:

Query27SPTMEAVEASTASHPH42

SP++T+PH

Sbjct361SPSVNGRSYDITYPPH376

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