

BLAST Results

Needleman-Wunsch alignment of two sequences

X79493:D.melanogaster ey mRNA (exons 2-9)

RID

YXFF72XT114

(Expires on 10-02 03:32 am)

Query ID

X79493.1

Description

D.melanogaster ey mRNA (exons 2-9)

Molecule type

nucleic acid

Query Length

2848

Subject ID

AY707088.1

Description

Homo sapiens paired box gene 6 isoform a mRNA, complete cds

[See details](#)

Molecule type

nucleic acid

Subject Length

1269

Program

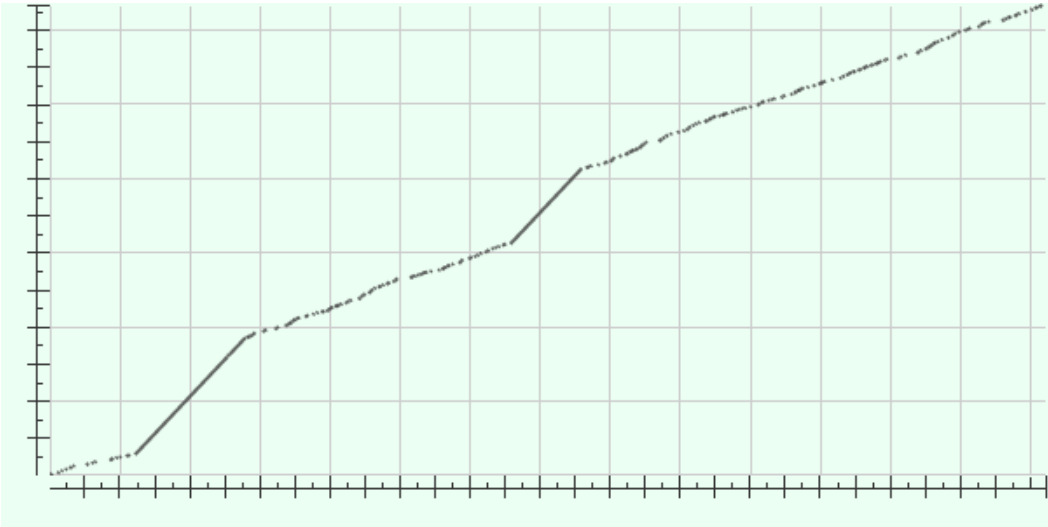
BLASTN 2.5.0+

Dot Matrix View



Plot of X79493.1 vs AY707088.1

[?]



Descriptions

Sequences producing significant alignments:

Description	Score	Percent Ident	Accession
Homo sapiens paired box gene 6 isoform a mRNA, complete cds	-5747.0	37%	AY707088.1

Alignments

Homo sapiens paired box gene 6 isoform a mRNA, complete cds
Sequence ID: **AY707088.1** Length: 1269 Number of Matches: 1
Range 1: 1 to 1269

NW Score	Identities	Gaps	Strand	Frame
-5747	1067/2849(37%)	1581/2849(55%)	Plus/Plus	

Features:

Query	1	TTTCGACGGCGTGCCTTTGGCTGAACACAGCAGTCTCTTGGCTAAAGCTTTCATGAGCAG	60
Sbjct	1	AT-GCA-----GAACA-----GTCAC-----AGC-----GGAG	22
Query	61	TGCATGTAATAAAAACTGAGATCCAACATATGTTTACATTGCAACCAACTCCAACCTGCTAT	120
Sbjct	23	TG-----AAT-----CAGCTC-----	33
Query	121	AGGCACCGTGGTCCCCCATGGTCAGCGGGAACATTGATAGAGCGCTGCCGTCTTTAGA	180
Sbjct	34	-GG-----TGGT-----GTCTTT-G-	46
Query	181	AGACATGGCTCACAAGGGTCACAGTGGAGTAAATCAGCTGGGTGGCGTTTTTGTGGAGG	240
Sbjct	47	-----TCA-----AC-----GGG---CG-----	56
Query	241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACGGCACATTCTGGAGCTCG	300
Sbjct	57	---GCCACTGCCGGACTCCACCCGGCAGAAAGATTGTAGAGCTAGCTCACAGCGGGGCCG	113
Query	301	GCCATGTGATATTTCTGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATCTCGG	360
Sbjct	114	GCCGTGCGACATTTCCCGAATTCTCGAGGTGTCCAACGGATGTGTGAGTAAATCTGGG	173
Query	361	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT	420
Sbjct	174	CAGGTATTACGAGACTGGCTCCATCAGACCAGGGCAATCGGTGGTAGTAAACCGAGAGT	233
Query	421	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTTAGCATATT	480
Sbjct	234	AGCGACTCCAGAAAGTTGTAAAGCAAAATAGCCAGTATAAGCGGGAGTGCCCGTCCATCTT	293
Query	481	TGCTTGGGAAATTCGGGATAGATTACT-TCAGGAGAACGTTTGTACTAACGATAATATAC	539
Sbjct	294	TGCTTGGGAAATCCGAGACAGATTACTGTCCG-AGGGGGTCTGTACCAACGATAACATAC	352
Query	540	CAAGTGTGTCTCAATAAACCGTGTATTGAGAACTTGGCTGCGCAAAAGGAGCAGCAAA	599
Sbjct	353	CAAGCGTGTATCAATAAAC-----A--GAG-----TT--CTTCGCAA-----	386
Query	600	GCACGGGATCCGGGAGCTCCAGCACATCCGCCGGCAACTCAATCAGCGCAAAAGTGTCTG	659
Sbjct	387	-----CCTGG--CT-----AGCG-AAAAG-----	402
Query	660	TCAGCATCGGTGGCAACGTGAGCAATGTGGCAAGCGGATCGAGAGGCACGTTGAGCTCTT	719
Sbjct	403	-----CAAC---AG--ATG-GGC--GCAGA-CG---GCA---TG-----	426
Query	720	CCACCGATCTTATGCAGACAGCCACTCCTCTTAACCTCTTCGAAAGCGGTGGCGCAACGA	779
Sbjct	427	-----TATG-ATA-----AACT-----AAG-----GA	442
Query	780	ACTCCGGGGAGGGTAGTGAACAGGAGGCGATTACGAGAAAGCTTCGGCTGTTAAATACTC	839
Sbjct	443	--T-----GT--TGAAC-GG--GC-----AGA--C--CGG-----AA-----	463
Query	840	AGCACGCTGCAGGACAGGACCACTGGAGCCTGCCAGAGCAGCGCCCTTGGTAGGTCAAT	899
Sbjct	464	-----GCTG--GGGC---ACC-----CGCCCT--GGTTGGT--AT	489
Query	900	CACCAACCACCTAGGAACCCGATCCAGCCACCCCAAGCTGGTGCACGGTAACCATCAGG	959
Sbjct	490	C-----CGGGGACTTCGGT--GCCA-----GG-GCA-----ACC-----	515
Query	960	CACTACAGCAGCATCAACAGCAGAGCTGGCCGCCCGTCACTATTCCGGATCTTGGTACC	1019
Sbjct	516	---TAC-GCA-----AGA-TGGCTGCC-----	532
Query	1020	CCACCTCTCTTAGCGAAATACCCATCTCATCGGCTCCCAATATCGCATCCGTTACGGCGT	1079
Sbjct	533	-----AGC-AA-----CA-----GG-----AA-----GGA--G---GG---	549
Query	1080	ATGCATCAGGACCTTCACTTGTCTACTCACTGAGTCCACCAACGACATCAAAAGCCTGG	1139
Sbjct	550	-----GGA-----GAG-----AAT-AC--CAA---CT--	565
Query	1140	CCAGTATCGGTCAACAGAGAACTGCCCGTTGCAACGGAGGACATACATTTAAAAAAG	1199
Sbjct	566	CCA-----TCA-----GTTCCAACGGAG-----AAG	586
Query	1200	AAC TTGATGGTCATCAGTCCGATGAAACGGGCTCCGGTGAAGGTGAAAACCTCAATGGTG	1259
Sbjct	587	A--TT-----CAG---ATGA---GGCTC-----AAA--TGCGA-----	609
Query	1260	GCGCTTCAAATATAGGAAACACTGAGGATGATCAAGCTCGGCTCATACTAAAAAGAAAGT	1319
Sbjct	610	---CTTCA-----G-----CTGA-----AGC--GG-----AAGC	628
Query	1320	TGCAACGCAATCGAACATCTTTCACGAACGACAGATAGACAGTCTTGAAAAAGAGTTTG	1379
Sbjct	629	TGCAAAAGAAATAGAACATCCTTTACCCAAGAGCAAATTGAGGCCCTGGAGAAAGAGTTTG	688
Query	1380	AACGAACACACTATCCAGATGTTTTGCCCGCGAACGTTTGGCTGGAAGATTGGGTTCG	1439
Sbjct	689	AGAGAACCCATTATCCAGATGTGTTTGCCCGAGAAAGACTAGCAGCCAAAATAGATCTAC	748
Query	1440	CAGAGGCAAGAAATCAGGTTTGGTTCTCAAACGTCGAGCAAAATGGCGTCGCGAGGAGA	1499
Sbjct	749	CTGAAGCAAGAAACAGGTATGGTTTCTAATCGAAGGGCCAAATGGAGAAGAGAAGAAA	808

```

Query 1500 AGCTGCGAAACCAGCGAAGAACACCAAATTCCACAGGAGCTAGTGCAACTTCTTCCTCTA 1559
Sbjct 809 AACTGAGGAATCAGAGAAGA-----CAGG--C-----CA----- 835

Query 1560 CATCGGCAACCGCCTCTTTGACTGACAGCCCTAACAGCCTAAGTGCTTGTTCCTCGCTGC 1619
Sbjct 836 -----GCAAC-----ACA--CCTA-----GT-CATATTCCT----- 858

Query 1620 TGTCCGGATCAGCTGGGGGTCCTCAGTCAGTACCATTAAATGGCTTATCGTCTCCAAGCA 1679
Sbjct 859 -----ATCAGC-----AGT-AGT-----TTCA--GC--A-----CCA-G-- 881

Query 1680 CATTGTCTACTAATGTCAATGCTCCAACGCTTGGCGCTGGGATCGATAGCTCTGAAAGCC 1739
Sbjct 882 ---TGTTCTACCAAC--CAAT--TCCA----- 900

Query 1740 CAACACCAATCCCGCACATTGCGCCTAGCTGCACCTCTGACAATGACAATGGTCGTCAAA 1799
Sbjct 901 CAAC-CCA---CCACAC---CGGTTT-----CCTC-----CTTCA-- 928

Query 1800 GTGAAGATTGCAGAAGAGTTTGTCTCCATGCCCACTTGGCGTTGGCGGGCATCAAAATA 1859
Sbjct 929 -----CA-----TCTGG-CTCCATG-----TTGG--GCCG-----AA---- 952

Query 1860 CTCATCATATCCAGAGCAATGGTCAACGCCAAGGTCATGCACTTGTTCCTGCCATTTTCGC 1919
Sbjct 953 -----CAGA-CA-----CA-GCCC---TCA--CA-----A----- 970

Query 1920 CACGACTCAATTTTAATAGTGGTAGTTTCGGCGCGATGTACTCCAACATGCATCATAACGG 1979
Sbjct 971 -AC-AC-C-----TA-----CAGCGC-----TC-----TGC-----CG- 990

Query 1980 CGTTATCCATGAGCGATTATATGCGGCGGTTACGCCGATTCGAGCTTTAACCACCTCAG 2039
Sbjct 991 -----CC-----TATG-----CCCAGCTT-----CAC-CA- 1009

Query 2040 CTGTCGGTCCGCTGGCTCCGCCATCGCCAATACCGCAACAGGGCGATCTTACCCCTTCCT 2099
Sbjct 1010 -----TGGC-----A-----AATA-----ACC--TGCCT 1026

Query 2100 CGTTATATCCGTGCCACATGACCCCTACGACCCCTCCGATGGCTCCCGCTCACCATCACA 2159
Sbjct 1027 -----ATG-----CAACCCCC---A-G--TCCC---CA----- 1045

Query 2160 TCGTGCCGGGTGACGGTGGCAGACCTGCGGGCGTTGGCCTAGGCAGTGGCCAATCTGCGA 2219
Sbjct 1046 ---GCC-----AGACCT-----CCT---CA-T---ACTC----- 1064

Query 2220 ATTTGGGAGCAAGCTGCAGCGGATCGGGATACGAAGTGCTATCTGCCTACGCGTTGCCAC 2279
Sbjct 1065 -----CTGCA-----TGCT---GCCAC-----CA- 1081

Query 2280 CGCCCCCTATGGCGTCGAGCTCTGCTGCTGATTCAAGCTTCTCAGCCGCTCCAGTGCCA 2339
Sbjct 1082 -GCC--T-----TCG-G-----TGAAT---G-----GGCG-G---AGT--- 1104

Query 2340 GCGCTAATGTGACCCACATCACACCATAGCCCAAGAATCATGCCCTCTCCGTGTTCAA 2399
Sbjct 1105 ---TA---TGA-----T---ACC-TA---CA-----CCCC---CC----- 1123

Query 2400 GCGCGAGCCACTTTGGAGTTGCTCAGATTCTGGGTTTTCTGTCGACCCGATTTACCGG 2459
Sbjct 1124 -----CACA--TATG-----CAGAC----- 1136

Query 2460 CTGTATCTTCGTATGCACATATGAGCTACAATTACGCGTCGTCGCTAACACCATGACGC 2519
Sbjct 1137 -----ACACATGA---ACA-----GTCAGC---CA--ATGG-GC 1161

Query 2520 CTTCTCCGCCAGCGGCACATCAGCACACGTGGCCCCGGGAAAAACAACAGTTCTTCGCCT 2579
Sbjct 1162 A--CCTC-G-----GGCAC-----CACTT-----CAACAG-----GACT 1187

Query 2580 CCTGTTTCTACTCACCGTGGGTCTAGGAACAGACTGGCGATTTGAGCAGAGAAGCACTGC 2639
Sbjct 1188 CAT--TTC-----CCCTGG-----TG-----TGT---CAG----- 1207

Query 2640 GAAAGGACTATTACATAGTTGAATGTATATCTAAAGGAGGCCATAATAAATCGAATTTA 2699
Sbjct 1208 -----TTCCA--GTTCAA-GT---TC-----CC----- 1224

Query 2700 CATATCTCTTGAAAAATAATGGAGTTGTAGAAAAATACATTTGTATGTATAAATTATAT 2759
Sbjct 1225 -----GGAAGT---GAA---CCT--G-----ATAT 1241

Query 2760 AGTTCGCCCCATTAAATCCAATCTATAGTGAGAATAATTGGTGAAATTAAATGATATA 2819
Sbjct 1242 -GT---CTCA-----ATACTG-----GCCAA-----GAT-TA 1263

Query 2820 ATTTTGACAAATAAAAAAAAAAAAAAAAAA 2848
Sbjct 1264 -----CAG-TAA 1269

```

