FGENESH 2.6 Prediction of potential genes in Trichinella_spiralis genomic DNA

Seg name: gb|SISJ02000053.1| Dmelanogaster01

Length of sequence: 2899

Number of predicted genes 1: in +chain 1, in -chain 0. Number of predicted exons 5: in +chain 5, in -chain 0.

Positions of predicted genes and exons: Variant 1 from 1, Score: 76.267493

	CDS	f	CDSi		CDSI	(CDSo	◆ Pc	lΑ	TSS	
	1	2		3	4						5
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227	400	600	800	1000	1200	1400	1600	1800	2000	2200	2400 2575
1 .	+ 1	CDSi	227	-	440	18.01	2	229 -	438	210	
1 .	+ 2	CDSi	575	_	731	8.70	5	576 -	731	156	
1	+ 3	CDSi	789	-	1164	37.46	7	789 -	1163	375	
1 -	+ 4	d CDSi	1217	-	1291	0.76	12	219 -	1290	72	
1	+ 5	CDSi	2130	_	2575	35.06	21	.32 -	2575	444	

Predicted protein(s):

>FGENESH: [mRNA] 1 5 exon (s) 227 - 2575 1266 bp, chain + AAAATTGTGGAGCAGAGCCTTGGTGCAGCCTTGGTGAAAACTCCCAAATTTGTGATACC CACTTTAATGATTCGCAGTGGAAGGCTGCACCTGCAAAAGGTCAGACATTTAAAAGGAGG CGACTCAACGCAGATGCCGTACCTAGTAAAGTGATAGAGCCTGAACCAGAAAAGATAAAA GAAGGCTATACCAGTGGGAGTACACAAACAGAAGCAGCAGCTGAGGGAGTCTCAACAGTT GGAGGAGTCTCTACGCAAAATCTTCACGGACACGCAGATACGGATACTGAAGAATGGTGG ACAAAGAGCTACGTTCAATTCCGACGACATTTCTACAGCTATTTGTCTCCACACCGCAGG CCTTCGAGCATGGTTATCAGATGTGGACATAAAAAGAGGGATGTTTGATGTGGTCATAGAC CTAATGGACAGTGATGGAGTTGATGACGCCGACAAGCTTTGCGTACTCGCTTTCGACGAG ATGAAGGTCGCTGCCTTCGAGTATGACAGTTCTGCTGATATTGTTTACGAGCCAAGC TTCGATTTTAATACCCGAATGGACCCGGATACTCTTAACAATATATTAAGGAAACTGCAT AGGAAAGGATATTTAGTAGTTGCTATTGTATCCGATTTAGGTACCGGAAACCAAAAGCTA TGGACAGAGCTCGGTATATCAGAATCAAAAACCTGGTTTAGCCATCCTGCAGATGACCAT TTAAAGATTTTCGTTTTTTCGGATACGCCACATTTAATTACCAGGAATACAGAAATGTTA AGAAATTCGGGAAATATCGAAGAGGACAACTCTGAAAGCTGGCTTAATTTAGATTTCAGT TCTAAAGAAAACGAAAATAAAAGTAAAGATGATGAGCCTGTCGATGATGAGCCTGTCGAT GAGATGTTAAGCAATATAGATTTCACCGAAATGGATGAGTTGACGGAGGATGCGATGGAA TATATCGCGGGCTATGTCATTAAAAAATTGAGAATCAGTGACAAAGTAAAAGAAAATTTG ACATTTACATACGTCGACGAGGTGTCTCACGGCGGACTTATTAAGCCGTCCGAAAAATTT CAAGAGAAGTTAAAAGAGCTAGAATGTATTTTTTTTGCATTATACAAATAATAATTTT GAAATTACAAATAATGTAAAGGAAAAATTAATATTAGCAGCGCGAAACGTCGATGTTGAT AAACAA

>FGENESH: 1 5 exon (s) 227 - 2575 422 aa, chain + KIVEQSLGCSLGENSQICDTHFNDSQWKAAPAKGQTFKRRRLNADAVPSKVIEPEPEKIK EGYTSGSTQTEAAAEGVSTVGGVSTQNLHGHADTDTEEWWTKSYVQFRRHFYSYLSPHRR PSSMVIRCGHKKRMFDVVIDLMDSDGVDDADKLCVLAFDEMKVAAAFEYDSSADIVYEPS DYVQLAIVRGLKKSWKQPVFFDFNTRMDPDTLNNILRKLHRKGYLVVAIVSDLGTGNQKL WTELGISESKTWFSHPADDHLKIFVFSDTPHLITRNTEMLRNSGNIEEDNSESWLNLDFS

SKENENKSKDDEPVDDEPVDEMLSNIDFTEMDELTEDAMEYIAGYVIKKLRISDKVKENL TFTYVDEVSHGGLIKPSEKFQEKLKELECIFLHYTNNNNFEITNNVKEKLILAARNVDVD KQ