FGENESH 2.6 Prediction of potential genes in Trichinella_spiralis genomic DNA

Seg name: gb|JAECYB010001729.1| Dwillistoni07

Length of sequence: 2853

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: 123.137097

C	DSf		CDSi		CDSI		CDSo	◆ Pol	A	TSS	
1			2		3		4			5	
1									<u> </u>		
199	400	600	800	1000	1200	1400	1600	1800	2000	2200	2529
1 +	1 (CDSi	199	-	390	18.53	20	00 -	388	189	
1 +	2 (CDSi	449	-	939	55.59	45	50 –	938	489	
1 +	3 (CDSi	1070	-	1114	5.79	107	/2 -	1113	42	
1 +	4 (CDSi	1168	-	1893	28.42	117	0 -	1892	723	
1 +	5 (CDSi	2084	-	2529	35.06	208	36 -	2529	444	

Predicted protein(s):

>FGENESH: [mRNA] 1 5 exon (s) 199 - 2529 1899 bp, chain + TTGGGTTATTTCCTTCTCCGGGAATCCCTATTCACCCACTTTAATGATTCGCAGTGG AAGGCTGCACCTGCAAAAGGTCAGACATTTAAAAGGAGGCGACTCAACGCAGATGCCGTA CCTAGTAAAGTGATAGAGCCTGAACCAGAAAAGATAAAAGAAGGCTATACCAGTGGGAGT ACACAAACAGAGTCCTGTTCATTGTTTAATGAAAATAAGAGCTTGAGGGAAAAAATTCGT ACTTTGGAGTACGAAATGCGTCGTTTAGAGCAGCAGCTGAGGGAGTCTCAACAGTTGGAG GAGTCTCTACGCAAAATCTTCACGGACACGCAGATACGGATACTGAAGAATGGTGGACAA AGAGCTACGTTCAATTCCGACGACATTTCTACAGCTATTTGTCTCCACACCGCAGGCCCT CGAGCGTATAACCATCTGTACAAAAAGGATTTCCTTTGCCCAGTCGTACGACTTTGTAC AGATGGTTATCAGATGTGGACATAAAAAGAGGGATGTTTGGATGTGGTCATAGACCTAATG GACAGTGATGGAGTTGATGACGCCGACAAGCTTTGCGTACTCGCTTTCGACGAGATGAAG GTCGCTGCTTCGAGTATGACAGCTCTGCTGATATTGTTTACGAGCCAAGCGACTAT GTCCAACTGGCTATTGTTCGTGGTACCGGAAACCAAAAGCTATGGACAGAGCTCGGTATA TCAGAATCAAAAACCTGGTTTAGCCATCCTGCAGATGACCATTTAAAGATTTTCGTTTTT TCGGATACGCCACATTTAATTAAGTTAGTCCGTAACCACTATGTGGATTCCGGATTAACA ATAAATGGGAAAAAATTAACAAAAAAAAAAACAATTCAGGAGGCACTTCATCTTTGCAACAAG AAACAGAAGGTTAAATTGGCTACCCAGCTGTTTTCGAATACCACCGCTAGCTCGATCAGA CGCTGCTATTCATTGGGGTATGACATTGAAAATGCCACCGAAACTGCGGACTTCTTCAAA TTGATGAATGATTGGTTCGACATTTTTAATTCTAAATTGTCCACATCCAATTGCATTGAG TGCTCGCAACCTTATGGCAAGCAGTTGGATATACAGAATGATATTTTGAATCGAATGTCG GAAATTATGCGAACAGGAATTCTGGATAAACCCAAAAGGCTCCCATTTCAAAAAGGTATC ATTGTGAATAATGCTTCGCTTGATGGCTTGTATAAATATTTGCAAGAAAACTTCAGTATG CGATCGAGAGGTGGACAATTCGACCATCCCACTCCACTGCAGTTTAAGTATAGGTTAAGA AAATATATAATAGCCAGGAATACAGAAATGTTAAGAAATTCGGGAAATATCGAAGAGGAC AACTCTGAAAGCTGGCTTAATTTAGATTTCAGTTCTAAAGAAAACGAAAATAAAAGTAAA GATGATGAGCCTGTCGATGAGCCTGTCGATGAGATGTTAAGCAATATAGATTTCACC GAAATGGATGACTGACGGAGGATGCGATGGAATATATCGCGGGCTATGTCATTAAAAAA TTGAGAATCAGTGACAAAGTAAAAGAAAATTTGACATTTACATACGTCGACGAGGTGTCT
CACGGCGGACTTATTAAGCCGTCCGAAAAATTTCAAGAGAAGTTAAAAGAGCTAGAATGT
ATTTTTTTGCATTATACAAATAATAATTTTTGAAATTACAAATAATGTAAAGGAAAAA
TTAATATTAGCAGCGCGAAACGTCGATGTTGATAAACAA

>FGENESH: 1 5 exon (s) 199 - 2529 633 aa, chain +
LGYFPSLRESLFTHFNDSQWKAAPAKGQTFKRRRLNADAVPSKVIEPEPEKIKEGYTSGS
TQTESCSLFNENKSLREKIRTLEYEMRRLEQQLRESQQLEESLRKIFTDTQIRILKNGGQ
RATFNSDDISTAICLHTAGPRAYNHLYKKGFPLPSRTTLYRWLSDVDIKRGCLDVVIDLM
DSDGVDDADKLCVLAFDEMKVAAAFEYDSSADIVYEPSDYVQLAIVRGTGNQKLWTELGI
SESKTWFSHPADDHLKIFVFSDTPHLIKLVRNHYVDSGLTINGKKLTKKTIQEALHLCNK
SDLSILFKINENHINVRSLAKQKVKLATQLFSNTTASSIRRCYSLGYDIENATETADFFK
LMNDWFDIFNSKLSTSNCIECSQPYGKQLDIQNDILNRMSEIMRTGILDKPKRLPFQKGI
IVNNASLDGLYKYLQENFSMQYILTSRLNQDIVEHFFGSMRSRGGQFDHPTPLQFKYRLR
KYIIARNTEMLRNSGNIEEDNSESWLNLDFSSKENENKSKDDEPVDDEPVDEMLSNIDFT
EMDELTEDAMEYIAGYVIKKLRISDKVKENLTFTYVDEVSHGGLIKPSEKFQEKLKELEC
IFLHYTNNNNFEITNNVKEKLILAARNVDVDKQ