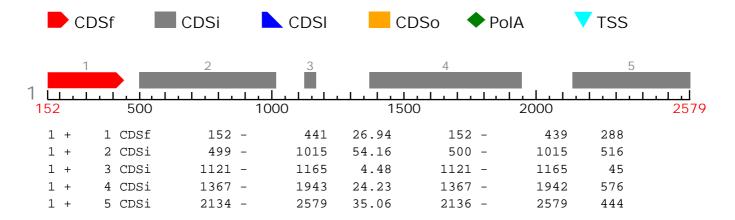
FGENESH 2.6 Prediction of potential genes in Trichinella_spiralis genomic DNA

Seg name: gb|CM027592.1| Dmelanogaster05

Length of sequence: 2903

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: 125.055750



Predicted protein(s):

>FGENESH: [mRNA] 1 5 exon (s) 152 - 2579 1875 bp, chain + AAGTGTGCTATTAAGAGAAAATTGTGGGAGCAGAGCCTTGGGTGCAGCCTTGGTGAAAAC TCCCAAATTTGTGATACCCACTTTAATGATTCGCAGTGGAAGGCTGCACCTGCAAAAGGT CAGACATTTAAAAGGAGGCGACTCAACGCAGATGCCGTACCTAGTAAAGTGATAGAGCCT GAACCAGAAAAGTAAAAGAAGGCTATACCAGTGGGAGTACACAAACAGAGTCCTGTTCA TTGTTTAATGAAAATAAGAGCTTGAGGGAAAAAATTCGTACTTTGGAGTACGAAATGCGT CGTTTAGAGCAGCTGAGGGAGTCTCAACAGTTGGAGGAGTCTCTACGCAAAATCTTC ACGGACACGCAGATACGGATACTGAAGAATGGTGGACAAAGAGCTACGTTCAATTCCGAC GACATTTCTACAGCTATTTGTCTCCACACCGCAGGCCCTCGAGCGTATAACCATCTGTAC AAAAAAGGATTTCCTTTGCCCAGTCGTACGACTTTGTACAGATGGTTATCAGATGTGGAC ATAAAAAGAGGATGTTTGGATGTGGTCATAGACCTAATGGACAGTGATGGAGTTGATGAC GACAGCTCTGCTGATATTGTTTACGAGCCAAGCGACTATGTCCAACTGGCTATTGTTCGT GGTCTAAAAAAATCGTGGAAGCAGCCAGTACCGGAAACCAAAAGCTATGGACAGAGCTCG GTATATCAGAATGAGGCACTTCATCTTTGCAACAAGTCCGATCTGTCTATCCTCTTTAAA ATTAATGAAAATCACATTAATGTTCGATCGCTCGCAAAACAGAAGGTTAAATTGGCTACC CAGCTGTTTTCGAATACCACCGCTAGCTCGATCAGACGCTGCTATTCATTGGGGTATGAC TTTAATTCTAAATTGTCCACATCCAATTGCATTGAGTGCTCGCAACCTTATGGCAAGCAG TTGGATATACAGAATGATATTTTGAATCGAATGTCGGAAATTATGCGAACAGGAATTCTG GATAAACCCAAAAGGCTCCCATTTCAAAAAGGTATCATTGTGAATAATGCTTCGCTTGAT GGCTTGTATAAATATTTGCAAGAAAACTTCAGTATGCAATACATATTAACAAGCCGTCTC AACCAAGACATTGTGGAGCATTTTTTTTGGCAGCATGCGATCGAGAGGTGGACAATTCGAC CATCCCACTCCACTGCAGTTTAAGTATAGGTTAAGAAAATATATAATAGCCAGGAATACA GAAATGTTAAGAAATTCGGGAAATATCGAAGAGGACAACTCTGAAAGCTGGCTTAATTTA GATTTCAGTTCTAAAGAAAACGAAAATAAAAGTAAAGATGATGAGCCTGTCGATGATGAG CCTGTCGATGAGATGTTAAGCAATATAGATTTCACCGAAATGGATGAGTTGACGGAGGAT GCGATGGAATATATCGCGGGCTATGTCATTAAAAAATTGAGAATCAGTGACAAAGTAAAA >FGENESH: 1 5 exon (s) 152 - 2579 625 aa, chain +
MKYCKFCCKAVTGVKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNDSQWKAAPAKG
QTFKRRRLNADAVPSKVIEPEPEKVKEGYTSGSTQTESCSLFNENKSLREKIRTLEYEMR
RLEQQLRESQQLEESLRKIFTDTQIRILKNGGQRATFNSDDISTAICLHTAGPRAYNHLY
KKGFPLPSRTTLYRWLSDVDIKRGCLDVVIDLMDSDGVDDADKLCVLAFDEMKVAAAFEY
DSSADIVYEPSDYVQLAIVRGLKKSWKQPVPETKSYGQSSVYQNEALHLCNKSDLSILFK
INENHINVRSLAKQKVKLATQLFSNTTASSIRRCYSLGYDIENATETADFFKLMNDWFDI
FNSKLSTSNCIECSQPYGKQLDIQNDILNRMSEIMRTGILDKPKRLPFQKGIIVNNASLD
GLYKYLQENFSMQYILTSRLNQDIVEHFFGSMRSRGGQFDHPTPLQFKYRLRKYIIARNT
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AMEYIAGYVIKKLRISDKVKENLTFTYVDEVSHGGLIKPSEKFQEKLKELECIFLHYTNN
NNFEITNNVKEKLILAARNVDVDKQ