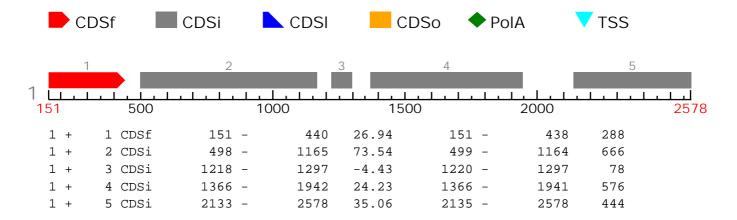
FGENESH 2.6 Prediction of potential genes in Trichinella_spiralis genomic DNA

Seg name: gb|CM027592.1| Dmelanogaster06

Length of sequence: 2902

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: 136.852246



Predicted protein(s):

>FGENESH: [mRNA] 1 5 exon (s) 151 - 2578 2061 bp, chain + AAGTGTGCTATTAAGAGAAAATTGTGGGAGCAGAGCCTTGGGTGCAGCCTTGGTGAAAAC TCCCAAATTTGTGATACCCACTTTAATGATTCGCAGTGGAAGGCTGCACCTGCAAAAGGT CAGACATTTAAAAGGAGGCGACTCAACGCAGATGCCGTACCTAGTAAAGTGATAGAGCCT GAACCAGAAAAGATAAAAGAAGGCTATACCAGTGGGAGTACACAAACAGAGTCCTGTTCA TTGTTTAATGAAAATAAGAGCTTGAGGGAAAAAATTCGTACTTTGGAGTACGAAATGCGT CGTTTAGAGCAGCTGAGGGAGTCTCAACAGTTGGAGGAGTCTCTACGCAAAATCTTC ACGGACACGCAGATACGGATACTGAAGAATGGTGGACAAAGAGCTACGTTCAATTCCGAC GACATTTCTACAGCTATTTGTCTCCACACCGCAGGCCCTCGAGCGTATAACCATCTGTAC AAAAAAGGATTTCCTTTGCCCAGTCGTACGACTTTGTACAGATGGTTATCAGATGTGGAC ATAAAAAGAGGATGTTTGGATGTGGTCATAGACCTAATGGACAGTGATGGAGTTGATGAC GACAGCTCTGCTGATATTGTTTACGAGCCAAGCGACTATGTCCAACTGGCTATTGTTCGT GGTCTAAAAAAATCGTGGAAGCAGCCAGTTTTTTTCGATTTTAATACCCGAATGGACCCG GATACTCTTAACAATATTAAGGAAACTGCATAGGAAAGGATATTTAGTAGTTGCTATT GTATCCGATTTAGGTACCGGAAACCAAAAGCTATGGACAGAGCTCGGTATATCAGAATCA AAAACCTGGTTTAGCCATCCTGCAGATGACCATTTAAAGATTTTCGTTTTTTCGGATACG CCACATTTAATTAAGTTAGAGGCACTTCATCTTTGCAACAAGTCCGATCTGTCTATCCTC GCTACCCAGCTGTTTTCGAATACCACCGCTAGCTCGATCAGACGCTGCTATTCATTGGGG GACATTTTTAATTCTAAATTGTCCACATCCAATTGCATTGAGTGCTCGCAACCTTATGGC AAGCAGTTGGATATACAGAATGATATTTTGAATCGAATGTCGGAAATTATGCGAACAGGA ATTCTGGATAAACCCAAAAGGCTCCCATTTCAAAAAGGTATCATTGTGAATAATGCTTCG CTTGATGGCTTGTATAAATATTTGCAAGAAAACTTCAGTATGCAATACATATTAACAAGC CGTCTCAACCAAGACATTGTGGAGCATTTTTTTTGGCAGCATGCGATCGAGAGGTGGACAA TTCGACCATCCCACTCCACTGCAGTTTAAGTATAGGTTAAGAAAATATATAATAGCCAGG AATACAGAAATGTTAAGAAATTCGGGAAATATCGAAGAGGACAACTCTGAAAGCTGGCTT >FGENESH: 1 5 exon (s) 151 - 2578 687 aa, chain +
MKYCKFCCKAVTGVKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNDSQWKAAPAKG
QTFKRRRLNADAVPSKVIEPEPEKIKEGYTSGSTQTESCSLFNENKSLREKIRTLEYEMR
RLEQQLRESQQLEESLRKIFTDTQIRILKNGGQRATFNSDDISTAICLHTAGPRAYNHLY
KKGFPLPSRTTLYRWLSDVDIKRGCLDVVIDLMDSDGVDDADKLCVLAFDEMKVAAAFEY
DSSADIVYEPSDYVQLAIVRGLKKSWKQPVFFDFNTRMDPDTLNNILRKLHRKGYLVVAI
VSDLGTGNQKLWTELGISESKTWFSHPADDHLKIFVFSDTPHLIKLEALHLCNKSDLSIL
FKINENHINVRSLAKQKVKLATQLFSNTTASSIRRCYSLGYDIENATETADFFKLMNDWF
DIFNSKLSTSNCIECSQPYGKQLDIQNDILNRMSEIMRTGILDKPKRLPFQKGIIVNNAS
LDGLYKYLQENFSMQYILTSRLNQDIVEHFFGSMRSRGGQFDHPTPLQFKYRLRKYIIAR
NTEMLRNSGNIEEDNSESWLNLDFSSKENENKSKDDEPVDDEPVDEMLSNIDFTEMDELT
EDAMEYIAGYVIKKLRISDKVKENLTFTYVDEVSHGGLIKPSEKFQEKLKELECIFLHYT
NNNNFEITNNVKEKLILAARNVDVDKQ