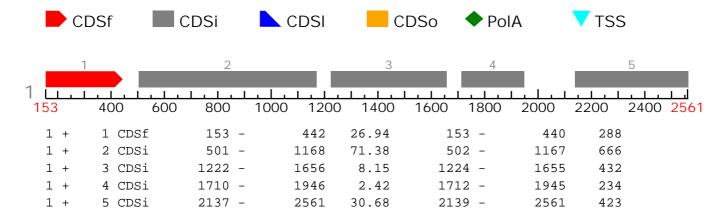
FGENESH 2.6 Prediction of potential genes in Trichinella\_spiralis genomic DNA

Seg name: gb|CM016475.1| Dmelanogaster21

Length of sequence: 2885

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: 121.385181



## Predicted protein(s):

>FGENESH: [mRNA] 1 5 exon (s) 153 - 2561 2055 bp, chain + AAGTGTGCTATTAAGAGAAAATTGTGGGAGCAGAGCCTTGGGTGCAGCCTTGGTGAAAAC TCCCAAATTTGTGATACCCACTTTAATGATTCGCAGTGGAAGGCTGCACCTGCAAAAGGT CAGACATTTAAAAGGAGGCGACTCAACGCAGATGCCGTACCTAGTAAAGTGATAGAGCCT GAACCAGAAAAGATAAAAGAAGGCTATACCAGTGGGAGTACACAAACAGAGTCCTGTTCA TTGTTTAATGAAAATAAGAACTTGAGGGAAAAAATTCGTACTTTGGAGTACGAAATGCGT CGTTTAGAGCAGCTGAGGGAGTCTCAACAGTTGGAGGAGTCTCTACGCAAAATCTTC ACGGACACGCAGATACGGATACTGAAGAATGGTGGACAAAGAGCTACGTTCAATTCCGAC GACATTTCTACAGCTATTTGTCTCCACACCGCAGGCCCTCGAGCGTATAACCATCTGTAC AAAAAAGGATTTCCTTTGCCCAGTCGTACGACTTTGTACAGATGGTTATCAGATGTGAAC ATAAAAAGAGGATGTTTGGATGTGGTCATAGACCTAATGGACAGTGATGGAGTTGATGAC GACAGCTCTGCTGATATTGTTTACGAGCCAAGCGACTATGTCCAACTGGCTATTGTTCGT GGTCTAAAAAAATCGTGGAAGCAGCCAGTTTTTTTCGATTTTAATACCCGAATGGACCCG GATACTCTTAACAATATTAAAGAAACTGCATAGGAAAGGATATTTAGTAGTTGCTATT GTATCCGATTTAGGTACCGGAAACCAAAAGCTATGGACAGAGCTCGGTATATCAGAATCA AAAACCTGGTTTAGCCATCCTGCAGATGACCATTTAAAGATTTTCGTTTTTTCGGATACG CCACATTTAATTAAGTTAGTCCGTAACCACTATGTGGATTCCGGATTAACAATAAATGGG AAAAAATTAACAAAAAAAACAATTCAGGAGGCACTTCATCTTTGCAACAAGTCCGATCTG GTTAAATTGGCTACCCAGCTGTTTTCGAATACCACCGCTAGCTCGATCAGACGCTGCTAT TCATTGGGGTATGACATTGAAAATGCCACCGAAACTGCGGACTTCTTCAAATTGATGAAT GATTGGTTCGACATTTTAATTCTAAATTGTCCACATCCAATTGCATTGAGTGCTCGCAAC CTTATGGCAAGCAGAATTCTGGATAAACCCAAAAGGCTCCCATTTCAAAAAGGTATCATT GTGAATAATGCTTCGCTTGATGGCTTGTATAAATATTTTGCAAGAAAACTTCAGTATGCAA TCGAGAGGTGGACAATTCGACCATCCCACTCCACTGCAGTTTAAGTATAGGTTAAGAAAA TATATAATAGCCAGGAATACAGAAATGTTAAGAAATTCGGGAAATATCGAAGAGGACAAC

>FGENESH: 1 5 exon (s) 153 - 2561 685 aa, chain +
MKYCKFCCKAVTGVKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNDSQWKAAPAKG
QTFKRRRLNADAVPSKVIEPEPEKIKEGYTSGSTQTESCSLFNENKNLREKIRTLEYEMR
RLEQQLRESQQLEESLRKIFTDTQIRILKNGGQRATFNSDDISTAICLHTAGPRAYNHLY
KKGFPLPSRTTLYRWLSDVNIKRGCLDVVIDLMDSDGVDDADKLCVLAFDEMKVAAAFEY
DSSADIVYEPSDYVQLAIVRGLKKSWKQPVFFDFNTRMDPDTLNNILKKLHRKGYLVVAI
VSDLGTGNQKLWTELGISESKTWFSHPADDHLKIFVFSDTPHLIKLVRNHYVDSGLTING
KKLTKKTIQEALHLCNKSDLSILFKINENHINVRSLAKQKVKLATQLFSNTTASSIRRCY
SLGYDIENATETADFFKLMNDWFDILILNCPHPIALSARNLMASRILDKPKRLPFQKGII
VNNASLDGLYKYLQENFSMQYILTSRLNQDIVEHFFGSMRSRGGQFDHPTPLQFKYRLRK
YIIARNTEMLRNSGNIEEDNSESWLNLDFSSKENENKSKDDEPVDDEPVDEMLSNIDFTE
MDELTEDAMEYIAGYVIKKLRISDKVKENLTFTYGLIKPSEKFQEKLKELECIFLHYTNN
NNFEITNNVKEKLILAARNVDVDKQ