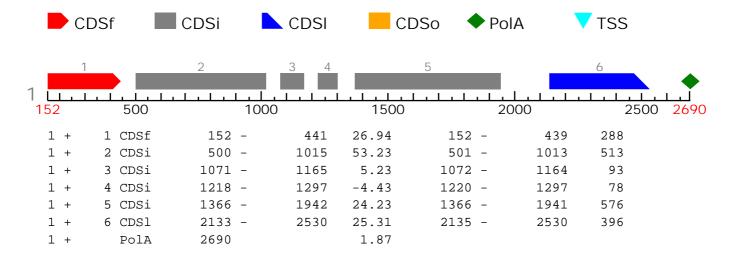
FGENESH 2.6 Prediction of potential genes in Trichinella_spiralis genomic DNA

Seg name: gb|CM027589.1| Dmelanogaster14

Length of sequence: 2900

Number of predicted genes 1: in +chain 1, in -chain 0. Number of predicted exons 6: in +chain 6, in -chain 0.

Positions of predicted genes and exons: Variant 1 from 1, Score: 122.034155



Predicted protein(s):

>FGENESH:[mRNA] 1 6 exon (s) 152 - 2530 1956 bp, chain + AAGTGTGCTATTAAGAGAAAATTGTGGGAGCAGAGCCTTGGGTGCAGCCTTGGTGAAAAC TCCCAAATTTGTGATACCCACTTTAATGATTCGCAGTGGAAGGCTGCACCTGCAAAAGGT CAGACATTTAAAAGGAGGCGACTCAACGCAGATGCCGTACCTAGTAAAGTGATAGAGCCT GAACCAGAAAAGATAAAAGAAGGCTATACCAGTGGGAGTACACAAACAGAGTCCTGTTCA TTGTTTAATGAAAATAAGAGCTTGAGGGAAAAAATTCGTACTTTGGAGTACGAAATGCGT CGTTTAGAGCAGCTGAGGGAGTCTCAACAGTTGGAGGAGTCTCTACGCAAAATCTTC ACGGACACGCAGATACGGATACTGAAGAATGGTGGACAAAGAGCTACGTTCAATTCCGAC GACATTTCTACAGCTATTTGTCTCCACACCGCAGGCCCTCGAGCGTATAACCATCTGTAC AAAAAAGGATTTCCTTTGCCCAGTCGTACGACTTTGTACAGATGGTTATCAGATGTGGAC ATAAAAAGAGGATGTTTGGATGTGGTCATAGACCTAATGGACAGTGATGGAGTTGATGAC GACAGCTCTGCTGATATTGTTTACGAGCCAAGCGACTATGTCCAACTGGCTATTGTTCGT GGTCTAAAAAATCGTGGAAGCAGCCAGAAACTGCATAGGAAAGGATATTTAGTAGTTGCT ATTGTATCCGATTTAGGTACCGGAAACCAAAAGCTATGGACAGAGCTCGGTATATCAGAA TCAAAAACCTGGTTTAGCCATCCTGCAGATGACCATTTAAAGATTTTCGTTTTTTCGGAT ACGCCACATTTAATTAAGTTAGAGGCACTTCATCTTTGCAACAAGTCCGATCTGTCTATC TTGGCTACCCAGCTGTTTTCGAATACCACCGCTAGCTCGATCAGACGCTGCTATTCATTG TTCGACATTTTTAATTCTAAATTGTCCACATCCAATTGCATTGAGTGCTCGCAACCTTAT GGCAAGCAGTTGGATATACAGAATGATATTTTGAATCGAATGTCGGAAATTATGCGAACA GGAATTCTGGATAAACCCAAAAGGCTCCCATTTCAAAAAGGTATCATTGTGAATAATGCT TCGCTTGATGGCTTGTATAAATATTTTGCAAGAAAACTTCAGTATGCAATACATATTAACA AGCCGTCTCAACCAAGACATTGTGGAGCATTTTTTTTGGCAGCATGCGATCGAGAGGTGGA CAATTCGACCATCCACTGCAGTTTAAGTATAGGTTAAGAAAATATATAATAGCC

>FGENESH: 1 6 exon (s) 152 - 2530 651 aa, chain +
MKYCKFCCKAVTGVKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNDSQWKAAPAKG
QTFKRRRLNADAVPSKVIEPEPEKIKEGYTSGSTQTESCSLFNENKSLREKIRTLEYEMR
RLEQQLRESQQLEESLRKIFTDTQIRILKNGGQRATFNSDDISTAICLHTAGPRAYNHLY
KKGFPLPSRTTLYRWLSDVDIKRGCLDVVIDLMDSDGVDDADKLCVLAFDEMKVAAAFEY
DSSADIVYEPSDYVQLAIVRGLKNRGSSQKLHRKGYLVVAIVSDLGTGNQKLWTELGISE
SKTWFSHPADDHLKIFVFSDTPHLIKLEALHLCNKSDLSILFKINENHINVRSLAKQKVK
LATQLFSNTTASSIRRCYSLGYDIENATETADFFKLMNDWFDIFNSKLSTSNCIECSQPY
GKQLDIQNDILNRMSEIMRTGILDKPKRLPFQKGIIVNNASLDGLYKYLQENFSMQYILT
SRLNQDIVEHFFGSMRSRGGQFDHPTPLQFKYRLRKYIIARNTEMLRNSGNIEEDNSESW
LNLDFSSKENENKSKDDEPVDDEPVDEMLSNIDFTEMDELTEDAMEYIAGYVIKKLRISD
KVKENLTFTYVDEVSHGGLIKPSEKFQEKLKELECIFCIIQIIIILKLQIM