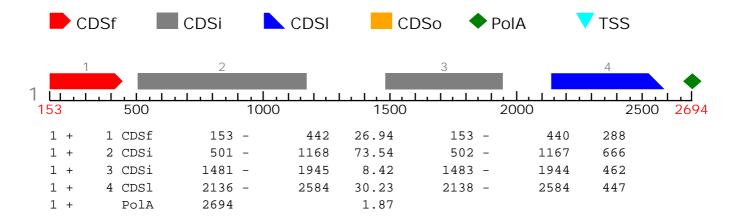
FGENESH 2.6 Prediction of potential genes in Trichinella_spiralis genomic DNA

Seg name: gb|CM016474.1| Dmelanogaster24

Length of sequence: 2904

Number of predicted genes 1: in +chain 1, in -chain 0. Number of predicted exons 4: in +chain 4, in -chain 0.

Positions of predicted genes and exons: Variant 1 from 1, Score: 129.599780



Predicted protein(s):

>FGENESH: [mRNA] 1 4 exon (s) 153 - 2584 1872 bp, chain + AAGTGTGCTATTAAGAGAAAATTGTGGGAGCAGAGCCTTGGGTGCAGCCTTGGTGAAAAC TCCCAAATTTGTGATACCCACTTTAATGATTCGCAGTGGAAGGCTGCACCTGCAAAAGGT CAGACATTTAAAAGGAGGCGACTCAACGCAGATGCCGTACCTAGTAAAGTGATAGAGCCT GAACCAGAAAAGATAAAAGAAGGCTATACCAGTGGGAGTACACAAACAGAGTCCTGTTCA TTGTTTAATGAAAATAAGAGCTTGAGGGAAAAAATTCGTACTTTGGAGTACGAAATGCGT CGTTTAGAGCAGCTGAGGGAGTCTCAACAGTTGGAGGAGTCTCTACGCAAAATCTTC ACGGACACGCAGATACGGATACTGAAGAATGGTGGACAAAGAGCTACGTTCAATTCCGAC GACATTTCTACAGCTATTTGTCTCCACACCGCAGGCCCTCGAGCGTATAACCATCTGTAC AAAAAAGGATTTCCTTTGCCCAGTCGTACGACTTTGTACAGATGGTTATCAGATGTGGAC ATAAAAAGAGGATGTTTGGATGTGGTCATAGACCTAATGGACAGTGATGGAGTTGATGAC GACAGCTCTGCTGATATTGTTTACGAGCCAAGCGACTATGTCCAACTGGCTATTGTTCGT GGTCTAAAAAAATCGTGGAAGCAGCCAGTTTTTTTCGATTTTAATACCCGAATGGACCCG GATACTCTTAACAATATTAAGGAAACTGCATAGGAAAGGATATTTAGTAGTTGCTATT GTATCCGATTTAGGTACCGGAAACCAAAAGCTATGGACAGAGCTCGGTATATCAGAATCT GTTTTCGAATACCACCATAGCTCGATCAGACGCTGCTATTCATTGGGGTATGACATTGAA TCTAAATTGTCCACATCCAATTGCATTGAGTGCTCGCAACCTTATGGCAAGCAGTTGGAT ATACAGAATGATATTTTGAATCGAATGTCGGAAATTATGCGAACAGGAATTCTGGATAAA CCCAAAAGGCTCCCATTTCAAAAAGGTATCATTGTGAATAATGCTTCGCTTGATGGCTTG TATAAATATTTGCAAGAAAACTTCAGTATGCAATACATATTAACAAACCGTCTCAACAAA GACATTGTGGAGCATTTTTTTGGCAGCATGCGATCGAGAGGTGGACAATTCGACCATCCC ACTCCACTGCAGTTTAAGTATAGGTTAAGAAAATATATAATAGCCAGGAATACAGAAATG TTAAGAAATTCGGGAAATATCGAAGAGGACAACTCTGAAAGCTGGCTTAATTTAGATTTC AGTTCTAAAGAAAACGAAAATAAAAGTAAAGATGATGAGCCTGTCGATGATGAGCCTGTC GATGAGATGTTAAGCAATATAGATTTCACCGAAATGGATGAGTTGACGGAGGATGCGATG GAATATATCGCGGGCTATGTCATTAAAAAATTGAGAATCAGTGACAAAGTAAAAGAAAAT

>FGENESH: 1 4 exon (s) 153 - 2584 623 aa, chain +
MKYCKFCCKAVTGVKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNDSQWKAAPAKG
QTFKRRRLNADAVPSKVIEPEPEKIKEGYTSGSTQTESCSLFNENKSLREKIRTLEYEMR
RLEQQLRESQQLEESLRKIFTDTQIRILKNGGQRATFNSDDISTAICLHTAGPRAYNHLY
KKGFPLPSRTTLYRWLSDVDIKRGCLDVVIDLMDSDGVDDADKLCVLAFDEMKVAAAFEY
DSSADIVYEPSDYVQLAIVRGLKKSWKQPVFFDFNTRMDPDTLNNILRKLHRKGYLVVAI
VSDLGTGNQKLWTELGISESVFEYHHSSIRRCYSLGYDIENATETADFFKLMNDWFDIFN
SKLSTSNCIECSQPYGKQLDIQNDILNRMSEIMRTGILDKPKRLPFQKGIIVNNASLDGL
YKYLQENFSMQYILTNRLNKDIVEHFFGSMRSRGGQFDHPTPLQFKYRLRKYIIARNTEM
LRNSGNIEEDNSESWLNLDFSSKENENKSKDDEPVDDEPVDEMLSNIDFTEMDELTEDAM
EYIAGYVIKKLRISDKVKENLTFTYVDEVSHGGLIKPSEKFQEKLKELECIFLHYTNNNN
FEITNNVKEKLILAAKTSMLINK