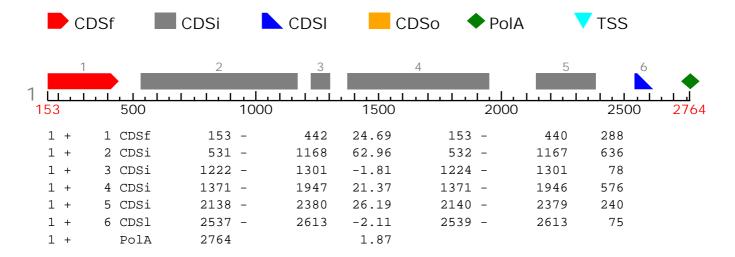
FGENESH 2.6 Prediction of potential genes in Trichinella_spiralis genomic DNA

Seg name: gb|JAECWJ010000002.1| Dsturtevanti02

Length of sequence: 2899

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: 121.597229



Predicted protein(s):

>FGENESH:[mRNA] 1 6 exon (s) 153 - 2613 1905 bp, chain + ATGAAATATTGCAAATTTTGCTGCAAAGCTGTGACTGGAGTGAAGTTAATTCATGTGCCG AAGTGTGCCATTAAAAGAAAATTGTGGGAGCAGAGCCTGGGGTGCAGCCTTGGTGAAAAC TCCCAAATTTGTGATACCCACTTTAATGGTTCGCAGTGGAAGTCTGCACCTGCAAAAGGT CAGACATTTAAAAGGAGGCGACTTAACGCAGATGCCGTACCTAGTAAAGTGATAGAGCCT GAACCAGAAAAGATAAAAGACGGCTTTGCAAGTGGGAGTACACAAACAGACTTAAGGGAA AAAATTCGTACTTTGGAGTACGAAATGCGTCGCTTAGAGCAGCAGCTGAAGGAGTCTCAA CAGTTGGAGGAGTCTCTACGCAAAATCTTCACGGAAACGCAGATACGGATACTGAAGAAT GGTGGACAAAGAGCGACGTTCAATGCCGATGACATTTGTACGGCTATTTGTCTCCACACT GCAGGCCCTCGAGCGTATAACCATCTGTACAAAAAAGGATTTCCTTTATCCATTCGTAGC ACTTTGTACAGATGGTTATCAGATGTGGAAATAAAAACAGGATGTTTGGATGTGGTCATA GACCTAATGGATAGTGATGGAGTTGATGACGCGGACAAGTTTTGCGTACTCGCTTTCGAC GAGATGAAGGTCGCTGCCTTCGAGTATGACAGCTCTGCTGATATTGTCTACGAGCCA AGCGACTATGTCCAACTGGCTATTGTTCGTGGTCTAAAGAAATCGTGGAAGCAGCCAGTT TTCTTCGATTTTAATACCCGAATGGACCCGGATAATCTTAACAACATATTAAGGAAACTG CATAGGAAAGGATATTTAGTAGTTGCTATTGTATCCGATTTAGGTACCGGAAACCAAAAG CTATGGACAGAACTCGGTATATCAGAATCAAAAACCTGGTTTAGCCATCCAGCAGATGAC CTTTGCAACAAGTCCGATCTGTCTATCCTGTTTAAAATTAATGAAAATCATATTAATGTT CGATCGCTCGCAAAACAGAAGGTTAAATTGGCTACCCAACTGTTTTCGAATACCACCGCT AGCTCCATCAGACGCTGCTATACATTGGGGCATCCCATTGAAAATGCCACCGAAACTGCG GACTTCTTCAAATTGATGATGATTGGTTCGACATTTTTTAATTCTAAATTGTCCACATCC AATTGCATTGAGTCCTCGCAACCTTATGGCAAGCAGTTGGATATACAGATTGACATTTTG AATCGAATGTCGGAGATTATGGAAACACGAATTCTGGATAAACCCAAAAGGCTCCCATTT CAAAAAGGGATCATTGTGAATAATGCTTCCCTGGATGGCTTGTATAAATATTTTGCAAGAA AACTTCAGTATGCAATACATAATAACAAGCCGTCTCAACCAAGACATTGTGGAGCATTTC TTTGGCAGCATGCGATCGAGAGGTGGACAATTCGACCATCCGACTCCACTGCAATTTAAG

>FGENESH: 1 6 exon (s) 153 - 2613 634 aa, chain +
MKYCKFCCKAVTGVKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNGSQWKSAPAKG
QTFKRRRLNADAVPSKVIEPEPEKIKDGFASGSTQTDLREKIRTLEYEMRRLEQQLKESQ
QLEESLRKIFTETQIRILKNGGQRATFNADDICTAICLHTAGPRAYNHLYKKGFPLSIRS
TLYRWLSDVEIKTGCLDVVIDLMDSDGVDDADKFCVLAFDEMKVAAAFEYDSSADIVYEP
SDYVQLAIVRGLKKSWKQPVFFDFNTRMDPDNLNNILRKLHRKGYLVVAIVSDLGTGNQK
LWTELGISESKTWFSHPADDHLKIFVFSDTPHLIKLEALQLCNKSDLSILFKINENHINV
RSLAKQKVKLATQLFSNTTASSIRRCYTLGHPIENATETADFFKLMNDWFDIFNSKLSTS
NCIESSQPYGKQLDIQIDILNRMSEIMETRILDKPKRLPFQKGIIVNNASLDGLYKYLQE
NFSMQYIITSRLNQDIVEHFFGSMRSRGGQFDHPTPLQFKYRLRKYIIARNTEMLRNAGN
VEEENSESWLNLDLSSKKKESKTKDDEPVDDEPVDDIISNIDVTEMDELTEDAMEYIAGC
HKKIKNQWQRKINISSAKRRCRYTSKIFIPLQRV