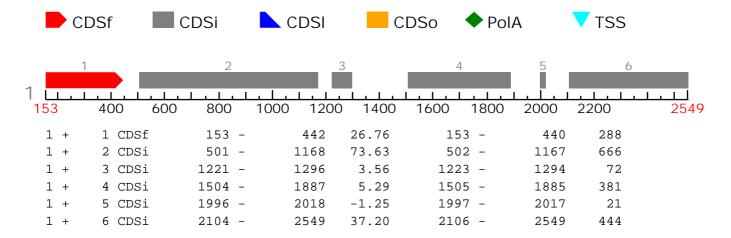
FGENESH 2.6 Prediction of potential genes in Trichinella_spiralis genomic DNA

Seg name: gb|JAECWI010000687.1| Dequinoxialis02

Length of sequence: 2860

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: 125.932068



Predicted protein(s):

>FGENESH:[mRNA] 1 6 exon (s) 153 - 2549 1887 bp, chain + AAGTGTGCTATTAAGAGAAAATTGTGGGAGCAGAGCCTTGGGTGCAGCCTTGGTGAAAAC TCCCAAATTTGTGATACCCACTTTAATGATTCGCAGTGGAAGGCTGCATCTGCAAAAGGT CAGACATTTAAAAGGAGGCGACTTAACGCAGATGCCGTACCTAGTAAAGTGATAGAGCCT TTGTTTAATGAAAATAAGAGCTTGAGGGAAAAAATTCGTACTTTGGAGTACGAAATGCGT CGCTTAGAGCAGCTGAGGGAGTCTCAACAGTTGGAGGAGTCTCTACGCAAAATCCTC ACGGACACGCAGATACGGATACTGAAGAATGGTGGACAAAGAGCTACGTTCAATTCCGAC GACATTTCTACAGCTATTTGTCTCCACACCGCAGGCCCTCGAGCGTATAACCATCTGTAC AAAAAAGGATTTCCTTTGCCCAGTCGTACCACTTTGTACAGATGGTTATCAGATGTGGAC ATAAAAAGAGGATGTTTGGATGTGGTCATAGACCTAATGGACAGTGATGGAGTTGATGAC GACAGCTCTGCTGATATTGTTTACGAGTCAAGCGACTATGTCCAACTGGCTATTGTTCGT GGTCTAAAAAAATCGTGGAAGCAGCCAGTTTTTTTCGATTTTAATACCCGAATGGACCCG GATACTCTTAACAATATTAAGGAAACTGCATAGGAAAGGATATTTAGTAGTTGCTATT GTATCCGATTTAGGTACTGGAAACCAAAAGCTATGGACAGAGCTCGGTATATCAGAATCA AAAACCTGGCTTAGCCATCCTGCAGATGACCATTTAAAGATTTTCGTTTTTTCGGATACG CCACATTTAATTAACTCGATCAGACGCTGCTATTCATTGGGGTATGACATTGAAAATGCC ACCGAAACTGCGGACTTCTTCAAATTGATGAATGATTGGTTCGACATTTTTAATTCTAAA TTGTCCACATCCAATTGCATTGAGTGCTCGCAACCTTATGGCAAGCAGTTGGATATACAG AATGATATTTTGAATAGAATGTCGGAAAGGCTCCCATTTCAAAAAGGTATCATTGTGAAT AATGCTTCGCTTGATGGCTTGTATAAATATTTTGCAAGAAAACTTCAGTATGCAATACATA TTAACAAGCTGTCTCAACCAAGACATTGTGGAGCATTTTTTTGGCAGCATGCGATCGAGA GGTGGACAATTCGACCATCCACTCCACTGCAGTTTAAGAAAGTTTCAGTTGAGAATGTA GCCAGGAATACAGAAATGTTAAGAAATTCGGGAAATATCGAAGAGGAAAACTCTGAAAGC TGGCTTAATTTAGACTTCAGTTCTAAAGAAAAGGAAAATAAGAGTAAAGATGATGAGCCT GTCGATGATGAGCCTGTCGATGAGATGTTAAGCAATATAGATGTCACCGGAATGGATGAG

>FGENESH: 1 6 exon (s) 153 - 2549 629 aa, chain +
MKYCKFCCKAVTGVKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNDSQWKAASAKG
QTFKRRRLNADAVPSKVIEPEPEKIKEGYTSGSKQTESCSLFNENKSLREKIRTLEYEMR
RLEQQLRESQQLEESLRKILTDTQIRILKNGGQRATFNSDDISTAICLHTAGPRAYNHLY
KKGFPLPSRTTLYRWLSDVDIKRGCLDVVIDLMDSDGVDDADKLCVLAFDEMKVAAAFEY
DSSADIVYESSDYVQLAIVRGLKKSWKQPVFFDFNTRMDPDTLNNILRKLHRKGYLVVAI
VSDLGTGNQKLWTELGISESKTWLSHPADDHLKIFVFSDTPHLINSIRRCYSLGYDIENA
TETADFFKLMNDWFDIFNSKLSTSNCIECSQPYGKQLDIQNDILNRMSERLPFQKGIIVN
NASLDGLYKYLQENFSMQYILTSCLNQDIVEHFFGSMRSRGGQFDHPTPLQFKKVSVENV
ARNTEMLRNSGNIEEENSESWLNLDFSSKEKENKSKDDEPVDDEPVDEMLSNIDVTGMDE
LTEDAMEYIAGYVIKKLRISDKVKENLTFTYVDEVSHGGLIKPSEKFQEKLKELECIFLH
YTNNNNFEITNNVKEKLILAAQNVDVDKQ