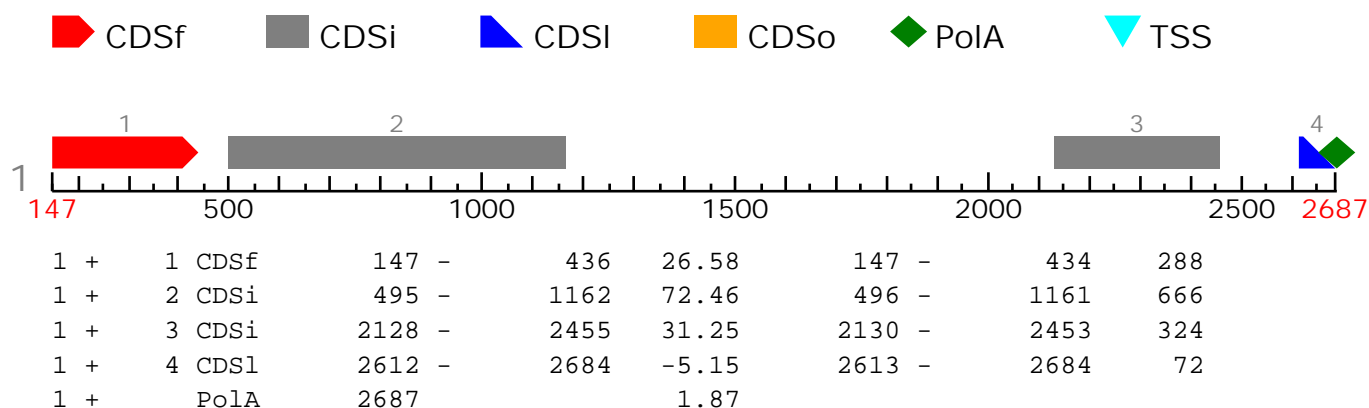


FGENESH 2.6 Prediction of potential genes in *Trichinella_spiralis* genomic DNA
 Seq name: gb|CM016479.2| *Dmelanogaster*17
 Length of sequence: 2897
 Number of predicted genes 1: in +chain 1, in -chain 0.
 Number of predicted exons 4: in +chain 4, in -chain 0.
 Positions of predicted genes and exons: Variant 1 from 1, Score:112.376233



Predicted protein(s):

```
>FGENESH:[mRNA] 1 4 exon (s) 147 - 2684 1359 bp, chain +
ATGAAATATTGCAAATTTTGCTGCAAAGCTGTGACTGGAGTAAAATTAATTCACGTGCCG
AAGTGTGCTATTAAGAGAAAATTGTGGGAGCAGAGCCTTGGGTGCAGCCTTGGTGAAAAC
TCCCAAATTTGTGATACCCACTTTAATGATTCTTGGTGAAGGCTGCACCTGCAAAAGGT
CAGACATTTAAAGGAGGCGACTCAACGCAGATGCCGTACCTAGTAAAGTGATAGAGCCT
GAACCAGAAAAGATAAAAAGAAGGCTATAACAGTGGGAGTACACAAACAGAGTCCTGTTCA
TTGTTTAAATGAAAATAAGAGCTTGAGGGAAAAAATTCGTACTTTGGAGTACGAAATGCGT
CGTTTAGAGTTGCTGCTGAGGGAGTCTCAACAGTTGGAGGAGTCTCTACGCAAAATCTTC
ACGGACACGCAGATACGGATACTGAAGAATGGTGGACAAAGAGCTACGTTCAATTCCGAC
GACATTTCTACAGCTATTTGTCTCCACACCGCAGGCCCTCGAGCGTATAACCATCTGTAC
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ATAAAAAGAGGATGTTTGGATGTGGTCATAGACCTAATGGACAGTGATGGAGTTGATGAC
GCCGACAAGCTTTGCGTACTCGCTTTTCGACGAGATGAAGGTCGCTGCTGCCTTCGAGTAT
GACAGCTCTGCTGATATTGTTTACGAGCCAAGCGACTATGTCCAAGTGGCTATTGTTTCGT
GGTCTAAAAAATCGTGGAAGCAGCCAGTTTTTTTTTCGATTTTAATACCCGAATGGACCCG
GATACTCTTAACAATATATTAAGGAACTGCATAGGAAAGGATATTTAGTAGTTGCTATT
GTATCCGATTTAGGTACCGGAAACCAAAGCTATGGACAGAGCTCGGTATATCAGAATCC
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CTTAATTTAGATTTTCAGTTCTAAAGAAAACGAAAATAAAAGTAAAGATGATGAGCCTGTC
GATGATGAGCCTGTTCGATGAGATGTTAAGCAATATAGATTTACCGGAAATGGATGAGTTG
ACGGAGGATGCGATGGAATATATCGCGGGCTATGTCAATAAAAAATTGAGAATCAGTGAC
AAAGTAAAGAAAAATTTGACATTTACATACGTCGACGAGGTGTCTCACGGCGGACTTATT
AAGCCGTCCGAAAAATTTCAAGAGAAAATTAAGTACTTCAACAAAAAAATTGAAATTAAA
AATCAAAAACAAAAGTTAATTGAAACTCCAAATTATTAA
```

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>FGENESH: 1 4 exon (s) 147 - 2684 452 aa, chain +
MKYCKFCCKAVTGVKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNDSWWKAAPAKG
QTFKRRRLNADAVPSKVIEPEPEKIKEGYTSGSTQTESCSLFNENKSLREKIRTLEYEMR
RLELLLLRESQQLEESLRKIFTDQIRILKNGGQRATFNSDDISTAICLHTAGPRAYNHLY
KKGFPPLPSRTTLYRWLSDVDIKRGCLDVVIDLMDSDGVDDADKLCVLAFFDEMKVAAAFY
```

DSSADIVYEPSDYVQLAIVRGLKKS WKQPVFFDFNTRMDPDTLNNILRKLHRKG YLVVAI
VSDLGTGNQKLWTELGI SE SRNTEMLRN SGNIEEDNSESWLN LDFSSKENENKSKDDEPV
DDEPVDEMLSNIDFTE MDELTEDAMEYIAGYVIKKLRISDKVKENLTFTYVDEVSHGGLI
KPSEKFQEKIKYFNKKIEIKNQKQKLIETPNY