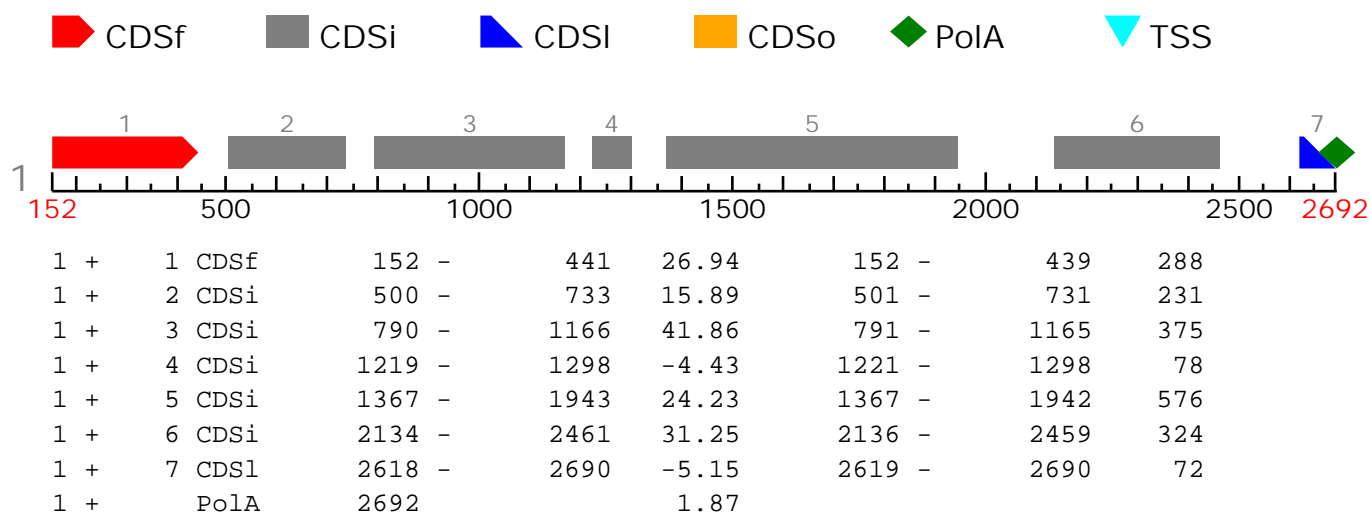


FGENESH 2.6 Prediction of potential genes in *Trichinella_spiralis* genomic DNA
 Seq name: gb|CM027589.1| *Dmelanogaster*13
 Length of sequence: 2902
 Number of predicted genes 1: in +chain 1, in -chain 0.
 Number of predicted exons 7: in +chain 7, in -chain 0.
 Positions of predicted genes and exons: Variant 1 from 1, Score:121.831091



Predicted protein(s):

```
>FGENESH:[mRNA] 1 7 exon (s) 152 - 2690 1959 bp, chain +
ATGAAATATTGCAAATTTTGCTGCAAAGCTGTGACTGGAGTAAAATTAATTCACGTGCCG
AAGTGTGCTATTAAGAGAAAATTGTGGGAGCAGAGCCTTGGGTGCAGCCTTGGTGAAAAC
TCCCAAATTTGTGATACCCACTTTAATGATTTCGAGTGAAGGCTGCACCTGCAAAAGGT
CAGACATTTAAAAGGAGGCGACTCAACGCAGATGCCGTACCTAGTAAAGTGATAGAGCCT
GAACCAGAAAAGATAAAAAGAAGGCTATAACAGTGGGAGTACACAAACAGAGTCCTGTTCA
TTGTTTAAATGAAAATAAGAGCTTGAGGGGAAAAAATTCGTACTTTGGAGTACGAAATGCGT
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ACGGACACGCAGATACGGATACTGAAGAATGGTGGACAAAGAGCTACGTTCAATTCCGAC
GACATTTCTACAGCTATTTGTCTCCACACCGCAGGCCCTCGAGCATGGTTATCAGATGTG
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TATGACAGCTCTGCTGATATTGTTTACGAGCCAAGCGACTATGTCCAACCTGGCTATTGTT
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ATTGTATCCGATTTAGGTACCGGAAACCAAAAGCTATGGACAGAGCTCGGTATATCAGAA
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GGCAAGCAGTTGGATATACAGAATGATATTTTGAATCGAATGTCGGAAATTATGCGAACA
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TCGCTTGATGGCTTGTATAAATATTTGCAAGAAAACCTTCAGTATGCAATACATATTAACA
AGCCGTCTCAACCAAGACATTGTGGAGCATTTTTTTTGGCAGCATGCGATCGAGAGGTGGA
```

CAATTCGACCATCCCACTCCACTGCAGTTTAAGTATAGGTAAAGAAAATATATAATAGCC
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CTTAATTTAGATTTTCAGTTCTAAAGAAAACGAAAATAAAAGTAAAGATGATGAGCCTGTC
GATGATGAGCCTGTCTGATGAGATGTTAAGCAATATAGATTTACCGAAATGGATGAGTTG
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AAGCCGTCCGAAAAATTTCAAGAGAAAATTAAGTACTTCAACAAAAAAATTGAAATTAAA
AATCAAAAACAAAAGTTAATTGAAACTCCAAATTATTAA

>FGENESH: 1 7 exon (s) 152 - 2690 652 aa, chain +

MKYCKFCKAVTGVKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNDSQWKAAPAKG
QTFKRRLNADAVPSKVIEPEPEKIKEGYTSGSTQTESCSLFNENKSLREKIRTLEYEMR
RLEQQQLRESQQLEESLRKIFTDTQIRILKNGGQRATFNSDDISTAICLHTAGPRAWLSDV
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RGLKKS WKQPVFDFNTRMDPDTLNNILRKLHRKGYLVVAIVSDLGTGNQKLWTELGISE
SKTWFSHPADDHLKIFVFS DTPHLIKLEALHLCNKSDLSILFKINENHINVRSLAKQKVK
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GKQLDIQNDILNRMSEIMRTGILDKPKRLPFQKGIIVNNASLDGLYKYLQENFSMQYILT
SRLNQDIVEHFFGSMRSRGGQFDHPTPLQFKYRLRKYIIARNTEMLRNSGNI EEDNSES
WLNLD FSSKENENKSKDDEPV DDEPVDEMLSNIDFTEMDELTE DAMEYIAGYVIKKLRISD
KVKENLTFTYVDEVSHGGLIKPSEKFQEKIKYFNKKIEIKNQKQKLIETPNY