

FGENESH 2.6 Prediction of potential genes in C_elegans genomic DNA

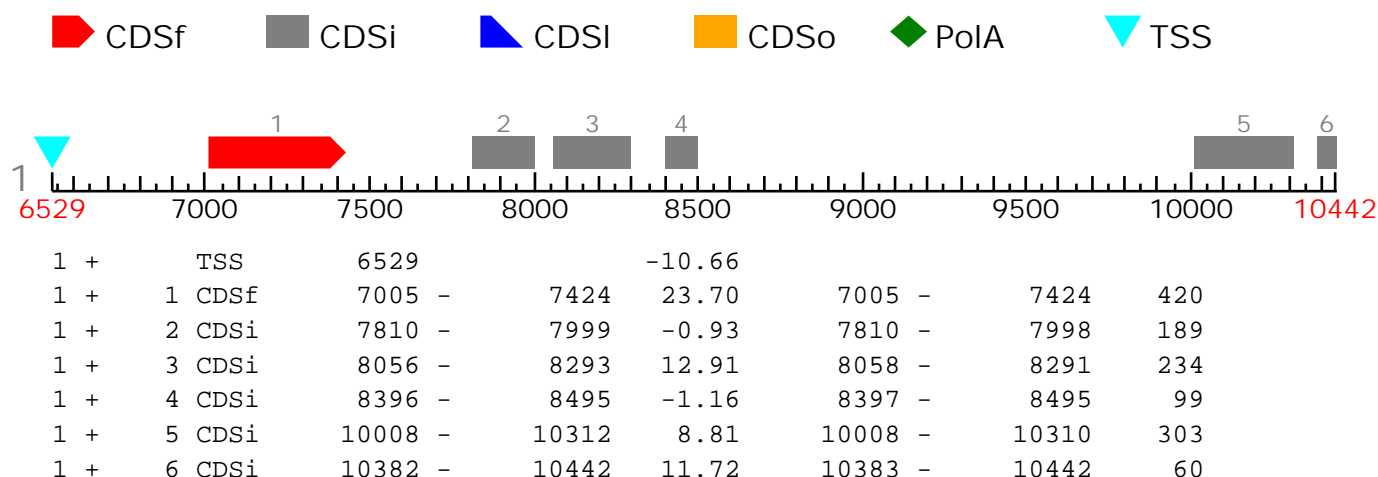
Seq name: Contig

Length of sequence: 10560

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: 30.690079



Predicted protein(s):

```
>FGENESH:[mRNA] 1 6 exon (s) 7005 - 10442 1314 bp, chain +
ATGGACGCTTCGGATGCCGCCGCTGGAATCTTTCTGCTTTTGTGGGAATTGTTGGATGT
GCTCTATATGTTTGATAGTTTGTCTCAATGTGGAGAATGGTTAATGAAATCGTTGGATTC
CGTTTTCTCATTTTCGCAAGCTCTCACGGATATTCTTCTGATGATCCAATTTGGCATTG
CCTGGAATTGTAATCTTGACTCAAAATGAAATCATCAATGAATCATGGCGATGGAACATT
CATATTTATTTGGATTTCACTTGGTGGGCAATGGTTTATCACTATACTGTTCATCGCGTGG
TCTCGTCTTGCTGCCGTTGAATGGCCGAATTGGTTCCGTACTCTGCCACATGGTACAAGT
ACAATGATTTGTGCAATTCCATGGTTCGCTGGTTTATTGCAAAGTCTAGTTGAGCATCAG
TTTGAATGGTTCACTCCTTTGTATTATTCTCCAACAAGATATGGAATGCATTCTAACTGG
GAGAAGTACGAAGTGTCTGGAACAAACACTTACTATATGATCTGTAATGTTATTCTGATG
GTTGTTCCGTTCCCATTTGTATGTTTTGGCACTGGGTGTTCTGTTCCAAAGACAGACTTCG
AGAAATTCTCAACTTCGATCGAAATACTCCACGCACCAATATCCACATCTTCATATGCT
GCACAACAACGACAATTGAGTATTGAAACTCGTCTTTTGGTTCCTTGTATCATCAATACA
ATCCTATTTCGTCGTTGGTCAAGTGTTTCAATGTTCCAAACACGGAAAATGGATG
AACTGGGCAGTTATGGTGGTGGTTTGCAACTAATTCTTTCGTGAACCTCTTCTTTATTTA
TTTTTCAGCAGCGTAATCCGTAAAGGAGTCCTGAGCAATTGTCTGGAAGAACTTCTCGCTT
TCTGCAATATAAATGACTACGAAATGCGATCCTCTCCAAGACATCTAAACTGCGCTCGT
CTCCAAGAGAAATTGGATAGTATGGTTCGGAAGAATGGGCCTGATCCGTCCACTTTTTAGC
CAGCTGTACCAGAACTAAGAGACATCACGTTTTGGGCTGGAAGCAAAAAAAGGCGTTG
GCTGACTGCAGAGTGATGAAGAGACAAATTGATGAACTGCTTGGAGACCAAGAAGAGGAG
TTGCCGGATACCAACCGTATGGGTCCCGCTATTGCCGGCATGCTCACGGCGGCAACTGGA
ACAGCCATCCTCCTCGTTATGCACCTCCATAAGATTCCGGTAGATGTCGATTGGTCGATC
GGTGCTCTATCTTCCAGTGCTGCTATCGTTGCCATTGTTGCTGTTGCCTATCCG
>FGENESH: 1 6 exon (s) 7005 - 10442 438 aa, chain +
MDASDAAAGIFLLLFGLVGCALYGLIVCSMWRMVNEIVGFRFLISQALTDILLMIQFGIW
PGIVILTQNEIINESWRWNIHIYLDFTWWAMVYHYTVIAWSRLAAVEWPWNWFRTPHGT
TMICAIPWFAGLLQSLVEHQFEWFTPLYSPTRYGMHSNWEKYELSGTNTYYMICNVILM
```

VVPFPLYVLALGVLFQRQTSRNSQLRSKYSHAPISTSSYAAQQRQLSIETRLLVPCIINT
ILFVVGQVFISQCSKHGKWMNWAVMVVFATNSFVNPLLYLFFSSVIRKGVLSNCRKNFSL
SAIYNDYEMRSSPRHLNCARLQEKLDSTMVGRMGLIRPLFSQLYQKLRDITFWAGSKKKAL
ADCRVMKRQIDELLGDQEEELPDTNRMGPAIAGMLTAATGTAILLVMHLHKIPVDVDWSI
GALSSSAAIVAIVAVAYP