FGENESH 2.6 Prediction of potential genes in Homo_sapiens genomic DNA

Seq name: test sequence Length of sequence: 75001

Number of predicted genes 1: in +chain 0, in -chain 1. Number of predicted exons 11: in +chain 0, in -chain 11.

Positions of predicted genes and exons: Variant 1 from 1, Score: 33.443375

CDSf		CDSi	CDSI		CDSo Pol	A	TSS	
1	: 	2345 67				1	8 9 	101
10823	20000	30000		40000	50000	6000	0	71414
1 -	PolA	10823		1.12				
1 -	1 CDSl	10882 -	11008	-4.60	10882 -	11007	126	
1 -	2 CDSi	22229 -	22338	6.83	22231 -	22338	108	
1 -	3 CDSi	23302 -	23358	3.99	23302 -	23358	57	
1 -	4 CDSi	24360 -	24435	0.91	24360 -	24434	75	
1 -	5 CDSi	25277 -	25401	1.05	25279 -	25401	123	
1 -	6 CDSi	27017 -	27151	5.79	27017 -	27151	135	
1 -	7 CDSi	27989 -	28100	9.92	27989 -	28099	111	
1 -	8 CDSi	62454 -	62565	1.57	62456 -	62563	108	
1 -	9 CDSi	64528 -	64650	5.21	64529 -	64648	120	
1 -	10 CDSi	69127 -	69226	2.59	69128 -	69226	99	
1 -	11 CDSf	69647 -	69751	15.53	69647 -	69751	105	
1 -	TSS	71414		-7.99				

Predicted protein(s):

>FGENESH:[mRNA] 1 11 exon (s) 10882 - 69751 1182 bp, chain -ATGGCGGCGAGCGCTGCGAGGCCTGCCAGTGGCTGGCGAGGCGAGAGTAGCGAGAGC GAGGATGATGGCTGGGAGATTGGGTATCTCGACCGGACGTCTCAGAAATTGAAAAGGCTA TTACCCATTGAAGAAAGAAAGAAAATTTAAGAAAGCAATGACCATCGGAGATGTTTCA ACTCCCCTTATGTATGCTGCTAGTGTTGCCAATGCAGAGCTGGTTCGGGTCCTTTTGGAC AGAGGTGCTAATGCAAGCTTTGAGAAGGATAAGCAAAGTATTTTGATAACTGCATGTTCT GCTCATGGCTCAGAGGAACAGATCTTGAAGTGTGTAGAACTACTACTTTCAAGAAATGCT GATCCAAATGTTGCTTGTAGGAGACTTATGACCCCAATCATGTATGCTGCTCGAGATGGT CACACCCAGGTTGTTGCTCTCTTGTTGCTCATGGAGCAGAAGTTAATACCCAGGATGAG AATGGTTACACTGCTTTAACGTGGGCAGCACGTCAGGGTCATAAAAATATAGTTTTGAAG TTGCTTGAACTTGGAGCTAATAAAATGCTACAAACCAAAGATGGAAAGATGCCAAGTGAG TTGGAAGGAAAACTTCAACAGCTAACTAAAGAAGACACTATTTGTAAAATATTGACAACA GATTCTGATAGAGAAAAAGATCACATTTTTAGTTCATATACAGCATTTGGAGATCTGGAA GTATTTTTACATGGTCTTGGACTTGAACATATGACAGATTTACTAAAGGAAAGGGATATA ACGTTAAGACATCTTTTGACCATGAGGGAAGATGAATTTACAAAGAATGGAATTACCAGT AAAGACCAGCAGAAAATTCTGGCTGCTCTTAAAGAACTACAGGTAGAAGAGATACAATTT GGAGAGCTATCTGAAGAGACAAAGTTGGAAATCAGTGGTGATGAGTTCCTCAACTTTCTT CTCAAATTAAATAACAGTGTGGCCATTTAATAACAGCTGTACAGAATGTTATTACTGAG TTACCTGTAAATTCTCAAAAGGTATTCTACAAAAGTTATTAA

>FGENESH: 1 11 exon (s) 10882 - 69751 393 aa, chain -

MAASALRGLPVAGGGESSESEDDGWEIGYLDRTSQKLKRLLPIEEKKEKFKKAMTIGDVS
LVQELLDSGISVDSNFQYGWTPLMYAASVANAELVRVLLDRGANASFEKDKQSILITACS
AHGSEEQILKCVELLLSRNADPNVACRRLMTPIMYAARDGHTQVVALLVAHGAEVNTQDE
NGYTALTWAARQGHKNIVLKLLELGANKMLQTKDGKMPSEIAKRNKHHEIFNLLSFTLNP
LEGKLQQLTKEDTICKILTTDSDREKDHIFSSYTAFGDLEVFLHGLGLEHMTDLLKERDI
TLRHLLTMREDEFTKNGITSKDQQKILAALKELQVEEIQFGELSEETKLEISGDEFLNFL
LKLNKQCGHLITAVQNVITELPVNSQKVFYKSY