

FGENESH 2.6 Prediction of potential genes in *C\_elegans* genomic DNA

Seq name: Omy\_NODE\_4d

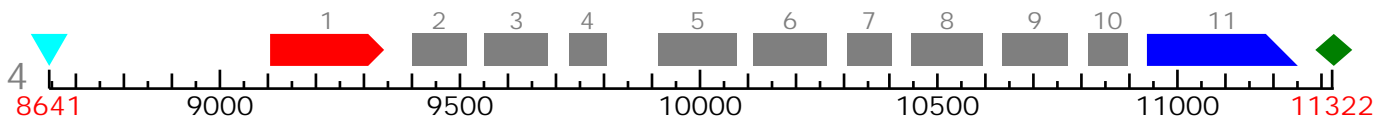
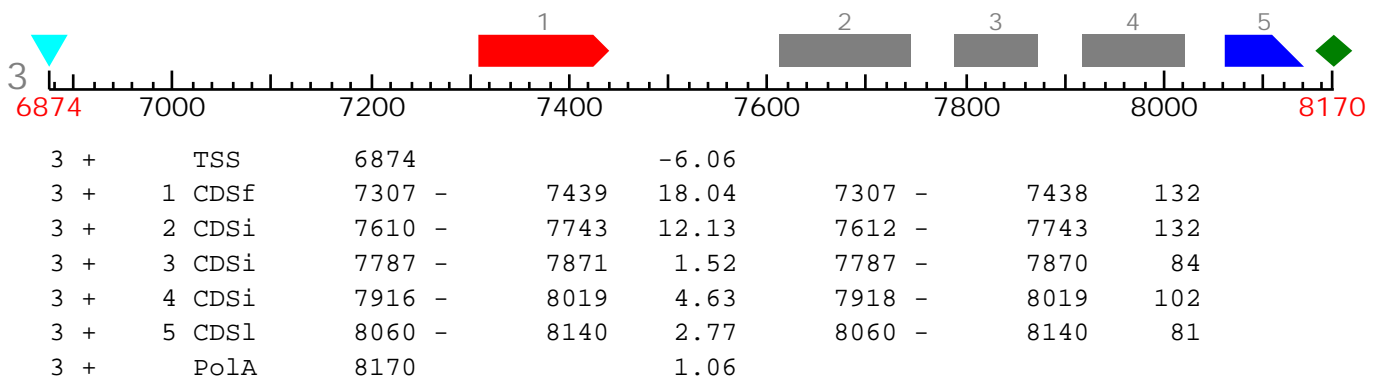
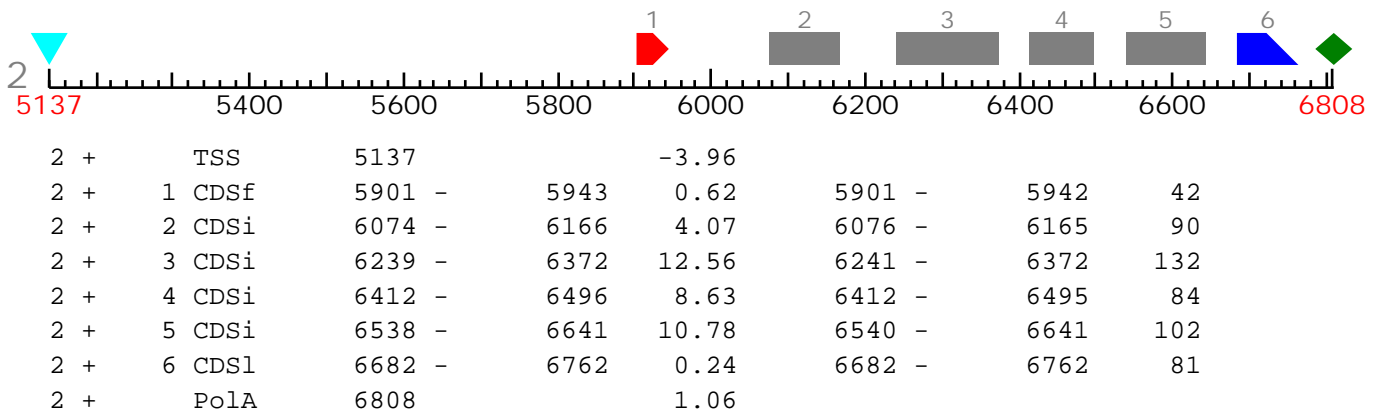
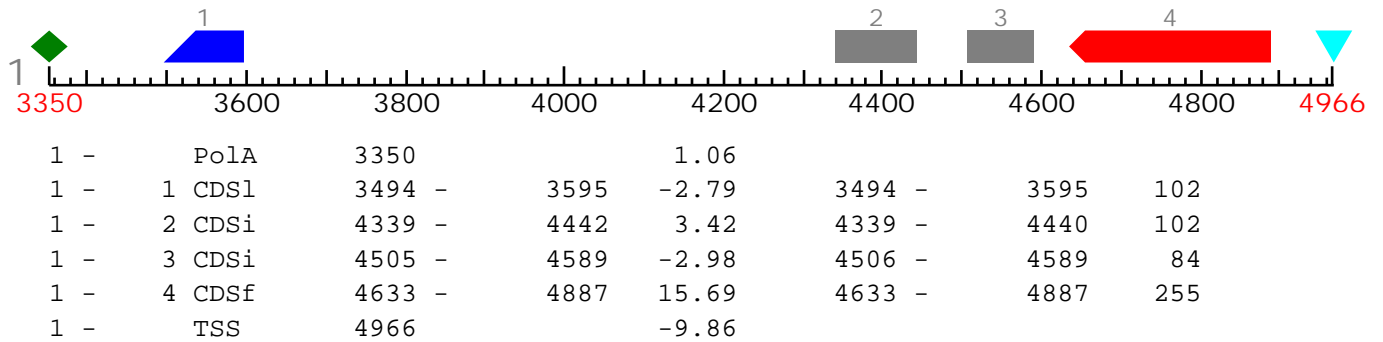
Length of sequence: 54160

Number of predicted genes 10: in +chain 7, in -chain 3.

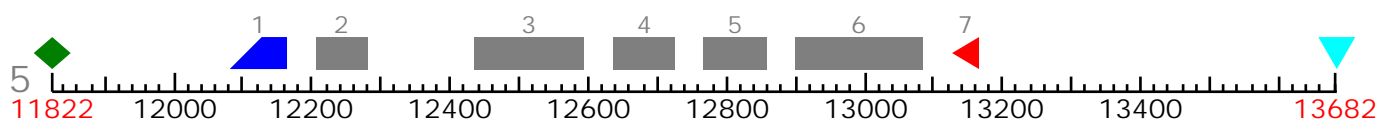
Number of predicted exons 132: in +chain 69, in -chain 63.

Positions of predicted genes and exons: Variant 1 from 1, Score: 620.796484

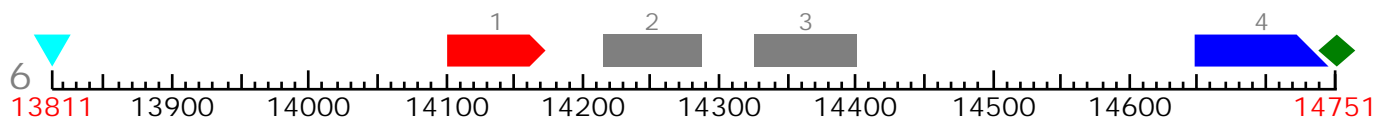
▶ CDSf   
  CDSi   
 ▶ CDSi   
  CDSo   
 ◆ PoIA   
 ▼ TSS



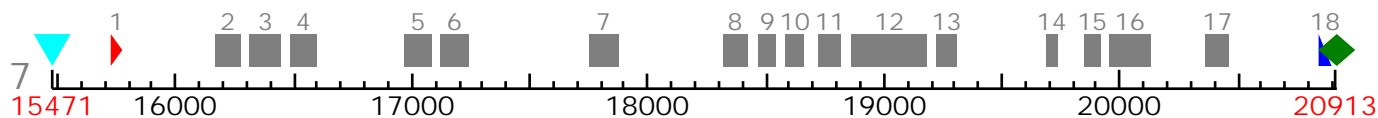
4 +	TSS	8641			-5.26			
4 +	1 CDSf	9102 -	9340	0.33	9102 -	9338	237	
4 +	2 CDSi	9398 -	9512	15.93	9399 -	9512	114	
4 +	3 CDSi	9550 -	9682	6.49	9550 -	9681	132	
4 +	4 CDSi	9725 -	9804	6.59	9727 -	9804	78	
4 +	5 CDSi	9913 -	10076	8.29	9913 -	10074	162	
4 +	6 CDSi	10111 -	10264	-0.51	10112 -	10264	153	
4 +	7 CDSi	10306 -	10398	9.55	10306 -	10398	93	
4 +	8 CDSi	10440 -	10590	-0.50	10440 -	10589	150	
4 +	9 CDSi	10630 -	10766	14.52	10632 -	10766	135	
4 +	10 CDSi	10809 -	10891	11.84	10809 -	10889	81	
4 +	11 CDSL	10932 -	11247	-3.33	10933 -	11247	315	
4 +	PolA	11322		1.06				



5 -	PolA	11822			-3.65			
5 -	1 CDSL	12079 -	12162	0.42	12079 -	12162	84	
5 -	2 CDSi	12204 -	12278	13.09	12204 -	12278	75	
5 -	3 CDSi	12433 -	12591	10.49	12433 -	12591	159	
5 -	4 CDSi	12635 -	12724	12.31	12635 -	12724	90	
5 -	5 CDSi	12765 -	12857	9.73	12765 -	12857	93	
5 -	6 CDSi	12898 -	13082	5.61	12898 -	13080	183	
5 -	7 CDSf	13125 -	13164	-1.68	13126 -	13164	39	
5 -	TSS	13682		-8.66				

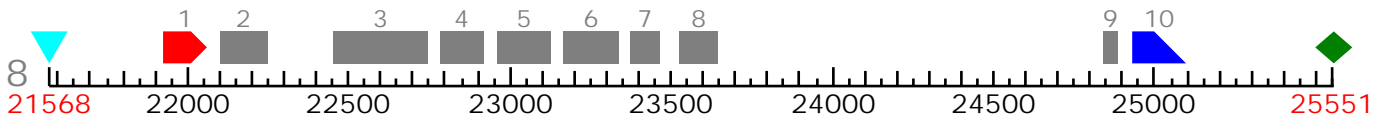


6 +	TSS	13811			-5.26			
6 +	1 CDSf	14100 -	14172	0.17	14100 -	14171	72	
6 +	2 CDSi	14214 -	14286	1.80	14216 -	14284	69	
6 +	3 CDSi	14325 -	14400	10.44	14326 -	14400	75	
6 +	4 CDSL	14647 -	14745	-0.03	14647 -	14745	99	
6 +	PolA	14751		1.06				

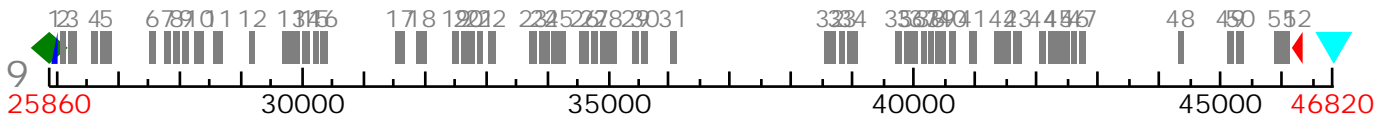


7 +	TSS	15471			-6.86			
7 +	1 CDSf	15719 -	15768	6.36	15719 -	15766	48	
7 +	2 CDSi	16161 -	16270	1.90	16162 -	16269	108	
7 +	3 CDSi	16308 -	16440	6.25	16310 -	16438	129	
7 +	4 CDSi	16479 -	16593	4.58	16480 -	16593	114	
7 +	5 CDSi	16962 -	17079	3.62	16962 -	17078	117	
7 +	6 CDSi	17115 -	17234	10.07	17117 -	17233	117	
7 +	7 CDSi	17745 -	17869	0.39	17747 -	17869	123	

7 +	8 CDSi	18312 -	18416	2.89	18312 -	18416	105
7 +	9 CDSi	18464 -	18538	0.30	18464 -	18538	75
7 +	10 CDSi	18577 -	18656	-3.68	18577 -	18654	78
7 +	11 CDSi	18718 -	18814	11.99	18719 -	18814	96
7 +	12 CDSi	18858 -	19176	4.70	18858 -	19175	318
7 +	13 CDSi	19216 -	19304	2.42	19218 -	19304	87
7 +	14 CDSi	19682 -	19729	0.43	19682 -	19729	48
7 +	15 CDSi	19843 -	19911	0.05	19843 -	19911	69
7 +	16 CDSi	19949 -	20123	-2.63	19949 -	20122	174
7 +	17 CDSi	20358 -	20456	5.19	20360 -	20455	96
7 +	18 CDSL	20836 -	20891	2.49	20838 -	20891	54
7 +	PolA	20913		1.06			

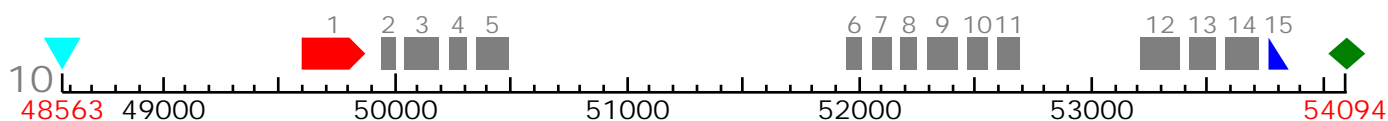


8 +	TSS	21568		-9.66			
8 +	1 CDSf	21921 -	22057	8.79	21921 -	22055	135
8 +	2 CDSi	22097 -	22244	30.43	22098 -	22244	147
8 +	3 CDSi	22449 -	22741	29.89	22449 -	22739	291
8 +	4 CDSi	22780 -	22915	18.43	22781 -	22915	135
8 +	5 CDSi	22957 -	23123	1.04	22957 -	23121	165
8 +	6 CDSi	23162 -	23334	3.39	23163 -	23333	171
8 +	7 CDSi	23370 -	23461	2.03	23372 -	23461	90
8 +	8 CDSi	23523 -	23641	10.36	23523 -	23639	117
8 +	9 CDSi	24836 -	24881	5.23	24837 -	24881	45
8 +	10 CDSL	24926 -	25093	10.78	24926 -	25093	168
8 +	PolA	25551		1.06			



9 -	PolA	25860		1.06			
9 -	1 CDSL	25895 -	25997	-0.14	25895 -	25996	102
9 -	2 CDSi	26040 -	26135	1.29	26042 -	26134	93
9 -	3 CDSi	26175 -	26308	4.11	26177 -	26308	132
9 -	4 CDSi	26556 -	26655	7.02	26556 -	26654	99
9 -	5 CDSi	26696 -	26890	7.14	26698 -	26889	192
9 -	6 CDSi	27491 -	27597	3.89	27493 -	27597	105
9 -	7 CDSi	27741 -	27852	5.15	27741 -	27851	111
9 -	8 CDSi	27891 -	27997	5.62	27893 -	27997	105
9 -	9 CDSi	28037 -	28146	4.98	28037 -	28144	108
9 -	10 CDSi	28232 -	28391	9.21	28233 -	28391	159
9 -	11 CDSi	28542 -	28700	-0.34	28542 -	28700	159
9 -	12 CDSi	29130 -	29219	2.64	29130 -	29219	90
9 -	13 CDSi	29662 -	29952	14.18	29662 -	29952	291
9 -	14 CDSi	29994 -	30121	2.40	29994 -	30119	126
9 -	15 CDSi	30162 -	30232	4.98	30163 -	30231	69
9 -	16 CDSi	30272 -	30400	0.24	30274 -	30399	126
9 -	17 CDSi	31511 -	31659	7.13	31513 -	31659	147

9 -	18	CDSi	31845 -	32022	4.01	31845 -	32021	177
9 -	19	CDSi	32445 -	32548	5.00	32447 -	32548	102
9 -	20	CDSi	32589 -	32810	10.48	32589 -	32810	222
9 -	21	CDSi	32849 -	32927	5.88	32849 -	32926	78
9 -	22	CDSi	33025 -	33141	7.57	33027 -	33140	114
9 -	23	CDSi	33697 -	33819	3.65	33699 -	33818	120
9 -	24	CDSi	33860 -	34024	9.00	33862 -	34023	162
9 -	25	CDSi	34063 -	34292	13.71	34065 -	34292	228
9 -	26	CDSi	34519 -	34668	8.55	34519 -	34668	150
9 -	27	CDSi	34708 -	34806	6.13	34708 -	34806	99
9 -	28	CDSi	34845 -	35114	2.20	34845 -	35114	270
9 -	29	CDSi	35375 -	35483	0.45	35375 -	35482	108
9 -	30	CDSi	35525 -	35629	2.68	35527 -	35628	102
9 -	31	CDSi	35989 -	36090	1.76	35991 -	36089	99
9 -	32	CDSi	38505 -	38698	1.36	38507 -	38698	192
9 -	33	CDSi	38751 -	38843	2.52	38751 -	38843	93
9 -	34	CDSi	38883 -	39060	1.84	38883 -	39059	177
9 -	35	CDSi	39668 -	39771	-0.69	39670 -	39771	102
9 -	36	CDSi	39819 -	40040	11.56	39819 -	40040	222
9 -	37	CDSi	40084 -	40162	3.13	40084 -	40161	78
9 -	38	CDSi	40202 -	40279	2.16	40204 -	40278	75
9 -	39	CDSi	40318 -	40496	3.75	40320 -	40496	177
9 -	40	CDSi	40537 -	40651	4.44	40537 -	40650	114
9 -	41	CDSi	40868 -	40987	3.92	40870 -	40986	117
9 -	42	CDSi	41290 -	41552	-0.74	41292 -	41552	261
9 -	43	CDSi	41589 -	41735	-0.27	41589 -	41735	147
9 -	44	CDSi	42018 -	42116	11.79	42018 -	42116	99
9 -	45	CDSi	42156 -	42502	11.05	42156 -	42500	345
9 -	46	CDSi	42541 -	42637	4.32	42542 -	42637	96
9 -	47	CDSi	42674 -	42779	1.27	42674 -	42778	105
9 -	48	CDSi	44276 -	44358	2.96	44278 -	44358	81
9 -	49	CDSi	45078 -	45191	1.79	45078 -	45191	114
9 -	50	CDSi	45233 -	45361	5.10	45233 -	45361	129
9 -	51	CDSi	45853 -	46098	10.05	45853 -	46098	246
9 -	52	CDSf	46136 -	46312	14.53	46136 -	46312	177
9 -		TSS	46820		-6.96			



10 +		TSS	48563		-6.36			
10 +	1	CDSf	49594 -	49868	8.06	49594 -	49866	273
10 +	2	CDSi	49936 -	49998	0.68	49937 -	49996	60
10 +	3	CDSi	50037 -	50187	23.66	50038 -	50187	150
10 +	4	CDSi	50229 -	50306	2.07	50229 -	50306	78
10 +	5	CDSi	50345 -	50486	11.26	50345 -	50485	141
10 +	6	CDSi	51940 -	52007	3.85	51942 -	52007	66
10 +	7	CDSi	52049 -	52133	0.67	52049 -	52132	84
10 +	8	CDSi	52174 -	52244	9.03	52176 -	52244	69
10 +	9	CDSi	52288 -	52419	10.51	52288 -	52419	132
10 +	10	CDSi	52458 -	52548	4.18	52458 -	52547	90
10 +	11	CDSi	52592 -	52687	11.70	52594 -	52686	93
10 +	12	CDSi	53206 -	53375	15.97	53208 -	53375	168

10 +	13 CDSi	53415 -	53530	-1.43	53415 -	53528	114
10 +	14 CDSi	53572 -	53715	2.69	53573 -	53713	141
10 +	15 CDS1	53757 -	53844	-2.45	53758 -	53844	87
10 +	PolA	54094		-0.44			

Predicted protein(s):

>FGENESH: 1 4 exon (s) 3494 - 4887 181 aa, chain -  
MDEVKTTFS DYPFGQIPVLEVDNFQIPQSI AIAIARYVARKTGHAGKNELEQALVDSFADQY  
KDYFTEVKPFFMIAFGIIPATEEEVNEKRKNLLGPARDQYFNLLTMYLKKSTTGFLAGGD  
LTYADLLL AENVTTFRNIDTDYTKGFPEISKLTCLVPGTGILVYNACSEQKLEKKVVFVH  
H

>FGENESH: 2 6 exon (s) 5901 - 6762 179 aa, chain +  
MVQYKLYYFFSRGLDFTFDQVPVLEVDSVQIPQSLAIYRFLAKKTGHCGKDDIEQAIVDA  
LADQHKDYYVATLPYFLAGLAI FPESEEEYVKAKYEQLVVPNRPNYLNYLTKFLRKSKTGF  
LAGGDLTFVDLMVAEYVTSIRAAIPDFTAGYPEVEAHVEKVISIPKLGKQWLDKRPVTPF

>FGENESH: 3 5 exon (s) 7307 - 8140 178 aa, chain +  
MVNYRLHYFFSRGLGEVGRQLFHLGGIPYEDVRYRSREQWPLVKEGHYKDDLEAGIIDAL  
ADLYKDYFKDTLPYYLSALEIFPETEEYVKAKYEELVVPARVKFFFTFLTYLQKSKTGYL  
AGGDL SFVDLIVAEHISTFRQVLPDYTAGFPEIEANVEKVRTNPKLKEWLEERPVTNF

>FGENESH: 4 11 exon (s) 9102 - 11247 554 aa, chain +  
MRLLLFSLVQCGLALNILVFLIGTNQFERNTFEFLAQQALRHHNVITVKPILIPPEPK  
LVKPKLHLVREKTLKNLLPRSLYEPELEKAGDVIPWQDTYEIEEYDKVYWTAHNASCYKML  
NSNLM DGLKKDSIDVAIAYS GNPCQLAL THVLGIPTIYYDVEGLSDETLVAAGAPLDLNQ  
PSSHCRLPDFPPYLRRLRNLG CYLKEYLVQSGLPVIPSLLSERYRGLDGPITRMWSEDT  
IKKRFPSFPDVNALKQDSVLYFANTDPLLELSRALPPTVIPVGGHLHDHPKPLFAPWNTT  
IESAEGLIVVSLGAQANSAGMSEQQAKSILGALS KLTKYRIYWRIGPNMVLPGVDEATV  
PSHINLTAFIPQNDLLAHKACKLFVTNGMSSLMEAVAYGVPVVGIPLYGSNLHNMEKVA  
NKGLGLIVTKSNLNEASLLKAMKSVLDGVKYKTVAKDMSKEFKSRASTPFNTALHYIEHV  
GRHHSAAFFSGNSCRCLFSQLNLDFFVLLFVILFVPPFYLPLALLKKCCFGKKTNVSDPKK  
SSEHKSSKESKKEK

>FGENESH: 5 7 exon (s) 12079 - 13164 241 aa, chain -  
MVLALSASFASNHSERPYESI EDFMEKYTFGDLFNEKYNEAVDSLITKYSMVAKMLDDEL  
IETKRQLRIVTMINELRKT LQEFDKESMFDSEKKQLRYDALMYNRLFTTIASSVVL SFEE  
KINLFDYVAIEYPEFLSICERSVEVAEDVEKMKPELRNVSQALRHAYLLVLRLOMEIHNE  
KLVAKIYEKLEELVRQFS PRDHKDLVRLLENYLAHDHEDFDEKLPFD SLIETYKNILFK  
K

>FGENESH: 6 4 exon (s) 14100 - 14745 106 aa, chain +  
MRLLA AVILLALFSSSFAIRCYSTAKIYGQKPKPSDAIDCPDDVKACLG VVYKGINGKMM  
HTSAWTC DYQHQVDTQGNTCKTSFEDDIQQTVCFCQTDLCNPITNV

>FGENESH: 7 18 exon (s) 15719 - 20891 660 aa, chain +  
MLFRRWTFNFC SLTAINFSTYFDQCDEL IASSVAVDV MYTNHADAVIGPSCSQPAMIAGV  
FGNLYNIP IVTWGSTTYSELLDIQRYPTV FVGSVSSVSVGVAIHRMFKAYKWTQFALIYS  
TREATKKCSSMRTDMSQAFSAISDKSVVMAFQGD LNEHSPERMKGLLQQAQR YARIFVLC  
MDDMTKRDFMLAADDLNMTTAEYAYVFTDIQSLGFRSLRTVHVGPDGHKSSVFYI IGLNS  
SELPHIYATITV DAYNSNKRVENS MASVRTNASSRTANSVRDRRRFGFFTLQGEIVVALR  
ITNRTTFNDQDKKELRQIRAFSMENLNKFVGLCLDGPDILFTWKFC SRGSLVDVINSTTF  
DMDFFFV FSLISDLTQGLEFLHSSTVKFHGRLTSETCLVDDR FQVKLAYFGMHKLPETT  
DGTTFISYEVMTLGDKLWTAPEVLREECSGSQAADIFGF AICSELLTRKHAYAIGGKD  
PEEIVYKVKRGLHPLFRPEVTVADSI EVGPGATSCHSPKGWSNSASRNVDLLNALYTTF

DAIIEENEVYKVETIGDGYLCASGLPTRIGNQHARRMAEMALALIKSVGSFKVPHLPDEK  
INIRVGIHCGSVVAGVVGLTMPRYCLFGDTVNTASRMESNGKHKEPGLYTAFAKAEQDVHL  
>FGENESH: 8 10 exon (s) 21921 - 25093 492 aa, chain +  
MIGIPYVDSVLRRLF SRKHVGDGADRLLSFATATLCGMFAILVCTKQYVGSMPMCWAPGEF  
RGGWDQYARDHCYIKNTYAVDFDINAFPDKEQRENHVQVNYQWVPLYLFLQAI VFYFPS  
YIWRKLYKNHGIQHADFKHKFLGIDVATVMDGSRKLRNLDSAAKEKELDYL SVSILETIR  
EQKARPFYKCFGLIAGNYSRVLTYKYIAVKLMYVVLV MNFYVCMFLNQHDSFWAIRGV  
QSLVTGDEWENSPSFRVSLCDFKIFDLGNVREFTVQCLLMNAVNEKVFFIQWFWLCMM  
LVITVCYNLQFVLSIASVSSRGLSIYRWLNHPNKKEIASGMTQKFAQLIGLDGFLVLYFI  
ESASGQRAASDFATYLF AKLKEDMEKEPELEKEPVYPAIPAYPSAPGAPEIVVGPVPEKEP  
IVVFGKEHVDRIGPKMVIVYAVCLLLLLTFSAMESWYISVVSQD TDWFATTILKPRFI  
T VTVSLHRDFSD

>FGENESH: 9 52 exon (s) 25895 - 46312 2487 aa, chain -  
MQLLNLF FLVGLVATAVHQHPITWRPSRRMTMAKSGELHAYLKFQEKLRVANLASLPQTV  
LDYGDYEYVANMTIGTPDQP FVIILDTGSSNLWVPATNCDKSC TGHSRFDMSKSSTWVKN  
GTAFTIEYQGNAAGTLEEDTVKGF SLESYTNKTEGISDTGT SFIGGVKSVTDELAKA  
AGASWHLLSQAYTIDCDATPPPLKVVIGSNTYSIDPVNYIVDP THRQHASSLWVEPTPLN  
FQVFTRLHKGSTNTSGTCFVQTSNLDGETTLKQRSVTDRWLDHSRRDLPINPSTFKVHCE  
EPNKDIDSITAWFEYEDGEEPIEKKNVLLRGSKLKNTAYVEGIVLYAGHDTKMMMNNGR  
APLKISDIERKTNFFILICLVILVAMVVIGCVLCGVFLGEYENPSFAIFIPWDSPPSPGKG  
AAISIGLFLICYQVMVPI SLYVTMEFVKLLQVYFIHGDI ELYDEENENSTDGAPLISRTL  
NNRCINYKNDEVASHFFRNILVNNTVVVNKGLEIEARAEENDLQI PLEAPIESPIELNPV  
GLIQQQVSVFIQNT EGEDI FYENVQIMTDQKKETVLD SFKRQFYEFCHLVSEWATRLIPP  
GNITEVNLVFPFDSERKMMSVVAKVDEKLILYTKGADSAVLQRQIMMDRTEERDRMLNQL  
RDDVEKDMTIIGVTGIEDKLQEDVSETITSLREAGIQVWVLTGDKLETAENIARSSGLFD  
DETGIFRINDTSDITSIEESKYNIILSTKVLPLLQDGNQQI IKILTRATCVLCYRMTPAH  
KASVAIAVKNYLKG NVLCIGDGANDVPMIQAANVGI GVRGKEGMQATMASDFAIGKFRFL  
KKLILVHGHWSYRRLALSFLYFLYKNMNLCFILFFYQFYCGNSGSYFMDTTYSVLYPIIF  
TSVQPVI VGLDQDSEAAVLLLEKPKLYSSGRLGQLYTYLLFFF CVLESIWQAAVIYFIPQ  
GAIWESDAARWTFGFYVATGMMFVNNAHLALEHILIGASFGISIGLHFTYFLSFYQVPP  
GYGNIVDLPTEVALDAISSAPFWYSMVITVVLSSIPSWRVIQANCVQDEPRHKLKNYRY  
VGNSITTTKYRGTSS FQKTSWKHIIVGDIIRVLDGHDIPADLLILRTSDRTGSCFVETS  
LDGETSLKQCSVPLRYIPFSEVGMVYAGHDTKVMNNGRAPLKVSAIERKTNGFIVVCL  
FILVAMITSSCILGSMFLSGELDPMAFFIPSNPNPTKAAILGIGKFLCYQVIVPISLY  
ITVEVIKLAQVFFMSQDLDLYDEENDYPINCRSLNIPEELGQITHILSDKTGTLTENIMI  
FRNCALDDEDYACDPEVESIQSCSQDSSSDGQSVIQQAPFVNTDSGMEVYMEDSTSLTP  
LQSSFHRCSSIIKGA FYDAREAIREYWETGTLRSTTSSEVFSKETKYHAESPDELALVEG  
AEMYGFSLEERTPTGVIIRNPNTYSERINVKLVL PFDKRKRMSVIVEEASGKFMMYTKG  
ADSAVLT SRFVKVYVWVMLRYNVVLSTEALKHIEDGDTSLIDLLKGSTSVLCYRMTPAE  
KASVVTTVKHHLK GKILAI GDGANDVPMIQA AHVGI GMKGKEGMQAAMACDFAIGKFCFL  
RKL LLLVHGHWCYERLALLFLYFLYKNTN NVFILFFYQFFCGVSGTY YVDSTYSLLYPIIF  
TGLQPILVGLDQDKRSQELMWNPKLYSAGRTGSSYTYVLF LFNVL DGWVQAAVIFVFPQ  
MNPVIAVCLVFFMFLHFAYFTA FYPLAVDAMRLATFWYSTFIVL FVSVLPRGIEVAPRTQ  
NLASFAYALDFATPATVSTLQCMKNAGYQAVFVRAYNPAGNGAFDRNAVTVNNAFTAQI  
GAEVFMTPQP VSSKTAATQMDEVIDGLISSITIRSIWIQVTSPLN WATNTAGNTNFVST  
LISRAKARGLAVGIY TNIDWSQITNNWQGAPSDV MLWYWTVLGPGVSGETGTNFADFRA  
FGNFRSATAKQFAQVESNSKDLNVMFDLPVADNDCFR AFNAIFLSFGVSCNVCGGPATGA  
PVTSAPTPGIHVKNLSRKWRIQFHEIQ LHQKDVPWFTLLKVS RDCSRNLCFHKKYRSMDG

MCNNLEQPLKGAFTPLPRLLPNDYDDGVNAVTDLSLRGLRPNPRVVSSRLLAMDQSIPLN  
VSSILMQFGQLVSHDITKNGLLHVCASCTNAQPNCASIPQRPFDGSPVGCFFPYTRSVHQC  
GTGFAGRPREQLNSNTAFIDASGNFNNRAHAPDILGDNRNFLITGLGALHTMFIRLHNRY  
QKHVDP SILNEFAGAAYRLHGLIQASYPLMDPNYRPFHQYDFRQGV LGPGNQQHVS DID  
SVLRGLIGTPAKAAQRLTSIVAERLGESFALAILSLQRVWLLQMDLYVGGLLEKPGQDA  
VMGPTFTCI IAEQFKRIRDGDRFYFENSGIFTSQQVIALRRVTL SWVICSNSDSMQRITP  
NVFFHDNGRNAIPCSSLQSLDLSPWRS

>FGENESH: 10 15 exon (s) 49594 - 53844 589 aa, chain +

MNFKLRSLLLIALRSVRRRAESPNSAAPP SHKNRRLPAARGGSYSSALTRLKSF AIMSSDHE  
EMLKRFFGPTLPTKEFVDQQISK SIGLPAETEDQINGLPLSKLLEQKSMTFNDLIFMPG  
YIYFGVADV SLETEVVKGIRVKLPFISSPMDTVTEAKMAITMALQGGLGVVHGNFQDPKK  
QVIEITRVKAFQEGFVLDPVCLKATAPVSEIFKKA EFGFKTFPVTEDGVLGSKFLGFIT  
KS NYVNI PVEDQQKLLIKDILPRGEMIAAGIGSSAFTVLRVMQENNL DVVPIVDVDMN L  
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WSGGVQHGLQDLGAKS IDDLHKMGDSGKLRGEVRTANAQAEGGVHSLDK