

FGENESH 2.6 Prediction of potential genes in Podospora_anserina genomic DNA

Seq name: All_nTARs

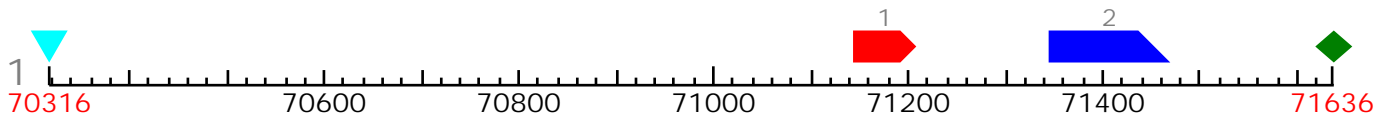
Length of sequence: 869610

Number of predicted genes 20: in +chain 9, in -chain 11.

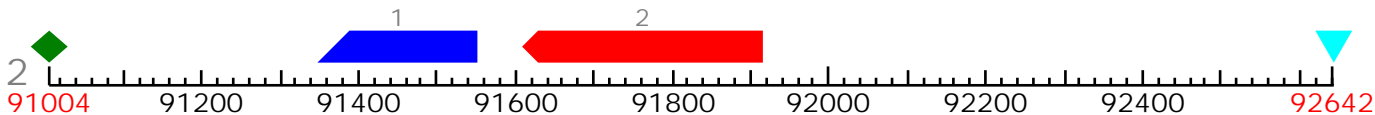
Number of predicted exons 50: in +chain 25, in -chain 25.

Positions of predicted genes and exons: Variant 1 from 1, Score:224.089307

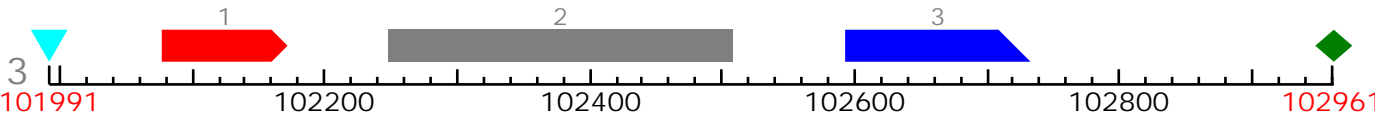
CDSf CDSi CDSl CDSo PoIA TSS



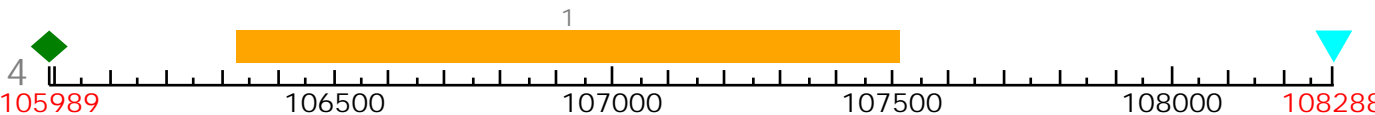
1 +	TSS	70316	-2.54				
1 +	1 CDSf	71142 -	71207	7.76	71142 -	71207	66
1 +	2 CDSl	71343 -	71468	1.77	71343 -	71468	126
1 +	PoIA	71636	1.87				



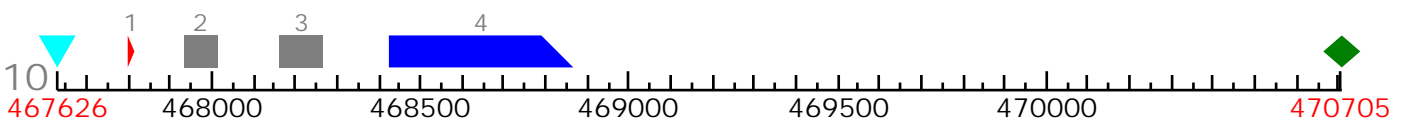
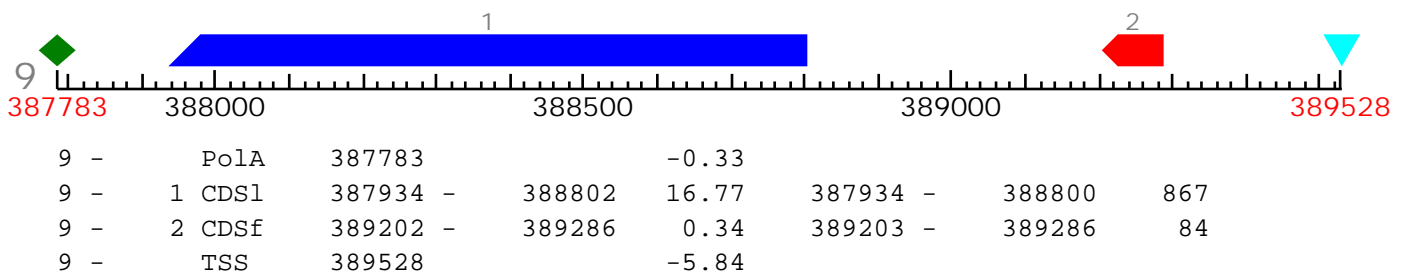
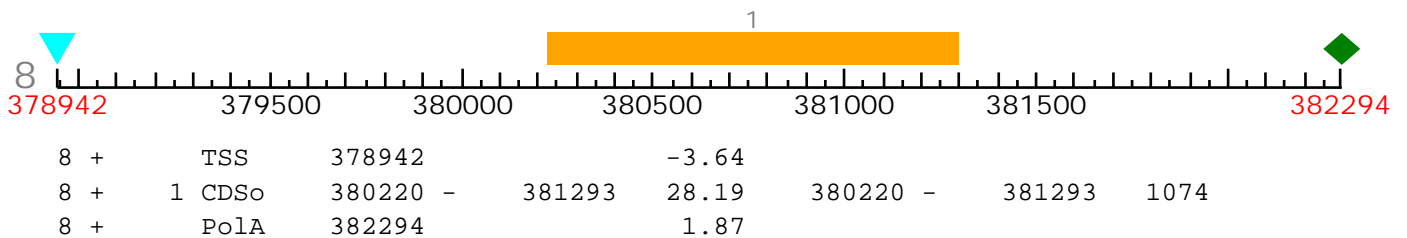
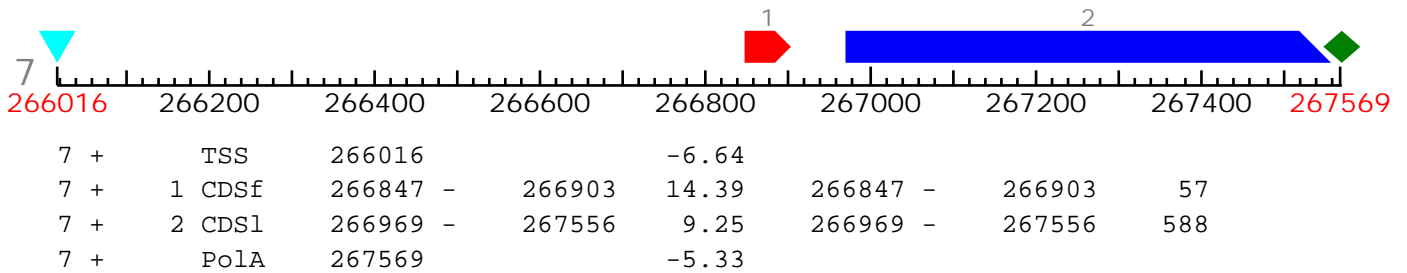
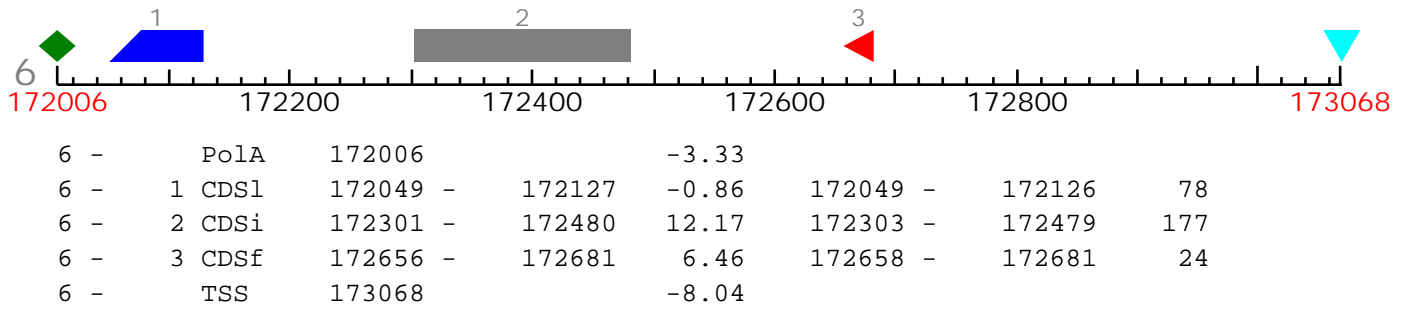
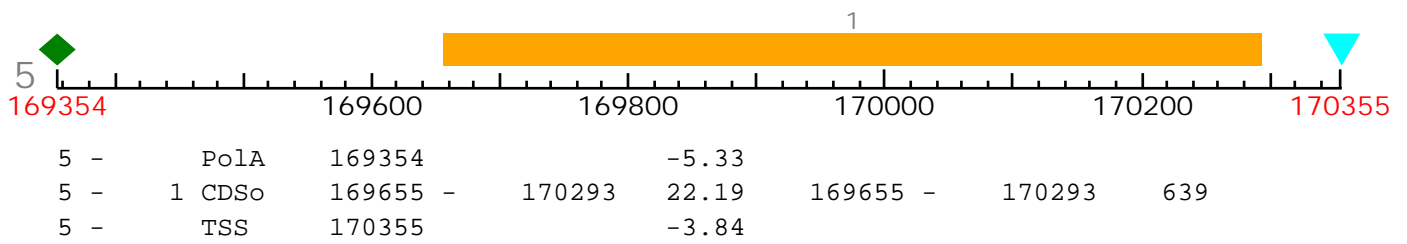
2 -	PoIA	91004	-0.33				
2 -	1 CDSl	91346 -	91550	-0.74	91346 -	91549	204
2 -	2 CDSf	91607 -	91914	16.70	91609 -	91914	306
2 -	TSS	92642	-6.24				



3 +	TSS	101991	-3.44				
3 +	1 CDSf	102076 -	102171	10.88	102076 -	102171	96
3 +	2 CDSi	102247 -	102507	4.41	102247 -	102507	261
3 +	3 CDSl	102592 -	102732	5.99	102592 -	102732	141
3 +	PoIA	102961	-2.93				



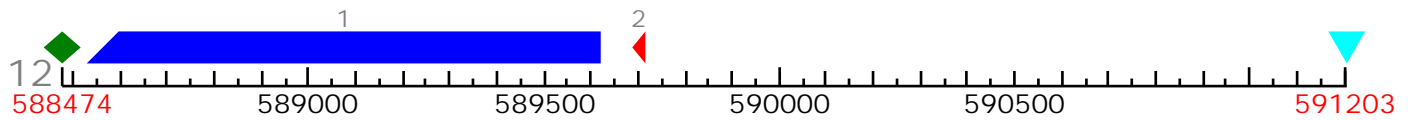
4 -	PoIA	105989	-3.33				
4 -	1 CDSo	106324 -	107511	22.60	106324 -	107511	1188
4 -	TSS	108288	-5.34				



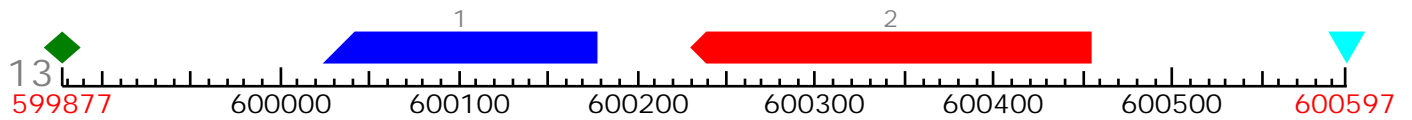
10 +	TSS	467626			-3.94			
10 +	1 CDSf	467795 -	467811	9.47	467795 -	467809	15	
10 +	2 CDSi	467929 -	468010	-2.21	467930 -	468010	81	
10 +	3 CDSi	468159 -	468264	2.35	468159 -	468263	105	
10 +	4 CDSL	468421 -	468863	25.09	468423 -	468863	441	
10 +	PoLA	470705		1.87				



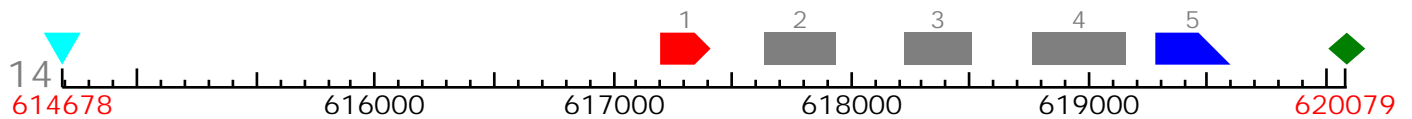
11 +	TSS	533135			-5.24			
11 +	1 CDSf	534161 -	534216	1.47	534161 -	534214	54	
11 +	2 CDSL	534734 -	534887	12.04	534735 -	534887	153	
11 +	PoLA	535000		1.87				



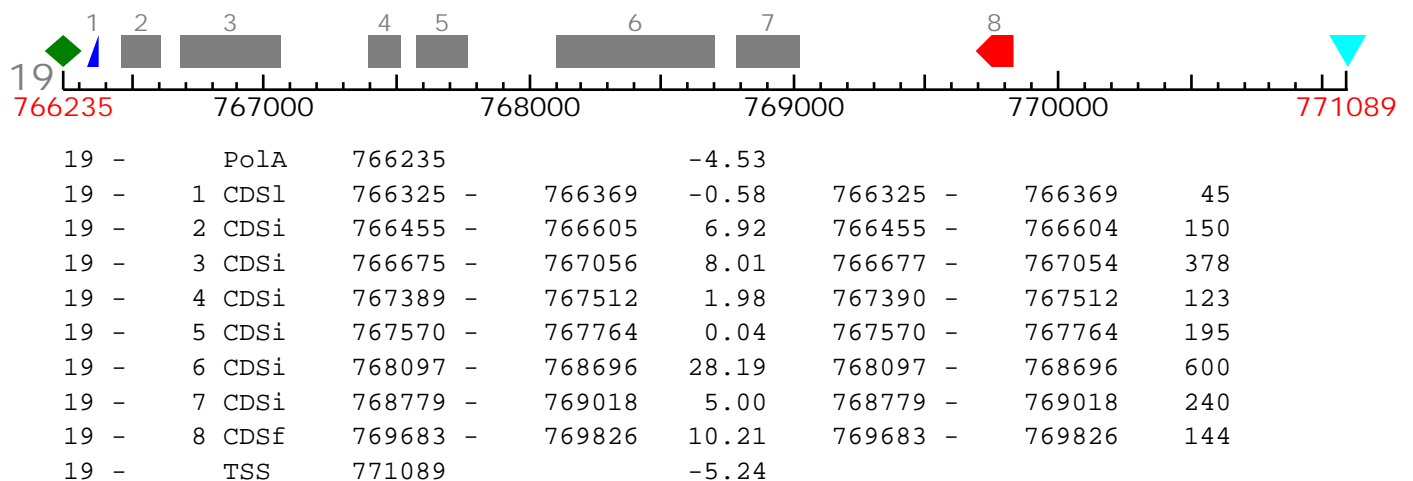
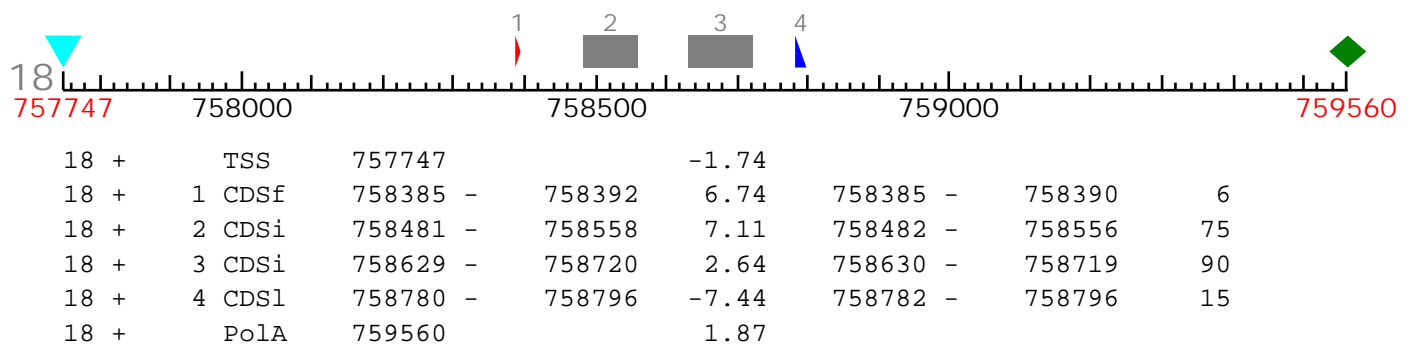
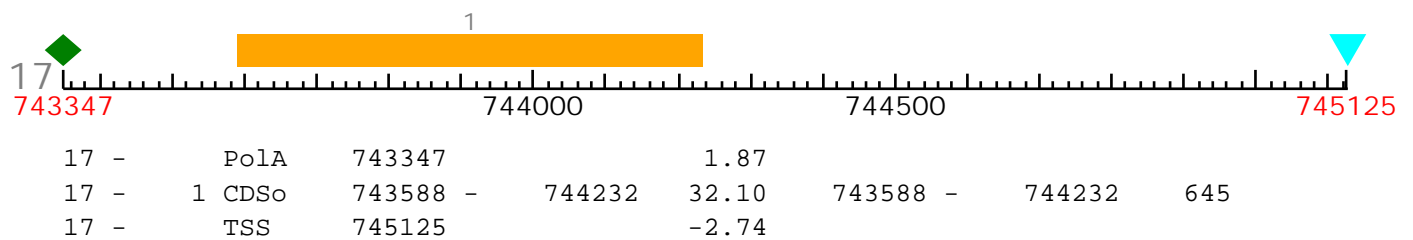
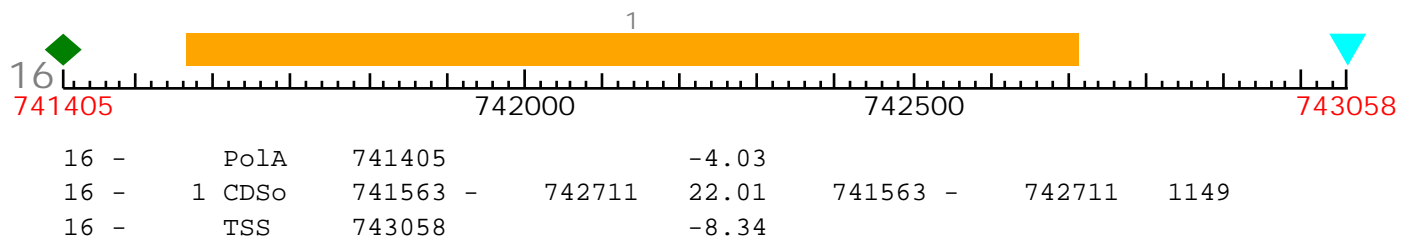
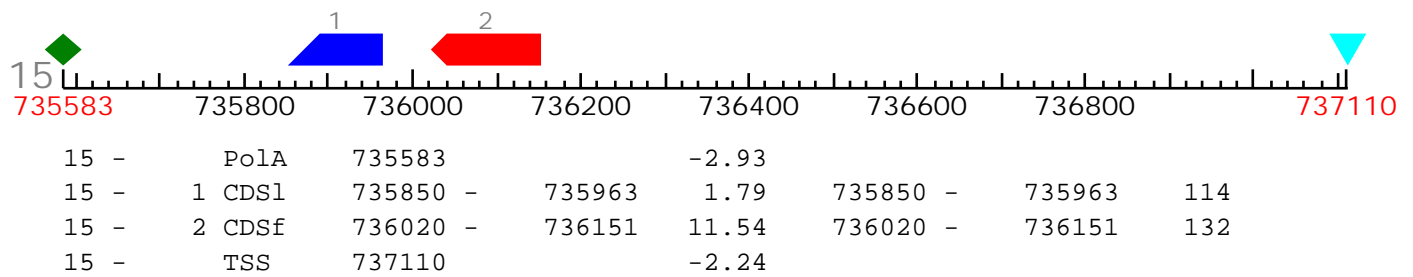
12 -	PoLA	588474			-4.93			
12 -	1 CDSL	588526 -	589618	59.96	588526 -	589617	1092	
12 -	2 CDSf	589685 -	589713	4.04	589687 -	589713	27	
12 -	TSS	591203		-5.24				



13 -	PoLA	599877			-5.13			
13 -	1 CDSL	600023 -	600177	-9.57	600023 -	600175	153	
13 -	2 CDSf	600229 -	600454	27.93	600230 -	600454	225	
13 -	TSS	600597		-7.04				



14 +	TSS	614678			-1.74			
14 +	1 CDSf	617192 -	617404	4.43	617192 -	617404	213	
14 +	2 CDSi	617631 -	617931	2.43	617631 -	617930	300	
14 +	3 CDSi	618218 -	618502	2.20	618220 -	618501	282	
14 +	4 CDSi	618756 -	619151	14.05	618758 -	619150	393	
14 +	5 CDSL	619274 -	619590	-2.37	619276 -	619590	315	
14 +	PoLA	620079		1.87				



ATTCTCCCAGATCTCGGCCTGTCTGGTTCGCACGATGTCGATTTTCGAGACCGAACTTCTC
GGCGAGTTGAGCCACGAATGCTTGTGCCGATATCACAGCGACGACGAAACTGCAAAGACC
TTGGTGGAGCAGTGGAAGACGGCTTTGAAGAAGGCTCGTTTCGCAATATCAGAAGACGGAG
CGAACTACATCAAAGGAATCTTTGAGCACGGATTCCGTGGCTCATCACGCTCGAACGCAG
TCGCCGCCCTGAGTTCCACAGAATCGGAGGAAACAACGGAAGTCATGCTCAAGGACCAC
CCGGAAGACTCTACGGTACTAAAGCAAGAGGCCATCGTTGAACAAACGATAGAGCAGTCA
ACATCTGCCAGTTCTCCTAGATTAAACTCCACCGAGTCAGCATCACCGCCAGCGGGAAAA
ACGCCCCCAAAGCTGGGCTTTTCTACCCCCGTTCCAGGCGCAACACCGTCCAAATCGCCA
GAAGTCAGCAAGTCTACACCTTTATTTGACTTCACCCAGCTCTTCCAGACCCCTGGCTCC
CACAAGCCTACAGTCAACCCACACAAAGGCACACCTGCCCCAGCGGCCTTCAAATATGAT
CAGTCTAGAACACCCGGCACCTCCAGCACAGCAGACATGTCGCACTCTTCAGTCGCAAGT
CTTAGCCCTAACGAGAATACCCCTGCCTTTGTCTTCACAAGTTCATCGACTCCTTCCAGG
CCTCCAGCCACCACAGAGGGGAGCCTTCCCAAGTCTGAAGATCCTTTCCGATACTCCGGG
AGCCCTATTTCGCGAGGCTGGGCAGCGAATTATAAAGAGTCTAAGGGAGATTGGGGACATG
GAAGTGCCGAACGAGCTAGACGGTGATATATCAGGGTTGGGGCAGAGTATTGAGAGATTG
CGGCTTCGTCTTGAGAAGGGACGCTCACTGTGCCTCAGTGGACCAGATGCGGGCTCTGAA
GGTGATGATGAGACTTCTGACCAGGATGGAAAAAGAAGGATGGAGTGA

>FGENESH: 4 1 exon (s) 106324 - 107511 395 aa, chain -
MADLIDLSQQSPSSLSPWEPSVLLQLWNPDVQAWSCLGWTRAERRCRRVLSQAKREATMR
ILPDLGLSGSHDVFETELLGELSHECLCRYHSDDETAKTLVEQWKTALKKARSQYQKTE
RTTSKESLSTDSVAHHARTQSPPLSSTESEETTEVMLKDHPEDSTVLKQEAIVEQTIEQS
TSASSPRLNSTESASPPAGKTPPKLGFSTPVPGATPSKSPEVSKSTPLFDFTQLFQTPGS
HKPTVNPCHKGTPAPAAFKYDQSRTPGTSSTADMSHSSVASLSPNENTPAFVFTSSSTPSR
PPATTEGSLPKSEDPFRYSGSPIREAGQRIIKSLREIGDMEVPNELDGDISGLGQSIERL
RLRLEKGRSLCLSGPDAGSEGDDETS DQDGKRRME

>FGENESH:[mRNA] 5 1 exon (s) 169655 - 170293 639 bp, chain -
ATGCCCCGCTCCGATATCACCATCGACCTGGACCGGAGCTCAACTCCGTTTCCGAGATCT
CGCCGCTCTGAGAGAGCCCACGAGCAGGTCGAGGACTTCAACCGGCGCAGCTCCTCGCCT
CGGAGATTTACCTCCACCCCGACCAGAAGCCGCGAGGCTGAGCCCCAGCCCGACTCGATAT
CGTTCTGCCGCCACAATCGCTCGCAGCCCTCCCAGATATCGTTCCCCTACCAGGATCACT
AGCGCTCCCCGCCCCCGCAGGATCAGCCCTAGTCCTCTTAGACATCGCTCCCCTATCCGA
CTCCCTAGCTCCACCTCCCGCCGTGCTCCCTTCCCCTCTCCCTATTTCAAGGAGACCCGT
ATCACCGAGGCTCGTCGCACTACCACGTACCACCCTACGAGCCCGGTGAGCCGCTACACC
GAGACTCGCACGACGTACCGCACTCCTATCTCCAGACCTCGCACTCCTCCTCGTGGCTCG
ATTGGCAGCCCCAGTCGGCGTATCACATCGCCGCGTCTTGTCGATATCAGGTCTTCTTCG
GAGATCTATAGCTCGTCTCGTCGATATGACTCGTACCCGTCGACAACCAGGAGCCCTGGC
CGCTCCACCGATAGAAGCCTGTTACCCGTCGCTATTAG

>FGENESH: 5 1 exon (s) 169655 - 170293 212 aa, chain -
MPASDITIDLDRSSTPFPRSRRSERAHEQVEDFNRRSSSPRRFTSTPTRSRRLSPSPTRY
RSAATIARSPPRYRSPTRITSAPRPRRISPSPLRHRSPIRLPSSTSRRAPFPSPYFKETR
ITEARRTTTTYHPTSPVSRYTETRTTYRTPISRPRTPPRGSIGSPSRRITSPRLVDIRSS
EIYSSSRRYDSYPSTTRSPGRSTDRLFTTRY

>FGENESH:[mRNA] 6 3 exon (s) 172049 - 172681 285 bp, chain -
ATGTCTGGATATCCTCCTCAGCAGGGTGGCTACTACCCCCAAGCCCCCTCCCCAGGGGTAC
CCTCCTCAGGGCTATCCCCCACC GGATGGAGGGTACCCCCACAGGGCTACCCTCCCCAG
GGCTATCCCCCTCCCCAGCAGCAGATGCAGTACCAGCAAGCGCCCCCTCCAAGGAGGAG
AAGAGCCACGGCTGCCTCTACACCTGCGTTGCTGCCATGTGCTGCTGCTGGCTCTGCGGA
GAGACCTGCGAATGCTGCCTCGAGTGCCTCGACTGCTGCTTCTAA

>FGENESH: 6 3 exon (s) 172049 - 172681 94 aa, chain -
MSGYPPQGGYYPQAPPQGYPPQGYPPPDGGYPPQGYPPQGYPPPQQMQYQQAPPPKEE
KSHGCLYTCVAAMCCCWLCGETCECCLECLDCCF

>FGENESH:[mRNA] 7 2 exon (s) 266847 - 267556 645 bp, chain +
ATGGCAAACATCAAGACGGAGACCGCGGATGAGGGTGTGACTGCTGCTGACCCCGGCGCT
ATCAAGAAAGCCCCATTTTCCATGACGGAGTCCGAGTTGCGAGAGATCTTGGTGCTGGCC
ATAGATCGCCACCCCGCAATACATCCCATTGTCCAACGGCACCTTGACAGGCTTCGGGAC
AACAATCTAGGCGGTTTCCAAGACGACTTTGAGAAAATCCGTTGCGAAGTTTACGCATGT
GCTTCAGAGCCTTGTTTTTCCGATCCCAAGGCAATCGGAGCATGCATCAAGCGATACTTT
GAGAAGCTTCTGAACGTGGCTACCCGAGAGTCGCCATATGAGACGAGGTA CTGGCGGTG
GAGTGGTTCTTCGCGTGCTGAACCTGCTTGTTTTACCAGCGATCCTCATGACGTGAGA
AAAGAGATCTGGAGTCATACAGATGGCTCTTGCTTGAAACTAGTGATGCTGGTTTGCCGC
TTCAGAACTGCTGAGAGAGGTGACTCCTTCGCGATCACAACAGCCTGATCATGCTCAAG
ATGGACTTGATCACAGCGAATGCCAAGGATCTCCCGGA ACTTCTTCGCGAATTCGAGCCA
ACTATCCACGTTATTAAGCTGGAGAGCTGAGTCAAGGGGCTAA

>FGENESH: 7 2 exon (s) 266847 - 267556 214 aa, chain +
MANIKTETADEGVTAADPGAIAKKAPFSMTESELREILVLAIDRHPAIIHPVQRHLDRLRD
NNLGGFQDDFEKIRCEVYACASEPCFSDPKAIGACIKRYFEKLLNVATRESPYETRYSAV
EWFLRVLNLLVFTSDPHDVRKEIWSHTDGSCLKLVMLVCRFRTAERGRLLRDHNSLIMLK
MDLITANAKDLPELLREFEPTIHVIKSWRAESRG

>FGENESH:[mRNA] 8 1 exon (s) 380220 - 381293 1074 bp, chain +
ATGGGATATGAGTGGAATGGGGACCCTACCATCCTCATCGTAGTCATTGCCTGCTCGGTA
TGCTTCGGATGGGTGCCCATCATCACCGTCGTCAGCATCGTCCGCCACTGCCGTGCCCGC
CTAAGGGCAAACGAGGCTCGAATGGTACCAATTCTGATGCCGAAAGTCAGGGAGGCAGA
CCCAGCACCGCTCCTGATGTGCCCAAGCCGCTCCAGACATATCACCCAGCTCAACCAAG
GGTCTCGAGAGGAGCGCGTCAAGTCGGACACGCAGCTCCGCTGATGGCTACGACCTCAA
CGTGTCGACACCAATTCTTCTGGAATCCCATCCGTCACTCCTTTCACTACGACAACGAA
TCGCTTTGGGGAGGAGACGGGCTGTCCAGGAGCAACAGTCGTCATCGGCCCCCGTACTTT
CCCACCCACGTACACAACACCACACCTTCACTCAGCCGCCAGCCTCCATCCGCTCTGTC
GCATCGAGCCATCGGCAACAGAGCCGGAGCCGCGAAGCTCAATGGCCAGCAACTCTGAC
AACGCACCGGCAGCCTTCCAGATCAATGACACCTACTACGACACTACACCGCTACCAAAT
GTGACGAGGACTGTAAACCCTGTCTGTCGCCAGCAGTAGTACGCCACCTCGTCAAAGGGG
CCAGGACAAGCTCCACAGCAACGTCAACAGAAGCAGCCAAAGCAAGACAATCCACACCCA
CCGCAGCGCAACCGCCGCACAAGGCACTCTCTTGACGCCCGCGGGGATTTCGATTCTCTA
ACCCGGGACATCTCCAGACCCAACACCTCCATGACAAGACGAGAAGTCGAAGAATACGAA
GACCTCGACAACCAGAAGCAAAAGGCCACCCACCGTAGCCACCGACACCCCGGCCAGGA
TCAGCATCACGGCGTGGCAGCCATTCAGCACCCGGCGGCAGCGAAGAGACTGACGATGAC
CTGTCCATGGCCGGGGCCTTGCCGCCTGCCAAGTTGCCCCCGAGGCGAGCATCGCTCCAT
GCACAAACATTTGAGCGTCCGGCATGGCTGCACGAGGAGCCCCACGCCATGTGA

>FGENESH: 8 1 exon (s) 380220 - 381293 357 aa, chain +
MGYEWNGDPTILIVVIACSVCFGWPIITVVSIVRHCRARLRKRGSGNGTNSDAESQGGR
PSTAPDVPKPLQTYHPSSTKGLERSASSRTRSSADGYDLKRVD TNSSWNPIRHSFHYDNE
SLWGGDGLSRNSRHRPPYFPTHVHNTTPSLSRPASIRSVASSHRQQSRSRSSMASNSD
NAPAAFQINDTYD TTPLPNVTRTVNPVVASSSTPTSSKGPQAPQQRQKQPKQDNPHP
PQRNRTRHSLDARGSDSLTRDISRPNTSMTRREVEEYEDLDNQKQKATHRSRHRPPRPG
SASRRGSHSAPGGSEETDDDL SMAGALPPAKLPPRRASLHAQTFERPAWLHEEPHAM

>FGENESH:[mRNA] 9 2 exon (s) 387934 - 389286 954 bp, chain -
ATGCATGATTGTGAATTTGAGGAAAACCCGGCAGGCTTTTGTTGCGCAGTAGAGACGGTG

GAGCTGCATGCGGCCGGTCGCTCATACTTTTACTCAAGCTTTGAGGGGGCTTCCTGTTAC
CGTCAAGACTTTGCCTTCTTTTCGAAACCTTCAACACATTTCACTGCGCAACTTCTTTGAT
GATCCAAACCGCTCACGCCAGCAGACTGTCCAGCTATTGCGCCACTCCCCGAATCTTCAC
CGGCTGGAACCTCGGCTTGTCTGCCAAAGCCGTTGTGCGACAGCTTGAACGCGAGGGCAGC
TTTGGCGTGTTTGTCCACTTCTTTGATCGGCTCTGTGATGAGTATGCCGAATCAGGAGGG
CAGCCTTTACGCCTCACACATTTGGGTCTCTTCGACGCTATGTGGGTATGGAAACCAGAG
TCGTTGAGGAAGAAGCCAGCCGATCTCGCCTTCTTCAAGAGGTCAGACTCAACACAGAG
ACTATCGAAGATTGCATCACCGACAATTTGGTTGACCTATTTCGACTCCGAGGCCCTTTTCG
GGCTATGCTGTCCTCGTTGAGACAGATAGAGGGTCTAAATATGGCCCTGCCTACCTGGTG
GGTGCCCCGGGAGTTGGAGATGCGTCGGCCCCGGACCCCGATGCAGTTGGCAGAAATGTCC
CTGGTCCTTGGAGGAACCTTGGGGCAATCAGAACTGTTGGCAGCAACCACGAGGCACTCA
CTACAGGGTCTGGTTGTAAACATGAACAGACCTGACCCACGCCGAAGCCTCGATTTTCTC
CTCGCCCCCTGCAGAACATGCACCGGCTTGCTCGGTTGTGGATTGTGTCTGCCAACATG
TACAAAGACCTTCTTTTATTGACAAAAGCCGCTCAGAAAGGCGGTTGTGCGGTTTCTCTGC
CTTGCGCTGCATCGTGATCGGGTGGCGCTGCTGGGAGGTAAGTGGCAGAATTAG

>FGENESH: 9 2 exon (s) 387934 - 389286 317 aa, chain -
MHDCEFEENPAGFCCAETVELHAAGRSYFYSSFEGASCYRQDFAFFRNLQHISLRNFFD
DPNRSRQQTVQLLRHSPNLHRLELGLSAKAVVRQLEREGSFVGFVHFFDRLCDEYAESGG
QPLRLTHLGLFDAMWVWKPESLRKKPADLAFLQEVRLNTETIEDCITDNLVDLFDSEALS
GYAVLVETDRGSKYGPAYLVGARELEMRRPRTPMQLAEMSLVLGGTWGNQKLLAATTRHS
LQGLVNMNRPDPRRSLDFLLAPLQNMHRLARLWIVSANMYKDLPLLTKAAQKGGCRVSC
LALHRDRVALLGGNWQN

>FGENESH:[mRNA] 10 4 exon (s) 467795 - 468863 648 bp, chain +
ATGGAGCCGAGGGAGACATATCGCGAGTTCGGTTCAAGAGCCGCAGGGAGGCATCGCAGA
AAGACGCTAGGCAGCACCCGGCAGACAGTTCGTGATAGTTGCAAAGTCAACGGCGGTAAC
GACGACACCTCTTGGTTGCGGACGCCGCCGCCGATTGTCCGTGCCAAAAGCTGCCGGTA
ACGACGGGCCTCCGGGAGGAAGAGTACGCGGGGAAGCAGACGCAGGCGAGGGAGGAGTCG
GACGGAATGTGGGTGGTGGTGGAAAGAAAAGAAGGTTTCGATCGCCAGCCTGGTGGTGAC
GGTTGTTTTTCAATCTGGGGAGAGGAAGAGGGGGTTTAGTGGGGGGTGGAGGAGTTGTCT
TCTACTACTACTACTACTACTACTACTACTACTGCTACTACTGCTACTACCACTACAACG
ACGACAACAGATGAAGAGGGGGGAGCACCGGGAGGAGCAACAAGAGACGGAAGAACTGGT
GGTTGTGGTGGTGGCAGTAAGGCGAGACCGCACAGCTTGGGGACGGTGGAGGAGAAGAAG
CCAAATAAGAAGATGGCGGGGGGACTACCCGGAGGTGTTGAGGAAGTTTAGCTTGCCGCTG
AGTGTGCAGGGGATTGGGAGCATGGGGTTGGGGTTTCCCATGCCGTAG

>FGENESH: 10 4 exon (s) 467795 - 468863 215 aa, chain +
MEPRETYREFGSRAAGRHRKTLGSTRQTVRDSCKVNGNDDTSWLRTPPPHCPCQKLPV
TTGLREEEYAGKQTQAREESDGMWVVERKEGFDRQPGGDGCFQSGERKRGFSGGWRRLS
STTTTTTTTTTATTATTTTTTTTTTDEEGEHREEQQETEETGGCGGGSKARPHSLGTVEEKK
PNKKMAGDYPEVLRKFSPLSVQGIGSMGLGFMP

>FGENESH:[mRNA] 11 2 exon (s) 534161 - 534887 210 bp, chain +
ATGGTCATATCGATGACACAGAGAAACATCCCCGGCATCTGGAGATCAGGGGGGGGGCGA
GGTCAAGACAACCTCAGCACCGCTGCCACAGCTGCAACAACAACAACAACAACAACAACA
CAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA
CCACAACCACAGCCACGACTGCAGCAATAA

>FGENESH: 11 2 exon (s) 534161 - 534887 69 aa, chain +
MVISMTQRNIPGIWRSGGGRGQDNSAPLPQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
PQPQPRLQQ

>FGENESH:[mRNA] 12 2 exon (s) 588526 - 589713 1122 bp, chain -

ATGTGTCAAGGAACCATCTACGACTTTTGGTGCCCCTGCATCTTCCACGCCCTTCAACC
TCCTTCTACCTCCAATTCGACATCCACCCCCCGACTTCAACTACACCTTCACCCGCCGC
CCCACCACCAACCTCTGAAAGCCCACCTGTCCAAAAGCTCCACAGCATCGTCTACAGC
CAGCACTGCGCCGCCTACAAGTTCTGCGACGACTACCTCCACTCCGAAGGCTTCAACCCC
GGCGATGTGTTTCGACATGGGCGGGCTGTGTCTGCTGGCCACCAAGTGACGTATGAAAGG
GAGGCGTTTATTTCTCACGGCTGTGTGATGCTTGTATCAGCGGGAAATGTGAGGAGAAT
ATGGAGTTTTCGGGGGTCAAGACTGTGAGGAGGAGTCGATATGGGTGGAGGAGTAGGGAG
GAGGAGAGGGAGGGGAAGAGGAGGAGCAGAAGTAGACCGGGGAGGGGGGTGAGTCCGGCG
GGGAGTGTGAGGAGCTTTGACTCTACGGGGAGGGGGAGGAGTTCATCTGTGGGGTCGACG
AGGACGGTGAAGGGGAGGGATATGGGGGTGGAAAAAGGGGGGGTGGCTGGGGAGGGGGAG
GGGAAGACGCTGGGGGCGATGAACCTGAAGAATTTGGTGGATAAGATGGTTCAAACGGTG
TCTGCGCTCCGGGTTGGTGGGGGTGCTGAGAGACAAGACCAGCCGCGCGTGATGCCTGCC
AGTGACCTCGAAGCCATGGCTGAAGAGTCGATGCCGACACCGCTGCCATCTCGACATAAA
CCTAGCGGGAAGAACCCTAGAAGATATGTTTGACAACAGCGGCCGGCCGGAGTATGACTCT
GACCAGGACACAGTGGTCGGTGCCTCAAAAACCTACGGAAAAGAAAAGCAAGGTAAATGGA
AAGACAATCGCTGCGGATGAGATTTCCGGGGTTATGCAGGAAATACCCACCGGCAGAAGC
AAGAGTCGCAAACGCCGCATGTGGACCGACCCAAGGACTGATGAAGAAGCATCTCGCGTA
CTGAGGTTTCTGAGACGGGGGAAGGGTGCTGCTCCCGTCGAGACTGGTAACTCACGAGAG
AGATCTCGAGGTCAAGGGTATGAGCGCATTACAATCGAATGA

>FGENESH: 12 2 exon (s) 588526 - 589713 373 aa, chain -
MCQGTIYDFWCPCIFHAPSTSFYLQFDIHPPDFNYTFTRRPTTNPLKAHLSKSSHSIVYS
QHCAAYKFCDDYLHSEGFNPGDVFDMGGLCPAGHQVTYEREAFISSRLCDACISGKCEEN
MEFAGVKTVRRSRYGWSREEEREGRKRRSRPGRGVSPAGSVRSFSDSTGRGRSSSVGST
RTVKGRDMGVEKGGVAGEGEGKTLGAMNLKNLVDKMOVQTVSALRVGGGAERQDQPRVMPA
SDLEAMAEESMPTPLPSRHKPSGKNLEDMFDNSGRPEYDSDQDTVVGASKTTEKSKVNG
KTIAADEISGVMQEIPTGRSKSRKRRMWTDPRTDEEASRVLRFLRRGKGAAPVETGNSRE
RSRGQGYERITIE

>FGENESH:[mRNA] 13 2 exon (s) 600023 - 600454 381 bp, chain -
ATGCAACTCACAAGATCCCTCTCCACCGCGCTCGTGGCCCTTCTTTTGTCCAGCATCGCA
ACTGGACACCGCATCCCAGCCCAATCAGAAGAGCTCCAGCTCCGAGACGCTGCTCCCGCC
GAGGTCAACGAGACCGGAACGCCGCTGTCTGCTCCTGTTGACGACACTCTGTCTGGCT
GATGTGATTGTGGATGAAACCGAGCATGGGTCCCTAGTGGGTAGAGCTGTTACCCCTCGT
CAGCTTGGAAGGGCAAAGGTGGAGGGAAAGGAAAGGGTGGTGGGAAAGGAAAGGGGGGA
GCCAAAGGGAAGGGTGGTGGCAAAGGAAAGGGGGGCAAGGGCAAGGGAGGGAAGGGAAAG
GGGGGCAAGGGCAAGGGTTAA

>FGENESH: 13 2 exon (s) 600023 - 600454 126 aa, chain -
MQLTRSLSTALVALLLSSIATGHRIPAQSEELQLRDAAPAEVNETGTPPVVLPVDDTLA
DVIVDETEHGSVLGRAVHPRQLGKGKGGGKGKGGGKGKGGAAGKGGGKGKGKGKGKGK
GGKGKG

>FGENESH:[mRNA] 14 5 exon (s) 617192 - 619590 1512 bp, chain +
ATGACACCCGACGTTGACAAACCAACCGCACAAATCCCAATCTACAAAAGCAATTATCC
GTCGAGCGAGAGGAGAAGGAGCTGAAGGAAGCTCAATACCAGTTCAGAATTCAGGAACTG
CAGGATGAAATCAACAGTCTTCGGGACAACGAGCACGAAAGCATCAGCACCGGCTGTCTC
CAACCTGAACCTGGCACGACAAGTGTCAACCGGGAAGACATTGTGGTGAGGGCGATGCTC
CGTGGAACAAGTCCAGCTATGCTACATCAAGAGGGGACCATTGCCTTGCCACTGTCTGAA
TCTCCCAGGTTGTCTGTGTCTCATTCGGAGGATCATTATGAATGGAAAGACAACATAACG
GCCTTGGCGCTGACAAGCCAGGGTGAAGACACTCCGAAAGTAGCCTACAAAGTTGAGGAG
GGAAGTCAGAACGATGAGTCCGATTTTGACGAGGTTGACTACCGCATCCCTATGAAAGGA

AAGGAAAAGTGGAAAGCGGCCGTGACAAGCGAAAGATACAAGTATCGCGAACAGAAGGAC
CGAGAATATCGTGAGGCCTTGAACAAACAACATGTCGATGGCAGTGATCGCATTTCTTAGG
ATGGATGAGCTGGTCGCTGAAGGGAATCAGCCATGGAGTACATTCAATATGAGGCATACG
TTGAAGGCCACTACTGCCCATGACATTCCGTTACAGAGCTCTAAATCGCACCCCGTGGAG
AGCCATGACGTCCCCCTCAGCGATCATGATTGGATATCTGGGAAACATCCAGACGATCCA
AGGGCTGAAGATCGTTTGGCGCCGGAAGATGTGGATGTGAAGCTTGCACCCTTGAAGGAC
GACACTGCCATGGGTTCCGTACCTGATTTAGGATATGGATTGCCCAGGGAATTGTCTATT
AGGCCCCAAAACGAGTCAAAGACGGACGATGGCAATATACAGGAAGATCAGTCTGATAAT
CAGACAGTTTATTTCGGACGATGGCAGCATTTGATGGTGACATCCTCAATGTCTGCAAGACT
GAGCTGGCCGATTCCCTTGCCAATCATATCCGCCAGCTGGAGGTAGGACCGGAAGGCTAT
GCCAACATCACCAGGAAGCTACCCCGTTGCTCAAAGCCTTCGCCTTGAGAGTAGGAATC
CAGGCTCATCGCGGATGCCGAGGGATGCTATGTTCTTTGTGCACAAGTATCGCGACGAAG
CCGGCATCAGAATATAATGGGACTAGCACTGAAGCCCTGGGATCACGGATCATAAACTGG
ATTCAACATGATGAAGACAGTGACAGCACTGGACTCGAGCAGCAACCTTCCAAAGAGACA
CCAGATGAACTACCAGTTGAAGTTGAAGCCGACGGAATTAACCTTCCTGCCGGACGACCAC
CAAGGATTGGCCACCAGAGAAACCATCATTCATCCAACCTTTGGAGAACACAGCGGTGTA
TCCTGGTTGCTGGCACTGTGGTGTGAGACCCCTAAATTATGGTCTTTTGGAATGGTCATA
GTTGCCATCTAA

>FGENESH: 14 5 exon (s) 617192 - 619590 503 aa, chain +
MTPDVKPNRTIPNLQQLSVEREEKELKEAQYQFRIQELQDEINSLRDNEHESISTGCP
QPEPGTTSVNREDIVVRAMLRGTSPAMLHQEGTIALPLSESPRLSVSHSEHDHYEWDNIT
ALALTSQGEDTPKVAYKVEEGSQNDESDFDEVDIRIPMKGKEKWKA AVTSERYKYREQD
REYREALNKQHVDGSDRILRMDELVAEGNQPWSTFNMRTLKATTAHDIPLQSSKSHPVE
SHDVPLSDHDWISGKHPDDPRAEDRLAPEDVDVKLAPLKDDTAMGSVPDLGYGLPRELSI
RPQNESKTDDGNIQEDQSDNQTVYSDDGSIDGDILNVCKTELADSLANHIRQLEVGPEGY
ANITRKLPLPKAFALRVGIQAHRGCRGMLCSLCTSIATKPASEYNGTSTEALGSRIINW
IQHDESDSDSTGLEQQPSKETPDELPVEVEADGINFLPDDHQGLAHQRNHHSSNFGEHSGV
SWLLALWCETPKLWSFGMVIVAI

>FGENESH:[mRNA] 15 2 exon (s) 735850 - 736151 246 bp, chain -
ATGACGGAGGATTTGCATCGCGATATTACCGAACGACTCCGCTGTCTCGAACTCCAGATC
CGGATCACAAGCCATATGTTTCATTGGAGTGGCACAGAATGCGGGGGATGACCCCAACAT
CTCGTCAAAGTTAAAGACGAGATGCTTGGGAAGTTGCAGGAGATGAGATATGAGGAGGAA
CGTCTGGCCCGGAGAGGCTAGCTGCGCTCAAACAAAGAGTGCCATCTGCGGGTAATTCT
GATTAG

>FGENESH: 15 2 exon (s) 735850 - 736151 81 aa, chain -
MTEDLHRDITERLRCLQLIRITSHMFIGVAQNAGDDPTNLVKVKDEMLGKLQEMRYEEE
RLARERLAALKQRVPSAGNSD

>FGENESH:[mRNA] 16 1 exon (s) 741563 - 742711 1149 bp, chain -
ATGTCAGCTCCATTACTGATGCACCCTGCTGAGCCTGCCACCGCCGACAACACCAAGCCA
AGGCTAGCTTGTCCCTTCTTCCGTTATGATCCATGTCGCCATTACGCGTGCGCCAGTTAC
GAGCTGAAGGGCTTCGAGGCGGTCAAGAAGCACCTCGAGAGGAAACACATCCTGAAGAAT
CACTGCGCCCGTTGCTTCAGGTCGTTTGAAAGTGAGGATGCAAGAAACAACCACATCGTG
AGCGAGTGCTGCTCAATCGCGCTTGGCCGCGACGAAATAACATACGACGAATGGACCAGA
GCGCGGCGGTGCCCTAGAACGAAGTCCTGTGAAGTGAAGTGGAAGTGGTTGTGGACGACA
TTCTTCAAGCTCCCAGCACTGCCTCGAGAGCTTGTCTATTTTCAAGATGCTGTCGTGGAG
GCCAAAACGTTTTGATCGACCCTGTTACCATACAGTCAGTTCTCAAGGCGCGACTGCAC
CTTGATCAACAGGAAATTTTCATCAGTAGCCGACGAGGTTGCGGAAGCCTTGCTCCGTAAA
AATTCCGGTGCAAGACCTTATCGCGTCTGCGACAGCGAGGGTGGCGGTGACAATGGGATA

CCGGCTAACTTGAAAGCCTCGGGGTATGGGTCTATGGGTGGAGGGGCGCAGAAATGGAA
GCAGAGGCCGTTGCTTTTGCCCTTCCACCAGCGCGACACGCATTGCTTCCAGAAGAACCA
TGTCTCCCAATCATCGGAGAATCTTCTCCTCACCCCTGCCGCTGCGGTACAGTCTGTACCC
CCTCTGCCAACCAGCTTTAGCCTCGGACCGATATTGGTACCTCAACAACCAGCGTCCACC
AGCGGCGGGGGCCCTGAAACAAACACCTTCGACGCTTGGCGAACCGTGTGTTTGGTCCCT
TGGGCGACCGCGGATGGGATCTTGGCAAGGTTGATGGAAGACCCGATTTTCATGGTTTAAA
CCGGATGGTCCCAAGTGGAGTGACGTTTACGACCACATCGACCGGGATGCTCTGAGGAAG
TTCTGGGGCCCTTGGAACACACCGGCAGTACAGGTTTTCGATACCGATCCGGTCCACCCAT
GTCCAAAGCCTGGCCGCAATAGAATCCAAGCTGTTTCGATTTTCGAGGTCGCAGGCATCCGG
CCTTCATAG

>FGENESH: 16 1 exon (s) 741563 - 742711 382 aa, chain -
MSAPLLMHPAEPATADNTKPRLLACPFPRYDPCRHYACASYELKGFEAVKKHLERKHILKN
HCARCFRSFESEDARNNHIVSECCSIALGRDEITYDEWTRARRCPRTKSCVKKWKLWTT
FFKLPLALPRELVYFQDAVVEAKNVLIDPVTIQSVLKARLHLDQQEISSVADEVREALLRK
NSGARPYRVCDSEGGGDNIGIPANLKASGYGSMGGGAAEMEAEAVAFALPPARHALLPEEP
CLPIIGESSPHPAAAVSPVTPPLTSFSLGPLVLPQQPASTSGGGPETNTFDWRTVCLVP
WATADGILARLMEDPISWFKPDGPKWSDVYDHIDRDALRKFWALGNTPAVQVSIPIRSTH
VQSLAAIESKLFDFEVAGIRPS

>FGENESH:[mRNA] 17 1 exon (s) 743588 - 744232 645 bp, chain -
ATGGACACCAAGGACGAAGACTCAGCCCAACAACAATCATCACCACTCCTCCCATATCA
AACCACCCACCATCATCCAGACCCAGAACCCCAATCCTCCTCAAACCTAGAAACAAACCTC
CCCCTCGTACACACCAGCTCAACCCCCCGAGACGACCCCCCAAGAAACCTGGGACTACCCA
ACCTCCCTCCGCCAACTCACCGCCCTCCTCCTCTTCACCCTCCAACTCCTCATCCTCATA
ACTTACCACCCCAGCTTCTCCTCCTCCTCCCCATCCCCGGCCCCCTATCCAACCACCAC
TGCTCCTACTAGCCGACACGATCATCACCTGTCTGGCAATCATAATATCGAGTTATGTC
CACTTTTGCATCGCCAGCCTGGACTGTGAGCTACTAGAACAGGGTTGGAAGCCCGTATAC
TTTTACATCATGGCCGCGGACGAGACGGTGATTTTGCTGGCGGCGGCGAGCTCAGGATTG
GAGAATGTTTGCTCGTGGGGGTTGTTTGTGTGACGGTGGGGAGTTGGTATGTGGGTTGG
AGGTTGGGGGCCGTGGAGGTGTTGAGTAGGAGGTTGTTTAGGGCCGAGGGTTGGGAGTTT
GGGCAGGGGGAGGGGGAGGAGGGGGAGGGGTTTGCGGGTGGTGTAG

>FGENESH: 17 1 exon (s) 743588 - 744232 214 aa, chain -
MDTKDEDSAQQQSSPLLPISNHPPSSRPRTPIILLKLETNLPLVTPAQPPETTPQETWDYP
TSLRQLTALLLFTLQLLILITYHPSFLSLPIPGPLSNHHCLLLADTIITCLAIIISSYV
HFCIASLDCELLEQGWKPVYFYIMAADETVILLAAASSGLENVCSWGLFVVTVGSWYVGW
RLGAVEVLSRRLFRAEGWEFGQGEEGEGRGLRVV

>FGENESH:[mRNA] 18 4 exon (s) 758385 - 758796 195 bp, chain +
ATGGCTTGACTCCACGGCAGGCAACCCTCAGAGTTTGCCCTTGTTTCATGAGGCACTC
CCTCGCGATATCCACTTGCCTACTTGTATACACGCCAGCCCTAAGCGCAAGACAGTCTCT
TCGTCCGACACCAAGCCGCGGCGGTTCTTGTACACACACAAGGTGTCACAAGCGGGCCG
AGAGCTTGTGGGTGA

>FGENESH: 18 4 exon (s) 758385 - 758796 64 aa, chain +
MACDSHGRQPSEFALVHEALPRDIHLPTCIHASPKRKTVSSSDTKPRRFLHTQGVTSGP
RACG

>FGENESH:[mRNA] 19 8 exon (s) 766325 - 769826 1881 bp, chain -
ATGGTGGAGGGTGTGAGGGCATTGACAAACTTGACTGGAAAGACGATGTCGCATTCTGC
TCACTGACGGAGGATATGGAAGAGGCAGTCGGGCCGGGGACGAGGTCTTCGTCTGCTCA
AATCAAGATGGGATGACGGGCAGTTGGGAAATGATTACAAACAGTAGCTCGTTTGGAGCG
CCCCCTATCACTAGCGAACTCTTTGAGAATGCCAACGAAGAGCCCATGATAGATCCAGCA

GTACTAGGGGACACATGGAGTCAAATGAAGGCTTGGGCCACTTTATGTGGCATCAAAGAT
GATCCCATAGCACCTGGTATAGCTGAGTTGCTGGAAATCGAGGAGCAAGAAAGTGGAGAT
GGCGGCTTCTGTTGCTACGGGACTATCAGCCATGCCGAAGTGAAGCTGGTTGGTAACCTG
GCCGAGTCCAGAGACAGGCTTCTGAATAACGAGCATGTTTCAAGTCAATTTGCTGTCATCAA
CACGACGACTACTTGATGGTCATATTTTCAGATAATCACATATTCGCCCAGGTGAATGAG
GCTGTATCACAAGCTCTCACTTCGCTGTTCAACAAGTTCAAGTTTTTCGAAGTGAAGGCG
TTTGCCCAAATAGGGGAAAATACAGAGCCTCTTTTACCAGTCACACACTCCTGGCCAGGCA
AAGCTACGAGTGGACATCAACATATACGGATCTGCTGCCGATGCCGATGCCGTAGGGCTT
TATCTCGGCAGCACTGCCAAGCTGTACCTTCAAGACCCCGAATATGGCACCAGAAAACATC
GAGTATCTGAACAGGCAGTTGATTCACTTCCCCGGTTTTGAAGAACCCTAAAGTCTTTGCC
GGGCCCCGGGCGGATTTTGCTAACAAGACCAGCAAAGCCTTGCAGGGTGTGCGTTCCCAA
CGCGAACACTTTGACCAAACGCTCTCGCAAATCTTGCTGACCAGTCGCAGTCATCATGTA
CTTGTTGGTTGGAAGAAATCAAAAACGACCCCAAGACAACACTTTTCAAGGCAGCGTGTGAA
ATCCGCGCAAACCTTCGGATGGTGCCTCACAGCTACTCCCATTCAGAACCGGCTGGAAGAG
CTCGGGTCGCCCTTGCTTTCCCTACCAATCGACCAGCTACAAAACCGGGCCATGTTCAAG
AAGAAGATCATGGATGCGTCTTCGCCAGATGCACATACTATGCTCGAGCTGCCTCCGATT
GAGGAACGCTACCACTACATCACGCTCTCCCAAGAGGAAAGAAACCGCTATGACAAGACA
GCTGCTGACATGAGCAACTGGATCAATCACAAAACCGGCTTACACGTCCTGACGCCAAAT
AGCGGTGACGACAACAATGACAAGGTGGACCATTTTCGATCTATCAGGAGTCTCATCGAAA
ATCGAAGTCCTGATCCGCCACCTCCAGCAAACCCCAAGAGACACGAAGAGGTACGTCGGC
TCTGCTAGACTGGCCGAAGTCCTTGAGAACCAAGCTTACATCAACTCACCAGCATTTGTA
TTTTCTGCTGGACAAAACCTGGACCTGGTCGCACTCCATCTCACTCGGATGAAGATC
CTTCATCAACGAATTGACGGCAGGCAAAAACCTGGCAGAAAGACAGCACAAACATGAGCCGT
TTTGTGTCTGACGAGGGCACCTCCGTTCCAGTTCTGCTCACGACTACCGGTGTCGGTGCA
TTCGGGCTCAACCTCACAGCTGCTAACCACGTCTACATTCTCGAGCCCCAGTGGAACCCA
AGCGTCGAGAGTCAAGCCCTCAGTCGTGTTGCCCCGCGTGGTCAGAAGAAGACTGTCCTA
GTCACAAGATACCTGGTTTCATGGCACCGTGGAGATTCTCCGCAAATGCGCCTGGCGGAG
GCAGGATGGGCAACTCCCTAG

>FGENESH: 19 8 exon (s) 766325 - 769826 626 aa, chain -
MVEGVRAFDKLDWKDDVAFCSLTEDMEEAVGPGDEVFVCSNQDGMTGSWEMIHNSSSFGA
PPITSELFENANEEPMIDPAVLGDTWSQMKAWATLCGIKDDPIAPGIAELLEIEEQESGD
GGFCCYGTISHAEVKLVGNLAESRDRLNNEHVQSFVAVIKHDDYLMVIFSDNHIFAQVNE
AVSQALTSLFNKFKFFFEVKAFAQIGKIQSLFYQSHTPGQAKLRVDINIYGSAADADAVGL
YLGSTAKLYLQDPEYGTENIEYLNRLIHFPGFEEPKVFAAGPGADFANKTSKALQGVRSQ
REHFDQTLSQLLLTSRSHHVLVVGRNQKRPQTTLFKAACEIRANFGWCLTATPIQNRLEE
LGSPLAFLPIDQLQNRAMFKKKIMDASSPDAHTMLELPPIEERYHYITLSQEERNRYDKT
AADMSNWINHKTGLHVLTPNSGDDNNDKVDHFDLSGVSSKIEVLIRHLQQTTPRDTKRYVG
SARLAEVLENQAYINSPSIVFSCWTKTLDLVALHLTRMKILHQRIDGRQKLAERQHNMSR
FVSDEGTSVPVLLTTTGVGAFGLNLTAANHVIILEPQWNPSVESQALSRVARRGQKKTVL
VTRYLVHGTVEILRKMLAEAGWATP

>FGENESH:[mRNA] 20 2 exon (s) 858154 - 858417 159 bp, chain +
ATGCCTCCAAAAATTTTGAGCGAGAAGCATGAAGCATTGCGGCAAGACGTGAACGCAAAG
ATGAACAAGTTTGAAGTGAATCAATCGCAAGGTGGACGACCACATGCAGTTGCGGGAT
ATGTTTCATGATCGTCGTGAGGCTACTTCGTTTAGTTGA

>FGENESH: 20 2 exon (s) 858154 - 858417 52 aa, chain +
MPPKILSEKHEALRQDVNAKMNFELRINRKVDDHMQLRDMFHDRREATSFS