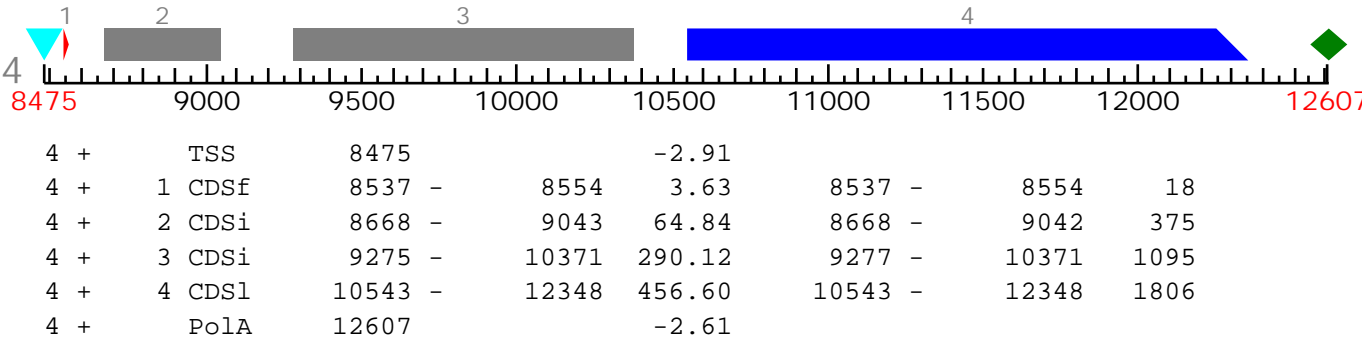
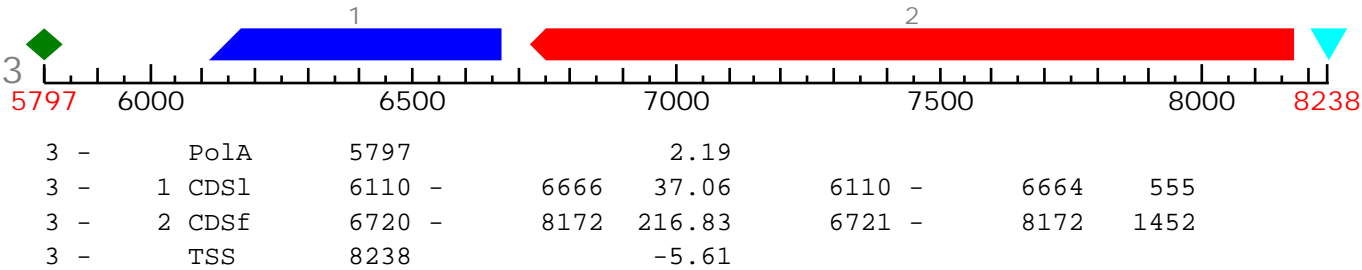
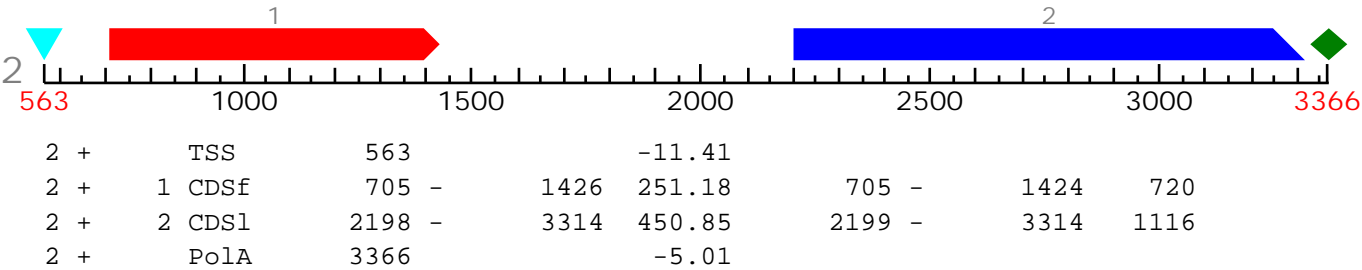
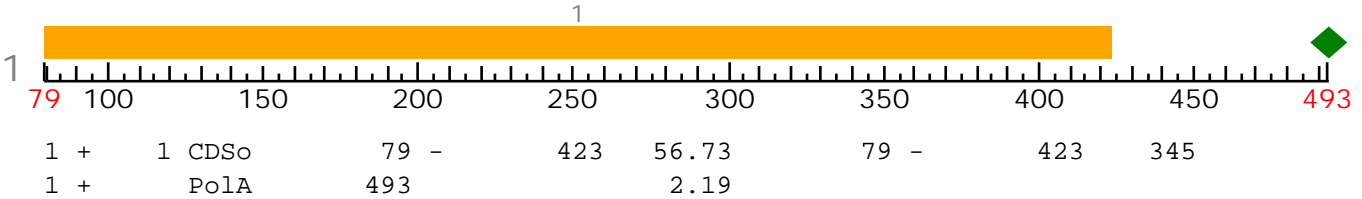
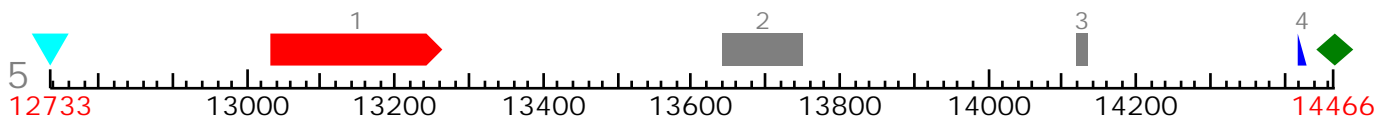


FGENESH 2.6 Prediction of potential genes in Triticum genomic DNA
Seq name: region6
Length of sequence: 15001
Number of predicted genes 5: in +chain 4, in -chain 1.
Number of predicted exons 13: in +chain 11, in -chain 2.
Positions of predicted genes and exons: Variant 1 from 1, Score:1813.750195

CDSf CDSi CDSl CDSo PolA TSS





5 +	TSS	12733			-7.61			
5 +	1 CDSf	13030 -	13262	22.47	13030 -	13260	231	
5 +	2 CDSi	13640 -	13749	14.97	13641 -	13748	108	
5 +	3 CDSi	14117 -	14132	3.67	14119 -	14130	12	
5 +	4 CDSl	14416 -	14428	1.35	14417 -	14428	12	
5 +	PolA	14466						-4.51

Predicted protein(s):

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>FGENESH:[mRNA] 1 1 exon (s) 79 - 423 345 bp, chain +
ATGGCCGGTGAACGAGACGCATTTTCAGCGCACGCAAGGTACAGGATGGGCCGGGGACAC
GGCTGGTTGGACGTAGTACAGCGAGAGACCGCCGAAACAGGGCCGGTGACACGCGTCGCG
CATCGGGGGCCTCCTCCGAGCCCGACGTGGCCGCGCGCGCCGCCCGCGCCAGCGCACACG
TCGCCGTCCACACGACGCTTCGAGGCCGGTTCACGCGTCGCCGTCCATTCCAGGCCCC
GGCCCCCGCGCCCGCGCCGCACCGCCTCACGTTGCCTTCACCGGCGGAGCACGCGCCACG
TCCGCCCCCACCGCGCGCGCGCCACCTTTCATCGCCACTATTTAA
>FGENESH: 1 1 exon (s) 79 - 423 114 aa, chain +
MAGERDAFSAHARYRMGRGHGWLDVVQRETAETGPVTRVAHRGPPPSPTWPRAPPAPAHT
SPSHTTLRGRFTRRRPFPFGPGRARAAPPHVAFTGGARATSAPTARAPPFIATI
>FGENESH:[mRNA] 2 2 exon (s) 705 - 3314 1839 bp, chain +
ATGGCCCTCAACCTGACCCACCAGACCGGCGCTGCGGCCATCGCGGCCACGCCGGCGCCG
GGCGCGCGCGCTTCGGTGTTCGCGGCGGCCTCGCCCGCCGCCGCCGCCGCCGGCTCC
GCCGTGGCGCCGGCGCAGGCGACCAGCCTGAGGATGCAGACGCAGCTGGTGGAGCCCGCG
CAGCCGCAGGCGCCGGAGATGTTCCAGGCCATGGCGCCCGACCAGCAGCAGCAGGGCGAG
GCCGCGCACCCGGACGCGGGCGGCGAGGAGGCACGCAAGGTGGGCGTGCCGGTGTTCGTG
ATGATGCCGCTGGACACGGTGC GCAAGGACGGCAGCGCGCTGAACCGGCGCAAGGCGGTG
CAGGCGTCCCTGGCGGCGCTCAAGAGCGCCGGCACGGCCGGCATCATGGTGGACGTGTGG
TGGGGCATCGCCGAGAGCGAGGGCCCCGGCCAGTACAACTTCGCCGGCTACATCGAGCTC
ATGGAGATGGCCAAGAAGGCCGGGCTCAAGGTGCAGGCCGTCATGTCTTTCCACCAGTGC
GGCGGCAACGTTCGAGACTCAGTCAAGTACGTCGTGCTCTGCTCCCTCTTCTCCATCCAG
TCCTCTGTCTATCCAAGTACACATATACGTACATGCATGCTGATCTTGATCATCCTTGCG
TACATTCTTGATATTTTTCATGATTCATGTACCATCGCATCTACGGGATGGACGCGTAC
ATCATACCACTTCCGAAATGGGTAACGGAGGAGATGGACAAGGACCAGGACCTGGCGTAC
ACGGACAGGTGCGGCCCGCCGGAACACGAGTACCTCTCGCTGGGCGCCGACACGATCCCG
GCCCTCAAGGGCCGCACCCCATCCAGTGCTACGCCGACTTCATGCGCGCCTTCCGCGAC
CACCTCGCGCCCTACATGGGCAACACCATCTGCGAGATCCAGGTGCGCATGGGCCCCGCC
GGCGAGCTCCGCTACCCCTCCTACCCGGAGAGCAACGGCACCTGGTCCTTCCCCGGCATC
GGCGAGTTCCAGTGCTACGACCGCTACATGCGCGCCAGCCTCAAGGCCGCCGCCGAGGCG
GTGGGCAGGCCCCGAGTGGGGCAACGCCGGCCCCGAGGACTCGGGCAGCTACAACCAGTGG
CCAGAGGACACCGGCTTCTTCCGCCGCGAGGGCGGCTGGAACACCGACTACGGCCAGTTC
TTCATGAGTTGGTACTCGCAGATGCTGATCGAGCACGGCGAGCGGATACTCTCCGCTGC
TCCTCCGTCTTCACGGGTACCCCTGGGGTCAAGGTCTCCGTCAAGGTGGCCGGCATCCAC
TGGCACTACGGCACCCGCTCCACGCGCCCGAGCTCACCGCCGGCTACTACAACACCAGG
AACCACGACGGGTACCTGCCCATCGCGCGCATGATCGGTGCGCCACGGCGCCGTGCTCAAC
TTCACCTGCGTGCAGATGCGCAACCACGAGCAGCCGACGCGCAGTGCATGCCCCGAG
GCGCTCGTGAGCCAGGTGGCCAGCGCCGCCAAGGAGGCCGGAGTGGGCCTCGCCGGGGAG
AACGCCCTACCCAGGTACGACGAGACGGCGCACGACCAGGTGCTGGCCACCGCGGCGGAG

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AAGGCTGAGGAGGACCGCATGGTCGCCTTCACCTACCTTCGCATGGGCCCCGACCTCTTC
CAGCCCGACAACCTGGCGCCGCTTCGCCGCGTTCGTCAAGCGCATGACGGAGACCGGCGTC
AGGGACGTGAGCCGGGAGCAGGTGGAGCGCAGGCTCAGGGCGTCGCCCACGCCACCCAG
GGCGTCATCCAGGAGGCCGCCGTCGCCCTCTGCAACTAA

>FGENESH: 2 2 exon (s) 705 - 3314 612 aa, chain +

MALNLTHQTGAAAIATPAPGARASVFAAASPAAGSAVAPAQATSLRMQTQLVEPA
QPQAPEMFQAMAPDQQQQGEAAHPDAGGEEARKVGVVPVFVMMPLDTRKDGSA LNRRKAV
QASLAALKSAGTAGIMVDVWWGIAESEGPQYNFAGYIELMEMAKKAGLKVQAVMSFHQC
GGNVGDSVKYVVLCSLFSIQSSVYPSTHIRTCLILILAYILVFFHDSMYHRIYGM DAY
I IPLPKWVTEEMDKDQDLAYTDRCGRRNIEYLSLGADTIPALKGRTP IQCYADFMRAFRD
HLAPYMGNTICEIQVGMGPAGELRYPSTPESNGTWSFPGIGEFQCYDRYMRASLKAAAEA
VGRPEWGNAGPEDSGSYNQWPEDTGFFRREGGWNTDYGQFFMSWYSQMLIEHGERILSAC
SSVFTGTTPGVKVS VKVAGIHWHYGTRSHAPELTAGYYNTRNHDGYLP IARMIGRHGAVLN
FTCVEMRNHEQPQDAQCMPEALVSQVASAAKEAGVGLAGENALPRYDETAHDQVLATAAE
KAEEDRMVAF TYLRMGPDLFQPDNWRRF AAFVKRMTETGVRDVSREQVEREAQGVAHATQ
GVIQEAAVALCN

>FGENESH:[mRNA] 3 2 exon (s) 6110 - 8172 2010 bp, chain -

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GTTGCCATCCCCGTGCTCCCCTTCAGCACGGCGGGGCTGTTCCGGTGAAC TGAAGAGCAAG
TGGGGGCTGCGCGGACGGCTCGACTACACACCTCTCCGCAACAACCGCTTCATGCTCGAA
TTCGAGCGTGAGGGCGATCGTCAGCACGTCCTGGAAAACGGCCCATGGACACACCGTAAG
GATGCATTCTCATTGTTCCCTTTGATGGACAGGGCAAGGCGTCGGACGTACCGGTGAAC
GTCATGCCAATCTGGGCACGCATCTATGATGTGCCACCTCTCATGCTGTCAGAAGAGATC
GGGTGGAAGCTAGGTGGCCTCTTGGGAAAAGTTCTCAGGGTAGATGCGGATAAGTTTGGG
AATATTTTCTCTGAATTTCTTTGTGTAAAGAGTTGAACATAATGTAAACACTCCTCTCCTG
CGTGAGATCAGTCCTAGAGAGTTAGGGGAGAAAGAGCATATGGACCTAGAGGTCAAGTAT
GAGAGAGCCCCACGATTTTGTATGTACTGTGGGCACATAGGTCATGGGGAAAGGGACTGC
AGGCTGCCGACGGATGATCAAGCAGAGAGGTTACGGGGGCGATGAGAGCATTGCCCTAT
AAATCAAGCAAAAACAAGTGCGGCTTCGTGGTACCAGACGCTTGTAGTGCCAGACGCTTC
CTGCAC TTTGGGTCTGAGTTGGACGGGGAGGCATGGACAGCCCCGGCCAAATTGGCCTGG
GAGAAGCTAGGCAGAGACAAGAAGGTGATGCATGCTCGATCACAGGAGATGGTAAGATGC
AGGGATATTCCAGATGATGTGCTGCTGGACCCGCTGTACAAGCGGCAATCGCAGCGGTT
AGCGCGCTTAGAGTGAGCGAAGACACTGGAAATGAAGGCACCAGGAAGACGAGCATCGGC
GAGAACACAAAGATGGCTCCGGCGAAACCCGCGCTGACCACGGCTTCTACTCCAACCATA
GCCATGGCTGACGCGGACACCTCGCCATCTACACCACCGGGTACAGGGGGCGGGGGGCGAC
ATCGACAAAACCCCGCTCGCACACACCATCGAGGATGCAGCAACCCCTCCCTACCCGCCG
GGTTTCGAGCCCGACTCTGTTAAGGCCTCTCCTGTGCTGCTACTGTTA ACTCAGTAGAG
ACGGAGACAAAGTCAGGGAAGTTGCATGCACCAAAGGAACAGGTCTCAAACCAAGGCA
AAATATATTAGCCAGCTCAAGGAAAGAAAGGAACCAGGGGAGACAAATTCAGTTCTAGGA
AAAAGAGGCACGGGTGACATGGCCACATCTACTGGGGCTATGGCTAGTGCGTCTGATGTA
ACAGGGGACATGTATAAGAAACAGAGAGCTGCTGTAGAGGAAGAGGATGAGAGAGCTGTA
GGAGAGATAGGTGAGCGCCCGTCAGGAGGAATGACGATCCTATGTTGGA ACTGCCGGGA
CTGGGCCACCCCGGACAGTTCTGTGAGCTTGTGTGCCTAGTGCGCACGTACCGCCCTCT
GTCGTGTT CATCTCTGAGACGCGGCAGTGTGAGGAGAGCGTCAAAAGAATAAGATGGAGG
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TTTTGGGATGAAAGTGTTGAAATAAAATTACTCTCCTATGGTTTGAGGTATATTGATGTG
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GAGCCGTGGATGATGATAGGAGACTTCAATGAAACATTATGGCAAAGTGAACATTTCTCT
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>FGENESH: 3 2 exon (s) 6110 - 8172 669 aa, chain -

MAIFCQKNEKGQSCHPLSIKVAIPVLPFSTAGLFGELKSKWGLRGRLDYTPLRNNRFMLE
FEREGDRQHVLENGPWTHRKDAFLIVPFDGQGKASDVPVNVMPIWARIYDVPPLMLSEEI
GWKLGGLLGKVLRLVDADKFGNIFSEFLCVRVEHNVNTPLLREISPRELGEKEHMDLEVKY
ERAPRFCMYCGHIGHGERDCRLPTDDQAERFTGAMRALPYKSSKNKCGFVVPDACSARRF
LHFGSELDGEAWTAPAKLAWEKLGDRDKVMHARSQEMVRCRDIPDDVLLDPAVQAAIAAV
SALRVSEDTGNEGTRKTSIGENTKMAPAKPALTTASTPTIAMADADTSPSTPPGTGAGGD
IDKTPLAHTIEDAATPPYPGFEFDSVKASPVAATVNSVETETKSGKLHAPKGTGLKTKA
KYISQLKERKEPGETNSVLGKRGTGDMATSTGAMASASDVTGDMYKKQRAAVEEEDERAV
GEIGERPSGGMTILCWNCRGLGHPGTVRELVLVRTYRPSVVFISETRQCEESVKRIRWR
LGLKNCITHDGMGKGAGIALFWDESVEIKLLSYGLRYIDVHMRMDPHGPMWRGTFVYGEF
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LHDLGYHGW

>FGENESH:[mRNA] 4 4 exon (s) 8537 - 12348 3297 bp, chain +
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GCCAGCGTCTGCCCCGCTCTGCAGCGTGCCGCGGTACGACCTGCCGTTCCGGCGACCCACA
CCACCTCCACCTCCGCCGCCCGCCGGTGCAGCCTCAGCCAGAGACTCGTCCCATTCCC
CTCCGCCCGTGTCATCATTCTCCCGCGGCAGTCACCTCCCGTGTCATTTCTGTGCACGGTCAG
CCACCGCCACCGCCACCACGACCGACATACTCGTGGCCACGCATTCCCACGCAGGCACGA
CAGCCGCCGCCACGGCCCGTGAATCTCGTGACGCTGGCAACCGGTCACCAGCCGCTGCA
TCAAACGAAGCAGTTGTTCATCAAGACGCGAAGCGAGTACCCGGCCATCGCCATGGATTTG
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CACAGTATGAGCGGGCAAAGTTGACGCTGTTGAAGCAGGCCATGCGGTTCTGTCATCGCC
AATCTCGGCCCGACGACCGCCTCTCCGTGCTGTCCTTCAACACGAAGGCGCGCCGGGTG
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GACCAGCGCCGGCACAGGAACGCCGTCTCGAGCGTCGTGCTCCTCTCTGATGGCCAGGAC
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ATCGGCGGGCTGCTCTCTGTCTGTGTCAGGAGGCTCGCATCGCCGTCGCGTGCCTGCAC
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CAAGAGATGCGCGGGCGCGTGTTCGAACCGACAGAGCTACGCGTTGTTCGGGTTCGGGCGTAC
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ACGTTCTCGTTCATCGAGAACGAGGCGGTGATCCAGGACGCGTTTGCCAGTGCATCGGC
AGGCTGCTCTCCGTCTGTGGTCCAGGGGGCTCGCATCGCCGTGCGGTGCGTGCACGCCGGG
GTCCGTCTCATGTTCGGTGAAGTCTAGCAGTTATGAGAGCCGCATCGACGAGGACGGCCGC
GCCGCCACGGTCTGTATCGGGGAACTCTACGCCGAGGAGGAGAGGCGTTTCTTGCTGTCT
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TTCAGCTACAGAAACGCGACGACCGGCGCGGACGTGAGCGTGACAACGGAGGACACAGTG
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CGCATCCGGGTGGAGGCGGCAGAGGACTTCACGGCGGCGAGGGCAGCGCGGAACGGGGC
GACCACCGGGAGGCGGTGAAGATACTCAACAACCGGCAGCGTGCAGTGGCGCTGTCACAG
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GGGCGCGTGGCGAACCGGCAGAGATACGCGCGGCCGGGTCCGGCGTACATGCTTTAG

>FGENESH: 4 4 exon (s) 8537 - 12348 1098 aa, chain +
MEIPDQTNPCAICLSGMGAGGGQATFTAECSTHFHSSCISASVCPLCSVPRYDLPFRRPT
PPPPPPPPVVRPQPETRPPIPLRPCIILPRQSPPVHFVHGQPPPPPPRPTYSWPRIPTQAR
QPPPRPVNLVHAGNRSPAAASNEAVVIKTRSEYPAIAMDLSSDNFAVLVHVQAPGMTDIT
AAGGDAPRAPVDLVTVLVDVSHMSGQKLTLKQAMRFVIANLGPDDRLSVVSFNTKARRV
TRLTRMSEAGKALSVSAVESLTAGGCTDIAEGLRMAAMVLDQRRHRNAVSSSVLLSDGQD
NYIMMRHQESSGVQANDYEDLVPPTFARTGADGEWSASIHTFGFGNDHDATAHVIAEAT
GGTFSFVENEAMIQDAFAQCIGLLSVVVQEARIAVACVHPGVRVMSVKSGSYESRIDED
GRAATVWVGELYADEERRFLILITVPRAEATDGDTTALLNVSFSCRDAATGMDVNVSAKD
TLVARPEHAVIDAKRSVEAELQEMRGRVSNRQSYALSGRAYMLAGISAHQQQRATSRQMNL
VEEMSVFEMAALVAAPPVKLASNEATLSYATPAMRAMLLRSRRAREASAEQGGQLQAE
YTGSSKHGQPTPPLTSSCPRLPTQLRPPPPPPMRIGHARPPTVVFDDDEQGGPASGPPAD
NRSPAAASNEAVVVKTRSEYPAIARDSSSENFAMLVHVQAPGMTDIMAVGGDASRAPVDL
VTVLVDVGGSMSGYKLALLKQAMRFIIANLGPDDRLSVVSFSSVARRRTRLTLMSETGKAL
SVSAVESLTAGGCTDIAEGLHMAAMVLDQRRHRNAVSSSVLLSDGPGSSGVRANNYEELV
PPSFARTGADGEWSAPIHTFGFGNDHDTAAMHAIADATGGTFSFIENEAVIQDAFAQCIG
RLLSVVVQGARIAVACVHAGVRLMSVKSSSYESRIDEDGRAATVCIGELYAEERRFLLS
LAVPRAEATDGDATLVKVVSFYNATTGADVSVTTEDTVVARPEHAPNASERSVEVERE
RIRVEAAEDFTAARAAERGDHREAVKILNNRQRAVALSQLSRDDDPVIMALEAEELWGM
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>FGENESH:[mRNA] 5 4 exon (s) 13030 - 14428 372 bp, chain +
ATGCCGGTGAATGGGAATATGGCCATGTTCAAGCGAGGACACCGGGCTCAGCTGCTTGTG
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AAGATGGTGAAGGAGGGTAGGGAGCTAAGAGGATACTGGTACCTGCTCCAGCGTGGAGC

TGCGCAATGCATGCGCTGTTGGAGTTAACCACGTCGGAGAGTCCATGCCCCGGTCTATACC
GCCGTTGAGGTCGGACCAGCGCCAACAGCGATGGTGGCCGGGCTCGTCAAAGTGCAGGTG
GCGATGGCGTCAGTGGGGCGGCGCATCCCCCGGGACAGCGAACGTGGGTCCTTCGTAAGG
AAAAAAAAGTAG

>FGENESH: 5 4 exon (s) 13030 - 14428 123 aa, chain +
MPVNGNMAMFKRGHRAQLLPETLVENMLFLAVGMRVELNKMVKEGRELRGYWYLLPAWS
CAMHALLELTTSSESPCPVYTAVEVGPAPTAMVAGLVKVQVAMASVGRRIPRDSERGSFVR
KKK