

FGENESH 2.6 Prediction of potential genes in Triticum genomic DNA

Seq name: region6

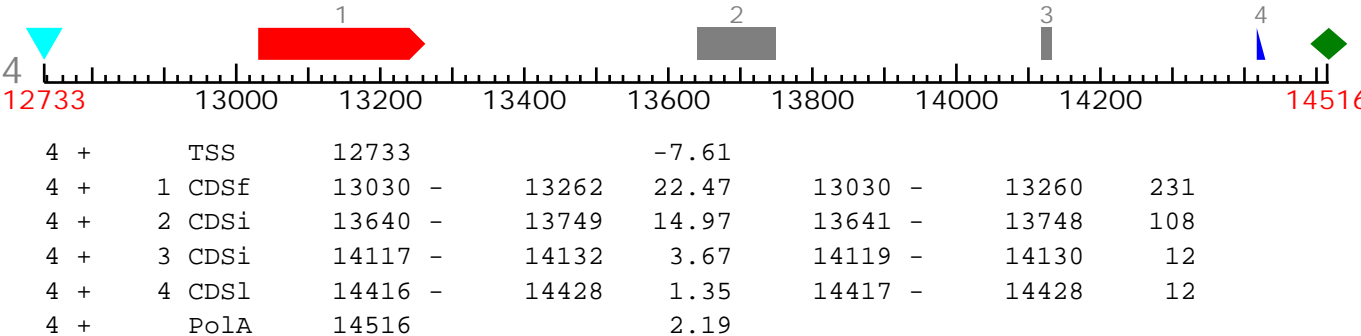
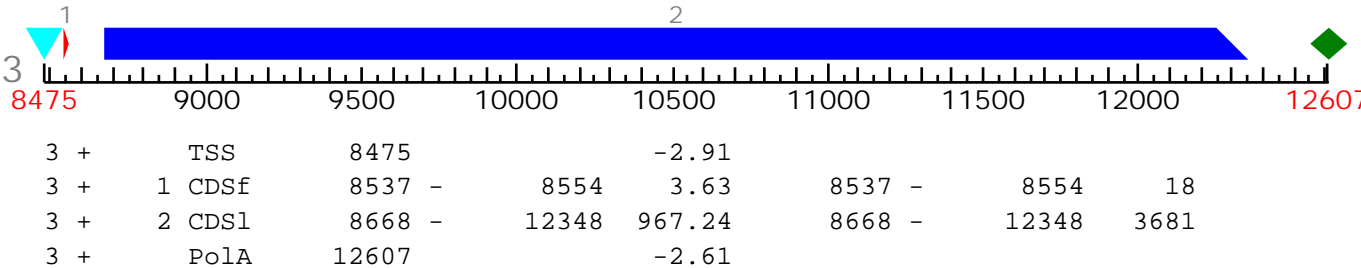
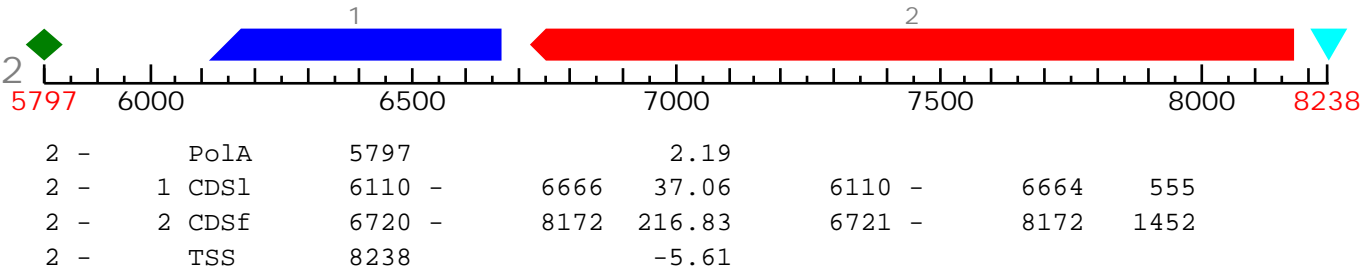
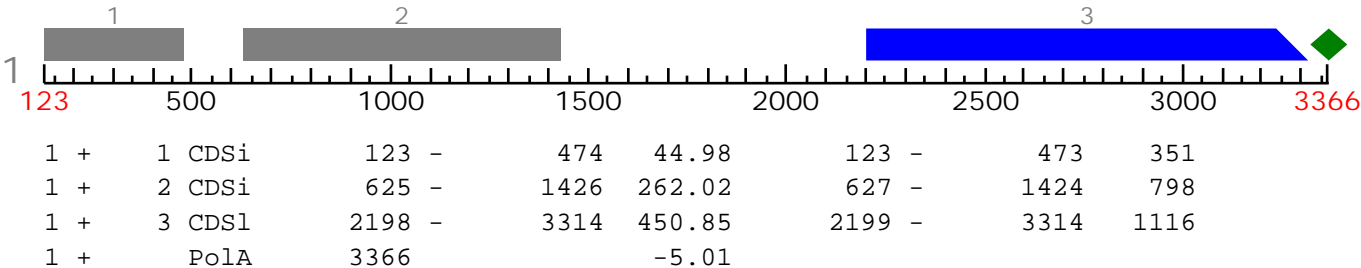
Length of sequence: 15001

Number of predicted genes 4: in +chain 3, in -chain 1.

Number of predicted exons 11: in +chain 9, in -chain 2.

Positions of predicted genes and exons: Variant 1 from 1, Score:1986.816602

► CDSf ■ CDSi ▲ CDSl ■ CDSo ◆ PolA ▼ TSS



Predicted protein(s):

>FGENESH:[mRNA] 1 3 exon (s) 123 - 3314 2271 bp, chain +
GATGGGCCCGGGGACACGGCTGGTTGGACGTAGTACAGCGAGAGACCGCCGAAACAGGGCC
GGTGACACGCGTCGCGCATCGGGGGCCTCCTCCGAGCCCGACGTGGCCGCGCGCGCCGCC
CGCGCCAGCGCACACGTCGCCGTCCCACACGACGCTTCGAGGCCGGTTCACGCGTCGCCG
TCCATTCCCAGGCCCGGCCCGCGCCCGCGCCGACCGCCTCACGTTGCCTTCACCGG
CGGAGCACGCGCCACGTCCGCCCCACCGCGCGCGCGCCACCTTTCATCGCCACTATTTA
ACCCCCATGCCCGCCTCCTCCATTGTCAGCCCCACCCATTTCTTCCCTTCGCGTCCGTC
GTCGTCGTCCAAGCTCTCCGTGCGACGCGCGCACGTGATCCGGCCCAGCCCGTCGTGTC
GTCGTCGTCCACATGGCCCTCAACCTGACCCACCAGACCGGCGCTGCGGCCATCGCGGCC
ACGCCGGCGCCGGGCGCGCGCGCTTCGGTGTTGCGGGCGGCCTCGCCCGCCGCCGCCGCC
GCCGCCGGCTCCGCCGTGGCGCCGGCGCAGGCGACCAGCCTGAGGATGCAGACGCAGCTG
GTGGAGCCCGCGCAGCCGCAGGCGCCGGAGATGTTCCAGGCCATGGCGCCCGACCAGCAG
CAGCAGGGCGAGGCCGCGCACCCGGACGCGGGCGGCGAGGAGGCACGCAAGGTGGGCGTG
CCGGTGTTCTGTGATGATGCCGCTGGACACGGTGCGCAAGGACGGCAGCGCGCTGAACCGG
CGCAAGGCGGTGCAGGCGTCCCTGGCGGCGCTCAAGAGCGCCGGCACGGCCGGCATCATG
GTGGACGTGTGGTGGGGCATCGCCGAGAGCGAGGGCCCCGGCCAGTACAACCTTCGCCGGC
TACATCGAGCTCATGGAGATGGCCAAGAAGGCCGGGCTCAAGGTGCAGGCCGTCATGTCT
TTCCACCAGTGCGGCGGCAACGTCGGAGACTCAGTCAAGTACGTGCTGCTCTGCTCCCTC
TTCTCCATCCAGTCCTCTGTCTATCCAAGTACACATATACGTACATGCATGCTGATCTTG
ATCATCCTTGCGTACATTCTTGTATTTTTTCCATGATTCCATGTACCATCGCATCTACGGG
ATGGACGCGTACATCATACTTCCGAAATGGGTAACGGAGGAGATGGACAAGGACCAG
GACCTGGCGTACACGGACAGGTGCGGCCCGCCGGAACCTACGAGTACCTCTCGCTGGGCGCC
GACACGATCCCGGCCCTCAAGGGCCGCACCCCATCCAGTGCTACGCCGACTTCATGCGC
GCCTTCCGCGACCACCTCGCGCCCTACATGGGCAACACCATCTGCGAGATCCAGGTGCGC
ATGGGCCCCCGCCGGCGAGCTCCGCTACCCCTCCTACCCGGAGAGCAACGGCACCTGGTCC
TTCCCCGGCATCGGCGAGTTCCAGTGCTACGACCGCTACATGCGCGCCAGCCTCAAGGCC
GCCGCCGAGGCGGTGGGCAGGCCCGAGTGGGGCAACGCCGCCCGAGGACTCGGGCAGC
TACAACCAGTGGCCAGAGGACACCGGCTTCTTCCGCCGCGAGGGCGGCTGGAACACCGAC
TACGGCCAGTTCTTCATGAGTTGGTACTCGCAGATGCTGATCGAGCACGGCGAGCGGATA
CTCTCCGCCTGCTCCTCCGTCTTCACGGGTACCCCTGGGGTCAAGGTCTCCGTCAAGGTG
GCCGGCATCCACTGGCACTACGGCACCCGCTCCCACGCGCCCGAGCTACCGCCGGCTAC
TACAACACCAGGAACCACGACGGGTACCTGCCCATCGCGCGCATGATCGGTGCCACGGC
GCCGTGCTCAACTTCACCTGCGTCGAGATGCGCAACCACGAGCAGCCGCAGGACGCGCAG
TGCATGCCCCGAGGCGCTCGTGAGCCAGGTGGCCAGCGCCGCCAAGGAGGCCGGAGTGGGC
CTCGCCGGGGAGAACGCCCTACCCAGGTACGACGAGACGGCGCACGACCAGGTGCTGGCC
ACCGCGGCGGAGAAGGCTGAGGAGGACCGCATGGTTCGCCTTCACCTACCTTCGCATGGGC
CCCGACCTCTTCCAGCCCGACAACCTGGCGCCGCTTCGCCGCGTTCGTCAAGCGCATGACG
GAGACCGGCGTCAGGGACGTGAGCCGGGAGCAGGTGGAGCGCGAGGCTCAGGGCGTCGCC
CACGCCACCCAGGGCGTCATCCAGGAGGCCGCCGTCGCCCTCTGCAACTAA

>FGENESH: 1 3 exon (s) 123 - 3314 756 aa, chain +
DGPGRTRLVGRSTARDRRNRAGDTRRASGASSEPDVAARAARASAHVAVPHDASRPVHASP
SIPRPRPPRPRRTASRCLHRRSTRHVRPHRARATFHRHYLTPMPASSIVSPTHFLPFASV
VVVQALRRTRARDPAQPVVVVVHMALNLTHQTGAAAIAATPAPGARASVFAAASPAAAA
AAGSAVAPAQATSLRMQTQLVEPAQPQAPEMFQAMAPDQQQQGEAAHPDAGGEEARKVGV
PVFVMMPLDTRKDGSLNRRKAVQASLAALKSAGTAGIMVDVWWGIAESEGPQGQYNFAG
YIELMEMAKKAGLKVQAVMSFHQCGGNVGDsvKYVVLCSLFSIQSSVYPSTHIRTCLIL
IILAYILVFFHDSMYHRIYGMDAYIIPLPKWVTEEMDKDQDLAYTDRCGRNRYEYLSLGA
DTIPALKGRTPIQCYADFMRAFRDHLAPYMGNTICEIQVGMGPAGELRYPSPYESNGTWS

FPGIGEFQCYDRYMRASLKAAAEAVGRPEWGNAGPEDSGSYNQWPEDTGFFRREGGWNTD
YGQFFMSWYSQMLIEHGERILSACSSVFTGTPGVKVSVKVAGIHWHYGTRSHAPELTAGY
YNTRNHDGYLPIARMIGRHGAVLNFTCVEMRNHEQPQDAQCMPEALVSQVASAAKEAGVG
LAGENALPRYDETAHDQVLATAAEKAEEDRMVAF'TYLRMGPDLFQPDNRRFAAFVKRMT
ETGVRDVSREQVEREAQGVAHATQGVIIQEAVALCN

>FGENESH:[mRNA] 2 2 exon (s) 6110 - 8172 2010 bp, chain -
ATGGCAATTTTCTGTCAAAAAAATGAAAAAGGACAAAGTTGCCATCCCCTATCAATTAAA
GTTGCCATCCCCGTGCTCCCCTTCAGCACGGCGGGGCTGTTTCGGTGAAGTGAAGAGCAAG
TGGGGGCTGCGCGGACGGCTCGACTACACACCTCTCCGCAACAACCGCTTCATGCTCGAA
TTCGAGCGTGAGGGCGATCGTCAGCACGTCCTGGAAAACGGCCCATGGACACACCGTAAG
GATGCATTCTCATTGTTCCCTTTGATGGACAGGGCAAGGCGTCGGACGTACCGGTGAAC
GTCATGCCAATCTGGGCACGCATCTATGATGTGCCACCTCTCATGCTGTCAGAAGAGATC
GGGTGGAAGCTAGGTGGCCTCTTGGGAAAAGTTCTCAGGGTAGATGCGGATAAGTTTGGG
AATATTTTCTCTGAATTTCTTTGTGTAAGAGTTGAACATAATGTAAACACTCCTCTCCTG
CGTGAGATCAGTCCTAGAGAGTTAGGGGAGAAAGAGCATATGGACCTAGAGGTCAAGTAT
GAGAGAGCCCCACGATTTTGTATGTACTGTGGGCACATAGGTCATGGGGAAAGGGACTGC
AGGCTGCCGACGGATGATCAAGCAGAGAGGTTACGGGGGCGATGAGAGCATTGCCCTAT
AAATCAAGCAAAAACAAGTGCGGCTTCGTGGTACCAGACGCTTGTAGTGCCAGACGCTTC
CTGCACTTTGGGTCTGAGTTGGACGGGGAGGCATGGACAGCCCCGGCCAAATTGGCCTGG
GAGAAGCTAGGCAGAGACAAGAAGGTGATGCATGCTCGATCACAGGAGATGGTAAGATGC
AGGGATATTCCAGATGATGTGCTGCTGGACCCGGCTGTACAAGCGGCAATCGCAGCGGTT
AGCGCGCTTAGAGTGAGCGAAGACACTGGAAATGAAGGCACCAGGAAGACGAGCATCGGC
GAGAACACAAAGATGGCTCCGGCGAAACCCGCGCTGACCACGGCTTCTACTCCAACCATA
GCCATGGCTGACGCGGACACCTCGCCATCTACACCACCGGGTACAGGGGCGGGGGGCGAC
ATCGACAAAACCCCGCTCGCACACACCATCGAGGATGCAGCAACCCCTCCCTACCCGCCG
GGTTTCGAGCCCGACTCTGTTAAGGCCTCTCCTGTCGCTGCTACTGTAACTCAGTAGAG
ACGGAGACAAAGTCAGGGAAGTTGCATGCACCAAAGGAACAGGTCTCAAAACCAAGGCA
AAATATATTAGCCAGCTCAAGGAAAGAAAGGAACCAGGGGAGACAAATTCAGTTCTAGGA
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ACAGGGGACATGTATAAGAAACAGAGAGCTGCTGTAGAGGAAGAGGATGAGAGAGCTGTA
GGAGAGATAGGTGAGCGCCCGTCAGGAGGAATGACGATCCTATGTTGGAAGTCCCAGGGA
CTGGGCCACCCCGGACAGTTTCGTGAGCTTGTGTGCCTAGTGCGCACGTACCGCCCTCT
GTCGTGTTTCATCTCTGAGACGCGGCAGTGTGAGGAGAGCGTCAAAGAATAAGATGGAGG
CTGGGCCTCAAAAAGTGCATCACCCACGATGGCATGGGAAAAGGTGCTGGTATAGCCCTG
TTTTGGGATGAAAGTGTTGAAATAAAATTACTCTCCTATGGTTTGAGGTATATTGATGTG
CATATGCGTATGGATCCCCATGGCCCGATGTGGCGGGGTACCTTTGTGTACGGCGAGCCT
AGAGCACATGAGAGGCATAACATGTGGAACCTGCTGAAAAGAATAAAACCAAAATCGATT
GAGCCGTGGATGATGATAGGAGACTTCAATGAAACATTATGGCAAAGTGAACATTTCTCT
GCAGCAAAAAGATCTGAAAGGTATATGGGCAATTTAGAGATGTACTGGCATACTGTAAT
CTTCATGATCTGGGTTACCATGGTTGGTAG

>FGENESH: 2 2 exon (s) 6110 - 8172 669 aa, chain -
MAIFCQKNEKGQSCHPLSIKVAIPVLPFSTAGLFGELKSKWGLRGRLDYTPLRNNRFMLE
FEREGDRQHVLNENGPWTHRKDAFLIVPFDGQKASDVPVNVMPIWARIYDVPPLMLSEEI
GWKLGLLLGKVLRLVDADKFGNIFSEFLCVRVEHNVNTPLLREISPRELGEKEHMDLEVKY
ERAPRFCMYCGHIGHGERDCRLPTDDQAERFTGAMRALPYKSSKNKCGFVVPDACSARRF
LHFGSELDDGEAWTAPAKLAWEKLGRDKKVMHARSQEMVRCRDIPDDVLLDPAVQAAIAAV
SALRVSEDTGNEGTRKTSIGENTKMAPAKPALTTASTPTIAMADADTSPSTPPGTGAGGD
IDKTPLAHTIEDAATPPYPGFEFDSVKASPVAATVNSVETETKSGKLHAPKGTGLKTKA

KYISQLKERKEPGETNSVLGKRGTGDMATSTGAMASASDVTGDMYKKQRAAVEEEDERAV
GEIGERPSGGMTILCWNCRGLGHPGTVRELVCLVRTYRPSVVFISETRQCEESVKRIRWR
LGLKNCITHDGMKGAGIALFWDESVEIKLLSYGLRYIDVHMRMDPHGPMWRGTFVYGEF
RAHERHNMWNLLKRIKPKSIEPWMMIGDFNETLWQSEHFSAAKRSESYMGNFRDVLAYCN
LHDLGYHGW

>FGENESH:[mRNA] 3 2 exon (s) 8537 - 12348 3699 bp, chain +
ATGGAGATCCCTGACCAGACCAATCCGTGCGCGATCTGTCTCAGCGGCATGGGCGCCGGC
GGTGGTCAGGCCACCTTCACGGCGGAGTGCTCCCACACGTTTCACTCCAGCTGCATCTCC
GCCAGCGTCTGCCCCTCTGCAGCGTGCCGCGGTACGACCTGCCGTTCCGGCGACCCACA
CCACCTCCACCTCCGCCGCCCCCGCCGGTGCGACCTCAGCCAGAGACTCGTCCCATTCCC
CTCCGCCCCGTGCATCATTCTCCCGCGGCAGTCACCTCCCGTGCAATTCGTGCACGGTCAG
CCACCGCCACCGCCACCACGACCGACATACTCGTGCCACGCATTCCCACGCAGGCACGA
CAGCCGCCGCCACGGCCCGTGAATCTCGTGACGGTCAGCCACCACCGCCGCCGCCGCCG
CCACCGCCCCCTGCGTCCCGTGCCACCGCCACCACCGCCCGTGCGTTCCGTGCCACGGCCA
CCACTAACATCGTTCGTGGCCGCGCTTGCCACGCAGCTACCTCCGCCGCTCCACCGCCG
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GTTGGTCCCGCCTCTGGGCGGCCAGCTGGCAACCGGTACCCAGCCGCTGCATCAAACGAA
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AACTTCGCCGTGCTCGTGACGTCCAGGCTCCCGGGATGACCGACATCACGGCAGCCGGT
GGCGACGCGCCGCGCGCGCCGGTGACCTCGTGACGGTTCTCGATGTCAGTCACAGTATG
AGCGGGCAAAGTTGACGCTGTTGAAGCAGGCCATGCGGTTTCGTTCATCGCCAATCTCGGC
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ACGCGCATGTCGGAGGCCGGGAAGGCCCTGTCCGTGAGCGCTGTGGAGTCCCTCACGGCG
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TTCTCGTTTCGTAGAGAACGAGGCGATGATCCAGGACGCGTTTCGCACAGTGCATCGGCGGG
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CGTGTCATGTCGGTCAAGTCCGGCAGTTACGAGAGCCGCATCGACGAGGACGGCCGCGCC
GCCACGGTCTGGGTTCGGAGAATACTACGCTGATGAGGAGAGGCGTTTCTTGCTGATCCTG
ACCGTGCCAAGAGCCGAAGCGACAGACGGTGACACCACCGCTCTGTTGAATGTGTATTTC
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GCATCAGCCGAGCAAGGGCAGCAACTACAAGCTGAAGAAGAATACACAGGAAGCTCTAAA
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GCGTCGAACGAAGCAGTTGTCTGTCGAAGACGCGGAGCGAGTACCCGGCCATCGCTAGGGAT
TCGTCCAGTGAAAACCTTCGCCATGCTCGTGACGTCCAGGCTCCCGGGATGACCGACATC

ATGGCGGTTGGTGGCGACGCGTCGCGCGCGCCGGTGGACCTCGTGACGGTTCTCGACGTC
GGTGGCAGCATGAGCGGGTACAAGCTGGCGCTGCTGAAGCAGGCCATGCGGTTTCATCATC
GCCAATCTTGGCCCCGGCGACCGCCTCTCCGTCTGTCTTCTCCTCCGTGGCGCGCCGC
CGGACCAGGCTCACGCTCATGTGCGGAGACCGGGAAGGCCCTGTCCGTGAGCGCCGTGGAG
TCCCTCACGGCGGGCGGCGGCACCGACATCGCCGAGGGGCTCCATATGGCAGCCATGGTA
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GGGTCATCCGGCGTCCGGGCCAACAACTACGAGGAGCTCGTCCCGCCCTCCTTCGCACGC
ACGGGAGCTGACGGCGAATGGTCAGCGCCGATCCACACGTTTCGGCTTCGGCAACGACCAC
GACACGGCCGCGATGCACGCCATCGCCGACGCGACGGGCGGCACGTTCTCGTTCATCGAG
AACGAGGCGGTGATCCAGGACGCGTTTGGCCAGTGCATCGGCAGGCTGCTCTCCGTCTGTG
GTCCAGGGGGCTCGCATCGCCGTGCGGTGCGTGACGCCGGGGTCCGTCTCATGTGCGGTG
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GGGGAActCTACGCCGAGGAGGAGAGGCGTTTCTTGCTGTCTCTGGCCGTGCCAAGAGCT
GAAGCAACAGACGGCGACACCGCTACTCTGGTGAAAGTGGTGTTTCAGCTACAGAAACGCG
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GCGCCGAACGCATCGGAGCGGTGCGTAGAGGTGGAGCGGAGCGCATCCGGGTGGAGGCG
GCAGAGGACTTCACGGCGGCGAGGGCAGCGGCGGAACGGGGCGACCACGGGAGGCGGTG
AAGATACTCAACAACCGGCAGCGTGCAGTGGCGCTGTACAGTTGTGCGCGGACGACGAC
CCCGTGATCATGGCGCTGGAGGCCGAGCTGTGGGGGATGTGCGGGCGCGTGGCGAACCGG
CAGAGATACGCGCGGCCGGGTCCGGCGTACATGCTTTAG

>FGENESH: 3 2 exon (s) 8537 - 12348 1232 aa, chain +
MEIPDQTNPCAICLSGMGAGGGQATFTAECSTHFHSSCISASVCPLCSVPRYDLPFRRPT
PPPPPPPPVVRPQPETRPIPLRPCIILPRQSPPVHFVHGQPPPPPPRPTYSWPRIPTQAR
QPPPRPVNLVHGQPPPPPPPPPLRPVPPPPPPVRSVPRPPLTSSWPRLPTQLPPPPPP
PPRVRISSQAQPQCSFDDDEQVGPASGPPAGNRSPAAASNEAVVIKTRSEYPAIAMDLSSD
NFAVLVHVQAPGMTDITAAGGDAPRAPVDLVTVLVDVSHMSGQKLTLKQAMRFVIANLG
PDDRLSVVSFNTKARRVTRLTRMSEAGKALSVS AVESLTAGGCTDIAEGLRMAAMVLDQR
RHRNAVSSSVLLSDGQDNYIMMRHQESSGVQANDYEDLVPPTFARTGADGEWSASIHFTG
FGNDHDATA MHVIAEATGGTFSFVENEAMIQDAFAQCIGLLSVVVQEARIAVACVHPGV
RVMSVKSGSYESRIDEDGRAATVWVGELYADEERRFLLILTVPRAEATDGD TTALLNVSF
SCRDAATGMDVNVSAKDTLVARPEHA VDAKRSVEVERERVRVDAEDIAAARAAAEERGEH
QEAVAILKNRQRAVALSEAASDGPVTMALEAELQEMRGRVSNRQSYALSGRAYMLAGIS
AHQQQRATSRQMN LVEEMSVEFMAALVAAPPVKLASNEATLSYATPAMRAMLLRSRRARE
ASAEQGGQLQAE E EYTGSSKHGQPTPPLTSSCPRLPTQLRPPPPPPMRIGHARPPTVVFD
DDEQGGPASGPPADNRSPAAASNEAVVVKTRSEYPAIARDSSSENFAMLVHVQAPGMTDI
MAVGGDASRAPVDLVTVLVDVGGSMSGYKLALLKQAMRF I IANLGP GDRLSVVSFS SVARR
RTRLTLMSETGKALSVS AVESLTAGGGTDIAEGLHMAAMVLDQRRHRNAVSSSVLLSDGP
GSSGVRANNYEELVPPSFARTGADGEWSAPIHFTGFGNDHDTAAMHAIADATGGTFSFIE
NEAVIQDAFAQCIGRLLSVVVQGARIAVACVHAGVRLMSVKSSSYESRIDEDGRAATVCI
GELYAE EERRFLLSLAVPRAEATDGD TATLVKVVS YRNATTGADVSVTTEDTVVARPEH
APNASERSVEVERERIRVEAAEDFTAARAAAE RGDHREAVKILNNRQRAVALS QLSRDDD
PVIMALEAELWGMCGRVANRQRYARPGPAYML

>FGENESH: [mRNA] 4 4 exon (s) 13030 - 14428 372 bp, chain +
ATGCCGGTGAATGGGAATATGGCCATGTTCAAGCGAGGACACCGGGCTCAGCTGCTTG
CCCGAGACGCTGGTCGAGAACATGCTATTCCTCGCTGTTGGCATGCGCGTGGA ACTCAAT
AAGATGGTGAAGGAGGGTAGGGAGCTAAGAGGATACTGGTACCTGCTCCCAGCGTGGAGC
TGCGCAATGCATGCGCTGTTGGAGTTAACCACGTCCGAGAGTCCATGCCCGGTCTATACC
GCCGTTGAGGTCGGACCAGCGCCAACAGCGATGGTGGCCGGGCTCGTCAAAGTGCAGGTG

GCGATGGCGTCAGTGGGGCGGCGCATCCCCGGGACAGCGAACGTGGGTCCTTCGTAAGG
AAAAAAAAGTAG

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