

Augustus [result display]

Your job id is AUG-736654824.

The [graphical](#) and [text results](#) are here

Calculating ...

```
# This output was generated with AUGUSTUS (version 3.3.1).
# AUGUSTUS is a gene prediction tool written by M. Stanke (mario.stanke@uni-greifswald.de),
# O. Keller, S. KÄnig, L. Gerischer, L. Romoth and Katharina Hoff.
# Please cite: Mario Stanke, Mark Diekhans, Robert Baertsch, David Haussler (2008),
# Using native and syntenically mapped cDNA alignments to improve de novo gene finding
# Bioinformatics 24: 637-644, doi 10.1093/bioinformatics/btn013
# Sources of extrinsic information: M E
# Setting lgroup1gene for E.
# reading in the file /data/www/augustus/webservice/data/AUG-736654824/hints.gff ...
# Have extrinsic information about 0 sequences (in the specified range).
# Initialising the parameters using config directory /data/www/augustus/augustus/config/ ...
# fly version. Using default transition matrix.
# Looks like /data/www/augustus/webservice/data/AUG-736654824/input.fa is in fasta format.
# We have hints for 0 sequences and for 0 of the sequences in the input set.
#
# ---- prediction on sequence number 1 (length = 2994, name = NT_033777.3:21378977-21381970) ----
#
# Constraints/Hints:
# (none)
# Predicted genes for sequence number 1 on both strands
# start gene g1
NT_033777.3:21378977-21381970 AUGUSTUS gene 166 2927 0.12 + . g1
NT_033777.3:21378977-21381970 AUGUSTUS transcript 166 2927 0.12 + . g1.t1
NT_033777.3:21378977-21381970 AUGUSTUS tss 166 166 . + . transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS exon 166 455 . + . transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS start_codon 271 273 . + 0 transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS initial 271 455 1 + 0 transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS internal 1358 1968 1 + 1 transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS terminal 2349 2851 0.79 + 2 transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS intron 456 1357 1 + . transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS intron 1969 2348 0.79 + . transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS CDS 271 455 1 + 0 transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS CDS 1358 1968 1 + 1 transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS exon 1358 1968 . + . transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS CDS 2349 2851 0.79 + 2 transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS exon 2349 2927 . + . transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS stop_codon 2849 2851 . + 0 transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:21378977-21381970 AUGUSTUS tss 2927 2927 . + . transcript_id "g1.t1"; gene_id "g1";
# coding sequence = [atgttgccagcaccatcagcagcaggctcaatcgggtggctactacgatcactacactcagtcacccagtcgggcagcc
# tgacgaacgcggatgccctgaacaccactccattttcggtcaaggatattcctgaacatggtaaccaaacggaggccctacgaaggttcctacgggcat
# atcgatggcggcgagctgctcggcgctcttcgccgctggtagtaccagaatccccaccagtagctcaaccaccagcagcatcagcaatccgagct
# gccgattccgcagcagaactgcatacacaacttggacgatggcgccaccacatcgtcgtccctatcgccactcttgccacccccgccgaccagc
# gtacggcgagataccaggactacggtagtgcggccacatgttccagcaccatcagggacatccccaccagagtttccagcactccgctcgccctac
# aacatgtccgcttcgagttctacgcggcgctcggccacggcctaccagacccccgccacctacaactacaactacgccggatcggtaggtgta
# cggtaggacccagccctcggcggtgggcatcaagagcgagtagatataccacgccatacgtcacgcccctcgccacccctggacctcaacagctccgctg
# aggtggacagcctgaagctcgcagcagaaagctgtgcgtcaatccccctgtgcagcgccctcatggagaccgtagcaactcgtcctccctaaggagc
# atctacggttcagatgagggcgccaaaaaattataaattatttactatattctcgatattggctattcttcagaggataacagccaggtgac
# ctctcgcgttcgagctgcgaaaaaacagcattcagtggggaacagcaatccggggagcaacagtggttccaccaagccccggatgaagcgaagcctc
# gcgtgctcttttccaggcacaggtcctggagctggagtgctcgttctgactcaaaaagtatctgacgggtcgaggagcgcgagataatcgcgaaaag
# cttaacctgtcggccaccaaagtgaagattgttccagaatcgccgctacaaatcgaacgtggcgacatcgactcgagggcatcgccaagcatct
# gaagttgaagtcgagccctggactcgccacttctctgcccccgccgattccaacacgtgagtggtggcccccaaccatgcagcaatcgagcagc
# agcagcagcatcatgcacagcagcaacagatgcagcacatgtag]
# protein sequence = [MLQHQQQAQSGGYDHYTQSPSPGSLTNADALNTPFSVKDILNMVNOQEAYEGSYGHIDGAATASALFAAGEYQNP
# HQYLNHQQHQSELPIPQQQLHHQHLDDGATTTSSSLSPLLPPPHQLYGGYQDYGMFAHMFQHHHGHPHQSFQHSASAYNMSAQFYAGASATAYQTP
# ATYNYNAGSGEVYGGATPSAVGKISEYIPTVYVTPSPDLNLSSAEVDSLQAPQKLCVNPLSQRMLMETASNSSLSRSIYGSDEGAKKIITIIIFYI
# LDIGYLSQVTSRSELKRNKISGNSNPGNSGSGTKPRMKRKRPRVLFSAQVLELECRFLKLYLGAEREIIAQKLNLSATQVQKIWFQNRRYKS
# KRGDIDCEGIAHLKLEPLDPSLPPPIPNHVMWPTMQSQQQQQHHAQQQQMHM]
# Evidence for and against this transcript:
# % of transcript supported by hints (any source): 0
# CDS exons: 0/3
# CDS introns: 0/2
# 5'UTR exons and introns: 0/1
# 3'UTR exons and introns: 0/1
# hint groups fully obeyed: 0
# incompatible hint groups: 0
# end gene g1
###
# command line:
# /data/www/augustus/augustus/bin/augustus --species=fly --strand=both --singlestrand=false --genemodel=partial --codingseq=on --hintsfile=/data/www
```

Done.

[submit another job](#)