Augustus [result display]

Your job id is AUG-1413868631.
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. König, 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
# No extrinsic information on sequences given.
# 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-1413868631/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 = 13738, name = NT_033777.3:c23141906-23128169) -----
#
# Constraints/Hints:
# (none)
# Predicted genes for sequence number 1 on both strands
# start gene g1
NT_033777.3:c23141906-23128169    AUGUSTUS          gene        96    13737   0.07   +   .   g1
NT_033777.3:c23141906-23128169    AUGUSTUS          transcript  96    13737   0.07   +   .   g1.t1
NT_033777.3:c23141906-23128169    AUGUSTUS          exon        96    865     .      +   .   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          start_codon 386   388     .      +   0   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          initial     386   865     0.96   +   0   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          internal    8644  8905    1      +   0   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          terminal    12496 13169   0.95   +   2   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          intron      866   8643    0.89   +   .   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          intron      8906  12495   0.98   +   .   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          CDS         386   865     0.96   +   0   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          CDS         8644  8905    1      +   0   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          exon        8644  8905    .      +   .   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          CDS         12496 13169   0.95   +   2   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          exon        12496 13737   .      +   .   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          stop_codon  13167 13169   .      +   0   transcript_id "g1.t1"; gene_id "g1";
NT_033777.3:c23141906-23128169    AUGUSTUS          tts         13737 13737   .      +   .   transcript_id "g1.t1"; gene_id "g1";
# coding sequence = [atggataaccacagctcagtgccttgggccagtgccgccagtgtcacctgtctctccctggatgccaaatgccacagtt
# ccagttccagttccagctccaaatccgcagcgagctccatctccgcaatcccgcaagaagaaacgcaaacgatgcgccacattgcgcatacgcagcgt
# tgcctcagcaggctgacctctctggtggccctgctgctgatcgtcttgccgatggtctttagcccggctcacagctgcggtcctggccgaggattggg
# tcgtcataggcgcgcaacctgtatccgctggtcctcaagcagacaattcccaatctatccgagtacacgaacagcgcctccggacctctggagggtg
# tgatccgtcgggactcgcccaaattcaaggacctcgtgcccaactacaacagggacatcctttttccgcgacgaggaaggcaccggagcggatcgcttg
# atgagcaagcgctgcaaggagaagctaaacgtgctggcctactcggtgatgaacgaatggcccggcatccgctgctggtcaccgagagctgggacga
# ggactaccatcacggccaggagtcgctccactacgagggccgagcggtgaccattgccacctccgatcgcgaccagtccaaatacggcatgctcgctc
# gcctggccgtcgaggctggattcgattgggtctcctacgtcagcaggcgccacatctactgctccgtcaagtcagattcgtcgatcagttcccacgtg
# cacggctgcttcacgccggagagcacagcgctgctggagagtggagtccggaagccgctcggcgagctctctatcggagatcgtgtttgagcatgac
# cgccaacggacaggccgtctacagcgaagtgatcctctttcatggaccgcaacatccgagcaagatgcaaaactttgtgcagctgcacacggacggtggag
# cagtgctcacggtgacgccggctcacctggttagcgtttggcagccggagagccagaagctcacgtttgtgtttgcggatcgcatcgaggagaagaac
# caggtgctcgtacgggatgtggagacgggcgagctgaggccccagcgagtcgtcaaggtgggcagtgtgcgcagtaagggcgtggtcgcgccgctgac
# ccgcgagggcaccattgtggtcaactcggtggccgccagttgctatgcggtgatcaacagccagtcgctggcccactgggactggctccccatgcgcc
# tgctgtccacgctggaggcgtggctgcccgccaaggagcagttgcacagttcgccgaaggtggtgagctcggcgcagcagcagaatggcatccattgg
# tatgccaatgcgctctacaaggtcaaggactacgttctgccgcagagctggcgccacgattga]
# protein sequence = [MDNHSSVPWASAASVTCLSLDAKCHSSSSSSSSKSAASSISAIPQEETQTMRHIAHTQRCLSRLTSLVALLLIVLPMV
# FSPAHSCGPGRGLGRHRARNLYPLVLKQTIPNLSEYTNSASGPLEGVIRRDSPKFKDLVPNYNRDILFRDEEGTGADRLMSKRCKEKLNVLAYSVMNE
# WPGIRLLVTESWDEDYHHGQESLHYEGRAVTIATSDRDQSKYGMLARLAVEAGFDWVSYVSRRHIYCSVKSDSSISSHVHGCFTPESTALLESGVRKP
# LGELSIGDRVLSMTANGQAVYSEVILFMDRNLEQMQNFVQLHTDGGAVLTVTPAHLVSVWQPESQKLTFVFADRIEEKNQVLVRDVETGELRPQRVVK
# VGSVRSKGVVAPLTREGTIVVNSVAASCYAVINSQSLAHWGLAPMRLLSTLEAWLPAKEQLHSSPKVVSSAQQQNGIHWYANALYKVKDYVLPQSWRH
# D]
# end gene g1
###
# command line:
# /data/www/augustus/augustus/bin/augustus --species=fly --strand=both --singlestrand=false --genemodel=partial --codingseq=on --sample=100 --keep_v
```

Done.

submit another job