

### Calculating ...

 $\frac{1}{2}$

3/24/2019

Augustus: result display

NT\_037436.4:c18846267-18828632

AUGUSTUS

internal

15534

15992

1

+

1

transcript\_id "g2.t2"; gene\_id "g2";

NT\_037436.4:c18846267-18828632

AUGUSTUS

internal

16311

16689

1

+

1

transcript\_id "g2.t2"; gene\_id "g2";

NT\_037436.4:c18846267-18828632

AUGUSTUS

terminal

16755

17045

0.99

+

0

transcript\_id "g2.t2"; gene\_id "g2";

NT\_037436.4:c18846267-18828632

AUGUSTUS

CDS

14314

14321

0.29

+

0

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NT\_037436.4:c18846267-18828632

AUGUSTUS

CDS

14647

14773

0.94

+

1

transcript\_id "g2.t2"; gene\_id "g2";

NT\_037436.4:c18846267-18828632

AUGUSTUS

CDS

15027

15175

1

+

0

transcript\_id "g2.t2"; gene\_id "g2";

NT\_037436.4:c18846267-18828632

AUGUSTUS

CDS

15240

15428

0.97

+

1

transcript\_id "g2.t2"; gene\_id "g2";

NT\_037436.4:c18846267-18828632

AUGUSTUS

CDS

15534

15992

1

+

1

transcript\_id "g2.t2"; gene\_id "g2";

NT\_037436.4:c18846267-18828632

AUGUSTUS

CDS

16311

16689

1

+

1

transcript\_id "g2.t2"; gene\_id "g2";

NT\_037436.4:c18846267-18828632

AUGUSTUS

CDS

16755

17045

0.99

+

0

transcript\_id "g2.t2"; gene\_id "g2";

NT\_037436.4:c18846267-18828632

AUGUSTUS

stop\_codon

17043

17045

.

+

0

transcript\_id "g2.t2"; gene\_id "g2";

# coding sequence = [atggaaattgaaattggcgaacaacccagcctcgggtgaagtgctccaacttcttcgctaaccactggaagggttgg

# ttgtgttctcgggtgccgctgctatgtctgcctgttatgtctgctaacaaggcgccagctcggatcagacttggcgttgctacttcaaggatacgcctg

# gtgatgttcatggcgccattatggtcgccctggctgtggagtactgtaacttacacaaacgtcttgccttgagggtaatccagatcgtgggctgcag

# tccccgcagattacactttggcctcatcatggttacaatgtttttagcatgtggatttcgaacgccctgtactgccatgatgtgtccgattatcc

# aagccgtgtcggaggagctgcaggctcagggtgtctgcaaaatcaaccatgagcctcaataccaatcgttggaggcaacaagaaaaacaacagggat

# gagccaccataacccaccaagatcactctgtgtactatctgggcattgcctacgcctcctcgctgggtggctgtggaaacctatcggaaactgccac

# caatcttaccttcaaggcatctacagggtcgttttcaagaactccaccgaacagatggacttccccaccttcatgtttctactcggtgccatccatgt

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# cattgctggaatcggtccgaccatcattaccatcatcacctctgtttgttttctgccaacctggggcctggtcgtctatccgaaccttaactcgttcc

# ccgaatgggctcagatttatgcccgcgagcactgggaaacaagacgcactag]

# protein sequence = [MEIEIGEQPPVKCSNFFANHWKGLVVFLVPLLCLPVMLLNEGASSDQTCRLYFKDTLVMFMGGIMVALAVEYCNLH

# KRLALRVIQIVGCSRRRLHFGILIMVTMFLSMWISNAECTAMMCPIIQAVLEELQAQGVCKINHEPQYQIVGGNKKNNEDEPPYPKTKITLCYVLGIAYA

# SSLGGCGTIIGTATNLTFKGIYEAFKKNSTEQMDFFTFFMYSVPSMLVYLLTFVFLQWHFMGLWRPKSKEAQEVQRGREGADVAKKVIDQRYKDLGP

# MSIHEIQVMILFIFMVVMYFTRKPGIFLGWADLLNSKDIRNSMPTIFVVVMCFMLPANYAFRLYCTRGGPVPTGTPSLITWKFIQTKVPWGLVFL

# GGGFALAEGSKQSGMAKLIGNALIGLVLPNSVLLLVILVAVFLTAFSSNVAIANIIPVLAEMSIAIEIHPLYLILPAGLACSMAFHLPVSTPPNA

# LVAGYANIRTKDMAIAGTGTIIITILFVFCQTWGLVVYPNLNSFPEWAQIYAAAAALGNKTH]

# end gene g2

###

# command line:

# /data/www/augustus/augustus/bin/augustus --species=human --strand=both --singlestrand=false --genemodel=partial --codingseq=on --sample=100 --keep

Done.

[submit another job](#)