GeneVision Analysis Report

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User: Mariem

1. General Information

Analyzed sequence: Available in appendix Predicted genes: Available in appendix Protein sequences: Available in appendix

Tools used:

Gene prediction: AUGUSTUS

• Functional annotation: DeepGOPlus + QuickGO

• Structural modeling: ESMAtlas

2. Sequence Data

Number of predicted genes: 1
Number of protein sequences: 1
Total input sequence length: 2344 bp

3. Results Summary

Gene ID	Position	Score	GO Term	Function	Description
gene1	445 - 1848	0.87	GO:0005575	cellular_component	A macromolecular machine's location within a cell, like on the cell membrane or inside a mitochondrion. This location can also include virus parts or large protein complexes.

Appendix - Sequence Contents

A1. Input Sequence

>input_sequence

CGGCGCTCCCTGTTGCCGGGCCCTGAGCAAGTGGCTTCATGAACCCCGTGACGTTGGCCA TGGAGATAAGACCACTGGGTGATGGTTTAAGGAAGATAACGTGTAAAGGGCTAAGGACTG TCGGTGGAAATCAGGGGTGCAGGAGAAATGGATAAACAGCCAGAGGTCAACTCGGACTTT GTACATAGGACATGGTGCCAGGCCCTGCCAGGAAGTGCAGATCGAAGCTAGGCTCACGAG GAGGCTGGAGGTGGGGGGGGGGGCAACGGATGGACATGGACTTCCTGGGCTGGGCTC TGTGACAGCAGAGTAGACTCTGTCCTGGGACTTGGTGGTGCTACCCTTGGCCTCCCACAG TCCTGCCACCTGCTGCCGCCACCATGCTGCCCCCTGGGACTGCGACCCTCTTGACTCTG CTCCTGGCAGCTGGCTCGCTGGGCCAGAAGCCTCAGAGGCCACGCCGGCCCGCATCCCCC AGAGGGAGGCAGGTAGAAGTTGTGGGAGGGGTAGAGGGAGACAGGTAGAAGTTGTTGCGG GGGAGAGGAAGCAGGTGAAGTTGTGGGGGGTGTAGAGGGAAGCAGGTGAGGGGCCCTCC CACAGTGCCCTCGAGTTCTCCCATGGTCTGCCCCCAGTTTGCAGGGACCTGGCTCCTTGT GGCTGTGGGCTCCGCTTGCCGTTTCCTGCAGGAGCAGGCCACCGGGCCGAGGCCACCAC CCCAGAGCAGCCCTGCACCCTAACCCCAACCCTCCTCTCAGCCCCGGACTTCAGCCCTG CTCTGGCCCCTGACCCCACCCCGGCTGTGGCCTGGACTAGGATTCCTGGTTGGGGTCTCC CAGCCTGTGGTGCCTCCCCCGCCCCCCAGGGATGGGATCTGCTGGCAGGTGCGCCAG $\tt CTCTATGGAGACACAGGGGTCCTCGGCCGCTTCCTGCTTCAAGGTGAGGCAGGGGCTGCA$ GGTCATGTGGGTGGGGATGACGCAGCCACTGTGGCTCTCTGACATGGCTACTGTGGCTC TGCCCAGCCCGAGGCGCCCGAGGGGCTGTGCACGTGGTTGTCGCTGAGACCGACTACCAG AGTTTCGCTGTCCTGTACCTGGAGCGGGCGGGCAGCTGTCAGTGAAGCTCTACGGTATG $\tt CGAGGGGCTGGGTGAGCCATGGGGACACACTTCCTTTCTCCCATCCTGATCCTCCTGCTA$ AGCAGGGGCCCAGGGAGTAGTGACAGACAGGCCTGGTGTGGGAGCAGGAGGAGGGCCCC GAGGGGCAGGGGACACAGACCCCGTTCCCAGAGCCCTCCACGCCGCCTGGTGCCAGGA CCCCAGGAACCCTGTCTGCCCTGCAGCCCGCTCGCTCCCTGTGAGCGACTCGGTCCTGAG TGGGTTTGAGCAGCGGGTCCAGGAGGCCCACCTGACTGAGGACCAGATCTTCTACTTCCC CAAGTACGGTGAGTGTCCCCAGCAGGTCCCCAGCTCAGCCACCCCACTCTCTGGCTGAT GTCCAGCCTGACCCTGCCTTGGCGCCCCAGGCTTCTGCGAGGCTGCAGACCAGTTCCAC GTCCTGGACGGTGAGTGCACAGCGGGGGCAAGCATGGCGGCGTGGTGAGGGGGGCCACTC GCACCGGCTGAGTCTCGTCTGCTGCAGAAGTGAGGAGGTGAGGCCGGCACACAGCTCC AGTGCTGAGAAGTCAGTGCCCCGAGAGACGACCCCACCAGTGGGGTGCCCGCTGCCTGTC CTCCGTGAAACCAGCCTCAGATCAGGGCCCTGCCACCCAGGGCAGGGGATCTTCTGCCGG ${\tt CTGCCCAGAGGACAGTGGGTGGAGTGGTACCTACTTATTAAATGTCTCAGACCCCTCTC}$ TGACTCTTCTGTCCACTCTGGACCGGCGCCAGTACCACCAAGGCCCTCTCTGCCCCCACC $\tt CCGCCTCTTTAAAAGCCCGGCGCTCCCTGTTGGCTGGAGTCCACGCAGGGTCACTGGGCC$ GATTTCGGCTCTTGGGATTTGGGAGGGGAGATCCTCTCTGGCATATGCCATCTTGTGCCC TGCTGGACCTGGGGGCGTCCACGTCACTCCAAGGCTGCTCTTGCCTGGGCCATGCCTGCA GCCC

A2. Predicted Genes

>gene1

A3. Protein Sequences

>gene1

MLPPGTATLLTLLLAAGSLGQKPQRPRRPASPISTIQPKANFDAQQEQGHRAEATTLHVA PQGTAMAVSTFRKLDGICWQVRQLYGDTGVLGRFLLQARGARGAVHVVVAETDYQSFAVL YLERAGQLSVKLYARSLPVSDSVLSGFEQRVQEAHLTEDQIFYFPKYGFCEAADQFHVLD GECTAGASMAAW