

# GeneVision Analysis Report

**File name:** genevision\_report\_2025-05-08.pdf

**Generation date:** May 08, 2025

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## 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	This refers to the specific place within a cell (or virus) where a group of molecules works together to perform a task. These places can be physical structures like the cell membrane, organelles like mitochondria, or molecular complexes like the clathrin complex.

# Appendix - Sequence Contents

## A1. Input Sequence

```
>input_sequence
AGCGGGCGGGCGGTTCGTGGGCGGGGTTGCAGGCGAGGCTCAACGAACGCTGGTCTGACCGT
CGGCGCTCCCTGTTGCCGGGCCCTGAGCAAGTGGCTTCATGAACCCCGTGACGTTGGCCA
TGGAGATAAGACCACTGGGTGATGGTTTAAGGAAGATAACGTGTAAAGGGCTAAGGACTG
TCGGTGGAAATCAGGGGTGCAGGAGAAATGGATAAACAGCCAGAGGTCAACTCGGACTTT
GTACATAGGACATGGTGCCAGGCCCTGCCAGGAAGTGCAGATCGAAGCTAGGCTCACGAG
GAGGCTGGAGGTGGGGGGTGGGGAGGCAACGGATGGACATGGACTTCCTGGGCTGGGCTC
TGTGACAGCAGAGTAGACTCTGTCTGGGACTTGGTGGTGCTACCCCTTGGCCTCCACAG
TCCTGCCACCCTGTCTGCCGCCACCATGTCTGCCCCCTGGGACTGCGACCCCTTGACTCTG
CTCCTGGCAGCTGGCTCGCTGGGCCAGAAGCCTCAGAGGCCACGCCGGCCCCGCATCCCCC
ATCAGCACCATCCAGCCCAAGGCCAATTTTGATGCGCAGCAGGTAGAAGTTGGGGGGGGT
AGAGGGAGGCAGGTAGAAGTTGTGGGAGGGGTAGAGGGAGACAGGTAGAAGTTGTTGCGG
GGGAGAGGGAAGCAGGTGAAGTTGTGGGGGGTGTAGAGGGAAGCAGGTGAGGGGGCCCTCC
CACAGTGCCCTCGAGTTCTCCCATGGTCTGCCCCCAGTTTGACAGGGACCTGGCTCCTTGT
GGCTGTGGGCTCCGCTTGCCGTTTCTGTCAGGAGCAGGGCCACCGGGCCGAGGCCACCAC
ACTGCATGTGGCTCCCCAGGGCACAGCCATGGCTGTGAGTACCTTCCGAAAGCTGTGAGT
CCCAGAGCAGCCCTGCACCCTAACCCCAACCCCTCCTCTCAGCCCCCGGACTTCAGCCCTG
CTCTGGCCCCCTGACCCCCACCCCGGCTGTGGCCTGGACTAGGATTCTTGTTGGGGTCTCC
CAGCCTGTGGTGCCTCCTCCCCGCCCCCCCCAGGGATGGGATCTGCTGGCAGGTGCGCCAG
CTCTATGGAGACACAGGGGTCTCTCGGCCGCTTCTGCTTCAAGGTGAGGCAGGGGCTGCA
GGTCATGTGGGTGGGGGATGACGCAGCCACTGTGGCTCTCTGACATGGCTACTGTGGCTC
TGCCCAGCCCGAGGCGCCCGAGGGGCTGTGCACGTGGTTGTGCTGAGACCGACTACCAG
AGTTTCGCTGTCTGTACCTGGAGCGGGCGGGGCAGCTGTGAGTGAAGCTCTACGGTATG
TGGGGGCCAGCCTCTGTGACCAGGCAGGCGCTCAAGCTCTGCACACTCACTGGGCCACCC
CGAGGGGCTGGGTGAGCCATGGGGACACACTTCTTTCTCCCATCCTGATCCTCCTGCTA
AGCAGGGGCCCAGGGAGTAGTGACAGACAGGCCTGGTGTGGGAGCAGGGAGGAGGGCCCC
GAGGGGCAGGGGACACACAGACACCCCGTTCCAGAGCCCTCCACGCCCGCTGGTGCCAGGA
CCCCAGGAACCCTGTCTGCCCTGCAGCCCGCTCGCTCCCTGTGAGCGACTCGGTCTGAG
TGGGTTTGTAGCAGCGGGTCCAGGAGGCCACCTGACTGAGGACCAGATCTTCTACTTCCC
CAAGTACGGTGAGTGTCCCCAGCAGGTCCCCAGCTCAGCCACCCCCACTCTCTGGCTGAT
GTCCAGCCTGACCCCTGCCTTGGCGCCCCAGGCTTCTGCGAGGCTGCAGACCAGTTCCAC
GTCCTGGACGGTGAGTGACAGCGGGGGCAAGCATGGCGGCGTGGTGAGGGGGGCCACTC
GCACCGGCTGAGTCTCGTCTCTGCTGTCAGAAAGTGAGGAGGTGAGGCCGGGCACACAGTCC
AGTGCTGAGAAGTCAGTGCCCCGAGAGACGACCCACCAGTGGGGTGCCCGCTGCCCTGTC
CTCCGTGAAACCAGCCTCAGATCAGGGCCCTGCCACCCAGGGCAGGGGATCTTCTGCCGG
CTGCCCCAGAGGACAGTGGGTGGAGTGGTACCTACTTATTAATGTCTCAGACCCCTCTC
TGACTCTTCTGTCCACTCTGGACCGGCGCCAGTACCACCAAGGCCCTCTCTGCCCCCACC
CCGCTCTTTAAAGCCCGGCGCTCCCTGTTGGCTGGAGTCCACGCAGGGTCACTGGGCC
GATTTTCGGCTCTTGGGATTTGGGAGGGGAGATCCTCTCTGGCATATGCCATCTTGTGCC
TGCTGGACCTGGGGGCGTCCACGTCACTCCAAGGCTGCTCTTGCTGGGCCATGCCTGCA
GCCC
```

## A2. Predicted Genes

```
>gene1
ATGCTGCCCCCTGGGACTGCGACCCCTTTGACTCTGCTCCTGGCAGCTGGCTCGCTGGGC
CAGAAGCCTCAGAGGCCACGCCGGCCCGCATCCCCATCAGCACCATCCAGCCCAAGGCC
AATTTTGATGCGCAGCAGGAGCAGGGCCACCGGGCCGAGGCCACCACACTGCATGTGGCT
CCCCAGGGCACAGCCATGGCTGTGAGTACCTTCCGAAAGCTGGATGGGATCTGCTGGCAG
GTCCGCCAGCTCTATGGAGACACAGGGGTCTCTGGCCGCTTCTGCTTCAAGCCCCGAGGC
GCCCCGAGGGCTGTGCACGTGGTTGTGCTGAGACCGACTACCAGAGTTTCGCTGTCTCTG
TACCTGGAGCGGGCGGGCAGCTGTGAGTGAAGCTCTACGCCCCGCTCGCTCCCTGTGAGC
GACTCGGTCTGAGTGGGTTTGTAGCAGCGGGTCCAGGAGGCCACCTGACTGAGGACCAG
ATCTTCTACTTCCCCAAGTACGGCTTCTGCGAGGCTGCAGACCAGTTCACGTCTTGAC
GGTGAGTGACAGCGGGGCAAGCATGGCGGCGTGGTGA
```

## A3. Protein Sequences

```
>gene1
MLPPGTATLLTLLLAAGSLGQKPQRPRRPASPISTIQPKANFDAQQEQGHRAEATTLHVA
PQGTAMAVSTFRKLDGICWQVRQLYGDTGVLGRFLLQARGARGAVHVVAETDYQSFAVL
YLERAGQLSVKLYARSLPVSDSVLSGFQQRVQEAHLTEDQIFYFPKYGFCEAADQFHVLD
GECTAGASMAAW
```