

Task 3: Protein Structure Prediction

Human Cytochrome c (P15954-Cytochrome c oxidase subunit 7C)

Introduction

Cytochrome c is a small, soluble electron transport protein found in mitochondria. It plays a crucial role in the electron transport chain and apoptosis signaling. The protein contains a heme prosthetic group that binds iron and allows electron transfer.

Procedure

1. Sequence Retrieval

1. Open UniProt (<https://www.uniprot.org>).
2. Search for “Human Cytochrome c” or CYCS.
3. Open the protein entry → click FASTA → copy or download the sequence in FASTA format.

2. Structure Prediction

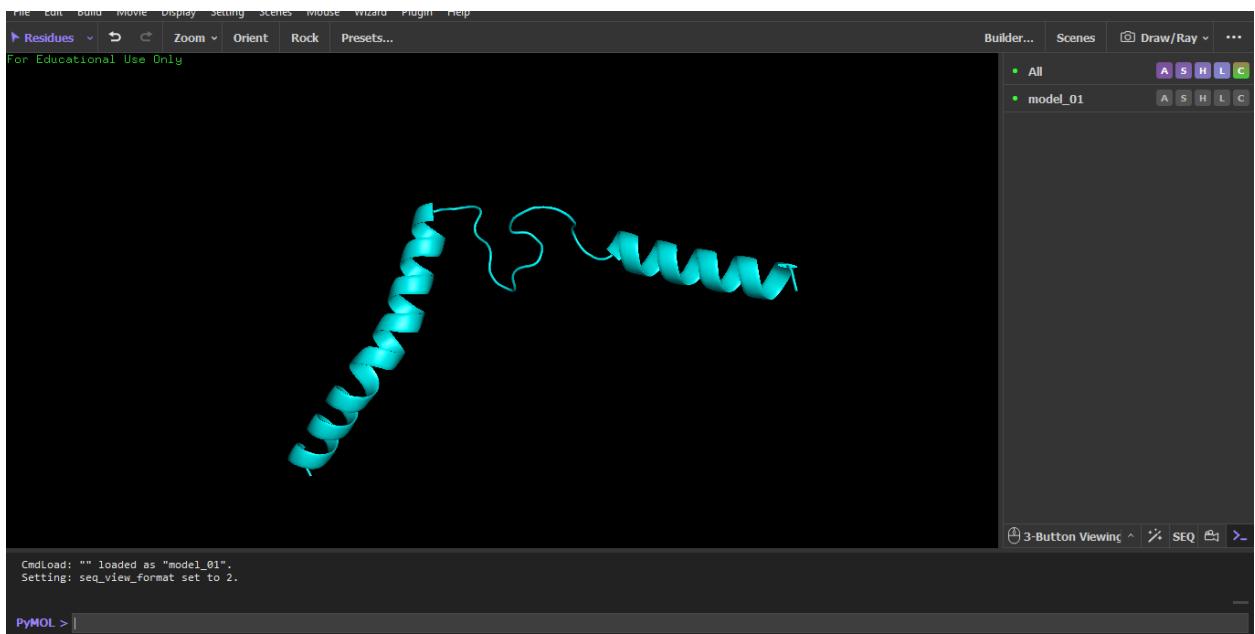
SWISS-MODEL

1. Go to SWISS-MODEL (<https://swissmodel.expasy.org/>).
2. Paste the Cytochrome c FASTA sequence.
3. Click Build Model → wait for the predicted 3D structure.



Structure Visualization

1. Open PyMOL
2. Load the PDB file of Cytochrome c.
3. Rotate and zoom to examine the globular structure.



Results / Structural Features

The image is a ribbon diagram representation of a protein structure, likely generated using a SWISS-MODEL. The entire protein appears to be composed of a single, highly regular alpha helix. This is represented by the continuous, tightly coiled ribbon structure, which is the defining visual characteristic of an α -helix in this representation. The structure is visually **very short** compared to other protein subunits typically seen in complex structures, which is consistent with COX7C being one of the smaller, nuclear-encoded subunits of Complex IV.