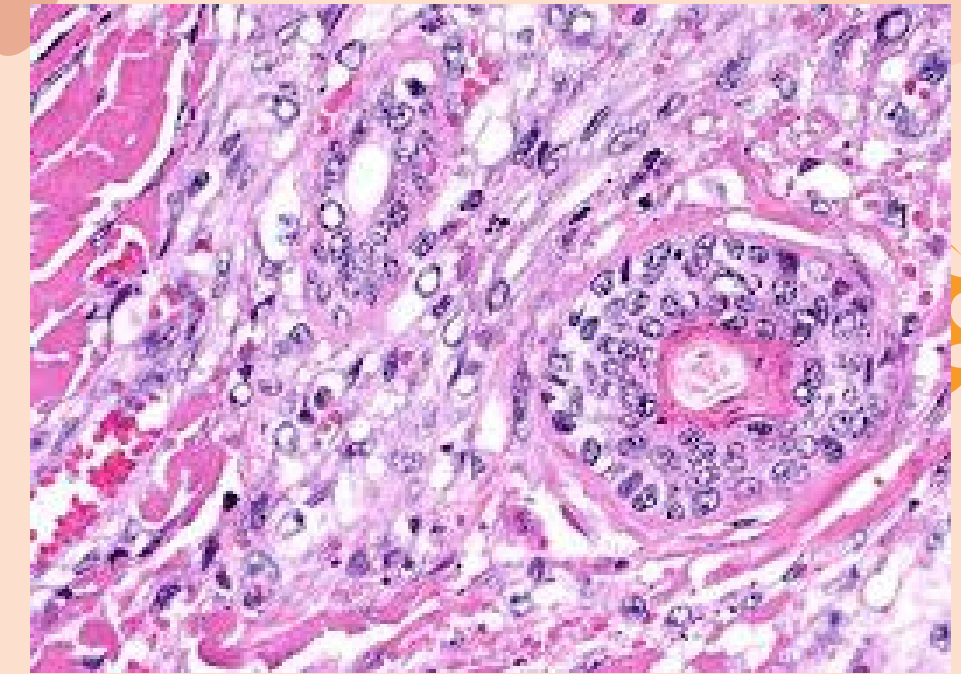


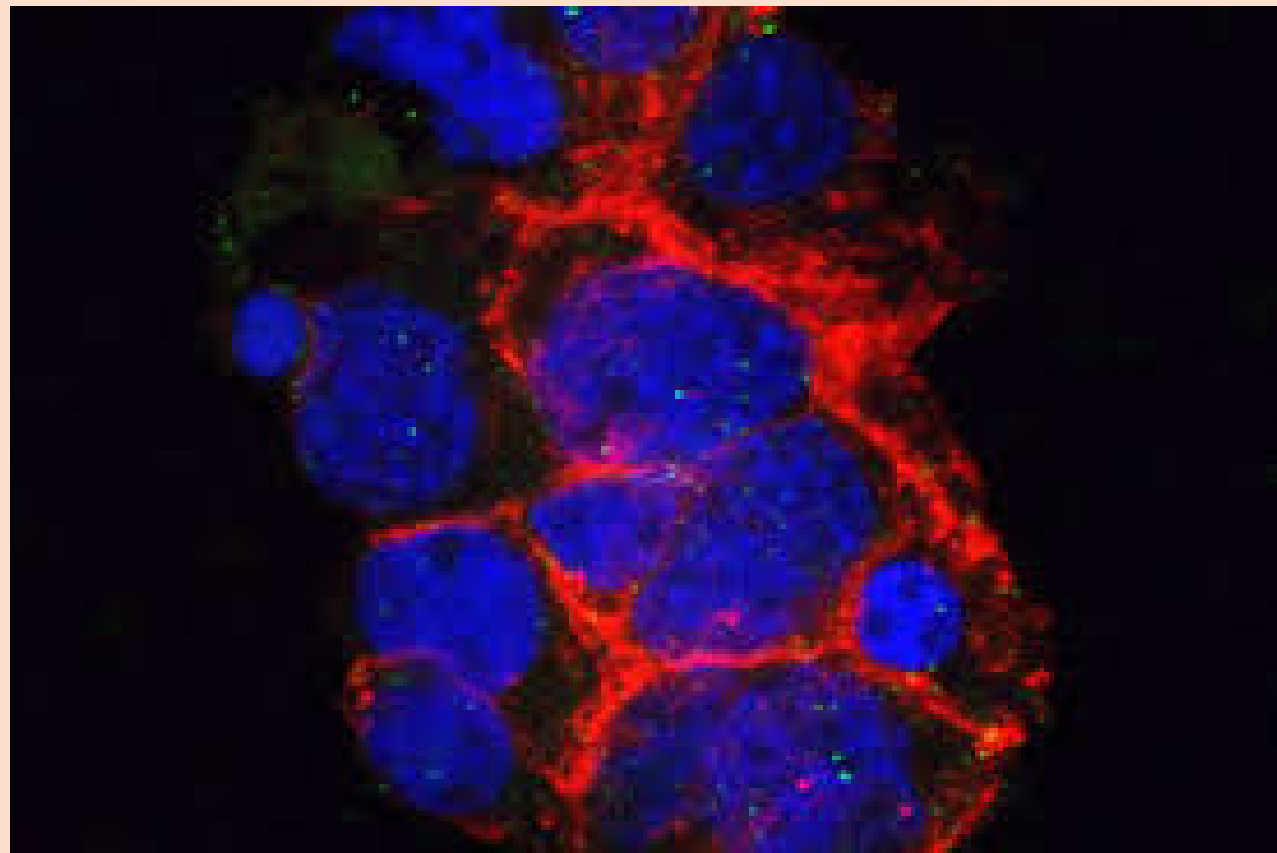
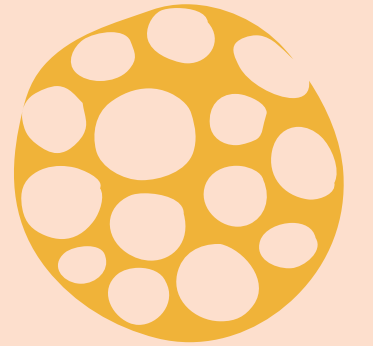
↘ Endoplasmic reticulum ↘ Autophagosome ↘ Virion



Structural and Functional Characterization of Hypothetical Proteins of Lumpy Skin Disease Virus Toward Identification of Vaccine Targets



Lumpy Skin Disease Overview



***Poxviridae* family**

Encodes over 150 proteins, many classified as hypothetical with unknown functions

Methodology



UniProt

CD-HIT



InterPro
Classification of protein families



AlphaFold 3

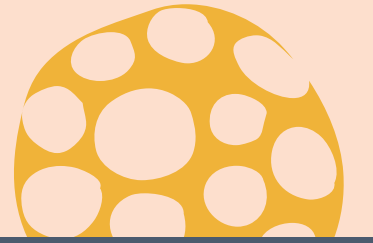
VAST: Vector Alignment Search Tool

DeepFRI

VaxiJen v2.0

DEG BLAST

Methodology



Advanced Search

Searching in
UniProtKB

Organism [OS]
Lumpy skin disease virus (LSDV) [59509] **Remove**

AND Protein Existence [PE]
Predicted **Remove**

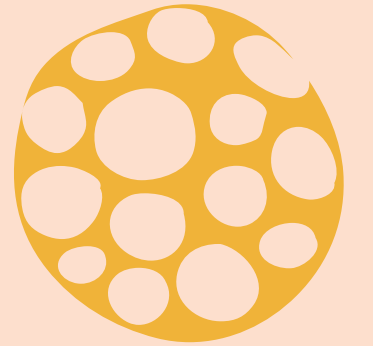
NOT Function [CC]
enzyme Evidence: Any **Remove**

NOT Gene Ontology [GO]
0009986 Evidence: Any assertion method **Remove**

Add Field **Cancel** **Search**

*Type * in the search box to search for all values for the selected field.*

Methodology



CD-HIT

Clustering of
sequences

VAST

Functional
Prediction of true
hypothetical
proteins

InterProScan

Functional
Analysis of true
hypothetical
proteins

DeepERI

VaxiJen

Antigenicity

Alpha Fold

Structural
Prediction of true
hypothetical
proteins

DEG BLAST

Non-Homology
Check of true
hypothetical
proteins



Vaccine Target Identification



Cellular Localization

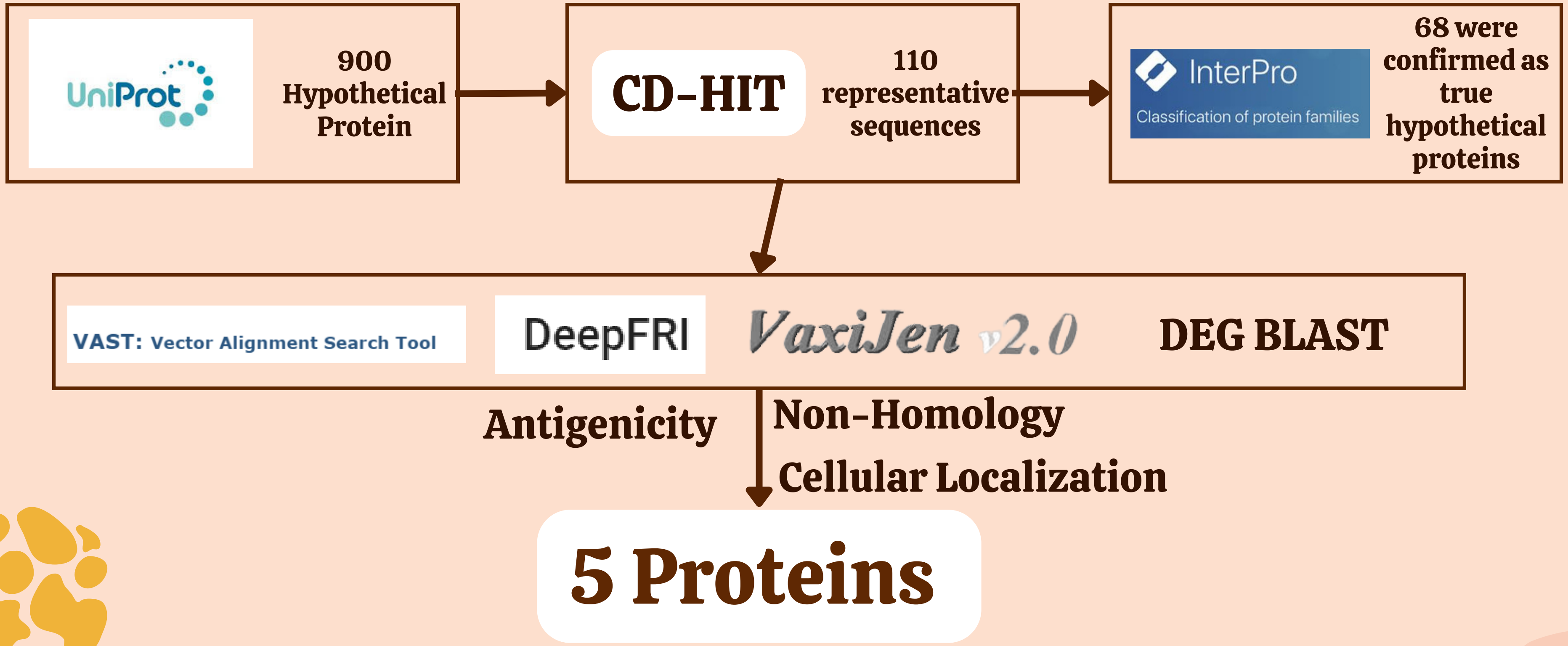
Non-Homology 



Antigenicity



Results



900
Hypothetical
Protein

CD-HIT

110
representative
sequences

InterPro
Classification of protein families

68 were
confirmed as
true
hypothetical
proteins

VAST: Vector Alignment Search Tool

DeepFRI

VaxiJen v2.0

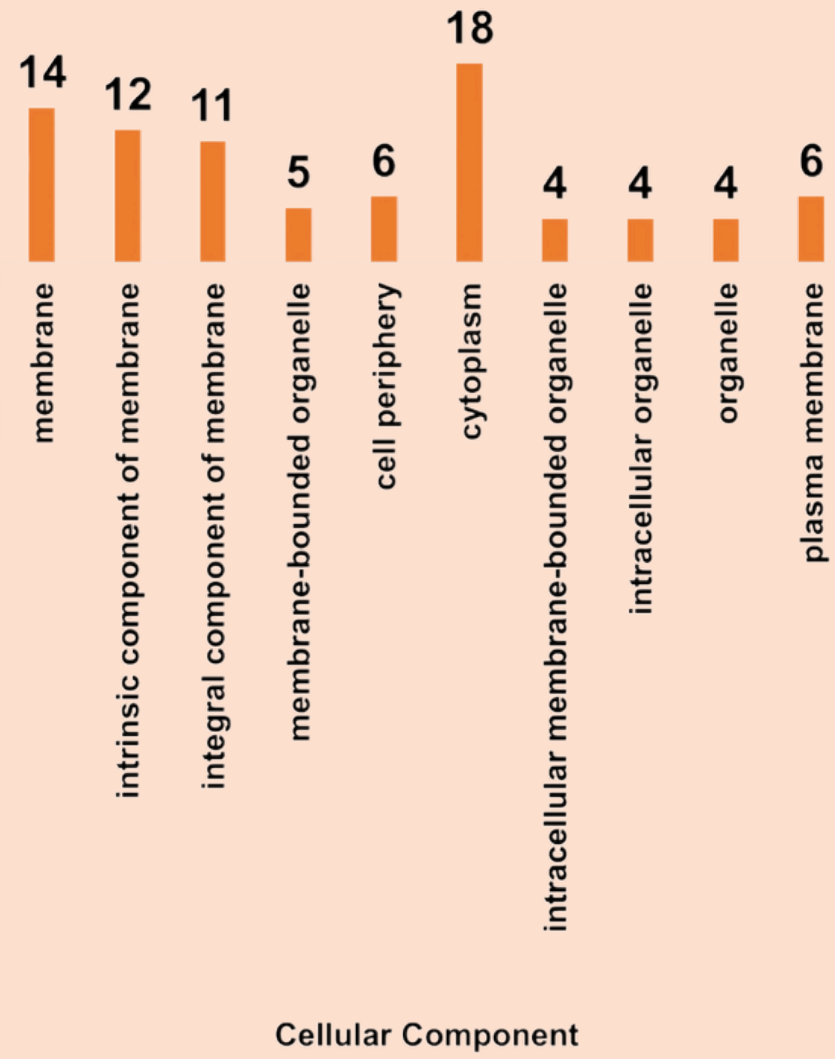
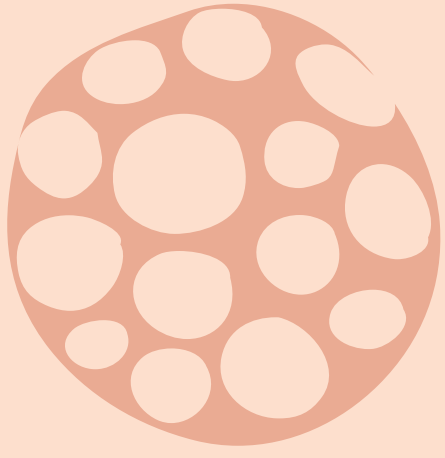
DEG BLAST

Antigenicity

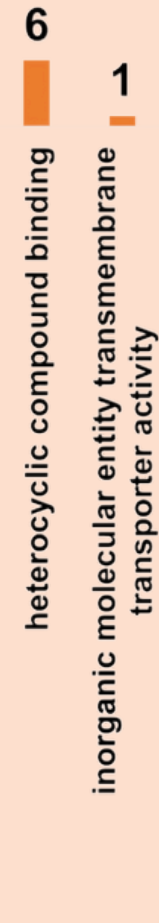
Non-Homology

Cellular Localization

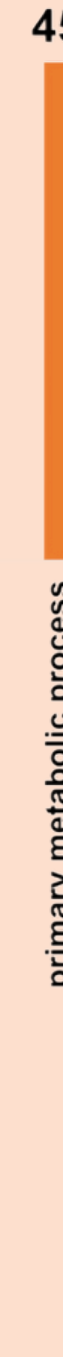
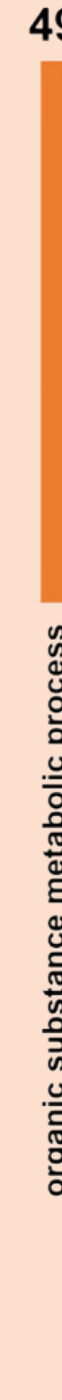
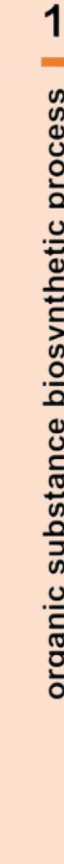
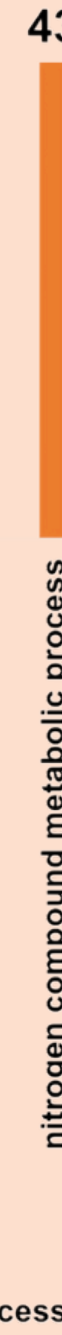
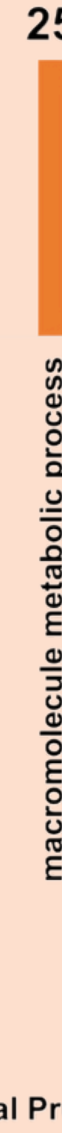
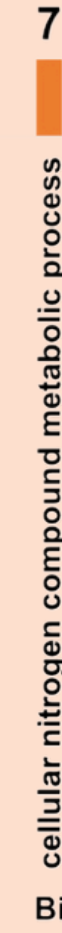
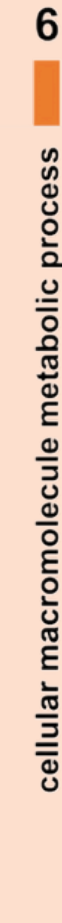
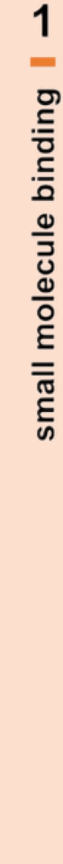
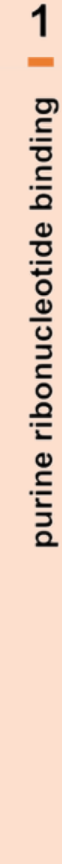
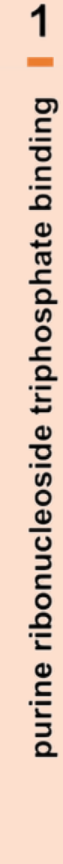
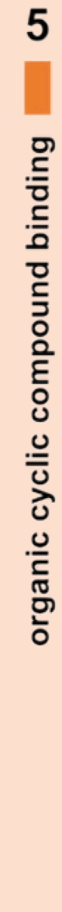
5 Proteins



Cellular Component


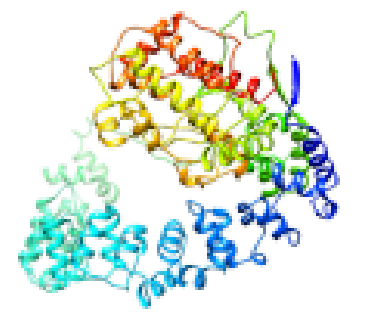
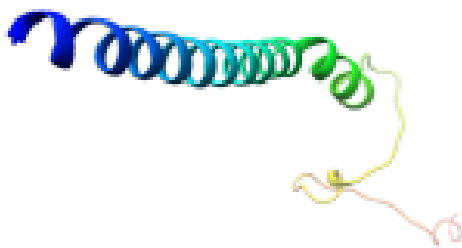

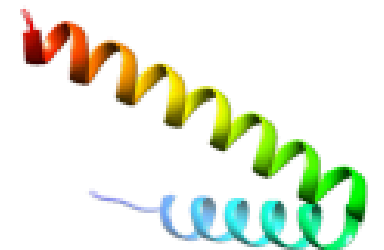


Molecular Function



Biological Process



Structure	Uniprot ID	Length	Putative function
	A0A1B3B604	86	Stathmin-like protein
	A0A1B3B618	684	Lysine-specific histone demethylase
	A0A1B3B6C9	91	Mediator complex subunit-4
	A0A1C9HHG4	67	Signaling helix coiled-coil domain of the beta-1 subunit of the soluble guanylyl cyclase
	A0A1C9HHX0	53	Human respiratory syncytial virus A2 phosphoprotein-like