Modeling of fowl adenovirus 4 hexon protein

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ABSTRACT

Modeling of fowl adenovirus 4 hexon protein was done using SWISS-MODEL software. Valuable structural details and reacting sites could be elucidated.

Key words: Modeling, FAV4, hexon, protein

INTRODUCTION

Fowl adenovirus 4 (FAV 4) is an important pathogen of birds specially the broiler birds and causes serious disease conditions including fatality. The FAV4 hexon protein is important in producing disease and is also important in the development of protective immunity. Therefore, it is useful to understand the structural details of the fav4 protein.

MATERIALS AND METHODS

Protein

The E3W8N8_9ADEN E3W8N8 fav4 hexon protein amino acid sequence was obtained from GenBank and used for modelling.

Modelling software

https://swissmodel.expasy.org was reached to model the protein.

RESULTS AND DISCUSSION

Project summary

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KFRQTVVAPTRNVTTEKAQRLQIRFYPIQTDDTSTGYRVRYNINVGDGWVLDMGSTYFDIKGILDRGPSFKPYCGTAYNPLAPKESMF  120
NNWSETAPGQNVSASGQLSNVYTNTSTSKDTT                                                          0

AAQVTKISGVFPNPNQGPGRNPLRRVENANTGVLGRFAKSQYNYAYGAYVKPVAADGSQSLTQTPYWIMDNTGTNYLGAVAVEDYTNS  240
LSYPDTIVVPPPEDYDDYNIGTTRALRPNYIG                                                          0

FRDNFINLLYHDSGVCSGTLNSERSGMNVVVELPDRNTELSYQYMLADMMSRHH                                    294
```

Template Results

A total of 179 templates were found to match the target sequence. This list was filtered by a heuristic down to 50. The top templates are:

Template	Sequence Identity	Biounit Oligo State	Description
2iny.1	74.74	homo-trimer	Hexon protein Nanoporous Crystals of Chicken Embryo Lethal Orphan (CELO) Adenovirus Major Coat Protein, Hexon

Template	Sequence Identity	Biounit Oligo State	Description
2iny.1	76.71	homo-trimer	Hexon protein Nanoporous Crystals of Chicken Embryo Lethal Orphan (CELO) Adenovirus Major Coat Protein, Hexon
6qi5.1	42.55	hetero-20-mer	Hexon protein Near Atomic Structure of an Atadenovirus Shows a possible gene duplication event and Intergenera Variations in Cementing Proteins
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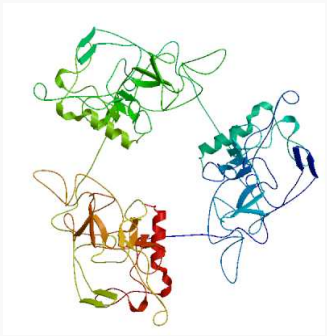
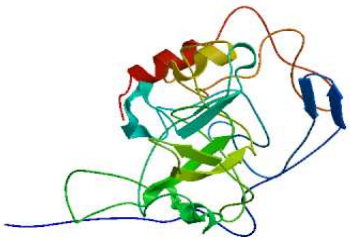
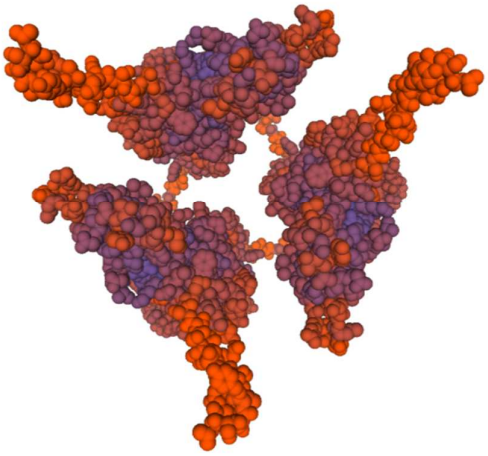
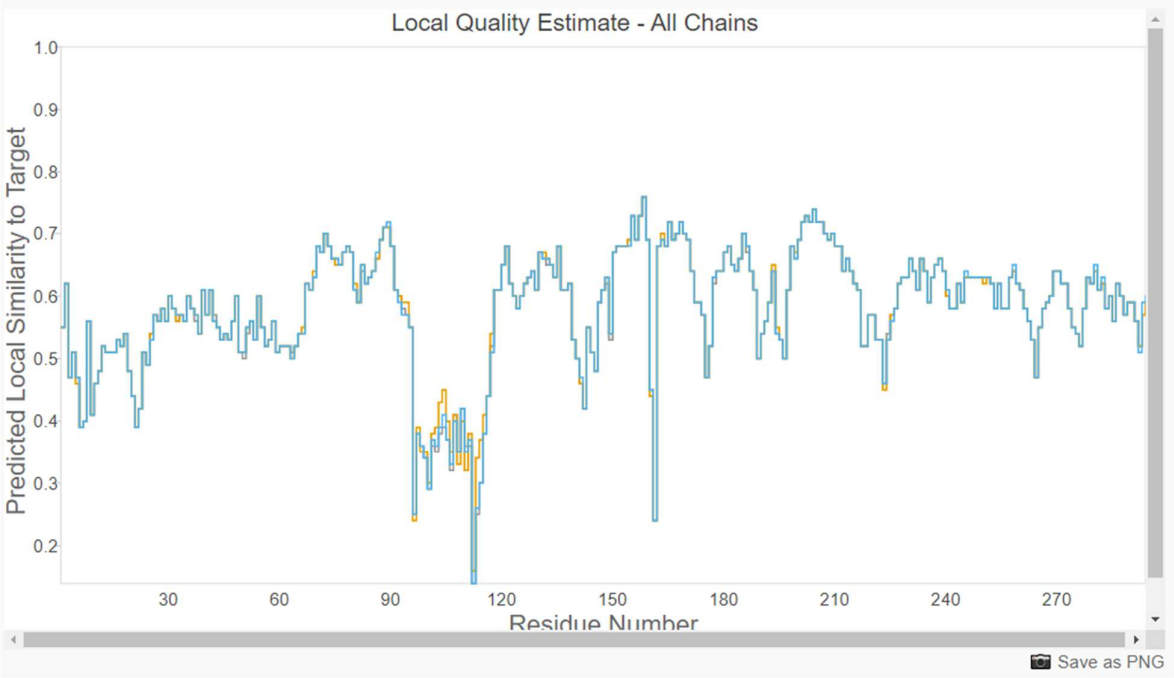
Model Results

	Id	Template	GMQE	QMEANDisCo Global	Oligo State	Ligands
	01	2iny.1.A	0.73	0.58 ± 0.05	homo-trimer	-
	02	6qi5.1.E	0.56	± 0.05	monomer	-



Spacefill model



It is apparent that two models could be constructed and structural details could be elucidated.

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