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Modeling of canine adenovirus 2 hexon protein

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ABSTRACT

Modelling of cav2 hexon protein was done using SWISS-MODEL software and structural details could be visualized and a 3-D image was obtained.

Key words: Modelling, adenovirus, hexon, protein

INTRODUCTION

Canine adenovirus (CAV), a non-enveloped dsDNA virus, is a member of the genus Mastadenovirus under the family Adenoviridae. Based on genetic and antigenic characteristics, canine adenoviruses are divided into two types: canine adenovirus type 1 (CAV-1) and canine adenovirus type 2 (CAV-2). Although CAV-1 affects the digestive tract and causes infectious canine hepatitis (ICH) accompanied by uveitis and interstitial nephritis in dogs, CAV-2 is mainly associated with respiratory type of disease. Modeling of cav2 hexon protein may provide valuable data on its structure.

MATERIALS AND METHODS

Protein sequence

Canine adenovirus 2 hexon gene sequence was downloaded GenBank: EU794687, 12718 bp DNA linear and the amino acid sequence was used for modelling.

Modelling software

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

RESULTS AND DISCUSSION

The results obtained are given below.

Target

MATPSMLPQWSYMHIAGQDAAEYLSPALVQFAQATSSYFKLDNKFRNPTVAPTHDVTTERSQRLQLRFV 120
PVMQEDGQYTYKTRFQLAVGDNRVLDMASTYFDIRGTLDRGPSFKPYSGTA

YNALAPKAGANNCLFNGQGANINTLAQVPSAGAITVNGQAAVTNNTYQPEPQLGPESWVDGSLAELGDA 240
SGRALKASTPRMPCYGSYAPPTNENGGQATGPVESRFYKVTTNNNNEADAM

LYTEDVNLQAPDTHLVHQVPEGQVTGVQGLGQQAAPNRPNYIGFRDNFIGLMYYNSNGNLGVLAGQSSQ 360
LNAVVDLQDRNTELSYQLLLDALTDRSRYFSMWNQAVDSYDQDVRIIDNHG

VEDDMPNYCYPLSGMGPLTNMTTMKVNNQNFQAENANVGPIQKIGFGNVEAMEINLNANLFKSFLYSNV 480
ALYLPDAFKYTPENIVAPANVNTYAYMNVRLPAANLIDTFVNIGARWSPDV

MDTVNPFNHHRNAGLRYRSQLLGNGRYCSFHIQVPQKFFAIKNLLLLPGTYTYEWSFRKDVNMILQSSLG 600
NDLRVDGATINIQSINLYASFFPMAHNTASTLEAMLRNDVNDQSFADYLS

SANMLYPIPANTTNLPISIPARNWAGFRGWSFTRIKQRETPALGSPYDPYFTYSGSIPYLDATFYLSHTFRR
VSIMFDSSVSWPGNDRLLTPNEFEIKRYVDGEGYNVAQSNMTKDWFMV 720

QMLAHYNIGYQGYHLPESYKDRMYSFLRNFEPMCRQLVDVANYAAYQPVTVGHQHNNSGYASALSAFN
PREGHPYPANWPYPLIGANAVPTVTQKKFLCDRSLWRIPFSSNFMSMGTLTD 840

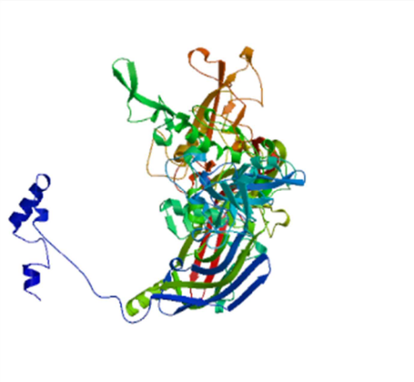
LGQNLLYSNSAHALDMTFEVDAMNEPTLLYVLFEVFDVARVHQPHRGVIEVVYLRTPFSAGNATT 905

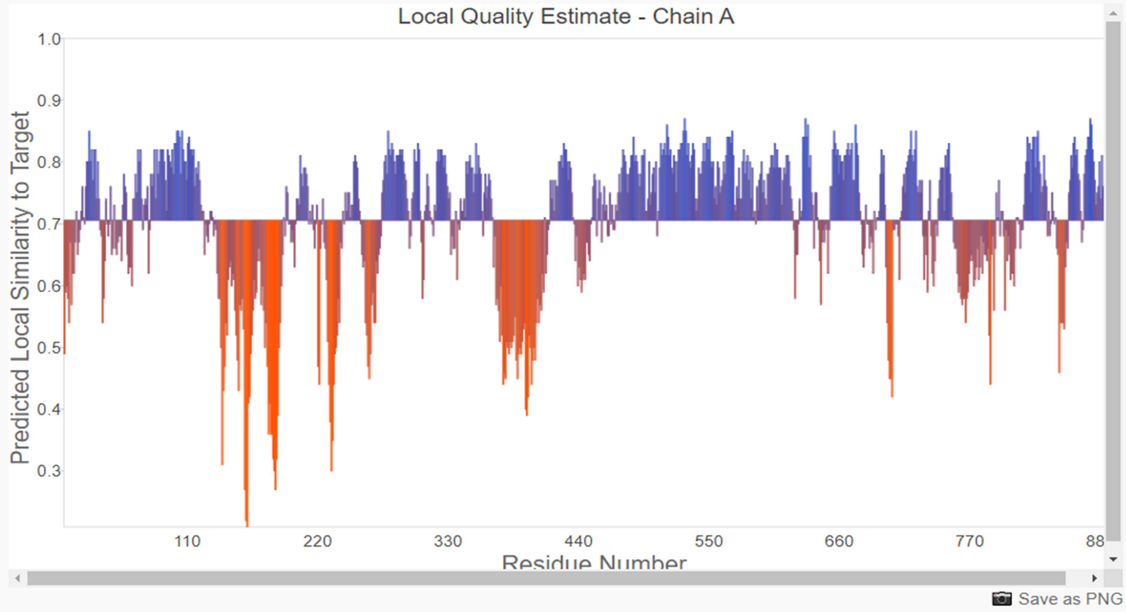
Template Results

A total of 361 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
1p2z.1	71.75	homo-trimer	Hexon protein Refinement of Adenovirus Type 2 Hexon with CNS
2obe.1	71.59	homo-trimer	Hexon protein Crystal Structure of Chimpanzee Adenovirus (Type 68/Simian 25) Major Coat Protein Hexon
6b1t.1	71.37	hetero-25-mer	Hexon protein Improved cryoEM structure of human adenovirus type 5 with atomic details of minor proteins VI and VII
6b1t.1	71.37	hetero-25-mer	Hexon protein Improved cryoEM structure of human adenovirus type 5 with atomic details of minor proteins VI and VII
6b1t.1	71.37	hetero-25-mer	Hexon protein Improved cryoEM structure of human adenovirus type 5 with atomic details of minor proteins VI and VII

Model Results

	Id	Template	GMQE	QMEANDisCo Global	Oligo State	Ligands
	01	1p2z.1.A	0.73	0.71 ± 0.05	monomer	



QMEANDisCo Global: ± 0.05

QMEAN Z-Scores

QMEAN	-2.03
Cβ	-2.19
All Atom	-1.97
solvation	-2.46
torsion	-0.79

★Comparison with Non-redundantSet of PDB StructuresNormalized QMEAN4Protein Size (Residues)

Fig. CAV2 hexon protein as ball and stick(A) and as spacefill (B) model.

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