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Modeling of canine adenovirus1 hexon protein

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Abstract

Modeling of CAV1 hexon protein was done using SWISS-MODEL software. Valuable structural properties could be elucidated.

Key words: Modeling, CAV1, penton, protein.

Introduction

Canine adenovirus-1 (CAV-1), 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 cav1 hexon protein may provide valuable data on its structure.

Materials and Methods

Protein sequence

Canine adenovirus-1 strain 574-2013-RS hexon gene,complete cds GenBank: KP840549.1 linear 2718 bp DNA was downloaded and the amino acid sequence was used for modelling.

Modelling software

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

Results and Discussion

Project Summary

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MATPSMLPQWSYMHIAGQDAAEYLSPALVQFAQATSSYFKLDNKFRNPTVAPTHDVTTERSQRLQ  120
LRFVPVMQEDGQYTYKTRFQLAVGDNRVLDMASTYFDIRGTLDRGPSFKPYSGTA

YNALAPRAGANNCLFNGSGANINTLAQVPFAGAITVNGQAAVTDNTYQPEPQLGPESWVDGTLAD  240
LGDASGRALKASTPRMPCYGSYAPPTNENGGQATGAVERRFYKVTTNNNNEADAL

LYTEDVNLQTPDTHLVHQVSDDQVTGVQGLGQQAAPNRPNYIGFRDNFIGLMYYNSNGNLGVLAG  360
QSSQLNAVVDLQDRNTELSYQLLLDALTDRSRYFSMWNQAVDSYDQDVRIIDNHG
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VEDDMPNYCFPLSGMGPLTNMTAMKVNSQNFQTDNTNVGPIQKIGFGNVEAMEINLNANLFKGFL
YSNVALYLPDAYKYTPDNIVAPANANTYAYMNVRLPAANLIDTFVNIGARWSPDV 480

MDSVNPFNHHRNAGLRYRSQLLGNGRYCSFHIQVPQKFFAIKNLLLLPGTYTYEWSFRKDVNMIL
QSSLGNDLRVDGASINIQSINLYASFFPMAHNTASTLEAMLRNDVNDQSFADYLS 600

AANMLYPIPANTTNLPISIPARNWAGFRGWSFTRIKQRETPALGSPYDPYFTYSGSIPYLDSTFY
LSHTFRRVSIMFDSSVSWPGNDRLLTPNEFEIKRYVDGEGYNVAQSNMTKDWFLV 720

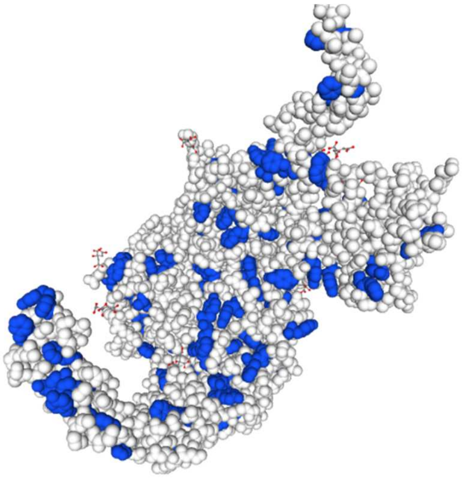
QMLAHYNIGYQGYHLPESYKDRMYSFLRNFEPMCRQLVDVTNYATYQSVTVGHQHNNSGYASALS
TFNPREGHPYPANWPYPLIGVNAVPTVTQKKFLCDRTLWRIPFSSNFMSMGTLTD 840

LGQNLLYSNSAHALDMTFEVDAMNEPTLLYVLFEVFDVARVHQPHRGVIEVVYLRTPFSAGNATT 905

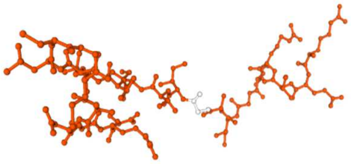
Template Results

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	72.64	homo-trimer	Hexon protein Refinement of Adenovirus Type 2 Hexon with CNS
2obe.1	72.59	homo-trimer	Hexon protein Crystal Structure of Chimpanzee Adenovirus (Type 68/Simian 25) Major Coat Protein Hexon
1p2z.1	72.89	homo-trimer	Hexon protein Refinement of Adenovirus Type 2 Hexon with CNS
6b1t.1	72.25	hetero-25-mer	Hexon protein Improved cryoEM structure of human adenovirus type 5 with atomic details of minor proteins VI and VII
6b1t.1	72.25	hetero-25-mer	Hexon protein Improved cryoEM structure of human adenovirus type 5 with atomic details of minor proteins VI and VII



Spacefill model



Ball + stick model

It is evident that valuable structural parameters could be obtained.

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