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Modeling of canine distemper virus hemagglutinin protein

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ABSTRACT

Modeling of canine distemper virus hemagglutinin protein was done using SWISS-MODEL software. Structural details could be elucidated.

Key words: Modeling, canine distemper virus, hemagglutinin, protein.

INTRODUCTION

Canine distemper virus (CDV) is an important pathogen of dogs and causes serious disease conditions including fatality. The H protein plays an important role in induction of immune response. Therefore it is useful to understand the structural details of the H protein.

MATERIALS AND METHODS

Protein

Canine distemper virus strain TW/05-YY hemagglutinin (H) gene, complete cds. GenBank: EU296493.1 1824 bp cRNA 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

Project summary

MLSYQDKVGAFYKDTARANSSKLSLVTEEQGGRRPPYLLFVLLILLIGILALLAITGVRFHQVSTS 120
NMEFSRLLKEDMEKSEAVHHQVIDVLTPLFKIIGDEIGLRLPQKLNEIKQFILQ

KTNFFNPNREFDFRDLHWCINPPSKIKVNFTNYCDTVGVKNSIASAANPIILSALSGARGDIFPPY 240
RCSGATTSVGRVFPLSVSLSMSLISRTSEIINMLTAISDGVYGKTYLLVPDYIE

GEFDSQKIRVFEIGFIKRWLNNMPLLQTTNYMVLPETSKAKVCTIAVGELTLASLCVGESTVLLY 360
HDSNGSQNGILVVTLGIFGPTPMDQVGEVIPIAHPSVERIHITNHRGFIKDSVVT

WMVPVLVSEKQEEQKNCLESACQRKSYPMCNQTSWEPFGGGQLPSYGRLTLPLDPSVDLQLNI 480
SFTYGPVILNGDGMDYYESPLLESGWLTIPPKNGTVLGLINKASRGDQFTVTPHVLT

FAPRESSGNCYLPIQTSQIMDKDVLTESNLVVLPTQNFRYVIATYDISRGDHAIVYYVYDPIRTIF 600
YTYPFRLTTKGRPDFLRIECFVWDDDLWCHQFYRFEANITNSTTSVENLVRIRF

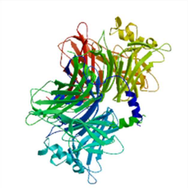
SCNRARP 60

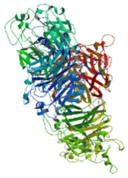
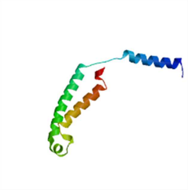
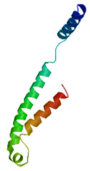
Template Results

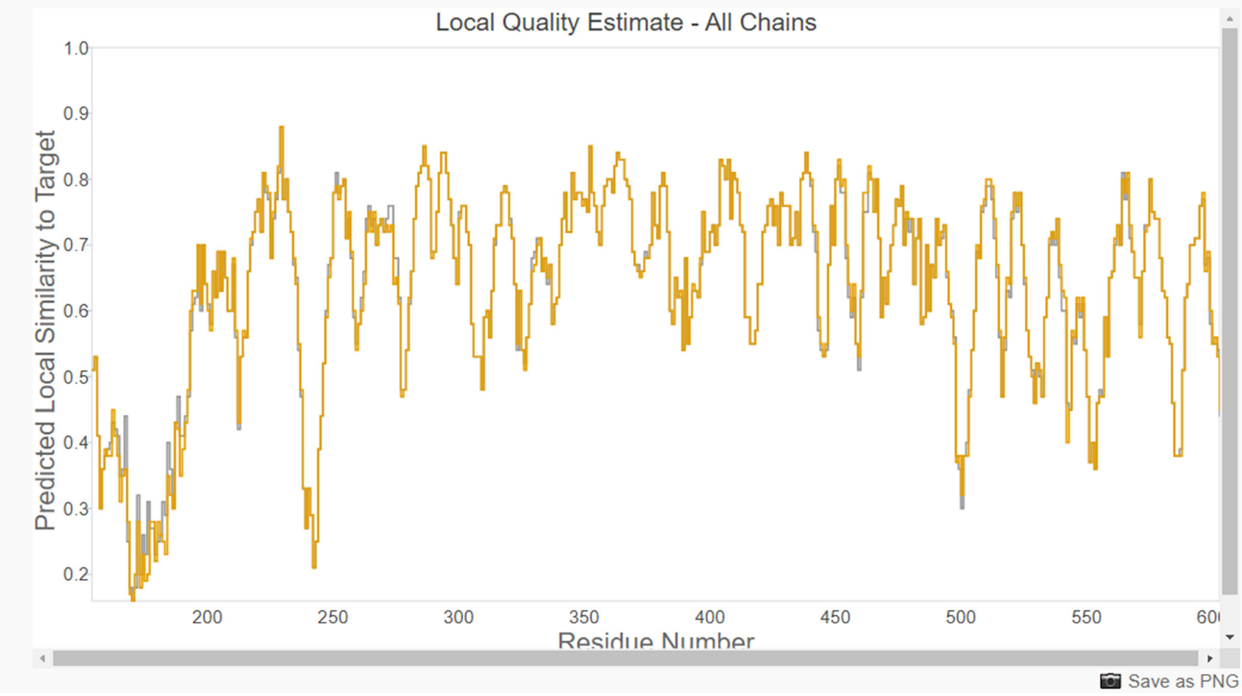
A total of 80 templates were found to match the target sequence. This list was filtered by a heuristic down to 24. The top templates are:

Template	Sequence Identity	Biounit Oligo State	Description
2zb5.1	33.41	homo-dimer	Hemagglutinin protein Crystal structure of the measles virus hemagglutinin (complex-sugar-type)
2zb5.1	34.51	homo-dimer	Hemagglutinin protein Crystal structure of the measles virus hemagglutinin (complex-sugar-type)
2zb6.1	33.41	homo-dimer	Hemagglutinin protein Crystal structure of the measles virus hemagglutinin (oligo-sugar type)
2zb6.1	34.51	homo-dimer	Hemagglutinin protein Crystal structure of the measles virus hemagglutinin (oligo-sugar type)
3alx.1	36.54	homo-tetramer	Hemagglutinin,LINKER,CDw150 Crystal structure of the measles virus hemagglutinin bound to its cellular receptor SLAM (MV-H(L482R)-SLAM(N102H/R108Y) fusion)

Model Results

Id	Template	GMQE	QMEANDisCo Global
	01	2zb5.1.A	0.58

Id	Template	GMQE	QMEANDisCo Global
	02	7bwu.1.A	0.29
	03	3on0.1.A	0.04
	04	3on0.1.C	0.04



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

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