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Modeling of infectious bursal disease virus VP2 protein

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ABSTRACT

Modeling of infectious bursal disease virus VP2 protein was done using SWISS-MODEL software. Structural details could be elucidated.

Key words: Modeling, IBD virus, vp2, protein

INTRODUCTION

Infectious bursal disease virus (IBDV) is an important pathogen of chicken and causes fatality as well as drop in egg production. VP 2 protein plays an important role in induction of immune response. Therefore it is useful to understand the structural details of the VP 2 protein.

MATERIALS AND METHODS

Protein

IBD virus vp2 gene sequence was downloaded GenBank: GenBank: OM307063.1 linear 3121 bp RNA 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

RSLLMPTTGPASIPDDTLEKHTLRSETSTYNLTVGDTGSGLIVFFPGFPGSIVGAHYTLQSDGNYKFDQMLL
TAQNLPASYNYCRLVSRSLTVRSSTLPGGVYALNGTINAVTFQGSLSE 120

LTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGLDPKMVATCDSSDRPRV
YTITAADNYQFSSQYKTGGVTITLFSANIDAITSLSVGGELVFKTSIQNL 240

VLGATIYLIGFDGTAVITRAVAANNGLTAGIDNLMPFNLVIPTSEITQPITSIKLEIVTSKSDGQVGEQMSWS
ASGSLAVTIHGGNYPGALRPVTLVAYERVAKGSVVTVAGVSNFELIP 360

NPELAKNLVTEYGRFDPGAMNYTKLILSERDRLGIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFK
DIIRAIRRIAVPVVSTLFPPAAPLAHAIGEGVDYLLGDEAQAASGTARAA 480

SGK 483

Template results

A total of 34 templates were found to match the target sequence. This list was filtered by a heuristic down to 8. The top templates are:

Template	Sequence Identity	Biounit Oligo State	Description
2df7.1	95.13	homo-60-mer	structural polyprotein VP2 Crystal structure of infectious bursal disease virus VP2 subviral particle
2df7.1	95.19	homo-60-mer	structural polyprotein VP2 Crystal structure of infectious bursal disease virus VP2 subviral particle
2df7.1	95.13	homo-60-mer	structural polyprotein VP2 Crystal structure of infectious bursal disease virus VP2 subviral particle
3fbm.1	95.59	homo-60-mer	Polyprotein D431N Mutant VP2 Protein of Infectious Bursal Disease Virus; Derived T=1 Particles
2df7.1	95.19	homo-60-mer	structural polyprotein VP2 Crystal structure of infectious bursal disease virus VP2 subviral particle

Model results Id	Template	GMQE	QMEANDisCo Global	Oligo State	Ligands	Oligo State	Ligands
01	2df7.1.A	0.78	0.84 ± 0.050	homo-60-mer	20 x CA		20 x CA

QMEAN Z-Scores

QMEAN	-0.28
Cβ	-0.83
All Atom	-0.93
solvation	-1.40
torsion	0.33

Template

2df7.1.A structural polyprotein VP2 Crystal structure of infectious bursal disease virus VP2 subviral particle

Seq Identity 95.13%

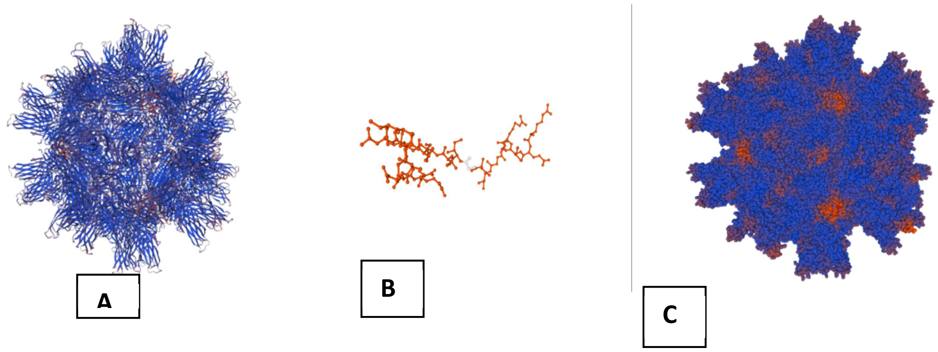
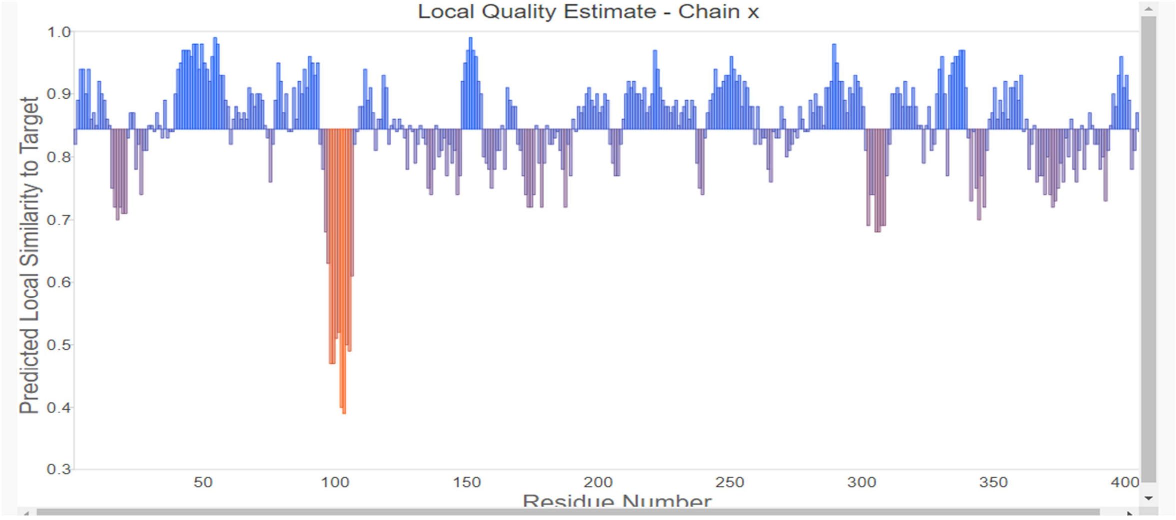


Fig. IBD VP2 A-cartoon, B- ball &



It is evident that details of the protein structure could be deduced.

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