



Modeling of human herpesvirus 8 glycoprotein gp35/37

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Abstract

Modeling of human herpesvirus 8 glycoprotein gp35/37 was done and valuable information about its structural details was revealed.

Key words: Modeling, human herepesvirus, glycoprotein, gp35/37 protein

Introduction

Viral proteins play an important role in their actions and study of their structural details would be of great importance.

Materials and Methods

Protein

The amino acid sequence of human herpesvirus 8 glycoprotein gp35/37 GenBank: AF009173.1 protein sequence was downloaded from GenBank and used for modeling.

Modelling software

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

Project Summary

Targe	MSSTQIRTEIPVALLILCLCLVACHANCPTYRSHLGFWQEGWSGQVYQDWLGRMNC SYEN	90
t 1	MTALEAVSLNGTRLAAGSPSSEYPNVSVSV	
Targe	EDTSASGSGEDAIDESGSGEEERPVTSHVTFMTQSVQATTELTDALISAFSGSYSSGEP S	18
t 1	RTTRIRVSPVAENGRNSGASNRV PFSATT	0
Targe	TTRGRDAHYN AEIRTHLYILWAVGLLLGLVLILYLCVPRCRRKPYIV	22
t 1		8

Template Results

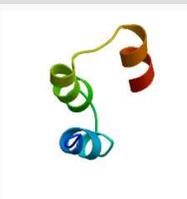
A total of 23 templates were found to match the target sequence. This list was filtered by a heuristic down to 10. The top templates are:

Template	Sequence Identity	Biounit Oligo State	Description
6jmq.1	38.24	hetero-tetramer	4F2 cell-surface antigen heavy chain LAT1-CD98hc complex bound to MEM-108 Fab

Template	Sequence Identity	Biounit Oligo State	Description
8kdh.1	38.24	hetero-dimer	4F2 cell-surface antigen heavy chain Structure of LAT1-CD98hc in complex with BCH, focused on T
8kdi.1	38.24	hetero-tetramer	4F2 cell-surface antigen heavy chain Structure of apo inward-open LAT1-CD98hc-Fab170 in nanodisc
7dcv.1	39.29	monomer	Programmed cell death 1 ligand 1 Structure of the transmembrane domain of human PD-L1
8kdp.1	38.24	hetero-dimer	4F2 cell-surface antigen heavy chain Structure of apo outward-open LAT1-CD98h in nanodisc, focus

[Show full template details](#)

Model Results

	Id	Template	GMQE	QMEANDisCo Global	Oligo St
	02	1utr.1.A	0.07	0.32 ± 0.12	monome
	01	6jmq.1.B	0.01	± 0.12	monome

References

Berman H, Henrick K, Nakamura H, Markley JL. 2007. The worldwide Protein Data Bank (wwPDB): ensuring a single, uniform archive of PDB data. *Nucleic Acids Res.* 35: D301-303.

Bertoni M, Kiefer F, Biasini M, Bordoli L, Schwede T. 2017. Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. *Scientific Reports* 7.



Bienert S, Waterhouse A, de Beer TAP, Tauriello G, Studer G, Bordoli L, Schwede T. 2017. The SWISS-MODEL Repository - new features and functionality. *Nucleic Acids Res.* 45: D313-D319.

Bordoli L, Schwede T. 2012. Automated protein structure modeling with SWISS-MODEL Workspace and the Protein Model Portal. *Methods Mol. Biol.* 857:107-136.

Guex N, Peitsch MC, Schwede T. 2009. Automated comparative protein structure modeling with you SWISS-MODEL and Swiss-PdbViewer: A historical perspective. *Electrophoresis* 30: S162-S173.

Mariani V, Biasini M, Barbato A, Schwede T. 2013. IDDT: a local superposition-free score for comparing protein structures and models using distance difference tests. *Bioinformatics* 29: 2722-2728.

Mirdita M, von den Driesch L, Galiez C, Martin MJ, Söding J, Steinegger M *Uniclust databases of clustered and deeply annotated protein sequences and alignments.* *Nucleic Acids Res.* 45, D170–D176. (2016)

Schwede T, Kopp J, Guex N, Peitsch MC. 2003. SWISS-MODEL: an automated protein homology- modeling server. *Nucleic Acids Res.* 31: 3381-3385.

Steinegger M, Meier M, Mirdita M, Vöhringer H, Haunsberger S J, Söding J. 2019. HH-suite3 for fast remote homology detection and deep protein annotation. *BMC Bioinformatics* 20, 473.

Studer G, Rempfer C, Waterhouse AM, Gumienny R, Haas J, Schwede T. 2020. QMEANDisCo – distance constraints applied on model quality estimation. *Bioinformatics* 36: 1765-1771.

Studer G, Tauriello G, Bienert S, Biasini M, Johner N, Schwede T. 2021. ProMod3 - A versatile homology modelling toolbox. *PLOS Comp. Biol.* 17: e1008667.

Waterhouse A, Bertoni M, Bienert S, Studer G, Tauriello G, Gumienny R, Heer FT, de Beer TAP, Rempfer C, Bordoli L, Lepore R, Schwede T. 2018. SWISS-MODEL: homology modelling of protein structures and complexes. *Nucleic Acids Res* 46(W1): W296-W303.