19.6 Devi & Rai, 2026 Biotechnology International 19:26-30.
https://www.biotechnologyinternational.org

# Modeling of human betaherpesvirus 6B U85 glycoprotein

**Soni Devi, Anant Rai**

BTS institute, 197 Mundia Ahmednagar, Pilibhit Road, Bareilly-243122,
Correspondence: anant1948@zohomail.in

## Abstract

**Modeling of human betaherpesvirus 6B U85 glycoprotein was done and valuable information about its structural details was revealed.**

**Key words: Modeling, human betaherepesvirus, glycoprotein,**

## 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 signal transducing membrane glycoprotein sequence was downloaded from GenBank: AB190768.1
and used for modeling.

### Modelling software

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

### Template Search

Template search with BLAST and HHblits has been performed against the SWISS-MODEL template library (SMTL, last update: 2026-03-11, last included PDB release: 2026-03-06).

The target sequence was searched with BLAST against the primary amino acid sequence contained in the SMTL. A total of 1 template was found.

An initial HHblits profile has been built using the procedure outlined in (Steinegger et al.), followed by 1 iteration of HHblits against Uniclust30 (Mirdita, von den Driesch et al.). The obtained profile has then be searched against all profiles of the SMTL. A total of 16972 templates were found.

### Template Selection

For each identified template, the template's quality has been predicted from features of the target-template alignment. The templates with the highest quality have then been selected for model building.

## Model Building

Models are built based on the target-template alignment using ProMod3 (Studer et al.). Coordinates which are conserved between the target and the template are copied from the template to the model. Insertions and deletions are remodelled using a fragment library. Side chains are then rebuilt. Finally, the geometry of the resulting model is regularized by using a force field.

## Model Quality Estimation

The global and per-residue model quality has been assessed using the QMEAN scoring function (Studer et al.).

## Ligand Modelling

Ligands present in the template structure are transferred by homology to the model when the following criteria are met: (a) The ligands are annotated as biologically relevant in the template library, (b) the ligand is in contact with the model, (c) the ligand is not clashing with the protein, (d) the residues in contact with the ligand are conserved between the target and the template. If any of these four criteria is not satisfied, a certain ligand will not be included in the model. The model summary includes information on why and which ligand has not been included.

## Oligomeric State Conservation

The quaternary structure annotation of the template is used to model the target sequence in its oligomeric form. The method (Bertoni et al.) is based on a supervised machine learning algorithm, Support Vector Machines (SVM), which combines interface conservation, structural clustering, and other template features to provide a quaternary structure quality estimate (QSQE). The QSQE score is a number between 0 and 1, reflecting the expected accuracy of the interchain contacts for a model built based a given alignment and template. Higher numbers indicate higher reliability. This complements the GMQE score which estimates the accuracy of the tertiary structure of the resulting model.

## Results and Discussion

### Project Summary

```
Target 1 MSPLMLRLLPLLCIIISAHFVPRPETSPSLVYEIGSTVTFHCRLNTTTNIQSVSWYNKSR 90
         LISNHEVQNMDNLSFTDDGYVFIHELNKIN

Target 1 NLDVDSKLYFHIKHDRTTSLLKIKARSTYDATCLTCTFTVDNEKTSATSCLKLIMKPIVV 180
         LYFRYLNNFLDVTCTVTSYPKPNVVIKFLG

Target 1 EVYKRDIPMVRQNENGSSTVSVSFTFKRRTKLEFVGKTISCLASSWFTNQKASALVTSGE 270
         HTVQNHDEYSKEAVKGSNSDEIVFTWIVPL

Target 1 ILILIISVMVILISMCIVAFKS                                       292
```

### Template Results

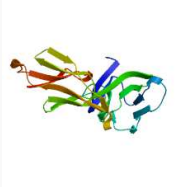
A total of 16845 templates were found to match the target sequence. This list was filtered by a heuristic down to 50. The top templates are:

| Template | Sequence Identity | Biounit Oligo State | Description |
|---|---|---|---|
| A0A126LB32.1 | 91.72 | monomer | U85<br>AlphaFold DB model of A0A126LB32_HUMAN (gene: U85, organism: Hom |
| 4utb.2 | 12.50 | hetero-trimer | BROADLY NEUTRALIZING HUMAN ANTIBODY EDE2 A11<br>Crystal structure of dengue 2 virus envelope glycoprotein in complex with t neutralizing human antibody EDE2 A11 |
| 6ldx.1 | 16.02 | hetero-trimer | Fab light chain<br>Structure antibody E6 in complex with methylated peptide |
| 4fmk.1 | 15.90 | homo-dimer | Poliovirus receptor-related protein 2<br>Crystal structure of mouse nectin-2 extracellular fragment D1-D2 |
| 4fs0.1 | 15.66 | monomer | Poliovirus receptor-related protein 2<br>Crystal structure of mutant F136D of mouse nectin-2 extracellular fragment |

Show full template details

## Model Results

| | Id | Template | GMQE | QMEANDisCo Global | Oligo |
|---|---|---|---|---|---|
| | 01 | A0A126LB32.1.A | 0.75 | | mono |
| | 02 | 4utb.2.B | 0.34 | ± 0.06 | mono |

| | Id | Template | GMQE | QMEANDisCo Global | Oligo |
|---|---|---|---|---|---|
|  | 03 | 6yjp.3.A | 0.33 | 0.48 ± 0.06 | mono |
| | 04 | 4ozh.1.D | 0.32 | ± 0.06 | mono |

**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. lDDT: 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
2 Steinegger M, Meier M, Mirdita M, Vöhringer H, Haunsberger SJ, 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.