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Research Article

MODELING OF RABIES GLYCOPROTEIN USING SWISS-MODEL

Hiteshwari Singh Chauhan[1] and Anant Rai[2]*

[1]Invertis University, Bareilly, [2]Institute of Biotechnology & IT, Mudiya Ahmadnagar, Bareilly-243122, UP, India.

***Corresponding author: raia48@gmail.com**

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ABSTRACT

The modelling of rabies glycoprotein was done using Swiss-Model software. The unique structural details could be observed an analysed.

Keywords: Rabies, glycoprotein, modeling, Swiss-Model.

INTRODUCTION

Rabies is a very important infectious disease of man and animals which is transmissible from dog to man. The glycoprotein of rabies virus is important in its infection process and the antibodies produced by glycoprotein are able to neutralize the virus. Therefore understanding of the structural details of this protein may provide valuable information in understanding the immune responses against rabies and develop efficient advanced vaccines.

MATERIALS AND METHODS

Rabies virus gp gene for glycoprotein, genomic RNA GenBank: AJ489620.1 was used for obtaining amino acid sequence and modeling (Table 1).

Table 1: Primary amino acid sequence of rabies glycoprotein (G).

MVPQALLFVPLLVFPLCFGKFPIYTIPDKLGPWSPIDIHHLSCPNNLVVEDEGCTNLSG
FSYMELKVGYILAIKMNGFTCTGVVTEAETYTNFVGYVTTT
FKRKHFRPTPDACRAAYNWKMAGDPRYEESLHNPYPDYRWLRTVKTTKESLVIISPS
VADLDPYDRSLHSRVFPSGKCSGVAVSSTYCSTNHDYTIWMPE
NPRLGMSCDIFTNSRGKRASKGSETCGFVDERGLYKSLKGACKLKLCGVLGLRLMD
GTWVAMQTSNETKWCPPDQLVNLHDFRSDEIEHLVVEELVRKRE

ECLDALESIMTTKSVSFRRLSHLRKLVPGFGKAYTIFNKTLMEADAHYKSVRTWNEI
LPSKGCLRVGGRCHPHVNGVFFNGIILGPDGNVLIPEMQSSLL
QQHMELLESSVIPLVHPLADPSTVFKDGDEAEDFVEVHLPDVHNQVSGVDLGLPNW
GKYVLLSAGALTALMLIIFLMTCCRRVNRSEPTQHNLRGTGREV
SVTSQSGKIISSWESHKSGGETRL

Modeling

The SWISS-MODEL template library (SMTL version 2019-05-15, PDB release 2019-05-10) was searched with BLAST (Camacho *et al*., 2009) and HHBlits (Remmert *et al*., 2012) for evolutionary related structures matching the target sequence in Table 1. Overall 45 templates were found. The target sequence was searched with BLAST against the primary amino acid sequence contained in the SMTL. 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. Models are built based on the target-template alignment using ProMod3. 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. In case loop modelling with ProMod3 fails, an alternative model is built with PROMOD-II (Guex *et al*., 1999, 2009; Guex and Peitsch, 1996, 1997). The global and per-residue model quality has been assessed using the QMEAN scoring function (Benkert *et al*., 2011). For improved performance, weights of the individual QMEAN terms have been trained specifically for SWISS-MODEL. 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.

The quaternary structure annotation of the template is used to model the target sequence in its oligomeric form. The method (Bertoni *et al*., 2017) 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

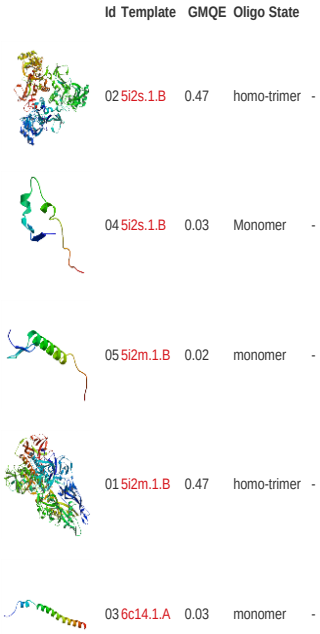

Fig. 1. Results obtained in Swiss-modeling of rabies G

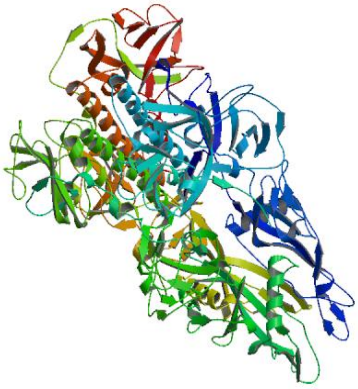

Fig. 2. Model 01 seen in spdbv 4.01

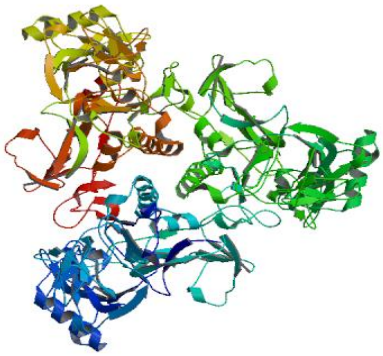

Fig. 3. Model 02 seen in spdbv 4.01.

Swiss-model and spdbv 4.01 are being extensively used in protein modeling and viewing of protein models and structures (Bertoni *et al*., 2017; Bienert *et al*., 2017; Carson, 1987; Guex, 1996; Guex, N. and Peitsch, 1996, 1997; Guex *et al*., 1999; 2009; Johansson, *et al*., 2012; Schwede *et al*., 2003; Waterhouse *et al*., 2018; url: http://www.expasy.org/spdbv/)

CONCLUSION

The model of rabies glycoprotein has been successfully constructed ad the structural details have been clearly visualised and studied.

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