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Modeling of virulent rabies virus glycoprotein

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ABSTRACT

Modeling of virulent rabies virus glycoprotein was done using SWISS-MODEL software and valuable structural details were studied. The reacting sites in the protein could be visualised.

Key words: Modeling, rabies, virus, virulent strain, glycoprotein

INTRODUCTION

Rabies virus is very important since it causes infection in animals and man and is fatal. Glycoprotein is responsible for its infectious property and is responsible for producing neutralizing antibodies and thus plays role in protection.

MATERIALS AND METHODS

Protein

Rabies virus strain virulent glycoprotein (G) gene, genomic RNA was downloaded GenBank: EF151231.1 linear 1575 bp cRNA and amino acid sequence was used for modelling.

Modelling software

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

RESULTS AND DISCUSSION

Project summary

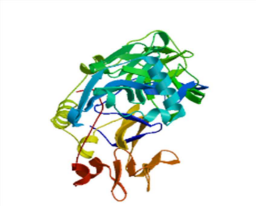
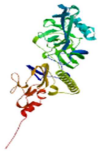
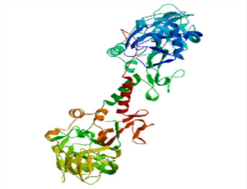
MVPQALLFVPLLVFPLCFGKFPIYTIPDKLGPWSPIDIHHLSCPNNLVVEDEGCTNLSGFSYMELKVGYISAIKMNGFTCTGV VTEADTYTNFVGYVTTTFKRKHFRPTPDACRAAYNWK	120
MAGDPRYEESLHNPYPDYHLLRTVKTTKESLVIISPSVADLDPYDKSLHSRVFPSGKCSGITISSTYCSTNHDYTIWMPENPR LGTSCDIFTNSRGKRASKGGKTCGFVDERGLYKSLKG	240
ACKLKLCGVLGLRLMDGTWVAMQTSNETKWCPPDQLVNLHDFRSDEIEHLVVEELVKKREECLDALESIMTTKSVSFRRL SHLRKLVPGFGKAYTIFNKTLMEADAHYKSVRTWNEIIPS	360
KGCLRVGGRCHPHVKGVFFNGIILGPDGHVLIPEMQSSLLRQHMELLESSVIPLMHPLADPSTVFKDGDEAEDFVEVHLPDV HKQISGVDLGLPSWGKYVLVSAGVLVVLMLTIFIITCC	480
GRVHRPKSTQHGLGGTGRKVSVTSQSGKVISSWESYKSGGETRL	524

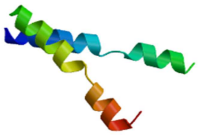
Template Results

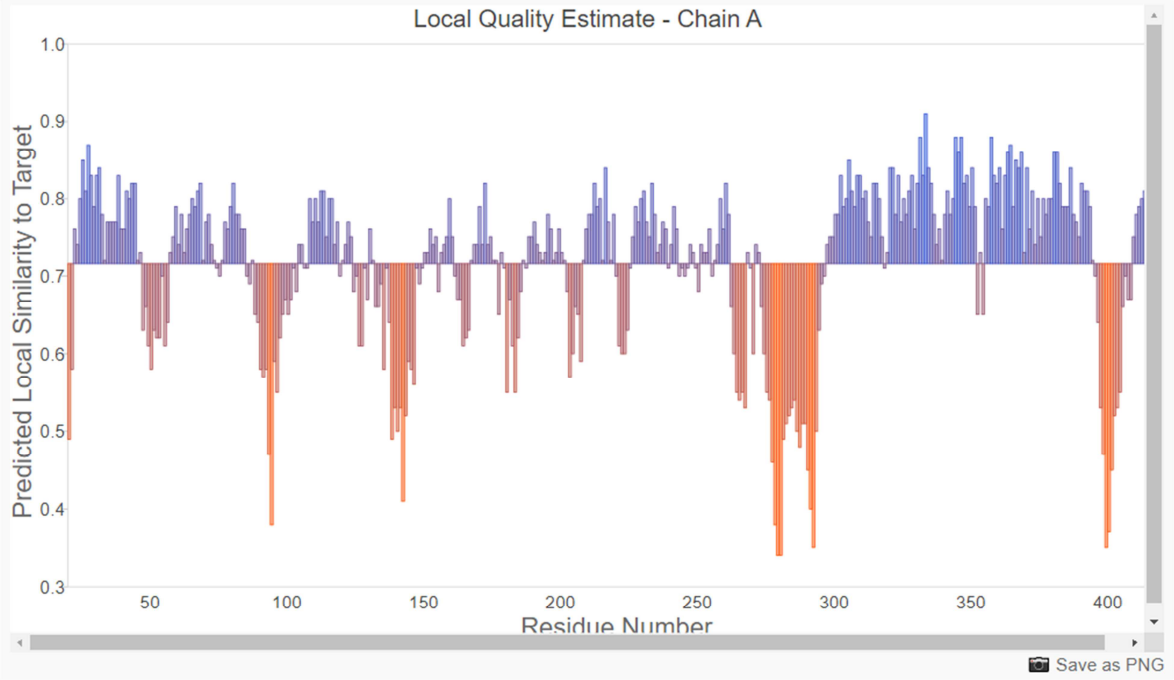
A total of 106 templates were found to match the target sequence. This list was filtered by a heuristic down to 35. The top templates are:

Template	Sequence Identity	Biounit Oligo State	Description
6lgx.1	90.30	homo-dimer	Glycoprotein,Glycoprotein,Glycoprotein Structure of Rabies virus glycoprotein at basic pH
6lgx.1	92.15	homo-dimer	Glycoprotein,Glycoprotein,Glycoprotein Structure of Rabies virus glycoprotein at basic pH
6lgx.1	92.15	homo-dimer	Glycoprotein,Glycoprotein,Glycoprotein Structure of Rabies virus glycoprotein at basic pH
6lgx.1	90.30	homo-dimer	Glycoprotein,Glycoprotein,Glycoprotein Structure of Rabies virus glycoprotein at basic pH
6lgw.2	90.23	hetero-trimer	Glycoprotein,Glycoprotein,Glycoprotein Structure of Rabies virus glycoprotein in complex with neutralizing antibody 523-11 at acidic pH

Model Results

	Id	Template	GMQE	QMEANDisCo Global	Oligo State	Ligands
	03	7u9g.1.A	0.68	± 0.05	monomer	-
	02	6lgw.2.C	0.65	± 0.05	monomer	-
	01	6lgx.1.A	0.63	± 0.05	homo-dimer	-

	Id	Template	GMQE	QMEANDisCo Global	Oligo State	Ligands
	04	1afo.1.A	0.00	± 0.11	homo-dimer	-



It may be seen that valuable models were constructed and the structural details and binding sites could be visualized.

REFERENCES

Berman, H., Westbrook J., Feng Z., Gilliland G., Bhat T. N., Weissig I., Shindyalov I., Bourne P. E. 2000. The Proten Data Bank. Nucleic Acids Res, 28: 235-242.

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

Bienert, S., Waterhouse, A., de Beer, T.A.P., 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.

Grosdidier A, Zoete V, Michielin O. 2011. SwissDock, a protein-small molecule docking web service based on EADock DSS. Nucleic Acids Res, 39: W270-7.

Grosdidier A, Zoete V, Michielin O. 2011. Fast docking using the CHARMM force field with EADock DSS. J Comput Chem. 32: 2149-2159.

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

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., Tauriello, G., Bienert, S., Waterhouse, A.M., Bertoni, M., Bordoli, L., Schwede, T., Lepore, R. 2019. Modeling of Protein Tertiary and Quaternary Structures Based on Evolutionary Information. Methods Mol. Biol. 1851: 301-316.

The UniProt Consortium. 2017. UniProt: the universal protein knowledgebase. Nucleic Acids Res. 45: D158-D169.

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