

Antiviral Targets via Geometry

Robert Penner*

**Institut des Hautes Etudes Scientifiques, France.*

Published December 12th, 2020

ABSTRACT

Just as Ramachandran plots capture normative behavior for conformational angles, new 3-dimensional plots describe the geometry of protein backbone hydrogen bonds. These new plots likewise provide a distribution that elucidates regions of likely/unlikely geometry. A well-known Ansatz in protein theory posits proportionality between differences of free energies of protein details and differences of logarithms of their probabilities as determined by this distribution. This is the basis for the novel method of backbone free energy prediction applied here. The input to the method is a protein PDB file and the output provides a numerical estimate of the inherent backbone free energy nearby each amino acid residue. This method is applied to a wide class of viral glycoproteins, from which there are two overriding conclusions: 1) in known cases, the method effectively pinpoints both fusion peptides and receptor binding domains; 2) in particular cases where pre- and post-fusion conformations of fusion peptides can be compared, the method identifies regions primed for large conformational changes. In both instances, the method thus provides a means for de novo prediction. The technique is finally specialized to the seven human coronavirus spike glycoproteins represented in the PDB to align regions of high free energy, and five such conserved sites of interest for antiviral attack are uncovered. These may be especially promising since they are likely to be preserved under viral mutation owing to their conservation across different coronaviruses. They are also unlikely to be widely present in the host proteome owing to their rarity in the PDB itself, and hence drugs/vaccines targeting them are less likely to induce host side-effects.

Keywords: Backbone hydrogen bond, Free energy, Glycoprotein, Fusion peptide, Receptor binding domain, Antiviral target

Corresponding author: Robert Penner, Institut des Hautes Etudes Scientifiques, France Le Bois Marie, 35 Route des Chartres, 91440 Bures-sur-Yvette, France, E-mail: rpenner@ihes.fr

Citation: Penner R. (2020) Antiviral Targets via Geometry. J Infect Dis Res, 3(S3): 24.

Copyright: ©2020 Penner R. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

