

# Viral and Host Genetic and Epigenetic Biomarkers Related to SARS-CoV-2 Cell Entry, Infection Rate, and Disease Severity

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## Methodology:

### *Figure preparation*

PDB files were downloaded from PDB base: <https://www.rcsb.org/> (accessed 15 December 2021). PDB files were opened with a Swiss-Prot PDB viewer, and the 3D structure was presented in ribbons.

### *Gene ontology analysis*

Gene ontology analysis was performed with the WEBGESTALT program, freely available online. Additional settings: Method of interest: Over-representation analysis, Functional database: Gene ontology. We performed three separate tests: Cellular Component, Biological Process, and Molecular function. Reference list: Illumina humanht 12v3.

### *miRNA analysis*

Into program search miRBASE ([mirbase.org](http://mirbase.org)), we inserted several times parts of virus RNA (1000 nt) due to size restriction. Settings: Search sequences: mature miRNA, Search method: BlastN, E-value cut off: 10, Maximum no. of hits: 100, Show results only from specific organisms: human has been checked. The program found a new set of 24 miRNAs that bind to virus RNA coding and non-coding regions. The list of miRNA was additionally analyzed with sFold program (<https://sfold.wadsworth.org/cgi-bin/index.pl> (accessed 15 December 2021)). Settings: Algorithm used: StarMir, Model for prediction: V-CLIP based model (Human), microRNA list was copied, virus RNA sequence pasted. Results of duplex formation and bond energy were presented in the form of tables, figures.