Doctoral School of Information and Biomedical Technologies
Polish Academy of Sciences (TIB PAN)

SUBJECT: Biomechanics of the SARS-CoV-2 Variants by Molecular Simulations

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DESCRIPTION: The PhD studies will be focused on the molecular biomechanics of the SARS-CoV-2 virion which is responsible for the COVID-19 pandemic. Here we plan to investigate by molecular dynamics (MD) simulation the SARS-CoV-2 spike (S) glycoprotein, taking in consideration all possible variants as well as the interaction with the human angiotensin-converting enzyme 2 (hACE2) receptor. The latter protein considered the entry door of the virion into cells [1]. The full-length S protein will be probed under *in silico* single-molecule force spectroscopy (SMFS) [2]. The results of the nanomechanical analysis will be correlated with the immune evasion which has been reported in last variants, such as Omicron BA.1 and BA.4. This work will employ a multiscale approach that will combine explicit (all-atom MD) and coarse-grained (structure-based model) approaches for the design of protein complexes. In addition, we plan to validate the computational findings with experimental SMFS data. The combined framework will improve the predictability power of the computational analysis [3.4]. The selected person will participate in the ongoing research in the field of the nanomechanics of biomolecular complexes as well as in the development of novel biophysical strategies to inhibit the virus-cell interaction. The PhD candidate will participate in a few training schools (e.g. BioExcel or CECAM) and international conferences in the area of biomolecular modelling. Furthermore, it is expected to report findings in several international scientific journals with high impact factors.

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2. Moreira R.A., Chwastyk M, Baker J.L., Guzman H.V., Poma A.B., Quantitative determination of mechanical stability in the novel coronavirus spike protein, *Nanoscale* 12(31):16409-16413 (2020). doi:10.1039/D0NR03969A

3. Liu S., Moreira R.A., Dujmović A., Liu H., Yang B., Poma A.B., Nash M.A., Mapping Mechanostable Pulling Geometries of a Therapeutic Anticalin/CTLA-4 Protein Complex, *Nano Letters* 22(1), 179-187 (2022). doi:10.1021/acs.nanolett.1c03584

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