

Inferring the stabilization effects of SARS-CoV-2 variant receptor

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Mutational Effect of Some Major COVID-19 Variants on Binding of the S Protein to ACE2. <i>Biomolecules</i> , 2022, 12, 572.	4.0	8
2	Shape Complementarity Optimization of Antibody–Antigen Interfaces: The Application to SARS-CoV-2 Spike Protein. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	3.5	5
3	Assessment of mutations on RBD in the Spike protein of SARS-CoV-2 Alpha, Delta and Omicron variants. <i>Scientific Reports</i> , 2022, 12, .	3.3	53
4	Bioinformatic and Experimental Analysis of T Cell Immune Reactivity to SARS-CoV-2 and its Variants. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	6
5	Spatial organization of hydrophobic and charged residues affects protein thermal stability and binding affinity. <i>Scientific Reports</i> , 2022, 12, .	3.3	21
6	Molecular dynamics simulations highlight the altered binding landscape at the spike-ACE2 interface between the Delta and Omicron variants compared to the SARS-CoV-2 original strain. <i>Computers in Biology and Medicine</i> , 2022, 149, 106035.	7.0	14
7	Tracking mutational semantics of SARS-CoV-2 genomes. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
8	Structural plasticity of omicron BA.5 and BA.2.75 for enhanced ACE-dependent entry into cells. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 10762-10773.	3.5	2
9	Is BF.7 more infectious than other Omicron subtypes: Insights from structural and simulation studies of BF.7 spike RBD variant. <i>International Journal of Biological Macromolecules</i> , 2023, 238, 124154.	7.5	4
10	Investigating the competition between ACE2 natural molecular interactors and SARS-CoV-2 candidate inhibitors. <i>Chemico-Biological Interactions</i> , 2023, 374, 110380.	4.0	1
11	The role of macrophages in the tumor microenvironment and tumor metabolism. <i>Seminars in Immunopathology</i> , 2023, 45, 187-201.	6.1	7
12	Dynamical changes of SARS-CoV-2 spike variants in the highly immunogenic regions impact the viral antibodies escaping. <i>Proteins: Structure, Function and Bioinformatics</i> , 2023, 91, 1116-1129.	2.6	2
13	Electrostatic complementarity at the interface drives transient protein-protein interactions. <i>Scientific Reports</i> , 2023, 13, .	3.3	5
14	Differences in the organization of interface residues tunes the stability of the SARS-CoV-2 spike-ACE2 complex. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	3.5	3
15	Molecular dynamics analysis of superoxide dismutase 1 mutations suggests decoupling between mechanisms underlying ALS onset and progression. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 5296-5308.	4.1	1
16	Design of protein-binding peptides with controlled binding affinity: the case of SARS-CoV-2 receptor binding domain and angiotensin-converting enzyme 2 derived peptides. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	3.5	0
17	Two Receptor Binding Strategy of SARS-CoV-2 Is Mediated by Both the N-Terminal and Receptor-Binding Spike Domain. <i>Journal of Physical Chemistry B</i> , 2024, 128, 451-464.	2.6	1
18	Computational evidences of a misfolding event in an aggregation-prone light chain preceding the formation of the non-native pathogenic dimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 0, , .	2.6	0

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19	Single-Molecule Investigation of the Binding Interface Stability of SARS-CoV-2 Variants with ACE2. ACS Nanoscience Au, 2024, 4, 136-145.	4.8	0