

Interactions of the Receptor Binding Domain of SARS-CoV-2 from Molecular Docking Analysis and Molecular Dynamics

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Natural Bioactive Molecules: An Alternative Approach to the Treatment and Control of COVID-19. International Journal of Molecular Sciences, 2021, 22, 12638.	4.1	45
3	A rigorous framework for detecting SARS-CoV-2 spike protein mutational ensemble from genomic and structural features. Current Research in Structural Biology, 2021, 3, 290-300.	2.2	17
4	Fruit Bromelain-Derived Peptide Potentially Restrains the Attachment of SARS-CoV-2 Variants to hACE2: A Pharmacoinformatics Approach. Molecules, 2022, 27, 260.	3.8	21
5	Prion-like Domains in Spike Protein of SARS-CoV-2 Differ across Its Variants and Enable Changes in Affinity to ACE2. Microorganisms, 2022, 10, 280.	3.6	25
6	The Omicron (B.1.1.529) variant of SARS-CoV-2 binds to the hACE2 receptor more strongly and escapes the antibody response: Insights from structural and simulation data. International Journal of Biological Macromolecules, 2022, 200, 438-448.	7.5	64
7	Computational prediction of the effect of mutations in the receptor-binding domain on the interaction between SARS-CoV-2 and human ACE2. Molecular Diversity, 2022, 26, 3309-3324.	3.9	17
8	A computational comparative analysis of the binding mechanism of molnupiravir's active metabolite to RNA-dependent RNA polymerase of wild-type and Delta subvariant AY.4 of SARS-CoV-2. Journal of Cellular Biochemistry, 2022, 123, 807-818.	2.6	24
9	Can the SARS-CoV-2 Omicron Variant Confer Natural Immunity against COVID-19?. Molecules, 2022, 27, 2221.	3.8	12
10	Appraisal of Bioactive Compounds of Betel Fruit as Antimalarial Agents by Targeting Plasmeprin 1 and 2: A Computational Approach. Pharmaceuticals, 2021, 14, 1285.	3.8	3
11	Insights into the Binding of Receptor-Binding Domain (RBD) of SARS-CoV-2 Wild Type and B.1.620 Variant with hACE2 Using Molecular Docking and Simulation Approaches. Biology, 2021, 10, 1310.	2.8	5
12	Changes in Receptor Binding Domain of the Covid-19 during Pandemic; a Review Study. Pizhish-i Salamat, 2021, 7, 75-86.	0.1	0
13	Investigation of the binding and dynamic features of A.30 variant revealed higher binding of RBD for hACE2 and escapes the neutralizing antibody: A molecular simulation approach. Computers in Biology and Medicine, 2022, 146, 105574.	7.0	4
14	An Insight Based on Computational Analysis of the Interaction between the Receptor-Binding Domain of the Omicron Variants and Human Angiotensin-Converting Enzyme 2. Biology, 2022, 11, 797.	2.8	10
15	Comparative overview of emerging RNA viruses: Epidemiology, pathogenesis, diagnosis and current treatment. Annals of Medicine and Surgery, 2022, 79, .	1.1	7
16	Characterization of mutations modulating enhanced transmissibility of SARS-CoV-2 B.1.617+ (Delta) variant using In Silico tools. Gene Reports, 2022, 27, 101636.	0.8	0
17	Deciphering the Impact of Mutations on the Binding Efficacy of SARS-CoV-2 Omicron and Delta Variants With Human ACE2 Receptor. Frontiers in Chemistry, 0, 10, .	3.6	12
18	Modeling Kaempferol as a Potential Pharmacological Agent for COVID-19/PF Co-Occurrence Based on Bioinformatics and System Pharmacological Tools. Frontiers in Pharmacology, 0, 13, .	3.5	8
19	Modern drug discovery applications for the identification of novel candidates for COVID-19 infections. Annals of Medicine and Surgery, 2022, 80, .	1.1	11

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20	Coronavirus Disease 2019 (COVID-19). <i>Biology</i> , 2022, 11, 1250.	2.8	2
21	Variations in Cell Surface ACE2 Levels Alter Direct Binding of SARS-CoV-2 Spike Protein and Viral Infectivity: Implications for Measuring Spike Protein Interactions with Animal ACE2 Orthologs. <i>Journal of Virology</i> , 2022, 96, .	3.4	3
22	Most frequently harboured missense variants of hACE2 across different populations exhibit varying patterns of binding interaction with spike glycoproteins of emerging SARS-CoV-2 of different lineages. <i>Computers in Biology and Medicine</i> , 2022, 148, 105903.	7.0	5
23	Omicron variant (B.1.1.529) and its sublineages: What do we know so far amid the emergence of recombinant variants of SARS-CoV-2?. <i>Biomedicine and Pharmacotherapy</i> , 2022, 154, 113522.	5.6	56
24	Boosting the detection performance of severe acute respiratory syndrome coronavirus 2 test through a sensitive optical biosensor with new superior antibody. <i>Bioengineering and Translational Medicine</i> , 2023, 8, .	7.1	2
25	Ultra-Large-Scale Screening of Natural Compounds and Free Energy Calculations Revealed Potential Inhibitors for the Receptor-Binding Domain (RBD) of SARS-CoV-2. <i>Molecules</i> , 2022, 27, 7317.	3.8	3
26	SARS-CoV-2 Variants Show a Gradual Declining Pathogenicity and Pro-Inflammatory Cytokine Stimulation, an Increasing Antigenic and Anti-Inflammatory Cytokine Induction, and Rising Structural Protein Instability: A Minimal Number Genome-Based Approach. <i>Inflammation</i> , 2023, 46, 297-312.	3.8	12
27	Insights from computational studies on the potential of natural compounds as inhibitors against SARS-CoV-2 spike omicron variant. <i>SAR and QSAR in Environmental Research</i> , 2022, 33, 953-968.	2.2	6
28	Molecular insights into the interaction of eighteen different variants of SARS-CoV-2 spike proteins with sixteen therapeutically important phytochemicals: in silico approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 12880-12907.	3.5	0
29	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
30	Impacts of SARS-CoV-2 on diabetes mellitus: A pre and post pandemic evaluation. <i>World Journal of Virology</i> , 0, 12, 151-171.	2.9	0
31	Evaluation of Analytical and Clinical Performance and Usefulness in a Real-Life Hospital Setting of Two in-House Real-Time RT-PCR Assays to Track SARS-CoV-2 Variants of Concern. <i>Viruses</i> , 2023, 15, 1115.	3.3	2
32	Oxalic acid blocked the binding of spike protein from SARS-CoV-2 Delta (B.1.617.2) and Omicron (B.1.1.529) variants to human angiotensin-converting enzymes 2. <i>PLoS ONE</i> , 2023, 18, e0285722.	2.5	3
33	Immunoinformatics-Driven Strategies for Advancing Epitope-Based Vaccine Design for West Nile Virus. <i>Journal of Pharmaceutical Sciences</i> , 2023, . .	3.3	0
34	Screening and identifying natural products with SARS-CoV-2 infection inhibitory activity from medicinal fungi. <i>Biosafety and Health</i> , 2024, 6, 12-20.	2.7	0
35	In Silico Therapeutic Study: The Next Frontier in the Fight against SARS-CoV-2 and Its Variants. , 2024, 3, 54-69.		0
36	Interaction analysis of SARS-CoV-2 omicron BA1 and BA2 of RBD with fifty monoclonal antibodies: Molecular dynamics approach. <i>Journal of Molecular Graphics and Modelling</i> , 2024, 128, 108719.	2.4	0
37	Binding behavior of receptor binding domain of the SARS-CoV-2 virus and ivermectin. <i>Scientific Reports</i> , 2024, 14, .	3.3	0

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38	Insights from <i>in silico</i> study of receptor energetics of SARS-CoV-2 variants. Physical Chemistry Chemical Physics, 2024, 26, 8794-8806.	2.8	0