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Real-Time Conformational Dynamics of SARS-CoV-2 Spikes on Virus Particles

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122	Cryo-EM Structures of SARS-CoV-2 Spike without and with ACE2 Reveal a pH-Dependent Switch to Mediate Endosomal Positioning of Receptor-Binding Domains. <i>Cell Host and Microbe</i> , 2020 , 28, 867-879	9.€§ ^{.4}	168
121	FRETing over SARS-CoV-2: Conformational Dynamics of the Spike Glycoprotein. <i>Cell Host and Microbe</i> , 2020 , 28, 778-779	23.4	1
120	Characterization of Structural and Energetic Differences between Conformations of the SARS-CoV-2 Spike Protein. 2020 , 13,		33
119	Single-Molecule FRET Imaging of Virus Spike-Host Interactions. 2021 , 13,		5
118	Kobophenol A Inhibits Binding of Host ACE2 Receptor with Spike RBD Domain of SARS-CoV-2, a Lead Compound for Blocking COVID-19. 2021 , 12, 1793-1802		33
117	A glycan gate controls opening of the SARS-CoV-2 spike protein. 2021 ,		22
116	Potent neutralizing nanobodies resist convergent circulating variants of SARS-CoV-2 by targeting novel and conserved epitopes. 2021 ,		7
115	Live Imaging of SARS-CoV-2 Infection in Mice Reveals Neutralizing Antibodies Require Fc Function for Optimal Efficacy. 2021 ,		10
114	The great escape? SARS-CoV-2 variants evading neutralizing responses. <i>Cell Host and Microbe</i> , 2021 , 29, 322-324	23.4	48
113	A single BNT162b2 mRNA dose elicits antibodies with Fc-mediated effector functions and boost pre-existing humoral and T cell responses. 2021 ,		19
112	Can ketone bodies inactivate coronavirus spike protein? The potential of biocidal agents against SARS-CoV-2. 2021 , 43, e2000312		2
111	Single-Molecular Fister Resonance Energy Transfer Measurement on Structures and Interactions of Biomolecules. 2021 , 12,		6
110	Integrated Biophysical Modeling of the SARS-CoV-2 Spike Protein Binding and Allosteric Interactions with Antibodies. 2021 , 125, 4596-4619		16
109	Role of Serine Proteases and Host Cell Receptors Involved in Proteolytic Activation, Entry of SARS-CoV-2 and Its Current Therapeutic Options. 2021 , 14, 1883-1892		5
108	SARS-CoV-2 simulations go exascale to predict dramatic spike opening and cryptic pockets across the proteome. 2021 , 13, 651-659		62
107	Structure-based design of a highly stable, covalently-linked SARS-CoV-2 spike trimer with improved structural properties and immunogenicity.		9
106	Structural and Biophysical Characterization of the HCV E1E2 Heterodimer for Vaccine Development. 2021 , 13,		O

(2021-2021)

105	Does Trypsin Oral Spray (Viruprotect/ColdZyme) Protect against COVID-19 and Common Colds or Induce Mutation? Caveats in Medical Device Regulations in the European Union. 2021 , 18,	1
104	Cooperative multivalent receptor binding promotes exposure of the SARS-CoV-2 fusion machinery core. 2021 ,	1
103	Probing Affinity, Avidity, Anti-Cooperativity, and Competition in Antibody and Receptor Binding to the SARS-CoV-2 Spike by Single Particle Mass Analyses.	1
102	Landscape-Based Mutational Sensitivity Cartography and Network Community Analysis of the SARS-CoV-2 Spike Protein Structures: Quantifying Functional Effects of the Circulating D614G Variant. 2021 , 6, 16216-16233	3
101	Development and optimization of heavy metal lead biosensors in biomedical and environmental applications. 2021 , 84, 745-753	3
100	Different Neutralization Sensitivity of SARS-CoV-2 Cell-to-Cell and Cell-Free Modes of Infection to Convalescent Sera. 2021 , 13,	7
99	An infectivity-enhancing site on the SARS-CoV-2 spike protein targeted by antibodies. 2021 , 184, 3452-3466	.e1 8 6
98	Computational analysis of protein stability and allosteric interaction networks in distinct conformational forms of the SARS-CoV-2 spike D614G mutant: reconciling functional mechanisms through allosteric model of spike regulation. 2021 , 1-18	3
97	SARS-CoV-2 RNAemia and proteomic trajectories inform prognostication in COVID-19 patients admitted to intensive care. 2021 , 12, 3406	41
96	Trendbericht Biochemie: Einzelmolek [Fret-Spektroskopie. 2021, 69, 54-55	
96 95	Trendbericht Biochemie: Einzelmolek Fret-Spektroskopie. 2021, 69, 54-55 Identification of Human SARS-CoV-2 Monoclonal Antibodies from Convalescent Patients Using EBV Immortalization. 2021, 10,	0
	Identification of Human SARS-CoV-2 Monoclonal Antibodies from Convalescent Patients Using EBV	
95	Identification of Human SARS-CoV-2 Monoclonal Antibodies from Convalescent Patients Using EBV Immortalization. 2021 , 10,	
95 94	Identification of Human SARS-CoV-2 Monoclonal Antibodies from Convalescent Patients Using EBV Immortalization. 2021 , 10, The Next Frontier for Designing Switchable Proteins: Rational Enhancement of Kinetics. 2021 , 125, 9069-90	77 1
95 94 93	Identification of Human SARS-CoV-2 Monoclonal Antibodies from Convalescent Patients Using EBV Immortalization. 2021, 10, The Next Frontier for Designing Switchable Proteins: Rational Enhancement of Kinetics. 2021, 125, 9069-90. The SARS-CoV-2 spike reversibly samples an open-trimer conformation exposing novel epitopes. Free Energy Landscapes from SARS-CoV-2 Spike Glycoprotein Simulations Suggest that RBD	77 ₁
95 94 93 92	Identification of Human SARS-CoV-2 Monoclonal Antibodies from Convalescent Patients Using EBV Immortalization. 2021, 10, The Next Frontier for Designing Switchable Proteins: Rational Enhancement of Kinetics. 2021, 125, 9069-90. The SARS-CoV-2 spike reversibly samples an open-trimer conformation exposing novel epitopes. Free Energy Landscapes from SARS-CoV-2 Spike Glycoprotein Simulations Suggest that RBD Opening Can Be Modulated via Interactions in an Allosteric Pocket. 2021, 143, 11349-11360	77 ₁
95 94 93 92 91	Identification of Human SARS-CoV-2 Monoclonal Antibodies from Convalescent Patients Using EBV Immortalization. 2021, 10, The Next Frontier for Designing Switchable Proteins: Rational Enhancement of Kinetics. 2021, 125, 9069-90. The SARS-CoV-2 spike reversibly samples an open-trimer conformation exposing novel epitopes. Free Energy Landscapes from SARS-CoV-2 Spike Glycoprotein Simulations Suggest that RBD Opening Can Be Modulated via Interactions in an Allosteric Pocket. 2021, 143, 11349-11360 A Tethered Ligand Assay to Probe SARS-CoV-2:ACE2 Interactions. Dynamics of SARS-CoV-2 Spike Proteins in Cell Entry: Control Elements in the Amino-Terminal	77 1 3 13

87	SARS-CoV-2 spike opening dynamics and energetics reveal the individual roles of glycans and their collective impact.	2
86	A glycan gate controls opening of the SARS-CoV-2 spike protein. 2021 , 13, 963-968	63
85	DNA Aptamers Block the Receptor Binding Domain at the Spike Protein of SARS-CoV-2. 2021 , 8, 713003	5
84	Structural Basis and Mode of Action for Two Broadly Neutralizing Antibodies Against SARS-CoV-2 Emerging Variants of Concern. 2021 ,	5
83	Live imaging of SARS-CoV-2 infection in mice reveals that neutralizing antibodies require Fc function for optimal efficacy. 2021 , 54, 2143-2158.e15	37
82	Atomistic Simulations and In Silico Mutational Profiling of Protein Stability and Binding in the SARS-CoV-2 Spike Protein Complexes with Nanobodies: Molecular Determinants of Mutational Escape Mechanisms. 2021 , 6, 26354-26371	2
81	An anti-SARS-CoV-2 non-neutralizing antibody with Fc-effector function defines a new NTD epitope and delays neuroinvasion and death in K18-hACE2 mice.	4
80	Integrating single-molecule spectroscopy and simulations for the study of intrinsically disordered proteins. 2021 , 193, 116-135	6
79	Potential natural candidates in the treatment of coronavirus infections. 2021 , 28, 5704-5713	
78	Modeling biomolecular kinetics with large-scale simulation. 2021 , 72, 95-102	
78 77	Modeling biomolecular kinetics with large-scale simulation. 2021 , 72, 95-102 Dynamic Network Modeling of Allosteric Interactions and Communication Pathways in the SARS-CoV-2 Spike Trimer Mutants: Differential Modulation of Conformational Landscapes and Signal Transmission via Cascades of Regulatory Switches. 2021 , 125, 850-873	18
	Dynamic Network Modeling of Allosteric Interactions and Communication Pathways in the SARS-CoV-2 Spike Trimer Mutants: Differential Modulation of Conformational Landscapes and	18
77	Dynamic Network Modeling of Allosteric Interactions and Communication Pathways in the SARS-CoV-2 Spike Trimer Mutants: Differential Modulation of Conformational Landscapes and Signal Transmission via Cascades of Regulatory Switches. 2021 , 125, 850-873 An infectivity-enhancing site on the SARS-CoV-2 spike protein is targeted by COVID-19 patient	
77 76	Dynamic Network Modeling of Allosteric Interactions and Communication Pathways in the SARS-CoV-2 Spike Trimer Mutants: Differential Modulation of Conformational Landscapes and Signal Transmission via Cascades of Regulatory Switches. 2021 , 125, 850-873 An infectivity-enhancing site on the SARS-CoV-2 spike protein is targeted by COVID-19 patient antibodies.	3
77 76 75	Dynamic Network Modeling of Allosteric Interactions and Communication Pathways in the SARS-CoV-2 Spike Trimer Mutants: Differential Modulation of Conformational Landscapes and Signal Transmission via Cascades of Regulatory Switches. 2021, 125, 850-873 An infectivity-enhancing site on the SARS-CoV-2 spike protein is targeted by COVID-19 patient antibodies. Differential Dynamic Behavior of Prefusion Spike Proteins of SARS Coronaviruses 1 and 2. 2021,	1
77 76 75	Dynamic Network Modeling of Allosteric Interactions and Communication Pathways in the SARS-CoV-2 Spike Trimer Mutants: Differential Modulation of Conformational Landscapes and Signal Transmission via Cascades of Regulatory Switches. 2021, 125, 850-873 An infectivity-enhancing site on the SARS-CoV-2 spike protein is targeted by COVID-19 patient antibodies. Differential Dynamic Behavior of Prefusion Spike Proteins of SARS Coronaviruses 1 and 2. 2021, Replication and single-cycle delivery of SARS-CoV-2 replicons. 2021, 374, 1099-1106 Predicting Mutational Effects on Receptor Binding of the Spike Protein of SARS-CoV-2 Variants.	3 1 7
77 76 75 74 73	Dynamic Network Modeling of Allosteric Interactions and Communication Pathways in the SARS-CoV-2 Spike Trimer Mutants: Differential Modulation of Conformational Landscapes and Signal Transmission via Cascades of Regulatory Switches. 2021, 125, 850-873 An infectivity-enhancing site on the SARS-CoV-2 spike protein is targeted by COVID-19 patient antibodies. Differential Dynamic Behavior of Prefusion Spike Proteins of SARS Coronaviruses 1 and 2. 2021, Replication and single-cycle delivery of SARS-CoV-2 replicons. 2021, 374, 1099-1106 Predicting Mutational Effects on Receptor Binding of the Spike Protein of SARS-CoV-2 Variants. 2021, 143, 17646-17654 Temporal-Geographical Dispersion of SARS-CoV-2 Spike Glycoprotein Variant Lineages and Their	3 1 7

69	Probing Affinity, Avidity, Anticooperativity, and Competition in Antibody and Receptor Binding to the SARS-CoV-2 Spike by Single Particle Mass Analyses. 2021 , 7, 1863-1873	2
68	Glycosylation and disulfide bonding of wild-type SARS-CoV-2 spike glycoprotein. 2021 , JVI0162621	2
67	Evaluating Humoral Immunity against SARS-CoV-2: Validation of a Plaque-Reduction Neutralization Test and a Multilaboratory Comparison of Conventional and Surrogate Neutralization Assays. 2021 , e0088621	6
66	Structural basis and mode of action for two broadly neutralizing antibodies against SARS-CoV-2 emerging variants of concern 2021 , 110210	26
65	Antibacterial, antibiofilm, anti-inflammatory, and wound healing effects of nanoscale multifunctional cationic alternating copolymers 2021 , 119, 105550	3
64	Conformational Flexibility and Local Frustration in the Functional States of the SARS-CoV-2 Spike B.1.1.7 and B.1.351 Variants: Mutation-Induced Allosteric Modulation Mechanism of Functional Dynamics and Protein Stability 2022 , 23,	O
63	A Fc-enhanced NTD-binding non-neutralizing antibody delays virus spread and synergizes with a nAb to protect mice from lethal SARS-CoV-2 infection 2022 , 110368	10
62	Aspects of the physiochemical properties of SARS-CoV-2 to prevent S-protein receptor binding using Arabic gum. 2022 , 11, 150-163	
61	VE607 Stabilizes SARS-CoV-2 Spike In the "RBD-up" Conformation and Inhibits Viral Entry 2022,	
60	Cholesterol-Rich Lipid Rafts as Platforms for SARS-CoV-2 Entry 2021 , 12, 796855	5
59	SARS-CoV-2 Variants Increase Kinetic Stability of Open Spike Conformations as an Evolutionary	
	Strategy 2022 , e0322721	3
58	Strategy 2022, e0322721 Cooperative multivalent receptor binding promotes exposure of the SARS-CoV-2 fusion machinery core 2022, 13, 1002	3
58 57	Cooperative multivalent receptor binding promotes exposure of the SARS-CoV-2 fusion machinery	
	Cooperative multivalent receptor binding promotes exposure of the SARS-CoV-2 fusion machinery core 2022 , 13, 1002 Allosteric Determinants of the SARS-CoV-2 Spike Protein Binding with Nanobodies: Examining	3
57	Cooperative multivalent receptor binding promotes exposure of the SARS-CoV-2 fusion machinery core 2022 , 13, 1002 Allosteric Determinants of the SARS-CoV-2 Spike Protein Binding with Nanobodies: Examining Mechanisms of Mutational Escape and Sensitivity of the Omicron Variant 2022 , 23, Analysis of the Neutralizing Activity of Antibodies Targeting Open or Closed SARS-CoV-2 Spike	3 0
<i>57</i> <i>56</i>	Cooperative multivalent receptor binding promotes exposure of the SARS-CoV-2 fusion machinery core 2022, 13, 1002 Allosteric Determinants of the SARS-CoV-2 Spike Protein Binding with Nanobodies: Examining Mechanisms of Mutational Escape and Sensitivity of the Omicron Variant 2022, 23, Analysis of the Neutralizing Activity of Antibodies Targeting Open or Closed SARS-CoV-2 Spike Protein Conformations 2022, 23, Structural and Computational Studies of the SARS-CoV-2 Spike Protein Binding Mechanisms with	3 0
57 56 55	Cooperative multivalent receptor binding promotes exposure of the SARS-CoV-2 fusion machinery core 2022, 13, 1002 Allosteric Determinants of the SARS-CoV-2 Spike Protein Binding with Nanobodies: Examining Mechanisms of Mutational Escape and Sensitivity of the Omicron Variant 2022, 23, Analysis of the Neutralizing Activity of Antibodies Targeting Open or Closed SARS-CoV-2 Spike Protein Conformations 2022, 23, Structural and Computational Studies of the SARS-CoV-2 Spike Protein Binding Mechanisms with Nanobodies: From Structure and Dynamics to Avidity-Driven Nanobody Engineering 2022, 23,	3 0 3

51	The SARS-CoV-2 spike reversibly samples an open-trimer conformation exposing novel epitopes 2022 ,	6
50	Conformational dynamics and allosteric modulation of the SARS-CoV-2 spike 2022, 11,	3
49	The inherent flexibility of receptor binding domains in SARS-CoV-2 spike protein 2022, 11,	3
48	Prefusion Spike Protein Conformational Changes Are Slower in SARS-CoV-2 than in SARS-CoV-1 2022 , 101814	3
47	Landscape-Based Protein Stability Analysis and Network Modeling of Multiple Conformational States of the SARS-CoV-2 Spike D614G Mutant: Conformational Plasticity and Frustration-Induced Allostery as Energetic Drivers of Highly Transmissible Spike Variants 2022 ,	О
46	Millisecond dynamic of SARS-CoV-2 spike and its interaction with ACE2 receptor and small extracellular vesicles. 2021 , 10, e12170	5
45	Allosteric Determinants of the SARS-CoV-2 Spike Protein Binding with Nanobodies: Examining Mechanisms of Mutational Escape and Sensitivity of the Omicron Variant.	
44	Design, immunogenicity, and efficacy of a pan-sarbecovirus dendritic-cell targeting vaccine.	
43	Conformational Flexibility and Local Frustration in the Functional States of the SARS-CoV-2 Spike B.1.1.7 and B.1.351 Variants: Mutation-Induced Allosteric Modulation Mechanism of Functional Dynamics and Protein Stability.	0
42	The Landscape-Based Protein Stability Analysis and Network Modeling of Multiple Conformational States of the SARS-CoV-2 Spike D614 Mutant: Conformational Plasticity and Frustration-Driven Allostery as Energetic Drivers of Highly Transmissible Spike Variant.	
41	Biosensor-Enabled Deconvolution of the Avidity-Induced Affinity Enhancement for the SARS-CoV-2 Spike Protein and ACE2 Interaction 2021 ,	1
40	Hierarchical Computational Modeling and Dynamic Network Analysis of Allosteric Regulation in the SARS-CoV-2 Spike Omicron Trimer Structures: Omicron Mutations Cooperate to Allosterically Control Balance of Protein Stability and Conformational Adaptability.	
39	Computer Simulations and Network-Based Profiling of Binding and Allosteric Interactions of SARS-CoV-2 Spike Variant Complexes and the Host Receptor: Dissecting the Mechanistic Effects of the Delta and Omicron Mutations 2022 , 23,	1
38	Isolation, characterization, and structure-based engineering of a neutralizing nanobody against SARS-CoV-2 2022 ,	О
37	Anti-Fungal Drug Anidulafungin Inhibits SARS-CoV-2 Spike-Induced Syncytia Formation by Targeting ACE2-Spike Protein Interaction 2022 , 13, 866474	1
36	Application of Coarse-Grained (CG) Models to Explore Conformational Pathway of Large-Scale Protein Machines. 2022 , 24, 620	0
35	An electrostatically-steered conformational selection mechanism promotes SARS-CoV-2 Spike protein variation. 2022 , 167637	O
34	Uncovering the structural flexibility of SARS-CoV-2 glycoprotein spike variants.	

33	Human interaction targets of SARS-COV-2 spike protein: A systematic review. 2022 , 20, 1721727X2210953	О
32	VE607 Stabilizes SARS-CoV-2 Spike In the R BD-uplConformation and Inhibits Viral Entry. 2022 , 104528	1
31	Integrating Conformational Dynamics and Perturbation-Based Network Modeling for Mutational Profiling of Binding and Allostery in the SARS-CoV-2 Spike Variant Complexes with Antibodies: Balancing Local and Global Determinants of Mutational Escape Mechanisms.	
30	Structural Plasticity and Immune Evasion of SARS-CoV-2 Spike Variants. 2022 , 14, 1255	1
29	Frustration-driven allosteric regulation and signal transmission in the SARS-CoV-2 spike omicron trimer structures: a crosstalk of the omicron mutation sites allosterically regulates tradeoffs of protein stability and conformational adaptability.	2
28	Integrating Conformational Dynamics and Perturbation-Based Network Modeling for Mutational Profiling of Binding and Allostery in the SARS-CoV-2 Spike Variant Complexes with Antibodies: Balancing Local and Global Determinants of Mutational Escape Mechanisms. 2022 , 12, 964	
27	Coronaviruses. 2023 , 277-306	
26	Serum cytokine/chemokine profile and clinical/paraclinical data in COVID-19 deceased and recovered patients. 2022 , 20, 1721727X2211254	O
25	Atomistic Simulations and Network-Based Energetic Profiling of Binding and Allostery in the SARS-CoV-2 Spike Omicron BA.1, BA.1.1, BA.2 and BA.3 Subvariant Complexes with the Host Receptor: Revealing Hidden Functional Roles of the Binding Hotspots in Mediating Epistatic Effects	О
24	Probing Mechanisms of Binding and Allostery in the SARS-CoV-2 Spike Omicron Variant Complexes with the Host Receptor: Revealing Functional Roles of the Binding Hotspots in Mediating Epistatic Effects and Communication with Allosteric Pockets. 2022 , 23, 11542	2
23	Energetics of Spike Protein Opening of SARS-CoV-1 and SARS-CoV-2 and Its Variants of Concern: Implications in Host Receptor Scanning and Transmission.	0
22	One-pot synthesis, molecular docking, ADMET, and DFT studies of novel pyrazolines as promising SARS-CoV-2 main protease inhibitors.	2
21	MVsim is a toolset for quantifying and designing multivalent interactions. 2022, 13,	О
20	Acriflavine and Proflavine Hemisulfate as potential antivirals by targeting Mpro. 2022 , 106185	O
19	Temperature Influences the Interaction between SARS-CoV-2 Spike from Omicron Subvariants and Human ACE2. 2022 , 14, 2178	O
18	Membrane attachment and fusion of HIV-1, influenza A, and SARS-CoV-2: resolving the mechanisms with biophysical methods. 2022 , 14, 1109-1140	O
17	The ACE-2 receptor accelerates but is not biochemically required for SARS-CoV-2 membrane fusion.	O
16	SARS-CoV-2 spike opening dynamics and energetics reveal the individual roles of glycans and their collective impact. 2022 , 5,	3

15	Micro-second Time-resolved X-ray Single-molecule Internal Motions of SARS-CoV-2 Spike Variants.	O
14	Conformational stability of SARS-CoV-2 glycoprotein spike variants. 2023 , 26, 105696	O
13	Molecular basis for antiviral activity of two pediatric neutralizing antibodies targeting SARS-CoV-2 Spike RBD. 2023 , 26, 105783	О
12	Identification of an immunogenic epitope and protective antibody against the furin cleavage site of SARS-CoV-2. 2023 , 87, 104401	O
11	Atomic-level characterization of the conformational transition pathways in SARS-CoV-1 and SARS-CoV-2 spike proteins.	0
10	A cell-free platform to measure coronavirus membrane fusion. 2023 , 4, 102189	O
9	Omicron mutations increase interdomain interactions and reduce epitope exposure in the SARS-CoV-2 spike. 2023 , 26, 105981	O
8	Exploring and Learning the Universe of Protein Allostery Using Artificial Intelligence Augmented Biophysical and Computational Approaches. 2023 , 63, 1413-1428	O
7	Coarse-Grained Molecular Simulations and Ensemble-Based Mutational Profiling of Protein Stability in the Different Functional Forms of the SARS-CoV-2 Spike Trimers: Balancing Stability and Adaptability in BA.1, BA.2 and BA.2.75 Variants.	О
6	An intact amber-free HIV-1 system for in-virus protein bioorthogonal click labeling that delineates envelope conformational dynamics.	O
5	Polarimetric imaging for the detection of synthetic models of SARS-CoV-2: A proof of concept. 2023 , 302, 108567	O
4	Structural dynamics in the evolution of SARS-CoV-2 spike glycoprotein. 2023 , 14,	O
3	Balancing Functional Tradeoffs between Protein Stability and ACE2 Binding in the SARS-CoV-2 Omicron BA.2, BA.2.75 and XBB Lineages : Dynamics-Based Network Models Reveal Epistatic Effects Modulating Compensatory Dynamic and Energetic Changes.	O
2	Intranasal trimeric sherpabody inhibits SARS-CoV-2 including recent immunoevasive Omicron subvariants. 2023 , 14,	O
1	Coarse-Grained Molecular Simulations and Ensemble-Based Mutational Profiling of Protein Stability in the Different Functional Forms of the SARS-CoV-2 Spike Trimers: Balancing Stability and Adaptability in BA.1, BA.2 and BA.2.75 Variants. 2023 , 24, 6642	О