

Reza Khayat

List of Publications by Year in descending order

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citing authors

#	ARTICLE	IF	CITATIONS
1	A Structural Perspective of Reps from CRESS-DNA Viruses and Their Bacterial Plasmid Homologues. <i>Viruses</i> , 2022, 14, 37.	3.3	11
2	It is all about the Structure. <i>Viral Immunology</i> , 2021, 34, 1-2.	1.3	1
3	Mechanism of DNA Interaction and Translocation by the Replicase of a Circular Rep-Encoding Single-Stranded DNA Virus. <i>MBio</i> , 2021, 12, e0076321.	4.1	12
4	Constant pH molecular dynamics of porcine circovirus 2 capsid protein reveals a mechanism for capsid assembly. <i>Physical Chemistry Chemical Physics</i> , 2021, 23, 24617-24626.	2.8	1
5	Cryo-electron microscopy structure of the 70S ribosome from <i>Enterococcus faecalis</i> . <i>Scientific Reports</i> , 2020, 10, 16301.	3.3	15
6	Structural characterization of the PCV2d virus-like particle at 3.3 Å resolution reveals differences to PCV2a and PCV2b capsids, a tetranucleotide, and an N-terminus near the icosahedral 3-fold axes. <i>Virology</i> , 2019, 537, 186-197.	2.4	12
7	The Arginines in the N-Terminus of the Porcine Circovirus 2 Virus-like Particles Are Responsible for Disrupting the Membranes at Neutral and Acidic pH. <i>Journal of Molecular Biology</i> , 2019, 431, 3261-3274.	4.2	4
8	Porcine Circovirus 2 Uses a Multitude of Weak Binding Sites To Interact with Heparan Sulfate, and the Interactions Do Not Follow the Symmetry of the Capsid. <i>Journal of Virology</i> , 2019, 93, .	3.4	25
9	Sequential Protein Expression and Capsid Assembly in Cell: Toward the Study of Multiprotein Viral Capsids Using Solid-State Nuclear Magnetic Resonance Techniques. <i>Biochemistry</i> , 2018, 57, 1568-1571.	2.5	1
10	164. Reporting the High-resolution Structure of the Enterococcal Ribosome: A New Template for Antibiotic Discovery. <i>Open Forum Infectious Diseases</i> , 2018, 5, S15-S16.	0.9	0
11	All-Atom Molecular Dynamics Simulations of Entire Virus Capsid Reveal the Role of Ion Distribution in Capsid's Stability. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 779-784.	4.6	42
12	Receptor Recognition by Porcine Circovirus 2. <i>Microscopy and Microanalysis</i> , 2016, 22, 1108-1109.	0.4	0
13	In silico analysis of surface structure variation of PCV2 capsid resulting from loop mutations of its capsid protein (Cap). <i>Journal of General Virology</i> , 2016, 97, 3331-3344.	2.9	24
14	Architecture of a dsDNA Viral Capsid in Complex with Its Maturation Protease. <i>Structure</i> , 2014, 22, 230-237.	3.3	34
15	Structural Characterization of Cleaved, Soluble HIV-1 Envelope Glycoprotein Trimers. <i>Journal of Virology</i> , 2013, 87, 9865-9872.	3.4	71
16	Supersite of immune vulnerability on the glycosylated face of HIV-1 envelope glycoprotein gp120. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 796-803.	8.2	314
17	Broadly Neutralizing Antibody PGT121 Allosterically Modulates CD4 Binding via Recognition of the HIV-1 gp120 V3 Base and Multiple Surrounding Glycans. <i>PLoS Pathogens</i> , 2013, 9, e1003342.	4.7	267
18	Influences on Trimerization and Aggregation of Soluble, Cleaved HIV-1 SOSIP Envelope Glycoprotein. <i>Journal of Virology</i> , 2013, 87, 9873-9885.	3.4	76

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19	Highly Conserved Protective Epitopes on Influenza B Viruses. <i>Science</i> , 2012, 337, 1343-1348.	12.6	705
20	Partial Enzymatic Deglycosylation Preserves the Structure of Cleaved Recombinant HIV-1 Envelope Glycoprotein Trimers. <i>Journal of Biological Chemistry</i> , 2012, 287, 24239-24254.	3.4	50
21	A Virus-Like Particle That Elicits Cross-Reactive Antibodies to the Conserved Stem of Influenza Virus Hemagglutinin. <i>Journal of Virology</i> , 2012, 86, 11686-11697.	3.4	71
22	Cross-neutralization of influenza A viruses mediated by a single antibody loop. <i>Nature</i> , 2012, 489, 526-532.	27.8	434
23	The Prohead-I Structure of Bacteriophage HK97: Implications for Scaffold-Mediated Control of Particle Assembly and Maturation. <i>Journal of Molecular Biology</i> , 2011, 408, 541-554.	4.2	58
24	Pass the Jelly Rolls. <i>Structure</i> , 2011, 19, 904-906.	3.3	12
25	A Potent and Broad Neutralizing Antibody Recognizes and Penetrates the HIV Glycan Shield. <i>Science</i> , 2011, 334, 1097-1103.	12.6	644
26	The 2.3-Angstrom Structure of Porcine Circovirus 2. <i>Journal of Virology</i> , 2011, 85, 7856-7862.	3.4	154
27	Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. <i>Nature</i> , 2011, 480, 336-343.	27.8	794
28	P22 Coat Protein Structures Reveal a Novel Mechanism for Capsid Maturation: Stability without Auxiliary Proteins or Chemical Crosslinks. <i>Structure</i> , 2010, 18, 390-401.	3.3	136
29	In Vivo Assembly of an Archaeal Virus Studied with Whole-Cell Electron Cryotomography. <i>Structure</i> , 2010, 18, 1579-1586.	3.3	60
30	The Architecture and Chemical Stability of the Archaeal <i>Sulfolobus</i> Turreted Icosahedral Virus. <i>Journal of Virology</i> , 2010, 84, 9575-9583.	3.4	33
31	Subunits fold at position-dependent rates during maturation of a eukaryotic RNA virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14111-14115.	7.1	19
32	An automated procedure for detecting protein folds from sub-nanometer resolution electron density. <i>Journal of Structural Biology</i> , 2010, 170, 513-521.	2.8	8
33	Structural and Functional Studies of Archaeal Viruses. <i>Journal of Biological Chemistry</i> , 2009, 284, 12599-12603.	3.4	96
34	Dissecting the Functional Domains of a Nonenveloped Virus Membrane Penetration Peptide. <i>Journal of Virology</i> , 2009, 83, 6929-6933.	3.4	28
35	The P22 Tail Machine at Subnanometer Resolution Reveals the Architecture of an Infection Conduit. <i>Structure</i> , 2009, 17, 789-799.	3.3	63
36	Engineering d-amino acid containing novel protease inhibitors using catalytic site architecture. <i>Bioorganic and Medicinal Chemistry</i> , 2006, 14, 214-236.	3.0	11

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37	Characterization of the Archaeal Thermophile Sulfolobus Turreted Icosahedral Virus Validates an Evolutionary Link among Double-Stranded DNA Viruses from All Domains of Life. <i>Journal of Virology</i> , 2006, 80, 7625-7635.	3.4	86
38	Structure of an archaeal virus capsid protein reveals a common ancestry to eukaryotic and bacterial viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18944-18949.	7.1	169
39	Crystal structures of MTH1187 and its yeast ortholog YBL001c. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 478-480.	2.6	8
40	Structural Studies of Herpesvirus Proteases. <i>Protein and Peptide Letters</i> , 2001, 8, 333-342.	0.9	9
41	A T14C Variant of <i>Azotobacter vinelandii</i> Ferredoxin I Undergoes Facile [3Fe-4S] ₀ to [4Fe-4S] ₂₊ Conversion in Vitro but Not in Vivo. <i>Journal of Biological Chemistry</i> , 1998, 273, 33692-33701.	3.4	21