

Young-jun Park

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

15,191
citations

159585

30
h-index

315739

38
g-index

54
all docs

54
docs citations

54
times ranked

24618
citing authors

#	ARTICLE	IF	CITATIONS
1	Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry. <i>Science</i> , 2022, 375, 449-454.	12.6	108
2	Structure-based design of stabilized recombinant influenza neuraminidase tetramers. <i>Nature Communications</i> , 2022, 13, 1825.	12.8	21
3	Multivalent designed proteins neutralize SARS-CoV-2 variants of concern and confer protection against infection in mice. <i>Science Translational Medicine</i> , 2022, 14, eabn1252.	12.4	68
4	Structure, receptor recognition, and antigenicity of the human coronavirus CCoV-HuPn-2018 spike glycoprotein. <i>Cell</i> , 2022, 185, 2279-2291.e17.	28.9	25
5	Quadrivalent influenza nanoparticle vaccines induce broad protection. <i>Nature</i> , 2021, 592, 623-628.	27.8	180
6	Design of multi-scale protein complexes by hierarchical building block fusion. <i>Nature Communications</i> , 2021, 12, 2294.	12.8	48
7	Structural basis for broad coronavirus neutralization. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 478-486.	8.2	152
8	Generation of ordered protein assemblies using rigid three-body fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	25
9	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , 2021, 597, 97-102.	27.8	385
10	Lectins enhance SARS-CoV-2 infection and influence neutralizing antibodies. <i>Nature</i> , 2021, 598, 342-347.	27.8	230
11	Mapping Neutralizing and Immunodominant Sites on the SARS-CoV-2 Spike Receptor-Binding Domain by Structure-Guided High-Resolution Serology. <i>Cell</i> , 2020, 183, 1024-1042.e21.	28.9	1,195
12	De novo design of picomolar SARS-CoV-2 miniprotein inhibitors. <i>Science</i> , 2020, 370, 426-431.	12.6	464
13	Cross-neutralization of SARS-CoV-2 by a human monoclonal SARS-CoV antibody. <i>Nature</i> , 2020, 583, 290-295.	27.8	1,695
14	Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. <i>Cell</i> , 2020, 181, 281-292.e6.	28.9	6,979
15	Tailored design of protein nanoparticle scaffolds for multivalent presentation of viral glycoprotein antigens. <i>ELife</i> , 2020, 9, .	6.0	123
16	Suppressor Mutations in Type II Secretion Mutants of <i>Vibrio cholerae</i> : Inactivation of the VesC Protease. <i>MSphere</i> , 2020, 5, .	2.9	2
17	Cryo-EM Structure of Nipah Virus Fusion Glycoprotein in Complex with a Monoclonal Antibody Reveals Mechanism of Neutralization. <i>Microscopy and Microanalysis</i> , 2019, 25, 1328-1329.	0.4	0
18	Unexpected Receptor Functional Mimicry Elucidates Activation of Coronavirus Fusion. <i>Cell</i> , 2019, 176, 1026-1039.e15.	28.9	558

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19	Structures of MERS-CoV spike glycoprotein in complex with sialoside attachment receptors. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1151-1157.	8.2	218
20	An antibody against the F glycoprotein inhibits Nipah and Hendra virus infections. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 980-987.	8.2	69
21	Structure of the type VI secretion system TssKâ€“TssFâ€“TssG baseplate subcomplex revealed by cryo-electron microscopy. <i>Nature Communications</i> , 2018, 9, 5385.	12.8	37
22	Bifunctional Immunity Proteins Protect Bacteria against FtsZ-Targeting ADP-Ribosylating Toxins. <i>Cell</i> , 2018, 175, 1380-1392.e14.	28.9	109
23	Hexamers of the Type II Secretion ATPase GspE from <i>Vibrio cholerae</i> with Increased ATPase Activity. <i>Structure</i> , 2013, 21, 1707-1717.	3.3	60
24	Crystal structure of a heterodimer of editosome interaction proteins in complex with two copies of a cross-reacting nanobody. <i>Nucleic Acids Research</i> , 2012, 40, 1828-1840.	14.5	35
25	Explorations of linked editosome domains leading to the discovery of motifs defining conserved pockets in editosome OB-folds. <i>Journal of Structural Biology</i> , 2012, 180, 362-373.	2.8	6
26	The structure of the C-terminal domain of the largest editosome interaction protein and its role in promoting RNA binding by RNA-editing ligase L2. <i>Nucleic Acids Research</i> , 2012, 40, 6966-6977.	14.5	19
27	Structures of a key interaction protein from the <i>Trypanosoma brucei</i> editosome in complex with single domain antibodies. <i>Journal of Structural Biology</i> , 2011, 174, 124-136.	2.8	27
28	A Protein-Protein Interaction Map of Trypanosome $\frac{1}{4}$ 20S Editosomes. <i>Journal of Biological Chemistry</i> , 2010, 285, 5282-5295.	3.4	46
29	Histone chaperone specificity in Rtt109 activation. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 957-964.	8.2	62
30	Histone chaperones in nucleosome eviction and histone exchange. <i>Current Opinion in Structural Biology</i> , 2008, 18, 282-289.	5.7	175
31	A \hat{I}^2 -Hairpin Comprising the Nuclear Localization Sequence Sustains the Self-associated States of Nucleosome Assembly Protein 1. <i>Journal of Molecular Biology</i> , 2008, 375, 1076-1085.	4.2	43
32	A Thermodynamic Model for Nap1-Histone Interactions. <i>Journal of Biological Chemistry</i> , 2008, 283, 32412-32418.	3.4	83
33	Structure and function of nucleosome assembly proteinsThis paper is one of a selection of papers published in this Special Issue, entitled 27th International West Coast Chromatin and Chromosome Conference, and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2006, 84, 549-549.	2.0	133
34	The structure of nucleosome assembly protein 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1248-1253.	7.1	178
35	Nucleosome Assembly Protein 1 Exchanges Histone H2A-H2B Dimers and Assists Nucleosome Sliding*. <i>Journal of Biological Chemistry</i> , 2005, 280, 1817-1825.	3.4	159
36	A New Fluorescence Resonance Energy Transfer Approach Demonstrates That the Histone Variant H2AZ Stabilizes the Histone Octamer within the Nucleosome. <i>Journal of Biological Chemistry</i> , 2004, 279, 24274-24282.	3.4	193

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37	Nucleosomes containing the histone variant H2A.Bbd organize only 118 base pairs of DNA. EMBO Journal, 2004, 23, 3314-3324.	7.8	181
38	Preferential Binding of the Histone (H3-H4) ₂ Tetramer by NAP1 Is Mediated by the Amino-terminal Histone Tails. Journal of Biological Chemistry, 2003, 278, 44574-44583.	3.4	98