

Young-jun Park

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

50
papers

9,415
citations

28
h-index

54
g-index

54
ext. papers

12,665
ext. citations

21.2
avg, IF

7.19
L-index

#	Paper	IF	Citations
50	Structural changes in the SARS-CoV-2 spike E406W mutant escaping a clinical monoclonal antibody cocktail. 2022 ,		2
49	Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry.. <i>Science</i> , 2022 , 375, eabm8143	33.3	23
48	Structure-based design of stabilized recombinant influenza neuraminidase tetramers.. <i>Nature Communications</i> , 2022 , 13, 1825	17.4	0
47	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	17.5	3
46	Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry 2021 ,		7
45	Structural basis for broad coronavirus neutralization 2021 ,		14
44	Quadrivalent influenza nanoparticle vaccines induce broad protection. <i>Nature</i> , 2021 , 592, 623-628	50.4	40
43	Design of multi-scale protein complexes by hierarchical building block fusion. <i>Nature Communications</i> , 2021 , 12, 2294	17.4	14
42	Antibodies to the SARS-CoV-2 receptor-binding domain that maximize breadth and resistance to viral escape 2021 ,		12
41	Structural basis for broad coronavirus neutralization. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 478-486	17.6	65
40	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,	11.5	6
39	Multivalent designed proteins protect against SARS-CoV-2 variants of concern 2021 ,		4
38	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , 2021 , 597, 97-102	50.4	118
37	Lectins enhance SARS-CoV-2 infection and influence neutralizing antibodies. <i>Nature</i> , 2021 , 598, 342-347	50.4	63
36	Cross-neutralization of SARS-CoV-2 by a human monoclonal SARS-CoV antibody. <i>Nature</i> , 2020 , 583, 290-301	30.1	1028
35	Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. <i>Cell</i> , 2020 , 181, 281-292.e6	56.2	4571
34	Tailored design of protein nanoparticle scaffolds for multivalent presentation of viral glycoprotein antigens. <i>ELife</i> , 2020 , 9,	8.9	51

33	Structural and functional analysis of a potent sarbecovirus neutralizing antibody 2020 ,		42
32	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	56.2	601
31	De novo design of picomolar SARS-CoV-2 miniprotein inhibitors. <i>Science</i> , 2020 , 370, 426-431	33.3	219
30	Unexpected Receptor Functional Mimicry Elucidates Activation of Coronavirus Fusion. <i>Cell</i> , 2019 , 176, 1026-1039.e15	56.2	416
29	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	0.5	
28	Structures of MERS-CoV spike glycoprotein in complex with sialoside attachment receptors. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 1151-1157	17.6	161
27	An antibody against the F glycoprotein inhibits Nipah and Hendra virus infections. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 980-987	17.6	28
26	Structure of the type VI secretion system TssK-TssF-TssG baseplate subcomplex revealed by cryo-electron microscopy. <i>Nature Communications</i> , 2018 , 9, 5385	17.4	20
25	Bifunctional Immunity Proteins Protect Bacteria against FtsZ-Targeting ADP-Ribosylating Toxins. <i>Cell</i> , 2018 , 175, 1380-1392.e14	56.2	62
24	Hexamers of the type II secretion ATPase GspE from <i>Vibrio cholerae</i> with increased ATPase activity. <i>Structure</i> , 2013 , 21, 1707-17	5.2	51
23	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, 362-73	3.4	4
22	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, 6966-77	20.1	16
21	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, 1828-40	20.1	26
20	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, 124-36	3.4	23
19	A protein-protein interaction map of trypanosome ~20S editosomes. <i>Journal of Biological Chemistry</i> , 2010 , 285, 5282-95	5.4	40
18	Histone chaperone specificity in Rtt109 activation. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 957-64	17.6	56
17	Histone chaperones in nucleosome eviction and histone exchange. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 282-9	8.1	158
16	A beta-hairpin comprising the nuclear localization sequence sustains the self-associated states of nucleosome assembly protein 1. <i>Journal of Molecular Biology</i> , 2008 , 375, 1076-85	6.5	33

15	A thermodynamic model for Nap1-histone interactions. <i>Journal of Biological Chemistry</i> , 2008 , 283, 32412-54	70
14	The structure of nucleosome assembly protein 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 1248-53	11.5 155
13	Structure and function of nucleosome assembly proteins. <i>Biochemistry and Cell Biology</i> , 2006 , 84, 549-583.6	112
12	Nucleosome assembly protein 1 exchanges histone H2A-H2B dimers and assists nucleosome sliding. <i>Journal of Biological Chemistry</i> , 2005 , 280, 1817-25	5.4 144
11	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, 24274-82	5.4 177
10	Nucleosomes containing the histone variant H2A.Bbd organize only 118 base pairs of DNA. <i>EMBO Journal</i> , 2004 , 23, 3314-24	13 162
9	Preferential binding of the histone (H3-H4) ₂ tetramer by NAP1 is mediated by the amino-terminal histone tails. <i>Journal of Biological Chemistry</i> , 2003 , 278, 44574-83	5.4 87
8	Structure, receptor recognition and antigenicity of the human coronavirus CCoV-HuPn-2018 spike glycoprotein	
7	Tailored Design of Protein Nanoparticle Scaffolds for Multivalent Presentation of Viral Glycoprotein Antigens	7
6	Structure, function and antigenicity of the SARS-CoV-2 spike glycoprotein	126
5	Elicitation of broadly protective immunity to influenza by multivalent hemagglutinin nanoparticle vaccines	15
4	Generation of ordered protein assemblies using rigid three-body fusion	4
3	Hierarchical design of multi-scale protein complexes by combinatorial assembly of oligomeric helical bundle and repeat protein building blocks	4
2	Membrane lectins enhance SARS-CoV-2 infection and influence the neutralizing activity of different classes of antibodies	18
1	Imprinted antibody responses against SARS-CoV-2 Omicron sublineages	5