

Guang-Wen Lu

List of Publications by Citations

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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.

51
papers

4,910
citations

24
h-index

57
g-index

57
ext. papers

6,591
ext. citations

14.1
avg, IF

5.82
L-index

#	Paper	IF	Citations
51	Structural and Functional Basis of SARS-CoV-2 Entry by Using Human ACE2. <i>Cell</i> , 2020 , 181, 894-904.e9	56.2	1513
50	Cryo-EM structures of MERS-CoV and SARS-CoV spike glycoproteins reveal the dynamic receptor binding domains. <i>Nature Communications</i> , 2017 , 8, 15092	17.4	484
49	Molecular basis of binding between novel human coronavirus MERS-CoV and its receptor CD26. <i>Nature</i> , 2013 , 500, 227-31	50.4	466
48	Bat-to-human: spike features determining host jump of coronaviruses SARS-CoV, MERS-CoV, and beyond. <i>Trends in Microbiology</i> , 2015 , 23, 468-78	12.4	363
47	A vaccine targeting the RBD of the S protein of SARS-CoV-2 induces protective immunity. <i>Nature</i> , 2020 , 586, 572-577	50.4	348
46	Bat origins of MERS-CoV supported by bat coronavirus HKU4 usage of human receptor CD26. <i>Cell Host and Microbe</i> , 2014 , 16, 328-37	23.4	198
45	Ebola Viral Glycoprotein Bound to Its Endosomal Receptor Niemann-Pick C1. <i>Cell</i> , 2016 , 164, 258-268	56.2	165
44	SARS-CoV-2 M inhibitors with antiviral activity in a transgenic mouse model. <i>Science</i> , 2021 , 371, 1374-1378	59.3	124
43	A humanized neutralizing antibody against MERS-CoV targeting the receptor-binding domain of the spike protein. <i>Cell Research</i> , 2015 , 25, 1237-49	24.7	116
42	Middle East respiratory syndrome coronavirus and bat coronavirus HKU9 both can utilize GRP78 for attachment onto host cells. <i>Journal of Biological Chemistry</i> , 2018 , 293, 11709-11726	5.4	114
41	Recombinant Receptor Binding Domain Protein Induces Partial Protective Immunity in Rhesus Macaques Against Middle East Respiratory Syndrome Coronavirus Challenge. <i>EBioMedicine</i> , 2015 , 2, 1438-46	8.8	87
40	SARS-CoV-2 Omicron variant: Characteristics and prevention.. <i>MedComm</i> , 2021 ,	2.2	85
39	Molecular characterization of the monoclonal antibodies composing ZMAb: a protective cocktail against Ebola virus. <i>Scientific Reports</i> , 2014 , 4, 6881	4.9	74
38	MERS-CoV spike protein: Targets for vaccines and therapeutics. <i>Antiviral Research</i> , 2016 , 133, 165-77	10.8	72
37	Binding of herpes simplex virus glycoprotein D to nectin-1 exploits host cell adhesion. <i>Nature Communications</i> , 2011 , 2, 577	17.4	66
36	Tailoring subunit vaccine immunity with adjuvant combinations and delivery routes using the Middle East respiratory coronavirus (MERS-CoV) receptor-binding domain as an antigen. <i>PLoS ONE</i> , 2014 , 9, e112602	3.7	64
35	Carcinoembryonic Antigen-Related Cell Adhesion Molecule 5 Is an Important Surface Attachment Factor That Facilitates Entry of Middle East Respiratory Syndrome Coronavirus. <i>Journal of Virology</i> , 2016 , 90, 9114-27	6.6	56

34	Genomic monitoring of SARS-CoV-2 uncovers an Nsp1 deletion variant that modulates type I interferon response. <i>Cell Host and Microbe</i> , 2021 , 29, 489-502.e8	23.4	47
33	Crystal structure of SARS-CoV-2 nsp10/nsp16 2FO-methylase and its implication on antiviral drug design. <i>Signal Transduction and Targeted Therapy</i> , 2020 , 5, 131	21	46
32	Crystal structure of herpes simplex virus 2 gD bound to nectin-1 reveals a conserved mode of receptor recognition. <i>Journal of Virology</i> , 2014 , 88, 13678-88	6.6	29
31	The two-component system Ihk/Irr contributes to the virulence of <i>Streptococcus suis</i> serotype 2 strain 05ZYH33 through alteration of the bacterial cell metabolism. <i>Microbiology (United Kingdom)</i> , 2012 , 158, 1852-1866	2.9	28
30	hNUDT16: a universal decapping enzyme for small nucleolar RNA and cytoplasmic mRNA. <i>Protein and Cell</i> , 2011 , 2, 64-73	7.2	27
29	Crystal structure of SARS-CoV-2 nsp10 bound to nsp14-ExoN domain reveals an exoribonuclease with both structural and functional integrity. <i>Nucleic Acids Research</i> , 2021 , 49, 5382-5392	20.1	27
28	Structural basis of nectin-1 recognition by pseudorabies virus glycoprotein D. <i>PLoS Pathogens</i> , 2017 , 13, e1006314	7.6	26
27	Discovery of Potent and Selective Inhibitors of Cdc2-Like Kinase 1 (CLK1) as a New Class of Autophagy Inducers. <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 6337-6352	8.3	24
26	Two classes of protective antibodies against Pseudorabies virus variant glycoprotein B: Implications for vaccine design. <i>PLoS Pathogens</i> , 2017 , 13, e1006777	7.6	22
25	Structural and functional analysis of an anchorless fibronectin-binding protein FBPS from Gram-positive bacterium <i>Streptococcus suis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 13869-13874	11.5	21
24	PILR and PILR have a siglec fold and provide the basis of binding to sialic acid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 8221-6	11.5	19
23	Structural Analysis of Rabies Virus Glycoprotein Reveals pH-Dependent Conformational Changes and Interactions with a Neutralizing Antibody. <i>Cell Host and Microbe</i> , 2020 , 27, 441-453.e7	23.4	18
22	Molecular basis of binding between the global post-transcriptional regulator CsrA and the T3SS chaperone CesT. <i>Nature Communications</i> , 2018 , 9, 1196	17.4	17
21	Structural basis of collagen recognition by human osteoclast-associated receptor and design of osteoclastogenesis inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 1038-43	11.5	17
20	Active DNA unwinding and transport by a membrane-adapted helicase nanopore. <i>Nature Communications</i> , 2019 , 10, 5083	17.4	16
19	From Lead to Drug Candidate: Optimization of 3-(Phenylethynyl)-1H-pyrazolo[3,4-d]pyrimidin-4-amine Derivatives as Agents for the Treatment of Triple Negative Breast Cancer. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 9788-9805	8.3	14
18	Putative Receptor Binding Domain of Bat-Derived Coronavirus HKU9 Spike Protein: Evolution of Betacoronavirus Receptor Binding Motifs. <i>Biochemistry</i> , 2016 , 55, 5977-5988	3.2	14
17	A bivalent recombinant vaccine targeting the S1 protein induces neutralizing antibodies against both SARS-CoV-2 variants and wild-type of the virus. <i>MedComm</i> , 2021 , 2, 430	2.2	13

16	Molecular Basis of Binding between Middle East Respiratory Syndrome Coronavirus and CD26 from Seven Bat Species. <i>Journal of Virology</i> , 2020 , 94,	6.6	12
15	A novel "open-form" structure of sortaseC from <i>Streptococcus suis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2764-9	4.2	12
14	The NS1 gene from bat-derived influenza-like virus H17N10 can be rescued in influenza A PR8 backbone. <i>Journal of General Virology</i> , 2016 , 97, 1797-1806	4.9	11
13	Structure of the S1 subunit C-terminal domain from bat-derived coronavirus HKU5 spike protein. <i>Virology</i> , 2017 , 507, 101-109	3.6	9
12	Cationic nanocarriers as potent adjuvants for recombinant S-RBD vaccine of SARS-CoV-2. <i>Signal Transduction and Targeted Therapy</i> , 2020 , 5, 291	21	7
11	Crystal structure of Usutu virus envelope protein in the pre-fusion state. <i>Virology Journal</i> , 2018 , 15, 183	6.1	7
10	Spike protein of SARS-CoV-2 Omicron (B.1.1.529) variant have a reduced ability to induce the immune response.. <i>Signal Transduction and Targeted Therapy</i> , 2022 , 7, 119	21	5
9	Crystal structure of bovine herpesvirus 1 glycoprotein D bound to nectin-1 reveals the basis for its low-affinity binding to the receptor. <i>Science Advances</i> , 2020 , 6, eaba5147	14.3	4
8	Crystal structure of PA0833 periplasmic domain from <i>Pseudomonas aeruginosa</i> reveals an unexpected enlarged peptidoglycan binding pocket. <i>Biochemical and Biophysical Research Communications</i> , 2019 , 511, 875-881	3.4	3
7	In vitro transcriptome analysis of two Chinese isolates of <i>Streptococcus suis</i> serotype 2. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 266-75	6.5	3
6	Flagella hook protein FlgE is a novel vaccine candidate of <i>Pseudomonas aeruginosa</i> identified by a genomic approach. <i>Vaccine</i> , 2021 , 39, 2386-2395	4.1	3
5	S19W, T27W, and N330Y mutations in ACE2 enhance SARS-CoV-2 S-RBD binding toward both wild-type and antibody-resistant viruses and its molecular basis. <i>Signal Transduction and Targeted Therapy</i> , 2021 , 6, 343	21	3
4	Crystal structure of the S1 subunit N-terminal domain from DcCoV UAE-HKU23 spike protein. <i>Virology</i> , 2019 , 535, 74-82	3.6	2
3	The novel regulators CheP and CheQ control the core chemotaxis operon cheVAW in <i>Campylobacter jejuni</i> . <i>Molecular Microbiology</i> , 2019 , 111, 145-158	4.1	2
2	Characterization of SARS-CoV-2 Omicron spike RBD reveals significantly decreased stability, severe evasion of neutralizing-antibody recognition but unaffected engagement by decoy ACE2 modified for enhanced RBD binding.. <i>Signal Transduction and Targeted Therapy</i> , 2022 , 7, 56	21	1
1	Intranasal administration of a recombinant RBD vaccine induces long-term immunity against Omicron-included SARS-CoV-2 variants.. <i>Signal Transduction and Targeted Therapy</i> , 2022 , 7, 159	21	0