

Guang-Wen Lu

List of Publications by Year in descending order

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54
papers

7,855
citations

172207

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155451

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all docs

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docs citations

57
times ranked

14158
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and Functional Basis of SARS-CoV-2 Entry by Using Human ACE2. <i>Cell</i> , 2020, 181, 894-904.e9.	13.5	2,443
2	Cryo-EM structures of MERS-CoV and SARS-CoV spike glycoproteins reveal the dynamic receptor binding domains. <i>Nature Communications</i> , 2017, 8, 15092.	5.8	649
3	A vaccine targeting the RBD of the S protein of SARS-CoV-2 induces protective immunity. <i>Nature</i> , 2020, 586, 572-577.	13.7	630
4	Molecular basis of binding between novel human coronavirus MERS-CoV and its receptor CD26. <i>Nature</i> , 2013, 500, 227-231.	13.7	582
5	Bat-to-human: spike features determining "host jump"™ of coronaviruses SARS-CoV, MERS-CoV, and beyond. <i>Trends in Microbiology</i> , 2015, 23, 468-478.	3.5	521
6	SARS-CoV-2 Omicron variant: Characteristics and prevention. <i>MedComm</i> , 2021, 2, 838-845.	3.1	364
7	SARS-CoV-2 M ^{pro} inhibitors with antiviral activity in a transgenic mouse model. <i>Science</i> , 2021, 371, 1374-1378.	6.0	324
8	Bat Origins of MERS-CoV Supported by Bat Coronavirus HKU4 Usage of Human Receptor CD26. <i>Cell Host and Microbe</i> , 2014, 16, 328-337.	5.1	252
9	Ebola Viral Glycoprotein Bound to Its Endosomal Receptor Niemann-Pick C1. <i>Cell</i> , 2016, 164, 258-268.	13.5	226
10	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.	1.6	153
11	A humanized neutralizing antibody against MERS-CoV targeting the receptor-binding domain of the spike protein. <i>Cell Research</i> , 2015, 25, 1237-1249.	5.7	137
12	Recombinant Receptor Binding Domain Protein Induces Partial Protective Immunity in Rhesus Macaques Against Middle East Respiratory Syndrome Coronavirus Challenge. <i>EBioMedicine</i> , 2015, 2, 1438-1446.	2.7	102
13	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.	5.1	95
14	MERS-CoV spike protein: Targets for vaccines and therapeutics. <i>Antiviral Research</i> , 2016, 133, 165-177.	1.9	94
15	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.	6.5	94
16	Binding of herpes simplex virus glycoprotein D to nectin-1 exploits host cell adhesion. <i>Nature Communications</i> , 2011, 2, 577.	5.8	93
17	Molecular Characterization of the Monoclonal Antibodies Composing ZMAb: A Protective Cocktail Against Ebola Virus. <i>Scientific Reports</i> , 2014, 4, 6881.	1.6	90
18	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.	1.1	74

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19	Crystal structure of SARS-CoV-2 nsp10/nsp16 2â€²-O-methylase and its implication on antiviral drug design. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 131.	7.1	72
20	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, 9114-9127.	1.5	68
21	Structural basis of nectin-1 recognition by pseudorabies virus glycoprotein D. <i>PLoS Pathogens</i> , 2017, 13, e1006314.	2.1	55
22	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.	5.1	49
23	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.	2.9	40
24	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, 13678-13688.	1.5	38
25	A bivalent recombinant vaccine targeting the S1 protein induces neutralizing antibodies against both SARSâ€CoVâ€2 variants and wildâ€type of the virus. <i>MedComm</i> , 2021, 2, 430-441.	3.1	37
26	hNUDT16: a universal decapping enzyme for small nucleolar RNA and cytoplasmic mRNA. <i>Protein and Cell</i> , 2011, 2, 64-73.	4.8	36
27	The two-component system <i>lhk/lrr</i> 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.	0.7	36
28	Spike protein of SARSâ€CoVâ€2 Omicron (B.1.1.529) variant has a reduced ability to induce the immune response. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 119.	7.1	35
29	Two classes of protective antibodies against Pseudorabies virus variant glycoprotein B: Implications for vaccine design. <i>PLoS Pathogens</i> , 2017, 13, e1006777.	2.1	34
30	Molecular basis of binding between the global post-transcriptional regulator CsrA and the T3SS chaperone CesT. <i>Nature Communications</i> , 2018, 9, 1196.	5.8	34
31	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.	7.1	31
32	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.	3.3	27
33	PILRÎ± and PILRÎ² 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, 8221-8226.	3.3	25
34	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, 1038-1043.	3.3	25
35	Active DNA unwinding and transport by a membrane-adapted helicase nanopore. <i>Nature Communications</i> , 2019, 10, 5083.	5.8	25
36	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.	7.1	24

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37	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.	2.9	23
38	Putative Receptor Binding Domain of Bat-Derived Coronavirus HKU9 Spike Protein: Evolution of Betacoronavirus Receptor Binding Motifs. <i>Biochemistry</i> , 2016, 55, 5977-5988.	1.2	22
39	Cationic nanocarriers as potent adjuvants for recombinant S-RBD vaccine of SARS-CoV-2. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 291.	7.1	22
40	Histones released by NETosis enhance the infectivity of SARS-CoV-2 by bridging the spike protein subunit 2 and sialic acid on host cells. , 2022, 19, 577-587.		22
41	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.	7.1	21
42	Molecular Basis of Binding between Middle East Respiratory Syndrome Coronavirus and CD26 from Seven Bat Species. <i>Journal of Virology</i> , 2020, 94, .	1.5	16
43	A novel "open" structure of sortaseC from <i>Streptococcus suis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2764-2769.	1.5	13
44	Structure of the S1 subunit C-terminal domain from bat-derived coronavirus HKU5 spike protein. <i>Virology</i> , 2017, 507, 101-109.	1.1	13
45	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.	1.3	12
46	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.	1.7	10
47	Crystal structure of Usutu virus envelope protein in the pre-fusion state. <i>Virology Journal</i> , 2018, 15, 183.	1.4	9
48	Crystal structure of the S1 subunit N-terminal domain from DcCoV UAE-HKU23 spike protein. <i>Virology</i> , 2019, 535, 74-82.	1.1	9
49	The novel regulators CheP and CheQ control the core chemotaxis operon <i>cheVAW</i> in <i>Campylobacter jejuni</i> . <i>Molecular Microbiology</i> , 2019, 111, 145-158.	1.2	8
50	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.	4.7	8
51	A Potent Neutralizing Nanobody Targeting the Spike Receptor-Binding Domain of SARS-CoV-2 and the Structural Basis of Its Intimate Binding. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	7
52	An engineered 5-helix bundle derived from SARS-CoV-2 S2 pre-binds sarbecoviral spike at both serological- and endosomal-pH to inhibit virus entry. <i>Emerging Microbes and Infections</i> , 2022, 11, 1920-1935.	3.0	7
53	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.	1.0	6
54	In vitro Transcriptome Analysis of Two Chinese Isolates of <i>Streptococcus suis</i> Serotype 2. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 266-275.	3.0	4