Hongmin Li

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6551388/publications.pdf

Version: 2024-02-01

		76326	82547
95	5,560	40	72
papers	citations	h-index	g-index

96	96	96	5889
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Inteins as Drug Targets and Therapeutic Tools. Frontiers in Molecular Biosciences, 2022, 9, 821146.	3.5	10
2	Antiviral Agents against Flavivirus Protease: Prospect and Future Direction. Pathogens, 2022, 11, 293.	2.8	16
3	Editorial of Special Column on Antiviral Drug Discovery and Pharmacology. Acta Pharmaceutica Sinica B, 2022, 12, 1540-1541.	12.0	0
4	Allosteric inhibitors of the main protease of SARS-CoV-2. Antiviral Research, 2022, 205, 105381.	4.1	23
5	The nucleocapsid protein of zoonotic betacoronaviruses is an attractive target for antiviral drug discovery. Life Sciences, 2021, 282, 118754.	4.3	8
6	Drug repurposing approach to combating coronavirus: Potential drugs and drug targets. Medicinal Research Reviews, 2021, 41, 1375-1426.	10.5	28
7	Small-molecule inhibitors for the Prp8 intein as antifungal agents. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	15
8	Design, synthesis and biological evaluation of 7H-pyrrolo[2,3-d]pyrimidine derivatives containing 1,8-naphthyridine-4-one fragment. European Journal of Medicinal Chemistry, 2021, 215, 113273.	5.5	6
9	An alternative domain-swapped structure of the Pyrococcus horikoshii PolII mini-intein. Scientific Reports, 2021, 11, 11680.	3.3	1
10	In vitro and in vivo characterization of erythrosin B and derivatives against Zika virus. Acta Pharmaceutica Sinica B, 2021, , .	12.0	10
11	Methylene blue is a potent and broad-spectrum inhibitor against Zika virus in vitro and in vivo. Emerging Microbes and Infections, 2020, 9, 2404-2416.	6.5	26
12	Prospect of SARS-CoV-2 spike protein: Potential role in vaccine and therapeutic development. Virus Research, 2020, 288, 198141.	2.2	116
13	Conditional DnaB Protein Splicing Is Reversibly Inhibited by Zinc in Mycobacteria. MBio, 2020, 11, .	4.1	16
14	Targeting Crucial Host Factors of SARS-CoV-2. ACS Infectious Diseases, 2020, 6, 2844-2865.	3.8	28
15	JMX0207, a Niclosamide Derivative with Improved Pharmacokinetics, Suppresses Zika Virus Infection Both In Vitro and In Vivo. ACS Infectious Diseases, 2020, 6, 2616-2628.	3.8	32
16	Crystal structure and transient dimerization for the FKBP12 protein from the pathogenic fungus Candida auris. Biochemical and Biophysical Research Communications, 2020, 525, 1103-1108.	2.1	1
17	Broad Spectrum Antiviral Agent Niclosamide and Its Therapeutic Potential. ACS Infectious Diseases, 2020, 6, 909-915.	3.8	252
18	Spliceosomal Prp8 intein at the crossroads of protein and RNA splicing. PLoS Biology, 2019, 17, e3000104.	5.6	28

#	Article	IF	Citations
19	General Base Swap Preserves Activity and Expands Substrate Tolerance in Hedgehog Autoprocessing. Journal of the American Chemical Society, 2019, 141, 18380-18384.	13.7	6
20	Cisplatin protects mice from challenge of Cryptococcus neoformans by targeting the Prp8 intein. Emerging Microbes and Infections, 2019, 8, 895-908.	6.5	20
21	Contributions of Hepatic and Intestinal Metabolism to the Disposition of Niclosamide, a Repurposed Drug with Poor Bioavailability. Drug Metabolism and Disposition, 2019, 47, 756-763.	3.3	24
22	Hectd3 promotes pathogenic Th17 lineage through Stat3 activation and Malt1 signaling in neuroinflammation. Nature Communications, 2019, 10, 701.	12.8	57
23	Analysis of Proteinâ€Protein Interactions by Split Luciferase Complementation Assay. Current Protocols in Toxicology / Editorial Board, Mahin D Maines (editor-in-chief) [et Al], 2019, 82, e90.	1.1	10
24	Structure of an engineered intein reveals thiazoline ring and provides mechanistic insight. Biotechnology and Bioengineering, 2019, 116, 709-721.	3.3	1
25	Erythrosin B is a potent and broad-spectrum orthosteric inhibitor of the flavivirus NS2B-NS3 protease. Antiviral Research, 2018, 150, 217-225.	4.1	61
26	Mycobacterial DnaB helicase intein as oxidative stress sensor. Nature Communications, 2018, 9, 4363.	12.8	26
27	Existing drugs as broad-spectrum and potent inhibitors for Zika virus by targeting NS2B-NS3 interaction. Cell Research, 2017, 27, 1046-1064.	12.0	153
28	Flavivirus NS2B/NS3 Protease: Structure, Function, and Inhibition. , 2017, , 163-188.		13
29	A conformational switch high-throughput screening assay and allosteric inhibition of the flavivirus NS2B-NS3 protease. PLoS Pathogens, 2017, 13, e1006411.	4.7	116
30	Exploring Intein Inhibition by Platinum Compounds as an Antimicrobial Strategy. Journal of Biological Chemistry, 2016, 291, 22661-22670.	3.4	32
31	Novel Broad Spectrum Inhibitors Targeting the Flavivirus Methyltransferase. PLoS ONE, 2015, 10, e0130062.	2.5	58
32	Coupling of Conformational Transitions in the N-terminal Domain of the 51-kDa FK506-binding Protein (FKBP51) Near Its Site of Interaction with the Steroid Receptor Proteins. Journal of Biological Chemistry, 2015, 290, 15746-15757.	3.4	18
33	Transcription Factor Bcl11b Controls Identity and Function of Mature Type 2 Innate Lymphoid Cells. Immunity, 2015, 43, 354-368.	14.3	137
34	Identification and Characterization of Novel Broad-Spectrum Inhibitors of the Flavivirus Methyltransferase. ACS Infectious Diseases, 2015, 1, 340-349.	3.8	51
35	Zinc Inhibits Hedgehog Autoprocessing. Journal of Biological Chemistry, 2015, 290, 11591-11600.	3.4	15
36	5â€²-Silylated 3â€²-1,2,3-triazolyl Thymidine Analogues as Inhibitors of West Nile Virus and Dengue Virus. Journal of Medicinal Chemistry, 2015, 58, 4016-4028.	6.4	67

#	Article	IF	Citations
37	Refolding of a fully functional flavivirus methyltransferase revealed that Sâ€adenosyl methionine but not Sâ€adenosyl homocysteine is copurified with flavivirus methyltransferase. Protein Science, 2015, 24, 117-128.	7.6	14
38	Structural basis of conformational transitions in the active site and 80â€²s loop in the FK506-binding protein FKBP12. Biochemical Journal, 2014, 458, 525-536.	3.7	15
39	Crystal structure and conformational flexibility of the unligated FK506-binding protein FKBP12.6. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 636-646.	2.5	5
40	Inexpensive electronics and software for photon statistics and correlation spectroscopy. American Journal of Physics, 2014, 82, 712-722.	0.7	7
41	The HECTD3 E3 Ubiquitin Ligase Suppresses Cisplatin-Induced Apoptosis via Stabilizing MALT1. Neoplasia, 2013, 15, 39-IN15.	5.3	36
42	Selective inhibition of the West Nile virus methyltransferase by nucleoside analogs. Antiviral Research, 2013, 97, 232-239.	4.1	51
43	The flavivirus protease as a target for drug discovery. Virologica Sinica, 2013, 28, 326-336.	3.0	47
44	Pfit Is a Structurally Novel Crohn's Disease-Associated Superantigen. PLoS Pathogens, 2013, 9, e1003837.	4.7	4
45	Analysing the visible conformational substates of the FK506-binding protein FKBP12. Biochemical Journal, 2013, 453, 371-380.	3.7	19
46	The HECTD3 E3 ubiquitin ligase facilitates cancer cell survival by promoting K63-linked polyubiquitination of caspase-8. Cell Death and Disease, 2013, 4, e935-e935.	6.3	45
47	S-Adenosyl-Homocysteine Is a Weakly Bound Inhibitor for a Flaviviral Methyltransferase. PLoS ONE, 2013, 8, e76900.	2.5	18
48	Functional Interaction of CD154 Protein with Î±5Î²1 Integrin Is Totally Independent from Its Binding to Î±IIbÎ²3 Integrin and CD40 Molecules. Journal of Biological Chemistry, 2012, 287, 18055-18066.	3.4	29
49	Flavivirus RNA cap methyltransferase: structure, function, and inhibition. Frontiers in Biology, 2010, 5, 286-303.	0.7	62
50	Structural and Functional Analyses of a Conserved Hydrophobic Pocket of Flavivirus Methyltransferase. Journal of Biological Chemistry, 2010, 285, 32586-32595.	3.4	52
51	Crystal Structure of the Mycoplasma arthritidis-Derived Mitogen in Apo Form Reveals a 3D Domain-Swapped Dimer. Journal of Molecular Biology, 2010, 399, 367-376.	4.2	3
52	Separate molecules of West Nile virus methyltransferase can independently catalyze the N7 and 2â€²-O methylations of viral RNA cap. Virology, 2008, 377, 1-6.	2.4	33
53	West Nile Virus Methyltransferase Catalyzes Two Methylations of the Viral RNA Cap through a Substrate-Repositioning Mechanism. Journal of Virology, 2008, 82, 4295-4307.	3.4	105
54	Structure and Function of Flavivirus NS5 Methyltransferase. Journal of Virology, 2007, 81, 3891-3903.	3.4	324

#	Article	IF	Citations
55	Zinc Induces Dimerization of the Class II Major Histocompatibility Complex Molecule That Leads to Cooperative Binding to a Superantigen. Journal of Biological Chemistry, 2007, 282, 5991-6000.	3.4	17
56	Distinct RNA Elements Confer Specificity to Flavivirus RNA Cap Methylation Events. Journal of Virology, 2007, 81, 4412-4421.	3.4	109
57	Mutagenesis, biochemical, and biophysical characterization of Mycoplasma arthritidis-derived mitogen. Molecular Immunology, 2007, 44, 763-773.	2.2	6
58	NMR and X-ray analysis of structural additivity in metal binding site-swapped hybrids of rubredoxin. BMC Structural Biology, 2007, 7, 81.	2.3	1
59	Crystal structure of a complete ternary complex of TCR, superantigen and peptide-MHC. Nature Structural and Molecular Biology, 2007, 14, 169-171.	8.2	39
60	A single point mutation changes the crystallization behavior ofMycoplasma arthritidis-derived mitogen. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 238-241.	0.7	4
61	West Nile Virus 5â€²-Cap Structure Is Formed by Sequential Guanine N-7 and Ribose 2â€²-O Methylations by Nonstructural Protein 5. Journal of Virology, 2006, 80, 8362-8370.	3.4	329
62	Crystal structures of T cell receptor Î² chains related to rheumatoid arthritis. Protein Science, 2005, 14, 3025-3038.	7.6	10
63	The Structure of the Candida albicans Ess1 Prolyl Isomerase Reveals a Well-Ordered Linker that Restricts Domain Mobility,. Biochemistry, 2005, 44, 6180-6189.	2.5	46
64	Crystal Structure of Mycoplasma arthritidis Mitogen Complexed with HLA-DR1 Reveals a Novel Superantigen Fold and a Dimerized Superantigen-MHC Complex. Structure, 2004, 12, 277-288.	3.3	20
65	Crystallization and preliminary crystallographic analysis ofMycoplasma arthritidis-derived mitogen complexed with peptide/MHC class II antigen. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 353-356.	2.5	5
66	X-ray snapshots of the maturation of an antibody response to a protein antigen. Nature Structural and Molecular Biology, 2003, 10, 482-488.	8.2	151
67	Crystal structure of pokeweed antiviral protein with well-defined sugars from seeds at 1.8Ã... resolution. Journal of Structural Biology, 2003, 141, 171-178.	2.8	16
68	Immunoassay Targeting Nonstructural Protein 5 To Differentiate West Nile Virus Infection from Dengue and St. Louis Encephalitis Virus Infections and from Flavivirus Vaccination. Journal of Clinical Microbiology, 2003, 41, 4217-4223.	3.9	113
69	The Human Polymeric Immunoglobulin Receptor Binds to Streptococcus pneumoniae via Domains 3 and 4. Journal of Biological Chemistry, 2003, 278, 48178-48187.	3.4	65
70	Conservation of Nonpeptide Antigen Recognition by Rhesus Monkey VÎ³2VÎ´2 T Cells. Journal of Immunology, 2003, 170, 3696-3706.	0.8	52
71	Three-dimensional Structure of Human Î³-Glutamyl Hydrolase. Journal of Biological Chemistry, 2002, 277, 24522-24529.	3.4	28
72	Structures of Two Streptococcal Superantigens Bound to TCR Î² Chains Reveal Diversity in the Architecture of T Cell Signaling Complexes. Structure, 2002, 10, 687-699.	3.3	116

#	Article	IF	Citations
73	Involvement of zinc in the binding ofMycoplasma arthritidis-derived mitogen to the proximity of the HLA-DR binding groove regardless of histidine 81 of the Î² chain. European Journal of Immunology, 2002, 32, 50-58.	2.9	17
74	Crystal Structure of a Superantigen Bound to the High-Affinity, Zinc-Dependent Site on MHC Class II. Immunity, 2001, 14, 93-104.	14.3	134
75	Superantigen Recognition by Î³Î´ T Cells. Immunity, 2001, 14, 331-344.	14.3	50
76	Structural Features of Nonpeptide Prenyl Pyrophosphates That Determine Their Antigenicity for Human Î³Î´ T Cells. Journal of Immunology, 2001, 167, 36-41.	0.8	74
77	Crystal structure determination of a neutral neurotoxin BmK M4 fromButhus martensii Karsch at 0.20 nm. Science in China Series C: Life Sciences, 2000, 43, 39-46.	1.3	1
78	Structural basis for the binding of an immunodominant peptide from myelin basic protein in different registers by two HLA-DR2 proteins. Journal of Molecular Biology, 2000, 304, 177-188.	4.2	131
79	Three-Dimensional Structures of the Free and Antigen-Bound Fab from Monoclonal Antilysozyme Antibody HyHEL-63â€‚â€¡. Biochemistry, 2000, 39, 6296-6309.	2.5	94
80	A series of bioactivity-variant neurotoxins from scorpionButhus martensiiKarsch: purification, crystallization and crystallographic analysis. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 341-344.	2.5	9
81	Structure of an insulin dimer in an orthorhombic crystal: the structure analysis of a human insulin mutant (B9 Serâ†'Glu). Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1524-1532.	2.5	29
82	THE STRUCTURAL BASIS OF T CELL ACTIVATION BY SUPERANTIGENS. Annual Review of Immunology, 1999, 17, 435-466.	21.8	294
83	Crystal structures of two Î±-like scorpion toxins: non-proline cis peptide bonds and implications for new binding site selectivity on the sodium channel 1 1Edited by R. Huber. Journal of Molecular Biology, 1999, 292, 125-135.	4.2	81
84	Structure of the VÎ´ domain of a human Î³Î´ T-cell antigen receptor. Nature, 1998, 391, 502-506.	27.8	121
85	Imperfect interfaces. Nature Structural Biology, 1998, 5, 412-414.	9.7	31
86	Structure-function studies of T-cell receptor-superantigen interactions. Immunological Reviews, 1998, 163, 177-186.	6.0	48
87	Crystal structure of pokeweed antiviral protein from seeds ofPhytolacca americana at 0.25 nm. Science in China Series C: Life Sciences, 1998, 41, 413-418.	1.3	0
88	Crystallization and preliminary crystallographic analyses of pokeweed antiviral protein from seeds. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 137-139.	2.5	5
89	Three-Dimensional Structure of the Complex between a T Cell Receptor Î² Chain and the Superantigen Staphylococcal Enterotoxin B. Immunity, 1998, 9, 807-816.	14.3	188
90	Three-dimensional structure of H-2Dd complexed with an immunodominant peptide from human immunodeficiency virus envelope glycoprotein 120. Journal of Molecular Biology, 1998, 283, 179-191.	4.2	71

#	Article	IF	Citations
91	A Mutational Analysis of Binding Interactions in an Antigenâ^'Antibody Proteinâ^'Protein Complexâ€. Biochemistry, 1998, 37, 7981-7991.	2.5	157
92	A Mutational Analysis of the Binding of Staphylococcal Enterotoxins B and C3 to the T Cell Receptor Î² Chain and Major Histocompatibility Complex Class II. Journal of Experimental Medicine, 1998, 187, 823-833.	8.5	145
93	Dual conformations of a T cell receptor VÎ± homodimer: implications for variability in VÎ±VÎ² domain association 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 1997, 269, 385-394.	4.2	18
94	Crystal Structure of an Acidic Neurotoxin from ScorpionButhus martensiiKarsch at 1.85 Ã... Resolution. Journal of Molecular Biology, 1996, 261, 415-431.	4.2	89
95	Crystal structure of a T-cell receptor Î²-chain complexed with a superantigen. Nature, 1996, 384, 188-192.	27.8	295