

Huilin Li

List of Publications by Year in descending order

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103
papers

6,025
citations

76196

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82410

72
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118
all docs

118
docs citations

118
times ranked

5476
citing authors

#	ARTICLE	IF	CITATIONS
1	A double-hexameric MCM2-7 complex is loaded onto origin DNA during licensing of eukaryotic DNA replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20240-20245.	3.3	465
2	Diamond family of nanoparticle superlattices. <i>Science</i> , 2016, 351, 582-586.	6.0	331
3	Inhibitors selective for mycobacterial versus human proteasomes. <i>Nature</i> , 2009, 461, 621-626.	13.7	213
4	ATPase-dependent cooperative binding of ORC and Cdc6 to origin DNA. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 965-971.	3.6	198
5	Lattice engineering through nanoparticle-DNA frameworks. <i>Nature Materials</i> , 2016, 15, 654-661.	13.3	198
6	Fiber Formation across the Bacterial Outer Membrane by the Chaperone/Usher Pathway. <i>Cell</i> , 2008, 133, 640-652.	13.5	194
7	Structure of eukaryotic CMG helicase at a replication fork and implications to replisome architecture and origin initiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E697-E706.	3.3	176
8	Ordered three-dimensional nanomaterials using DNA-prescribed and valence-controlled material voxels. <i>Nature Materials</i> , 2020, 19, 789-796.	13.3	172
9	Crystal structure of the FimD usher bound to its cognate FimC-FimH substrate. <i>Nature</i> , 2011, 474, 49-53.	13.7	170
10	The architecture of a eukaryotic replisome. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 976-982.	3.6	161
11	Structure of the eukaryotic replicative CMG helicase suggests a pumpjack motion for translocation. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 217-224.	3.6	130
12	Structural basis of Mcm2-7 replicative helicase loading by ORC-Cdc6 and Cdt1. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 316-324.	3.6	130
13	Cryo-EM structure of a helicase loading intermediate containing ORC-Cdc6-Cdt1-MCM2-7 bound to DNA. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 944-951.	3.6	122
14	Structure of the Mycobacterium tuberculosis proteasome and mechanism of inhibition by a peptidyl boronate. <i>Molecular Microbiology</i> , 2006, 59, 1417-1428.	1.2	120
15	Characterization of a Mycobacterium tuberculosis proteasomal ATPase homologue. <i>Molecular Microbiology</i> , 2004, 55, 561-571.	1.2	119
16	Depupylation of Prokaryotic Ubiquitin-like Protein from Mycobacterial Proteasome Substrates. <i>Molecular Cell</i> , 2010, 39, 821-827.	4.5	110
17	Binding-induced folding of prokaryotic ubiquitin-like protein on the Mycobacterium proteasomal ATPase targets for degradation. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1352-1357.	3.6	109
18	A unique DNA entry gate serves for regulated loading of the eukaryotic replicative helicase MCM2-7 onto DNA. <i>Genes and Development</i> , 2014, 28, 1653-1666.	2.7	105

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19	Structure of the ER membrane complex, a transmembrane-domain insertase. <i>Nature</i> , 2020, 584, 475-478.	13.7	102
20	<i>Mycobacterium tuberculosis</i> prcBA genes encode a gated proteasome with broad oligopeptide specificity. <i>Molecular Microbiology</i> , 2006, 59, 1405-1416.	1.2	98
21	The atomic structure of a eukaryotic oligosaccharyltransferase complex. <i>Nature</i> , 2018, 555, 328-333.	13.7	97
22	Structural and mechanistic insights into Mcm2-7 double-hexamer assembly and function. <i>Genes and Development</i> , 2014, 28, 2291-2303.	2.7	96
23	Structure of an Ancient Respiratory System. <i>Cell</i> , 2018, 173, 1636-1649.e16.	13.5	92
24	O-Glycosylation modulates the stability of epidermal growth factor-like repeats and thereby regulates Notch trafficking. <i>Journal of Biological Chemistry</i> , 2017, 292, 15964-15973.	1.6	82
25	The ring-shaped hexameric helicases that function at DNA replication forks. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 122-130.	3.6	78
26	Cryo-EM structure of Mcm2-7 double hexamer on DNA suggests a lagging-strand DNA extrusion model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9529-E9538.	3.3	76
27	ATP hydrolysis-coupled peptide translocation mechanism of <i>Mycobacterium tuberculosis</i> ClpB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9560-E9569.	3.3	72
28	The architecture of the DNA replication origin recognition complex in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10326-10331.	3.3	70
29	Quaternary organization of a phytochrome dimer as revealed by cryoelectron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10872-10877.	3.3	69
30	The Outer Membrane Usher Forms a Twin-pore Secretion Complex. <i>Journal of Molecular Biology</i> , 2004, 344, 1397-1407.	2.0	67
31	The Eukaryotic CMG Helicase at the Replication Fork: Emerging Architecture Reveals an Unexpected Mechanism. <i>BioEssays</i> , 2018, 40, 1700208.	1.2	66
32	Structural Insights on the <i>Mycobacterium tuberculosis</i> Proteasomal ATPase Mpa. <i>Structure</i> , 2009, 17, 1377-1385.	1.6	65
33	Cdc6-Induced Conformational Changes in ORC Bound to Origin DNA Revealed by Cryo-Electron Microscopy. <i>Structure</i> , 2012, 20, 534-544.	1.6	60
34	Notch-modifying xylosyltransferase structures support an SNI-like retaining mechanism. <i>Nature Chemical Biology</i> , 2015, 11, 847-854.	3.9	60
35	Fellutamide B is a potent inhibitor of the <i>Mycobacterium tuberculosis</i> proteasome. <i>Archives of Biochemistry and Biophysics</i> , 2010, 501, 214-220.	1.4	57
36	Structure of the polymerase μ holoenzyme and atomic model of the leading strand replisome. <i>Nature Communications</i> , 2020, 11, 3156.	5.8	57

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37	Oligosaccharyltransferase directly binds to ribosome at a location near the translocon-binding site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6945-6949.	3.3	56
38	Autoinhibition and activation mechanisms of the eukaryotic lipid flippase Drs2p-Cdc50p. <i>Nature Communications</i> , 2019, 10, 4142.	5.8	51
39	DNA unwinding mechanism of a eukaryotic replicative CMG helicase. <i>Nature Communications</i> , 2020, 11, 688.	5.8	50
40	Structure of the Oligosaccharyl Transferase Complex at 12 Å.. Resolution. <i>Structure</i> , 2008, 16, 432-440.	1.6	45
41	Crystallographic study of FABP5 as an intracellular endocannabinoid transporter. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 290-298.	2.5	44
42	Structure of the active form of human origin recognition complex and its ATPase motor module. <i>ELife</i> , 2017, 6, .	2.8	44
43	The Origin Recognition Complex: A Biochemical and Structural View. <i>Sub-Cellular Biochemistry</i> , 2012, 62, 37-58.	1.0	42
44	Ctf4 organizes sister replisomes and Pol δ into a replication factory. <i>ELife</i> , 2019, 8, .	2.8	42
45	Structural mechanism of helicase loading onto replication origin DNA by ORC-Cdc6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17747-17756.	3.3	41
46	Structure of eukaryotic DNA polymerase ϵ bound to the PCNA clamp while encircling DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30344-30353.	3.3	41
47	Structure and activation mechanism of the hexameric plasma membrane H ⁺ -ATPase. <i>Nature Communications</i> , 2021, 12, 6439.	5.8	41
48	An adenosine triphosphate-independent proteasome activator contributes to the virulence of <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1763-72.	3.3	40
49	Transport mechanism of P4 ATPase phosphatidylcholine flippases. <i>ELife</i> , 2020, 9, .	2.8	40
50	Photosensing and Thermosensing by Phytochrome B Require Both Proximal and Distal Allosteric Features within the Dimeric Photoreceptor. <i>Scientific Reports</i> , 2017, 7, 13648.	1.6	39
51	Structural basis for the assembly and gate closure mechanisms of the <i>Mycobacterium tuberculosis</i> 20S proteasome. <i>EMBO Journal</i> , 2010, 29, 2037-2047.	3.5	38
52	Structure of the eukaryotic protein O-mannosyltransferase Pmt1~Pmt2 complex. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 704-711.	3.6	38
53	The Eukaryotic Replisome Goes Under the Microscope. <i>Current Biology</i> , 2016, 26, R247-R256.	1.8	32
54	The Antinociceptive Agent SBFI-26 Binds to Anandamide Transporters FABP5 and FABP7 at Two Different Sites. <i>Biochemistry</i> , 2017, 56, 3454-3462.	1.2	31

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55	Fatty-acid-binding protein inhibition produces analgesic effects through peripheral and central mechanisms. <i>Molecular Pain</i> , 2017, 13, 174480691769700.	1.0	31
56	SAR studies on truxillic acid mono esters as a new class of antinociceptive agents targeting fatty acid binding proteins. <i>European Journal of Medicinal Chemistry</i> , 2018, 154, 233-252.	2.6	31
57	Cdc6 ATPase activity disengages Cdc6 from the pre-replicative complex to promote DNA replication. <i>ELife</i> , 2015, 4, .	2.8	30
58	Plant phytochrome B is an asymmetric dimer with unique signalling potential. <i>Nature</i> , 2022, 604, 127-133.	13.7	29
59	The structure of ORC-Cdc6 on an origin DNA reveals the mechanism of ORC activation by the replication initiator Cdc6. <i>Nature Communications</i> , 2021, 12, 3883.	5.8	28
60	The pilus usher controls protein interactions via domain masking and is functional as an oligomer. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 540-546.	3.6	27
61	The Pup-Proteasome System of <i>Mycobacterium tuberculosis</i> . <i>Sub-Cellular Biochemistry</i> , 2013, 66, 267-295.	1.0	26
62	Structure of the respiratory MBS complex reveals iron-sulfur cluster catalyzed sulfane sulfur reduction in ancient life. <i>Nature Communications</i> , 2020, 11, 5953.	5.8	26
63	Structural analysis of the dodecameric proteasome activator PafE in <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1983-92.	3.3	21
64	<i>Mycobacterium tuberculosis</i> Proteasome Accessory Factor A (PafA) Can Transfer Prokaryotic Ubiquitin-Like Protein (Pup) between Substrates. <i>MBio</i> , 2017, 8, .	1.8	21
65	<i>Mycobacterium tuberculosis</i> proteasomal ATPase Mpa has a $\hat{2}$ -grasp domain that hinders docking with the proteasome core protease. <i>Molecular Microbiology</i> , 2017, 105, 227-241.	1.2	21
66	Handover mechanism of the growing pilus by the bacterial outer-membrane usher FimD. <i>Nature</i> , 2018, 562, 444-447.	13.7	21
67	Architecture of the <i>Saccharomyces cerevisiae</i> Replisome. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1042, 207-228.	0.8	20
68	DNA is loaded through the 9-1-1 DNA checkpoint clamp in the opposite direction of the PCNA clamp. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 376-385.	3.6	19
69	Cryo-EM is uncovering the mechanism of eukaryotic protein N-glycosylation. <i>FEBS Journal</i> , 2019, 286, 1638-1644.	2.2	16
70	Evolution of DNA replication origin specification and gene silencing mechanisms. <i>Nature Communications</i> , 2020, 11, 5175.	5.8	16
71	Cryoelectron microscopy structure and mechanism of the membrane-associated electron-bifurcating flavoprotein Fix/EtfABCX. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	16
72	Proteasome substrate capture and gate opening by the accessory factor PafE from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 4713-4723.	1.6	15

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73	Structure and electron transfer pathways of an electron-bifurcating NiFe-hydrogenase. <i>Science Advances</i> , 2022, 8, eabm7546.	4.7	15
74	Structural Basis for the Species-Selective Binding of N,C-Capped Dipeptides to the <i>Mycobacterium tuberculosis</i> Proteasome. <i>Biochemistry</i> , 2017, 56, 324-333.	1.2	14
75	Identification of Fatty Acid Binding Protein 5 Inhibitors Through Similarity-Based Screening. <i>Biochemistry</i> , 2019, 58, 4304-4316.	1.2	14
76	Selective Phenylimidazole-Based Inhibitors of the <i>Mycobacterium tuberculosis</i> Proteasome. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9246-9253.	2.9	14
77	Evolution of complex λ -like respiratory complexes. <i>Journal of Biological Chemistry</i> , 2021, 296, 100740.	1.6	14
78	Structural basis of the P4B ATPase lipid flippase activity. <i>Nature Communications</i> , 2021, 12, 5963.	5.8	14
79	Structural basis for aggregate dissolution and refolding by the <i>Mycobacterium tuberculosis</i> ClpB-DnaK bi-chaperone system. <i>Cell Reports</i> , 2021, 35, 109166.	2.9	13
80	Cryo-EM structures reveal that RFC recognizes both the 3'- and 5'-DNA ends to load PCNA onto gaps for DNA repair. <i>ELife</i> , 0, 11, .	2.8	13
81	The eukaryotic CMG helicase pumpjack and integration into the replisome. <i>Nucleus</i> , 2016, 7, 146-154.	0.6	11
82	Highly specific monoclonal antibodies for allosteric inhibition and immunodetection of the human pancreatic zinc transporter ZnT8. <i>Journal of Biological Chemistry</i> , 2018, 293, 16206-16216.	1.6	11
83	Novel autoantibodies to the β -cell surface epitopes of ZnT8 in patients progressing to type-1 diabetes. <i>Journal of Autoimmunity</i> , 2021, 122, 102677.	3.0	11
84	Processive dynamics of the usher assembly platform during uropathogenic <i>Escherichia coli</i> P pilus biogenesis. <i>Nature Communications</i> , 2021, 12, 5207.	5.8	11
85	Molecular mechanisms of eukaryotic origin initiation, replication fork progression, and chromatin maintenance. <i>Biochemical Journal</i> , 2020, 477, 3499-3525.	1.7	11
86	Cryo-EM structures of the endoplasmic reticulum membrane complex. <i>FEBS Journal</i> , 2021, , .	2.2	9
87	Macrocyclic Peptides that Selectively Inhibit the <i>Mycobacterium tuberculosis</i> Proteasome. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 6262-6272.	2.9	9
88	An Abundant and Diverse New Family of Electron Bifurcating Enzymes With a Non-canonical Catalytic Mechanism. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
89	Water skating: How polymerase sliding clamps move on DNA. <i>FEBS Journal</i> , 2021, 288, 7256-7262.	2.2	8
90	Anatomy of a twin DNA replication factory. <i>Biochemical Society Transactions</i> , 2020, 48, 2769-2778.	1.6	8

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91	Recent Progress in Structural Studies on the GT-C Superfamily of Protein Glycosyltransferases. <i>Sub-Cellular Biochemistry</i> , 2021, 96, 259-271.	1.0	7
92	<i>Pseudomonas aeruginosa</i> C-Terminal Processing Protease CtpA Assembles into a Hexameric Structure That Requires Activation by a Spiral-Shaped Lipoprotein-Binding Partner. <i>MBio</i> , 2022, 13, e0368021.	1.8	7
93	Structure of the human GlcNAc-1-phosphotransferase $\hat{1}\pm\hat{2}$ subunits reveals regulatory mechanism for lysosomal enzyme glycan phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 348-356.	3.6	6
94	Protein N-glycosylation and O-mannosylation are catalyzed by two evolutionarily related GT-C glycosyltransferases. <i>Current Opinion in Structural Biology</i> , 2021, 68, 66-73.	2.6	5
95	Biology and Biochemistry of Bacterial Proteasomes. <i>Sub-Cellular Biochemistry</i> , 2019, 93, 339-358.	1.0	5
96	Characterization of Guided Entry of Tail-Anchored Proteins 3 Homologues in <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	4
97	The mycobacterial proteasomal ATPase Mpa forms a gapped ring to engage the 20S proteasome. <i>Journal of Biological Chemistry</i> , 2021, 296, 100713.	1.6	4
98	Structural Analysis of <i>Mycobacterium tuberculosis</i> Homologues of the Eukaryotic Proteasome Assembly Chaperone 2 (PAC2). <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	3
99	Cryo-EM of dynamic protein complexes in eukaryotic DNA replication. <i>Protein Science</i> , 2017, 26, 40-51.	3.1	3
100	DNA replication from two different worlds. <i>Science</i> , 2019, 363, 814-815.	6.0	2
101	A transmission electron microscopy study of ferroelectric domains in a modified lead zirconate titanate ceramic. <i>Journal of Physics Condensed Matter</i> , 1993, 5, 5037-5044.	0.7	0
102	Cryo-EM Studies of Respiratory Complexes in a Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> Suggest an Evolutionary Path to Modern-Day Complex I. <i>Microscopy and Microanalysis</i> , 2019, 25, 1354-1355.	0.2	0
103	Mathematical description of eukaryotic chromosome replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4776-4778.	3.3	0