

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
g-index

118
all docs

118
docs citations

118
times ranked

5476
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Pseudomonas aeruginosa C-Terminal Processing Protease CtpA Assembles into a Hexameric Structure That Requires Activation by a Spiral-Shaped Lipoprotein-Binding Partner. MBio, 2022, 13, e0368021. | 1.8 | 7 |
| 2 | Structure and electron transfer pathways of an electron-bifurcating NiFe-hydrogenase. Science Advances, 2022, 8, eabm7546. | 4.7 | 15 |
| 3 | Structure of the human GlcNAc-1-phosphotransferase $\hat{1}\pm\hat{1}^2$ subunits reveals regulatory mechanism for lysosomal enzyme glycan phosphorylation. Nature Structural and Molecular Biology, 2022, 29, 348-356. | 3.6 | 6 |
| 4 | DNA is loaded through the 9-1-1 DNA checkpoint clamp in the opposite direction of the PCNA clamp. Nature Structural and Molecular Biology, 2022, 29, 376-385. | 3.6 | 19 |
| 5 | Plant phytochrome B is an asymmetric dimer with unique signalling potential. Nature, 2022, 604, 127-133. | 13.7 | 29 |
| 6 | Evolution of complex $\hat{1}\hat{1}$ -like respiratory complexes. Journal of Biological Chemistry, 2021, 296, 100740. | 1.6 | 14 |
| 7 | The mycobacterial proteasomal ATPase Mpa forms a gapped ring to engage the 20S proteasome. Journal of Biological Chemistry, 2021, 296, 100713. | 1.6 | 4 |
| 8 | Water skating: How polymerase sliding clamps move on DNA. FEBS Journal, 2021, 288, 7256-7262. | 2.2 | 8 |
| 9 | Cryo-EM structures of the endoplasmic reticulum membrane complex. FEBS Journal, 2021, , . | 2.2 | 9 |
| 10 | Structural basis for aggregate dissolution and refolding by the Mycobacterium tuberculosis ClpB-DnaK bi-chaperone system. Cell Reports, 2021, 35, 109166. | 2.9 | 13 |
| 11 | Macrocyclic Peptides that Selectively Inhibit the <i>Mycobacterium tuberculosis</i> Proteasome. Journal of Medicinal Chemistry, 2021, 64, 6262-6272. | 2.9 | 9 |
| 12 | Protein N-glycosylation and O-mannosylation are catalyzed by two evolutionarily related GT-C glycosyltransferases. Current Opinion in Structural Biology, 2021, 68, 66-73. | 2.6 | 5 |
| 13 | The structure of ORC-Cdc6 on an origin DNA reveals the mechanism of ORC activation by the replication initiator Cdc6. Nature Communications, 2021, 12, 3883. | 5.8 | 28 |
| 14 | Novel autoantibodies to the $\hat{1}^2$ -cell surface epitopes of ZnT8 in patients progressing to type-1 diabetes. Journal of Autoimmunity, 2021, 122, 102677. | 3.0 | 11 |
| 15 | Processive dynamics of the usher assembly platform during uropathogenic Escherichia coli P pilus biogenesis. Nature Communications, 2021, 12, 5207. | 5.8 | 11 |
| 16 | Recent Progress in Structural Studies on the GT-C Superfamily of Protein Glycosyltransferases. Sub-Cellular Biochemistry, 2021, 96, 259-271. | 1.0 | 7 |
| 17 | Cryoelectron microscopy structure and mechanism of the membrane-associated electron-bifurcating flavoprotein Fix/EtfABCX. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 16 |
| 18 | Structural basis of the P4B ATPase lipid flippase activity. Nature Communications, 2021, 12, 5963. | 5.8 | 14 |

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|----|--|------|-----------|
| 19 | Structure and activation mechanism of the hexameric plasma membrane H ⁺ -ATPase. <i>Nature Communications</i> , 2021, 12, 6439. | 5.8 | 41 |
| 20 | Evolution of DNA replication origin specification and gene silencing mechanisms. <i>Nature Communications</i> , 2020, 11, 5175. | 5.8 | 16 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | Structure of the ER membrane complex, a transmembrane-domain insertase. <i>Nature</i> , 2020, 584, 475-478. | 13.7 | 102 |
| 25 | Structure of the polymerase δ holoenzyme and atomic model of the leading strand replisome. <i>Nature Communications</i> , 2020, 11, 3156. | 5.8 | 57 |
| 26 | Ordered three-dimensional nanomaterials using DNA-prescribed and valence-controlled material voxels. <i>Nature Materials</i> , 2020, 19, 789-796. | 13.3 | 172 |
| 27 | DNA unwinding mechanism of a eukaryotic replicative CMG helicase. <i>Nature Communications</i> , 2020, 11, 688. | 5.8 | 50 |
| 28 | Molecular mechanisms of eukaryotic origin initiation, replication fork progression, and chromatin maintenance. <i>Biochemical Journal</i> , 2020, 477, 3499-3525. | 1.7 | 11 |
| 29 | Anatomy of a twin DNA replication factory. <i>Biochemical Society Transactions</i> , 2020, 48, 2769-2778. | 1.6 | 8 |
| 30 | Transport mechanism of P4 ATPase phosphatidylcholine flippases. <i>ELife</i> , 2020, 9, . | 2.8 | 40 |
| 31 | Structure of the eukaryotic protein O-mannosyltransferase Pmt1 $\hat{\sim}$ Pmt2 complex. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 704-711. | 3.6 | 38 |
| 32 | 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 |
| 33 | Identification of Fatty Acid Binding Protein 5 Inhibitors Through Similarity-Based Screening. <i>Biochemistry</i> , 2019, 58, 4304-4316. | 1.2 | 14 |
| 34 | Autoinhibition and activation mechanisms of the eukaryotic lipid flippase Drs2p-Cdc50p. <i>Nature Communications</i> , 2019, 10, 4142. | 5.8 | 51 |
| 35 | Selective Phenylimidazole-Based Inhibitors of the <i>Mycobacterium tuberculosis</i> Proteasome. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9246-9253. | 2.9 | 14 |
| 36 | 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 |

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|----|---|------|-----------|
| 37 | Mathematical description of eukaryotic chromosome replication. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4776-4778. | 3.3 | 0 |
| 38 | DNA replication from two different worlds. Science, 2019, 363, 814-815. | 6.0 | 2 |
| 39 | Cryo-EM is uncovering the mechanism of eukaryotic protein N-glycosylation. FEBS Journal, 2019, 286, 1638-1644. | 2.2 | 16 |
| 40 | Biology and Biochemistry of Bacterial Proteasomes. Sub-Cellular Biochemistry, 2019, 93, 339-358. | 1.0 | 5 |
| 41 | Ctf4 organizes sister replisomes and Pol δ into a replication factory. ELife, 2019, 8, . | 2.8 | 42 |
| 42 | Proteasome substrate capture and gate opening by the accessory factor PafE from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2018, 293, 4713-4723. | 1.6 | 15 |
| 43 | The ring-shaped hexameric helicases that function at DNA replication forks. Nature Structural and Molecular Biology, 2018, 25, 122-130. | 3.6 | 78 |
| 44 | The Eukaryotic CMG Helicase at the Replication Fork: Emerging Architecture Reveals an Unexpected Mechanism. BioEssays, 2018, 40, 1700208. | 1.2 | 66 |
| 45 | The atomic structure of a eukaryotic oligosaccharyltransferase complex. Nature, 2018, 555, 328-333. | 13.7 | 97 |
| 46 | ATP hydrolysis-coupled peptide translocation mechanism of <i>Mycobacterium tuberculosis</i> ClpB. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9560-E9569. | 3.3 | 72 |
| 47 | Handover mechanism of the growing pilus by the bacterial outer-membrane usher FimD. Nature, 2018, 562, 444-447. | 13.7 | 21 |
| 48 | Highly specific monoclonal antibodies for allosteric inhibition and immunodetection of the human pancreatic zinc transporter ZnT8. Journal of Biological Chemistry, 2018, 293, 16206-16216. | 1.6 | 11 |
| 49 | SAR studies on truxillic acid mono esters as a new class of antinociceptive agents targeting fatty acid binding proteins. European Journal of Medicinal Chemistry, 2018, 154, 233-252. | 2.6 | 31 |
| 50 | Structure of an Ancient Respiratory System. Cell, 2018, 173, 1636-1649.e16. | 13.5 | 92 |
| 51 | Structure of eukaryotic CMG helicase at a replication fork and implications to replisome architecture and origin initiation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E697-E706. | 3.3 | 176 |
| 52 | <i>Mycobacterium tuberculosis</i> Proteasome Accessory Factor A (PafA) Can Transfer Prokaryotic Ubiquitin-Like Protein (Pup) between Substrates. MBio, 2017, 8, . | 1.8 | 21 |
| 53 | Structural basis of Mcm2-7 replicative helicase loading by ORC-Cdc6 and Cdt1. Nature Structural and Molecular Biology, 2017, 24, 316-324. | 3.6 | 130 |
| 54 | Structural Analysis of Mycobacterium tuberculosis Homologues of the Eukaryotic Proteasome Assembly Chaperone 2 (PAC2). Journal of Bacteriology, 2017, 199, . | 1.0 | 3 |

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|----|--|------|-----------|
| 55 | <i>Mycobacterium tuberculosis</i> proteasomal ATPase Mpa has a Î²-grasp domain that hinders docking with the proteasome core protease. <i>Molecular Microbiology</i> , 2017, 105, 227-241. | 1.2 | 21 |
| 56 | 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 |
| 57 | Fatty-acid-binding protein inhibition produces analgesic effects through peripheral and central mechanisms. <i>Molecular Pain</i> , 2017, 13, 174480691769700. | 1.0 | 31 |
| 58 | 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 |
| 59 | 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 |
| 60 | 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 |
| 61 | 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 |
| 62 | Cryo-EM of dynamic protein complexes in eukaryotic DNA replication. <i>Protein Science</i> , 2017, 26, 40-51. | 3.1 | 3 |
| 63 | Architecture of the <i>Saccharomyces cerevisiae</i> Replisome. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1042, 207-228. | 0.8 | 20 |
| 64 | Structure of the active form of human origin recognition complex and its ATPase motor module. <i>ELife</i> , 2017, 6, . | 2.8 | 44 |
| 65 | The Eukaryotic Replisome Goes Under the Microscope. <i>Current Biology</i> , 2016, 26, R247-R256. | 1.8 | 32 |
| 66 | 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 |
| 67 | The eukaryotic CMG helicase pumpjack and integration into the replisome. <i>Nucleus</i> , 2016, 7, 146-154. | 0.6 | 11 |
| 68 | Lattice engineering through nanoparticle-DNA frameworks. <i>Nature Materials</i> , 2016, 15, 654-661. | 13.3 | 198 |
| 69 | 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 |
| 70 | Diamond family of nanoparticle superlattices. <i>Science</i> , 2016, 351, 582-586. | 6.0 | 331 |
| 71 | 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 |
| 72 | 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 |

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|----|--|------|-----------|
| 73 | Notch-modifying xylosyltransferase structures support an SNI-like retaining mechanism. <i>Nature Chemical Biology</i> , 2015, 11, 847-854. | 3.9 | 60 |
| 74 | The architecture of a eukaryotic replisome. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 976-982. | 3.6 | 161 |
| 75 | Cdc6 ATPase activity disengages Cdc6 from the pre-replicative complex to promote DNA replication. <i>ELife</i> , 2015, 4, . | 2.8 | 30 |
| 76 | Crystallographic study of FABP5 as an intracellular endocannabinoid transporter. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 290-298. | 2.5 | 44 |
| 77 | 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 |
| 78 | Structural and mechanistic insights into Mcm2-7 double-hexamer assembly and function. <i>Genes and Development</i> , 2014, 28, 2291-2303. | 2.7 | 96 |
| 79 | 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 |
| 80 | The Pup-Proteasome System of <i>Mycobacterium tuberculosis</i> . <i>Sub-Cellular Biochemistry</i> , 2013, 66, 267-295. | 1.0 | 26 |
| 81 | The Origin Recognition Complex: A Biochemical and Structural View. <i>Sub-Cellular Biochemistry</i> , 2012, 62, 37-58. | 1.0 | 42 |
| 82 | 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 |
| 83 | Crystal structure of the FimD usher bound to its cognate FimC-FimH substrate. <i>Nature</i> , 2011, 474, 49-53. | 13.7 | 170 |
| 84 | Binding-induced folding of prokaryotic ubiquitin-like protein on the <i>Mycobacterium</i> proteasomal ATPase targets substrates for degradation. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1352-1357. | 3.6 | 109 |
| 85 | 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 |
| 86 | 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 |
| 87 | Depupylation of Prokaryotic Ubiquitin-like Protein from <i>Mycobacterial</i> Proteasome Substrates. <i>Molecular Cell</i> , 2010, 39, 821-827. | 4.5 | 110 |
| 88 | 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 |
| 89 | 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 |
| 90 | 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 |

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| 91 | Structural Insights on the Mycobacterium tuberculosis Proteasomal ATPase Mpa. Structure, 2009, 17, 1377-1385. | 1.6 | 65 |
| 92 | Inhibitors selective for mycobacterial versus human proteasomes. Nature, 2009, 461, 621-626. | 13.7 | 213 |
| 93 | Structure of the Oligosaccharyl Transferase Complex at 12 Å.. Resolution. Structure, 2008, 16, 432-440. | 1.6 | 45 |
| 94 | Fiber Formation across the Bacterial Outer Membrane by the Chaperone/Usher Pathway. Cell, 2008, 133, 640-652. | 13.5 | 194 |
| 95 | The architecture of the DNA replication origin recognition complex in <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10326-10331. | 3.3 | 70 |
| 96 | Mycobacterium tuberculosis prcBA genes encode a gated proteasome with broad oligopeptide specificity. Molecular Microbiology, 2006, 59, 1405-1416. | 1.2 | 98 |
| 97 | Structure of the Mycobacterium tuberculosis proteasome and mechanism of inhibition by a peptidyl boronate. Molecular Microbiology, 2006, 59, 1417-1428. | 1.2 | 120 |
| 98 | ATPase-dependent cooperative binding of ORC and Cdc6 to origin DNA. Nature Structural and Molecular Biology, 2005, 12, 965-971. | 3.6 | 198 |
| 99 | Characterization of a Mycobacterium tuberculosis proteasomal ATPase homologue. Molecular Microbiology, 2004, 55, 561-571. | 1.2 | 119 |
| 100 | The Outer Membrane Usher Forms a Twin-pore Secretion Complex. Journal of Molecular Biology, 2004, 344, 1397-1407. | 2.0 | 67 |
| 101 | A transmission electron microscopy study of ferroelectric domains in a modified lead zirconate titanate ceramic. Journal of Physics Condensed Matter, 1993, 5, 5037-5044. | 0.7 | 0 |
| 102 | An Abundant and Diverse New Family of Electron Bifurcating Enzymes With a Non-canonical Catalytic Mechanism. Frontiers in Microbiology, 0, 13, . | 1.5 | 9 |
| 103 | Cryo-EM structures reveal that RFC recognizes both the 3' and 5' DNA ends to load PCNA onto gaps for DNA repair. ELife, 0, 11, . | 2.8 | 13 |