Jianlin Lei

List of Publications by Year
in descending order

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66	7,673	66234 42	102304 66
papers	citations	h-index	g-index

71	71	71	10055
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Cryo-EM structure of the nuclear ring from Xenopus laevis nuclear pore complex. Cell Research, 2022, 32, 349-358.	5.7	19
2	Cryo-EM structure of the inner ring from the Xenopus laevis nuclear pore complex. Cell Research, 2022, 32, 451-460.	5.7	15
3	Structure of the cytoplasmic ring of the <i>Xenopus laevis</i> nuclear pore complex. Science, 2022, 376, .	6.0	44
4	Mechanism of spliceosome remodeling by the ATPase/helicase Prp2 and its coactivator Spp2. Science, 2021, 371, .	6.0	35
5	Structural basis of human monocarboxylate transporter 1 inhibition by anti-cancer drug candidates. Cell, 2021, 184, 370-383.e13.	13.5	143
6	Structure of human Na _v 1.5 reveals the fast inactivation-related segments as a mutational hotspot for the long QT syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	44
7	Structure of the activated human minor spliceosome. Science, 2021, 371, .	6.0	43
8	Comparative structural analysis of human Na _v 1.1 and Na _v 1.5 reveals mutational hotspots for sodium channelopathies. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	56
9	A structure of human Scap bound to Insig-2 suggests how their interaction is regulated by sterols. Science, 2021, 371, .	6.0	44
10	Structural Basis for Pore Blockade of the Human Cardiac Sodium Channel Na_v1.5 by the Antiarrhythmic Drug Quinidine**. Angewandte Chemie, 2021, 133, 11575-11581.	1.6	6
11	Structural Basis for Pore Blockade of the Human Cardiac Sodium Channel Na_v1.5 by the Antiarrhythmic Drug Quinidine**. Angewandte Chemie - International Edition, 2021, 60, 11474-11480.	7.2	63
12	Structural basis of Î³-secretase inhibition and modulation by small molecule drugs. Cell, 2021, 184, 521-533.e14.	13.5	100
13	Structural insight into the substrate recognition and transport mechanism of the human LAT2â€“4F2hc complex. Cell Discovery, 2020, 6, 82.	3.1	13
14	Molecular Architecture of the SARS-CoV-2 Virus. Cell, 2020, 183, 730-738.e13.	13.5	793
15	Structural insights into the gating mechanism of human SLC26A9 mediated by its C-terminal sequence. Cell Discovery, 2020, 6, 55.	3.1	43
16	Molecular architecture of the luminal ring of the Xenopus laevis nuclear pore complex. Cell Research, 2020, 30, 532-540.	5.7	51
17	Structure of the cytoplasmic ring of the Xenopus laevis nuclear pore complex by cryo-electron microscopy single particle analysis. Cell Research, 2020, 30, 520-531.	5.7	51
18	Cryo-EM structure of the human heteromeric amino acid transporter b ^{0,+} AT-rBAT. Science Advances, 2020, 6, eaay6379.	4.7	27

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19	Modulation of cardiac ryanodine receptor 2 by calmodulin. Nature, 2019, 572, 347-351.	13.7	110
20	Structure and mechanogating of the mammalian tactile channel PIEZO2. Nature, 2019, 573, 225-229.	13.7	218
21	Structure of the African swine fever virus major capsid protein p72. Cell Research, 2019, 29, 953-955.	5.7	70
22	Molecular Basis for Ligand Modulation of a Mammalian Voltage-Gated Ca2+ Channel. Cell, 2019, 177, 1495-1506.e12.	13.5	172
23	Single particle cryo-EM reconstruction of 52â€‰kDa streptavidin at 3.2 Angstrom resolution. Nature Communications, 2019, 10, 2386.	5.8	106
24	Architecture of Saccharomyces cerevisiae SAGA complex. Cell Discovery, 2019, 5, 25.	3.1	21
25	Structures of the Catalytically Activated Yeast Spliceosome Reveal the Mechanism of Branching. Cell, 2019, 177, 339-351.e13.	13.5	64
26	Structure of the human LAT1â€“4F2hc heteromeric amino acid transporter complex. Nature, 2019, 568, 127-130.	13.7	217
27	Structures of the human spliceosomes before and after release of the ligated exon. Cell Research, 2019, 29, 274-285.	5.7	74
28	Structures of human Na _v 1.7 channel in complex with auxiliary subunits and animal toxins. Science, 2019, 363, 1303-1308.	6.0	318
29	Molecular basis for pore blockade of human Na ⁺ channel Na _v 1.2 by the Î¼-conotoxin KIIIA. Science, 2019, 363, 1309-1313.	6.0	197
30	Molecular basis for allosteric regulation of the type 2 ryanodine receptor channel gating by key modulators. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25575-25582.	3.3	39
31	Cryo-EM structures of apo and antagonist-bound human Cav3.1. Nature, 2019, 576, 492-497.	13.7	116
32	Structural basis of Notch recognition by human Î³-secretase. Nature, 2019, 565, 192-197.	13.7	194
33	Recognition of the amyloid precursor protein by human Î³-secretase. Science, 2019, 363, .	6.0	229
34	Cryo-EM structure of the polycystic kidney disease-like channel PKD2L1. Nature Communications, 2018, 9, 1192.	5.8	45
35	Structure of the human activated spliceosome in three conformational states. Cell Research, 2018, 28, 307-322.	5.7	163
36	Chaperonin-GroEL as a Smart Hydrophobic Drug Delivery and Tumor Targeting Molecular Machine for Tumor Therapy. Nano Letters, 2018, 18, 921-928.	4.5	44

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37	Structure of a human catalytic step I spliceosome. Science, 2018, 359, 537-545.	6.0	118
38	Structures of the human pre-catalytic spliceosome and its precursor spliceosome. Cell Research, 2018, 28, 1129-1140.	5.7	85
39	Structure of the human plasma membrane Ca2+-ATPase 1 in complex with its obligatory subunit neuroplastin. Nature Communications, 2018, 9, 3623.	5.8	71
40	Structure of the human voltage-gated sodium channel Na _v 1.4 in complex with Î²1. Science, 2018, 362, .	6.0	333
41	The application of CorrSightâ„¢ in correlative light and electron microscopy of vitrified biological specimens. Biophysics Reports, 2018, 4, 143-152.	0.2	2
42	Structures of the fully assembled <i>Saccharomyces cerevisiae</i> spliceosome before activation. Science, 2018, 360, 1423-1429.	6.0	77
43	Structural basis for the recognition of Sonic Hedgehog by human Patched1. Science, 2018, 361, .	6.0	168
44	Structural basis for the modulation of voltage-gated sodium channels by animal toxins. Science, 2018, 362, .	6.0	200
45	Structure of the human PKD1-PKD2 complex. Science, 2018, 361, .	6.0	173
46	Structural snapshot of cytoplasmic pre-60S ribosomal particles bound by Nmd3, Lsg1, Tif6 and Reh1. Nature Structural and Molecular Biology, 2017, 24, 214-220.	3.6	94
47	An Atomic Structure of the Human Spliceosome. Cell, 2017, 169, 918-929.e14.	13.5	215
48	Structure of the Human Lipid Exporter ABCA1. Cell, 2017, 169, 1228-1239.e10.	13.5	214
49	Near-Atomic Resolution Structure Determination in Over-Focus with Volta Phase Plate by Cs-Corrected Cryo-EM. Structure, 2017, 25, 1623-1630.e3.	1.6	34
50	Structure of an Intron Lariat Spliceosome from Saccharomyces cerevisiae. Cell, 2017, 171, 120-132.e12.	13.5	77
51	Structure of the Nav1.4-Î²1 Complex from Electric Eel. Cell, 2017, 170, 470-482.e11.	13.5	272
52	Structure of the Post-catalytic Spliceosome from Saccharomyces cerevisiae. Cell, 2017, 171, 1589-1598.e8.	13.5	76
53	Biological cryoâ€electron microscopy in China. Protein Science, 2017, 26, 16-31.	3.1	3
54	Diverse roles of assembly factors revealed by structures of late nuclear pre-60S ribosomes. Nature, 2016, 534, 133-137.	13.7	193

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55	The architecture of the mammalian respirasome. Nature, 2016, 537, 639-643.	13.7	311
56	Structural dynamics of the yeast Shwachman-Diamond syndrome protein (Sdo1) on the ribosome and its implication in the 60S subunit maturation. Protein and Cell, 2016, 7, 187-200.	4.8	8
57	Structure of the eukaryotic MCM complex at 3.8 Ã…. Nature, 2015, 524, 186-191.	13.7	207
58	HflX is a ribosome-splitting factor rescuing stalled ribosomes under stress conditions. Nature Structural and Molecular Biology, 2015, 22, 906-913.	3.6	88
59	Structural insights into the function of a unique tandem GTPase EngA in bacterial ribosome assembly. Nucleic Acids Research, 2014, 42, 13430-13439.	6.5	38
60	Structural and Functional Insights into the Mode of Action of a Universally Conserved Obg GTPase. PLoS Biology, 2014, 12, e1001866.	2.6	108
61	Structural basis for interaction of a cotranslational chaperone with the eukaryotic ribosome. Nature Structural and Molecular Biology, 2014, 21, 1042-1046.	3.6	61
62	Structural insights into the assembly of the 30S ribosomal subunit in vivo: functional role of S5 and location of the 17S rRNA precursor sequence. Protein and Cell, 2014, 5, 394-407.	4.8	26
63	Dissecting the in vivo assembly of the 30S ribosomal subunit reveals the role of RimM and general features of the assembly process. Nucleic Acids Research, 2013, 41, 2609-2620.	6.5	72
64	Cryo-EM structures of the late-stage assembly intermediates of the bacterial 50S ribosomal subunit. Nucleic Acids Research, 2013, 41, 7073-7083.	6.5	56
65	Structural basis for the function of a small GTPase RsgA on the 30S ribosomal subunit maturation revealed by cryoelectron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13100-13105.	3.3	57
66	Automated acquisition of cryo-electron micrographs for single particle reconstruction on an FEI Tecnai electron microscope. Journal of Structural Biology, 2005, 150, 69-80.	1.3	230