

# Jianlin Lei

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6885890/publications.pdf>

Version: 2024-02-01

66  
papers

7,673  
citations

66234

42  
h-index

102304

66  
g-index

71  
all docs

71  
docs citations

71  
times ranked

10055  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Architecture of the SARS-CoV-2 Virus. <i>Cell</i> , 2020, 183, 730-738.e13.	13.5	793
2	Structure of the human voltage-gated sodium channel Na <sup>v</sup> 1.4 in complex with Î²1. <i>Science</i> , 2018, 362, .	6.0	333
3	Structures of human Na <sup>v</sup> 1.7 channel in complex with auxiliary subunits and animal toxins. <i>Science</i> , 2019, 363, 1303-1308.	6.0	318
4	The architecture of the mammalian respirasome. <i>Nature</i> , 2016, 537, 639-643.	13.7	311
5	Structure of the Nav1.4-Î²1 Complex from Electric Eel. <i>Cell</i> , 2017, 170, 470-482.e11.	13.5	272
6	Automated acquisition of cryo-electron micrographs for single particle reconstruction on an FEI Tecnai electron microscope. <i>Journal of Structural Biology</i> , 2005, 150, 69-80.	1.3	230
7	Recognition of the amyloid precursor protein by human Î³-secretase. <i>Science</i> , 2019, 363, .	6.0	229
8	Structure and mechanogating of the mammalian tactile channel PIEZO2. <i>Nature</i> , 2019, 573, 225-229.	13.7	218
9	Structure of the human LAT1-4F2hc heteromeric amino acid transporter complex. <i>Nature</i> , 2019, 568, 127-130.	13.7	217
10	An Atomic Structure of the Human Spliceosome. <i>Cell</i> , 2017, 169, 918-929.e14.	13.5	215
11	Structure of the Human Lipid Exporter ABCA1. <i>Cell</i> , 2017, 169, 1228-1239.e10.	13.5	214
12	Structure of the eukaryotic MCM complex at 3.8 Å... <i>Nature</i> , 2015, 524, 186-191.	13.7	207
13	Structural basis for the modulation of voltage-gated sodium channels by animal toxins. <i>Science</i> , 2018, 362, .	6.0	200
14	Molecular basis for pore blockade of human Na <sup>v</sup> channel Na <sup>v</sup> 1.2 by the Î¼-conotoxin KIIIA. <i>Science</i> , 2019, 363, 1309-1313.	6.0	197
15	Structural basis of Notch recognition by human Î³-secretase. <i>Nature</i> , 2019, 565, 192-197.	13.7	194
16	Diverse roles of assembly factors revealed by structures of late nuclear pre-60S ribosomes. <i>Nature</i> , 2016, 534, 133-137.	13.7	193
17	Structure of the human PKD1-PKD2 complex. <i>Science</i> , 2018, 361, .	6.0	173
18	Molecular Basis for Ligand Modulation of a Mammalian Voltage-Gated Ca <sup>2+</sup> Channel. <i>Cell</i> , 2019, 177, 1495-1506.e12.	13.5	172

#	ARTICLE	IF	CITATIONS
19	Structural basis for the recognition of Sonic Hedgehog by human Patched1. <i>Science</i> , 2018, 361, .	6.0	168
20	Structure of the human activated spliceosome in three conformational states. <i>Cell Research</i> , 2018, 28, 307-322.	5.7	163
21	Structural basis of human monocarboxylate transporter 1 inhibition by anti-cancer drug candidates. <i>Cell</i> , 2021, 184, 370-383.e13.	13.5	143
22	Structure of a human catalytic step I spliceosome. <i>Science</i> , 2018, 359, 537-545.	6.0	118
23	Cryo-EM structures of apo and antagonist-bound human Cav3.1. <i>Nature</i> , 2019, 576, 492-497.	13.7	116
24	Modulation of cardiac ryanodine receptor 2 by calmodulin. <i>Nature</i> , 2019, 572, 347-351.	13.7	110
25	Structural and Functional Insights into the Mode of Action of a Universally Conserved Obg GTPase. <i>PLoS Biology</i> , 2014, 12, e1001866.	2.6	108
26	Single particle cryo-EM reconstruction of 52 kDa streptavidin at 3.2 Angstrom resolution. <i>Nature Communications</i> , 2019, 10, 2386.	5.8	106
27	Structural basis of $\hat{3}$ -secretase inhibition and modulation by small molecule drugs. <i>Cell</i> , 2021, 184, 521-533.e14.	13.5	100
28	Structural snapshot of cytoplasmic pre-60S ribosomal particles bound by Nmd3, Lsg1, Tif6 and Reh1. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 214-220.	3.6	94
29	HflX is a ribosome-splitting factor rescuing stalled ribosomes under stress conditions. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 906-913.	3.6	88
30	Structures of the human pre-catalytic spliceosome and its precursor spliceosome. <i>Cell Research</i> , 2018, 28, 1129-1140.	5.7	85
31	Structure of an Intron Lariat Spliceosome from <i>Saccharomyces cerevisiae</i> . <i>Cell</i> , 2017, 171, 120-132.e12.	13.5	77
32	Structures of the fully assembled <i>Saccharomyces cerevisiae</i> spliceosome before activation. <i>Science</i> , 2018, 360, 1423-1429.	6.0	77
33	Structure of the Post-catalytic Spliceosome from <i>Saccharomyces cerevisiae</i> . <i>Cell</i> , 2017, 171, 1589-1598.e8.	13.5	76
34	Structures of the human spliceosomes before and after release of the ligated exon. <i>Cell Research</i> , 2019, 29, 274-285.	5.7	74
35	Dissecting the in vivo assembly of the 30S ribosomal subunit reveals the role of RimM and general features of the assembly process. <i>Nucleic Acids Research</i> , 2013, 41, 2609-2620.	6.5	72
36	Structure of the human plasma membrane Ca <sup>2+</sup> -ATPase 1 in complex with its obligatory subunit neuroplastin. <i>Nature Communications</i> , 2018, 9, 3623.	5.8	71

#	ARTICLE	IF	CITATIONS
37	Structure of the African swine fever virus major capsid protein p72. <i>Cell Research</i> , 2019, 29, 953-955.	5.7	70
38	Structures of the Catalytically Activated Yeast Spliceosome Reveal the Mechanism of Branching. <i>Cell</i> , 2019, 177, 339-351.e13.	13.5	64
39	Structural Basis for Pore Blockade of the Human Cardiac Sodium Channel Na <sup>v</sup> 1.5 by the Antiarrhythmic Drug Quinidine**. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 11474-11480.	7.2	63
40	Structural basis for interaction of a cotranslational chaperone with the eukaryotic ribosome. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1042-1046.	3.6	61
41	Structural basis for the function of a small GTPase RsgA on the 30S ribosomal subunit maturation revealed by cryoelectron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13100-13105.	3.3	57
42	Cryo-EM structures of the late-stage assembly intermediates of the bacterial 50S ribosomal subunit. <i>Nucleic Acids Research</i> , 2013, 41, 7073-7083.	6.5	56
43	Comparative structural analysis of human Na <sup>v</sup> 1.1 and Na <sup>v</sup> 1.5 reveals mutational hotspots for sodium channelopathies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	56
44	Molecular architecture of the luminal ring of the <i>Xenopus laevis</i> nuclear pore complex. <i>Cell Research</i> , 2020, 30, 532-540.	5.7	51
45	Structure of the cytoplasmic ring of the <i>Xenopus laevis</i> nuclear pore complex by cryo-electron microscopy single particle analysis. <i>Cell Research</i> , 2020, 30, 520-531.	5.7	51
46	Cryo-EM structure of the polycystic kidney disease-like channel PKD2L1. <i>Nature Communications</i> , 2018, 9, 1192.	5.8	45
47	Chaperonin-GroEL as a Smart Hydrophobic Drug Delivery and Tumor Targeting Molecular Machine for Tumor Therapy. <i>Nano Letters</i> , 2018, 18, 921-928.	4.5	44
48	Structure of human Na <sup>v</sup> 1.5 reveals the fast inactivation-related segments as a mutational hotspot for the long QT syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	44
49	A structure of human Scap bound to Insig-2 suggests how their interaction is regulated by sterols. <i>Science</i> , 2021, 371, .	6.0	44
50	Structure of the cytoplasmic ring of the <i>Xenopus laevis</i> nuclear pore complex. <i>Science</i> , 2022, 376, .	6.0	44
51	Structural insights into the gating mechanism of human SLC26A9 mediated by its C-terminal sequence. <i>Cell Discovery</i> , 2020, 6, 55.	3.1	43
52	Structure of the activated human minor spliceosome. <i>Science</i> , 2021, 371, .	6.0	43
53	Molecular basis for allosteric regulation of the type 2 ryanodine receptor channel gating by key modulators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25575-25582.	3.3	39
54	Structural insights into the function of a unique tandem GTPase EngA in bacterial ribosome assembly. <i>Nucleic Acids Research</i> , 2014, 42, 13430-13439.	6.5	38

#	ARTICLE	IF	CITATIONS
55	Mechanism of spliceosome remodeling by the ATPase/helicase Prp2 and its coactivator Spp2. <i>Science</i> , 2021, 371, .	6.0	35
56	Near-Atomic Resolution Structure Determination in Over-Focus with Volta Phase Plate by Cs-Corrected Cryo-EM. <i>Structure</i> , 2017, 25, 1623-1630.e3.	1.6	34
57	Cryo-EM structure of the human heteromeric amino acid transporter b <sup>0,+</sup> AT-rBAT. <i>Science Advances</i> , 2020, 6, eaay6379.	4.7	27
58	Structural insights into the assembly of the 30S ribosomal subunit in vivo: functional role of S5 and location of the 17S rRNA precursor sequence. <i>Protein and Cell</i> , 2014, 5, 394-407.	4.8	26
59	Architecture of <i>Saccharomyces cerevisiae</i> SAGA complex. <i>Cell Discovery</i> , 2019, 5, 25.	3.1	21
60	Cryo-EM structure of the nuclear ring from <i>Xenopus laevis</i> nuclear pore complex. <i>Cell Research</i> , 2022, 32, 349-358.	5.7	19
61	Cryo-EM structure of the inner ring from the <i>Xenopus laevis</i> nuclear pore complex. <i>Cell Research</i> , 2022, 32, 451-460.	5.7	15
62	Structural insight into the substrate recognition and transport mechanism of the human LAT2 <sup>Δ</sup> 4F2hc complex. <i>Cell Discovery</i> , 2020, 6, 82.	3.1	13
63	Structural dynamics of the yeast Shwachman-Diamond syndrome protein (Sdo1) on the ribosome and its implication in the 60S subunit maturation. <i>Protein and Cell</i> , 2016, 7, 187-200.	4.8	8
64	Structural Basis for Pore Blockade of the Human Cardiac Sodium Channel Na <sub>v</sub> 1.5 by the Antiarrhythmic Drug Quinidine**. <i>Angewandte Chemie</i> , 2021, 133, 11575-11581.	1.6	6
65	Biological cryo-electron microscopy in China. <i>Protein Science</i> , 2017, 26, 16-31.	3.1	3
66	The application of CorrSight <sup>™</sup> in correlative light and electron microscopy of vitrified biological specimens. <i>Biophysics Reports</i> , 2018, 4, 143-152.	0.2	2