

Xiao-chen Bai

List of Publications by Year in descending order

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66
papers

10,541
citations

57631

44
h-index

110170

64
g-index

80
all docs

80
docs citations

80
times ranked

14056
citing authors

#	ARTICLE	IF	CITATIONS
1	Synergistic activation of the insulin receptor via two distinct sites. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 357-368.	3.6	36
2	Activation of STING by targeting a pocket in the transmembrane domain. <i>Nature</i> , 2022, 604, 557-562.	13.7	71
3	Molecular mechanism of the wake-promoting agent TAK-925. <i>Nature Communications</i> , 2022, 13, .	5.8	12
4	SNARE assembly enlightened by cryo-EM structures of a synaptobrevinâ€“Munc18-1â€“syntaxin-1 complex. <i>Science Advances</i> , 2022, 8, .	4.7	40
5	Cryo-electron Microscopic Analysis of Single-Pass Transmembrane Receptors. <i>Chemical Reviews</i> , 2022, 122, 13952-13988.	23.0	7
6	Cryo-EM structure of the Hippo signaling integrator human STRIPAK. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 290-299.	3.6	36
7	Seeing Atoms by Single-Particle Cryo-EM. <i>Trends in Biochemical Sciences</i> , 2021, 46, 253-254.	3.7	16
8	Architecture of the Sema3A/PlexinA4/Neuropilin tripartite complex. <i>Nature Communications</i> , 2021, 12, 3172.	5.8	24
9	Scap structures highlight key role for rotation of intertwined luminal loops in cholesterol sensing. <i>Cell</i> , 2021, 184, 3689-3701.e22.	13.5	18
10	Structural basis of the activation of c-MET receptor. <i>Nature Communications</i> , 2021, 12, 4074.	5.8	64
11	Characterization of the subunit composition and structure of adult human glycine receptors. <i>Neuron</i> , 2021, 109, 2707-2716.e6.	3.8	32
12	A structural model of a Rasâ€“Raf signalosome. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 847-857.	3.6	44
13	Structures and Mechanisms in the cGAS-STING Innate Immunity Pathway. <i>Immunity</i> , 2020, 53, 43-53.	6.6	325
14	Structural and Mechanistic Regulation of the Pro-degenerative NAD Hydrolase SARM1. <i>Cell Reports</i> , 2020, 32, 107999.	2.9	94
15	Cryo-EM structure of the human cohesin-NIPBL-DNA complex. <i>Science</i> , 2020, 368, 1454-1459.	6.0	171
16	Structure of a D2 dopamine receptorâ€“G-protein complex in a lipid membrane. <i>Nature</i> , 2020, 584, 125-129.	13.7	128
17	Cryo-EM structure of the PlexinC1/A39R complex reveals inter-domain interactions critical for ligand-induced activation. <i>Nature Communications</i> , 2020, 11, 1953.	5.8	13
18	Cryo-EM structures of human ZnT8 in both outward- and inward-facing conformations. <i>ELife</i> , 2020, 9, .	2.8	46

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19	Structural insights into the Ca ²⁺ -dependent gating of the human mitochondrial calcium uniporter. <i>ELife</i> , 2020, 9, .	2.8	34
20	Structural basis of the activation of type 1 insulin-like growth factor receptor. <i>Nature Communications</i> , 2019, 10, 4567.	5.8	117
21	Cryo-EM structures of the human cation-chloride cotransporter KCC1. <i>Science</i> , 2019, 366, 505-508.	6.0	61
22	Structural Mechanism of EMRE-Dependent Gating of the Human Mitochondrial Calcium Uniporter. <i>Cell</i> , 2019, 177, 1252-1261.e13.	13.5	108
23	Cryo-EM structures of STING reveal its mechanism of activation by cyclic GMP&. <i>Nature</i> , 2019, 567, 389-393.	13.7	392
24	Structural basis of STING binding with and phosphorylation by TBK1. <i>Nature</i> , 2019, 567, 394-398.	13.7	540
25	Structural mechanisms of phospholipid activation of the human TPC2 channel. <i>ELife</i> , 2019, 8, .	2.8	103
26	Structural and functional characterization of an otopetrin family proton channel. <i>ELife</i> , 2019, 8, .	2.8	20
27	Cryo-EM analyses reveal the common mechanism and diversification in the activation of RET by different ligands. <i>ELife</i> , 2019, 8, .	2.8	37
28	Activation mechanism of the insulin receptor revealed by cryo-EM structure of the fully liganded receptor&ligand complex. <i>ELife</i> , 2019, 8, .	2.8	123
29	Structural insights into the voltage and phospholipid activation of the mammalian TPC1 channel. <i>Nature</i> , 2018, 556, 130-134.	13.7	153
30	Cryo-EM structure of the adenosine A2A receptor coupled to an engineered heterotrimeric G protein. <i>ELife</i> , 2018, 7, .	2.8	219
31	Cryo-EM structure of a fungal mitochondrial calcium uniporter. <i>Nature</i> , 2018, 559, 570-574.	13.7	125
32	Mechanistic insights into caspase-9 activation by the structure of the apoptosome holoenzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1542-1547.	3.3	95
33	Structure of a spliceosome remodelled for exon ligation. <i>Nature</i> , 2017, 542, 377-380.	13.7	160
34	Cryo-EM structure of a metazoan separase&securin complex at near-atomic resolution. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 414-418.	3.6	65
35	Structure of the MacAB&TolC ABC-type tripartite multidrug efflux pump. <i>Nature Microbiology</i> , 2017, 2, 17070.	5.9	140
36	Mefloquine targets the <i>Plasmodium falciparum</i> 80S ribosome to inhibit protein synthesis. <i>Nature Microbiology</i> , 2017, 2, 17031.	5.9	128

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37	Structure of mammalian endolysosomal TRPML1 channel in nanodiscs. <i>Nature</i> , 2017, 550, 415-418.	13.7	244
38	Structures of the human mitochondrial ribosome in native states of assembly. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 866-869.	3.6	140
39	Structures of the calcium-activated, non-selective cation channel TRPM4. <i>Nature</i> , 2017, 552, 205-209.	13.7	158
40	Structure of β -Secretases and Implications for Drug Development. <i>Alzheimer's and Dementia</i> , 2016, 12, P161.	0.4	0
41	The Central domain of RyR1 is the transducer for long-range allosteric gating of channel opening. <i>Cell Research</i> , 2016, 26, 995-1006.	5.7	93
42	The Sac3 TPR-like region in the <i>Saccharomyces cerevisiae</i> TREX-2 complex is more extensive but independent of the CID region. <i>Journal of Structural Biology</i> , 2016, 195, 316-324.	1.3	3
43	Design of a molecular support for cryo-EM structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7456-E7463.	3.3	93
44	Cryo-EM structure of the yeast U4/U6.U5 tri-snRNP at 3.7 Å... resolution. <i>Nature</i> , 2016, 530, 298-302.	13.7	184
45	Sampling the conformational space of the catalytic subunit of human β -secretase. <i>ELife</i> , 2015, 4, .	2.8	556
46	Structure of the apoptosome: mechanistic insights into activation of an initiator caspase from <i>Drosophila</i> . <i>Genes and Development</i> , 2015, 29, 277-287.	2.7	55
47	The architecture of the spliceosomal U4/U6.U5 tri-snRNP. <i>Nature</i> , 2015, 523, 47-52.	13.7	195
48	An atomic structure of human β -secretase. <i>Nature</i> , 2015, 525, 212-217.	13.7	490
49	Atomic structure of the apoptosome: mechanism of cytochrome <i>c</i> - and dATP-mediated activation of Apaf-1. <i>Genes and Development</i> , 2015, 29, 2349-2361.	2.7	201
50	Structure of the rabbit ryanodine receptor RyR1 at near-atomic resolution. <i>Nature</i> , 2015, 517, 50-55.	13.7	391
51	How cryo-EM is revolutionizing structural biology. <i>Trends in Biochemical Sciences</i> , 2015, 40, 49-57.	3.7	709
52	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Science</i> , 2014, 343, 1485-1489.	6.0	521
53	Initiation of Translation by Cricket Paralysis Virus IRES Requires Its Translocation in the Ribosome. <i>Cell</i> , 2014, 157, 823-831.	13.5	211
54	Structure of the large ribosomal subunit from human mitochondria. <i>Science</i> , 2014, 346, 718-722.	6.0	260

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55	Three-dimensional structure of human β -secretase. <i>Nature</i> , 2014, 512, 166-170.	13.7	317
56	Cryo-EM structure of the <i>Plasmodium falciparum</i> 80S ribosome bound to the anti-protozoan drug emetine. <i>ELife</i> , 2014, 3, .	2.8	274
57	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Microscopy and Microanalysis</i> , 2014, 20, 1252-1253.	0.2	1
58	Molecular Architecture of a Eukaryotic Translational Initiation Complex. <i>Science</i> , 2013, 342, 1240585.	6.0	120
59	Ribosome structures to near-atomic resolution from thirty thousand cryo-EM particles. <i>ELife</i> , 2013, 2, e00461.	2.8	378
60	Cryo-EM structure of a 3D DNA-origami object. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20012-20017.	3.3	219
61	Structural characterization of full-length NSF and 20S particles. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 268-275.	3.6	46
62	Characterization of the Structure and Function of <i>Escherichia coli</i> DegQ as a Representative of the DegQ-like Proteases of Bacterial HtrA Family Proteins. <i>Structure</i> , 2011, 19, 1328-1337.	1.6	37
63	Two types of oligomeric structures of DegP in protein quality control. <i>FASEB Journal</i> , 2011, 25, 905.5.	0.2	0
64	Cellular Internalization of Exosomes Occurs Through Phagocytosis. <i>Traffic</i> , 2010, 11, 675-687.	1.3	757
65	Bowl-shaped oligomeric structures on membranes as DegP's new functional forms in protein quality control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4858-4863.	3.3	64
66	Overexpression of complexin in PC12 cells inhibits exocytosis by preventing SNARE complex recycling. <i>Biochemistry (Moscow)</i> , 2007, 72, 439-444.	0.7	11