

Maojun Yang

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

5,246
citations

126708

33
h-index

123241

61
g-index

63
all docs

63
docs citations

63
times ranked

7947
citing authors

#	ARTICLE	IF	CITATIONS
1	The coupling mechanism of mammalian mitochondrial complex I. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 172-182.	3.6	45
2	A SYBR Gold-based Label-free in vitro Dicing Assay. <i>Bio-protocol</i> , 2022, 12, e4382.	0.2	1
3	AcrIF5 specifically targets DNA-bound CRISPR-Cas surveillance complex for inhibition. <i>Nature Chemical Biology</i> , 2022, 18, 670-677.	3.9	10
4	Structural basis for the catalytic activity of filamentous human serine beta-lactamase-like protein LACTB. <i>Structure</i> , 2022, 30, 685-696.e5.	1.6	8
5	Insights into the inhibition of type I-F CRISPR-Cas system by a multifunctional anti-CRISPR protein AcrIF24. <i>Nature Communications</i> , 2022, 13, 1931.	5.8	16
6	Discovery of small-molecule activators of nicotinamide phosphoribosyltransferase (NAMPT) and their preclinical neuroprotective activity. <i>Cell Research</i> , 2022, 32, 570-584.	5.7	27
7	Structure of intact human MCU supercomplex with the auxiliary MICU subunits. <i>Protein and Cell</i> , 2021, 12, 220-229.	4.8	34
8	The structural basis of function and regulation of neuronal cotransporters NKCC1 and KCC2. <i>Communications Biology</i> , 2021, 4, 226.	2.0	48
9	Structure of the full-length human Pannexin1 channel and insights into its role in pyroptosis. <i>Cell Discovery</i> , 2021, 7, 30.	3.1	14
10	Molecular insights into the human ABCB6 transporter. <i>Cell Discovery</i> , 2021, 7, 55.	3.1	18
11	Insights into the dual functions of AcrIF14 during the inhibition of type I-F CRISPR-Cas surveillance complex. <i>Nucleic Acids Research</i> , 2021, 49, 10178-10191.	6.5	9
12	Mechanism of siRNA production by a plant Dicer-RNA complex in dicing-competent conformation. <i>Science</i> , 2021, 374, 1152-1157.	6.0	58
13	Cryo-EM structures and transport mechanism of human P5B type ATPase ATP13A2. <i>Cell Discovery</i> , 2021, 7, 106.	3.1	16
14	Atomic structure of human TOM core complex. <i>Cell Discovery</i> , 2020, 6, 67.	3.1	67
15	Molecular insights into the human CLC-7/Ostm1 transporter. <i>Science Advances</i> , 2020, 6, eabb4747.	4.7	31
16	Distinct structural modulation of photosystem I and lipid environment stabilizes its tetrameric assembly. <i>Nature Plants</i> , 2020, 6, 314-320.	4.7	30
17	Research journey of respirasome. <i>Protein and Cell</i> , 2020, 11, 318-338.	4.8	22
18	Cryo-EM structure of the mammalian ATP synthase tetramer bound with inhibitory protein IF1. <i>Science</i> , 2019, 364, 1068-1075.	6.0	145

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19	Structure and mechanism of mitochondrial electron transport chain. <i>Biomedical Journal</i> , 2018, 41, 9-20.	1.4	133
20	UQCRCFS1N assembles mitochondrial respiratory complex-III into an asymmetric 21-subunit dimer. <i>Protein and Cell</i> , 2018, 9, 586-591.	4.8	8
21	A binding-block ion selective mechanism revealed by a Na/K selective channel. <i>Protein and Cell</i> , 2018, 9, 629-639.	4.8	14
22	Structural basis of ubiquitin modification by the Legionella effector SdeA. <i>Nature</i> , 2018, 557, 674-678.	13.7	69
23	Structure of the intact 14-subunit human cytochrome c oxidase. <i>Cell Research</i> , 2018, 28, 1026-1034.	5.7	159
24	Cryo-EM structure of the ASIC1a-mambalgin-1 complex reveals that the peptide toxin mambalgin-1 inhibits acid-sensing ion channels through an unusual allosteric effect. <i>Cell Discovery</i> , 2018, 4, 27.	3.1	28
25	Temperature-dependent ESR and computational studies on antiferromagnetic electron transfer in the yeast NADH dehydrogenase Ndi1. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 4849-4854.	1.3	8
26	Structural insights into the coordination of plastid division by the ARC6-PDV2 complex. <i>Nature Plants</i> , 2017, 3, 17011.	4.7	29
27	Determining EGFR-TKI sensitivity of G719X and other uncommon EGFR mutations in non-small cell lung cancer: Perplexity and solution. <i>Oncology Reports</i> , 2017, 37, 1347-1358.	1.2	63
28	Target Elucidation by Cocrystal Structures of NADH-Ubiquinone Oxidoreductase of <i>Plasmodium falciparum</i> (<i>Pf</i> NDH2) with Small Molecule To Eliminate Drug-Resistant Malaria. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 1994-2005.	2.9	51
29	Architecture of Human Mitochondrial Respiratory Megacomplex I ₂ III ₂ IV ₂ . <i>Cell</i> , 2017, 170, 1247-1257.e12.	13.5	362
30	Cryo-EM structures of the mammalian endo-lysosomal TRPML1 channel elucidate the combined regulation mechanism. <i>Protein and Cell</i> , 2017, 8, 834-847.	4.8	39
31	Identification of Intracellular β -Barrel Residues Involved in Ion Selectivity in the Mechanosensitive Channel of <i>Thermoanaerobacter tengcongensis</i> . <i>Frontiers in Physiology</i> , 2017, 8, 832.	1.3	2
32	Structural basis of the interaction between the meningitis pathogen <i>Streptococcus suis</i> adhesin Fhb and its human receptor. <i>FEBS Letters</i> , 2016, 590, 1384-1392.	1.3	11
33	Structure of Mammalian Respiratory Supercomplex I ₁ III ₂ IV ₁ . <i>Cell</i> , 2016, 167, 1598-1609.e10.	13.5	311
34	TMCO1 Is an ER Ca ²⁺ Load-Activated Ca ²⁺ Channel. <i>Cell</i> , 2016, 165, 1454-1466.	13.5	112
35	The architecture of the mammalian respirasome. <i>Nature</i> , 2016, 537, 639-643.	13.7	311
36	Amazing structure of respirasome: unveiling the secrets of cell respiration. <i>Protein and Cell</i> , 2016, 7, 854-865.	4.8	38

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37	Crystal structures of Bbp from <i>Staphylococcus aureus</i> reveal the ligand binding mechanism with Fibrinogen $\hat{1}\pm$. <i>Protein and Cell</i> , 2015, 6, 757-766.	4.8	16
38	Expression, purification, crystallization and structure determination of the N terminal domain of Fhb, a factor H binding protein from <i>Streptococcus suis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 466, 413-417.	1.0	4
39	Structure of the eukaryotic MCM complex at 3.8 Å... <i>Nature</i> , 2015, 524, 186-191.	13.7	207
40	Structural basis for substrate specificity of an amino acid ABC transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5243-5248.	3.3	49
41	Architecture of the mammalian mechanosensitive Piezo1 channel. <i>Nature</i> , 2015, 527, 64-69.	13.7	363
42	Functional and Structural Characterization of the Antiphagocytic Properties of a Novel Transglutaminase from <i>Streptococcus suis</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 19081-19092.	1.6	22
43	Structural insights into the TRIM family of ubiquitin E3 ligases. <i>Cell Research</i> , 2014, 24, 762-765.	5.7	118
44	Planar substrate-binding site dictates the specificity of ECF-type nickel/cobalt transporters. <i>Cell Research</i> , 2014, 24, 267-277.	5.7	39
45	Structural basis for hijacking CBF $\hat{1}^2$ and CUL5 E3 ligase complex by HIV-1 Vif. <i>Nature</i> , 2014, 505, 229-233.	13.7	185
46	Hat2p recognizes the histone H3 tail to specify the acetylation of the newly synthesized H3/H4 heterodimer by the Hat1p/Hat2p complex. <i>Genes and Development</i> , 2014, 28, 1217-1227.	2.7	33
47	Structures of SdrD from <i>Staphylococcus aureus</i> reveal the molecular mechanism of how the cell surface receptors recognize their ligands. <i>Protein and Cell</i> , 2013, 4, 277-285.	4.8	30
48	Perilipin1 promotes unilocular lipid droplet formation through the activation of Fsp27 in adipocytes. <i>Nature Communications</i> , 2013, 4, 1594.	5.8	200
49	Crystal Structures Reveal the Multi-Ligand Binding Mechanism of <i>Staphylococcus aureus</i> ClfB. <i>PLoS Pathogens</i> , 2012, 8, e1002751.	2.1	51
50	Structural insight into the type-II mitochondrial NADH dehydrogenases. <i>Nature</i> , 2012, 491, 478-482.	13.7	105
51	When MAGE meets RING: insights into biological functions of MAGE proteins. <i>Protein and Cell</i> , 2011, 2, 7-12.	4.8	46
52	MAGE-RING Protein Complexes Comprise a Family of E3 Ubiquitin Ligases. <i>Molecular Cell</i> , 2010, 39, 963-974.	4.5	388
53	Insights into Mad2 Regulation in the Spindle Checkpoint Revealed by the Crystal Structure of the Symmetric Mad2 Dimer. <i>PLoS Biology</i> , 2008, 6, e50.	2.6	86
54	p31comet Blocks Mad2 Activation through Structural Mimicry. <i>Cell</i> , 2007, 131, 744-755.	13.5	172

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55	Mechanistic Analysis of a Suicide Inactivator of Histone Demethylase LSD1. <i>Biochemistry</i> , 2007, 46, 6892-6902.	1.2	87
56	Structural Basis for the Inhibition of the LSD1 Histone Demethylase by the Antidepressant trans-2-Phenylcyclopropylamine. <i>Biochemistry</i> , 2007, 46, 8058-8065.	1.2	213
57	Structural basis of histone demethylation by LSD1 revealed by suicide inactivation. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 535-539.	3.6	170
58	Structural Basis for CoREST-Dependent Demethylation of Nucleosomes by the Human LSD1 Histone Demethylase. <i>Molecular Cell</i> , 2006, 23, 377-387.	4.5	306
59	Crystallization and preliminary crystallographic analysis of RSB-66, a novel round spermatid-specific protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1853-1855.	2.5	4
60	Crystallization and preliminary crystallographic analysis of the extracellular fragment of Fc ϵ RI/CD89. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2251-2253.	2.5	2