

Jianping Ding

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

63

papers

4,230

citations

21

h-index

65

g-index

68

ext. papers

4,904

ext. citations

13.7

avg, IF

4.67

L-index

#	Paper	IF	Citations
63	Tet-mediated formation of 5-carboxylcytosine and its excision by TDG in mammalian DNA. <i>Science</i> , 2011 , 333, 1303-7	33.3	1980
62	Glioma-derived mutations in IDH1 dominantly inhibit IDH1 catalytic activity and induce HIF-1alpha. <i>Science</i> , 2009 , 324, 261-5	33.3	884
61	Structures of human cytosolic NADP-dependent isocitrate dehydrogenase reveal a novel self-regulatory mechanism of activity. <i>Journal of Biological Chemistry</i> , 2004 , 279, 33946-57	5.4	278
60	Negative feedback-defective PRPS1 mutants drive thiopurine resistance in relapsed childhood ALL. <i>Nature Medicine</i> , 2015 , 21, 563-71	50.5	106
59	Molecular mechanisms of "off-on switch" of activities of human IDH1 by tumor-associated mutation R132H. <i>Cell Research</i> , 2010 , 20, 1188-200	24.7	90
58	Crystal structure of the Ego1-Ego2-Ego3 complex and its role in promoting Rag GTPase-dependent TORC1 signaling. <i>Cell Research</i> , 2015 , 25, 1043-59	24.7	57
57	Mutation of Gly-11 on the dimer interface results in the complete crystallographic dimer dissociation of severe acute respiratory syndrome coronavirus 3C-like protease: crystal structure with molecular dynamics simulations. <i>Journal of Biological Chemistry</i> , 2008 , 283, 554-564	5.4	57
56	Ego3 functions as a homodimer to mediate the interaction between Gtr1-Gtr2 and Ego1 in the ego complex to activate TORC1. <i>Structure</i> , 2012 , 20, 2151-60	5.2	51
55	Crystal structure of DNA cytidine deaminase ABOBEC3G catalytic deamination domain suggests a binding mode of full-length enzyme to single-stranded DNA. <i>Journal of Biological Chemistry</i> , 2015 , 290, 4010-21	5.4	44
54	Structural basis of intramitochondrial phosphatidic acid transport mediated by Ups1-Mdm35 complex. <i>EMBO Reports</i> , 2015 , 16, 813-23	6.5	42
53	Crystal structures of isocitrate decarboxylases reveal a novel catalytic mechanism of 5-carboxyl-uracil decarboxylation and shed light on the search for DNA decarboxylase. <i>Cell Research</i> , 2013 , 23, 1296-309	24.7	42
52	A vitamin-C-derived DNA modification catalysed by an algal TET homologue. <i>Nature</i> , 2019 , 569, 581-585	50.4	41
51	Regulation of the histone acetyltransferase activity of hMOF via autoacetylation of Lys274. <i>Cell Research</i> , 2011 , 21, 1262-6	24.7	38
50	Molecular mechanism for Rabex-5 GEF activation by Rabaptin-5. <i>ELife</i> , 2014 , 3,	8.9	31
49	Structural studies of <i>Saccharomyces cerevisiae</i> mitochondrial NADP-dependent isocitrate dehydrogenase in different enzymatic states reveal substantial conformational changes during the catalytic reaction. <i>Protein Science</i> , 2008 , 17, 1542-54	6.3	30
48	LRCH1 interferes with DOCK8-Cdc42-induced T cell migration and ameliorates experimental autoimmune encephalomyelitis. <i>Journal of Experimental Medicine</i> , 2017 , 214, 209-226	16.6	29
47	Salvianolic acid B inhibits platelets as a P2Y12 antagonist and PDE inhibitor: evidence from clinic to laboratory. <i>Thrombosis Research</i> , 2014 , 134, 866-76	8.2	28

46	Structural basis for Ragulator functioning as a scaffold in membrane-anchoring of Rag GTPases and mTORC1. <i>Nature Communications</i> , 2017 , 8, 1394	17.4	28
45	Crystal structures of human NUDT5 reveal insights into the structural basis of the substrate specificity. <i>Journal of Molecular Biology</i> , 2006 , 364, 1021-33	6.5	28
44	Molecular dynamics of HIV-1 reverse transcriptase indicates increased flexibility upon DNA binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 45, 176-82	4.2	28
43	Conotoxin D-GeXXA utilizes a novel strategy to antagonize nicotinic acetylcholine receptors. <i>Scientific Reports</i> , 2015 , 5, 14261	4.9	25
42	Structural basis of immunosuppression by the therapeutic antibody daclizumab. <i>Cell Research</i> , 2010 , 20, 1361-71	24.7	21
41	Structural insight into the arginine-binding specificity of CASTOR1 in amino acid-dependent mTORC1 signaling. <i>Cell Discovery</i> , 2016 , 2, 16035	22.3	20
40	Molecular mechanism of the allosteric regulation of the α -heterodimer of human NAD-dependent isocitrate dehydrogenase. <i>Scientific Reports</i> , 2017 , 7, 40921	4.9	18
39	Human antibody 3E1 targets the HA stem region of H1N1 and H5N6 influenza A viruses. <i>Nature Communications</i> , 2016 , 7, 13577	17.4	18
38	The α and β subunits play distinct functional roles in the α -heterotetramer of human NAD-dependent isocitrate dehydrogenase. <i>Scientific Reports</i> , 2017 , 7, 41882	4.9	17
37	Structural insight into human N6amt1-Trm112 complex functioning as a protein methyltransferase. <i>Cell Discovery</i> , 2019 , 5, 51	22.3	13
36	Structural basis for the functional role of the Shu complex in homologous recombination. <i>Nucleic Acids Research</i> , 2017 , 45, 13068-13079	20.1	12
35	Insights into the inhibitory mechanisms of NADH on the α -heterodimer of human NAD-dependent isocitrate dehydrogenase. <i>Scientific Reports</i> , 2018 , 8, 3146	4.9	12
34	Subdomain II of β -isopropylmalate synthase is essential for activity: inferring a mechanism of feedback inhibition. <i>Journal of Biological Chemistry</i> , 2014 , 289, 27966-78	5.4	12
33	Structural insights into the functions of the FANCM-FAAP24 complex in DNA repair. <i>Nucleic Acids Research</i> , 2013 , 41, 10573-83	20.1	11
32	Structural and mechanistic insights into regulation of HBO1 histone acetyltransferase activity by BRPF2. <i>Nucleic Acids Research</i> , 2017 , 45, 5707-5719	20.1	10
31	Crystal structure of the WOPR-DNA complex and implications for Wor1 function in white-opaque switching of <i>Candida albicans</i> . <i>Cell Research</i> , 2014 , 24, 1108-20	24.7	10
30	Cbln1 and Cbln4 Are Structurally Similar but Differ in GluD2 Binding Interactions. <i>Cell Reports</i> , 2017 , 20, 2328-2340	10.6	10
29	Structural basis for Sfm1 functioning as a protein arginine methyltransferase. <i>Cell Discovery</i> , 2015 , 1, 15037	22.3	10

28	Structure-based Mechanistic Insights into Terminal Amide Synthase in Nosiheptide-Represented Thiopeptides Biosynthesis. <i>Scientific Reports</i> , 2015 , 5, 12744	4.9	10
27	Aldolase B suppresses hepatocellular carcinogenesis by inhibiting G6PD and pentose phosphate pathways. <i>Nature Cancer</i> , 2020 , 1, 735-747	15.4	9
26	Structure basis of the FERM domain of kindlin-3 in supporting integrin $\alpha\text{IIb}\beta\text{3}$ activation in platelets. <i>Blood Advances</i> , 2020 , 4, 3128-3135	7.8	9
25	Structural insights into the EGO-TC-mediated membrane tethering of the TORC1-regulatory Rag GTPases. <i>Science Advances</i> , 2019 , 5, eaax8164	14.3	7
24	Molecular basis for the function of the α heterodimer of human NAD-dependent isocitrate dehydrogenase. <i>Journal of Biological Chemistry</i> , 2019 , 294, 16214-16227	5.4	7
23	Structural insights into the activation of USP46 by WDR48 and WDR20. <i>Cell Discovery</i> , 2019 , 5, 34	22.3	6
22	Structural basis for self-cleavage prevention by tag:anti-tag pairing complementarity in type VI Cas13 CRISPR systems. <i>Molecular Cell</i> , 2021 , 81, 1100-1115.e5	17.6	6
21	Crystal structure of the Rab9A-RUTBC2 RBD complex reveals the molecular basis for the binding specificity of Rab9A with RUTBC2. <i>Structure</i> , 2014 , 22, 1408-20	5.2	5
20	Molecular basis for the substrate specificity and catalytic mechanism of thymine-7-hydroxylase in fungi. <i>Nucleic Acids Research</i> , 2015 , 43, 10026-38	20.1	5
19	HBO1 is a versatile histone acyltransferase critical for promoter histone acylations. <i>Nucleic Acids Research</i> , 2021 , 49, 8037-8059	20.1	5
18	Crystal Structure of Cytidine Deaminase Human APOBEC3F Chimeric Catalytic Domain in Complex with DNA. <i>Chinese Journal of Chemistry</i> , 2018 , 36, 1241-1248	4.9	5
17	Role of Rab5 in the formation of macrophage-derived foam cell. <i>Lipids in Health and Disease</i> , 2017 , 16, 170	4.4	4
16	Structural basis for targeting BIG1 to Golgi apparatus through interaction of its DCB domain with Arl1. <i>Journal of Molecular Cell Biology</i> , 2016 , 8, 459-461	6.3	3
15	Molecular basis for the recognition of CCN1 by monoclonal antibody 093G9. <i>Journal of Molecular Recognition</i> , 2017 , 30, e2645	2.6	2
14	Molecular mechanism of the dual regulatory roles of ATP on the α heterodimer of human NAD-dependent isocitrate dehydrogenase. <i>Scientific Reports</i> , 2020 , 10, 6225	4.9	2
13	Structure and allosteric regulation of human NAD-dependent isocitrate dehydrogenase. <i>Cell Discovery</i> , 2020 , 6, 94	22.3	2
12	Structure, substrate specificity, and catalytic mechanism of human D-2-HGDH and insights into pathogenicity of disease-associated mutations. <i>Cell Discovery</i> , 2021 , 7, 3	22.3	2
11	Unique binding pattern for a lineage of human antibodies with broad reactivity against influenza A virus. <i>Nature Communications</i> , 2022 , 13, 2378	17.4	2

10	Crystal Structures of Arabidopsis thaliana Nudix Hydrolase NUDT7 Reveal a Previously Unobserved Conformation. <i>Molecular Plant</i> , 2015 , 8, 1557-9	14.4	1
9	Nde1 is a Rab9 effector for loading late endosomes to cytoplasmic dynein motor complex. <i>Structure</i> , 2021 ,	5.2	1
8	Molecular mechanism for vitamin C-derived C-glyceryl-methylcytosine DNA modification catalyzed by algal TET homologue CMD1. <i>Nature Communications</i> , 2021 , 12, 744	17.4	1
7	AKT2 reduces IFN β production to modulate antiviral responses and systemic lupus erythematosus.. <i>EMBO Journal</i> , 2022 , e108016	13	1
6	Staurosporine targets the Hippo pathway to inhibit cell growth. <i>Journal of Molecular Cell Biology</i> , 2018 , 10, 267-269	6.3	0
5	New exon and accelerated evolution of placental gene Nrk occurred in the ancestral lineage of placental mammals. <i>Placenta</i> , 2021 , 114, 14-21	3.4	0
4	Identification and Tetramer Structure of Hemin-Binding Protein SPD_0310 Linked to Iron Homeostasis and Virulence of Streptococcus pneumoniae.. <i>MSystems</i> , 2022 , e0022122	7.6	0
3	Molecular basis for the functions of dominantly active Y35N and inactive D60K Rheb mutants in mTORC1 signaling. <i>Journal of Molecular Cell Biology</i> , 2020 , 12, 741-744	6.3	
2	Molecular basis of the activation of the Rabex-5 GEF activity by Rabaptin-5 in endocytosis (802.27). <i>FASEB Journal</i> , 2014 , 28, 802.27	0.9	
1	Crystal structures of S6K1 provide insights into the regulation mechanism of S6K1 by the hydrophobic motif. <i>FASEB Journal</i> , 2013 , 27, lb133	0.9	