Jianping Ding

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/971316/jianping-ding-publications-by-year.pdf
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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	AKT2 reduces IFN▯ production to modulate antiviral responses and systemic lupus erythematosus.. *EMBO Journal*, **2022**, e108016	13	1
62	Identification and Tetramer Structure of Hemin-Binding Protein SPD_0310 Linked to Iron Homeostasis and Virulence of Streptococcus pneumoniae.. *MSystems*, **2022**, e0022122	7.6	0
61	Unique binding pattern for a lineage of human antibodies with broad reactivity against influenza A virus.. *Nature Communications*, **2022**, 13, 2378	17.4	2
60	Nde1 is a Rab9 effector for loading late endosomes to cytoplasmic dynein motor complex. *Structure*, **2021**,	5.2	1
59	Structural basis for self-cleavage prevention by tag:anti-tag pairing complementarity in type VI Cas13 CRISPR systems. *Molecular Cell*, **2021**, 81, 1100-1115.e5	17.6	6
58	HBO1 is a versatile histone acyltransferase critical for promoter histone acylations. *Nucleic Acids Research*, **2021**, 49, 8037-8059	20.1	5
57	Molecular mechanism for vitamin C-derived C-glyceryl-methylcytosine DNA modification catalyzed by algal TET homologue CMD1. *Nature Communications*, **2021**, 12, 744	17.4	1
56	New exon and accelerated evolution of placental gene Nrk occurred in the ancestral lineage of placental mammals. *Placenta*, **2021**, 114, 14-21	3.4	0
55	Structure, substrate specificity, and catalytic mechanism of human D-2-HGDH and insights into pathogenicity of disease-associated mutations. *Cell Discovery*, **2021**, 7, 3	22.3	2
54	Molecular basis for the functions of dominantly active Y35N and inactive D60K Rheb mutants in mTORC1 signaling. *Journal of Molecular Cell Biology*, **2020**, 12, 741-744	6.3	
53	Aldolase B suppresses hepatocellular carcinogenesis by inhibiting G6PD and pentose phosphate pathways.. *Nature Cancer*, **2020**, 1, 735-747	15.4	9
52	Molecular mechanism of the dual regulatory roles of ATP on the ▯heterodimer of human NAD-dependent isocitrate dehydrogenase. *Scientific Reports*, **2020**, 10, 6225	4.9	2
51	Structure and allosteric regulation of human NAD-dependent isocitrate dehydrogenase. *Cell Discovery*, **2020**, 6, 94	22.3	2
50	Structure basis of the FERM domain of kindlin-3 in supporting integrin ▯b▯3 activation in platelets. *Blood Advances*, **2020**, 4, 3128-3135	7.8	9
49	Structural insight into human N6amt1-Trm112 complex functioning as a protein methyltransferase. *Cell Discovery*, **2019**, 5, 51	22.3	13
48	Structural insights into the EGO-TC-mediated membrane tethering of the TORC1-regulatory Rag GTPases. *Science Advances*, **2019**, 5, eaax8164	14.3	7
47	A vitamin-C-derived DNA modification catalysed by an algal TET homologue. *Nature*, **2019**, 569, 581-585	50.4	41

46	Structural insights into the activation of USP46 by WDR48 and WDR20. *Cell Discovery*, **2019**, 5, 34	22.3	6
45	Molecular basis for the function of the □heterodimer of human NAD-dependent isocitrate dehydrogenase. *Journal of Biological Chemistry*, **2019**, 294, 16214-16227	5.4	7
44	Insights into the inhibitory mechanisms of NADH on the □heterodimer of human NAD-dependent isocitrate dehydrogenase. *Scientific Reports*, **2018**, 8, 3146	4.9	12
43	Staurosporine targets the Hippo pathway to inhibit cell growth. *Journal of Molecular Cell Biology*, **2018**, 10, 267-269	6.3	0
42	Crystal Structure of Cytidine Deaminase Human APOBEC3F Chimeric Catalytic Domain in Complex with DNA. *Chinese Journal of Chemistry*, **2018**, 36, 1241-1248	4.9	5
41	The □and □subunits play distinct functional roles in the □heterotetramer of human NAD-dependent isocitrate dehydrogenase. *Scientific Reports*, **2017**, 7, 41882	4.9	17
40	Molecular mechanism of the allosteric regulation of the □heterodimer of human NAD-dependent isocitrate dehydrogenase. *Scientific Reports*, **2017**, 7, 40921	4.9	18
39	Structural and mechanistic insights into regulation of HBO1 histone acetyltransferase activity by BRPF2. *Nucleic Acids Research*, **2017**, 45, 5707-5719	20.1	10
38	Molecular basis for the recognition of CCN1 by monoclonal antibody 093G9. *Journal of Molecular Recognition*, **2017**, 30, e2645	2.6	2
37	LRCH1 interferes with DOCK8-Cdc42-induced T cell migration and ameliorates experimental autoimmune encephalomyelitis. *Journal of Experimental Medicine*, **2017**, 214, 209-226	16.6	29
36	Structural basis for the functional role of the Shu complex in homologous recombination. *Nucleic Acids Research*, **2017**, 45, 13068-13079	20.1	12
35	Role of Rab5 in the formation of macrophage-derived foam cell. *Lipids in Health and Disease*, **2017**, 16, 170	4.4	4
34	Cbln1 and Cbln4 Are Structurally Similar but Differ in GluD2 Binding Interactions. *Cell Reports*, **2017**, 20, 2328-2340	10.6	10
33	Structural basis for Ragulator functioning as a scaffold in membrane-anchoring of Rag GTPases and mTORC1. *Nature Communications*, **2017**, 8, 1394	17.4	28
32	Human antibody 3E1 targets the HA stem region of H1N1 and H5N6 influenza A viruses. *Nature Communications*, **2016**, 7, 13577	17.4	18
31	Structural insight into the arginine-binding specificity of CASTOR1 in amino acid-dependent mTORC1 signaling. *Cell Discovery*, **2016**, 2, 16035	22.3	20
30	Structural basis for targeting BIG1 to Golgi apparatus through interaction of its DCB domain with Arl1. *Journal of Molecular Cell Biology*, **2016**, 8, 459-461	6.3	3
29	Crystal structure of DNA cytidine deaminase ABOBEC3G catalytic deamination domain suggests a binding mode of full-length enzyme to single-stranded DNA. *Journal of Biological Chemistry*, **2015**, 290, 4010-21	5.4	44

28	Crystal structure of the Ego1-Ego2-Ego3 complex and its role in promoting Rag GTPase-dependent TORC1 signaling. *Cell Research*, **2015**, 25, 1043-59	24.7	57
27	Negative feedback-defective PRPS1 mutants drive thiopurine resistance in relapsed childhood ALL. *Nature Medicine*, **2015**, 21, 563-71	50.5	106
26	Crystal Structures of Arabidopsis thaliana Nudix Hydrolase NUDT7 Reveal a Previously Unobserved Conformation. *Molecular Plant*, **2015**, 8, 1557-9	14.4	1
25	Conotoxin □D-GeXXA utilizes a novel strategy to antagonize nicotinic acetylcholine receptors. *Scientific Reports*, **2015**, 5, 14261	4.9	25
24	Structural basis for Sfm1 functioning as a protein arginine methyltransferase. *Cell Discovery*, **2015**, 1, 15037	22.3	10
23	Structure-based Mechanistic Insights into Terminal Amide Synthase in Nosiheptide-Represented Thiopeptides Biosynthesis. *Scientific Reports*, **2015**, 5, 12744	4.9	10
22	Molecular basis for the substrate specificity and catalytic mechanism of thymine-7-hydroxylase in fungi. *Nucleic Acids Research*, **2015**, 43, 10026-38	20.1	5
21	Structural basis of intramitochondrial phosphatidic acid transport mediated by Ups1-Mdm35 complex. *EMBO Reports*, **2015**, 16, 813-23	6.5	42
20	Crystal structure of the WOPR-DNA complex and implications for Wor1 function in white-opaque switching of Candida albicans. *Cell Research*, **2014**, 24, 1108-20	24.7	10
19	Crystal structure of the Rab9A-RUTBC2 RBD complex reveals the molecular basis for the binding specificity of Rab9A with RUTBC2. *Structure*, **2014**, 22, 1408-20	5.2	5
18	Salvianolic acid B inhibits platelets as a P2Y12 antagonist and PDE inhibitor: evidence from clinic to laboratory. *Thrombosis Research*, **2014**, 134, 866-76	8.2	28
17	Subdomain II of □isopropylmalate synthase is essential for activity: inferring a mechanism of feedback inhibition. *Journal of Biological Chemistry*, **2014**, 289, 27966-78	5.4	12
16	Molecular mechanism for Rabex-5 GEF activation by Rabaptin-5. *ELife*, **2014**, 3,	8.9	31
15	Molecular basis of the activation of the Rabex-5 GEF activity by Rabaptin-5 in endocytosis (802.27). *FASEB Journal*, **2014**, 28, 802.27	0.9	
14	Crystal structures of isoorotate decarboxylases reveal a novel catalytic mechanism of 5-carboxyl-uracil decarboxylation and shed light on the search for DNA decarboxylase. *Cell Research* , **2013**, 23, 1296-309	24.7	42
13	Structural insights into the functions of the FANCM-FAAP24 complex in DNA repair. *Nucleic Acids Research*, **2013**, 41, 10573-83	20.1	11
12	Crystal structures of S6K1 provide insights into the regulation mechanism of S6K1 by the hydrophobic motif. *FASEB Journal*, **2013**, 27, lb133	0.9	
11	Ego3 functions as a homodimer to mediate the interaction between Gtr1-Gtr2 and Ego1 in the ego complex to activate TORC1. *Structure*, **2012**, 20, 2151-60	5.2	51

10	Tet-mediated formation of 5-carboxylcytosine and its excision by TDG in mammalian DNA. *Science*, **2011**, 333, 1303-7	33.3	1980
9	Regulation of the histone acetyltransferase activity of hMOF via autoacetylation of Lys274. *Cell Research*, **2011**, 21, 1262-6	24.7	38
8	Molecular mechanisms of "off-on switch" of activities of human IDH1 by tumor-associated mutation R132H. *Cell Research*, **2010**, 20, 1188-200	24.7	90
7	Structural basis of immunosuppression by the therapeutic antibody daclizumab. *Cell Research*, **2010** , 20, 1361-71	24.7	21
6	Glioma-derived mutations in IDH1 dominantly inhibit IDH1 catalytic activity and induce HIF-1alpha. *Science*, **2009**, 324, 261-5	33.3	884
5	Structural studies of Saccharomyces cerevesiae mitochondrial NADP-dependent isocitrate dehydrogenase in different enzymatic states reveal substantial conformational changes during the catalytic reaction. *Protein Science*, **2008**, 17, 1542-54	6.3	30
4	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. *Journal of Biological Chemistry*, **2008**, 283, 554-564	5.4	57
3	Crystal structures of human NUDT5 reveal insights into the structural basis of the substrate specificity. *Journal of Molecular Biology*, **2006**, 364, 1021-33	6.5	28
2	Structures of human cytosolic NADP-dependent isocitrate dehydrogenase reveal a novel self-regulatory mechanism of activity. *Journal of Biological Chemistry*, **2004**, 279, 33946-57	5.4	278
1	Molecular dynamics of HIV-1 reverse transcriptase indicates increased flexibility upon DNA binding. *Proteins: Structure, Function and Bioinformatics*, **2001**, 45, 176-82	4.2	28