Ziguo Zhang

List of Publications by Year
in descending order

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47	6,279	136740	223531
papers	citations	32 h-index	46 g-index

50	50	50	7918
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structure of the human inner kinetochore bound to a centromeric CENP-A nucleosome. Science, 2022, 376, 844-852.	6.0	40
2	Structure of the SARS-CoV-2 RNA-dependent RNA polymerase in the presence of favipiravir-RTP. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	144
3	Molecular mechanisms of APC/C release from spindle assembly checkpoint inhibition by APC/C SUMOylation. Cell Reports, 2021, 34, 108929.	2.9	12
4	Structure of the DOCK2â˜ELMO1 complex provides insights into regulation of the auto-inhibited state. Nature Communications, 2020, 11, 3464.	5.8	34
5	Crystal structure of the Cenp-HIKHead-TW sub-module of the inner kinetochore CCAN complex. Nucleic Acids Research, 2020, 48, 11172-11184.	6.5	16
6	Structure of the inner kinetochore CCAN complex assembled onto a centromeric nucleosome. Nature, 2019, 574, 278-282.	13.7	113
7	Architecture of the CBF3â€“centromere complex of the budding yeast kinetochore. Nature Structural and Molecular Biology, 2018, 25, 1103-1110.	3.6	23
8	Cryo-EM structure of a metazoan separaseâ€“securin complex at near-atomic resolution. Nature Structural and Molecular Biology, 2017, 24, 414-418.	3.6	65
9	Molecular mechanism of APC/C activation by mitotic phosphorylation. Nature, 2016, 533, 260-264.	13.7	159
10	WD40 domain of Apc1 is critical for the coactivator-induced allosteric transition that stimulates APC/C catalytic activity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10547-10552.	3.3	16
11	Molecular basis of APC/C regulation by the spindle assembly checkpoint. Nature, 2016, 536, 431-436.	13.7	178
12	Recombinant expression and reconstitution of multiprotein complexes by the USER cloning method in the insect cell-baculovirus expression system. Methods, 2016, 95, 13-25.	1.9	49
13	Atomic structure of the APC/C and its mechanism of protein ubiquitination. Nature, 2015, 522, 450-454.	13.7	208
14	Atomic-Resolution Structures of the APC/C Subunits Apc4 and the Apc5 N-Terminal Domain. Journal of Molecular Biology, 2015, 427, 3300-3315.	2.0	10
15	Molecular architecture and mechanism of the anaphase-promoting complex. Nature, 2014, 513, 388-393.	13.7	180
16	Mechanism of farnesylated CAAX protein processing by the intramembrane protease Rce1. Nature, 2013, 504, 301-305.	13.7	155
17	The Four Canonical TPR Subunits of Human APC/C Form Related Homo-Dimeric Structures and Stack in Parallel to Form a TPR Suprahelix. Journal of Molecular Biology, 2013, 425, 4236-4248.	2.0	20
18	Insights into Degron Recognition by APC/C Coactivators from the Structure of an Acm1-Cdh1 Complex. Molecular Cell, 2013, 50, 649-660.	4.5	115

#	Article	IF	Citations
19	Recombinant expression, reconstitution and structure of human anaphase-promoting complex (APC/C). Biochemical Journal, 2013, 449, 365-371.	1.7	48
20	Building a pseudo-atomic model of the anaphase-promoting complex. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2236-2243.	2.5	7
21	Structure of the mitotic checkpoint complex. Nature, 2012, 484, 208-213.	13.7	270
22	Mechanism of Isoprenylcysteine Carboxyl Methylation from the Crystal Structure of the Integral Membrane Methyltransferase ICMT. Molecular Cell, 2011, 44, 997-1004.	4.5	49
23	Structures of APC/CCdh1 with substrates identify Cdh1 and Apc10 as the D-box co-receptor. Nature, 2011, 470, 274-278.	13.7	176
24	Structural basis for the subunit assembly of the anaphase-promoting complex. Nature, 2011, 470, 227-232.	13.7	150
25	Multiple Factors Confer Specific Cdc42 and Rac Protein Activation by Dedicator of Cytokinesis (DOCK) Nucleotide Exchange Factors. Journal of Biological Chemistry, 2011, 286, 25341-25351.	1.6	81
26	Powdery mildew fungal effector candidates share N-terminal Y/F/WxC-motif. BMC Genomics, 2010, 11, 317.	1.2	177
27	The APC/C subunit Cdc16/Cut9 is a contiguous tetratricopeptide repeat superhelix with a homo-dimer interface similar to Cdc27. EMBO Journal, 2010, 29, 3733-3744.	3.5	68
28	Molecular Structure of the N-terminal Domain of the APC/C Subunit Cdc27 Reveals a Homo-dimeric Tetratricopeptide Repeat Architecture. Journal of Molecular Biology, 2010, 397, 1316-1328.	2.0	29
29	Activation of Rho GTPases by DOCK Exchange Factors Is Mediated by a Nucleotide Sensor. Science, 2009, 325, 1398-1402.	6.0	103
30	A proteomics study of barley powdery mildew haustoria. Proteomics, 2009, 9, 3222-3232.	1.3	56
31	A Lesion-Mimic Syntaxin Double Mutant in Arabidopsis Reveals Novel Complexity of Pathogen Defense Signaling. Molecular Plant, 2008, 1, 510-527.	3.9	76
32	A Novel Role for Catalase B in the Maintenance of Fungal Cell-Wall Integrity During Host Invasion in the Rice Blast Fungus Magnaporthe grisea. Molecular Plant-Microbe Interactions, 2007, 20, 568-580.	1.4	77
33	A SNARE-protein has opposing functions in penetration resistance and defence signalling pathways. Plant Journal, 2007, 49, 302-312.	2.8	172
34	Blumeria graminis secretes an extracellular catalase during infection of barley: potential role in suppression of host defence. Molecular Plant Pathology, 2004, 5, 537-547.	2.0	66
35	Quinoxyfen perturbs signal transduction in barley powdery mildew (Blumeria graminis f.sp. hordei). Molecular Plant Pathology, 2003, 4, 177-186.	2.0	34
36	A "Step Down" PCR-Based Technique for Walking Into and the Subsequent Direct-Sequence Analysis of Flanking Genomic DNA. , 2002, 192, 343-350.		7

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37	Expression and sequence analysis of the Blumeria graminis mitogen-activated protein kinase genes, mpk 1 and mpk 2. Gene, 2001, 266, 57-65.	1.0	28
38	The barley powdery mildew protein kinase C gene,pkc1 andpkc-like gene, are differentially expressed during morphogenesis. Molecular Plant Pathology, 2001, 2, 327-337.	2.0	14
39	Differential expression of two Blumeria graminis chitin synthase genes. Molecular Plant Pathology, 2000, 1, 125-138.	2.0	25
40	Walking into the unknown: a â€˜step downâ€™ PCR-based technique leading to the direct sequence analysis of flanking genomic DNA. Gene, 2000, 253, 145-150.	1.0	62
41	An epidermis/papilla-specific oxalate oxidase-like protein in the defence response of barley attacked by the powdery mildew fungus. Plant Molecular Biology, 1998, 36, 101-112.	2.0	134
42	Molecular Characterization of the Oxalate Oxidase Involved in the Response of Barley to the Powdery Mildew Fungus1. Plant Physiology, 1998, 117, 33-41.	2.3	139
43	Subcellular localization of H2O2 in plants. H2O2 accumulation in papillae and hypersensitive response during the barley-powdery mildew interaction. Plant Journal, 1997, 11, 1187-1194.	2.8	2,406
44	Ethanol increases sensitivity of oxalate oxidase assays and facilitates direct activity staining in SDS gels. Plant Molecular Biology Reporter, 1996, 14, 266-272.	1.0	35
45	Germin-like oxalate oxidase, a H2O2-producing enzyme, accumulates in barley attacked by the powdery mildew fungus. Plant Journal, 1995, 8, 139-145.	2.8	192
46	Conditions inducing fertility alteration and ecological adaptation of photoperiod-sensitive genic male-sterile rice. Field Crops Research, 1994, 38, 111-120.	2.3	9
47	Two Photoperiodicâ€Reactions in Photoperiodâ€Sensitive Genic Maleâ€Sterile Rice. Crop Science, 1993, 33, 651-660.	0.8	47