Kang Zhou

List of Publications by Year
in descending order

23 papers	638 citations	687363 13 h-index	642732 23 g-index
25 all docs	25 docs citations	25 times ranked	1143 citing authors

#	Article	IF	Citations
1	The Î±-synuclein hereditary mutation E46K unlocks a more stable, pathogenic fibril structure. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3592-3602.	7.1	122
2	N-Terminal Domain of Bombyx mori Fibroin Mediates the Assembly of Silk in Response to pH Decrease. Journal of Molecular Biology, 2012, 418, 197-207.	4.2	107
3	Different functional states of fusion protein gB revealed on human cytomegalovirus by cryo electron tomography with Volta phase plate. PLoS Pathogens, 2018, 14, e1007452.	4.7	80
4	Structural basis for STAT2 suppression by flavivirus NS5. Nature Structural and Molecular Biology, 2020, 27, 875-885.	8.2	40
5	Characterization of the First Fungal Glycosyl Hydrolase Family 19 Chitinase (NbchiA) from Nosema bombycis (Nb). Journal of Eukaryotic Microbiology, 2016, 63, 37-45.	1.7	34
6	Conservative transcription in three steps visualized in a double-stranded RNA virus. Nature Structural and Molecular Biology, 2019, 26, 1023-1034.	8.2	33
7	Atomic structures of anthrax toxin protective antigen channels bound to partially unfolded lethal and edema factors. Nature Communications, 2020, 11, 840.	12.8	28
8	Crystal structures and catalytic mechanism of theC-methyltransferase Coq5 provide insights into a key step of the yeast coenzyme Q synthesis pathway. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2085-2092.	2.5	22
9	Structure of the gas vesicle protein GvpF from the cyanobacteriumMicrocystis aeruginosa. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3013-3022.	2.5	22
10	pH-dependent gating mechanism of the Helicobacter pylori urea channel revealed by cryo-EM. Science Advances, 2019, 5, eaav8423.	10.3	20
11	Crystal structure of juvenile hormone epoxide hydrolase from the silkwormBombyx mori. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3224-3229.	2.6	18
12	Structure of the adenylationâ€“peptidyl carrier protein didomain of theMicrocystis aeruginosamicrocystin synthetase McyG. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 873-881.	2.5	18
13	Structural insights into the catalytic mechanism of the yeast pyridoxal 5-phosphate synthase Snz1. Biochemical Journal, 2010, 432, 445-454.	3.7	17
14	Crystal structure of caspase-11 CARD provides insights into caspase-11 activation. Cell Discovery, 2020, 6, 70.	6.7	14
15	Crystal structure of yeast monothiol glutaredoxin Grx6 in complex with a glutathione-coordinated [2Feâ€“2S] cluster. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 732-737.	0.8	12
16	A novel point mutation of acetylcholinesterase in a trichlorfon-resistant strain of the oriental fruit fly Bactrocera dorsalis (Diptera: Tephritidae). Applied Entomology and Zoology, 2014, 49, 129-137.	1.2	10
17	Atomic Structures of Anthrax Prechannel Bound with Full-Length Lethal and Edema Factors. Structure, 2020, 28, 879-887.e3.	3.3	8
18	Structural insights into the catalysis and substrate specificity of cyanobacterial aspartate racemase McyF. Biochemical and Biophysical Research Communications, 2019, 514, 1108-1114.	2.1	6

#	Article	IF	Citations
19	Locations and in situ structure of the polymerase complex inside the virion of vesicular stomatitis virus. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2111948119.	7.1	6
20	Structure and Catalytic Mechanism of Yeast 4-Amino-4-deoxychorismate Lyase. Journal of Biological Chemistry, 2013, 288, 22985-22992.	3.4	5
21	Structures of an all-Î± protein running along the DNA major groove. Nucleic Acids Research, 2016, 44, 3936-3945.	14.5	5
22	High-resolution crystal structure ofStreptococcus agalactiaeglyceraldehyde-3-phosphate dehydrogenase. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 236-244.	0.8	5
23	Structural and biochemical analyses of Microcystis aeruginosa O-acetylserine sulfhydrylases reveal a negative feedback regulation of cysteine biosynthesis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 308-315.	2.3	4