Jianhua He

List of Publications by Year in descending order

37 papers	695 citations	759233 12 h-index	580821 25 g-index
38 all docs	38 docs citations	38 times ranked	1519 citing authors

#	Article	IF	Citations
1	Molecular determinants of human neutralizing antibodies isolated from a patient infected with Zika virus. Science Translational Medicine, 2016, 8, 369ra179.	12.4	194
2	Structural basis for reversible amyloids of hnRNPA1 elucidates their role in stress granule assembly. Nature Communications, 2019, 10, 2006.	12.8	157
3	Automatic crystal centring procedure at the SSRF macromolecular crystallography beamline. Journal of Synchrotron Radiation, 2016, 23, 1323-1332.	2.4	61
4	Discovery of potent N-(isoxazol-5-yl)amides as HSP90 inhibitors. European Journal of Medicinal Chemistry, 2014, 87, 765-781.	5.5	33
5	Pyrethroid Carboxylesterase PytH from Sphingobium faniae JZ-2: Structure and Catalytic Mechanism. Applied and Environmental Microbiology, 2020, 86, .	3.1	25
6	Crystal Structure and Function of PqqF Protein in the Pyrroloquinoline Quinone Biosynthetic Pathway. Journal of Biological Chemistry, 2016, 291, 15575-15587.	3.4	23
7	Structural insight into the cooperation of chloroplast chaperonin subunits. BMC Biology, 2016, 14, 29.	3.8	21
8	Crystal structure and enantioselectivity of terpene cyclization in SAM-dependent methyltransferase TleD. Biochemical Journal, 2016, 473, 4385-4397.	3.7	18
9	Crystal structure of the Vibrio cholerae VqmAâ€“ligandâ€“DNA complex provides insight into ligand-binding mechanisms relevant for drug design. Journal of Biological Chemistry, 2019, 294, 2580-5171.	3.4	18
10	Shanghai synchrotron radiation facility. National Science Review, 2014, 1, 171-172.	9.5	17
11	Identification of a new series of potent diphenol HSP90 inhibitors by fragment merging and structure-based optimization. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 2525-2529.	2.2	16
12	Crystal structure of the catalytic domain of PigE: A transaminase involved in the biosynthesis of 2-methyl-3-n-amyl-pyrrole (MAP) from Serratia sp. FS14. Biochemical and Biophysical Research Communications, 2014, 447, 178-183.	2.1	12
13	Myroilysin Is a New Bacterial Member of the M12A Family of Metzincin Metallopeptidases and Is Activated by a Cysteine Switch Mechanism. Journal of Biological Chemistry, 2017, 292, 5195-5206.	3.4	11
14	Structural and mechanistic insights into the biosynthesis of CDP-archaeol in membranes. Cell Research, 2017, 27, 1378-1391.	12.0	10
15	Large conformation shifts of Vibrio cholerae VqmA dimer in the absence of target DNA provide insight into DNA-binding mechanisms of LuxR-type receptors. Biochemical and Biophysical Research Communications, 2019, 520, 399-405.	2.1	9
16	Crystal structure and biochemical studies of the bifunctional DNA primase-polymerase from phage NrS-1. Biochemical and Biophysical Research Communications, 2019, 510, 573-579.	2.1	9
17	Functional Partition of Cpn60Î± and Cpn60Î² Subunits in Substrate Recognition and Cooperation with Co-chaperonins. Molecular Plant, 2016, 9, 1210-1213.	8.3	8
18	Mini-beam modes on standard MX beamline BL17U at SSRF. Review of Scientific Instruments, 2017, 88, 073301.	1.3	7

#	Article	IF	Citations
19	Expression, crystallization and preliminary crystallographic data analysis of VioD, a hydroxylase in the violacein-biosynthesis pathway. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 149-152.	0.8	6
20	Crystal structures of phage NrS-1 N300-dNTPs-Mg2+ complex provide molecular mechanisms for substrate specificity. Biochemical and Biophysical Research Communications, 2019, 515, 551-557.	2.1	6
21	Crystal structures of the kinase domain of PpkA, a key regulatory component of T6SS, reveal a general inhibitory mechanism. Biochemical Journal, 2018, 475, 2209-2224.	3.7	5
22	Crystal structure details of Vibrio fischeri DarR and mutant DarR-M202I from LTTR family reveals their activation mechanism. International Journal of Biological Macromolecules, 2021, 183, 2354-2363.	7.5	5
23	Status of the crystallography beamlines at SSRF. European Physical Journal Plus, 2015, 130, 1.	2.6	4
24	PEPTIDE NANOFILAMENTS USED FOR REPLICA-MOLDING: A COMBINATION OF "BOTTOM-UP" AND "TOP-DOWN". Surface Review and Letters, 2007, 14, 301-307.	1.1	3
25	Crystal structure of the periplasmic domain of TssL, a key membrane component of Type VI secretion system. International Journal of Biological Macromolecules, 2018, 120, 1474-1479.	7.5	3
26	Design of new sub-micron protein crystallography beamline at SSRF. AIP Conference Proceedings, 2019, , .	0.4	3
27	Microplates for Crystal Growth and in situ Data Collection at a Synchrotron Beamline. Crystals, 2020, 10, 798.	2.2	3
28	Expression, crystallization and preliminary crystallographic data analysis of PigI, a putative<scp>L</scp>-prolyl-AMP ligase from the prodigiosin synthetic pathway inSerratia. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 624-627.	0.8	2
29	Crystal structure of mature myroilysin and implication for its activation mechanism. International Journal of Biological Macromolecules, 2020, 156, 1556-1564.	7.5	2
30	Novel combined crystallization plate for high-throughput crystal screening and in situ data collection at a crystallography beamline. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 319-327.	0.8	1
31	Structural Study of the Complex of cblC Methylmalonic Aciduria and Homocystinuria-Related Protein MMACHC with Cyanocobalamin. Crystals, 2022, 12, 468.	2.2	1
32	SSRF in Full Commissioning. Synchrotron Radiation News, 2008, 21, 20-23.	0.8	0
33	Synchrotron Radiation Facilities in China. Synchrotron Radiation News, 2009, 22, 17-22.	0.8	0
34	Recognition of outer membrane proteins using adaptive neuro-fuzzy inference systems. , 2014, , .		0
35	The crystal structure of MreC provides insights into polymer formation. FEBS Open Bio, 2021, , .	2.3	0
36	Crystal structures of TTHA1265 and TTHA1264/TTHA1265 complex reveal an intrinsic heterodimeric assembly. International Journal of Biological Macromolecules, 2022, 207, 424-433.	7.5	0

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37	Translesion synthesis of apurinic/apyrimidic site analogues by Y-family DNA polymerase Dbh from <italic>Sulfolobus acidocaldarius</italic>. Acta Biochimica Et Biophysica Sinica, 2022, , .	2.0	0