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List of Publications by Year
in descending order

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49 papers	2,531 citations	361413 20 h-index	223800 46 g-index
49 all docs	49 docs citations	49 times ranked	5881 citing authors

#	Article	IF	Citations
1	Structural and biochemical analysis of the PTPN4 PDZ domain bound to the C-terminal tail of the human papillomavirus E6 oncoprotein. Journal of Microbiology, 2022, 60, 395-401.	2.8	6
2	Eif2b3 mutants recapitulate phenotypes of vanishing white matter disease and validate novel disease alleles in zebrafish. Human Molecular Genetics, 2021, 30, 331-342.	2.9	8
3	Crystal structure of human LC8 bound to a peptide from Ebola virus VP35. Journal of Microbiology, 2021, 59, 410-416.	2.8	4
4	Molecular Analysis of the Interaction between Human PTPN21 and the Oncoprotein E7 from Human Papillomavirus Genotype 18. Molecules and Cells, 2021, 44, 26-37.	2.6	13
5	Crystallization and preliminary diffraction analysis of the phosphatase domain of PTPN14 in the human papillomavirus E7 binding-defective mutant form. Biodesign, 2021, 9, 63-66.	0.4	0
6	The transcription factor PITX1 drives astrocyte differentiation by regulating the SOX9 gene. Journal of Biological Chemistry, 2020, 295, 13677-13690.	3.4	10
7	Requirement of the Cep57-Cep63 Interaction for Proper Cep152 Recruitment and Centriole Duplication. Molecular and Cellular Biology, 2020, 40, .	2.3	25
8	Nurr1 performs its anti-inflammatory function by regulating RasGRP1 expression in neuro-inflammation. Scientific Reports, 2020, 10, 10755.	3.3	17
9	Structural and Biochemical Characterization of the Two Drosophila Low Molecular Weight-Protein Tyrosine Phosphatases DARP and Primo-1. Molecules and Cells, 2020, 43, 1035-1045.	2.6	0
10	Crystal Structure of the YAPâ€binding Domain of Human TEAD1. Bulletin of the Korean Chemical Society, 2019, 40, 74-77.	1.9	2
11	Structural basis for recognition of the tumor suppressor protein PTPN14 by the oncoprotein E7 of human papillomavirus. PLoS Biology, 2019, 17, e3000367.	5.6	45
12	Structural and Physiological Exploration of Salmonella Typhi YfdX Uncovers Its Dual Function in Bacterial Antibiotic Stress and Virulence. Frontiers in Microbiology, 2019, 9, 3329.	3.5	15
13	Disordered region of cereblon is required for efficient degradation by proteolysis-targeting chimera. Scientific Reports, 2019, 9, 19654.	3.3	26
14	Oligomer Model of PB1 Domain of p62/SQSTM1 Based on Crystal Structure of Homo-Dimer and Calculation of Helical Characteristics. Molecules and Cells, 2019, 42, 729-738.	2.6	2
15	Identification of N-(5-(phenoxymethyl)-1,3,4-thiadiazol-2-yl)acetamide derivatives as novel protein tyrosine phosphatase epsilon inhibitors exhibiting anti-osteoclastic activity. Bioorganic and Medicinal Chemistry, 2018, 26, 5204-5211.	3.0	2
16	Structural study reveals the temperature-dependent conformational flexibility of Tk-PTP, a protein tyrosine phosphatase from Thermococcus kodakaraensis KOD1. PLoS ONE, 2018, 13, e0197635.	2.5	9
17	Methyl 3-(3-(4-(2,4,4-Trimethylpentan-2-yl)phenoxy)-propanamido)benzoate as a Novel and Dual Malate Dehydrogenase (MDH) 1/2 Inhibitor Targeting Cancer Metabolism. Journal of Medicinal Chemistry, 2017, 60, 8631-8646.	6.4	24
18	Crystal structures of two forms of the Acanthamoeba polyphaga mimivirus Rab GTPase. Archives of Virology, 2017, 162, 3407-3416.	2.1	5

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19	Two-track virtual screening approach to identify both competitive and allosteric inhibitors of human small C-terminal domain phosphatase 1. Journal of Computer-Aided Molecular Design, 2017, 31, 743-753.	2.9	5
20	The Discovery of Novel Protein Tyrosine Phosphatase Îµ Inhibitors Using a Highâ€throughput Screening Approach. Bulletin of the Korean Chemical Society, 2017, 38, 44-53.	1.9	1
21	Structural and biochemical analysis of atypically low dephosphorylating activity of human dual-specificity phosphatase 28. PLoS ONE, 2017, 12, e0187701.	2.5	3
22	Structural Study of the HD-PTP Bro1 Domain in a Complex with the Core Region of STAM2, a Subunit of ESCRT-0. PLoS ONE, 2016, 11, e0149113.	2.5	20
23	Discovery of Novel Striatalâ€enriched Protein Tyrosine Phosphatase Inhibitors Through Structureâ€based Virtual Screening. Bulletin of the Korean Chemical Society, 2016, 37, 1783-1788.	1.9	2
24	High-resolution crystal structure of the PDZ1 domain of human protein tyrosine phosphatase PTP-Bas. Biochemical and Biophysical Research Communications, 2016, 478, 1205-1210.	2.1	3
25	Mitochondrial Akt Regulation of Hypoxic Tumor Reprogramming. Cancer Cell, 2016, 30, 257-272.	16.8	158
26	Crystal structure of SP-PTP, a low molecular weight protein tyrosine phosphatase from Streptococcus pyogenes. Biochemical and Biophysical Research Communications, 2016, 478, 1217-1222.	2.1	7
27	Identification of novel protein tyrosine phosphatase sigma inhibitors promoting neurite extension. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 87-93.	2.2	6
28	Identification of a Highly Conserved Hypothetical Protein TON_0340 as a Probable Manganese-Dependent Phosphatase. PLoS ONE, 2016, 11, e0167549.	2.5	1
29	Structural analysis of the poloâ€box domain of human Poloâ€like kinase 2. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1201-1208.	2.6	9
30	Conversion of cell-survival activity of Akt into apoptotic death of cancer cells by two mutations on the BIM BH3 domain. Cell Death and Disease, 2015, 6, e1804-e1804.	6.3	8
31	The family-wide structure and function of human dual-specificity protein phosphatases. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 421-435.	2.5	34
32	Discovery of novel protein tyrosine phosphatase sigma inhibitors through the virtual screening with modified scoring function. Medicinal Chemistry Research, 2014, 23, 1016-1022.	2.4	2
33	Molecular basis for unidirectional scaffold switching of human Plk4 in centriole biogenesis. Nature Structural and Molecular Biology, 2014, 21, 696-703.	8.2	94
34	Identification of novel PTPRQ phosphatase inhibitors based on the virtual screening with docking simulations. Theoretical Biology and Medical Modelling, 2013, 10, 49.	2.1	7
35	Structural basis of intersubunit recognition in elongin BCâ€“cullin 5â€“SOCS box ubiquitinâ€“protein ligase complexes. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1587-1597.	2.5	32
36	Structural basis for the dephosphorylating activity of PTPRQ towards phosphatidylinositide substrates. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1522-1529.	2.5	8

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37	VipD of Legionella pneumophila Targets Activated Rab5 and Rab22 to Interfere with Endosomal Trafficking in Macrophages. PLoS Pathogens, 2012, 8, e1003082.	4.7	89
38	Phosphoinositides Differentially Regulate Protrudin Localization through the FYVE Domain. Journal of Biological Chemistry, 2012, 287, 41268-41276.	3.4	33
39	Crystal structure of DeSIâ€1, a novel deSUMOylase belonging to a putative isopeptidase superfamily. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2099-2104.	2.6	29
40	Evidence that inhibition of BAX activation by BCL-2 involves its tight and preferential interaction with the BH3 domain of BAX. Cell Research, 2011, 21, 627-641.	12.0	245
41	Downregulation of autophagy by Bcl-2 promotes MCF7 breast cancer cell growth independent of its inhibition of apoptosis. Cell Death and Differentiation, 2011, 18, 452-464.	11.2	55
42	Crystal structure of the MukB hinge domain with coiledâ€coil stretches and its functional implications. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1483-1490.	2.6	28
43	Structural insights into the dual nucleotide exchange and GDI displacement activity of SidM/DrrA. EMBO Journal, 2010, 29, 496-504.	7.8	66
44	Structural Studies of a Bacterial Condensin Complex Reveal ATP-Dependent Disruption of Intersubunit Interactions. Cell, 2009, 136, 85-96.	28.9	145
45	Crystal Structures and Enzyme Mechanisms of a Dual Fucose Mutarotase/Ribose Pyranase. Journal of Molecular Biology, 2009, 391, 178-191.	4.2	8
46	Structural and Biochemical Bases for the Inhibition of Autophagy and Apoptosis by Viral BCL-2 of Murine Î³-Herpesvirus 68. PLoS Pathogens, 2008, 4, e25.	4.7	174
47	An insight into the mechanistic role of Beclin 1 and its inhibition by prosurvival Bcl-2 family proteins. Autophagy, 2008, 4, 519-520.	9.1	41
48	UVRAG: A New Player in Autophagy and Tumor Cell Growth. Autophagy, 2007, 3, 69-71.	9.1	60
49	Autophagic and tumour suppressor activity of a novel Beclin1-binding protein UVRAG. Nature Cell Biology, 2006, 8, 688-698.	10.3	945