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List of Publications by Year in descending order

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28 papers	2,249 citations	361388 20 h-index	501174 28 g-index
33 all docs	33 docs citations	33 times ranked	3454 citing authors

#	Article	IF	Citations
1	CryoEM of RUVBL1â€“RUVBL2â€“ZNHIT2, a complex that interacts with pre-mRNA-processing-splicing factor 8. Nucleic Acids Research, 2022, 50, 1128-1146.	14.5	6
2	Cryoâ€EM structure of metazoan TRAPPIII, the multiâ€subunit complex that activates the GTPase Rab1. EMBO Journal, 2021, 40, e107608.	7.8	26
3	Structure of the TELO2-TTI1-TTI2 complex and its function in TOR recruitment to the R2TP chaperone. Cell Reports, 2021, 36, 109317.	6.4	20
4	Phosphorylation-dependent BRD4 dimerization and implications for therapeutic inhibition of BET family proteins. Communications Biology, 2021, 4, 1273.	4.4	10
5	Mechanistic Insights into Regulation of the ALC1 Remodeler by the Nucleosome Acidic Patch. Cell Reports, 2020, 33, 108529.	6.4	20
6	Inter-membrane association of the Sec and BAM translocons for bacterial outer-membrane biogenesis. ELife, 2020, 9, .	6.0	39
7	Structures of Respiratory Supercomplex I+III2 Reveal Functional and Conformational Crosstalk. Molecular Cell, 2019, 75, 1131-1146.e6.	9.7	148
8	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. Analytical Chemistry, 2019, 91, 6953-6961.	6.5	100
9	Activation of the Endonuclease that Defines mRNA 3â€² Ends Requires Incorporation into an 8-Subunit Core Cleavage and Polyadenylation Factor Complex. Molecular Cell, 2019, 73, 1217-1231.e11.	9.7	70
10	Architecture of the mycobacterial type VII secretion system. Nature, 2019, 576, 321-325.	27.8	89
11	Structure of the Fanconi anaemia monoubiquitin ligase complex. Nature, 2019, 575, 234-237.	27.8	80
12	RPAP3 provides a flexible scaffold for coupling HSP90 to the human R2TP co-chaperone complex. Nature Communications, 2018, 9, 1501.	12.8	54
13	Crystal structure of the N-terminal domain of human Timeless and its interaction with Tipin. Nucleic Acids Research, 2017, 45, 5555-5563.	14.5	18
14	Architecture of eukaryotic mRNA 3â€²-end processing machinery. Science, 2017, 358, 1056-1059.	12.6	124
15	The Structure of the R2TP Complex Defines a Platform for Recruiting Diverse Client Proteins to the HSP90 Molecular Chaperone System. Structure, 2017, 25, 1145-1152.e4.	3.3	48
16	Atomic structure of the entire mammalian mitochondrial complex I. Nature, 2016, 538, 406-410.	27.8	427
17	Purification of Ovine Respiratory Complex I Results in a Highly Active and Stable Preparation. Journal of Biological Chemistry, 2016, 291, 24657-24675.	3.4	26
18	BEAR, a Novel Virtual Screening Methodology for Drug Discovery. Journal of Biomolecular Screening, 2011, 16, 129-133.	2.6	35

#	Article	IF	Citations
19	Fast and accurate predictions of binding free energies using MMâ€PBSA and MMâ€GBSA. Journal of Computational Chemistry, 2010, 31, 797-810.	3.3	569
20	A computational workflow for the design of irreversible inhibitors of protein kinases. Journal of Computer-Aided Molecular Design, 2010, 24, 183-194.	2.9	11
21	Exploring the Binding Site of C-Terminal Hsp90 Inhibitors. Journal of Chemical Information and Modeling, 2010, 50, 1522-1528.	5.4	27
22	Design and Discovery of Plasmepsinâ€...II Inhibitors Using an Automated Workflow on Largeâ€Scale Grids. ChemMedChem, 2009, 4, 1164-1173.	3.2	41
23	Binding Estimation after Refinement, a New Automated Procedure for the Refinement and Rescoring of Docked Ligands in Virtual Screening. Chemical Biology and Drug Design, 2009, 73, 283-286.	3.2	101
24	WISDOM-II: Screening against multiple targets implicated in malaria using computational grid infrastructures. Malaria Journal, 2009, 8, 88.	2.3	29
25	Inâ€...vitro Effects of Plasmodium falciparum Dihydrofolate Reductase Inhibitors on Normal and Cancer Cell Proliferation. ChemMedChem, 2008, 3, 421-424.	3.2	1
26	Structural Models and Binding Site Prediction of the Câ€terminal Domain of Human Hsp90: A New Target for Anticancer Drugs. Chemical Biology and Drug Design, 2008, 71, 420-433.	3.2	26
27	Validation of an automated procedure for the prediction of relative free energies of binding on a set of aldose reductase inhibitors. Bioorganic and Medicinal Chemistry, 2007, 15, 7865-7877.	3.0	97
28	Structure of the TELO2-TTI1-TTI2 Complex and its Function in TOR Recruitment to the R2TP Chaperone. SSRN Electronic Journal, 0, , .	0.4	0