

May Marsh

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

1,783
citations

394286

19
h-index

477173

29
g-index

31
all docs

31
docs citations

31
times ranked

3245
citing authors

#	ARTICLE	IF	CITATIONS
1	A new tubulin-binding site and pharmacophore for microtubule-destabilizing anticancer drugs. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13817-13821.	3.3	229
2	Serial millisecond crystallography for routine room-temperature structure determination at synchrotrons. Nature Communications, 2017, 8, 542.	5.8	203
3	An automated microseed matrix-screening method for protein crystallization. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 550-554.	2.5	175
4	Structural Basis of Microtubule Stabilization by Laulimalide and Peloruside...A. Angewandte Chemie - International Edition, 2014, 53, 1621-1625.	7.2	154
5	Using a Fragment-Based Approach To Target Protein-Protein Interactions. ChemBioChem, 2013, 14, 332-342.	1.3	115
6	Microseed matrix screening for optimization in protein crystallization: what have we learned?. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1117-1126.	0.4	93
7	Biophysical and computational fragment-based approaches to targeting protein-protein interactions: applications in structure-guided drug discovery. Quarterly Reviews of Biophysics, 2012, 45, 383-426.	2.4	90
8	Targeting Protein-Protein Interactions and Fragment-Based Drug Discovery. Topics in Current Chemistry, 2011, 317, 145-179.	4.0	88
9	An enantioselective artificial Suzukiase based on the biotin-streptavidin technology. Chemical Science, 2016, 7, 673-677.	3.7	86
10	Structural basis for ~ 10 promoter element melting by environmentally induced sigma factors. Nature Structural and Molecular Biology, 2014, 21, 269-276.	3.6	82
11	Thermodynamic Properties of Water Molecules at a Protein-Protein Interaction Surface. Journal of Chemical Theory and Computation, 2011, 7, 3514-3522.	2.3	46
12	NMR-Based Determination of the 3D Structure of the Ligand-Protein Interaction Site without Protein Resonance Assignment. Journal of the American Chemical Society, 2016, 138, 4393-4400.	6.6	46
13	Comprehensive Analysis of Binding Sites in Tubulin. Angewandte Chemie - International Edition, 2021, 60, 13331-13342.	7.2	44
14	Structural Insights into Plasticity and Discovery of Remdesivir Metabolite GS-441524 Binding in SARS-CoV-2 Macrodomein. ACS Medicinal Chemistry Letters, 2021, 12, 603-609.	1.3	29
15	Crystal Structures of Fungal Tectonin in Complex with O-Methylated Glycans Suggest Key Role in Innate Immune Defense. Structure, 2018, 26, 391-402.e4.	1.6	28
16	A small-molecule inhibitor of the BRCA2-RAD51 interaction modulates RAD51 assembly and potentiates DNA damage-induced cell death. Cell Chemical Biology, 2021, 28, 835-847.e5.	2.5	27
17	Structural and Spectroscopic Consequences of Hexacoordination of a Bacteriochlorophyll Cofactor in the <i>Rhodobacter sphaeroides</i> Reaction Center. Biochemistry, 2010, 49, 1882-1892.	1.2	21
18	Crystal structures of Cg1458 reveal a catalytic lid domain and a common catalytic mechanism for the FAH family. Biochemical Journal, 2013, 449, 51-60.	1.7	21

#	ARTICLE	IF	CITATIONS
19	Structure of Bacterial Glutathione-S-Transferase Maleyl Pyruvate Isomerase and Implications for Mechanism of Isomerisation. <i>Journal of Molecular Biology</i> , 2008, 384, 165-177.	2.0	20
20	Structure-activity relationship of the peptide binding motif mediating the BRCA2:RAD51 protein-protein interaction. <i>FEBS Letters</i> , 2016, 590, 1094-1102.	1.3	20
21	The Structure of Ca ²⁺ Sensor Case16 Reveals the Mechanism of Reaction to Low Ca ²⁺ Concentrations. <i>Sensors</i> , 2010, 10, 8143-8160.	2.1	18
22	Engineering Archeal Surrogate Systems for the Development of Protein-Protein Interaction Inhibitors against Human RAD51. <i>Journal of Molecular Biology</i> , 2016, 428, 4589-4607.	2.0	13
23	Demonstration of femtosecond X-ray pump X-ray probe diffraction on protein crystals. <i>Structural Dynamics</i> , 2018, 5, 054303.	0.9	11
24	Comprehensive Analysis of Binding Sites in Tubulin. <i>Angewandte Chemie</i> , 2021, 133, 13443-13454.	1.6	7
25	ATP half-sites in RadA and RAD51 recombinases bind nucleotides. <i>FEBS Open Bio</i> , 2016, 6, 372-385.	1.0	5
26	Crystal structure of the pheromone Er-13 from the ciliate <i>Euplotes raikovi</i> , with implications for a protein-protein association model in pheromone/receptor interactions. <i>Journal of Structural Biology</i> , 2022, 214, 107812.	1.3	5
27	Elucidation of a nutlin-derivative-HDM2 complex structure at the interaction site by NMR molecular replacement: A straightforward derivation. <i>Journal of Magnetic Resonance Open</i> , 2022, 10-11, 100032.	0.5	1
28	Optimizing the Growth of Endothiapepsin Crystals for Serial Crystallography Experiments. <i>Journal of Visualized Experiments</i> , 2021, , .	0.2	0