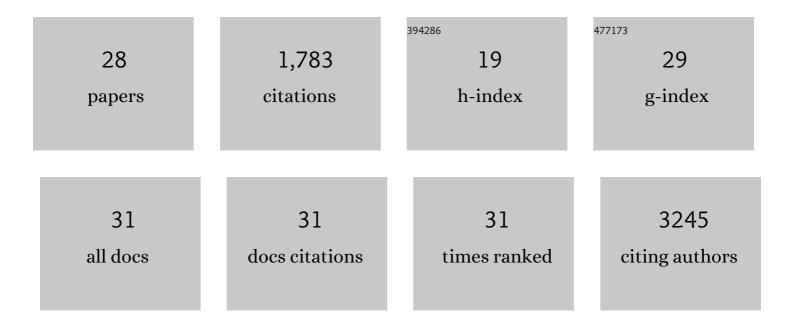
May Marsh

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Crystal structure of the pheromone Er-13 from the ciliate Euplotes raikovi, with implications for a protein–protein association model in pheromone/receptor interactions. Journal of Structural Biology, 2022, 214, 107812.	1.3	5
2	Elucidation of a nutlin-derivative—HDM2 complex structure at the interaction site by NMR molecular replacement: A straightforward derivation. Journal of Magnetic Resonance Open, 2022, 10-11, 100032.	0.5	1
3	Optimizing the Growth of Endothiapepsin Crystals for Serial Crystallography Experiments. Journal of Visualized Experiments, 2021, , .	0.2	0
4	Structural Insights into Plasticity and Discovery of Remdesivir Metabolite GS-441524 Binding in SARS-CoV-2 Macrodomain. ACS Medicinal Chemistry Letters, 2021, 12, 603-609.	1.3	29
5	Comprehensive Analysis of Binding Sites in Tubulin. Angewandte Chemie - International Edition, 2021, 60, 13331-13342.	7.2	44
6	Comprehensive Analysis of Binding Sites in Tubulin. Angewandte Chemie, 2021, 133, 13443-13454.	1.6	7
7	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
8	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
9	Demonstration of femtosecond X-ray pump X-ray probe diffraction on protein crystals. Structural Dynamics, 2018, 5, 054303.	0.9	11
10	Serial millisecond crystallography for routine room-temperature structure determination at synchrotrons. Nature Communications, 2017, 8, 542.	5.8	203
11	Engineering Archeal Surrogate Systems for the Development of Protein–Protein Interaction Inhibitors against Human RAD51. Journal of Molecular Biology, 2016, 428, 4589-4607.	2.0	13
12	Structureâ€activity relationship of the peptide bindingâ€motif mediating the BRCA2:RAD51 protein–protein interaction. FEBS Letters, 2016, 590, 1094-1102.	1.3	20
13	ATP halfâ€sites in RadA and RAD51 recombinases bind nucleotides. FEBS Open Bio, 2016, 6, 372-385.	1.0	5
14	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
15	An enantioselective artificial Suzukiase based on the biotin–streptavidin technology. Chemical Science, 2016, 7, 673-677.	3.7	86
16	Structural basis for â^'10 promoter element melting by environmentally induced sigma factors. Nature Structural and Molecular Biology, 2014, 21, 269-276.	3.6	82
17	Structural Basis of Microtubule Stabilization by Laulimalide and Pelorusideâ€A. Angewandte Chemie - International Edition, 2014, 53, 1621-1625.	7.2	154
18	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

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#	Article	IF	CITATIONS
19	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
20	Using a Fragmentâ€Based Approach To Target Protein–Protein Interactions. ChemBioChem, 2013, 14, 332-342.	1.3	115
21	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
22	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
23	Thermodynamic Properties of Water Molecules at a Protein–Protein Interaction Surface. Journal of Chemical Theory and Computation, 2011, 7, 3514-3522.	2.3	46
24	Targeting Protein–Protein Interactions and Fragment-Based Drug Discovery. Topics in Current Chemistry, 2011, 317, 145-179.	4.0	88
25	The Structure of Ca2+ Sensor Case16 Reveals the Mechanism of Reaction to Low Ca2+ Concentrations. Sensors, 2010, 10, 8143-8160.	2.1	18
26	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
27	Structure of Bacterial Glutathione-S-Transferase Maleyl Pyruvate Isomerase and Implications for Mechanism of Isomerisation. Journal of Molecular Biology, 2008, 384, 165-177.	2.0	20
28	An automated microseed matrix-screening method for protein crystallization. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 550-554.	2.5	175