

Andrew S Arvai

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

22 papers	2,650 citations	17 h-index	22 g-index
22 ext. papers	2,884 ext. citations	15.8 avg, IF	4.07 L-index

#	Paper	IF	Citations
22	Fragment- and structure-based drug discovery for developing therapeutic agents targeting the DNA Damage Response. <i>Progress in Biophysics and Molecular Biology</i> , 2021 , 163, 130-142	4.7	8
21	Targeting SARS-CoV-2 Nsp3 macrodomain structure with insights from human poly(ADP-ribose) glycohydrolase (PARG) structures with inhibitors. <i>Progress in Biophysics and Molecular Biology</i> , 2021 , 163, 171-186	4.7	20
20	An effective human uracil-DNA glycosylase inhibitor targets the open pre-catalytic active site conformation. <i>Progress in Biophysics and Molecular Biology</i> , 2021 , 163, 143-159	4.7	9
19	Human XPG nuclease structure, assembly, and activities with insights for neurodegeneration and cancer from pathogenic mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 14127-14138	11.5	24
18	Targeting Allostery with Avatars to Design Inhibitors Assessed by Cell Activity: Dissecting MRE11 Endo- and Exonuclease Activities. <i>Methods in Enzymology</i> , 2018 , 601, 205-241	1.7	17
17	Phosphate steering by Flap Endonuclease 1 promotes 5Yflap specificity and incision to prevent genome instability. <i>Nature Communications</i> , 2017 , 8, 15855	17.4	53
16	Self-Assembly of the Cephalopod Protein Reflectin. <i>Advanced Materials</i> , 2016 , 28, 8405-8412	24	31
15	The nucleotide-dependent interaction of FlaH and FlaI is essential for assembly and function of the archaeellum motor. <i>Molecular Microbiology</i> , 2016 , 99, 674-85	4.1	43
14	Bioinspired Films: Self-Assembly of the Cephalopod Protein Reflectin (Adv. Mater. 38/2016). <i>Advanced Materials</i> , 2016 , 28, 8553-8553	24	
13	DNA double-strand break repair pathway choice is directed by distinct MRE11 nuclease activities. <i>Molecular Cell</i> , 2014 , 53, 7-18	17.6	371
12	Structural and functional characterization of a conserved pair of bacterial cellulose-oxidizing lytic polysaccharide monooxygenases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 8446-51	11.5	191
11	Ultrahigh resolution and full-length pilin structures with insights for filament assembly, pathogenic functions, and vaccine potential. <i>Journal of Biological Chemistry</i> , 2011 , 286, 44254-44265	5.4	48
10	Anchored plasticity opens doors for selective inhibitor design in nitric oxide synthase. <i>Nature Chemical Biology</i> , 2008 , 4, 700-7	11.7	156
9	Reaction intermediates in the catalytic mechanism of Escherichia coli MutY DNA glycosylase. <i>Journal of Biological Chemistry</i> , 2004 , 279, 46930-9	5.4	46
8	Structures of tetrahydrobiopterin binding-site mutants of inducible nitric oxide synthase oxygenase dimer and implicated roles of Trp457. <i>Biochemistry</i> , 2001 , 40, 12826-32	3.2	31
7	Protein mimicry of DNA from crystal structures of the uracil-DNA glycosylase inhibitor protein and its complex with Escherichia coli uracil-DNA glycosylase. <i>Journal of Molecular Biology</i> , 1999 , 287, 331-46	6.5	114
6	MutY catalytic core, mutant and bound adenine structures define specificity for DNA repair enzyme superfamily. <i>Nature Structural Biology</i> , 1998 , 5, 1058-64		273

5	Structure of Haemophilus influenzae Fe(+3)-binding protein reveals convergent evolution within a superfamily. <i>Nature Structural and Molecular Biology</i> , 1997 , 4, 919-24	17.6	162
4	A nucleotide-flipping mechanism from the structure of human uracil-DNA glycosylase bound to DNA. <i>Nature</i> , 1996 , 384, 87-92	50.4	479
3	Crystallization and preliminary crystallographic study of human CksHs1: a cell cycle regulatory protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 21, 70-3	4.2	7
2	Crystal structure and mutational analysis of human uracil-DNA glycosylase: structural basis for specificity and catalysis. <i>Cell</i> , 1995 , 80, 869-78	56.2	336
1	Crystal structure of human uracil-DNA glycosylase in complex with a protein inhibitor: protein mimicry of DNA. <i>Cell</i> , 1995 , 82, 701-8	56.2	231