

Alan Brown

List of Publications by Year in descending order

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43
papers

5,399
citations

159525

30
h-index

254106

43
g-index

48
all docs

48
docs citations

48
times ranked

7388
citing authors

#	ARTICLE	IF	CITATIONS
1	Ciliary central apparatus structure reveals mechanisms of microtubule patterning. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 483-492.	3.6	33
2	Structures of VWF tubules before and after concatemerization reveal a mechanism of disulfide bond exchange. <i>Blood</i> , 2022, 140, 1419-1430.	0.6	10
3	Structures of radial spokes and associated complexes important for ciliary motility. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 29-37.	3.6	81
4	Structure of a microtubule-bound axonemal dynein. <i>Nature Communications</i> , 2021, 12, 477.	5.8	54
5	Cryo-EM structure of an activated GPCR-G protein complex in lipid nanodiscs. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 258-267.	3.6	71
6	Cryo-EM structure of cortical microtubules from human parasite <i>Toxoplasma gondii</i> identifies their microtubule inner proteins. <i>Nature Communications</i> , 2021, 12, 3065.	5.8	48
7	De novo identification of mammalian ciliary motility proteins using cryo-EM. <i>Cell</i> , 2021, 184, 5791-5806.e19.	13.5	73
8	Structure of CRL2Lrr1, the E3 ubiquitin ligase that promotes DNA replication termination in vertebrates. <i>Nucleic Acids Research</i> , 2021, 49, 13194-13206.	6.5	4
9	Primary Cilia: A Closer Look at the Antenna of Cells. <i>Current Biology</i> , 2020, 30, R1494-R1496.	1.8	4
10	Structure and activation mechanism of the BBSome membrane protein trafficking complex. <i>ELife</i> , 2020, 9, .	2.8	62
11	Structure of the Decorated Ciliary Doublet Microtubule. <i>Cell</i> , 2019, 179, 909-922.e12.	13.5	186
12	Mechanism of ribosome stalling during translation of a poly(A) tail. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1132-1140.	3.6	114
13	Structural Patching Fosters Divergence of Mitochondrial Ribosomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 207-219.	3.5	56
14	Structures of translationally inactive mammalian ribosomes. <i>ELife</i> , 2018, 7, .	2.8	85
15	Tiny crystals have big potential for determining structures of small molecules. <i>Nature</i> , 2018, 564, 348-349.	13.7	4
16	Ribosomes and cryo-EM: a duet. <i>Current Opinion in Structural Biology</i> , 2018, 52, 1-7.	2.6	24
17	The structure of the yeast mitochondrial ribosome. <i>Science</i> , 2017, 355, 528-531.	6.0	161
18	Mefloquine targets the <i>Plasmodium falciparum</i> 80S ribosome to inhibit protein synthesis. <i>Nature Microbiology</i> , 2017, 2, 17031.	5.9	128

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19	Structures of the human mitochondrial ribosome in native states of assembly. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 866-869.	3.6	140
20	Translational termination without a stop codon. <i>Science</i> , 2016, 354, 1437-1440.	6.0	72
21	Ribosome-dependent activation of stringent control. <i>Nature</i> , 2016, 534, 277-280.	13.7	200
22	Decoding Mammalian Ribosome-mRNA States by Translational GTPase Complexes. <i>Cell</i> , 2016, 167, 1229-1240.e15.	13.5	191
23	Organization and Regulation of Mitochondrial Protein Synthesis. <i>Annual Review of Biochemistry</i> , 2016, 85, 77-101.	5.0	221
24	Structure and Assembly Pathway of the Ribosome Quality Control Complex. <i>Molecular Cell</i> , 2015, 57, 433-444.	4.5	165
25	Mechanistic Origin of Microtubule Dynamic Instability and Its Modulation by EB Proteins. <i>Cell</i> , 2015, 162, 849-859.	13.5	367
26	Structural basis for stop codon recognition in eukaryotes. <i>Nature</i> , 2015, 524, 493-496.	13.7	237
27	Tools for macromolecular model building and refinement into electron cryo-microscopy reconstructions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 136-153.	2.5	537
28	The structure of the human mitochondrial ribosome. <i>Science</i> , 2015, 348, 95-98.	6.0	432
29	Mapping the Binding Site of a Cross-Reactive <i>Plasmodium falciparum</i> PfEMP1 Monoclonal Antibody Inhibitory of ICAM-1 Binding. <i>Journal of Immunology</i> , 2015, 195, 3273-3283.	0.4	25
30	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Science</i> , 2014, 343, 1485-1489.	6.0	521
31	From (+)-epigallocatechin gallate to a simplified synthetic analogue as a cytoadherence inhibitor for <i>P. falciparum</i> . <i>RSC Advances</i> , 2014, 4, 4769-4781.	1.7	13
32	Structure of the large ribosomal subunit from human mitochondria. <i>Science</i> , 2014, 346, 718-722.	6.0	260
33	The crystal structure of fibroblast growth factor 18 (FGF18). <i>Protein and Cell</i> , 2014, 5, 343-347.	4.8	8
34	Cryo-EM structure of the <i>Plasmodium falciparum</i> 80S ribosome bound to the anti-protozoan drug emetine. <i>ELife</i> , 2014, 3, .	2.8	274
35	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Microscopy and Microanalysis</i> , 2014, 20, 1252-1253.	0.2	1
36	Cooperative Heparin-Mediated Oligomerization of Fibroblast Growth Factor-1 (FGF1) Precedes Recruitment of FGFR2 to Ternary Complexes. <i>Biophysical Journal</i> , 2013, 104, 1720-1730.	0.2	42

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37	Molecular Mechanism of SSR128129E, an Extracellularly Acting, Small-Molecule, Allosteric Inhibitor of FGF Receptor Signaling. <i>Cancer Cell</i> , 2013, 23, 489-501.	7.7	125
38	A Novel Domain Cassette Identifies <i>Plasmodium falciparum</i> PfEMP1 Proteins Binding ICAM-1 and Is a Target of Cross-Reactive, Adhesion-Inhibitory Antibodies. <i>Journal of Immunology</i> , 2013, 190, 240-249.	0.4	101
39	Molecular Architecture of a Complex between an Adhesion Protein from the Malaria Parasite and Intracellular Adhesion Molecule 1. <i>Journal of Biological Chemistry</i> , 2013, 288, 5992-6003.	1.6	37
40	Structure of the trypanosome haptoglobin-hemoglobin receptor and implications for nutrient uptake and innate immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1905-1910.	3.3	81
41	Carbohydrate binding molecules in malaria pathology. <i>Current Opinion in Structural Biology</i> , 2010, 20, 560-566.	2.6	17
42	Structural interactomics: informatics approaches to aid the interpretation of genetic variation and the development of novel therapeutics. <i>Molecular BioSystems</i> , 2009, 5, 1456.	2.9	8
43	Analysis of Cooperativity by Isothermal Titration Calorimetry. <i>International Journal of Molecular Sciences</i> , 2009, 10, 3457-3477.	1.8	122