

Neil Shaw

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8484819/publications.pdf>

Version: 2024-02-01

46
papers

2,281
citations

257357

24
h-index

233338

45
g-index

47
all docs

47
docs citations

47
times ranked

5098
citing authors

#	ARTICLE	IF	CITATIONS
1	Double lock of a potent human therapeutic monoclonal antibody against SARS-CoV-2. National Science Review, 2021, 8, nwaa297.	4.6	24
2	Structural basis for neutralization of SARS-CoV-2 and SARS-CoV by a potent therapeutic antibody. Science, 2020, 369, 1505-1509.	6.0	358
3	Crystal Structure of ATP-Bound Human ABCF1 Demonstrates a Unique Conformation of ABC Proteins. Structure, 2018, 26, 1259-1265.e3.	1.6	14
4	Expression, purification and crystallization of phosphoribosyl transferase from a mycobacteriophage. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 161-165.	0.4	1
5	Structural view of the helicase reveals that Zika virus uses a conserved mechanism for unwinding RNA. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 205-213.	0.4	7
6	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. Nature Communications, 2017, 8, 14.	5.8	117
7	Crystal structure of Rv1220c, a SAM-dependent O ⁶ -methyltransferase from Mycobacterium tuberculosis. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 315-320.	0.4	2
8	New insights into the structural basis of DNA recognition by HINa and HINb domains of IFI16. Journal of Molecular Cell Biology, 2016, 8, 51-61.	1.5	48
9	Structural views of quinone oxidoreductase from Mycobacterium tuberculosis reveal large conformational changes induced by the co-factor. FEBS Journal, 2015, 282, 2697-2707.	2.2	8
10	Studies on Inhibition of Proliferation of Enterovirus-71 by Compound YZ-LY-0. International Journal of Biological Sciences, 2015, 11, 1337-1347.	2.6	3
11	Structural View and Substrate Specificity of Papain-like Protease from Avian Infectious Bronchitis Virus. Journal of Biological Chemistry, 2015, 290, 7160-7168.	1.6	28
12	Structural basis and functional analysis of the SARS coronavirus nsp14-nsp10 complex. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9436-9441.	3.3	431
13	Molecular basis for the inhibition of β^2 -hydroxyacyl-ACP dehydratase HadAB complex from Mycobacterium tuberculosis by flavonoid inhibitors. Protein and Cell, 2015, 6, 504-517.	4.8	28
14	Mechanism of Dephosphorylation of Glucosyl-3-phosphoglycerate by a Histidine Phosphatase. Journal of Biological Chemistry, 2014, 289, 21242-21251.	1.6	9
15	Introductory Biology Students'™ Conceptual Models and Explanations of the Origin of Variation. CBE Life Sciences Education, 2014, 13, 529-539.	1.1	43
16	Crystal structure of the N-terminal methyltransferase-like domain of anamorsin. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1066-1071.	1.5	12
17	Role of the HIN Domain in Regulation of Innate Immune Responses. Molecular and Cellular Biology, 2014, 34, 2-15.	1.1	36
18	Mechanism of the Rpn13-induced activation of Uch37. Protein and Cell, 2014, 5, 616-630.	4.8	27

#	ARTICLE	IF	CITATIONS
19	Structural analysis of asparaginyl endopeptidase reveals the activation mechanism and a reversible intermediate maturation stage. <i>Cell Research</i> , 2014, 24, 344-358.	5.7	86
20	Homotypic dimerization of a maltose kinase for molecular scaffolding. <i>Scientific Reports</i> , 2014, 4, 6418.	1.6	7
21	Binding of bacterial secondary messenger molecule c di-GMP is a STING operation. <i>Protein and Cell</i> , 2013, 4, 117-129.	4.8	18
22	Structural basis for termination of AIM2-mediated signaling by p202. <i>Cell Research</i> , 2013, 23, 855-858.	5.7	38
23	Structure of the Leanyer orthobunyavirus nucleoprotein-RNA complex reveals unique architecture for RNA encapsidation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9054-9059.	3.3	59
24	Structure of Severe Fever with Thrombocytopenia Syndrome Virus Nucleocapsid Protein in Complex with Suramin Reveals Therapeutic Potential. <i>Journal of Virology</i> , 2013, 87, 6829-6839.	1.5	67
25	Studies of Human 2,4-Dienoyl CoA Reductase Shed New Light on Peroxisomal $\hat{2}$ -Oxidation of Unsaturated Fatty Acids. <i>Journal of Biological Chemistry</i> , 2012, 287, 28956-28965.	1.6	17
26	Structural View of a Non Pfam Singleton and Crystal Packing Analysis. <i>PLoS ONE</i> , 2012, 7, e31673.	1.1	2
27	Structural Analysis of the STING Adaptor Protein Reveals a Hydrophobic Dimer Interface and Mode of Cyclic di-GMP Binding. <i>Immunity</i> , 2012, 36, 1073-1086.	6.6	282
28	Structural insights into a human anti-IFN antibody exerting therapeutic potential for systemic lupus erythematosus. <i>Journal of Molecular Medicine</i> , 2012, 90, 837-846.	1.7	25
29	S-SAD phasing study of death receptor 6 and its solution conformation revealed by SAXS. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 521-530.	2.5	24
30	Conversion of α -D-ribose 5-phosphate to α -D-xylulose 5-phosphate: new insights from structural and biochemical studies on human RPE. <i>FASEB Journal</i> , 2011, 25, 497-504.	0.2	28
31	An efficient strategy for high throughput screening of recombinant integral membrane protein expression and stability. <i>Protein Expression and Purification</i> , 2011, 78, 6-13.	0.6	27
32	Crystal structure of a novel non-Pfam protein PF2046 solved using low resolution B-factor sharpening and multi-crystal averaging methods. <i>Protein and Cell</i> , 2010, 1, 453-458.	4.8	13
33	Structure-function analysis of human α -prostaglandin D synthase bound with fatty acid molecules. <i>FASEB Journal</i> , 2010, 24, 4668-4677.	0.2	1
34	Structure-function analysis of human β -prostaglandin D synthase bound with fatty acid molecules. <i>FASEB Journal</i> , 2010, 24, 4668-4677.	0.2	40
35	Structural Basis and Catalytic Mechanism for the Dual Functional Endo- $\hat{2}$ -N-Acetylglucosaminidase A. <i>PLoS ONE</i> , 2009, 4, e4658.	1.1	52
36	Structural insight into acute intermittent porphyria. <i>FASEB Journal</i> , 2009, 23, 396-404.	0.2	45

#	ARTICLE	IF	CITATIONS
37	Crystal structure of human esterase D: a potential genetic marker of retinoblastoma. <i>FASEB Journal</i> , 2009, 23, 1441-1446.	0.2	31
38	Structural Basis for the Inhibition of Human 5,10-Methenyltetrahydrofolate Synthetase by N10-Substituted Folate Analogues. <i>Cancer Research</i> , 2009, 69, 7294-7301.	0.4	16
39	Purification, crystallization and preliminary crystallographic analysis of the non-Pfam protein AF1514 from <i>Archeoglobus fulgidus</i> DSM 4304. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 91-93.	0.7	0
40	Crystal structure solution of a ParB-like nuclease at atomic resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 263-267.	1.5	7
41	Crystal structure of a novel non-Pfam protein AF1514 from <i>Archeoglobus fulgidus</i> DSM 4304 solved by SAD using a Cr K α source. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 2109-2113.	1.5	8
42	Crystal structure of an aerobic FMN-dependent azoreductase (AzoA) from <i>Enterococcus faecalis</i> . <i>Archives of Biochemistry and Biophysics</i> , 2007, 463, 68-77.	1.4	66
43	Structure of the hypothetical protein PF0899 from <i>Pyrococcus furiosus</i> at 1.85 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 549-552.	0.7	6
44	(NZ)CH...O Contacts assist crystallization of a ParB-like nuclease. <i>BMC Structural Biology</i> , 2007, 7, 46.	2.3	17
45	Characterization of a corrinoid protein involved in the C1 metabolism of strict anaerobic bacterium <i>Moorella thermoacetica</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 167-176.	1.5	28
46	The multifunctional human p100 protein 'hooks' methylated ligands. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 779-784.	3.6	72