

Neil Shaw

List of Publications by Year in descending order

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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	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
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	Structural Analysis of the STING Adaptor Protein Reveals a Hydrophobic Dimer Interface and Mode of Cyclic di-GMP Binding. Immunity, 2012, 36, 1073-1086.	6.6	282
4	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. Nature Communications, 2017, 8, 14.	5.8	117
5	Structural analysis of asparaginyl endopeptidase reveals the activation mechanism and a reversible intermediate maturation stage. Cell Research, 2014, 24, 344-358.	5.7	86
6	The multifunctional human p100 protein 'hooks' methylated ligands. Nature Structural and Molecular Biology, 2007, 14, 779-784.	3.6	72
7	Structure of Severe Fever with Thrombocytopenia Syndrome Virus Nucleocapsid Protein in Complex with Suramin Reveals Therapeutic Potential. Journal of Virology, 2013, 87, 6829-6839.	1.5	67
8	Crystal structure of an aerobic FMN-dependent azoreductase (AzoA) from Enterococcus faecalis. Archives of Biochemistry and Biophysics, 2007, 463, 68-77.	1.4	66
9	Structure of the Leanyer orthobunyavirus nucleoprotein-RNA complex reveals unique architecture for RNA encapsidation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9054-9059.	3.3	59
10	Structural Basis and Catalytic Mechanism for the Dual Functional Endo-Î²-N-Acetylglucosaminidase A. PLoS ONE, 2009, 4, e4658.	1.1	52
11	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
12	Structural insight into acute intermittent porphyria. FASEB Journal, 2009, 23, 396-404.	0.2	45
13	Introductory Biology Students's™ Conceptual Models and Explanations of the Origin of Variation. CBE Life Sciences Education, 2014, 13, 529-539.	1.1	43
14	Structure-function analysis of human I-prostaglandin D synthase bound with fatty acid molecules. FASEB Journal, 2010, 24, 4668-4677.	0.2	40
15	Structural basis for termination of AIM2-mediated signaling by p202. Cell Research, 2013, 23, 855-858.	5.7	38
16	Role of the HIN Domain in Regulation of Innate Immune Responses. Molecular and Cellular Biology, 2014, 34, 2-15.	1.1	36
17	Crystal structure of human esterase D: a potential genetic marker of retinoblastoma. FASEB Journal, 2009, 23, 1441-1446.	0.2	31
18	Characterization of a corrinoid protein involved in the C1 metabolism of strict anaerobic bacterium Moorella thermoacetica. Proteins: Structure, Function and Bioinformatics, 2007, 67, 167-176.	1.5	28

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19	Conversion of ribulose 5-phosphate to 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
20	Structural View and Substrate Specificity of Papain-like Protease from Avian Infectious Bronchitis Virus. <i>Journal of Biological Chemistry</i> , 2015, 290, 7160-7168.	1.6	28
21	Molecular basis for the inhibition of \hat{I}^2 -hydroxyacyl-ACP dehydratase HadAB complex from <i>Mycobacterium tuberculosis</i> by flavonoid inhibitors. <i>Protein and Cell</i> , 2015, 6, 504-517.	4.8	28
22	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
23	Mechanism of the Rpn13-induced activation of Uch37. <i>Protein and Cell</i> , 2014, 5, 616-630.	4.8	27
24	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
25	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
26	Double lock of a potent human therapeutic monoclonal antibody against SARS-CoV-2. <i>National Science Review</i> , 2021, 8, nwa297.	4.6	24
27	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
28	(NZ)CH...O Contacts assist crystallization of a ParB-like nuclease. <i>BMC Structural Biology</i> , 2007, 7, 46.	2.3	17
29	Studies of Human 2,4-Dienoyl CoA Reductase Shed New Light on Peroxisomal \hat{I}^2 -Oxidation of Unsaturated Fatty Acids. <i>Journal of Biological Chemistry</i> , 2012, 287, 28956-28965.	1.6	17
30	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
31	Crystal Structure of ATP-Bound Human ABCF1 Demonstrates a Unique Conformation of ABC Proteins. <i>Structure</i> , 2018, 26, 1259-1265.e3.	1.6	14
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	Crystal structure of the N-terminal methyltransferase-like domain of anamorsin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1066-1071.	1.5	12
34	Mechanism of Dephosphorylation of Glucosyl-3-phosphoglycerate by a Histidine Phosphatase. <i>Journal of Biological Chemistry</i> , 2014, 289, 21242-21251.	1.6	9
35	Crystal structure of a novel non-Pfam protein AF1514 from <i>Archeoglobus fulgidus</i> DSM 4304 solved by S-SAD using a Cr X-ray source. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 2109-2113.	1.5	8
36	Structural views of quinone oxidoreductase from <i>Mycobacterium tuberculosis</i> reveal large conformational changes induced by the co-factor. <i>FEBS Journal</i> , 2015, 282, 2697-2707.	2.2	8

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37	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
38	Homotypic dimerization of a maltose kinase for molecular scaffolding. <i>Scientific Reports</i> , 2014, 4, 6418.	1.6	7
39	Structural view of the helicase reveals that <i>Zika virus</i> uses a conserved mechanism for unwinding RNA. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 205-213.	0.4	7
40	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
41	Studies on Inhibition of Proliferation of Enterovirus-71 by Compound YZ-LY-0. <i>International Journal of Biological Sciences</i> , 2015, 11, 1337-1347.	2.6	3
42	Structural View of a Non Pfam Singleton and Crystal Packing Analysis. <i>PLoS ONE</i> , 2012, 7, e31673.	1.1	2
43	Crystal structure of Rv1220c, a SAM-dependent <i>O</i> -methyltransferase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 315-320.	0.4	2
44	Structure-function analysis of human prostaglandin D synthase bound with fatty acid molecules. <i>FASEB Journal</i> , 2010, 24, 4668-4677.	0.2	1
45	Expression, purification and crystallization of phosphoribosyl transferase from a mycobacteriophage. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 161-165.	0.4	1
46	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