

David R Cooper

List of Publications by Year in descending order

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39
papers

1,988
citations

394421

19
h-index

315739

38
g-index

42
all docs

42
docs citations

42
times ranked

3370
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimal structure determination from sub-optimal diffraction data. <i>Protein Science</i> , 2022, 31, 259-268.	7.6	6
2	Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2-related structural models. <i>Protein Science</i> , 2021, 30, 115-124.	7.6	15
3	Synchrotron radiation as a tool for macromolecular X-Ray Crystallography: A XXI century perspective. <i>Nuclear Instruments & Methods in Physics Research B</i> , 2021, 489, 30-40.	1.4	3
4	Rapid response to emerging biomedical challenges and threats. <i>IUCrJ</i> , 2021, 8, 395-407.	2.2	5
5	virusMED: an atlas of hotspots of viral proteins. <i>IUCrJ</i> , 2021, 8, 931-942.	2.2	5
6	State-of-the-Art Data Management: Improving the Reproducibility, Consistency, and Traceability of Structural Biology and in Vitro Biochemical Experiments. <i>Methods in Molecular Biology</i> , 2021, 2199, 209-236.	0.9	5
7	Structural and biochemical analysis of <i>Bacillus Anthracis</i> prephenate dehydrogenase reveals an unusual mode of inhibition by tyrosine via the ACT domain. <i>FEBS Journal</i> , 2020, 287, 2235-2255.	4.7	3
8	Albumin-Based Transport of Nonsteroidal Anti-Inflammatory Drugs in Mammalian Blood Plasma. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 6847-6862.	6.4	37
9	Structure-based design approach to rational site-directed mutagenesis of β -lactoglobulin. <i>Journal of Structural Biology</i> , 2020, 210, 107493.	2.8	12
10	Molecular determinants of vascular transport of dexamethasone in COVID-19 therapy. <i>IUCrJ</i> , 2020, 7, 1048-1058.	2.2	12
11	Pyrimidine biosynthesis in pathogens – Structures and analysis of dihydroorotases from <i>Yersinia pestis</i> and <i>Vibrio cholerae</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 136, 1176-1187.	7.5	17
12	The Integrated Resource for Reproducibility in Macromolecular Crystallography: Experiences of the first four years. <i>Structural Dynamics</i> , 2019, 6, 064301.	2.3	25
13	ACT domain of <i>Bacillus anthracis</i> prephenate dehydrogenase acts as tyrosine sensor and inhibits the enzyme via a mechanical switch. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, a341-a341.	0.1	0
14	Molstack – Interactive visualization tool for presentation, interpretation, and validation of macromolecules and electron density maps. <i>Protein Science</i> , 2018, 27, 86-94.	7.6	31
15	Differences in substrate specificity of <i>V. cholerae</i> FabH enzymes suggest new approaches for the development of novel antibiotics and biofuels. <i>FEBS Journal</i> , 2018, 285, 2900-2921.	4.7	3
16	Databases, Repositories, and Other Data Resources in Structural Biology. <i>Methods in Molecular Biology</i> , 2017, 1607, 643-665.	0.9	6
17	CheckMyMetal: a macromolecular metal-binding validation tool. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 223-233.	2.3	268
18	A public database of macromolecular diffraction experiments. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C627-C627.	0.1	1

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19	A public database of macromolecular diffraction experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1181-1193.	2.3	103
20	Validation of metal-binding sites in macromolecular structures with the CheckMyMetal web server. <i>Nature Protocols</i> , 2014, 9, 156-170.	12.0	254
21	A multi-faceted analysis of RutD reveals a novel family of $\hat{1}\pm/\hat{1}^2$ hydrolases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2359-2368.	2.6	7
22	Structure of a short-chain dehydrogenase/reductase from <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 632-637.	0.7	3
23	X-ray crystallography: assessment and validation of protein-small molecule complexes for drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2011, 6, 771-782.	5.0	53
24	The structure of DinB from <i>Geobacillus stearothermophilus</i> : a representative of a unique four-helix-bundle superfamily. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 219-224.	0.7	14
25	Structure of <i>Thermotoga maritima</i> TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn ²⁺ -binding FCD domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 356-365.	2.5	31
26	Structure and Function of <i>Bacillus subtilis</i> YphP, a Prokaryotic Disulfide Isomerase with a CXC Catalytic Motif. <i>Biochemistry</i> , 2009, 48, 8664-8671.	2.5	37
27	Protein crystallization by surface entropy reduction: optimization of the SER strategy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 636-645.	2.5	146
28	Structure of the <i>Bacillus subtilis</i> OhrB hydroperoxide-resistance protein in a fully oxidized state. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1269-1273.	2.5	4
29	The Structure of the Coiled-Coil Domain of Ndel1 and the Basis of Its Interaction with Lis1, the Causal Protein of Miller-Dieker Lissencephaly. <i>Structure</i> , 2007, 15, 1467-1481.	3.3	74
30	Toward rational protein crystallization: A Web server for the design of crystallizable protein variants. <i>Protein Science</i> , 2007, 16, 1569-1576.	7.6	247
31	The DC-module of doublecortin: Dynamics, domain boundaries, and functional implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 874-882.	2.6	15
32	The Structure of the N-Terminal Domain of the Product of the Lissencephaly Gene Lis1 and Its Functional Implications. <i>Structure</i> , 2004, 12, 987-998.	3.3	106
33	The Crystal Structure of the Reduced, Zn ²⁺ -Bound Form of the <i>B. subtilis</i> Hsp33 Chaperone and Its Implications for the Activation Mechanism. <i>Structure</i> , 2004, 12, 1901-1907.	3.3	77
34	The Structure and Ligand Binding Properties of the <i>B. subtilis</i> YkoF Gene Product, a Member of a Novel Family of Thiamin/HMP-binding Proteins. <i>Journal of Molecular Biology</i> , 2004, 343, 395-406.	4.2	43
35	PDZ Tandem of Human Syntenin. <i>Structure</i> , 2003, 11, 459-468.	3.3	90
36	Molecular Roots of Degenerate Specificity in Syntenin's PDZ2 Domain. <i>Structure</i> , 2003, 11, 845-853.	3.3	83

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37	Crystallization of butyrate kinase 2 from <i>Thermotoga maritima</i> mediated by vapor diffusion of acetic acid. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1100-1102.	2.5	5
38	The structure of the FERM domain of merlin, the neurofibromatosis type 2 gene product. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 381-391.	2.5	45
39	Urkinase: Structure of Acetate Kinase, a Member of the ASKHA Superfamily of Phosphotransferases. <i>Journal of Bacteriology</i> , 2001, 183, 680-686.	2.2	97