

# David R Cooper

## List of Publications by Year in descending order

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39  
papers

1,988  
citations

394286

19  
h-index

315616

38  
g-index

42  
all docs

42  
docs citations

42  
times ranked

3370  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>CheckMyMetal</i> : a macromolecular metal-binding validation tool. Acta Crystallographica Section D: Structural Biology, 2017, 73, 223-233.	1.1	268
2	Validation of metal-binding sites in macromolecular structures with the CheckMyMetal web server. Nature Protocols, 2014, 9, 156-170.	5.5	254
3	Toward rational protein crystallization: A Web server for the design of crystallizable protein variants. Protein Science, 2007, 16, 1569-1576.	3.1	247
4	Protein crystallization by surface entropy reduction: optimization of the SER strategy. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 636-645.	2.5	146
5	The Structure of the N-Terminal Domain of the Product of the Lissencephaly Gene Lis1 and Its Functional Implications. Structure, 2004, 12, 987-998.	1.6	106
6	A public database of macromolecular diffraction experiments. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1181-1193.	1.1	103
7	Urkinase: Structure of Acetate Kinase, a Member of the ASKHA Superfamily of Phosphotransferases. Journal of Bacteriology, 2001, 183, 680-686.	1.0	97
8	PDZ Tandem of Human Syntenin. Structure, 2003, 11, 459-468.	1.6	90
9	Molecular Roots of Degenerate Specificity in Syntenin's PDZ2 Domain. Structure, 2003, 11, 845-853.	1.6	83
10	The Crystal Structure of the Reduced, Zn <sup>2+</sup> -Bound Form of the B. subtilis Hsp33 Chaperone and Its Implications for the Activation Mechanism. Structure, 2004, 12, 1901-1907.	1.6	77
11	The Structure of the Coiled-Coil Domain of Ndel1 and the Basis of Its Interaction with Lis1, the Causal Protein of Miller-Dieker Lissencephaly. Structure, 2007, 15, 1467-1481.	1.6	74
12	X-ray crystallography: assessment and validation of protein-small molecule complexes for drug discovery. Expert Opinion on Drug Discovery, 2011, 6, 771-782.	2.5	53
13	The structure of the FERM domain of merlin, the neurofibromatosis type 2 gene product. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 381-391.	2.5	45
14	The Structure and Ligand Binding Properties of the B.subtilis YkoF Gene Product, a Member of a Novel Family of Thiamin/HMP-binding Proteins. Journal of Molecular Biology, 2004, 343, 395-406.	2.0	43
15	Structure and Function of Bacillus subtilis YphP, a Prokaryotic Disulfide Isomerase with a CXC Catalytic Motif. Biochemistry, 2009, 48, 8664-8671.	1.2	37
16	Albumin-Based Transport of Nonsteroidal Anti-Inflammatory Drugs in Mammalian Blood Plasma. Journal of Medicinal Chemistry, 2020, 63, 6847-6862.	2.9	37
17	Structure of <i>Thermotoga maritima</i> TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn <sup>2+</sup> -binding FCD domains. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 356-365.	2.5	31
18	Molstack: Interactive visualization tool for presentation, interpretation, and validation of macromolecules and electron density maps. Protein Science, 2018, 27, 86-94.	3.1	31

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19	The Integrated Resource for Reproducibility in Macromolecular Crystallography: Experiences of the first four years. <i>Structural Dynamics</i> , 2019, 6, 064301.	0.9	25
20	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.	3.6	17
21	The DC-module of doublecortin: Dynamics, domain boundaries, and functional implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 874-882.	1.5	15
22	Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2-related structural models. <i>Protein Science</i> , 2021, 30, 115-124.	3.1	15
23	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
24	Structure-based design approach to rational site-directed mutagenesis of $\beta$ -lactoglobulin. <i>Journal of Structural Biology</i> , 2020, 210, 107493.	1.3	12
25	Molecular determinants of vascular transport of dexamethasone in COVID-19 therapy. <i>IUCr</i> , 2020, 7, 1048-1058.	1.0	12
26	A multi-faceted analysis of RutD reveals a novel family of $\beta$ -hydrolases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2359-2368.	1.5	7
27	Databases, Repositories, and Other Data Resources in Structural Biology. <i>Methods in Molecular Biology</i> , 2017, 1607, 643-665.	0.4	6
28	Optimal structure determination from sub-optimal diffraction data. <i>Protein Science</i> , 2022, 31, 259-268.	3.1	6
29	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
30	Rapid response to emerging biomedical challenges and threats. <i>IUCr</i> , 2021, 8, 395-407.	1.0	5
31	virusMED: an atlas of hotspots of viral proteins. <i>IUCr</i> , 2021, 8, 931-942.	1.0	5
32	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.	0.4	5
33	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
34	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
35	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.	2.2	3
36	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.	2.2	3

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37	Synchrotron radiation as a tool for macromolecular X-Ray Crystallography: A XXI century perspective. Nuclear Instruments & Methods in Physics Research B, 2021, 489, 30-40.	0.6	3
38	A public database of macromolecular diffraction experiments. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C627-C627.	0.0	1
39	ACT domain of Bacillus anthracis prephenate dehydrogenase acts as tyrosine sensor and inhibits the enzyme via a mechanical switch. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a341-a341.	0.0	0