Kevin Cowtan

List of Publications by Year
in descending order

57 papers	66,743 citations	212478 28 h-index	175968 55 g-index
60 all docs	60 docs citations	60 times ranked	67837 citing authors

#	Article	IF	Citations
1	Coot: model-building tools for molecular graphics. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2126-2132.	2.5	26,736
2	Features and development of Coot. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 486-501.	2.5	22,799
3	Overview of theCCP4 suite and current developments. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 235-242.	2.5	11,098
4	TheBuccaneersoftware for automated model building. 1. Tracing protein chains. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1002-1011.	2.5	1,725
5	Developments in theCCP4 molecular-graphics project. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2288-2294.	2.5	516
6	Coverage bias in the HadCRUT4 temperature series and its impact on recent temperature trends. Quarterly Journal of the Royal Meteorological Society, 2014, 140, 1935-1944.	1.0	477
7	Recent developments in classical density modification. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 470-478.	2.5	407
8	CCP4i2: the new graphical user interface to theCCP4 program suite. Acta Crystallographica Section D: Structural Biology, 2018, 74, 68-84.	1.1	382
9	Privateer: software for the conformational validation of carbohydrate structures. Nature Structural and Molecular Biology, 2015, 22, 833-834.	3.6	301
10	Miscellaneous Algorithms for Density Modification. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 487-493.	2.5	260
11	Density modification for macromolecular phase improvement. Progress in Biophysics and Molecular Biology, 1999, 72, 245-270.	1.4	242
12	TheCCP4 molecular-graphics project. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1955-1957.	2.5	193
13	Fitting molecular fragments into electron density. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 83-89.	2.5	170
14	Robust comparison of climate models with observations using blended land air and ocean sea surface temperatures. Geophysical Research Letters, 2015, 42, 6526-6534.	1.5	139
15	[4] Combining constraints for electron-density modification. Methods in Enzymology, 1997, 277, 53-64.	0.4	109
16	Reconciled climate response estimates from climate models and the energy budget of Earth. Nature Climate Change, 2016, 6, 931-935.	8.1	107
17	Error estimation and bias correction in phase-improvement calculations. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1555-1567.	2.5	100
18	Assessing recent warming using instrumentally homogeneous sea surface temperature records. Science Advances, 2017, 3, e1601207.	4.7	98

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19	Completion of autobuilt protein models using a database of protein fragments. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 328-335.	2.5	78
20	Carbohydrate anomalies in the PDB. Nature Chemical Biology, 2015, 11, 303-303.	3.9	74
21	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	9.0	73
22	A Limited Role for Unforced Internal Variability in Twentieth-Century Warming. Journal of Climate, 2019, 32, 4893-4917.	1.2	68
23	General quadratic functions in real and reciprocal space and their application to likelihood phasing. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1612-1621.	2.5	66
24	Modified Phased Translation Functions and their Application to Molecular-Fragment Location. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 750-756.	2.5	65
25	From crystal to structure with CCP4. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 233-234.	2.5	57
26	Three-dimensional structures of two heavily N-glycosylatedAspergillussp. family GH3 Î²-<scp>D</scp>-glucosidases. Acta Crystallographica Section D: Structural Biology, 2016, 72, 254-265.	1.1	38
27	Global temperature definition affects achievement of long-term climate goals. Environmental Research Letters, 2018, 13, 054004.	2.2	36
28	Carbohydrate structure: the rocky road to automation. Current Opinion in Structural Biology, 2017, 44, 39-47.	2.6	31
29	Evaluating biases in sea surface temperature records using coastal weather stations. Quarterly Journal of the Royal Meteorological Society, 2018, 144, 670-681.	1.0	29
30	Current approaches for automated model building into cryo-EM maps using Buccaneer with CCP-EM. Acta Crystallographica Section D: Structural Biology, 2020, 76, 531-541.	1.1	29
31	Evaluating the impact of U.S. Historical Climatology Network homogenization using the U.S. Climate Reference Network. Geophysical Research Letters, 2016, 43, 1695-1701.	1.5	24
32	A fluctuation in surface temperature in historical context: reassessment and retrospective on the evidence. Environmental Research Letters, 2018, 13, 123008.	2.2	23
33	Fast Fourier feature recognition. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1435-1444.	2.5	22
34	Automated nucleic acid chain tracing in real time. IUCrJ, 2014, 1, 387-392.	1.0	19
35	The â€˜pauseâ€™ in global warming in historical context: (II). Comparing models to observations. Environmental Research Letters, 2018, 13, 123007.	2.2	17
36	Predicting protein model correctness in Coot using machine learning. Acta Crystallographica Section D: Structural Biology, 2020, 76, 713-723.	1.1	17

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37	Generic representation and evaluation of properties as a function of position in reciprocal space. Journal of Applied Crystallography, 2002, 35, 655-663.	1.9	16
38	Statistical analysis of coverage error in simple global temperature estimators. Dynamics and Statistics of the Climate System, 2018, 3, .	0.8	11
39	Comparison of automated crystallographic model-building pipelines. Acta Crystallographica Section D: Structural Biology, 2019, 75, 1119-1128.	1.1	11
40	Pacific variability reconciles observed and modelled global mean temperature increase since 1950. Climate Dynamics, 2021, 56, 613-634.	1.7	11
41	Shift-field refinement of macromolecular atomic models. Acta Crystallographica Section D: Structural Biology, 2020, 76, 1192-1200.	1.1	10
42	Likelihood weighting of partial structure factors using spline coefficients. Journal of Applied Crystallography, 2005, 38, 193-198.	1.9	7
43	Atomic model validation using the CCP-EM software suite. Acta Crystallographica Section D: Structural Biology, 2022, 78, 152-161.	1.1	7
44	Automating tasks in protein structure determination with the clipper python module. Protein Science, 2018, 27, 207-216.	3.1	6
45	Macromolecular refinement by model morphing using non-atomic parameterizations. Acta Crystallographica Section D: Structural Biology, 2018, 74, 125-131.	1.1	6
46	Reply to Comment on â€˜Quantifying the consensus on anthropogenic global warming in the scientific literatureâ€™. Environmental Research Letters, 2015, 10, 039002.	2.2	5
47	Eigensystem analysis of the refinement of a small metalloprotein. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 842-856.	2.5	4
48	Comment on "Cosmic-ray-driven reaction and greenhouse effect of halogenated molecules: Culprits for atmospheric ozone depletion and global climate change". International Journal of Modern Physics B, 2014, 28, 1482003.	1.0	4
49	IceBreaker: Software for high-resolution single-particle cryo-EM with non-uniform ice. Structure, 2022, 30, 522-531.e4.	1.6	4
50	An Overview of Some Developments in Crystallographic Computing Methods Worldwide. Crystallography Reviews, 2003, 9, 73-80.	0.4	3
51	On a minimal model for estimating climate sensitivity. Ecological Modelling, 2015, 297, 20-25.	1.2	3
52	Ligand Electron Density Shape Recognition Using 3D Zernike Descriptors. Lecture Notes in Computer Science, 2009, , 125-136.	1.0	3
53	Comment on â€œThe Impact of Recent Forcing and Ocean Heat Uptake Data on Estimates of Climate Sensitivityâ€• Journal of Climate, 2020, 33, 391-396.	1.2	2
54	Pairwise running of automated crystallographic model-building pipelines. Acta Crystallographica Section D: Structural Biology, 2020, 76, 814-823.	1.1	2

#	Article	IF	Citations
55	Predicting the performance of automated crystallographic model-building pipelines. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1591-1601.	1.1	2
56	Comment on â€œQuantitatively evaluating the effects of CO2 emission on temperature riseâ€• Quaternary International, 2014, 336, 176-179.	0.7	0
57	Structural barriers to scientific progress. Acta Crystallographica Section D: Structural Biology, 2020, 76, 908-911.	1.1	0