Martyn D Winn

List of Publications by Year
in descending order

32 papers	38,662 citations	331670 21 h-index	395702 33 g-index
36 all docs	36 docs citations	36 times ranked	40858 citing authors

#	Article	IF	Citations
1	Atomic model validation using the CCP-EM software suite. Acta Crystallographica Section D: Structural Biology, 2022, 78, 152-161.	2.3	7
2	Small molecules enhance the potency of natural antimicrobial peptides. Biophysical Journal, 2022, 121, 491-501.	0.5	2
3	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	19.0	73
4	Redeployment of automated MrBUMP search-model identification for map fitting in cryo-EM. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1378-1385.	2.3	3
5	Comparing Cryo-EM Reconstructions and Validating Atomic Model Fit Using Difference Maps. Journal of Chemical Information and Modeling, 2020, 60, 2552-2560.	5.4	29
6	Modulation of Antimicrobial Peptide Potency in Stressed Lipid Bilayers. Physical Review Letters, 2019, 122, 208103.	7.8	13
7	West-Life: A Virtual Research Environment for structural biology. Journal of Structural Biology: X, 2019, 1, 100006.	1.3	2
8	CCP4i2: the new graphical user interface to theCCP4 program suite. Acta Crystallographica Section D: Structural Biology, 2018, 74, 68-84.	2.3	382
9	Tuneable poration: host defense peptides as sequence probes for antimicrobial mechanisms. Scientific Reports, 2018, 8, 14926.	3.3	24
10	Distributed computing for macromolecular crystallography. Acta Crystallographica Section D: Structural Biology, 2018, 74, 143-151.	2.3	54
11	Ensembles generated from crystal structures of single distant homologues solve challenging molecular-replacement cases inAMPLE. Acta Crystallographica Section D: Structural Biology, 2018, 74, 183-193.	2.3	16
12	Recent developments inMrBUMP: better search-model preparation, graphical interaction with search models, and solution improvement and assessment. Acta Crystallographica Section D: Structural Biology, 2018, 74, 167-182.	2.3	35
13	Improved metrics for comparing structures of macromolecular assemblies determined by 3D electron-microscopy. Journal of Structural Biology, 2017, 199, 12-26.	2.8	56
14	Recent developments in theCCP-EMsoftware suite. Acta Crystallographica Section D: Structural Biology, 2017, 73, 469-477.	2.3	280
15	Refinement of atomic models in high resolution EM reconstructions using Flex-EM and local assessment. Methods, 2016, 100, 42-49.	3.8	101
16	Residue contacts predicted by evolutionary covariance extend the application ofab initiomolecular replacement to larger and more challenging protein folds. IUCrJ, 2016, 3, 259-270.	2.2	17
17	Collaborative Computational Project for Electron cryo-Microscopy. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 123-126.	2.5	84
18	Exploring the speed and performance of molecular replacement withAMPLEusingQUARK ab initioprotein models. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 338-343.	2.5	25

#	Article	IF	Citations
19	MRC2014: Extensions to the MRC format header for electron cryo-microscopy and tomography. Journal of Structural Biology, 2015, 192, 146-150.	2.8	59
20	Routine phasing of coiled-coil protein crystal structures withAMPLE. IUCrJ, 2015, 2, 198-206.	2.2	24
21	Application of theAMPLEcluster-and-truncate approach to NMR structures for molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2194-2201.	2.5	13
22	Data management challenges in three-dimensional EM. Nature Structural and Molecular Biology, 2012, 19, 1203-1207.	8.2	49
23	AMPLE: a cluster-and-truncate approach to solve the crystal structures of small proteins using rapidly computedab initiomodels. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1622-1631.	2.5	109
24	Overview of theCCP4 suite and current developments. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 235-242.	2.5	11,098
25	REFMAC5 for the refinement of macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 355-367.	2.5	7,247
26	Evaluating the solution fromMrBUMPandBALBES. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 313-323.	2.5	23
27	The CCP4 software suite - current status and future developments. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s127-s127.	0.3	2
28	MrBUMP: an automated pipeline for molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 119-124.	2.5	148
29	Molecular replacement usingab initiopolyalanine models generated withROSETTA. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1288-1291.	2.5	30
30	Phasercrystallographic software. Journal of Applied Crystallography, 2007, 40, 658-674.	4.5	17,782
31	Automated search-model discovery and preparation for structure solution by molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 447-457.	2.5	144
32	Macromolecular TLS Refinement in REFMAC at Moderate Resolutions. Methods in Enzymology, 2003, 374, 300-321.	1.0	725