

# Martyn D Winn

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

38,662  
citations

331538

21  
h-index

395590

33  
g-index

36  
all docs

36  
docs citations

36  
times ranked

40858  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Phaser</i> crystallographic software. <i>Journal of Applied Crystallography</i> , 2007, 40, 658-674.	1.9	17,782
2	Overview of the <i>CCP4</i> suite and current developments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 235-242.	2.5	11,098
3	<i>REFMAC5</i> for the refinement of macromolecular crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 355-367.	2.5	7,247
4	Macromolecular TLS Refinement in <i>REFMAC</i> at Moderate Resolutions. <i>Methods in Enzymology</i> , 2003, 374, 300-321.	0.4	725
5	<i>CCP4</i> <i>i2</i> : the new graphical user interface to the <i>CCP4</i> program suite. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 68-84.	1.1	382
6	Recent developments in the <i>CCP-EM</i> software suite. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 469-477.	1.1	280
7	<i>MrBUMP</i> : an automated pipeline for molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 119-124.	2.5	148
8	Automated search-model discovery and preparation for structure solution by molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 447-457.	2.5	144
9	<i>AMPLE</i> : a cluster-and-truncate approach to solve the crystal structures of small proteins using rapidly computed <i>ab initio</i> models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1622-1631.	2.5	109
10	Refinement of atomic models in high resolution EM reconstructions using <i>Flex-EM</i> and local assessment. <i>Methods</i> , 2016, 100, 42-49.	1.9	101
11	Collaborative Computational Project for Electron cryo-Microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 123-126.	2.5	84
12	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	9.0	73
13	MRC2014: Extensions to the MRC format header for electron cryo-microscopy and tomography. <i>Journal of Structural Biology</i> , 2015, 192, 146-150.	1.3	59
14	Improved metrics for comparing structures of macromolecular assemblies determined by 3D electron-microscopy. <i>Journal of Structural Biology</i> , 2017, 199, 12-26.	1.3	56
15	Distributed computing for macromolecular crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 143-151.	1.1	54
16	Data management challenges in three-dimensional EM. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1203-1207.	3.6	49
17	Recent developments in <i>MrBUMP</i> : better search-model preparation, graphical interaction with search models, and solution improvement and assessment. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 167-182.	1.1	35
18	Molecular replacement using <i>ab initio</i> polyalanine models generated with <i>ROSETTA</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1288-1291.	2.5	30

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19	Comparing Cryo-EM Reconstructions and Validating Atomic Model Fit Using Difference Maps. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2552-2560.	2.5	29
20	Exploring the speed and performance of molecular replacement with <i>AMPLE</i> using <i>QUARK</i> ab initio protein models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 338-343.	2.5	25
21	Tuneable poration: host defense peptides as sequence probes for antimicrobial mechanisms. <i>Scientific Reports</i> , 2018, 8, 14926.	1.6	24
22	Routine phasing of coiled-coil protein crystal structures with <i>AMPLE</i> . <i>IUCr</i> , 2015, 2, 198-206.	1.0	24
23	Evaluating the solution from <i>MrBUMP</i> and <i>BALBES</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 313-323.	2.5	23
24	Residue contacts predicted by evolutionary covariance extend the application of ab initio molecular replacement to larger and more challenging protein folds. <i>IUCr</i> , 2016, 3, 259-270.	1.0	17
25	Ensembles generated from crystal structures of single distant homologues solve challenging molecular-replacement cases in <i>AMPLE</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 183-193.	1.1	16
26	Application of the <i>AMPLE</i> cluster-and-truncate approach to NMR structures for molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2194-2201.	2.5	13
27	Modulation of Antimicrobial Peptide Potency in Stressed Lipid Bilayers. <i>Physical Review Letters</i> , 2019, 122, 208103.	2.9	13
28	Atomic model validation using the <i>CCP-EM</i> software suite. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 152-161.	1.1	7
29	Redeployment of automated <i>MrBUMP</i> search-model identification for map fitting in cryo-EM. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1378-1385.	1.1	3
30	West-Life: A Virtual Research Environment for structural biology. <i>Journal of Structural Biology: X</i> , 2019, 1, 100006.	0.7	2
31	The CCP4 software suite - current status and future developments. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s127-s127.	0.3	2
32	Small molecules enhance the potency of natural antimicrobial peptides. <i>Biophysical Journal</i> , 2022, 121, 491-501.	0.2	2