

Matthew W. Bowler

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/7403391/matthew-w-bowler-publications-by-year.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

75
papers

2,542
citations

28
h-index

49
g-index

90
ext. papers

2,998
ext. citations

7.4
avg, IF

4.78
L-index

#	Paper	IF	Citations
75	Structural insights into the substrate-bound condensation domains of non-ribosomal peptide synthetase AmbB.. <i>Scientific Reports</i> , 2022 , 12, 5353	4.9	
74	Finding order in chaos - nanocrystals in amorphous protein gels. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021 , 77, 386-387	1.1	
73	Cross-Reactive SARS-CoV-2 Neutralizing Antibodies From Deep Mining of Early Patient Responses. <i>Frontiers in Immunology</i> , 2021 , 12, 678570	8.4	9
72	A plant-like mechanism coupling m6A reading to polyadenylation safeguards transcriptome integrity and developmental gene partitioning in. <i>ELife</i> , 2021 , 10,	8.9	3
71	Structural and functional comparison of fumarylacetoacetate domain containing protein 1 in human and mouse. <i>Bioscience Reports</i> , 2020 , 40,	4.1	1
70	Fully Autonomous Characterization and Data Collection from Crystals of Biological Macromolecules. <i>Journal of Visualized Experiments</i> , 2019 ,	1.6	1
69	A molecular mechanism for transthyretin amyloidogenesis. <i>Nature Communications</i> , 2019 , 10, 925	17.4	54
68	MXCuBE2: the dawn of MXCuBE Collaboration. <i>Journal of Synchrotron Radiation</i> , 2019 , 26, 393-405	2.4	14
67	A comparative anatomy of protein crystals: lessons from the automatic processing of 56 000 samples. <i>IUCrJ</i> , 2019 , 6, 822-831	4.7	5
66	Controlled dehydration, structural flexibility and gadolinium MRI contrast compound binding in the human plasma glycoprotein afamin. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019 , 75, 1071-1083	5.5	2
65	van der Waals Contact between Nucleophile and Transferring Phosphorus Is Insufficient To Achieve Enzyme Transition-State Architecture. <i>ACS Catalysis</i> , 2018 , 8, 8140-8153	13.1	10
64	Structural basis for reactivating the mutant TERT promoter by cooperative binding of p52 and ETS1. <i>Nature Communications</i> , 2018 , 9, 3183	17.4	28
63	A new MR-SAD algorithm for the automatic building of protein models from low-resolution X-ray data and a poor starting model. <i>IUCrJ</i> , 2018 , 5, 166-171	4.7	12
62	Structural basis for Scc3-dependent cohesin recruitment to chromatin. <i>ELife</i> , 2018 , 7,	8.9	43
61	Structural basis for the bi-functionality of human oxaloacetate decarboxylase FAHD1. <i>Biochemical Journal</i> , 2018 , 475, 3561-3576	3.8	8
60	Multi-position data collection and dynamic beam sizing: recent improvements to the automatic data-collection algorithms on MASSIF-1. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 433-440	5.5	22
59	Assessing the Influence of Mutation on GTPase Transition States by Using X-ray Crystallography, F NMR, and DFT Approaches. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 9732-9735	16.4	6

58	Assessing the Influence of Mutation on GTPase Transition States by Using X-ray Crystallography, 19F NMR, and DFT Approaches. <i>Angewandte Chemie</i> , 2017 , 129, 9864-9867	3.6	1
57	FlexED8: the first member of a fast and flexible sample-changer family for macromolecular crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 841-851	5.5	7
56	Observing enzyme ternary transition state analogue complexes by F NMR spectroscopy. <i>Chemical Science</i> , 2017 , 8, 8427-8434	9.4	1
55	Raoult's law revisited: accurately predicting equilibrium relative humidity points for humidity control experiments. <i>Journal of Applied Crystallography</i> , 2017 , 50, 631-638	3.8	6
54	Cyanine Conformational Restraint in the Far-Red Range. <i>Journal of the American Chemical Society</i> , 2017 , 139, 12406-12409	16.4	75
53	Computational design of amyloid self-assembling peptides bearing aromatic residues and the cell adhesive motif Arg-Gly-Asp. <i>Molecular Systems Design and Engineering</i> , 2017 , 2, 321-335	4.6	12
52	Structural Evidence for a Role of the Multi-functional Human Glycoprotein Afamin in Wnt Transport. <i>Structure</i> , 2017 , 25, 1907-1915.e5	5.2	21
51	Self-Assembled Amyloid Peptides with Arg-Gly-Asp (RGD) Motifs As Scaffolds for Tissue Engineering. <i>ACS Biomaterials Science and Engineering</i> , 2017 , 3, 1404-1416	5.5	28
50	Structural basis for blocking PD-1-mediated immune suppression by therapeutic antibody pembrolizumab. <i>Cell Research</i> , 2017 , 27, 147-150	24.7	71
49	Structural Basis for the Subversion of MAP Kinase Signaling by an Intrinsically Disordered Parasite Secreted Agonist. <i>Structure</i> , 2017 , 25, 16-26	5.2	26
48	Towards a compact and precise sample holder for macromolecular crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 829-840	5.5	6
47	Structural basis for specific recognition of pre-snRNA by Gemin5. <i>Cell Research</i> , 2016 , 26, 1353-1356	24.7	12
46	Structural basis of suppression of host translation termination by Moloney Murine Leukemia Virus. <i>Nature Communications</i> , 2016 , 7, 12070	17.4	20
45	Fully automatic macromolecular crystallography: the impact of MASSIF-1 on the optimum acquisition and quality of data. <i>Crystallography Reviews</i> , 2016 , 22, 233-249	1.3	28
44	RoboDiff: combining a sample changer and goniometer for highly automated macromolecular crystallography experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 966-75	5.5	25
43	ISPyB for BioSAXS, the gateway to user autonomy in solution scattering experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 76-85		45
42	The status of the macromolecular crystallography beamlines at the European Synchrotron Radiation Facility. <i>European Physical Journal Plus</i> , 2015 , 130, 1	3.1	25
41	MASSIF-1: a beamline dedicated to the fully automatic characterization and data collection from crystals of biological macromolecules. <i>Journal of Synchrotron Radiation</i> , 2015 , 22, 1540-7	2.4	90

40	Fully automatic characterization and data collection from crystals of biological macromolecules. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 1757-67		72
39	Purification and characterization of DR_2577 (SlpA) a major S-layer protein from <i>Deinococcus radiodurans</i> . <i>Frontiers in Microbiology</i> , 2015 , 6, 414	5.7	14
38	The sweet quartet: Binding of fucose to the norovirus capsid. <i>Virology</i> , 2015 , 483, 203-8	3.6	39
37	Automation and Experience of Controlled Crystal Dehydration: Results from the European Synchrotron HC1 Collaboration. <i>Crystal Growth and Design</i> , 2015 , 15, 1043-1054	3.5	27
36	New features of the cell wall of the radio-resistant bacterium <i>Deinococcus radiodurans</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 1978-84	3.8	32
35	Fluorophosphonates reveal how a phosphomutase conserves transition state conformation over hexose recognition in its two-step reaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 12384-9	11.5	38
34	Measurement of the intrinsic variability within protein crystals: implications for sample-evaluation and data-collection strategies. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 127-32	1.1	10
33	Lsm2 and Lsm3 bridge the interaction of the Lsm1-7 complex with Pat1 for decapping activation. <i>Cell Research</i> , 2014 , 24, 233-46	24.7	35
32	Conformational dynamics in phosphoglycerate kinase, an open and shut case?. <i>FEBS Letters</i> , 2013 , 587, 1878-83	3.8	11
31	Automatic processing of macromolecular crystallography X-ray diffraction data at the ESRF. <i>Journal of Applied Crystallography</i> , 2013 , 46, 804-810	3.8	77
30	QsIA disrupts LasR dimerization in antiactivation of bacterial quorum sensing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 20765-70	11.5	30
29	Recent progress in robot-based systems for crystallography and their contribution to drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2013 , 8, 835-47	6.2	18
28	The Upgrade Programme for the Structural Biology beamlines at the European Synchrotron Radiation Facility [High throughput sample evaluation and automation. <i>Journal of Physics: Conference Series</i> , 2013 , 425, 012001	0.3	25
27	Le rayonnement synchrotron : comprendre la relation structure-fonction des macromolécules biologiques 2013 , 48-53	0.1	1
26	The use of workflows in the design and implementation of complex experiments in macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 975-84		32
25	Charge-Balanced Metal Fluoride Complexes for Protein Kinase A with Adenosine Diphosphate and Substrate Peptide SP20. <i>Angewandte Chemie</i> , 2012 , 124, 12408-12411	3.6	6
24	Charge-balanced metal fluoride complexes for protein kinase A with adenosine diphosphate and substrate peptide SP20. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 12242-5	16.4	23
23	Reflections on biocatalysis involving phosphorus. <i>Biochemistry (Moscow)</i> , 2012 , 77, 1083-96	2.9	7

22	Structural basis of the PNR2-mediated link between mrna surveillance and decapping. <i>Structure</i> , 2012 , 20, 2025-37	5.2	52
21	Measurement of the equilibrium relative humidity for common precipitant concentrations: facilitating controlled dehydration experiments. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 111-4		27
20	The Ighmbp2 helicase structure reveals the molecular basis for disease-causing mutations in DMSA1. <i>Nucleic Acids Research</i> , 2012 , 40, 11009-22	20.1	30
19	Near attack conformers dominate β -phosphoglucomutase complexes where geometry and charge distribution reflect those of substrate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 6910-5	11.5	41
18	Crystal structures of Lsm3, Lsm4 and Lsm5/6/7 from <i>Schizosaccharomyces pombe</i> . <i>PLoS ONE</i> , 2012 , 7, e36768	3.7	12
17	Inducing phase changes in crystals of macromolecules: status and perspectives for controlled crystal dehydration. <i>Journal of Structural Biology</i> , 2011 , 175, 236-43	3.4	49
16	Interaction of human 3-phosphoglycerate kinase with its two substrates: is substrate antagonism a kinetic advantage?. <i>Journal of Molecular Biology</i> , 2011 , 409, 742-57	6.5	11
15	Direct cryocooling of naked crystals: are cryoprotection agents always necessary?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 902-6		42
14	A spring-loaded release mechanism regulates domain movement and catalysis in phosphoglycerate kinase. <i>Journal of Biological Chemistry</i> , 2011 , 286, 14040-8	5.4	46
13	Atomic details of near-transition state conformers for enzyme phosphoryl transfer revealed by MgF-3 rather than by phosphoranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 4555-60	11.5	72
12	Transition state analogue structures of human phosphoglycerate kinase establish the importance of charge balance in catalysis. <i>Journal of the American Chemical Society</i> , 2010 , 132, 6507-16	16.4	70
11	Why did Nature select phosphate for its dominant roles in biology?. <i>New Journal of Chemistry</i> , 2010 , 34, 784	3.6	114
10	Diffraction cartography: applying microbeams to macromolecular crystallography sample evaluation and data collection. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 855-64		88
9	MxCuBE: a synchrotron beamline control environment customized for macromolecular crystallography experiments. <i>Journal of Synchrotron Radiation</i> , 2010 , 17, 700-7	2.4	148
8	Improving diffraction by humidity control: a novel device compatible with X-ray beamlines. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009 , 65, 1237-46		91
7	MgF(3)(-) and alpha-galactose 1-phosphate in the active site of beta-phosphoglucomutase form a transition state analogue of phosphoryl transfer. <i>Journal of the American Chemical Society</i> , 2009 , 131, 16334-5	16.4	28
6	Ground state structure of F1-ATPase from bovine heart mitochondria at 1.9 Å resolution. <i>Journal of Biological Chemistry</i> , 2007 , 282, 14238-42	5.4	158
5	How azide inhibits ATP hydrolysis by the F-ATPases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 8646-9	11.5	181

4	Reproducible improvements in order and diffraction limit of crystals of bovine mitochondrial F(1)-ATPase by controlled dehydration. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 991-5		24
3	Increasing the diffraction limit and internal order of a membrane protein crystal by dehydration. <i>Journal of Structural Biology</i> , 2003 , 141, 97-102	3-4	24
2	Controlled dehydration, structural flexibility, and Gadolinium MRI contrast compound binding in human plasma glycoprotein afamin		1
1	Deep mining of early antibody response in COVID-19 patients yields potent neutralisers and reveals high level of convergence		3