

Matthew W. Bowler

List of Publications by Year in descending order

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77
papers

3,351
citations

136885

32
h-index

161767

54
g-index

90
all docs

90
docs citations

90
times ranked

4639
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural insights into the substrate-bound condensation domains of non-ribosomal peptide synthetase AmbB. <i>Scientific Reports</i> , 2022, 12, 5353.	1.6	3
2	Cross-Reactive SARS-CoV-2 Neutralizing Antibodies From Deep Mining of Early Patient Responses. <i>Frontiers in Immunology</i> , 2021, 12, 678570.	2.2	16
3	A plant-like mechanism coupling m6A reading to polyadenylation safeguards transcriptome integrity and developmental gene partitioning in <i>Toxoplasma</i> . <i>ELife</i> , 2021, 10, .	2.8	19
4	Finding order in chaos “ nanocrystals in amorphous protein gels. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 386-387.	0.4	0
5	Structural and functional comparison of fumarylacetoacetate domain containing protein 1 in human and mouse. <i>Bioscience Reports</i> , 2020, 40, .	1.1	2
6	<i>MXCuBE2</i>: the dawn of <i>MXCuBE</i> Collaboration. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 393-405.	1.0	30
7	CrystalDirect-To-Beam: Opening the shortest path from crystal to data. <i>AIP Conference Proceedings</i> , 2019, , .	0.3	1
8	Fully Autonomous Characterization and Data Collection from Crystals of Biological Macromolecules. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	2
9	A molecular mechanism for transthyretin amyloidogenesis. <i>Nature Communications</i> , 2019, 10, 925.	5.8	92
10	A comparative anatomy of protein crystals: lessons from the automatic processing of 56â€¦000 samples. <i>IUCr</i> , 2019, 6, 822-831.	1.0	7
11	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.	1.1	2
12	Structural basis for the bi-functionality of human oxaloacetate decarboxylase FAHD1. <i>Biochemical Journal</i> , 2018, 475, 3561-3576.	1.7	13
13	A novel amyloid designable scaffold and potential inhibitor inspired by <scp>GAIIG</scp> of amyloid beta and the <scp>HIV</scp>â€œ V3 loop. <i>FEBS Letters</i> , 2018, 592, 1777-1788.	1.3	18
14	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.	1.1	34
15	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.	5.5	12
16	Structural basis for reactivating the mutant TERT promoter by cooperative binding of p52 and ETS1. <i>Nature Communications</i> , 2018, 9, 3183.	5.8	52
17	A new MR-SAD algorithm for the automatic building of protein models from low-resolution X-ray data and a poor starting model. <i>IUCr</i> , 2018, 5, 166-171.	1.0	33
18	Structural basis for Scc3-dependent cohesin recruitment to chromatin. <i>ELife</i> , 2018, 7, .	2.8	69

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19	Assessing the Influence of Mutation on GTPase Transition States by Using X-ray Crystallography, ¹⁹ F-NMR, and DFT Approaches. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 9732-9735.	7.2	9
20	Assessing the Influence of Mutation on GTPase Transition States by Using X-ray Crystallography, ¹⁹ F-NMR, and DFT Approaches. <i>Angewandte Chemie</i> , 2017, 129, 9864-9867.	1.6	1
21	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.	1.1	13
22	Observing enzyme ternary transition state analogue complexes by ¹⁹ F NMR spectroscopy. <i>Chemical Science</i> , 2017, 8, 8427-8434.	3.7	2
23	Cyanine Conformational Restraint in the Far-Red Range. <i>Journal of the American Chemical Society</i> , 2017, 139, 12406-12409.	6.6	125
24	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.	1.7	14
25	Structural Evidence for a Role of the Multi-functional Human Glycoprotein Afamin in Wnt Transport. <i>Structure</i> , 2017, 25, 1907-1915.e5.	1.6	29
26	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.	2.6	38
27	Structural basis for blocking PD-1-mediated immune suppression by therapeutic antibody pembrolizumab. <i>Cell Research</i> , 2017, 27, 147-150.	5.7	111
28	Structural Basis for the Subversion of MAP Kinase Signaling by an Intrinsically Disordered Parasite Secreted Agonist. <i>Structure</i> , 2017, 25, 16-26.	1.6	41
29	Raoult's law revisited: accurately predicting equilibrium relative humidity points for humidity control experiments. <i>Journal of Applied Crystallography</i> , 2017, 50, 631-638.	1.9	8
30	Towards a compact and precise sample holder for macromolecular crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 829-840.	1.1	8
31	Automated data collection based on RoboDiff at the ESRF beamline MASSIF-1. <i>AIP Conference Proceedings</i> , 2016, , .	0.3	0
32	Structural basis for specific recognition of pre-snRNA by Gemin5. <i>Cell Research</i> , 2016, 26, 1353-1356.	5.7	23
33	Structural basis of suppression of host translation termination by Moloney Murine Leukemia Virus. <i>Nature Communications</i> , 2016, 7, 12070.	5.8	27
34	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.	0.4	37
35	RoboDiff: combining a sample changer and goniometer for highly automated macromolecular crystallography experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 966-975.	1.1	35
36	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, 1540-1547.	1.0	133

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37	Fully automatic characterization and data collection from crystals of biological macromolecules. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1757-1767.	2.5	102
38	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.	1.5	20
39	The sweet quartet: Binding of fucose to the norovirus capsid. <i>Virology</i> , 2015, 483, 203-208.	1.1	46
40	Automation and Experience of Controlled Crystal Dehydration: Results from the European Synchrotron HC1 Collaboration. <i>Crystal Growth and Design</i> , 2015, 15, 1043-1054.	1.4	33
41	ISPyB for BioSAXS, the gateway to user autonomy in solution scattering experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 76-85.	2.5	56
42	The status of the macromolecular crystallography beamlines at the European Synchrotron Radiation Facility. <i>European Physical Journal Plus</i> , 2015, 130, 1.	1.2	31
43	Lsm2 and Lsm3 bridge the interaction of the Lsm1-7 complex with Pat1 for decapping activation. <i>Cell Research</i> , 2014, 24, 233-246.	5.7	43
44	New features of the cell wall of the radio-resistant bacterium <i>Deinococcus radiodurans</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 1978-1984.	1.4	60
45	$\hat{\Gamma}$ -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, 12384-12389.	3.3	42
46	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, 127-132.	0.4	12
47	Conformational dynamics in phosphoglycerate kinase, an open and shut case?. <i>FEBS Letters</i> , 2013, 587, 1878-1883.	1.3	18
48	Automatic processing of macromolecular crystallography X-ray diffraction data at the ESRF. <i>Journal of Applied Crystallography</i> , 2013, 46, 804-810.	1.9	107
49	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, 20765-20770.	3.3	44
50	Recent progress in robot-based systems for crystallography and their contribution to drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2013, 8, 835-847.	2.5	19
51	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	35
52	Le rayonnement synchrotron : comprendre la relation structure-fonction des macromolécules biologiques. , 2013, , 48-53.	0.1	1
53	The Ighmbp2 helicase structure reveals the molecular basis for disease-causing mutations in DMSA1. <i>Nucleic Acids Research</i> , 2012, 40, 11009-11022.	6.5	46
54	Near attack conformers dominate $\hat{\Gamma}$ -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, 6910-6915.	3.3	47

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55	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, 975-984.	2.5	37
56	Charge-Balanced Metal Fluoride Complexes for Protein Kinase...A with Adenosine Diphosphate and Substrate Peptide SP20. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 12242-12245.	7.2	26
57	Reflections on biocatalysis involving phosphorus. <i>Biochemistry (Moscow)</i> , 2012, 77, 1083-1096.	0.7	7
58	Structural Basis of the PNRC2-Mediated Link between mRNA Surveillance and Decapping. <i>Structure</i> , 2012, 20, 2025-2037.	1.6	59
59	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, 111-114.	0.7	29
60	Crystal Structures of Lsm3, Lsm4 and Lsm5/6/7 from <i>Schizosaccharomyces pombe</i> . <i>PLoS ONE</i> , 2012, 7, e36768.	1.1	16
61	Inducing phase changes in crystals of macromolecules: Status and perspectives for controlled crystal dehydration. <i>Journal of Structural Biology</i> , 2011, 175, 236-243.	1.3	51
62	Interaction of Human 3-Phosphoglycerate Kinase with Its Two Substrates: Is Substrate Antagonism a Kinetic Advantage?. <i>Journal of Molecular Biology</i> , 2011, 409, 742-757.	2.0	14
63	Direct cryocooling of naked crystals: are cryoprotection agents always necessary?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 902-906.	2.5	46
64	A Spring-loaded Release Mechanism Regulates Domain Movement and Catalysis in Phosphoglycerate Kinase. <i>Journal of Biological Chemistry</i> , 2011, 286, 14040-14048.	1.6	53
65	Diffraction cartography: applying microbeams to macromolecular crystallography sample evaluation and data collection. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 855-864.	2.5	93
66	<i>MxCuBE</i> : a synchrotron beamline control environment customized for macromolecular crystallography experiments. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 700-707.	1.0	193
67	Atomic details of near-transition state conformers for enzyme phosphoryl transfer revealed by MgF ₃ - rather than by phosphoranates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4555-4560.	3.3	74
68	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, 6507-6516.	6.6	79
69	Why did Nature select phosphate for its dominant roles in biology?. <i>New Journal of Chemistry</i> , 2010, 34, 784.	1.4	146
70	MX automation: towards a new sample holder standard for frozen crystals. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s9-s9.	0.3	1
71	Diffraction cartography: multi-crystal and multi-position data collection. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s9-s10.	0.3	1
72	Improving diffraction by humidity control: a novel device compatible with X-ray beamlines. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1237-1246.	2.5	109

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73	MgF ₃ ⁺ and β -Galactose 1-Phosphate in the Active Site of β -Phosphoglucomutase Form a Transition State Analogue of Phosphoryl Transfer. <i>Journal of the American Chemical Society</i> , 2009, 131, 16334-16335.	6.6	29
74	Ground State Structure of F1-ATPase from Bovine Heart Mitochondria at 1.9 Å Resolution. <i>Journal of Biological Chemistry</i> , 2007, 282, 14238-14242.	1.6	176
75	Reproducible improvements in order and diffraction limit of crystals of bovine mitochondrial F1-ATPase by controlled dehydration. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 991-995.	2.5	30
76	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, 8646-8649.	3.3	220
77	Increasing the diffraction limit and internal order of a membrane protein crystal by dehydration. <i>Journal of Structural Biology</i> , 2003, 141, 97-102.	1.3	26