Matthew W. Bowler

List of Publications by Year
in descending order

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77 papers	3,351 citations	136740 32 h-index	161609 54 g-index
90 all docs	90 docs citations	90 times ranked	4639 citing authors

#	Article	IF	Citations
1	How azide inhibits ATP hydrolysis by the F-ATPases. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8646-8649.	3.3	220
2	<i>MxCuBE</i>: a synchrotron beamline control environment customized for macromolecular crystallography experiments. Journal of Synchrotron Radiation, 2010, 17, 700-707.	1.0	193
3	Ground State Structure of F1-ATPase from Bovine Heart Mitochondria at 1.9 AÃ¥ Resolution. Journal of Biological Chemistry, 2007, 282, 14238-14242.	1.6	176
4	Why did Nature select phosphate for its dominant roles in biology?. New Journal of Chemistry, 2010, 34, 784.	1.4	146
5	MASSIF-1: a beamline dedicated to the fully automatic characterization and data collection from crystals of biological macromolecules. Journal of Synchrotron Radiation, 2015, 22, 1540-1547.	1.0	133
6	Cyanine Conformational Restraint in the Far-Red Range. Journal of the American Chemical Society, 2017, 139, 12406-12409.	6.6	125
7	Structural basis for blocking PD-1-mediated immune suppression by therapeutic antibody pembrolizumab. Cell Research, 2017, 27, 147-150.	5.7	111
8	Improving diffraction by humidity control: a novel device compatible with X-ray beamlines. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1237-1246.	2.5	109
9	Automatic processing of macromolecular crystallography X-ray diffraction data at the ESRF. Journal of Applied Crystallography, 2013, 46, 804-810.	1.9	107
10	Fully automatic characterization and data collection from crystals of biological macromolecules. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1757-1767.	2.5	102
11	Diffraction cartography: applying microbeams to macromolecular crystallography sample evaluation and data collection. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 855-864.	2.5	93
12	A molecular mechanism for transthyretin amyloidogenesis. Nature Communications, 2019, 10, 925.	5.8	92
13	Transition State Analogue Structures of Human Phosphoglycerate Kinase Establish the Importance of Charge Balance in Catalysis. Journal of the American Chemical Society, 2010, 132, 6507-6516.	6.6	79
14	Atomic details of near-transition state conformers for enzyme phosphoryl transfer revealed by MgF3- rather than by phosphoranes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4555-4560.	3.3	74
15	Structural basis for Scc3-dependent cohesin recruitment to chromatin. ELife, 2018, 7, .	2.8	69
16	New features of the cell wall of the radio-resistant bacterium Deinococcus radiodurans. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 1978-1984.	1.4	60
17	Structural Basis of the PNRC2-Mediated Link between mRNA Surveillance and Decapping. Structure, 2012, 20, 2025-2037.	1.6	59
18	ISPyB for BioSAXS, the gateway to user autonomy in solution scattering experiments. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 76-85.	2.5	56

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19	A Spring-loaded Release Mechanism Regulates Domain Movement and Catalysis in Phosphoglycerate Kinase. Journal of Biological Chemistry, 2011, 286, 14040-14048.	1.6	53
20	Structural basis for reactivating the mutant TERT promoter by cooperative binding of p52 and ETS1. Nature Communications, 2018, 9, 3183.	5.8	52
21	Inducing phase changes in crystals of macromolecules: Status and perspectives for controlled crystal dehydration. Journal of Structural Biology, 2011, 175, 236-243.	1.3	51
22	Near attack conformers dominate Î²-phosphoglucomutase complexes where geometry and charge distribution reflect those of substrate. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6910-6915.	3.3	47
23	Direct cryocooling of naked crystals: are cryoprotection agents always necessary?. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 902-906.	2.5	46
24	The Ighmbp2 helicase structure reveals the molecular basis for disease-causing mutations in DMSA1. Nucleic Acids Research, 2012, 40, 11009-11022.	6.5	46
25	The sweet quartet: Binding of fucose to the norovirus capsid. Virology, 2015, 483, 203-208.	1.1	46
26	QslA disrupts LasR dimerization in antiactivation of bacterial quorum sensing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20765-20770.	3.3	44
27	Lsm2 and Lsm3 bridge the interaction of the Lsm1-7 complex with Pat1 for decapping activation. Cell Research, 2014, 24, 233-246.	5.7	43
28	Î±-Fluorophosphonates reveal how a phosphomutase conserves transition state conformation over hexose recognition in its two-step reaction. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12384-12389.	3.3	42
29	Structural Basis for the Subversion of MAP Kinase Signaling by an Intrinsically Disordered Parasite Secreted Agonist. Structure, 2017, 25, 16-26.	1.6	41
30	Self-Assembled Amyloid Peptides with Arg-Gly-Asp (RGD) Motifs As Scaffolds for Tissue Engineering. ACS Biomaterials Science and Engineering, 2017, 3, 1404-1416.	2.6	38
31	The use of workflows in the design and implementation of complex experiments in macromolecular crystallography. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 975-984.	2.5	37
32	Fully automatic macromolecular crystallography: the impact of MASSIF-1 on the optimum acquisition and quality of data. Crystallography Reviews, 2016, 22, 233-249.	0.4	37
33	The Upgrade Programme for the Structural Biology beamlines at the European Synchrotron Radiation Facility â€“ High throughput sample evaluation and automation. Journal of Physics: Conference Series, 2013, 425, 012001.	0.3	35
34	RoboDiff: combining a sample changer and goniometer for highly automated macromolecular crystallography experiments. Acta Crystallographica Section D: Structural Biology, 2016, 72, 966-975.	1.1	35
35	Multi-position data collection and dynamic beam sizing: recent improvements to the automatic data-collection algorithms on MASSIF-1. Acta Crystallographica Section D: Structural Biology, 2018, 74, 433-440.	1.1	34
36	Automation and Experience of Controlled Crystal Dehydration: Results from the European Synchrotron HC1 Collaboration. Crystal Growth and Design, 2015, 15, 1043-1054.	1.4	33

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37	A new MR-SAD algorithm for the automatic building of protein models from low-resolution X-ray data and a poor starting model. IUCrJ, 2018, 5, 166-171.	1.0	33
38	The status of the macromolecular crystallography beamlines at the European Synchrotron Radiation Facility. European Physical Journal Plus, 2015, 130, 1.	1.2	31
39	Reproducible improvements in order and diffraction limit of crystals of bovine mitochondrial F1-ATPase by controlled dehydration. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 991-995.	2.5	30
40	<i>MXCuBE2</i>: the dawn of <i>MXCuBE</i> Collaboration. Journal of Synchrotron Radiation, 2019, 26, 393-405.	1.0	30
41	MgF₃^{âˆ’} and Î±-Galactose 1-Phosphate in the Active Site of Î²-Phosphoglucomutase Form a Transition State Analogue of Phosphoryl Transfer. Journal of the American Chemical Society, 2009, 131, 16334-16335.	6.6	29
42	Measurement of the equilibrium relative humidity for common precipitant concentrations: facilitating controlled dehydration experiments. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 111-114.	0.7	29
43	Structural Evidence for a Role of the Multi-functional Human Glycoprotein Afamin in Wnt Transport. Structure, 2017, 25, 1907-1915.e5.	1.6	29
44	Structural basis of suppression of host translation termination by Moloney Murine Leukemia Virus. Nature Communications, 2016, 7, 12070.	5.8	27
45	Increasing the diffraction limit and internal order of a membrane protein crystal by dehydration. Journal of Structural Biology, 2003, 141, 97-102.	1.3	26
46	Chargeâ€Balanced Metal Fluoride Complexes for Protein Kinaseâ€…A with Adenosine Diphosphate and Substrate Peptide SP20. Angewandte Chemie - International Edition, 2012, 51, 12242-12245.	7.2	26
47	Structural basis for specific recognition of pre-snRNA by Gemin5. Cell Research, 2016, 26, 1353-1356.	5.7	23
48	Purification and characterization of DR_2577 (SlpA) a major S-layer protein from Deinococcus radiodurans. Frontiers in Microbiology, 2015, 6, 414.	1.5	20
49	Recent progress in robot-based systems for crystallography and their contribution to drug discovery. Expert Opinion on Drug Discovery, 2013, 8, 835-847.	2.5	19
50	A plant-like mechanism coupling m6A reading to polyadenylation safeguards transcriptome integrity and developmental gene partitioning in Toxoplasma. ELife, 2021, 10, .	2.8	19
51	Conformational dynamics in phosphoglycerate kinase, an open and shut case?. FEBS Letters, 2013, 587, 1878-1883.	1.3	18
52	A novel amyloid designable scaffold and potential inhibitor inspired by <scp>GAIIG</scp> of amyloid beta and the <scp>HIV</scp>â€1 V3 loop. FEBS Letters, 2018, 592, 1777-1788.	1.3	18
53	Cross-Reactive SARS-CoV-2 Neutralizing Antibodies From Deep Mining of Early Patient Responses. Frontiers in Immunology, 2021, 12, 678570.	2.2	16
54	Crystal Structures of Lsm3, Lsm4 and Lsm5/6/7 from Schizosaccharomyces pombe. PLoS ONE, 2012, 7, e36768.	1.1	16

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55	Interaction of Human 3-Phosphoglycerate Kinase with Its Two Substrates: Is Substrate Antagonism a Kinetic Advantage?. Journal of Molecular Biology, 2011, 409, 742-757.	2.0	14
56	Computational design of amyloid self-assembling peptides bearing aromatic residues and the cell adhesive motif Arg-Gly-Asp. Molecular Systems Design and Engineering, 2017, 2, 321-335.	1.7	14
57	FlexED8: the first member of a fast and flexible sample-changer family for macromolecular crystallography. Acta Crystallographica Section D: Structural Biology, 2017, 73, 841-851.	1.1	13
58	Structural basis for the bi-functionality of human oxaloacetate decarboxylase FAHD1. Biochemical Journal, 2018, 475, 3561-3576.	1.7	13
59	Measurement of the intrinsic variability within protein crystals: implications for sample-evaluation and data-collection strategies. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 127-132.	0.4	12
60	van der Waals Contact between Nucleophile and Transferring Phosphorus Is Insufficient To Achieve Enzyme Transition-State Architecture. ACS Catalysis, 2018, 8, 8140-8153.	5.5	12
61	Assessing the Influence of Mutation on GTPase Transition States by Using Xâ€ray Crystallography, ¹⁹Fâ€…NMR, and DFT Approaches. Angewandte Chemie - International Edition, 2017, 56, 9732-9735.	7.2	9
62	Raoult's law revisited: accurately predicting equilibrium relative humidity points for humidity control experiments. Journal of Applied Crystallography, 2017, 50, 631-638.	1.9	8
63	Towards a compact and precise sample holder for macromolecular crystallography. Acta Crystallographica Section D: Structural Biology, 2017, 73, 829-840.	1.1	8
64	Reflections on biocatalysis involving phosphorus. Biochemistry (Moscow), 2012, 77, 1083-1096.	0.7	7
65	A comparative anatomy of protein crystals: lessons from the automatic processing of 56â€…000 samples. IUCrJ, 2019, 6, 822-831.	1.0	7
66	Structural insights into the substrate-bound condensation domains of non-ribosomal peptide synthetase AmbB. Scientific Reports, 2022, 12, 5353.	1.6	3
67	Observing enzyme ternary transition state analogue complexes by ¹⁹F NMR spectroscopy. Chemical Science, 2017, 8, 8427-8434.	3.7	2
68	Fully Autonomous Characterization and Data Collection from Crystals of Biological Macromolecules. Journal of Visualized Experiments, 2019, , .	0.2	2
69	Structural and functional comparison of fumarylacetoacetate domain containing protein 1 in human and mouse. Bioscience Reports, 2020, 40, .	1.1	2
70	Controlled dehydration, structural flexibility and gadolinium MRI contrast compound binding in the human plasma glycoprotein afamin. Acta Crystallographica Section D: Structural Biology, 2019, 75, 1071-1083.	1.1	2
71	Assessing the Influence of Mutation on GTPase Transition States by Using Xâ€ray Crystallography, 19 Fâ€…NMR, and DFT Approaches. Angewandte Chemie, 2017, 129, 9864-9867.	1.6	1
72	CrystalDirect-To-Beam: Opening the shortest path from crystal to data. AIP Conference Proceedings, 2019, , .	0.3	1

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73	Le rayonnement synchrotron : comprendre la relation structure-fonction des macromolÃ©cules biologiques. , 2013, , 48-53.	0.1	1
74	MX automation: towards a new sample holder standard for frozen crystals. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s9-s9.	0.3	1
75	Diffraction cartography: multi-crystal and multi-position data collection. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s9-s10.	0.3	1
76	Automated data collection based on RoboDiff at the ESRF beamline MASSIF-1. AIP Conference Proceedings, 2016, , .	0.3	0
77	Finding order in chaos â€“ nanocrystals in amorphous protein gels. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 386-387.	0.4	0