Matthew W. Bowler

List of Publications by Citations

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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	How azide inhibits ATP hydrolysis by the F-ATPases. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 8646-9	11.5	181
74	Ground state structure of F1-ATPase from bovine heart mitochondria at 1.9 A resolution. *Journal of Biological Chemistry*, **2007**, 282, 14238-42	5.4	158
73	MxCuBE: a synchrotron beamline control environment customized for macromolecular crystallography experiments. *Journal of Synchrotron Radiation*, **2010**, 17, 700-7	2.4	148
72	Why did Nature select phosphate for its dominant roles in biology?. *New Journal of Chemistry*, **2010**, 34, 784	3.6	114
71	Improving diffraction by humidity control: a novel device compatible with X-ray beamlines. *Acta Crystallographica Section D: Biological Crystallography*, **2009**, 65, 1237-46		91
70	MASSIF-1: a beamline dedicated to the fully automatic characterization and data collection from crystals of biological macromolecules. *Journal of Synchrotron Radiation*, **2015**, 22, 1540-7	2.4	90
69	Diffraction cartography: applying microbeams to macromolecular crystallography sample evaluation and data collection. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 855-64		88
68	Automatic processing of macromolecular crystallography X-ray diffraction data at the ESRF. *Journal of Applied Crystallography*, **2013**, 46, 804-810	3.8	77
67	Cyanine Conformational Restraint in the Far-Red Range. *Journal of the American Chemical Society*, **2017**, 139, 12406-12409	16.4	75
66	Fully automatic characterization and data collection from crystals of biological macromolecules. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 1757-67		72
65	Atomic details of near-transition state conformers for enzyme phosphoryl transfer revealed by MgF-3 rather than by phosphoranes. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 4555-60	11.5	72
64	Structural basis for blocking PD-1-mediated immune suppression by therapeutic antibody pembrolizumab. *Cell Research*, **2017**, 27, 147-150	24.7	71
63	Transition state analogue structures of human phosphoglycerate kinase establish the importance of charge balance in catalysis. *Journal of the American Chemical Society*, **2010**, 132, 6507-16	16.4	70
62	A molecular mechanism for transthyretin amyloidogenesis. *Nature Communications*, **2019**, 10, 925	17.4	54
61	Structural basis of the PNRC2-mediated link between mrna surveillance and decapping. *Structure*, **2012**, 20, 2025-37	5.2	52
60	Inducing phase changes in crystals of macromolecules: status and perspectives for controlled crystal dehydration. *Journal of Structural Biology*, **2011**, 175, 236-43	3.4	49
59	A spring-loaded release mechanism regulates domain movement and catalysis in phosphoglycerate kinase. *Journal of Biological Chemistry*, **2011**, 286, 14040-8	5.4	46

58	ISPyB for BioSAXS, the gateway to user autonomy in solution scattering experiments. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 76-85		45
57	Structural basis for Scc3-dependent cohesin recruitment to chromatin. *ELife*, **2018**, 7,	8.9	43
56	Direct cryocooling of naked crystals: are cryoprotection agents always necessary?. *Acta Crystallographica Section D: Biological Crystallography*, **2011**, 67, 902-6		42
55	Near attack conformers dominate βphosphoglucomutase 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, 6910-5	11.5	41
54	The sweet quartet: Binding of fucose to the norovirus capsid. *Virology*, **2015**, 483, 203-8	3.6	39
53	αFluorophosphonates 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, 12384-9	11.5	38
52	Lsm2 and Lsm3 bridge the interaction of the Lsm1-7 complex with Pat1 for decapping activation. *Cell Research*, **2014**, 24, 233-46	24.7	35
51	New features of the cell wall of the radio-resistant bacterium Deinococcus radiodurans. *Biochimica Et Biophysica Acta - Biomembranes*, **2014**, 1838, 1978-84	3.8	32
50	The use of workflows in the design and implementation of complex experiments in macromolecular crystallography. *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 975-84		32
49	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, 20765-70	11.5	30
48	The Ighmbp2 helicase structure reveals the molecular basis for disease-causing mutations in DMSA1. *Nucleic Acids Research*, **2012**, 40, 11009-22	20.1	30
47	Fully automatic macromolecular crystallography: the impact of MASSIF-1 on the optimum acquisition and quality of data. *Crystallography Reviews*, **2016**, 22, 233-249	1.3	28
46	Structural basis for reactivating the mutant TERT promoter by cooperative binding of p52 and ETS1. *Nature Communications*, **2018**, 9, 3183	17.4	28
45	Self-Assembled Amyloid Peptides with Arg-Gly-Asp (RGD) Motifs As Scaffolds for Tissue Engineering. *ACS Biomaterials Science and Engineering*, **2017**, 3, 1404-1416	5.5	28
44	MgF(3)(-) and alpha-galactose 1-phosphate in the active site of beta-phosphoglucomutase form a transition state analogue of phosphoryl transfer. *Journal of the American Chemical Society*, **2009**, 131, 16334-5	16.4	28
43	Automation and Experience of Controlled Crystal Dehydration: Results from the European Synchrotron HC1 Collaboration. *Crystal Growth and Design*, **2015**, 15, 1043-1054	3.5	27
42	Measurement of the equilibrium relative humidity for common precipitant concentrations: facilitating controlled dehydration experiments. *Acta Crystallographica Section F: Structural Biology Communications*, **2012**, 68, 111-4		27
41	Structural Basis for the Subversion of MAP Kinase Signaling by an Intrinsically Disordered Parasite Secreted Agonist. *Structure*, **2017**, 25, 16-26	5.2	26

40	The status of the macromolecular crystallography beamlines at the European Synchrotron Radiation Facility. *European Physical Journal Plus*, **2015**, 130, 1	3.1	25
39	The Upgrade Programme for the Structural Biology beamlines at the European Synchrotron Radiation Facility High throughput sample evaluation and automation. *Journal of Physics: Conference Series*, **2013**, 425, 012001	0.3	25
38	RoboDiff: combining a sample changer and goniometer for highly automated macromolecular crystallography experiments. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 966-75	5.5	25
37	Reproducible improvements in order and diffraction limit of crystals of bovine mitochondrial F(1)-ATPase by controlled dehydration. *Acta Crystallographica Section D: Biological Crystallography*, **2006**, 62, 991-5		24
36	Increasing the diffraction limit and internal order of a membrane protein crystal by dehydration. *Journal of Structural Biology*, **2003**, 141, 97-102	3.4	24
35	Charge-balanced metal fluoride complexes for protein kinase A with adenosine diphosphate and substrate peptide SP20. *Angewandte Chemie - International Edition*, **2012**, 51, 12242-5	16.4	23
34	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	5.5	22
33	Structural Evidence for a Role of the Multi-functional Human Glycoprotein Afamin in Wnt Transport. *Structure*, **2017**, 25, 1907-1915.e5	5.2	21
32	Structural basis of suppression of host translation termination by Moloney Murine Leukemia Virus. *Nature Communications*, **2016**, 7, 12070	17.4	20
31	Recent progress in robot-based systems for crystallography and their contribution to drug discovery. *Expert Opinion on Drug Discovery*, **2013**, 8, 835-47	6.2	18
30	MXCuBE2: the dawn of MXCuBE Collaboration. *Journal of Synchrotron Radiation*, **2019**, 26, 393-405	2.4	14
29	Purification and characterization of DR_2577 (SlpA) a major S-layer protein from Deinococcus radiodurans. *Frontiers in Microbiology*, **2015**, 6, 414	5.7	14
28	Structural basis for specific recognition of pre-snRNA by Gemin5. *Cell Research*, **2016**, 26, 1353-1356	24.7	12
27	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	4.6	12
26	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	4.7	12
25	Crystal structures of Lsm3, Lsm4 and Lsm5/6/7 from Schizosaccharomyces pombe. *PLoS ONE*, **2012**, 7, e36768	3.7	12
24	Conformational dynamics in phosphoglycerate kinase, an open and shut case?. *FEBS Letters*, **2013**, 587, 1878-83	3.8	11
23	Interaction of human 3-phosphoglycerate kinase with its two substrates: is substrate antagonism a kinetic advantage?. *Journal of Molecular Biology*, **2011**, 409, 742-57	6.5	11

22	van der Waals Contact between Nucleophile and Transferring Phosphorus Is Insufficient To Achieve Enzyme Transition-State Architecture. *ACS Catalysis*, **2018**, 8, 8140-8153	13.1	10
21	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, 127-32	1.1	10
20	Cross-Reactive SARS-CoV-2 Neutralizing Antibodies From Deep Mining of Early Patient Responses. *Frontiers in Immunology*, **2021**, 12, 678570	8.4	9
19	Structural basis for the bi-functionality of human oxaloacetate decarboxylase FAHD1. *Biochemical Journal*, **2018**, 475, 3561-3576	3.8	8
18	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	5.5	7
17	Reflections on biocatalysis involving phosphorus. *Biochemistry (Moscow)*, **2012**, 77, 1083-96	2.9	7
16	Assessing the Influence of Mutation on GTPase Transition States by Using X-ray Crystallography, F NMR, and DFT Approaches. *Angewandte Chemie - International Edition*, **2017**, 56, 9732-9735	16.4	6
15	RaoultTs law revisited: accurately predicting equilibrium relative humidity points for humidity control experiments. *Journal of Applied Crystallography*, **2017**, 50, 631-638	3.8	6
14	Charge-Balanced Metal Fluoride Complexes for Protein Kinase A with Adenosine Diphosphate and Substrate Peptide SP20. *Angewandte Chemie*, **2012**, 124, 12408-12411	3.6	6
13	Towards a compact and precise sample holder for macromolecular crystallography. *Acta Crystallographica Section D: Structural Biology*, **2017**, 73, 829-840	5.5	6
12	A comparative anatomy of protein crystals: lessons from the automatic processing of 56 000 samples. *IUCrJ*, **2019**, 6, 822-831	4.7	5
11	Deep mining of early antibody response in COVID-19 patients yields potent neutralisers and reveals high level of convergence		3
10	A plant-like mechanism coupling m6A reading to polyadenylation safeguards transcriptome integrity and developmental gene partitioning in. *ELife*, **2021**, 10,	8.9	3
9	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	5.5	2
8	Assessing the Influence of Mutation on GTPase Transition States by Using X-ray Crystallography, 19F NMR, and DFT Approaches. *Angewandte Chemie*, **2017**, 129, 9864-9867	3.6	1
7	Observing enzyme ternary transition state analogue complexes by F NMR spectroscopy. *Chemical Science*, **2017**, 8, 8427-8434	9.4	1
6	Fully Autonomous Characterization and Data Collection from Crystals of Biological Macromolecules. *Journal of Visualized Experiments*, **2019**,	1.6	1
5	Controlled dehydration, structural flexibility, and Gadolinium MRI contrast compound binding in human plasma glycoprotein afamin		1

4	Structural and functional comparison of fumarylacetoacetate domain containing protein 1 in human and mouse. *Bioscience Reports*, **2020**, 40,	4.1	1
3	Le rayonnement synchrotron : comprendre la relation structure-fonction des macromolécules biologiques **2013**, 48-53	0.1	1
2	Finding order in chaos - nanocrystals in amorphous protein gels. *Acta Crystallographica Section F, Structural Biology Communications*, **2021**, 77, 386-387	1.1	
1	Structural insights into the substrate-bound condensation domains of non-ribosomal peptide synthetase AmbB.. *Scientific Reports*, **2022**, 12, 5353	4.9	