

Arwen R Pearson

List of Publications by Year in Descending Order

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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

1,862
citations

25
h-index

40
g-index

92
ext. papers

2,243
ext. citations

7
avg. IF

4.55
L-index

#	Paper	IF	Citations
75	Best practices for time-resolved serial synchrotron crystallography.. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022 , 78, 14-29	5.5	2
74	X-ray-Based Techniques to Study the Nano-Bio Interface. <i>ACS Nano</i> , 2021 , 15, 3754-3807	16.7	18
73	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. <i>Science</i> , 2021 , 372, 642-646	33.3	95
72	Probing the role of Val228 on the catalytic activity of Scytalidium catalase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021 , 1869, 140662	4	0
71	Using photocaging for fast time-resolved structural biology studies. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 1218-1232	5.5	3
70	Homogeneous batch micro-crystallization of proteins from ammonium sulfate. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 194-204	5.5	3
69	The HARE chip for efficient time-resolved serial synchrotron crystallography. <i>Journal of Synchrotron Radiation</i> , 2020 , 27, 360-370	2.4	20
68	3D-MiXD: 3D-printed X-ray-compatible microfluidic devices for rapid, low-consumption serial synchrotron crystallography data collection in flow. <i>IUCrJ</i> , 2020 , 7, 207-219	4.7	24
67	Structural Kinetics of MsbA Investigated by Stopped-Flow Time-Resolved Small-Angle X-Ray Scattering. <i>Structure</i> , 2020 , 28, 348-354.e3	5.2	15
66	Serial synchrotron crystallography for time-resolved structural biology. <i>Current Opinion in Structural Biology</i> , 2020 , 65, 168-174	8.1	21
65	Liquid application method for time-resolved analyses by serial synchrotron crystallography. <i>Nature Methods</i> , 2019 , 16, 979-982	21.6	41
64	Crystal structure of a domain-swapped photoactivatable sGFP variant provides evidence for GFP folding pathway. <i>FEBS Journal</i> , 2019 , 286, 2329-2340	5.7	2
63	Directed Assembly of Homopentameric Cholera Toxin B-Subunit Proteins into Higher-Order Structures Using Coiled-Coil Appendages. <i>Journal of the American Chemical Society</i> , 2019 , 141, 5211-5219	16.4	9
62	Synthesis and characterisation of α -carboxynitrobenzyl photocaged L-aspartates for applications in time-resolved structural biology.. <i>RSC Advances</i> , 2019 , 9, 8695-8699	3.7	4
61	Complex Interplay between Epitope Specificity and Isotype Dictates the Biological Activity of Anti-human CD40 Antibodies. <i>Cancer Cell</i> , 2018 , 33, 664-675.e4	24.3	48
60	Oxygen Activation Switch in the Copper Amine Oxidase of Escherichia coli. <i>Biochemistry</i> , 2018 , 57, 5301-5314	5.2	4
59	Identification of the site of oxidase substrate binding in Scytalidium thermophilum catalase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 979-985	5.5	3

58	Pathological macromolecular crystallographic data affected by twinning, partial-disorder and exhibiting multiple lattices for testing of data processing and refinement tools. <i>Scientific Reports</i> , 2018 , 8, 14876	4.9	8
57	Extending enzyme molecular recognition with an expanded amino acid alphabet. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 2610-2615	11.5	24
56	Preface to Special Topic: Transactions from the 66th Annual Meeting of the American Crystallographic Association. <i>Structural Dynamics</i> , 2017 , 4, 032001	3.2	
55	The Mechanism of Regulation of Pantothenate Biosynthesis by the PanD-PanZ Δ AcCoA Complex Reveals an Additional Mode of Action for the Antimetabolite N-Pentyl Pantothenamide (N5-Pan). <i>Biochemistry</i> , 2017 , 56, 4931-4939	3.2	12
54	Topological Dissection of the Membrane Transport Protein Mhp1 Derived from Cysteine Accessibility and Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 8844-8852	7.8	13
53	Fixed target combined with spectral mapping: approaching 100% hit rates for serial crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 944-55	5.5	54
52	Evaluation of fluoropyruvate as nucleophile in reactions catalysed by N-acetyl neuraminic acid lyase variants: scope, limitations and stereoselectivity. <i>Organic and Biomolecular Chemistry</i> , 2016 , 14, 105-12	3.9	17
51	The structure of the PanD/PanZ protein complex reveals negative feedback regulation of pantothenate biosynthesis by coenzyme A. <i>Chemistry and Biology</i> , 2015 , 22, 492-503		21
50	In pursuit of an accurate spatial and temporal model of biomolecules at the atomistic level: a perspective on computer simulation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 162-72		9
49	Using synchrotrons and XFELs for time-resolved X-ray crystallography and solution scattering experiments on biomolecules. <i>Current Opinion in Structural Biology</i> , 2015 , 35, 41-8	8.1	81
48	If You Can Get a Crystal Structure, Why Bother with Anything Else?. <i>Synchrotron Radiation News</i> , 2015 , 28, 10-14	0.6	4
47	Probing the molecular mechanisms in copper amine oxidases by generating heterodimers. <i>ChemBioChem</i> , 2015 , 16, 559-64	3.8	4
46	Reaction mechanism of N-acetylneuraminic acid lyase revealed by a combination of crystallography, QM/MM simulation, and mutagenesis. <i>ACS Chemical Biology</i> , 2014 , 9, 1025-32	4.9	36
45	Time-resolved crystallography using the Hadamard transform. <i>Nature Methods</i> , 2014 , 11, 1131-4	21.6	22
44	Limits of structural plasticity in a picornavirus capsid revealed by a massively expanded equine rhinitis A virus particle. <i>Journal of Virology</i> , 2014 , 88, 6093-9	6.6	16
43	Structure-guided design affirms inhibitors of hepatitis C virus p7 as a viable class of antivirals targeting virion release. <i>Hepatology</i> , 2014 , 59, 408-22	11.2	49
42	Threonine 57 is required for the post-translational activation of Escherichia coli aspartate β -decarboxylase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1166-72		5
41	Human cellular retinaldehyde-binding protein has secondary thermal 9-cis-retinal isomerase activity. <i>Journal of the American Chemical Society</i> , 2014 , 136, 137-46	16.4	11

40	Probing temperature- and solvent-dependent protein dynamics using terahertz time-domain spectroscopy. <i>Journal of Applied Crystallography</i> , 2014 , 47, 146-153	3.8	2
39	Combining Single Crystal UV/Vis Spectroscopy and Diffraction to Structurally Characterise Intermediates and Monitor Radiation Damage. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2014 , 253-259	0.1	
38	Packaging signals in single-stranded RNA viruses: nature's alternative to a purely electrostatic assembly mechanism. <i>Journal of Biological Physics</i> , 2013 , 39, 277-87	1.6	70
37	Dynamic structural science: recent developments in time-resolved spectroscopy and X-ray crystallography. <i>Biochemical Society Transactions</i> , 2013 , 41, 1260-4	5.1	10
36	Sequence-specific, RNA-protein interactions overcome electrostatic barriers preventing assembly of satellite tobacco necrosis virus coat protein. <i>Journal of Molecular Biology</i> , 2013 , 425, 1050-64	6.5	41
35	Investigating the active centre of the <i>Scytalidium thermophilum</i> catalase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 369-75		2
34	Structure, recombinant expression and mutagenesis studies of the catalase with oxidase activity from <i>Scytalidium thermophilum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 398-408		7
33	Effect of molecular size and particle shape on the terahertz absorption of a homologous series of tetraalkylammonium salts. <i>Analytical Chemistry</i> , 2013 , 85, 7926-34	7.8	10
32	Structural insights into the recovery of aldolase activity in N-acetylneuraminic acid lyase by replacement of the catalytically active lysine with Ethialysine by using a chemical mutagenesis strategy. <i>ChemBioChem</i> , 2013 , 14, 474-81	3.8	26
31	X-ray-excited optical luminescence of protein crystals: a new tool for studying radiation damage during diffraction data collection. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 505-10		9
30	Isolation of an asymmetric RNA uncoating intermediate for a single-stranded RNA plant virus. <i>Journal of Molecular Biology</i> , 2012 , 417, 65-78	6.5	27
29	Dissecting the mechanism of oxygen trafficking in a metalloenzyme. <i>Faraday Discussions</i> , 2011 , 148, 269-82; discussion 299-314	3.6	2
28	Applying broadband terahertz time-domain spectroscopy to the analysis of crystalline proteins: a dehydration study. <i>Journal of Applied Crystallography</i> , 2011 , 44, 129-133	3.8	13
27	Revealing low-dose radiation damage using single-crystal spectroscopy. <i>Journal of Synchrotron Radiation</i> , 2011 , 18, 367-73	2.4	17
26	Nature of the ferryl heme in compounds I and II. <i>Journal of Biological Chemistry</i> , 2011 , 286, 1260-8	5.4	81
25	All three domains of the hepatitis C virus nonstructural NS5A protein contribute to RNA binding. <i>Journal of Virology</i> , 2010 , 84, 9267-77	6.6	94
24	Exploring the roles of the metal ions in <i>Escherichia coli</i> copper amine oxidase. <i>Biochemistry</i> , 2010 , 49, 1268-80	3.2	26
23	Structural insight into methyl-coenzyme M reductase chemistry using coenzyme B analogues. <i>Biochemistry</i> , 2010 , 49, 7683-93	3.2	36

22	Structural insights into substrate specificity in variants of N-acetylneuraminic Acid lyase produced by directed evolution. <i>Journal of Molecular Biology</i> , 2010 , 404, 56-69	6.5	25
21	A comparative analysis of the fluorescence properties of the wild-type and active site mutants of the hepatitis C virus autoprotease NS2-3. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010 , 1804, 212-22	4	6
20	A new on-axis multimode spectrometer for the macromolecular crystallography beamlines of the Swiss Light Source. <i>Journal of Synchrotron Radiation</i> , 2009 , 16, 173-82	2.4	38
19	Crystallization and preliminary X-ray analysis of a bifunctional catalase-phenol oxidase from <i>Scytalidium thermophilum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 486-8		3
18	Structure of an <i>Escherichia coli</i> N-acetyl-D-neuraminic acid lyase mutant, E192N, in complex with pyruvate at 1.45 angstrom resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 1088-90		9
17	Combining X-ray crystallography and single-crystal spectroscopy to probe enzyme mechanisms. <i>Biochemical Society Transactions</i> , 2009 , 37, 378-81	5.1	30
16	Structure of a xenon derivative of <i>Escherichia coli</i> copper amine oxidase: confirmation of the proposed oxygen-entry pathway. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 1105-9		14
15	Exploring molecular oxygen pathways in <i>Hansenula polymorpha</i> copper-containing amine oxidase. <i>Journal of Biological Chemistry</i> , 2007 , 282, 17767-76	5.4	70
14	The crystal structure of cytochrome P460 of <i>Nitrosomonas europaea</i> reveals a novel cytochrome fold and heme-protein cross-link. <i>Biochemistry</i> , 2007 , 46, 8340-9	3.2	39
13	Tracking X-ray-derived redox changes in crystals of a methylamine dehydrogenase/amicyanin complex using single-crystal UV/Vis microspectrophotometry. <i>Journal of Synchrotron Radiation</i> , 2007 , 14, 92-8	2.4	31
12	Mechanistic possibilities in MauG-dependent tryptophan tryptophylquinone biosynthesis. <i>Biochemistry</i> , 2006 , 45, 13276-83	3.2	45
11	Isotope labeling studies reveal the order of oxygen incorporation into the tryptophan tryptophylquinone cofactor of methylamine dehydrogenase. <i>Journal of the American Chemical Society</i> , 2006 , 128, 12416-7	16.4	22
10	Expression, purification, crystallization and preliminary X-ray diffraction of a novel <i>Nitrosomonas europaea</i> cytochrome, cytochrome P460. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 395-8		8
9	MauG-dependent in vitro biosynthesis of tryptophan tryptophylquinone in methylamine dehydrogenase. <i>Journal of the American Chemical Society</i> , 2005 , 127, 8258-9	16.4	48
8	Active site aspartate residues are critical for tryptophan tryptophylquinone biogenesis in methylamine dehydrogenase. <i>Journal of Biological Chemistry</i> , 2005 , 280, 17392-6	5.4	15
7	Microspectrophotometry for structural enzymology. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 656-62		48
6	Further insights into quinone cofactor biogenesis: probing the role of mauG in methylamine dehydrogenase tryptophan tryptophylquinone formation. <i>Biochemistry</i> , 2004 , 43, 5494-502	3.2	76
5	Catching catalysis in the act: using single crystal kinetics to trap methylamine dehydrogenase reaction intermediates. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003 , 1647, 381-9	4	7

4	MauG, a novel diheme protein required for tryptophan tryptophylquinone biogenesis. <i>Biochemistry</i> , 2003 , 42, 7318-25	3.2	113
3	Understanding quinone cofactor biogenesis in methylamine dehydrogenase through novel cofactor generation. <i>Biochemistry</i> , 2003 , 42, 3224-30	3.2	20
2	Cryocrystallography of metalloprotein reaction intermediates. <i>Current Opinion in Chemical Biology</i> , 2002 , 6, 202-7	9.7	17
1	SARS-CoV-2 papain-like protease PLpro in complex with natural compounds reveal allosteric sites for antiviral drug design		3