

# Arwen R Pearson

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/1676830/arwen-r-pearson-publications-by-citations.pdf>

**Version:** 2024-04-25

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

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	MauG, a novel diheme protein required for tryptophan tryptophylquinone biogenesis. <i>Biochemistry</i> , <b>2003</b> , 42, 7318-25	3.2	113
74	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. <i>Science</i> , <b>2021</b> , 372, 642-646	33.3	95
73	All three domains of the hepatitis C virus nonstructural NS5A protein contribute to RNA binding. <i>Journal of Virology</i> , <b>2010</b> , 84, 9267-77	6.6	94
72	Using synchrotrons and XFELs for time-resolved X-ray crystallography and solution scattering experiments on biomolecules. <i>Current Opinion in Structural Biology</i> , <b>2015</b> , 35, 41-8	8.1	81
71	Nature of the ferryl heme in compounds I and II. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 1260-8	5.4	81
70	Further insights into quinone cofactor biogenesis: probing the role of mauG in methylamine dehydrogenase tryptophan tryptophylquinone formation. <i>Biochemistry</i> , <b>2004</b> , 43, 5494-502	3.2	76
69	Packaging signals in single-stranded RNA viruses: nature's alternative to a purely electrostatic assembly mechanism. <i>Journal of Biological Physics</i> , <b>2013</b> , 39, 277-87	1.6	70
68	Exploring molecular oxygen pathways in <i>Hansenula polymorpha</i> copper-containing amine oxidase. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 17767-76	5.4	70
67	Fixed target combined with spectral mapping: approaching 100% hit rates for serial crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2016</b> , 72, 944-55	5.5	54
66	Structure-guided design affirms inhibitors of hepatitis C virus p7 as a viable class of antivirals targeting virion release. <i>Hepatology</i> , <b>2014</b> , 59, 408-22	11.2	49
65	Complex Interplay between Epitope Specificity and Isotype Dictates the Biological Activity of Anti-human CD40 Antibodies. <i>Cancer Cell</i> , <b>2018</b> , 33, 664-675.e4	24.3	48
64	MauG-dependent in vitro biosynthesis of tryptophan tryptophylquinone in methylamine dehydrogenase. <i>Journal of the American Chemical Society</i> , <b>2005</b> , 127, 8258-9	16.4	48
63	Microspectrophotometry for structural enzymology. <i>Current Opinion in Structural Biology</i> , <b>2004</b> , 14, 656-62		48
62	Mechanistic possibilities in MauG-dependent tryptophan tryptophylquinone biosynthesis. <i>Biochemistry</i> , <b>2006</b> , 45, 13276-83	3.2	45
61	Liquid application method for time-resolved analyses by serial synchrotron crystallography. <i>Nature Methods</i> , <b>2019</b> , 16, 979-982	21.6	41
60	Sequence-specific, RNA-protein interactions overcome electrostatic barriers preventing assembly of satellite tobacco necrosis virus coat protein. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 1050-64	6.5	41
59	The crystal structure of cytochrome P460 of <i>Nitrosomonas europaea</i> reveals a novel cytochrome fold and heme-protein cross-link. <i>Biochemistry</i> , <b>2007</b> , 46, 8340-9	3.2	39

58	A new on-axis multimode spectrometer for the macromolecular crystallography beamlines of the Swiss Light Source. <i>Journal of Synchrotron Radiation</i> , <b>2009</b> , 16, 173-82	2.4	38
57	Reaction mechanism of N-acetylneuraminic acid lyase revealed by a combination of crystallography, QM/MM simulation, and mutagenesis. <i>ACS Chemical Biology</i> , <b>2014</b> , 9, 1025-32	4.9	36
56	Structural insight into methyl-coenzyme M reductase chemistry using coenzyme B analogues. <i>Biochemistry</i> , <b>2010</b> , 49, 7683-93	3.2	36
55	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> , <b>2007</b> , 14, 92-8	2.4	31
54	Combining X-ray crystallography and single-crystal spectroscopy to probe enzyme mechanisms. <i>Biochemical Society Transactions</i> , <b>2009</b> , 37, 378-81	5.1	30
53	Isolation of an asymmetric RNA uncoating intermediate for a single-stranded RNA plant virus. <i>Journal of Molecular Biology</i> , <b>2012</b> , 417, 65-78	6.5	27
52	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> , <b>2013</b> , 14, 474-81	3.8	26
51	Exploring the roles of the metal ions in Escherichia coli copper amine oxidase. <i>Biochemistry</i> , <b>2010</b> , 49, 1268-80	3.2	26
50	Structural insights into substrate specificity in variants of N-acetylneuraminic Acid lyase produced by directed evolution. <i>Journal of Molecular Biology</i> , <b>2010</b> , 404, 56-69	6.5	25
49	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> , <b>2017</b> , 114, 2610-2615	11.5	24
48	3D-MiXD: 3D-printed X-ray-compatible microfluidic devices for rapid, low-consumption serial synchrotron crystallography data collection in flow. <i>IUCrJ</i> , <b>2020</b> , 7, 207-219	4.7	24
47	Time-resolved crystallography using the Hadamard transform. <i>Nature Methods</i> , <b>2014</b> , 11, 1131-4	21.6	22
46	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> , <b>2006</b> , 128, 12416-7	16.4	22
45	The structure of the PanD/PanZ protein complex reveals negative feedback regulation of pantothenate biosynthesis by coenzyme A. <i>Chemistry and Biology</i> , <b>2015</b> , 22, 492-503		21
44	Serial synchrotron crystallography for time-resolved structural biology. <i>Current Opinion in Structural Biology</i> , <b>2020</b> , 65, 168-174	8.1	21
43	Understanding quinone cofactor biogenesis in methylamine dehydrogenase through novel cofactor generation. <i>Biochemistry</i> , <b>2003</b> , 42, 3224-30	3.2	20
42	The HARE chip for efficient time-resolved serial synchrotron crystallography. <i>Journal of Synchrotron Radiation</i> , <b>2020</b> , 27, 360-370	2.4	20
41	X-ray-Based Techniques to Study the Nano-Bio Interface. <i>ACS Nano</i> , <b>2021</b> , 15, 3754-3807	16.7	18

40	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> , <b>2016</b> , 14, 105-12	3.9	17
39	Revealing low-dose radiation damage using single-crystal spectroscopy. <i>Journal of Synchrotron Radiation</i> , <b>2011</b> , 18, 367-73	2.4	17
38	Cryocrystallography of metalloprotein reaction intermediates. <i>Current Opinion in Chemical Biology</i> , <b>2002</b> , 6, 202-7	9.7	17
37	Limits of structural plasticity in a picornavirus capsid revealed by a massively expanded equine rhinitis A virus particle. <i>Journal of Virology</i> , <b>2014</b> , 88, 6093-9	6.6	16
36	Active site aspartate residues are critical for tryptophan tryptophylquinone biogenesis in methylamine dehydrogenase. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 17392-6	5.4	15
35	Structural Kinetics of MsbA Investigated by Stopped-Flow Time-Resolved Small-Angle X-Ray Scattering. <i>Structure</i> , <b>2020</b> , 28, 348-354.e3	5.2	15
34	Structure of a xenon derivative of Escherichia coli copper amine oxidase: confirmation of the proposed oxygen-entry pathway. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2008</b> , 64, 1105-9		14
33	Topological Dissection of the Membrane Transport Protein Mhp1 Derived from Cysteine Accessibility and Mass Spectrometry. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 8844-8852	7.8	13
32	Applying broadband terahertz time-domain spectroscopy to the analysis of crystalline proteins: a dehydration study. <i>Journal of Applied Crystallography</i> , <b>2011</b> , 44, 129-133	3.8	13
31	The Mechanism of Regulation of Pantothenate Biosynthesis by the PanD-PanZ $\square$ AcCoA Complex Reveals an Additional Mode of Action for the Antimetabolite N-Pentyl Pantothenamide (N5-Pan). <i>Biochemistry</i> , <b>2017</b> , 56, 4931-4939	3.2	12
30	Human cellular retinaldehyde-binding protein has secondary thermal 9-cis-retinal isomerase activity. <i>Journal of the American Chemical Society</i> , <b>2014</b> , 136, 137-46	16.4	11
29	Dynamic structural science: recent developments in time-resolved spectroscopy and X-ray crystallography. <i>Biochemical Society Transactions</i> , <b>2013</b> , 41, 1260-4	5.1	10
28	Effect of molecular size and particle shape on the terahertz absorption of a homologous series of tetraalkylammonium salts. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 7926-34	7.8	10
27	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> , <b>2019</b> , 141, 5211-5219	16.4	9
26	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> , <b>2015</b> , 71, 162-72		9
25	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> , <b>2012</b> , 68, 505-10		9
24	Structure of an Escherichia coli 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> , <b>2009</b> , 65, 1088-90		9
23	Expression, purification, crystallization and preliminary X-ray diffraction of a novel Nitrosomonas europaea cytochrome, cytochrome P460. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2006</b> , 62, 395-8		8

22	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> , <b>2018</b> , 8, 14876	4.9	8
21	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> , <b>2013</b> , 69, 398-408		7
20	Catching catalysis in the act: using single crystal kinetics to trap methylamine dehydrogenase reaction intermediates. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2003</b> , 1647, 381-9	4	7
19	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> , <b>2010</b> , 1804, 212-22	4	6
18	Threonine 57 is required for the post-translational activation of <i>Escherichia coli</i> aspartate $\beta$ -decarboxylase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 1166-72		5
17	Synthesis and characterisation of $\beta$ -carboxynitrobenzyl photocaged L-aspartates for applications in time-resolved structural biology.. <i>RSC Advances</i> , <b>2019</b> , 9, 8695-8699	3.7	4
16	Oxygen Activation Switch in the Copper Amine Oxidase of <i>Escherichia coli</i> . <i>Biochemistry</i> , <b>2018</b> , 57, 5301-5314	5.14	4
15	If You Can Get a Crystal Structure, Why Bother with Anything Else?. <i>Synchrotron Radiation News</i> , <b>2015</b> , 28, 10-14	0.6	4
14	Probing the molecular mechanisms in copper amine oxidases by generating heterodimers. <i>ChemBioChem</i> , <b>2015</b> , 16, 559-64	3.8	4
13	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> , <b>2009</b> , 65, 486-8		3
12	Identification of the site of oxidase substrate binding in <i>Scytalidium thermophilum</i> catalase. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2018</b> , 74, 979-985	5.5	3
11	SARS-CoV-2 papain-like protease PLpro in complex with natural compounds reveal allosteric sites for antiviral drug design		3
10	Using photocaging for fast time-resolved structural biology studies. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 1218-1232	5.5	3
9	Homogeneous batch micro-crystallization of proteins from ammonium sulfate. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2021</b> , 77, 194-204	5.5	3
8	Crystal structure of a domain-swapped photoactivatable sfGFP variant provides evidence for GFP folding pathway. <i>FEBS Journal</i> , <b>2019</b> , 286, 2329-2340	5.7	2
7	Investigating the active centre of the <i>Scytalidium thermophilum</i> catalase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 369-75		2
6	Dissecting the mechanism of oxygen trafficking in a metalloenzyme. <i>Faraday Discussions</i> , <b>2011</b> , 148, 269-82; discussion 299-314	3.6	2
5	Best practices for time-resolved serial synchrotron crystallography.. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2022</b> , 78, 14-29	5.5	2

4	Probing temperature- and solvent-dependent protein dynamics using terahertz time-domain spectroscopy. <i>Journal of Applied Crystallography</i> , <b>2014</b> , 47, 146-153	3.8	2
3	Probing the role of Val228 on the catalytic activity of Scytalidium catalase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2021</b> , 1869, 140662	4	0
2	Preface to Special Topic: Transactions from the 66th Annual Meeting of the American Crystallographic Association. <i>Structural Dynamics</i> , <b>2017</b> , 4, 032001	3.2	
1	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> , <b>2014</b> , 253-259	0.1	