

Arwen R Pearson

List of Publications by Year in descending order

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86
papers

2,548
citations

185998

28
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214527

47
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92
all docs

92
docs citations

92
times ranked

3675
citing authors

#	ARTICLE	IF	CITATIONS
1	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. <i>Science</i> , 2021, 372, 642-646.	6.0	240
2	MauG, a Novel Diheme Protein Required for Tryptophan Tryptophylquinone Biogenesis. <i>Biochemistry</i> , 2003, 42, 7318-7325.	1.2	123
3	All Three Domains of the Hepatitis C Virus Nonstructural NS5A Protein Contribute to RNA Binding. <i>Journal of Virology</i> , 2010, 84, 9267-9277.	1.5	108
4	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, 41-48.	2.6	97
5	Nature of the Ferryl Heme in Compounds I and II. <i>Journal of Biological Chemistry</i> , 2011, 286, 1260-1268.	1.6	90
6	Packaging signals in single-stranded RNA viruses: nature's alternative to a purely electrostatic assembly mechanism. <i>Journal of Biological Physics</i> , 2013, 39, 277-287.	0.7	86
7	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.	7.7	78
8	Further Insights into Quinone Cofactor Biogenesis: Probing the Role of mauG in Methylamine Dehydrogenase Tryptophan Tryptophylquinone Formation. <i>Biochemistry</i> , 2004, 43, 5494-5502.	1.2	76
9	Exploring Molecular Oxygen Pathways in <i>Hansenula polymorpha</i> Copper-containing Amine Oxidase. <i>Journal of Biological Chemistry</i> , 2007, 282, 17767-17776.	1.6	76
10	Liquid application method for time-resolved analyses by serial synchrotron crystallography. <i>Nature Methods</i> , 2019, 16, 979-982.	9.0	74
11	Fixed target combined with spectral mapping: approaching 100% hit rates for serial crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 944-955.	1.1	71
12	Serial synchrotron crystallography for time-resolved structural biology. <i>Current Opinion in Structural Biology</i> , 2020, 65, 168-174.	2.6	62
13	X-ray-Based Techniques to Study the Nano-Bio Interface. <i>ACS Nano</i> , 2021, 15, 3754-3807.	7.3	60
14	Structure-guided design affirms inhibitors of hepatitis C virus p7 as a viable class of antivirals targeting virion release. <i>Hepatology</i> , 2014, 59, 408-422.	3.6	56
15	Structural Insight into Methyl-Coenzyme M Reductase Chemistry Using Coenzyme B Analogues. <i>Biochemistry</i> , 2010, 49, 7683-7693.	1.2	55
16	MauG-Dependent in Vitro Biosynthesis of Tryptophan Tryptophylquinone in Methylamine Dehydrogenase. <i>Journal of the American Chemical Society</i> , 2005, 127, 8258-8259.	6.6	52
17	Microspectrophotometry for structural enzymology. <i>Current Opinion in Structural Biology</i> , 2004, 14, 656-662.	2.6	51
18	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, 1050-1064.	2.0	50

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19	The Crystal Structure of Cytochrome P460 of <i>Nitrosomonas europaea</i> Reveals a Novel Cytochrome Fold and Heme α -Protein Cross-link. <i>Biochemistry</i> , 2007, 46, 8340-8349.	1.2	48
20	Mechanistic Possibilities in MauG-Dependent Tryptophan Tryptophylquinone Biosynthesis. <i>Biochemistry</i> , 2006, 45, 13276-13283.	1.2	45
21	3D-MiXD: 3D-printed X-ray-compatible microfluidic devices for rapid, low-consumption serial synchrotron crystallography data collection in flow. <i>IUCr</i> , 2020, 7, 207-219.	1.0	43
22	Reaction Mechanism of <i>N</i> -Acetylneuraminic Acid Lyase Revealed by a Combination of Crystallography, QM/MM Simulation, and Mutagenesis. <i>ACS Chemical Biology</i> , 2014, 9, 1025-1032.	1.6	41
23	A new on-axis multimode spectrometer for the macromolecular crystallography beamlines of the Swiss Light Source. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 173-182.	1.0	39
24	Using photocaging for fast time-resolved structural biology studies. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1218-1232.	1.1	39
25	The HARE chip for efficient time-resolved serial synchrotron crystallography. <i>Journal of Synchrotron Radiation</i> , 2020, 27, 360-370.	1.0	39
26	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, 92-98.	1.0	37
27	Combining X-ray crystallography and single-crystal spectroscopy to probe enzyme mechanisms. <i>Biochemical Society Transactions</i> , 2009, 37, 378-381.	1.6	31
28	Exploring the Roles of the Metal Ions in <i>Escherichia coli</i> Copper Amine Oxidase. <i>Biochemistry</i> , 2010, 49, 1268-1280.	1.2	30
29	Isolation of an Asymmetric RNA Uncoating Intermediate for a Single-Stranded RNA Plant Virus. <i>Journal of Molecular Biology</i> , 2012, 417, 65-78.	2.0	30
30	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.	6.2	30
31	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.	3.3	30
32	Time-resolved crystallography using the Hadamard transform. <i>Nature Methods</i> , 2014, 11, 1131-1134.	9.0	29
33	Structural Insights into Substrate Specificity in Variants of <i>N</i> -Acetylneuraminic Acid Lyase Produced by Directed Evolution. <i>Journal of Molecular Biology</i> , 2010, 404, 56-69.	2.0	28
34	Topological Dissection of the Membrane Transport Protein Mhp1 Derived from Cysteine Accessibility and Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 8844-8852.	3.2	28
35	Structural Kinetics of MsbA Investigated by Stopped-Flow Time-Resolved Small-Angle X-Ray Scattering. <i>Structure</i> , 2020, 28, 348-354.e3.	1.6	28
36	Structural Insights into the Recovery of Aldolase Activity in <i>N</i> -Acetylneuraminic Acid Lyase by Replacement of the Catalytically Active Lysine with ^{13}C -Thialysine by Using a Chemical Mutagenesis Strategy. <i>ChemBioChem</i> , 2013, 14, 474-481.	1.3	26

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37	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, 12416-12417.	6.6	23
38	Understanding Quinone Cofactor Biogenesis in Methylamine Dehydrogenase through Novel Cofactor Generation. <i>Biochemistry</i> , 2003, 42, 3224-3230.	1.2	21
39	Best practices for time-resolved serial synchrotron crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 14-29.	1.1	21
40	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, 6093-6099.	1.5	20
41	Cryocrystallography of metalloprotein reaction intermediates. <i>Current Opinion in Chemical Biology</i> , 2002, 6, 202-207.	2.8	19
42	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, 105-112.	1.5	19
43	Revealing low-dose radiation damage using single-crystal spectroscopy. <i>Journal of Synchrotron Radiation</i> , 2011, 18, 367-373.	1.0	18
44	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.	6.6	18
45	Hinge disulfides in human IgG2 CD40 antibodies modulate receptor signaling by regulation of conformation and flexibility. <i>Science Immunology</i> , 2022, 7, .	5.6	18
46	Active Site Aspartate Residues Are Critical for Tryptophan Tryptophylquinone Biogenesis in Methylamine Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2005, 280, 17392-17396.	1.6	15
47	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, 1105-1109.	0.7	15
48	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.	1.9	15
49	Human Cellular Retinaldehyde-Binding Protein Has Secondary Thermal 9- <i>cis</i> -Retinal Isomerase Activity. <i>Journal of the American Chemical Society</i> , 2014, 136, 137-146.	6.6	15
50	Effect of Molecular Size and Particle Shape on the Terahertz Absorption of a Homologous Series of Tetraalkylammonium Salts. <i>Analytical Chemistry</i> , 2013, 85, 7926-7934.	3.2	14
51	The Mechanism of Regulation of Pantothenate Biosynthesis by the PanD-PanZ-AcCoA Complex Reveals an Additional Mode of Action for the Antimetabolite <i>N</i> -Pentyl Pantothenamide (N5-Pan). <i>Biochemistry</i> , 2017, 56, 4931-4939.	1.2	14
52	Homogeneous batch micro-crystallization of proteins from ammonium sulfate. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 194-204.	1.1	12
53	Dynamic structural science: recent developments in time-resolved spectroscopy and X-ray crystallography. <i>Biochemical Society Transactions</i> , 2013, 41, 1260-1264.	1.6	11
54	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.	1.6	11

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55	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, 505-510.	2.5	10
56	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.	2.5	10
57	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, 162-172.	2.5	10
58	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, 381-389.	1.1	9
59	Structure of an <i>Escherichia coli</i> N-acetyl-D-neuraminic acid lyase mutant, E192N, in complex with pyruvate at 1.45 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1088-1090.	0.7	9
60	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, 395-398.	0.7	8
61	Oxygen Activation Switch in the Copper Amine Oxidase of <i>Escherichia coli</i> . <i>Biochemistry</i> , 2018, 57, 5301-5314.	1.2	8
62	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, 212-222.	1.1	6
63	Threonine 57 is required for the post-translational activation of <i>Escherichia coli</i> aspartate β -decarboxylase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1166-1172.	2.5	5
64	Probing the Molecular Mechanisms in Copper Amine Oxidases by Generating Heterodimers. <i>ChemBioChem</i> , 2015, 16, 559-564.	1.3	5
65	Crystal structure of a domain-swapped photoactivatable sfGFP variant provides evidence for GFP folding pathway. <i>FEBS Journal</i> , 2019, 286, 2329-2340.	2.2	5
66	Identification of the site of oxidase substrate binding in <i>Scytalidium thermophilum</i> catalase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 979-985.	1.1	5
67	If You Can Get a Crystal Structure, Why Bother with Anything Else?. <i>Synchrotron Radiation News</i> , 2015, 28, 10-14.	0.2	4
68	Synthesis and characterisation of β -carboxynitrobenzyl photocaged aspartates for applications in time-resolved structural biology. <i>RSC Advances</i> , 2019, 9, 8695-8699.	1.7	4
69	Probing temperature- and solvent-dependent protein dynamics using terahertz time-domain spectroscopy. <i>Journal of Applied Crystallography</i> , 2014, 47, 146-153.	1.9	4
70	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, 486-488.	0.7	3
71	Investigating the active centre of the <i>Scytalidium thermophilum</i> catalase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 369-375.	0.7	3
72	Probing the role of Val228 on the catalytic activity of <i>Scytalidium</i> catalase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140662.	1.1	3

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73	Dissecting the mechanism of oxygen trafficking in a metalloenzyme. Faraday Discussions, 2011, 148, 269-282.	1.6	2
74	Nature of the ferryl heme in Compounds I and II.. Journal of Biological Chemistry, 2011, 286, 18344.	1.6	1
75	Terahertz time-domain spectroscopy of lysozyme and mouse urinary protein single crystals. , 2013, , .		1
76	Capturing Functionally Relevant Protein Motions at the Atomic Level: Femtosecond Time Resolved Serial Crystallography of Ligand Dissociation of Carboxy-Myoglobin. Biophysical Journal, 2016, 110, 513a.	0.2	1
77	On Axis Resonance Raman Microspectroscopy Combined with Macromolecular Crystallography at the Swiss Light Source. , 2010, , .		0
78	Terahertz spectral measurements of a homologous organic series. , 2010, , .		0
79	Terahertz time-domain spectroscopy of protein single crystals. , 2010, , .		0
80	Calculation of terahertz active normal modes in organic crystals. , 2010, , .		0
81	Understanding the influence of morphology on the terahertz spectra of a powdered ionic crystalline system. , 2013, , .		0
82	Preface to Special Topic: Transactions from the 66th Annual Meeting of the American Crystallographic Association. Structural Dynamics, 2017, 4, 032001.	0.9	0
83	Structure, Substrate Recognition, and Mechanism of the Na ⁺ -Hydantoin Membrane Transport Protein, Mhp1. , 2019, , 1-12.		0
84	Experimental phasing and radiation damage. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, .	2.5	0
85	Combining Single Crystal UV/Vis Spectroscopy and Diffraction to Structurally Characterise Intermediates and Monitor Radiation Damage. NATO Science for Peace and Security Series A: Chemistry and Biology, 2014, , 253-259.	0.5	0
86	Structure, Substrate Recognition, and Mechanism of the Na ⁺ -Hydantoin Membrane Transport Protein, Mhp1. , 2019, , 1-12.		0