

# Gwyndaf Evans

## List of Publications by Year in descending order

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104  
papers

4,976  
citations

117453

34  
h-index

98622

67  
g-index

106  
all docs

106  
docs citations

106  
times ranked

7068  
citing authors

#	ARTICLE	IF	CITATIONS
1	Trapping and structural characterisation of a covalent intermediate in vitamin B <sub>6</sub> biosynthesis catalysed by the Pdx1 PLP synthase. RSC Chemical Biology, 2022, 3, 227-230.	2.0	0
2	<sc>DIALS</sc> as a toolkit. Protein Science, 2022, 31, 232-250.	3.1	55
3	A Sample Preparation Pipeline for Microcrystals at the VMXm Beamline. Journal of Visualized Experiments, 2021, , .	0.2	2
4	An on-demand, drop-on-drop method for studying enzyme catalysis by serial crystallography. Nature Communications, 2021, 12, 4461.	5.8	34
5	Machine learning applications in macromolecular X-ray crystallography. Crystallography Reviews, 2021, 27, 54-101.	0.4	8
6	Parakeet: a digital twin software pipeline to assess the impact of experimental parameters on tomographic reconstructions for cryo-electron tomography. Open Biology, 2021, 11, 210160.	1.5	5
7	A Workflow for Protein Structure Determination From Thin Crystal Lamella by Micro-Electron Diffraction. Frontiers in Molecular Biosciences, 2020, 7, 179.	1.6	21
8	Measuring energy-dependent photoelectron escape in microcrystals. IUCrJ, 2020, 7, 129-135.	1.0	9
9	The predictive power of data-processing statistics. IUCrJ, 2020, 7, 342-354.	1.0	7
10	Scanning electron microscopy as a method for sample visualization in protein X-ray crystallography. IUCrJ, 2020, 7, 500-508.	1.0	5
11	Scaling diffraction data in the <i>DIALS</i> software package: algorithms and new approaches for multi-crystal scaling. Acta Crystallographica Section D: Structural Biology, 2020, 76, 385-399.	1.1	107
12	High-throughput <i>in situ</i> experimental phasing. Acta Crystallographica Section D: Structural Biology, 2020, 76, 790-801.	1.1	6
13	Optical elements for dynamically broadening the focus of micro-focus optics at synchrotron x-ray sources. AIP Conference Proceedings, 2019, , .	0.3	0
14	New covariance-based methods for unconventional MR of transmembrane proteins. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e191-e191.	0.0	0
15	Combatting MX measurement errors at source. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e160-e160.	0.0	0
16	Machine learning for experimental phasing in MX. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e174-e174.	0.0	0
17	Measuring the dose: photoelectron escape in micro-crystals. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, e24-e24.	0.0	0
18	Towards in cellulose virus crystallography. Scientific Reports, 2018, 8, 3771.	1.6	11

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19	Improving signal strength in serial crystallography with <i>DIALS</i> geometry refinement. Acta Crystallographica Section D: Structural Biology, 2018, 74, 877-894.	1.1	49
20	Machining protein microcrystals for structure determination by electron diffraction. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9569-9573.	3.3	69
21	<i>DIALS</i> : implementation and evaluation of a new integration package. Acta Crystallographica Section D: Structural Biology, 2018, 74, 85-97.	1.1	811
22	Where is crystallography going?. Acta Crystallographica Section D: Structural Biology, 2018, 74, 152-166.	1.1	54
23	Scaling data in the DIALS framework. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e423-e423.	0.0	0
24	Using DIALS with DUI. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e148-e149.	0.0	0
25	Lysine relay mechanism coordinates intermediate transfer in vitamin B6 biosynthesis. Nature Chemical Biology, 2017, 13, 290-294.	3.9	16
26	An effective introduction to structural crystallography using 1D Gaussian atoms. European Journal of Physics, 2017, 38, 065501.	0.3	0
27	A Novel Approach to Data Collection for Difficult Structures: Data Management for Large Numbers of Crystals with the BLEND Software. Crystals, 2017, 7, 242.	1.0	6
28	<i>AUSPEX</i> : a graphical tool for X-ray diffraction data analysis. Acta Crystallographica Section D: Structural Biology, 2017, 73, 729-737.	1.1	16
29	Background modelling of diffraction data in the presence of ice rings. IUCrJ, 2017, 4, 626-638.	1.0	14
30	Maximum-likelihood methods in DIALS. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C340-C340.	0.0	0
31	Treatment of X-ray diffraction data at Diamond Light Source. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C628-C628.	0.0	0
32	<i>TakeTwo</i> : an indexing algorithm suited to still images with known crystal parameters. Acta Crystallographica Section D: Structural Biology, 2016, 72, 956-965.	1.1	35
33	Structural Biology with Microfocus Beamlines. Springer Protocols, 2016, , 241-273.	0.1	7
34	Applications of the BLEND Software to Crystallographic Data from Membrane Proteins. Advances in Experimental Medicine and Biology, 2016, 922, 119-135.	0.8	9
35	Structure of photosystem II and substrate binding at room temperature. Nature, 2016, 540, 453-457.	13.7	323
36	Development of a multi-lane X-ray mirror providing variable beam sizes. Review of Scientific Instruments, 2016, 87, 051802.	0.6	17

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37	On the release of <i>cppxfel</i> for processing X-ray free-electron laser images. <i>Journal of Applied Crystallography</i> , 2016, 49, 1065-1072.	1.9	28
38	Robust background modelling in <i>DIALS</i> . <i>Journal of Applied Crystallography</i> , 2016, 49, 1912-1921.	1.9	44
39	Imperfection and radiation damage in protein crystals studied with coherent radiation. <i>Journal of Synchrotron Radiation</i> , 2016, 23, 228-237.	1.0	5
40	Diffraction-geometry refinement in the <i>DIALS</i> framework. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 558-575.	1.1	158
41	TakeTwo: an indexing algorithm suited to still images with known crystal parameters. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s195-s195.	0.0	0
42	Two-dimensional spherical-polar visualization of data completeness using equal-volume units of reciprocal space. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s431-s432.	0.0	0
43	Background modelling in the presence of ice rings. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s162-s162.	0.0	0
44	MX data analysis developments at Diamond Light Source. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s18-s19.	0.0	0
45	Introducing DLUI, a graphical interface for <i>DIALS</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s189-s189.	0.0	4
46	<i>DIALS</i> – a new toolbox for diffraction image integration. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s504-s504.	0.0	1
47	The <i>DIALS</i> framework. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s501-s501.	0.0	0
48	VMXm: a new sub-micron beamline for macromolecular crystallography at Diamond Light Source. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s191-s191.	0.0	7
49	Multicrystal analysis with <i>DIALSandBLEND</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s185-s185.	0.0	0
50	Analysis of multi-crystal datasets with <i>xia2</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s19-s19.	0.0	0
51	In vacuo X-ray data collection from graphene-wrapped protein crystals. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s13-s13.	0.0	0
52	Structure of CPV17 polyhedrin determined by the improved analysis of serial femtosecond crystallographic data. <i>Nature Communications</i> , 2015, 6, 6435.	5.8	56
53	Data Analysis: Keeping Pace with Extraordinary Change. <i>Synchrotron Radiation News</i> , 2015, 28, 31-36.	0.2	1
54	A revised partiality model and post-refinement algorithm for X-ray free-electron laser data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1400-1410.	2.5	60

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55	Structure determination of an integral membrane protein at room temperature from crystals <i>in situ</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1228-1237.	2.5	36
56	Surface profiling of X-ray mirrors for shaping focused beams. <i>Optics Express</i> , 2015, 23, 1576.	1.7	14
57	Polyhedra structures and the evolution of the insect viruses. <i>Journal of Structural Biology</i> , 2015, 192, 88-99.	1.3	25
58	Application of In Situ Diffraction in High-Throughput Structure Determination Platforms. <i>Methods in Molecular Biology</i> , 2015, 1261, 233-253.	0.4	18
59	<i>In vacuo</i> X-ray data collection from graphene-wrapped protein crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2079-2088.	2.5	9
60	<i>dxtbx</i> : the diffraction experiment toolbox. <i>Journal of Applied Crystallography</i> , 2014, 47, 1459-1465.	1.9	29
61	New methods for indexing multi-lattice diffraction data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2652-2666.	2.5	56
62	Membrane protein structure determination – The next generation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 78-87.	1.4	190
63	Exploiting fast detectors to enter a new dimension in room-temperature crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1248-1256.	2.5	72
64	Collecting and analyzing diffraction data from multiple crystals. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C314-C314.	0.0	0
65	Micro-focused X-ray diffraction characterization of high-quality [6,6]-phenyl-C61-butyric acid methyl ester single crystals without solvent impurities. <i>Journal of Materials Chemistry C</i> , 2013, 1, 5619.	2.7	61
66	Visualization of membrane protein crystals in lipid cubic phase using X-ray imaging. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1252-1259.	2.5	22
67	Clustering procedures for the optimal selection of data sets from multiple crystals in macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1617-1632.	2.5	224
68	Automated processing of datasets obtained from multiple crystals. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s29-s30.	0.3	0
69	Diffraction data collection with a dynamically variable beam size. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s409-s409.	0.3	1
70	More haste and more speed: outrunning damage in room temperature MX. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s84-s84.	0.3	0
71	Visualisation of membrane protein crystals in lipid cubic phase using X-ray imaging. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s363-s363.	0.3	0
72	Two-dimensional algorithms in Dials project. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s397-s397.	0.3	0

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73	Automated processing of data sets obtained from multiple crystals. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s284-s284.	0.3	0
74	DXTBX: the diffraction experiment toolbox. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s393-s393.	0.3	0
75	Automated processing of datasets obtained from multiple crystals. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s142-s142.	0.3	0
76	The crystal structure of samarosporin I at atomic resolution. Journal of Peptide Science, 2012, 18, 678-684.	0.8	12
77	A sensor-adaptor mechanism for enterovirus uncoating from structures of EV71. Nature Structural and Molecular Biology, 2012, 19, 424-429.	3.6	347
78	<i>In situ</i> macromolecular crystallography using microbeams. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 592-600.	2.5	113
79	Outrunning free radicals in room-temperature macromolecular crystallography. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 810-818.	2.5	83
80	Macromolecular microcrystallography. Crystallography Reviews, 2011, 17, 105-142.	0.4	55
81	On the allowed values for the triclinic unit-cell angles. Acta Crystallographica Section A: Foundations and Advances, 2011, 67, 93-95.	0.3	7
82	The design of macromolecular crystallography diffraction experiments. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 261-270.	2.5	40
83	A novel technique combining high-resolution synchrotron x-ray microtomography and x-ray diffraction for characterization of micro particulates. Measurement Science and Technology, 2011, 22, 115703.	1.4	7
84	Estimation of errors in diffraction data measured by CCD area detectors. Journal of Applied Crystallography, 2010, 43, 1356-1371.	1.9	32
85	High-speed crystal detection and characterization using a fast-readout detector. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1032-1035.	2.5	63
86	Mammalian cell expression, purification, crystallization and microcrystal data collection of autotaxin/ENPP2, a secreted mammalian glycoprotein. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1130-1135.	0.7	25
87	How baculovirus polyhedra fit square pegs into round holes to robustly package viruses. EMBO Journal, 2010, 29, 505-514.	3.5	90
88	A comparison of muscle thin filament models obtained from electron microscopy reconstructions and low-angle X-ray fibre diagrams from non-overlap muscle. Journal of Structural Biology, 2006, 155, 273-284.	1.3	160
89	Data collection and analysis. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 0-0.	2.5	0
90	The Structural Biology Center 19ID undulator beamline: facility specifications and protein crystallographic results. Journal of Synchrotron Radiation, 2006, 13, 30-45.	1.0	143

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91	Vinculin activation by talin through helical bundle conversion. <i>Nature</i> , 2004, 427, 171-175.	13.7	219
92	SAD phasing with triiodide, softer X-rays and some help from radiation damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1429-1434.	2.5	19
93	Triiodide derivatization in protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1923-1929.	2.5	10
94	Triiodide derivatization and combinatorial counter-ion replacement: two methods for enhancing phasing signal using laboratory Cu K $\alpha$ X-ray equipment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 976-991.	2.5	47
95	CHOOCH: a program for deriving anomalous-scattering factors from X-ray fluorescence spectra. <i>Journal of Applied Crystallography</i> , 2001, 34, 82-86.	1.9	232
96	Modelling prior distributions of atoms for macromolecular refinement and completion. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1316-1323.	2.5	60
97	In-house low-resolution X-ray crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1304-1311.	2.5	2
98	Design of a vacuum-compatible high-precision monochromatic beam-position monitor for use with synchrotron radiation from 5 to 25 keV. <i>Journal of Synchrotron Radiation</i> , 2000, 7, 61-68.	1.0	47
99	A MAD experiment performed at the white line of the iridium LIII absorption edge in lysozyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 67-76.	2.5	2
100	Taking MAD to the extreme: ultrafast protein structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1168-1173.	2.5	101
101	MAD data collection – current trends. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1726-1732.	2.5	40
102	Characteristics and Crystal Structure of Bacterial Inosine-5'-monophosphate Dehydrogenase. <i>Biochemistry</i> , 1999, 38, 4691-4700.	1.2	169
103	Differential Signatures of Bacterial and Mammalian IMP Dehydrogenase Enzymes. <i>Current Medicinal Chemistry</i> , 1999, 6, 537-543.	1.2	24
104	Stabilization and calibration of X-ray wavelengths for anomalous diffraction measurements using synchrotron radiation. <i>Review of Scientific Instruments</i> , 1996, 67, 3428-3433.	0.6	8