

# Sean M Mcsweeney

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

3,123  
citations

201674

27  
h-index

214800

47  
g-index

52  
all docs

52  
docs citations

52  
times ranked

4439  
citing authors

#	ARTICLE	IF	CITATIONS
1	Upgraded ESRF BM29 beamline for SAXS on macromolecules in solution. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 660-664.	2.4	359
2	The "fingerprint"™ that X-rays can leave on structures. <i>Structure</i> , 2000, 8, 315-328.	3.3	302
3	Structural characterization of IrisFP, an optical highlighter undergoing multiple photo-induced transformations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18343-18348.	7.1	211
4	The ID23-2 structural biology microfocus beamline at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 107-118.	2.4	195
5	<i>iMxCuBE</i> : a synchrotron beamline control environment customized for macromolecular crystallography experiments. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 700-707.	2.4	193
6	ID29: a high-intensity highly automated ESRF beamline for macromolecular crystallography experiments exploiting anomalous scattering. <i>Journal of Synchrotron Radiation</i> , 2012, 19, 455-461.	2.4	172
7	The ID23-1 structural biology beamline at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2006, 13, 227-238.	2.4	140
8	ISPyB: an information management system for synchrotron macromolecular crystallography. <i>Bioinformatics</i> , 2011, 27, 3186-3192.	4.1	135
9	MASSIF-1: a beamline dedicated to the fully automatic characterization and data collection from crystals of biological macromolecules. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 1540-1547.	2.4	133
10	Automatic processing of macromolecular crystallography X-ray diffraction data at the ESRF. <i>Journal of Applied Crystallography</i> , 2013, 46, 804-810.	4.5	107
11	Diffraction cartography: applying microbeams to macromolecular crystallography sample evaluation and data collection. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 855-864.	2.5	93
12	The application of hierarchical cluster analysis to the selection of isomorphous crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 649-658.	2.5	80
13	ID30B " a versatile beamline for macromolecular crystallography experiments at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 1249-1260.	2.4	72
14	Colouring cryo-cooled crystals: online microspectrophotometry. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 163-172.	2.4	69
15	Structural basis for SARS-CoV-2 envelope protein recognition of human cell junction protein PALS1. <i>Nature Communications</i> , 2021, 12, 3433.	12.8	69
16	Crystal structure and DNA-binding analysis of RecO from <i>Deinococcus radiodurans</i> . <i>EMBO Journal</i> , 2005, 24, 906-918.	7.8	67
17	Evidence for the formation of disulfide radicals in protein crystals upon X-ray irradiation. <i>Journal of Synchrotron Radiation</i> , 2002, 9, 342-346.	2.4	63
18	A decade of user operation on the macromolecular crystallography MAD beamline ID14-4 at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 803-812.	2.4	54

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19	Inducing phase changes in crystals of macromolecules: Status and perspectives for controlled crystal dehydration. <i>Journal of Structural Biology</i> , 2011, 175, 236-243.	2.8	51
20	Automation of macromolecular crystallography beamlines. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 89, 124-152.	2.9	46
21	Structural and Functional Characterization of an SMC-like Protein RecN: New Insights into Double-Strand Break Repair. <i>Structure</i> , 2012, 20, 2076-2089.	3.3	43
22	Structural and Mutational Analyses of <i>Deinococcus radiodurans</i> UvrA2 Provide Insight into DNA Binding and Damage Recognition by UvrAs. <i>Structure</i> , 2009, 17, 547-558.	3.3	38
23	Structural basis for Ca <sup>2+</sup> -dependent activation of a plant metacaspase. <i>Nature Communications</i> , 2020, 11, 2249.	12.8	38
24	RoboDiff: combining a sample changer and goniometer for highly automated macromolecular crystallography experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 966-975.	2.3	35
25	Progress in research into radiation damage in cryo-cooled macromolecular crystals. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 1-3.	2.4	34
26	<i>MXCuBE2</i> : the dawn of <i>MXCuBE</i> Collaboration. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 393-405.	2.4	30
27	Sample manipulation and data assembly for robust microcrystal synchrotron crystallography. <i>IUCr</i> , 2018, 5, 238-246.	2.2	30
28	Crystal Structure of Maltooligosyltrehalose Trehalohydrolase from <i>Deinococcus radiodurans</i> in Complex with Disaccharides. <i>Journal of Molecular Biology</i> , 2005, 347, 949-963.	4.2	26
29	Online collection and analysis of X-ray fluorescence spectra on the macromolecular crystallography beamlines of the ESRF. <i>Journal of Applied Crystallography</i> , 2009, 42, 333-335.	4.5	24
30	FMX – the Frontier Microfocusing Macromolecular Crystallography Beamline at the National Synchrotron Light Source II. <i>Journal of Synchrotron Radiation</i> , 2021, 28, 650-665.	2.4	24
31	ID30A-3 (MASSIF-3) – a beamline for macromolecular crystallography at the ESRF with a small intense beam. <i>Journal of Synchrotron Radiation</i> , 2020, 27, 844-851.	2.4	23
32	Hepatitis C virus NS3/4A inhibitors and other drug-like compounds as covalent binders of SARS-CoV-2 main protease. <i>Scientific Reports</i> , 2022, 12, .	3.3	20
33	High-speed raster-scanning synchrotron serial microcrystallography with a high-precision piezo-scanner. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 1362-1370.	2.4	18
34	A self-supervised workflow for particle picking in cryo-EM. <i>IUCr</i> , 2020, 7, 719-727.	2.2	18
35	Structure of the Stress Response Protein DR1199 from <i>Deinococcus radiodurans</i> : A Member of the DJ-1 Superfamily. <i>Biochemistry</i> , 2008, 47, 11581-11589.	2.5	17
36	Synchrotron microcrystal native-SAD phasing at a low energy. <i>IUCr</i> , 2019, 6, 532-542.	2.2	14

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37	Robotic sample changers for macromolecular X-ray crystallography and biological small-angle X-ray scattering at the National Synchrotron Light Source II. <i>Journal of Synchrotron Radiation</i> , 2021, 28, 1649-1661.	2.4	11
38	AlphaFold Protein Structure Database for Sequence-Independent Molecular Replacement. <i>Crystals</i> , 2021, 11, 1227.	2.2	9
39	The crystal structure of DR2241 from <i>Deinococcus radiodurans</i> at 1.9 Å... resolution reveals a multi-domain protein with structural similarity to chelatases but also with two additional novel domains. <i>Journal of Structural Biology</i> , 2007, 159, 92-102.	2.8	7
40	High-resolution structure of the antibiotic resistance protein NimA from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 442-447.	0.7	7
41	Purification, crystallization and preliminary X-ray diffraction analysis of a hydroxycinnamoyl-CoA shikimate/quininate hydroxycinnamoyltransferase (HCT) from <i>Coffea canephora</i> involved in chlorogenic acid biosynthesis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 824-828.	0.7	7
42	PyMDA: microcrystal data assembly using Python. <i>Journal of Applied Crystallography</i> , 2020, 53, 277-281.	4.5	6
43	Structure of the dihydrolipoamide succinyltransferase catalytic domain from <i>Escherichia coli</i> in a novel crystal form: a tale of a common protein crystallization contaminant. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 616-624.	0.8	6
44	Cryo-EM structure of transmembrane AAA+ protease FtsH in the ADP state. <i>Communications Biology</i> , 2022, 5, 257.	4.4	4
45	Serial crystallography with multi-stage merging of thousands of images. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 281-288.	0.8	4
46	Expression, purification and preliminary structural analysis of the head domain of <i>Deinococcus radiodurans</i> RecN. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 81-84.	0.7	2
47	Searching for Needles in Haystacks: Automation and the Task of Crystal Structure Determination. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2013, , 47-57.	0.5	2