

Sean Mcsweeney

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11061370/publications.pdf>

Version: 2024-02-01

58
papers

3,150
citations

186265

28
h-index

161849

54
g-index

61
all docs

61
docs citations

61
times ranked

4534
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	AlphaFold Protein Structure Database for Sequence-Independent Molecular Replacement. <i>Crystals</i> , 2021, 11, 1227.	2.2	9
5	Structural basis for Ca ²⁺ -dependent activation of a plant metacaspase. <i>Nature Communications</i> , 2020, 11, 2249.	12.8	38
6	PyMDA: microcrystal data assembly using Python. <i>Journal of Applied Crystallography</i> , 2020, 53, 277-281.	4.5	6
7	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
8	<i>MXCuBE2</i>: the dawn of <i>MXCuBE</i> Collaboration. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 393-405.	2.4	30
9	Post-translational Protein Acetylation: An Elegant Mechanism for Bacteria to Dynamically Regulate Metabolic Functions. <i>Frontiers in Microbiology</i> , 2019, 10, 1604.	3.5	122
10	Synchrotron microcrystal native-SAD phasing at a low energy. <i>IUCrJ</i> , 2019, 6, 532-542.	2.2	14
11	Using sound pulses to solve the crystal-harvesting bottleneck. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 986-999.	2.3	7
12	ID30B – a versatile beamline for macromolecular crystallography experiments at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 1249-1260.	2.4	72
13	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
14	A new MR-SAD algorithm for the automatic building of protein models from low-resolution X-ray data and a poor starting model. <i>IUCrJ</i> , 2018, 5, 166-171.	2.2	33
15	Sample manipulation and data assembly for robust microcrystal synchrotron crystallography. <i>IUCrJ</i> , 2018, 5, 238-246.	2.2	30
16	NLSL-II biomedical beamlines for micro-crystallography, FMX, and for highly automated crystallography, AMX: New opportunities for advanced data collection. <i>AIP Conference Proceedings</i> , 2016, , .	0.4	6
17	Automated data collection based on RoboDiff at the ESRF beamline MASSIF-1. <i>AIP Conference Proceedings</i> , 2016, , .	0.4	0
18	Maintaining Microclimates during Nanoliter Chemical Dispensations Using Custom-Designed Source Plate Lids. <i>Journal of the Association for Laboratory Automation</i> , 2016, 21, 115-124.	2.8	3

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Purification and characterization of DR_2577 (SlpA) a major S-layer protein from <i>Deinococcus radiodurans</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 414.	3.5	20
22	BioSAXS Sample Changer: a robotic sample changer for rapid and reliable high-throughput X-ray solution scattering experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 67-75.	2.5	181
23	Purification, crystallization and preliminary crystallographic analysis of DR0248, an MNT-HEPN fused protein from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 49-53.	0.8	0
24	Structural and functional characterization of two unusual endonuclease III enzymes from <i>Deinococcus radiodurans</i> . <i>Journal of Structural Biology</i> , 2015, 191, 87-99.	2.8	20
25	ISPyB for BioSAXS, the gateway to user autonomy in solution scattering experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 76-85.	2.5	56
26	New features of the cell wall of the radio-resistant bacterium <i>Deinococcus radiodurans</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 1978-1984.	2.6	60
27	An "open" structure of the RecOR complex supports ssDNA binding within the core of the complex. <i>Nucleic Acids Research</i> , 2013, 41, 7972-7986.	14.5	19
28	Upgraded ESRF BM29 beamline for SAXS on macromolecules in solution. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 660-664.	2.4	359
29	A Structural Basis for the Biosynthesis of the Major Chlorogenic Acids Found in Coffee. <i>Plant Physiology</i> , 2012, 160, 249-260.	4.8	120
30	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
31	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
32	Expression, purification and preliminary structural analysis of the coiled-coil domain of <i>Deinococcus radiodurans</i> RecN. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 218-221.	0.7	2
33	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
34	Structure-function studies of an unusual 3-methyladenine DNA glycosylase II (AlkA) from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 703-712.	2.5	15
35	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
36	Purification, crystallization and preliminary X-ray diffraction analysis of a hydroxycinnamoyl-CoA shikimate/quinic acid 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

#	ARTICLE	IF	CITATIONS
37	The ID23-2 structural biology microfocus beamline at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 107-118.	2.4	195
38	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
39	Colouring cryo-cooled crystals: online microspectrophotometry. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 163-172.	2.4	69
40	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
41	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
42	Radiation stability of proteinase K crystals grown by LB nanotemplate method. <i>Journal of Structural Biology</i> , 2009, 168, 409-418.	2.8	23
43	Crystal structure and mutational study of RecOR provide insight into its mode of DNA binding. <i>EMBO Journal</i> , 2007, 26, 3260-3271.	7.8	41
44	The ID23-1 structural biology beamline at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2006, 13, 227-238.	2.4	140
45	The Crystal Structure of Mismatch-specific Uracil-DNA Glycosylase (MUG) from <i>Deinococcus radiodurans</i> Reveals a Novel Catalytic Residue and Broad Substrate Specificity. <i>Journal of Biological Chemistry</i> , 2006, 281, 569-577.	3.4	19
46	Crystal structure and DNA-binding analysis of RecO from <i>Deinococcus radiodurans</i> . <i>EMBO Journal</i> , 2005, 24, 906-918.	7.8	67
47	Automation of macromolecular crystallography beamlines. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 89, 124-152.	2.9	46
48	Automatic structure determination based on the single-wavelength anomalous diffraction technique away from an absorption edge. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 388-396.	2.5	8
49	Structure of the uracil-DNAN-glycosylase (UNG) from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1049-1056.	2.5	25
50	The Structure of the Organic Hydroperoxide Resistance Protein from <i>Deinococcus radiodurans</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 25830-25837.	3.4	36
51	Expression, purification, crystallization and preliminary crystal structure analysis of the <i>Deinococcus radiodurans</i> organic hydroperoxide-resistance protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 920-922.	2.5	2
52	Ligand-binding and metal-exchange crystallographic studies on shrimp alkaline phosphatase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1555-1561.	2.5	26
53	Specific Radiation Damage Can Be Used to Solve Macromolecular Crystal Structures. <i>Structure</i> , 2003, 11, 217-224.	3.3	141
54	The 1.9Å... Crystal Structure of Heat-labile Shrimp Alkaline Phosphatase. <i>Journal of Molecular Biology</i> , 2002, 318, 1265-1274.	4.2	94

#	ARTICLE	IF	CITATIONS
55	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
56	The C1 subunit of β -crustacyanin: the de novo phasing of the crystal structure of a 40 kDa homodimeric protein using the anomalous scattering from S atoms combined with direct methods. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1230-1237.	2.5	23
57	The Crystal Structure of an Asymmetric Complex of the Two Nucleotide Binding Components of Proton-Translocating Transhydrogenase. <i>Structure</i> , 2001, 9, 165-176.	3.3	59
58	The high-resolution structure of the NADP(H)-binding component (dIII) of proton-translocating transhydrogenase from human heart mitochondria. <i>Structure</i> , 2000, 8, 1-12.	3.3	180