

# Christoph Mueller-Dieckmann

## List of Publications by Year in descending order

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26  
papers

1,586  
citations

430874

18  
h-index

552781

26  
g-index

28  
all docs

28  
docs citations

28  
times ranked

2913  
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	<i>MxCuBE</i> : a synchrotron beamline control environment customized for macromolecular crystallography experiments. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 700-707.	2.4	193
3	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
4	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
5	<i>MeshAndCollect</i> : an automated multi-crystal data-collection workflow for synchrotron macromolecular crystallography beamlines. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2328-2343.	2.5	108
6	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
7	CM01: a facility for cryo-electron microscopy at the European Synchrotron. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 528-535.	2.3	83
8	ID30B "a versatile beamline for macromolecular crystallography experiments at the ESRF. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 1249-1260.	2.4	72
9	<i>In crystallo</i> optical spectroscopy ( <i>ic</i> OS) as a complementary tool on the macromolecular crystallography beamlines of the ESRF. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 15-26.	2.5	63
10	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
11	Hierarchical clustering for multiple-crystal macromolecular crystallography experiments: the <i>ccCluster</i> program. <i>Journal of Applied Crystallography</i> , 2017, 50, 1844-1851.	4.5	34
12	A new MR-SAD algorithm for the automatic building of protein models from low-resolution X-ray data and a poor starting model. <i>IUCr</i> , 2018, 5, 166-171.	2.2	33
13	The status of the macromolecular crystallography beamlines at the European Synchrotron Radiation Facility. <i>European Physical Journal Plus</i> , 2015, 130, 1.	2.6	31
14	<i>MXCuBE2</i> : the dawn of <i>MxCuBE</i> Collaboration. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 393-405.	2.4	30
15	Gas-sensitive biological crystals processed in pressurized oxygen and krypton atmospheres: deciphering gas channels in proteins using a novel 'soak-and-freeze' methodology. <i>Journal of Applied Crystallography</i> , 2016, 49, 1478-1487.	4.5	25
16	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
17	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
18	A simple and versatile microfluidic device for efficient biomacromolecule crystallization and structural analysis by serial crystallography. <i>IUCr</i> , 2019, 6, 454-464.	2.2	23

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19	Towards a high-throughput system for high-pressure cooling of cryoprotectant-free biological crystals. <i>Journal of Applied Crystallography</i> , 2014, 47, 584-592.	4.5	20
20	An inexpensive automatically operated device for the flash annealing of crystals of macromolecules. <i>Journal of Applied Crystallography</i> , 2009, 42, 125-128.	4.5	9
21	pH- and concentration-dependent supramolecular assembly of a fungal defensin plectasin variant into helical non-amyloid fibrils. <i>Nature Communications</i> , 2022, 13, .	12.8	9
22	Molecular comparison of Neanderthal and Modern Human adenylosuccinate lyase. <i>Scientific Reports</i> , 2018, 8, 18008.	3.3	6
23	High-pressure crystallography shows noble gas intervention into protein-lipid interaction and suggests a model for anaesthetic action. <i>Communications Biology</i> , 2022, 5, 360.	4.4	4
24	Fully Autonomous Characterization and Data Collection from Crystals of Biological Macromolecules. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	2
25	Structure Solution of the Fluorescent Protein Cerulean Using MeshAndCollect. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	1
26	CrystalDirect-To-Beam: Opening the shortest path from crystal to data. <i>AIP Conference Proceedings</i> , 2019, , .	0.4	1