

# Ricardo D Righetto

## List of Publications by Year in descending order

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Version: 2024-02-01

20  
papers

835  
citations

686830

13  
h-index

839053

18  
g-index

26  
all docs

26  
docs citations

26  
times ranked

1172  
citing authors

#	ARTICLE	IF	CITATIONS
1	Focus: The interface between data collection and data processing in cryo-EM. <i>Journal of Structural Biology</i> , 2017, 198, 124-133.	1.3	192
2	2dx – User-friendly image processing for 2D crystals. <i>Journal of Structural Biology</i> , 2007, 157, 64-72.	1.3	184
3	Deep learning improves macromolecule identification in 3D cellular cryo-electron tomograms. <i>Nature Methods</i> , 2021, 18, 1386-1394.	9.0	84
4	2dx_merge: Data management and merging for 2D crystal images. <i>Journal of Structural Biology</i> , 2007, 160, 375-384.	1.3	63
5	Ligand-induced structural changes in the cyclic nucleotide-modulated potassium channel MloK1. <i>Nature Communications</i> , 2014, 5, 3106.	5.8	59
6	Structural basis of Focal Adhesion Kinase activation on lipid membranes. <i>EMBO Journal</i> , 2020, 39, e104743.	3.5	47
7	2dx_automator: Implementation of a semiautomatic high-throughput high-resolution cryo-electron crystallography pipeline. <i>Journal of Structural Biology</i> , 2014, 186, 302-307.	1.3	29
8	3D reconstruction of two-dimensional crystals. <i>Archives of Biochemistry and Biophysics</i> , 2015, 581, 68-77.	1.4	27
9	Retrieving high-resolution information from disordered 2D crystals by single-particle cryo-EM. <i>Nature Communications</i> , 2019, 10, 1722.	5.8	25
10	Automatic recovery of missing amplitudes and phases in tilt-limited electron crystallography of two-dimensional crystals. <i>Physical Review E</i> , 2011, 84, 011916.	0.8	23
11	Robust image alignment for cryogenic transmission electron microscopy. <i>Journal of Structural Biology</i> , 2017, 197, 279-293.	1.3	23
12	High-Resolution Cryoelectron Microscopy Structure of the Cyclic Nucleotide-Modulated Potassium Channel MloK1 in a Lipid Bilayer. <i>Structure</i> , 2018, 26, 20-27.e3.	1.6	18
13	High-resolution cryo-EM structure of urease from the pathogen <i>Yersinia enterocolitica</i> . <i>Nature Communications</i> , 2020, 11, 5101.	5.8	17
14	MRCZ – A file format for cryo-TEM data with fast compression. <i>Journal of Structural Biology</i> , 2018, 201, 252-257.	1.3	11
15	Image processing techniques for high-resolution structure determination from badly ordered 2D crystals. <i>Journal of Structural Biology</i> , 2018, 203, 120-134.	1.3	9
16	Image Processing of 2D Crystal Images. <i>Methods in Molecular Biology</i> , 2013, 955, 171-194.	0.4	9
17	Merging of Image Data in Electron Crystallography. <i>Methods in Molecular Biology</i> , 2013, 955, 195-209.	0.4	6
18	Automation of Image Processing in Electron Crystallography. <i>Methods in Molecular Biology</i> , 2013, 955, 313-330.	0.4	5

#	ARTICLE	IF	CITATIONS
19	for High-Resolution. <i>Methods in Molecular Biology</i> , 2021, 2215, 267-284.	0.4	0
20	Expanding the arsenal of bacterial spearguns. <i>Nature Microbiology</i> , 2022, 7, 363-364.	5.9	0