

Ricardo D Righetto

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9215087/publications.pdf>

Version: 2024-02-01

20
papers

835
citations

687220

13
h-index

839398

18
g-index

26
all docs

26
docs citations

26
times ranked

1172
citing authors

#	ARTICLE	IF	CITATIONS
1	Expanding the arsenal of bacterial spearguns. <i>Nature Microbiology</i> , 2022, 7, 363-364.	5.9	0
2	Deep learning improves macromolecule identification in 3D cellular cryo-electron tomograms. <i>Nature Methods</i> , 2021, 18, 1386-1394.	9.0	84
3	for High-Resolution. <i>Methods in Molecular Biology</i> , 2021, 2215, 267-284.	0.4	0
4	High-resolution cryo-EM structure of urease from the pathogen <i>Yersinia enterocolitica</i> . <i>Nature Communications</i> , 2020, 11, 5101.	5.8	17
5	Structural basis of Focal Adhesion Kinase activation on lipid membranes. <i>EMBO Journal</i> , 2020, 39, e104743.	3.5	47
6	Retrieving high-resolution information from disordered 2D crystals by single-particle cryo-EM. <i>Nature Communications</i> , 2019, 10, 1722.	5.8	25
7	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
8	MRCZ "A file format for cryo-TEM data with fast compression. <i>Journal of Structural Biology</i> , 2018, 201, 252-257.	1.3	11
9	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
10	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
11	Robust image alignment for cryogenic transmission electron microscopy. <i>Journal of Structural Biology</i> , 2017, 197, 279-293.	1.3	23
12	3D reconstruction of two-dimensional crystals. <i>Archives of Biochemistry and Biophysics</i> , 2015, 581, 68-77.	1.4	27
13	Ligand-induced structural changes in the cyclic nucleotide-modulated potassium channel MloK1. <i>Nature Communications</i> , 2014, 5, 3106.	5.8	59
14	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
15	Image Processing of 2D Crystal Images. <i>Methods in Molecular Biology</i> , 2013, 955, 171-194.	0.4	9
16	Merging of Image Data in Electron Crystallography. <i>Methods in Molecular Biology</i> , 2013, 955, 195-209.	0.4	6
17	Automation of Image Processing in Electron Crystallography. <i>Methods in Molecular Biology</i> , 2013, 955, 313-330.	0.4	5
18	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

#	ARTICLE	IF	CITATIONS
19	2dx"User-friendly image processing for 2D crystals. Journal of Structural Biology, 2007, 157, 64-72.	1.3	184
20	2dx_merge: Data management and merging for 2D crystal images. Journal of Structural Biology, 2007, 160, 375-384.	1.3	63