

Matthew G Iadanza

List of Publications by Citations

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Version: 2024-04-29

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

18
papers

1,187
citations

12
h-index

19
g-index

19
ext. papers

1,596
ext. citations

13.3
avg, IF

4.66
L-index

#	Paper	IF	Citations
18	A new era for understanding amyloid structures and disease. <i>Nature Reviews Molecular Cell Biology</i> , 2018 , 19, 755-773	48.7	357
17	Three-dimensional electron crystallography of protein microcrystals. <i>ELife</i> , 2013 , 2, e01345	8.9	234
16	Lateral opening in the intact β barrel assembly machinery captured by cryo-EM. <i>Nature Communications</i> , 2016 , 7, 12865	17.4	117
15	The structure of a β microglobulin fibril suggests a molecular basis for its amyloid polymorphism. <i>Nature Communications</i> , 2018 , 9, 4517	17.4	85
14	pH-induced molecular shedding drives the formation of amyloid fibril-derived oligomers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 5691-6	11.5	81
13	Engineering the surface properties of a human monoclonal antibody prevents self-association and rapid clearance in vivo. <i>Scientific Reports</i> , 2016 , 6, 38644	4.9	66
12	The structure of purified kinetochores reveals multiple microtubule-attachment sites. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 925-9	17.6	63
11	A cryo-EM grid preparation device for time-resolved structural studies. <i>IUCrJ</i> , 2019 , 6, 1024-1031	4.7	42
10	Variations on Negative Stain Electron Microscopy Methods: Tools for Tackling Challenging Systems. <i>Journal of Visualized Experiments</i> , 2018 ,	1.6	35
9	Collection, pre-processing and on-the-fly analysis of data for high-resolution, single-particle cryo-electron microscopy. <i>Nature Protocols</i> , 2019 , 14, 100-118	18.8	31
8	Fibril structures of diabetes-related amylin variants reveal a basis for surface-templated assembly. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 1048-1056	17.6	29
7	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. <i>Communications Biology</i> , 2020 , 3, 766	6.7	13
6	A suite of software for processing MicroED data of extremely small protein crystals. <i>Journal of Applied Crystallography</i> , 2014 , 47, 1140-1145	3.8	12
5	MpUL-multi: Software for Calculation of Amyloid Fibril Mass per Unit Length from TB-TEM Images. <i>Scientific Reports</i> , 2016 , 6, 21078	4.9	10
4	Cryo-EM structures of an insecticidal Bt toxin reveal its mechanism of action on the membrane. <i>Nature Communications</i> , 2021 , 12, 2791	17.4	4
3	The role of membrane destabilisation and protein dynamics in BAM catalysed OMP folding. <i>Nature Communications</i> , 2021 , 12, 4174	17.4	4
2	Author response: Three-dimensional electron crystallography of protein microcrystals 2013 ,		2

1 A Cryo-EM Grid Preparation Device for Time-Resolved Structural Studies

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