

# Daniel Castaño-Díez

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2489145/publications.pdf>

Version: 2024-02-01

37  
papers

2,969  
citations

279798

23  
h-index

330143

37  
g-index

41  
all docs

41  
docs citations

41  
times ranked

5012  
citing authors

#	ARTICLE	IF	CITATIONS
1	Nanoscale architecture of a VAP-A-OSBP tethering complex at membrane contact sites. <i>Nature Communications</i> , 2021, 12, 3459.	12.8	29
2	Step-by-step guide to efficient subtomogram averaging of virus-like particles with Dynamo. <i>PLoS Biology</i> , 2021, 19, e3001318.	5.6	24
3	FTLD- $\tau$ DP assemblies seed neoaggregates with subtype-specific features via a prion-like cascade. <i>EMBO Reports</i> , 2021, 22, e53877.	4.5	14
4	The Dynamo Software Package for Cryo-electron Tomography and Subtomogram Averaging. <i>Microscopy and Microanalysis</i> , 2020, 26, 3142-3145.	0.4	6
5	“Differential Visual Proteomics” Enabling the Proteome-Wide Comparison of Protein Structures of Single-Cells. <i>Journal of Proteome Research</i> , 2019, 18, 3521-3531.	3.7	1
6	In situ structure determination by subtomogram averaging. <i>Current Opinion in Structural Biology</i> , 2019, 58, 68-75.	5.7	29
7	Lewy pathology in Parkinson’s disease consists of crowded organelles and lipid membranes. <i>Nature Neuroscience</i> , 2019, 22, 1099-1109.	14.8	604
8	Subtomogram averaging from cryo-electron tomograms. <i>Methods in Cell Biology</i> , 2019, 152, 217-259.	1.1	38
9	Live-Cell Structural Biology to Solve Biological Mechanisms: The Case of the Exocyst. <i>Structure</i> , 2019, 27, 886-892.	3.3	3
10	Cerebral Corpora amylacea are dense membranous labyrinths containing structurally preserved cell organelles. <i>Scientific Reports</i> , 2018, 8, 18046.	3.3	21
11	Protocols for Subtomogram Averaging of Membrane Proteins in the Dynamo Software Package. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 82.	3.5	33
12	Focus: The interface between data collection and data processing in cryo-EM. <i>Journal of Structural Biology</i> , 2017, 198, 124-133.	2.8	192
13	Cryo-EM structure of the extended type VI secretion system sheath-tube complex. <i>Nature Microbiology</i> , 2017, 2, 1507-1512.	13.3	107
14	Dynamo Catalogue: Geometrical tools and data management for particle picking in subtomogram averaging of cryo-electron tomograms. <i>Journal of Structural Biology</i> , 2017, 197, 135-144.	2.8	108
15	The <i>Dynamo</i> package for tomography and subtomogram averaging: components for <i>MATLAB</i> , GPU computing and EC2 Amazon Web Services. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 478-487.	2.3	33
16	Cryo-electron tomography reveals novel features of a viral RNA replication compartment. <i>ELife</i> , 2017, 6, .	6.0	89
17	The Structure of the Mouse Serotonin 5-HT <sub>3</sub> Receptor in Lipid Vesicles. <i>Structure</i> , 2016, 24, 165-170.	3.3	36
18	Insight into the Assembly of Viruses with Vertical Single $\beta$ -barrel Major Capsid Proteins. <i>Structure</i> , 2015, 23, 1866-1877.	3.3	29

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19	Structure of the Dodecameric Yersinia enterocolitica Secretin YscC and Its Trypsin-Resistant Core. <i>Structure</i> , 2013, 21, 2152-2161.	3.3	33
20	Mechanism of Membranous Tunnelling Nanotube Formation in Viral Genome Delivery. <i>PLoS Biology</i> , 2013, 11, e1001667.	5.6	75
21	Image Processing of 2D Crystal Images. <i>Methods in Molecular Biology</i> , 2013, 955, 171-194.	0.9	9
22	Merging of Image Data in Electron Crystallography. <i>Methods in Molecular Biology</i> , 2013, 955, 195-209.	0.9	6
23	Automation of Image Processing in Electron Crystallography. <i>Methods in Molecular Biology</i> , 2013, 955, 313-330.	0.9	5
24	In situ structural analysis of the Yersinia enterocolitica injectisome. <i>ELife</i> , 2013, 2, e00792.	6.0	109
25	Heritable yeast prions have a highly organized three-dimensional architecture with interfiber structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14906-14911.	7.1	38
26	LIMITING FACTORS IN SINGLE PARTICLE CRYO ELECTRON TOMOGRAPHY. <i>Computational and Structural Biotechnology Journal</i> , 2012, 1, e201207002.	4.1	28
27	Assessing the benefits of focal pair cryo-electron tomography. <i>Journal of Structural Biology</i> , 2012, 178, 88-97.	2.8	8
28	Dynamo: A flexible, user-friendly development tool for subtomogram averaging of cryo-EM data in high-performance computing environments. <i>Journal of Structural Biology</i> , 2012, 178, 139-151.	2.8	376
29	The three-dimensional molecular structure of the desmosomal plaque. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6480-6485.	7.1	71
30	3D Reconstruction from 2D Crystal Image and Diffraction Data. <i>Methods in Enzymology</i> , 2010, 482, 101-129.	1.0	19
31	Alignment of Cryo-Electron Tomography Datasets. <i>Methods in Enzymology</i> , 2010, 482, 343-367.	1.0	30
32	Alignator: A GPU powered software package for robust fiducial-less alignment of cryo tilt-series. <i>Journal of Structural Biology</i> , 2010, 170, 117-126.	2.8	59
33	Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.	12.6	440
34	Performance evaluation of image processing algorithms on the GPU. <i>Journal of Structural Biology</i> , 2008, 164, 153-160.	2.8	91
35	Radiation dose reduction and image enhancement in biological imaging through equally-sloped tomography. <i>Journal of Structural Biology</i> , 2008, 164, 221-227.	2.8	75
36	Reprint of "Fiducial-less alignment of cryo-sections". <i>J. Struct. Biol.</i> 159 (2007) 413-423. <i>Journal of Structural Biology</i> , 2008, 161, 249-259.	2.8	1

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37	Fiducial-less alignment of cryo-sections. <i>Journal of Structural Biology</i> , 2007, 159, 413-423.	2.8	55