

Michael A Cianfrocco

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3385584/publications.pdf>

Version: 2024-02-01

40
papers

1,365
citations

471061

17
h-index

454577

30
g-index

52
all docs

52
docs citations

52
times ranked

2218
citing authors

#	ARTICLE	IF	CITATIONS
1	Cloud computing platforms to support cryo-EM structure determination. Trends in Biochemical Sciences, 2022, 47, 103-105.	3.7	0
2	A kinesin-1 variant reveals motor-induced microtubule damage in cells. Current Biology, 2022, 32, 2416-2429.e6.	1.8	19
3	Measuring success for a future vision: Defining impact in science gateways/virtual research environments. Concurrency Computation Practice and Experience, 2021, 33, e6099.	1.4	12
4	Parthenolide Destabilizes Microtubules by Covalently Modifying Tubulin. Current Biology, 2021, 31, 900-907.e6.	1.8	15
5	Neuronal SETD2 activity links microtubule methylation to an anxiety-like phenotype in mice. Brain, 2021, 144, 2527-2540.	3.7	17
6	Molecular determinants for α -tubulin methylation by SETD2. Journal of Biological Chemistry, 2021, 297, 100898.	1.6	11
7	A mitochondrial membrane-bridging machinery mediates signal transduction of intramitochondrial oxidation. Nature Metabolism, 2021, 3, 1242-1258.	5.1	28
8	Kinesin-binding protein remodels the kinesin motor to prevent microtubule binding. Science Advances, 2021, 7, eabj9812.	4.7	10
9	The Huntingtin-interacting protein SETD2/HYPB is an actin lysine methyltransferase. Science Advances, 2020, 6, .	4.7	29
10	High-Throughput Cryo-EM Enabled by User-Free Preprocessing Routines. Structure, 2020, 28, 858-869.e3.	1.6	44
11	What Could Go Wrong? A Practical Guide to Single-Particle Cryo-EM: From Biochemistry to Atomic Models. Journal of Chemical Information and Modeling, 2020, 60, 2458-2469.	2.5	25
12	Miro: A molecular switch at the center of mitochondrial regulation. Protein Science, 2020, 29, 1269-1284.	3.1	39
13	Golgi-associated BICD adaptors couple ER membrane penetration and disassembly of a viral cargo. Journal of Cell Biology, 2020, 219, .	2.3	8
14	High-resolution cryo-EM using beam-image shift at 200 keV. IUCr, 2020, 7, 1179-1187.	1.0	14
15	Structural analyses of the PKA RII ² holoenzyme containing the oncogenic DnajB1-PKAc fusion protein reveal protomer asymmetry and fusion-induced allosteric perturbations in fibrolamellar hepatocellular carcinoma. PLoS Biology, 2020, 18, e3001018.	2.6	22
16	Title is missing!. , 2020, 18, e3001018.		0
17	Title is missing!. , 2020, 18, e3001018.		0
18	Title is missing!. , 2020, 18, e3001018.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 18, e3001018.		0
20	Title is missing!. , 2020, 18, e3001018.		0
21	Title is missing!. , 2020, 18, e3001018.		0
22	Reconstitution of Tubulin Methylation by SETD2. <i>Microscopy and Microanalysis</i> , 2019, 25, 1358-1359.	0.2	0
23	Cryo-electron microscopy structure and analysis of the P-Rex1-G1213 signaling scaffold. <i>Science Advances</i> , 2019, 5, eaax8855.	4.7	28
24	Building a Data-driven Workflow to Streamline Cryo-EM Data Processing. <i>Microscopy and Microanalysis</i> , 2019, 25, 1366-1367.	0.2	0
25	Cryo-EM structure of the human MLL1 core complex bound to the nucleosome. <i>Nature Communications</i> , 2019, 10, 5540.	5.8	47
26	Big data in cryoEM: automated collection, processing and accessibility of EM data. <i>Current Opinion in Microbiology</i> , 2018, 43, 1-8.	2.3	45
27	Structural Snapshots of a Dynamic Process in the Regulation of P-Rex, a Metastatic Factor. <i>Microscopy and Microanalysis</i> , 2018, 24, 1218-1219.	0.2	0
28	The Central Stalk Determines the Motility of Mitotic Kinesin-14 Homodimers. <i>Current Biology</i> , 2018, 28, 2302-2308.e3.	1.8	7
29	cryoem-cloud-tools: A software platform to deploy and manage cryo-EM jobs in the cloud. <i>Journal of Structural Biology</i> , 2018, 203, 230-235.	1.3	19
30	Lis1 Has Two Opposing Modes of Regulating Cytoplasmic Dynein. <i>Cell</i> , 2017, 170, 1197-1208.e12.	13.5	78
31	Structural basis for the initiation of eukaryotic transcription-coupled DNA repair. <i>Nature</i> , 2017, 551, 653-657.	13.7	151
32	Structure of Fam20A reveals a pseudokinase featuring a unique disulfide pattern and inverted ATP-binding. <i>ELife</i> , 2017, 6, .	2.8	29
33	Antigenic Characterization of the HCMV gH/gL/gO and Pentamer Cell Entry Complexes Reveals Binding Sites for Potently Neutralizing Human Antibodies. <i>PLoS Pathogens</i> , 2015, 11, e1005230.	2.1	65
34	Structural and biochemical studies of HCMV gH/gL/gO and Pentamer reveal mutually exclusive cell entry complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1767-1772.	3.3	129
35	Mechanism and Regulation of Cytoplasmic Dynein. <i>Annual Review of Cell and Developmental Biology</i> , 2015, 31, 83-108.	4.0	206
36	Low cost, high performance processing of single particle cryo-electron microscopy data in the cloud. <i>ELife</i> , 2015, 4, .	2.8	35

#	ARTICLE	IF	CITATIONS
37	Traffic control: adaptor proteins guide dynein's cargo takeoff. <i>EMBO Journal</i> , 2014, 33, 1845-1846.	3.5	4
38	Human TFIID Binds to Core Promoter DNA in a Reorganized Structural State. <i>Cell</i> , 2013, 152, 120-131.	13.5	110
39	Substrate-specific structural rearrangements of human Dicer. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 662-670.	3.6	89
40	Regulatory interplay between TFIID's conformational transitions and its modular interaction with core promoter DNA. <i>Transcription</i> , 2013, 4, 120-126.	1.7	6