Alex J Noble

List of Publications by Year in descending order

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361413 580821 2,379 26 20 25 h-index citations g-index papers 39 39 39 2978 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Positive-unlabeled convolutional neural networks for particle picking in cryo-electron micrographs. Nature Methods, 2019, 16, 1153-1160.	19.0	693
2	Topaz-Denoise: general deep denoising models for cryoEM and cryoET. Nature Communications, 2020, 11, 5208.	12.8	313
3	Routine single particle CryoEM sample and grid characterization by tomography. ELife, 2018, 7, .	6.0	216
4	Reducing effects of particle adsorption to the air–water interface in cryo-EM. Nature Methods, 2018, 15, 793-795.	19.0	167
5	Routine determination of ice thickness for cryo-EM grids. Journal of Structural Biology, 2018, 204, 38-44.	2.8	114
6	Visualization of clustered protocadherin neuronal self-recognition complexes. Nature, 2019, 569, 280-283.	27.8	86
7	ResLog plots as an empirical metric of the quality of cryo-EM reconstructions. Journal of Structural Biology, 2014, 185, 418-426.	2.8	72
8	Automated batch fiducial-less tilt-series alignment in Appion using Protomo. Journal of Structural Biology, 2015, 192, 270-278.	2.8	64
9	Eliminating effects of particle adsorption to the air/water interface in single-particle cryo-electron microscopy: Bacterial RNA polymerase and CHAPSO. Journal of Structural Biology: X, 2019, 1, 100005.	1.3	60
10	Structure of the gene therapy vector, adeno-associated virus with its cell receptor, AAVR. ELife, 2019, 8, .	6.0	60
11	A pseudoatomic model of the COPII cage obtained from cryo-electron microscopy and mass spectrometry. Nature Structural and Molecular Biology, 2013, 20, 167-173.	8.2	57
12	Characterization of the SARS-CoV-2 S Protein: Biophysical, Biochemical, Structural, and Antigenic Analysis. ACS Omega, 2021, 6, 85-102.	3.5	54
13	Big data in cryoEM: automated collection, processing and accessibility of EM data. Current Opinion in Microbiology, 2018, 43, 1-8.	5.1	45
14	Better, Faster, Cheaper: Recent Advances in Cryo–Electron Microscopy. Annual Review of Biochemistry, 2022, 91, 1-32.	11.1	45
15	Waffle Method: A general and flexible approach for improving throughput in FIB-milling. Nature Communications, 2022, 13, 1857.	12.8	43
16	Insights into the Mechanisms of Membrane Curvature and Vesicle Scission by the Small GTPase Sar1 in the Early Secretory Pathway. Journal of Molecular Biology, 2014, 426, 3811-3826.	4.2	40
17	Family-wide Structural and Biophysical Analysis of Binding Interactions among Non-clustered Î-Protocadherins. Cell Reports, 2020, 30, 2655-2671.e7.	6.4	35
18	Architecture of the human erythrocyte ankyrin-1 complex. Nature Structural and Molecular Biology, 2022, 29, 706-718.	8.2	33

#	Article	IF	CITATIONS
19	The influence of frame alignment with dose compensation on the quality of single particle reconstructions. Journal of Structural Biology, 2015, 192, 196-203.	2.8	30
20	The 2.8ÂÃ Electron Microscopy Structure of Adeno-Associated Virus-DJ Bound by a Heparinoid Pentasaccharide. Molecular Therapy - Methods and Clinical Development, 2017, 5, 1-12.	4.1	30
21	Label-free visual proteomics: Coupling MS- and EM-based approaches in structural biology. Molecular Cell, 2022, 82, 285-303.	9.7	21
22	Mechanisms of opening and closing of the bacterial replicative helicase. ELife, 2018, 7, .	6.0	16
23	TOPAZ: A Positive-Unlabeled Convolutional Neural Network CryoEM Particle Picker that can Pick Any Size and Shape Particle. Microscopy and Microanalysis, 2019, 25, 986-987.	0.4	14
24	Structural basis for the mechanisms of human presequence protease conformational switch and substrate recognition. Nature Communications, 2022, 13, 1833.	12.8	4
25	COPI gets a fancy new coat. Science, 2015, 349, 142-143.	12.6	1
26	ResLog Plots: A New Metric for the Quality of Cryo-EM Reconstructions. Microscopy and Microanalysis, 2014, 20, 1254-1255.	0.4	0