

# Josue Gomez-Blanco

## List of Publications by Year in descending order

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Version: 2024-02-01

28  
papers

1,867  
citations

471061

17  
h-index

552369

26  
g-index

31  
all docs

31  
docs citations

31  
times ranked

2933  
citing authors

#	ARTICLE	IF	CITATIONS
1	Localized reconstruction in Scipion expedites the analysis of symmetry mismatches in cryo-EM data. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 160, 43-52.	1.4	33
2	Local computational methods to improve the interpretability and analysis of cryo-EM maps. <i>Nature Communications</i> , 2021, 12, 1240.	5.8	36
3	Near-atomic structure of an adenovirus reveals a conserved capsid-binding motif and intergenera variations in cementing proteins. <i>Science Advances</i> , 2021, 7, .	4.7	9
4	DeepEMhancer: a deep learning solution for cryo-EM volume post-processing. <i>Communications Biology</i> , 2021, 4, 874.	2.0	561
5	Alternative conformations and motions adopted by 30S ribosomal subunits visualized by cryo-electron microscopy. <i>Rna</i> , 2020, 26, 2017-2030.	1.6	21
6	Deep Learning for Validating and Estimating Resolution of Cryo-Electron Microscopy Density Maps. <i>Molecules</i> , 2019, 24, 1181.	1.7	25
7	Role of Era in assembly and homeostasis of the ribosomal small subunit. <i>Nucleic Acids Research</i> , 2019, 47, 8301-8317.	6.5	34
8	Computational Methods to Process Highly Heterogeneous Cryo-EM Samples. <i>Microscopy and Microanalysis</i> , 2019, 25, 1292-1293.	0.2	0
9	A robust approach to ab initio cryo-electron microscopy initial volume determination. <i>Journal of Structural Biology</i> , 2019, 208, 107397.	1.3	10
10	MonoRes: Automatic and Accurate Estimation of Local Resolution for Electron Microscopy Maps. <i>Structure</i> , 2018, 26, 337-344.e4.	1.6	179
11	Using Scipion for stream image processing at cryo-EM facilities. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a161-a161.	0.0	0
12	Quantitative analysis of 3D alignment quality: its impact on soft-validation, particle pruning and homogeneity analysis. <i>Scientific Reports</i> , 2017, 7, 6307.	1.6	15
13	A review of resolution measures and related aspects in 3D Electron Microscopy. <i>Progress in Biophysics and Molecular Biology</i> , 2017, 124, 1-30.	1.4	30
14	Acquisition of functions on the outer capsid surface during evolution of double-stranded RNA fungal viruses. <i>PLoS Pathogens</i> , 2017, 13, e1006755.	2.1	26
15	Fast and automatic identification of particle tilt pairs based on Delaunay triangulation. <i>Journal of Structural Biology</i> , 2016, 196, 525-533.	1.3	4
16	Denosing of high-resolution single-particle electron-microscopy density maps by their approximation using three-dimensional Gaussian functions. <i>Journal of Structural Biology</i> , 2016, 194, 423-433.	1.3	16
17	Local analysis of strains and rotations for macromolecular electron microscopy maps. <i>Journal of Structural Biology</i> , 2016, 195, 123-128.	1.3	9
18	Heterodimers as the Structural Unit of the T=1 Capsid of the Fungal Double-Stranded RNA Rosellinia necatrix Quadriovirus 1. <i>Journal of Virology</i> , 2016, 90, 11220-11230.	1.5	17

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19	Foil-hole and data image quality assessment in 3DEM: Towards high-throughput image acquisition in the electron microscope. <i>Journal of Structural Biology</i> , 2016, 196, 515-524.	1.3	4
20	Asymmetric cryo-EM reconstruction of phage MS2 reveals genome structure in situ. <i>Nature Communications</i> , 2016, 7, 12524.	5.8	114
21	Scipion: A software framework toward integration, reproducibility and validation in 3D electron microscopy. <i>Journal of Structural Biology</i> , 2016, 195, 93-99.	1.3	474
22	Structural and functional insights into <i>Escherichia coli</i> $\alpha_2$ -macroglobulin endopeptidase snap-trap inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8290-8295.	3.3	34
23	Structural Basis for the Development of Avian Virus Capsids That Display Influenza Virus Proteins and Induce Protective Immunity. <i>Journal of Virology</i> , 2015, 89, 2563-2574.	1.5	20
24	Cryo-EM near-atomic structure of a dsRNA fungal virus shows ancient structural motifs preserved in the dsRNA viral lineage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7641-7646.	3.3	32
25	Chrysovirus Structure. <i>Advances in Virus Research</i> , 2013, 86, 87-108.	0.9	15
26	Semiautomatic, High-Throughput, High-Resolution Protocol for Three-Dimensional Reconstruction of Single Particles in Electron Microscopy. <i>Methods in Molecular Biology</i> , 2013, 950, 171-193.	0.4	25
27	Cryphonectria nitschkei Virus 1 Structure Shows that the Capsid Protein of Chrysoviruses Is a Duplicated Helix-Rich Fold Conserved in Fungal Double-Stranded RNA Viruses. <i>Journal of Virology</i> , 2012, 86, 8314-8318.	1.5	19
28	Epitope Insertion at the N-Terminal Molecular Switch of the Rabbit Hemorrhagic Disease Virus T=3 Capsid Protein Leads to Larger T=4 Capsids. <i>Journal of Virology</i> , 2012, 86, 6470-6480.	1.5	25