Roberto Marabini

List of Publications by Year
in descending order

99 papers	4,699 citations	186209 28 h-index	114418 63 g-index
105 all docs	105 docs citations	105 times ranked	4945 citing authors

#	Article	IF	Citations
1	On bias, variance, overfitting, gold standard and consensus in single-particle analysis by cryo-electron microscopy. Acta Crystallographica Section D: Structural Biology, 2022, 78, 410-423.	1.1	16
2	ScipionTomo: Towards cryo-electron tomography software integration, reproducibility, and validation. Journal of Structural Biology, 2022, 214, 107872.	1.3	19
3	Image Processing in Cryo-Electron Microscopy of Single Particles: The Power of Combining Methods. Methods in Molecular Biology, 2021, 2305, 257-289.	0.4	9
4	FSC-Q: a CryoEM map-to-atomic model quality validation based on the local Fourier shell correlation. Nature Communications, 2021, 12, 42.	5.8	28
5	Cryo-EM structure of enteric adenovirus HAdV-F41 highlights structural variations among human adenoviruses. Science Advances, 2021, 7, .	4.7	15
6	Algorithmic robustness to preferred orientations in single particle analysis by CryoEM. Journal of Structural Biology, 2021, 213, 107695.	1.3	18
7	Near-atomic structure of an atadenovirus reveals a conserved capsid-binding motif and intergenera variations in cementing proteins. Science Advances, 2021, 7, .	4.7	9
8	Cryo-EM density maps adjustment for subtraction, consensus and sharpening. Journal of Structural Biology, 2021, 213, 107780.	1.3	8
9	Advances in Xmipp for Cryo–Electron Microscopy: From Xmipp to Scipion. Molecules, 2021, 26, 6224.	1.7	22
10	Automatic local resolution-based sharpening of cryo-EM maps. Bioinformatics, 2020, 36, 765-772.	1.8	110
11	Measurement of local resolution in electron tomography. Journal of Structural Biology: X, 2020, 4, 100016.	0.7	10
12	Integration of Cryo-EM Model Building Software in *Scipion*. Journal of Chemical Information and Modeling, 2020, 60, 2533-2540.	2.5	24
13	Continuous flexibility analysis of SARS-CoV-2 spike prefusion structures. IUCrJ, 2020, 7, 1059-1069.	1.0	39
14	Survey of the analysis of continuous conformational variability of biological macromolecules by electron microscopy. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 19-32.	0.4	49
15	Validation of electron microscopy initial models via small angle X-ray scattering curves. Bioinformatics, 2019, 35, 2427-2433.	1.8	7
16	Flexible workflows for on-the-fly electron-microscopy single-particle image processing using *Scipion*. Acta Crystallographica Section D: Structural Biology, 2019, 75, 882-894.	1.1	14
17	MonoRes: Automatic and Accurate Estimation of Local Resolution for Electron Microscopy Maps. Structure, 2018, 26, 337-344.e4.	1.6	179
18	Blind estimation of DED camera gain in Electron Microscopy. Journal of Structural Biology, 2018, 203, 90-93.	1.3	7

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19	Map challenge: Analysis using a pair comparison method based on Fourier shell correlation. Journal of Structural Biology, 2018, 204, 527-542.	1.3	4
20	Using Scipion for stream image processing at Cryo-EM facilities. Journal of Structural Biology, 2018, 204, 457-463.	1.3	30
21	The first single particle analysis Map Challenge: A summary of the assessments. Journal of Structural Biology, 2018, 204, 291-300.	1.3	17
22	A new algorithm for high-resolution reconstruction of single particles by electron microscopy. Journal of Structural Biology, 2018, 204, 329-337.	1.3	28
23	XTEND: Extending the depth of field in cryo soft X-ray tomography. Scientific Reports, 2017, 7, 45808.	1.6	24
24	A review of resolution measures and related aspects in 3D Electron Microscopy. Progress in Biophysics and Molecular Biology, 2017, 124, 1-30.	1.4	30
25	A Survey of the Use of Iterative Reconstruction Algorithms in Electron Microscopy. BioMed Research International, 2017, 2017, 1-17.	0.9	29
26	Characterization of transfer function, resolution and depth of field of a soft X-ray microscope applied to tomography enhancement by Wiener deconvolution. Biomedical Optics Express, 2016, 7, 5092.	1.5	53
27	Fast and automatic identification of particle tilt pairs based on Delaunay triangulation. Journal of Structural Biology, 2016, 196, 525-533.	1.3	4
28	Local analysis of strains and rotations for macromolecular electron microscopy maps. Journal of Structural Biology, 2016, 195, 123-128.	1.3	9
29	Particle alignment reliability in single particle electron cryomicroscopy: a general approach. Scientific Reports, 2016, 6, 21626.	1.6	21
30	Scipion: A software framework toward integration, reproducibility and validation in 3D electron microscopy. Journal of Structural Biology, 2016, 195, 93-99.	1.3	474
31	The Electron Microscopy eXchange (EMX) initiative. Journal of Structural Biology, 2016, 194, 156-163.	1.3	12
32	System models for PET statistical iterative reconstruction: A review. Computerized Medical Imaging and Graphics, 2016, 48, 30-48.	3.5	35
33	Cryo-EM and the elucidation of new macromolecular structures: Random Conical Tilt revisited. Scientific Reports, 2015, 5, 14290.	1.6	16
34	Iterative reconstruction for pet scanners with continuous scintillators. , 2015, 2015, 2259-62.		0
35	Alignment of direct detection device micrographs using a robust Optical Flow approach. Journal of Structural Biology, 2015, 189, 163-176.	1.3	59
36	A statistical approach to the initial volume problem in Single Particle Analysis by Electron Microscopy. Journal of Structural Biology, 2015, 189, 213-219.	1.3	27

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37	A fast iterative convolution weighting approach for gridding-based direct Fourier three-dimensional reconstruction with correction for the contrast transfer function. Ultramicroscopy, 2015, 157, 79-87.	0.8	25
38	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359.	1.3	34
39	MRC2014: Extensions to the MRC format header for electron cryo-microscopy and tomography. Journal of Structural Biology, 2015, 192, 146-150.	1.3	59
40	Structures of Adenovirus Incomplete Particles Clarify Capsid Architecture and Show Maturation Changes of Packaging Protein L1 52/55k. Journal of Virology, 2015, 89, 9653-9664.	1.5	44
41	Three-dimensional reconstruction methods in Single Particle Analysis from transmission electron microscopy data. Archives of Biochemistry and Biophysics, 2015, 581, 39-48.	1.4	19
42	The soft x-ray transform. Inverse Problems, 2014, 30, 125015.	1.0	7
43	An image processing approach to the simulation of electron microscopy volumes of atomic structures. , 2014, , .		0
44	Efficient initial volume determination from electron microscopy images of single particles. Bioinformatics, 2014, 30, 2891-2898.	1.8	63
45	3D Cryo-Electron Reconstruction of BmrA, a Bacterial Multidrug ABC Transporter in an Inward-Facing Conformation and in a Lipidic Environment. Journal of Molecular Biology, 2014, 426, 2059-2069.	2.0	30
46	Interchanging Geometry Conventions in 3DEM: Mathematical Context for the Development of Standards. Applied and Numerical Harmonic Analysis, 2014, , 7-42.	0.1	8
47	Soft X-Ray Tomography Imaging for Biological Samples. Applied and Numerical Harmonic Analysis, 2014, , 187-220.	0.1	2
48	FASTDEF: Fast defocus and astigmatism estimation for high-throughput transmission electron microscopy. Journal of Structural Biology, 2013, 181, 136-148.	1.3	31
49	Particle quality assessment and sorting for automatic and semiautomatic particle-picking techniques. Journal of Structural Biology, 2013, 183, 342-353.	1.3	31
50	Xmipp 3.0: An improved software suite for image processing in electron microscopy. Journal of Structural Biology, 2013, 184, 321-328.	1.3	261
51	Semiautomatic, High-Throughput, High-Resolution Protocol for Three-Dimensional Reconstruction of Single Particles in Electron Microscopy. Methods in Molecular Biology, 2013, 950, 171-193.	0.4	25
52	A pattern matching approach to the automatic selection of particles from low-contrast electron micrographs. Bioinformatics, 2013, 29, 2460-2468.	1.8	73
53	On the development of three new tools for organizing and sharing information in three-dimensional electron microscopy. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 695-700.	2.5	5
54	Image processing for Cellular tomography using soft X-rays. , 2012, , .		0

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55	Image formation in cellular X-ray microscopy. Journal of Structural Biology, 2012, 178, 29-37.	1.3	30
56	Epitope Insertion at the N-Terminal Molecular Switch of the Rabbit Hemorrhagic Disease Virus T=3 Capsid Protein Leads to Larger T=4 Capsids. Journal of Virology, 2012, 86, 6470-6480.	1.5	25
57	Non-rigid consistent registration of 2D image sequences. Physics in Medicine and Biology, 2010, 55, 6215-6242.	1.6	16
58	A clustering approach to multireference alignment of single-particle projections in electron microscopy. Journal of Structural Biology, 2010, 171, 197-206.	1.3	188
59	Effects of the downsampling scheme on three-dimensional electron microscopy of single particles. , 2009, , .		1
60	A theoretical model for EM-ML reconstruction algorithms applied to rotating PET scanners. Physics in Medicine and Biology, 2009, 54, 1909-1934.	1.6	6
61	Exploiting desktop supercomputing for three-dimensional electron microscopy reconstructions using ART with blobs. Journal of Structural Biology, 2009, 165, 19-26.	1.3	16
62	Automatic particle selection from electron micrographs using machine learning techniques. Journal of Structural Biology, 2009, 167, 252-260.	1.3	52
63	Structure and Uncoating of Immature Adenovirus. Journal of Molecular Biology, 2009, 392, 547-557.	2.0	64
64	Volumetric restrictions in single particle 3DEM reconstruction. Pattern Recognition, 2008, 41, 616-626.	5.1	10
65	Image processing for electron microscopy single-particle analysis using XMIPP. Nature Protocols, 2008, 3, 977-990.	5.5	310
66	Localization of the N-Terminus of Minor Coat Protein IIIa in the Adenovirus Capsid. Journal of Molecular Biology, 2008, 383, 923-934.	2.0	37
67	Electron tomography of complex biological specimens on the Grid. Future Generation Computer Systems, 2007, 23, 435-446.	4.9	15
68	Algorithms for Three-dimensional Reconstruction From the Imperfect Projection Data Provided by Electron Microscopy. , 2007, , 217-243.		15
69	Image processing and 3-D reconstruction in electron microscopy. IEEE Signal Processing Magazine, 2006, 23, 84-94.	4.6	43
70	On the nature of 2D crystal unbending. Journal of Structural Biology, 2006, 156, 546-555.	1.3	9
71	Optimization problems in electron microscopy of single particles. Annals of Operations Research, 2006, 148, 133-165.	2.6	12
72	Consistent and Elastic Registration of Histological Sections Using Vector-Spline Regularization. Lecture Notes in Computer Science, 2006, , 85-95.	1.0	214

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73	Multiobjective algorithm parameter optimization using multivariate statistics in three-dimensional electron microscopy reconstruction. Pattern Recognition, 2005, 38, 2587-2601.	5.1	11
74	On the suitability of Biological structure determination by electron microscopy to Grid Computing. New Generation Computing, 2005, 23, 101-112.	2.5	8
75	Maximum-likelihood Multi-reference Refinement for Electron Microscopy Images. Journal of Molecular Biology, 2005, 348, 139-149.	2.0	239
76	Classification of single-projection reconstructions for cryo-electron microscopy data of icosahedral viruses. Journal of Structural Biology, 2005, 151, 79-91.	1.3	20
77	Transfer function restoration in 3D electron microscopy via iterative data refinement. Physics in Medicine and Biology, 2004, 49, 509-522.	1.6	15
78	THE POTENTIAL OF GRID COMPUTING IN THREE-DIMENSIONAL ELECTRON MICROSCOPY. Parallel Processing Letters, 2004, 14, 151-162.	0.4	3
79	Biological structure determination by EM is well suited to grid computing. New Generation Computing, 2004, 22, 187-188.	2.5	0
80	3-D Reconstruction of 2-D Crystals in Real Space. IEEE Transactions on Image Processing, 2004, 13, 549-561.	6.0	16
81	XMIPP: a new generation of an open-source image processing package for electron microscopy. Journal of Structural Biology, 2004, 148, 194-204.	1.3	434
82	Grid Computing in Structure Determination of Biological Specimens by Electron Microscope Tomography. Lecture Notes in Computer Science, 2004, , 171-181.	1.0	0
83	Three-dimensional reconstruction by ChahineÂs method from electron microscopic projections corrupted by instrumental aberrations. Inverse Problems, 2003, 19, 933-949.	1.0	14
84	The Effect of Overabundant Projection Directions on 3D Reconstruction Algorithms. Journal of Structural Biology, 2001, 133, 108-118.	1.3	74
85	Correlation of Topographic Surface and Volume Data from Three-Dimensional Electron Microscopy. Journal of Structural Biology, 2001, 136, 20-29.	1.3	9
86	Image processing approaches to biological three-dimensional electron microscopy. International Journal of Imaging Systems and Technology, 2000, 11, 12-29.	2.7	15
87	Discrete Tomography in Electron Microscopy. Applied and Numerical Harmonic Analysis, 1999, , 405-416.	0.1	18
88	Title is missing!. Neural Processing Letters, 1998, 8, 55-65.	2.0	12
89	3D reconstruction in electron microscopy using ART with smooth spherically symmetric volume elements (blobs). Ultramicroscopy, 1998, 72, 53-65.	0.8	157
90	A GA-optimized neural network for classification of biological particles from electron-microscopy images. Lecture Notes in Computer Science, 1997, , 1174-1182.	1.0	1

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91	Three-Dimensional Reconstruction from Reduced Sets of Very Noisy Images Acquired Following a Single-Axis Tilt Schema: Application of a New Three-Dimensional Reconstruction Algorithm and Objective Comparison with Weighted Backprojection. Journal of Structural Biology, 1997, 120, 363-371.	1.3	59
92	Proposal for a New Distributed Database of Macromolecular and Subcellular Structures from Different Areas of Microscopy. Journal of Structural Biology, 1996, 116, 161-166.	1.3	15
93	Xmipp: An Image Processing Package for Electron Microscopy. Journal of Structural Biology, 1996, 116, 237-240.	1.3	188
94	On a new computationally fast image invariant based on bispectral projections. Pattern Recognition Letters, 1996, 17, 959-967.	2.6	15
95	CNMA: a European initiative for OSI network management. IEEE Network, 1995, 9, 44-52.	4.9	2
96	Practical issues on invariant image averaging using the Bispectrum. Signal Processing, 1994, 40, 119-128.	2.1	5
97	Pattern recognition and classification of images of biological macromolecules using artificial neural networks. Biophysical Journal, 1994, 66, 1804-1814.	0.2	108
98	3D reconstruction of 2D crystals from projections in real space. , 0, , .		1
99	Volumetric constraints in 3D tomography applied to electron microscopy. , 0, , .		0