Carlos Oscar Sanchez Sorzano

List of Publications by Year
in descending order

241 papers	9,179 citations	57758 44 h-index	60623 81 g-index
260 all docs	260 docs citations	260 times ranked	10449 citing authors

#	Article	IF	Citations
1	DeepEMhancer: a deep learning solution for cryo-EM volume post-processing. Communications Biology, 2021, 4, 874.	4.4	561
2	Scipion: A software framework toward integration, reproducibility and validation in 3D electron microscopy. Journal of Structural Biology, 2016, 195, 93-99.	2.8	474
3	XMIPP: a new generation of an open-source image processing package for electron microscopy. Journal of Structural Biology, 2004, 148, 194-204.	2.8	434
4	Image processing for electron microscopy single-particle analysis using XMIPP. Nature Protocols, 2008, 3, 977-990.	12.0	310
5	TomoJ: tomography software for three-dimensional reconstruction in transmission electron microscopy. BMC Bioinformatics, 2007, 8, 288.	2.6	264
6	Elastic Registration of Biological Images Using Vector-Spline Regularization. IEEE Transactions on Biomedical Engineering, 2005, 52, 652-663.	4.2	263
7	Xmipp 3.0: An improved software suite for image processing in electron microscopy. Journal of Structural Biology, 2013, 184, 321-328.	2.8	261
8	Maximum-likelihood Multi-reference Refinement for Electron Microscopy Images. Journal of Molecular Biology, 2005, 348, 139-149.	4.2	239
9	<i>BRANCHED1</i>Promotes Axillary Bud Dormancy in Response to Shade in<i>Arabidopsis</i>Â Â. Plant Cell, 2013, 25, 834-850.	6.6	219
10	Consistent and Elastic Registration of Histological Sections Using Vector-Spline Regularization. Lecture Notes in Computer Science, 2006, , 85-95.	1.3	214
11	A clustering approach to multireference alignment of single-particle projections in electron microscopy. Journal of Structural Biology, 2010, 171, 197-206.	2.8	188
12	MonoRes: Automatic and Accurate Estimation of Local Resolution for Electron Microscopy Maps. Structure, 2018, 26, 337-344.e4.	3.3	179
13	Two-step demodulation based on the Gramâ€"Schmidt orthonormalization method. Optics Letters, 2012, 37, 443.	3.3	169
14	Two-step interferometry by a regularized optical flow algorithm. Optics Letters, 2011, 36, 3485.	3.3	124
15	Automatic local resolution-based sharpening of cryo-EM maps. Bioinformatics, 2020, 36, 765-772.	4.1	110
16	A Novel Poxvirus-Based Vaccine, MVA-CHIKV, Is Highly Immunogenic and Protects Mice against Chikungunya Infection. Journal of Virology, 2014, 88, 3527-3547.	3.4	101
17	Miro-1 Links Mitochondria and Microtubule Dynein Motors To Control Lymphocyte Migration and Polarity. Molecular and Cellular Biology, 2014, 34, 1412-1426.	2.3	100
18	Iterative Elastic 3D-to-2D Alignment Method Using Normal Modes for Studying Structural Dynamics of Large Macromolecular Complexes. Structure, 2014, 22, 496-506.	3.3	90

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19	Marker-free image registration of electron tomography tilt-series. BMC Bioinformatics, 2009, 10, 124.	2.6	88
20	Endosomal clathrin drives actin accumulation at the immunological synapse. Journal of Cell Science, 2011, 124, 820-830.	2.0	80
21	COVID-19 Vaccine Candidates Based on Modified Vaccinia Virus Ankara Expressing the SARS-CoV-2 Spike Protein Induce Robust T- and B-Cell Immune Responses and Full Efficacy in Mice. Journal of Virology, 2021, 95, .	3.4	78
22	The Effect of Overabundant Projection Directions on 3D Reconstruction Algorithms. Journal of Structural Biology, 2001, 133, 108-118.	2.8	74
23	Immunogenic Profiling in Mice of a HIV/AIDS Vaccine Candidate (MVA-B) Expressing Four HIV-1 Antigens and Potentiation by Specific Gene Deletions. PLoS ONE, 2010, 5, e12395.	2.5	74
24	A pattern matching approach to the automatic selection of particles from low-contrast electron micrographs. Bioinformatics, 2013, 29, 2460-2468.	4.1	73
25	BIPSPI: a method for the prediction of partner-specific protein–protein interfaces. Bioinformatics, 2019, 35, 470-477.	4.1	73
26	Separating Actin-Dependent Chemokine Receptor Nanoclustering from Dimerization Indicates a Role for Clustering in CXCR4 Signaling and Function. Molecular Cell, 2018, 70, 106-119.e10.	9.7	70
27	A Candidate HIV/AIDS Vaccine (MVA-B) Lacking Vaccinia Virus Gene C6L Enhances Memory HIV-1-Specific T-Cell Responses. PLoS ONE, 2011, 6, e24244.	2.5	67
28	The HIV/AIDS Vaccine Candidate MVA-B Administered as a Single Immunogen in Humans Triggers Robust, Polyfunctional, and Selective Effector Memory T Cell Responses to HIV-1 Antigens. Journal of Virology, 2011, 85, 11468-11478.	3.4	63
29	Generalization of the Principal Component Analysis algorithm for interferometry. Optics Communications, 2013, 286, 130-134.	2.1	63
30	Efficient initial volume determination from electron microscopy images of single particles. Bioinformatics, 2014, 30, 2891-2898.	4.1	63
31	Improving Adaptive and Memory Immune Responses of an HIV/AIDS Vaccine Candidate MVA-B by Deletion of Vaccinia Virus Genes (C6L and K7R) Blocking Interferon Signaling Pathways. PLoS ONE, 2013, 8, e66894.	2.5	60
32	Alignment of direct detection device micrographs using a robust Optical Flow approach. Journal of Structural Biology, 2015, 189, 163-176.	2.8	59
33	Insertion of Vaccinia Virus C7L Host Range Gene into NYVAC-B Genome Potentiates Immune Responses against HIV-1 Antigens. PLoS ONE, 2010, 5, e11406.	2.5	59
34	Safety and immunogenicity of a modified vaccinia Ankara-based HIV-1 vaccine (MVA-B) in HIV-1-infected patients alone or in combination with a drug to reactivate latent HIV-1. Journal of Antimicrobial Chemotherapy, 2015, 70, 1833-1842.	3.0	56
35	Large T antigen on the simian virus 40 origin of replication: a 3D snapshot prior to DNA replication. EMBO Journal, 2003, 22, 6205-6213.	7.8	55
36	NFFinder: an online bioinformatics tool for searching similar transcriptomics experiments in the context of drug repositioning. Nucleic Acids Research, 2015, 43, W193-W199.	14.5	55

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37	Cryo-soft X-ray tomography as a quantitative three-dimensional tool to model nanoparticle:cell interaction. Journal of Nanobiotechnology, 2016, 14, 15.	9.1	54
38	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.	2.9	53
39	Identification of Chlamydomonas Central Core Centriolar Proteins Reveals a Role for Human WDR90 in Ciliogenesis. Current Biology, 2017, 27, 2486-2498.e6.	3.9	53
40	Automatic particle selection from electron micrographs using machine learning techniques. Journal of Structural Biology, 2009, 167, 252-260.	2.8	52
41	A Guided Tour of Selected Image Processing and Analysis Methods for Fluorescence and Electron Microscopy. IEEE Journal on Selected Topics in Signal Processing, 2016, 10, 6-30.	10.8	52
42	Spectral signal-to-noise ratio and resolution assessment of 3D reconstructions. Journal of Structural Biology, 2005, 149, 243-255.	2.8	51
43	Translocation dynamics of sorting nexin 27 in activated T cells. Journal of Cell Science, 2011, 124, 776-788.	2.0	49
44	Data management challenges in three-dimensional EM. Nature Structural and Molecular Biology, 2012, 19, 1203-1207.	8.2	49
45	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.	0.8	49
46	A method for estimating the CTF in electron microscopy based on ARMA models and parameter adjustment. Ultramicroscopy, 2003, 96, 17-35.	1.9	47
47	Fast, robust, and accurate determination of transmission electron microscopy contrast transfer function. Journal of Structural Biology, 2007, 160, 249-262.	2.8	47
48	Chromothripsis: Breakage-fusion-bridge over and over again. Cell Cycle, 2013, 12, 2016-2023.	2.6	46
49	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	14.5	46
50	*DeepRes*: a new deep-learning- and aspect-based local resolution method for electron-microscopy maps. IUCrJ, 2019, 6, 1054-1063.	2.2	45
51	Image processing and 3-D reconstruction in electron microscopy. IEEE Signal Processing Magazine, 2006, 23, 84-94.	5.6	43
52	Autofocused 3D Classification of Cryoelectron Subtomograms. Structure, 2014, 22, 1528-1537.	3.3	43
53	A Vaccine Based on a Modified Vaccinia Virus Ankara Vector Expressing Zika Virus Structural Proteins Controls Zika Virus Replication in Mice. Scientific Reports, 2018, 8, 17385.	3.3	43
54	A Human Multi-Epitope Recombinant Vaccinia Virus as a Universal T Cell Vaccine Candidate against Influenza Virus. PLoS ONE, 2011, 6, e25938.	2.5	42

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55	Fast and accurate conversion of atomic models into electron density maps. AIMS Biophysics, 2015, 2, 8-20.	0.6	42
56	Deletion of the Vaccinia Virus N2L Gene Encoding an Inhibitor of IRF3 Improves the Immunogenicity of Modified Vaccinia Virus Ankara Expressing HIV-1 Antigens. Journal of Virology, 2014, 88, 3392-3410.	3.4	41
57	A multiresolution approach to orientation assignment in 3D electron microscopy of single particles. Journal of Structural Biology, 2004, 146, 381-392.	2.8	40
58	Quadrature Component Analysis for interferometry. Optics and Lasers in Engineering, 2013, 51, 637-641.	3.8	40
59	High, Broad, Polyfunctional, and Durable T Cell Immune Responses Induced in Mice by a Novel Hepatitis C Virus (HCV) Vaccine Candidate (MVA-HCV) Based on Modified Vaccinia Virus Ankara Expressing the Nearly Full-Length HCV Genome. Journal of Virology, 2013, 87, 7282-7300.	3.4	39
60	Continuous flexibility analysis of SARS-CoV-2 spike prefusion structures. IUCrJ, 2020, 7, 1059-1069.	2.2	39
61	Removal of Vaccinia Virus Genes That Block Interferon Type I and II Pathways Improves Adaptive and Memory Responses of the HIV/AIDS Vaccine Candidate NYVAC-C in Mice. Journal of Virology, 2012, 86, 5026-5038.	3.4	38
62	Quantitative morphometrical characterization of human pronuclear zygotes. Human Reproduction, 2008, 23, 1983-1992.	0.9	37
63	*Deep Consensus*, a deep learning-based approach for particle pruning in cryo-electron microscopy. IUCrJ, 2018, 5, 854-865.	2.2	37
64	System models for PET statistical iterative reconstruction: A review. Computerized Medical Imaging and Graphics, 2016, 48, 30-48.	5.8	35
65	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359.	2.8	34
66	Structural insights into influenza A virus ribonucleoproteins reveal a processive helical track as transcription mechanism. Nature Microbiology, 2020, 5, 727-734.	13.3	33
67	FASTDEF: Fast defocus and astigmatism estimation for high-throughput transmission electron microscopy. Journal of Structural Biology, 2013, 181, 136-148.	2.8	31
68	Particle quality assessment and sorting for automatic and semiautomatic particle-picking techniques. Journal of Structural Biology, 2013, 183, 342-353.	2.8	31
69	Distinct Roles of Vaccinia Virus NF-ÎºB Inhibitor Proteins A52, B15, and K7 in the Immune Response. Journal of Virology, 2017, 91, .	3.4	31
70	Image formation in cellular X-ray microscopy. Journal of Structural Biology, 2012, 178, 29-37.	2.8	30
71	High Quality Long-Term CD4+ and CD8+ Effector Memory Populations Stimulated by DNA-LACK/MVA-LACK Regimen in Leishmania major BALB/c Model of Infection. PLoS ONE, 2012, 7, e38859.	2.5	30
72	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.	4.2	30

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73	Virological and Immunological Characterization of Novel NYVAC-Based HIV/AIDS Vaccine Candidates Expressing Clade C Trimeric Soluble gp140(ZM96) and Gag(ZM96)-Pol-Nef(CN54) as Virus-Like Particles. Journal of Virology, 2015, 89, 970-988.	3.4	30
74	Coarse-Graining of Volumes for Modeling of Structure and Dynamics in Electron Microscopy: Algorithm to Automatically Control Accuracy of Approximation. IEEE Journal on Selected Topics in Signal Processing, 2016, 10, 161-173.	10.8	30
75	Pea PSII-LHCII supercomplexes form pairs by making connections across the stromal gap. Scientific Reports, 2017, 7, 10067.	3.3	30
76	A review of resolution measures and related aspects in 3D Electron Microscopy. Progress in Biophysics and Molecular Biology, 2017, 124, 1-30.	2.9	30
77	Using Scipion for stream image processing at Cryo-EM facilities. Journal of Structural Biology, 2018, 204, 457-463.	2.8	30
78	Deletion of the Viral Anti-Apoptotic Gene F1L in the HIV/AIDS Vaccine Candidate MVA-C Enhances Immune Responses against HIV-1 Antigens. PLoS ONE, 2012, 7, e48524.	2.5	30
79	A Survey of the Use of Iterative Reconstruction Algorithms in Electron Microscopy. BioMed Research International, 2017, 2017, 1-17.	1.9	29
80	Three-Dimensional Chemical Mapping by EFTEM-TomoJ Including Improvement of SNR by PCA and ART Reconstruction of Volume by Noise Suppression. Microscopy and Microanalysis, 2013, 19, 1669-1677.	0.4	28
81	A new algorithm for high-resolution reconstruction of single particles by electron microscopy. Journal of Structural Biology, 2018, 204, 329-337.	2.8	28
82	Measuring local-directional resolution and local anisotropy in cryo-EM maps. Nature Communications, 2020, 11, 55.	12.8	28
83	FSC-Q: a CryoEM map-to-atomic model quality validation based on the local Fourier shell correlation. Nature Communications, 2021, 12, 42.	12.8	28
84	Normalizing projection images: a study of image normalizing procedures for single particle three-dimensional electron microscopy. Ultramicroscopy, 2004, 101, 129-138.	1.9	27
85	A statistical approach to the initial volume problem in Single Particle Analysis by Electron Microscopy. Journal of Structural Biology, 2015, 189, 213-219.	2.8	27
86	MicrographCleaner: A python package for cryo-EM micrograph cleaning using deep learning. Journal of Structural Biology, 2020, 210, 107498.	2.8	27
87	Spline-based image-to-volume registration for three-dimensional electron microscopy. Ultramicroscopy, 2005, 103, 303-317.	1.9	26
88	Improving miRNA-mRNA interaction predictions. BMC Genomics, 2014, 15, S2.	2.8	26
89	NFÎºB activation by modified vaccinia virus as a novel strategy to enhance neutrophil migration and HIV-specific T-cell responses. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1333-E1342.	7.1	26
90	SPI-EM: Towards a Tool For Predicting CATH Superfamilies in 3D-EM Maps. Journal of Molecular Biology, 2005, 345, 759-771.	4.2	25

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91	Comparison of single‐particle analysis and electron tomography approaches: an overview. Journal of Microscopy, 2008, 232, 562-579.	1.8	25
92	Fringe pattern denoising by image dimensionality reduction. Optics and Lasers in Engineering, 2013, 51, 921-928.	3.8	25
93	Semiautomatic, High-Throughput, High-Resolution Protocol for Three-Dimensional Reconstruction of Single Particles in Electron Microscopy. Methods in Molecular Biology, 2013, 950, 171-193.	0.9	25
94	Deletion of the Vaccinia Virus Gene A46R, Encoding for an Inhibitor of TLR Signalling, Is an Effective Approach to Enhance the Immunogenicity in Mice of the HIV/AIDS Vaccine Candidate NYVAC-C. PLoS ONE, 2013, 8, e74831.	2.5	25
95	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.	1.9	25
96	StructMap: Elastic Distance Analysis of Electron Microscopy Maps for Studying Conformational Changes. Biophysical Journal, 2016, 110, 1753-1765.	0.5	25
97	XTEND: Extending the depth of field in cryo soft X-ray tomography. Scientific Reports, 2017, 7, 45808.	3.3	24
98	Hybrid Electron Microscopy Normal Mode Analysis with Scipion. Protein Science, 2020, 29, 223-236.	7.6	24
99	Integration of Cryo-EM Model Building Software in <i>Scipion</i>. Journal of Chemical Information and Modeling, 2020, 60, 2533-2540.	5.4	24
100	A Phase I Randomized Therapeutic MVA-B Vaccination Improves the Magnitude and Quality of the T Cell Immune Responses in HIV-1-Infected Subjects on HAART. PLoS ONE, 2015, 10, e0141456.	2.5	24
101	Improved Bayesian image denoising based on wavelets with applications to electron microscopy. Pattern Recognition, 2006, 39, 1205-1213.	8.1	23
102	Involvement of the Cellular Phosphatase DUSP1 in Vaccinia Virus Infection. PLoS Pathogens, 2013, 9, e1003719.	4.7	23
103	New vaccinia virus promoter as a potential candidate for future vaccines. Journal of General Virology, 2013, 94, 2771-2776.	2.9	22
104	Advances in Xmipp for Cryo–Electron Microscopy: From Xmipp to Scipion. Molecules, 2021, 26, 6224.	3.8	22
105	Measurement of the modulation transfer function of an X-ray microscope based on multiple Fourier orders analysis of a Siemens star. Optics Express, 2015, 23, 9567.	3.4	21
106	Particle alignment reliability in single particle electron cryomicroscopy: a general approach. Scientific Reports, 2016, 6, 21626.	3.3	21
107	Local resolution estimates of cryoEM reconstructions. Current Opinion in Structural Biology, 2020, 64, 74-78.	5.7	21
108	A novel method for improvement of visualization of power spectra for sorting cryo-electron micrographs and their local areas. Journal of Structural Biology, 2007, 157, 156-167.	2.8	20

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109	Safety and vaccine-induced HIV-1 immune responses in healthy volunteers following a late MVA-B boost 4 years after the last immunization. PLoS ONE, 2017, 12, e0186602.	2.5	20
110	Three-dimensional reconstruction methods in Single Particle Analysis from transmission electron microscopy data. Archives of Biochemistry and Biophysics, 2015, 581, 39-48.	3.0	19
111	Structural analysis of receptors and actin polarity in platelet protrusions. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
112	New insights into the role of endosomal proteins for African swine fever virus infection. PLoS Pathogens, 2022, 18, e1009784.	4.7	19
113	Hybrid Electron Microscopy Normal Mode Analysis graphical interface and protocol. Journal of Structural Biology, 2014, 188, 134-141.	2.8	18
114	3DBIONOTES v2.0: a web server for the automatic annotation of macromolecular structures. Bioinformatics, 2017, 33, 3655-3657.	4.1	18
115	Scipion web tools: Easy to use cryo€€EM image processing over the web. Protein Science, 2018, 27, 269-275.	7.6	18
116	Algorithmic robustness to preferred orientations in single particle analysis by CryoEM. Journal of Structural Biology, 2021, 213, 107695.	2.8	18
117	Shack€"Hartmann centroid detection using the spiral phase transform. Applied Optics, 2012, 51, 7362.	1.8	17
118	X-ray structure of full-length human RuvB-Like 2 €" mechanistic insights into coupling between ATP binding and mechanical action. Scientific Reports, 2018, 8, 13726.	3.3	17
119	The first single particle analysis Map Challenge: A summary of the assessments. Journal of Structural Biology, 2018, 204, 291-300.	2.8	17
120	Sensory Acceptance, Appetite Control and Gastrointestinal Tolerance of Yogurts Containing Coffee-Cascara Extract and Inulin. Nutrients, 2020, 12, 627.	4.1	17
121	3-D Reconstruction of 2-D Crystals in Real Space. IEEE Transactions on Image Processing, 2004, 13, 549-561.	9.8	16
122	Exploiting desktop supercomputing for three-dimensional electron microscopy reconstructions using ART with blobs. Journal of Structural Biology, 2009, 165, 19-26.	2.8	16
123	Non-rigid consistent registration of 2D image sequences. Physics in Medicine and Biology, 2010, 55, 6215-6242.	3.0	16
124	Error analysis of the principal component analysis demodulation algorithm. Applied Physics B: Lasers and Optics, 2014, 115, 355-364.	2.2	16
125	Cryo-EM and the elucidation of new macromolecular structures: Random Conical Tilt revisited. Scientific Reports, 2015, 5, 14290.	3.3	16
126	Denoising of high-resolution single-particle electron-microscopy density maps by their approximation using three-dimensional Gaussian functions. Journal of Structural Biology, 2016, 194, 423-433.	2.8	16

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127	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.	2.3	16
128	Transfer function restoration in 3D electron microscopy via iterative data refinement. Physics in Medicine and Biology, 2004, 49, 509-522.	3.0	15
129	Using neighborhood cohesiveness to infer interactions between protein domains. Bioinformatics, 2015, 31, 2545-2552.	4.1	15
130	3DIANA: 3D Domain Interaction Analysis: A Toolbox for Quaternary Structure Modeling. Biophysical Journal, 2016, 110, 766-775.	0.5	15
131	Quantitative analysis of 3D alignment quality: its impact on soft-validation, particle pruning and homogeneity analysis. Scientific Reports, 2017, 7, 6307.	3.3	15
132	Reconstruction From Multiple Particles for 3D Isotropic Resolution in Fluorescence Microscopy. IEEE Transactions on Medical Imaging, 2018, 37, 1235-1246.	8.9	15
133	Advances in image processing for single-particle analysis by electron cryomicroscopy and challenges ahead. Current Opinion in Structural Biology, 2018, 52, 127-145.	5.7	15
134	Algorithms for Three-dimensional Reconstruction From the Imperfect Projection Data Provided by Electron Microscopy. , 2007, , 217-243.		15
135	Three-dimensional reconstruction by ChahineÂs method from electron microscopic projections corrupted by instrumental aberrations. Inverse Problems, 2003, 19, 933-949.	2.0	14
136	Elastic image registration of 2-D gels for differential and repeatability studies. Proteomics, 2008, 8, 62-65.	2.2	14
137	Single-particle reconstruction using L2-gradient flow. Journal of Structural Biology, 2011, 176, 259-267.	2.8	14
138	3DEM Loupe: analysis of macromolecular dynamics using structures from electron microscopy. Nucleic Acids Research, 2013, 41, W363-W367.	14.5	14
139	Modification of promoter spacer length in vaccinia virus as a strategy to control the antigen expression. Journal of General Virology, 2015, 96, 2360-2371.	2.9	14
140	Flexible workflows for on-the-fly electron-microscopy single-particle image processing using <i>Scipion</i>. Acta Crystallographica Section D: Structural Biology, 2019, 75, 882-894.	2.3	14
141	Cryo-EM structure of a tetrameric photosystem I from Chroococcidiopsis TS-821, a thermophilic, unicellular, non-heterocyst-forming cyanobacterium. Plant Communications, 2022, 3, 100248.	7.7	14
142	3D electron microscopy of biological nanomachines: principles and applications. European Biophysics Journal, 2007, 36, 995-1013.	2.2	13
143	A GPU acceleration of 3-D Fourier reconstruction in cryo-EM. International Journal of High Performance Computing Applications, 2019, 33, 948-959.	3.7	13
144	Deletion of Vaccinia Virus A40R Gene Improves the Immunogenicity of the HIV-1 Vaccine Candidate MVA-B. Vaccines, 2020, 8, 70.	4.4	13

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145	Optimization problems in electron microscopy of single particles. Annals of Operations Research, 2006, 148, 133-165.	4.1	12
146	Comparing scientific performance among equals. Scientometrics, 2014, 101, 1731-1745.	3.0	12
147	Fast multiscale reconstruction for Cryo-EM. Journal of Structural Biology, 2018, 204, 543-554.	2.8	12
148	A Novel MVA-Based HIV Vaccine Candidate (MVA-gp145-GPN) Co-Expressing Clade C Membrane-Bound Trimeric gp145 Env and Gag-Induced Virus-Like Particles (VLPs) Triggered Broad and Multifunctional HIV-1-Specific T Cell and Antibody Responses. Viruses, 2019, 11, 160.	3.3	12
149	State-dependent sequential allostery exhibited by chaperonin TRiC/CCT revealed by network analysis of Cryo-EM maps. Progress in Biophysics and Molecular Biology, 2021, 160, 104-120.	2.9	12
150	Emerging Themes in CryoEMâ"€Single Particle Analysis Image Processing. Chemical Reviews, 2022, 122, 13915-13951.	47.7	12
151	Phan3D: design of biological phantoms in 3D electron microscopy. Bioinformatics, 2004, 20, 3286-3288.	4.1	11
152	Error analysis in the determination of the electron microscopical contrast transfer function parameters from experimental power Spectra. BMC Structural Biology, 2009, 9, 18.	2.3	11
153	Versatility of Approximating Single-Particle Electron Microscopy Density Maps Using Pseudoatoms and Approximation-Accuracy Control. BioMed Research International, 2016, 2016, 1-11.	1.9	11
154	Re-examining the spectra of macromolecules. Current practice of spectral quasi B-factor flattening. Journal of Structural Biology, 2020, 209, 107447.	2.8	11
155	DeepAlign, a 3D alignment method based on regionalized deep learning for Cryo-EM. Journal of Structural Biology, 2021, 213, 107712.	2.8	11
156	Enhancement of the HIV-1-Specific Immune Response Induced by an mRNA Vaccine through Boosting with a Poxvirus MVA Vector Expressing the Same Antigen. Vaccines, 2021, 9, 959.	4.4	11
157	Identification of incorrectly oriented particles in cryo-EM single particle analysis. Journal of Structural Biology, 2021, 213, 107771.	2.8	11
158	Volumetric restrictions in single particle 3DEM reconstruction. Pattern Recognition, 2008, 41, 616-626.	8.1	10
159	A Prime/Boost PfCS14K^{M}/MVA-sPfCS^{M}Vaccination Protocol Generates Robust CD8^{+}T Cell and Antibody Responses to Plasmodium falciparum Circumsporozoite Protein and Protects Mice against Malaria. Vaccine Journal, 2017, 24, .	3.1	10
160	Monocytes Phenotype and Cytokine Production in Human Immunodeficiency Virus-1 Infected Patients Receiving a Modified Vaccinia Ankara-Based HIV-1 Vaccine: Relationship to CD300 Molecules Expression. Frontiers in Immunology, 2017, 8, 836.	4.8	10
161	Removal of the C6 Vaccinia Virus Interferon-Î² Inhibitor in the Hepatitis C Vaccine Candidate MVA-HCV Elicited in Mice High Immunogenicity in Spite of Reduced Host Gene Expression. Viruses, 2018, 10, 414.	3.3	10
162	Structural basis for cooperativity of human monoclonal antibodies to meningococcal factor H-binding protein. Communications Biology, 2019, 2, 241.	4.4	10

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163	Measurement of local resolution in electron tomography. Journal of Structural Biology: X, 2020, 4, 100016.	1.3	10
164	Principal component analysis is limited to low-resolution analysis in cryoEM. Acta Crystallographica Section D: Structural Biology, 2021, 77, 835-839.	2.3	10
165	Adjuvant-like Effect of Vaccinia Virus 14K Protein: A Case Study with Malaria Vaccine Based on the Circumsporozoite Protein. Journal of Immunology, 2012, 188, 6407-6417.	0.8	9
166	Undergraduate Students Compete in the IEEE Signal Processing Cup: Part 1 [sp Education]. IEEE Signal Processing Magazine, 2015, 32, 123-125.	5.6	9
167	Local analysis of strains and rotations for macromolecular electron microscopy maps. Journal of Structural Biology, 2016, 195, 123-128.	2.8	9
168	Clathrin regulates lymphocyte migration by driving actin accumulation at the cellular leading edge. European Journal of Immunology, 2016, 46, 2376-2387.	2.9	9
169	Potent HIV-1-Specific CD8 T Cell Responses Induced in Mice after Priming with a Multiepitopic DNA-TMEP and Boosting with the HIV Vaccine MVA-B. Viruses, 2018, 10, 424.	3.3	9
170	Immune Modulation of NYVAC-Based HIV Vaccines by Combined Deletion of Viral Genes that Act on Several Signalling Pathways. Viruses, 2018, 10, 7.	3.3	9
171	Potent Anti-hepatitis C Virus (HCV) T Cell Immune Responses Induced in Mice Vaccinated with DNA-Launched RNA Replicons and Modified Vaccinia Virus Ankara-HCV. Journal of Virology, 2019, 93, .	3.4	9
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