

Carlos Oscar Sanchez Sorzano

List of Publications by Year in descending order

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Version: 2024-02-01

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	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542.	14.5	46
2	Cryo-EM structure of a tetrameric photosystem I from <i>Chroococcidiopsis</i> TS-821, a thermophilic, unicellular, non-heterocyst-forming cyanobacterium. <i>Plant Communications</i> , 2022, 3, 100248.	7.7	14
3	New insights into the role of endosomal proteins for African swine fever virus infection. <i>PLoS Pathogens</i> , 2022, 18, e1009784.	4.7	19
4	On bias, variance, overfitting, gold standard and consensus in single-particle analysis by cryo-electron microscopy. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 410-423.	2.3	16
5	Protein dynamics developments for the large scale and cryoEM: case study of <i>ProDy</i> 2.0. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 399-409.	2.3	7
6	Cryo-Electron Microscopy: The field of 1,000+ methods. <i>Journal of Structural Biology</i> , 2022, 214, 107861.	2.8	5
7	Emerging Themes in CryoEM Single Particle Analysis Image Processing. <i>Chemical Reviews</i> , 2022, 122, 13915-13951.	47.7	12
8	State-dependent sequential allostery exhibited by chaperonin TRiC/CCT revealed by network analysis of Cryo-EM maps. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 160, 104-120.	2.9	12
9	Image Processing in Cryo-Electron Microscopy of Single Particles: The Power of Combining Methods. <i>Methods in Molecular Biology</i> , 2021, 2305, 257-289.	0.9	9
10	FSC-Q: a CryoEM map-to-atomic model quality validation based on the local Fourier shell correlation. <i>Nature Communications</i> , 2021, 12, 42.	12.8	28
11	The combined vaccination protocol of DNA/MVA expressing Zika virus structural proteins as efficient inducer of T and B cell immune responses. <i>Emerging Microbes and Infections</i> , 2021, 10, 1441-1456.	6.5	6
12	Algorithmic robustness to preferred orientations in single particle analysis by CryoEM. <i>Journal of Structural Biology</i> , 2021, 213, 107695.	2.8	18
13	A Signal Processing Approach to Pharmacokinetic Data Analysis. <i>Pharmaceutical Research</i> , 2021, 38, 625-635.	3.5	2
14	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. <i>Journal of Virology</i> , 2021, 95, .	3.4	78
15	Neutrophil subtypes shape HIV-specific CD8 T-cell responses after vaccinia virus infection. <i>Npj Vaccines</i> , 2021, 6, 52.	6.0	6
16	Predicting MHC I restricted T cell epitopes in mice with NAP-CNB, a novel online tool. <i>Scientific Reports</i> , 2021, 11, 10780.	3.3	4
17	3DBionotes COVID-19 edition. <i>Bioinformatics</i> , 2021, 37, 4258-4260.	4.1	2
18	Cryo-EM and Single-Particle Analysis with Scipion. <i>Journal of Visualized Experiments</i> , 2021, , .	0.3	4

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19	Principal component analysis is limited to low-resolution analysis in cryoEM. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 835-839.	2.3	10
20	DeepAlign, a 3D alignment method based on regionalized deep learning for Cryo-EM. <i>Journal of Structural Biology</i> , 2021, 213, 107712.	2.8	11
21	Scipion PKPD: an Open-Source Platform for Biopharmaceutics, Pharmacokinetics and Pharmacodynamics Data Analysis. <i>Pharmaceutical Research</i> , 2021, 38, 1169-1178.	3.5	2
22	DeepEMhancer: a deep learning solution for cryo-EM volume post-processing. <i>Communications Biology</i> , 2021, 4, 874.	4.4	561
23	Enhancement of the HIV-1-Specific Immune Response Induced by an mRNA Vaccine through Boosting with a Poxvirus MVA Vector Expressing the Same Antigen. <i>Vaccines</i> , 2021, 9, 959.	4.4	11
24	ENRICH: A fast method to improve the quality of flexible macromolecular reconstructions. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 164, 92-100.	2.9	2
25	Identification of incorrectly oriented particles in cryo-EM single particle analysis. <i>Journal of Structural Biology</i> , 2021, 213, 107771.	2.8	11
26	Structural analysis of receptors and actin polarity in platelet protrusions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	19
27	Cryo-EM density maps adjustment for subtraction, consensus and sharpening. <i>Journal of Structural Biology</i> , 2021, 213, 107780.	2.8	8
28	Advances in Xmipp for Cryo-EM. <i>Electron Microscopy: From Xmipp to Scipion</i> . <i>Molecules</i> , 2021, 26, 6224.	3.8	22
29	Automatic local resolution-based sharpening of cryo-EM maps. <i>Bioinformatics</i> , 2020, 36, 765-772.	4.1	110
30	Hybrid Electron Microscopy Normal Mode Analysis with Scipion. <i>Protein Science</i> , 2020, 29, 223-236.	7.6	24
31	Re-examining the spectra of macromolecules. Current practice of spectral quasi B-factor flattening. <i>Journal of Structural Biology</i> , 2020, 209, 107447.	2.8	11
32	Measuring local-directional resolution and local anisotropy in cryo-EM maps. <i>Nature Communications</i> , 2020, 11, 55.	12.8	28
33	Measurement of local resolution in electron tomography. <i>Journal of Structural Biology: X</i> , 2020, 4, 100016.	1.3	10
34	Enhancement of HIV-1 Env-Specific CD8 T Cell Responses Using Interferon-Stimulated Gene 15 as an Immune Adjuvant. <i>Journal of Virology</i> , 2020, 95, .	3.4	6
35	Optimized Hepatitis C Virus (HCV) E2 Glycoproteins and their Immunogenicity in Combination with MVA-HCV. <i>Vaccines</i> , 2020, 8, 440.	4.4	8
36	Improvements on marker-free images alignment for electron tomography. <i>Journal of Structural Biology: X</i> , 2020, 4, 100037.	1.3	6

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37	Structural insights into influenza A virus ribonucleoproteins reveal a processive helical track as transcription mechanism. <i>Nature Microbiology</i> , 2020, 5, 727-734.	13.3	33
38	Sensory Acceptance, Appetite Control and Gastrointestinal Tolerance of Yogurts Containing Coffee-Cascara Extract and Inulin. <i>Nutrients</i> , 2020, 12, 627.	4.1	17
39	Local resolution estimates of cryoEM reconstructions. <i>Current Opinion in Structural Biology</i> , 2020, 64, 74-78.	5.7	21
40	FlexAlign: An Accurate and Fast Algorithm for Movie Alignment in Cryo-Electron Microscopy. <i>Electronics (Switzerland)</i> , 2020, 9, 1040.	3.1	5
41	Deletion of Vaccinia Virus A40R Gene Improves the Immunogenicity of the HIV-1 Vaccine Candidate MVA-B. <i>Vaccines</i> , 2020, 8, 70.	4.4	13
42	Integration of Cryo-EM Model Building Software in Scipion. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2533-2540.	5.4	24
43	MicrographCleaner: A python package for cryo-EM micrograph cleaning using deep learning. <i>Journal of Structural Biology</i> , 2020, 210, 107498.	2.8	27
44	Continuous flexibility analysis of SARS-CoV-2 spike prefusion structures. <i>IUCr</i> , 2020, 7, 1059-1069.	2.2	39
45	BIPSPi: a method for the prediction of partner-specific protein-protein interfaces. <i>Bioinformatics</i> , 2019, 35, 470-477.	4.1	73
46	Induction of Broad and Polyfunctional HIV-1-Specific T Cell Responses by the Multiepitopic Protein TMEP-B Vecteded by MVA Virus. <i>Vaccines</i> , 2019, 7, 57.	4.4	5
47	Structural basis for cooperativity of human monoclonal antibodies to meningococcal factor H-binding protein. <i>Communications Biology</i> , 2019, 2, 241.	4.4	10
48	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. <i>Journal of Virology</i> , 2019, 93, .	3.4	9
49	A GPU acceleration of 3-D Fourier reconstruction in cryo-EM. <i>International Journal of High Performance Computing Applications</i> , 2019, 33, 948-959.	3.7	13
50	Image Processing Protocol for the Analysis of the Diffusion and Cluster Size of Membrane Receptors by Fluorescence Microscopy. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	2
51	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. <i>Viruses</i> , 2019, 11, 160.	3.3	12
52	3DBIONOTES v3.0: crossing molecular and structural biology data with genomic variations. <i>Bioinformatics</i> , 2019, 35, 3512-3513.	4.1	9
53	An MVA Vector Expressing HIV-1 Envelope under the Control of a Potent Vaccinia Virus Promoter as a Promising Strategy in HIV/AIDS Vaccine Design. <i>Vaccines</i> , 2019, 7, 208.	4.4	5
54	Heterologous Combination of VSV-GP and NYVAC Vectors Expressing HIV-1 Trimeric gp145 Env as Vaccination Strategy to Induce Balanced B and T Cell Immune Responses. <i>Frontiers in Immunology</i> , 2019, 10, 2941.	4.8	9

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55	The Envelope-Based Fusion Antigen GP120C14K Forming Hexamer-Like Structures Triggers T Cell and Neutralizing Antibody Responses Against HIV-1. <i>Frontiers in Immunology</i> , 2019, 10, 2793.	4.8	2
56	Survey of the analysis of continuous conformational variability of biological macromolecules by electron microscopy. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 19-32.	0.8	49
57	Validation of electron microscopy initial models via small angle X-ray scattering curves. <i>Bioinformatics</i> , 2019, 35, 2427-2433.	4.1	7
58	<i>DeepRes</i>: a new deep-learning- and aspect-based local resolution method for electron-microscopy maps. <i>IUCrJ</i> , 2019, 6, 1054-1063.	2.2	45
59	Flexible workflows for on-the-fly electron-microscopy single-particle image processing using <i>Scipion</i>. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 882-894.	2.3	14
60	Separating Actin-Dependent Chemokine Receptor Nanoclustering from Dimerization Indicates a Role for Clustering in CXCR4 Signaling and Function. <i>Molecular Cell</i> , 2018, 70, 106-119.e10.	9.7	70
61	Reconstruction From Multiple Particles for 3D Isotropic Resolution in Fluorescence Microscopy. <i>IEEE Transactions on Medical Imaging</i> , 2018, 37, 1235-1246.	8.9	15
62	MonoRes: Automatic and Accurate Estimation of Local Resolution for Electron Microscopy Maps. <i>Structure</i> , 2018, 26, 337-344.e4.	3.3	179
63	Alignment of Tilt Series. <i>Biological and Medical Physics Series</i> , 2018, , 183-207.	0.4	0
64	Blind estimation of DED camera gain in Electron Microscopy. <i>Journal of Structural Biology</i> , 2018, 203, 90-93.	2.8	7
65	Scipion web tools: Easy to use cryo-EM image processing over the web. <i>Protein Science</i> , 2018, 27, 269-275.	7.6	18
66	Fast multiscale reconstruction for Cryo-EM. <i>Journal of Structural Biology</i> , 2018, 204, 543-554.	2.8	12
67	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. <i>Viruses</i> , 2018, 10, 424.	3.3	9
68	A Vaccine Based on a Modified Vaccinia Virus Ankara Vector Expressing Zika Virus Structural Proteins Controls Zika Virus Replication in Mice. <i>Scientific Reports</i> , 2018, 8, 17385.	3.3	43
69	Map challenge: Analysis using a pair comparison method based on Fourier shell correlation. <i>Journal of Structural Biology</i> , 2018, 204, 527-542.	2.8	4
70	Advances in image processing for single-particle analysis by electron cryomicroscopy and challenges ahead. <i>Current Opinion in Structural Biology</i> , 2018, 52, 127-145.	5.7	15
71	Using Scipion for stream image processing at Cryo-EM facilities. <i>Journal of Structural Biology</i> , 2018, 204, 457-463.	2.8	30
72	Removal of the C6 Vaccinia Virus Interferon- $\hat{1}$ 2 Inhibitor in the Hepatitis C Vaccine Candidate MVA-HCV Elicited in Mice High Immunogenicity in Spite of Reduced Host Gene Expression. <i>Viruses</i> , 2018, 10, 414.	3.3	10

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73	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
74	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
75	The first single particle analysis Map Challenge: A summary of the assessments. Journal of Structural Biology, 2018, 204, 291-300.	2.8	17
76	A new algorithm for high-resolution reconstruction of single particles by electron microscopy. Journal of Structural Biology, 2018, 204, 329-337.	2.8	28
77	<i>Deep Consensus</i>, a deep learning-based approach for particle pruning in cryo-electron microscopy. IUCr, 2018, 5, 854-865.	2.2	37
78	Improving 3D reconstructions of macromolecular conformations. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a155-a155.	0.1	0
79	Using Scipion for stream image processing at cryo-EM facilities. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a161-a161.	0.1	0
80	XTEND: Extending the depth of field in cryo soft X-ray tomography. Scientific Reports, 2017, 7, 45808.	3.3	24
81	Distinct Roles of Vaccinia Virus NF- β B Inhibitor Proteins A52, B15, and K7 in the Immune Response. Journal of Virology, 2017, 91, .	3.4	31
82	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
83	Pea PSII-LHCII supercomplexes form pairs by making connections across the stromal gap. Scientific Reports, 2017, 7, 10067.	3.3	30
84	Quantitative analysis of 3D alignment quality: its impact on soft-validation, particle pruning and homogeneity analysis. Scientific Reports, 2017, 7, 6307.	3.3	15
85	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
86	ScipionCloud: An integrative and interactive gateway for large scale cryo electron microscopy image processing on commercial and academic clouds. Journal of Structural Biology, 2017, 200, 20-27.	2.8	8
87	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
88	3DCONS-DB: A Database of Position-Specific Scoring Matrices in Protein Structures. Molecules, 2017, 22, 2230.	3.8	3
89	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
90	Electron Microscopy Structural Insights into CPAP Oligomeric Behavior: A Plausible Assembly Process of a Supramolecular Scaffold of the Centrosome. Frontiers in Molecular Biosciences, 2017, 4, 17.	3.5	5

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91	A Survey of the Use of Iterative Reconstruction Algorithms in Electron Microscopy. BioMed Research International, 2017, 2017, 1-17.	1.9	29
92	3DBIONOTES v2.0: a web server for the automatic annotation of macromolecular structures. Bioinformatics, 2017, 33, 3655-3657.	4.1	18
93	Gene signature associated with benign neurofibroma transformation to malignant peripheral nerve sheath tumors. PLoS ONE, 2017, 12, e0178316.	2.5	3
94	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
95	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
96	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
97	Fast and automatic identification of particle tilt pairs based on Delaunay triangulation. Journal of Structural Biology, 2016, 196, 525-533.	2.8	4
98	NYVAC vector modified by C7L viral gene insertion improves T cell immune responses and effectiveness against leishmaniasis. Virus Research, 2016, 220, 1-11.	2.2	4
99	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
100	Local analysis of strains and rotations for macromolecular electron microscopy maps. Journal of Structural Biology, 2016, 195, 123-128.	2.8	9
101	3DBIONOTES: A unified, enriched and interactive view of macromolecular information. Journal of Structural Biology, 2016, 194, 231-234.	2.8	7
102	Clastrin regulates lymphocyte migration by driving actin accumulation at the cellular leading edge. European Journal of Immunology, 2016, 46, 2376-2387.	2.9	9
103	Foil-hole and data image quality assessment in 3DEM: Towards high-throughput image acquisition in the electron microscope. Journal of Structural Biology, 2016, 196, 515-524.	2.8	4
104	Particle alignment reliability in single particle electron cryomicroscopy: a general approach. Scientific Reports, 2016, 6, 21626.	3.3	21
105	Scipion: A software framework toward integration, reproducibility and validation in 3D electron microscopy. Journal of Structural Biology, 2016, 195, 93-99.	2.8	474
106	StructMap: Elastic Distance Analysis of Electron Microscopy Maps for Studying Conformational Changes. Biophysical Journal, 2016, 110, 1753-1765.	0.5	25
107	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
108	3DIANA: 3D Domain Interaction Analysis: A Toolbox for Quaternary Structure Modeling. Biophysical Journal, 2016, 110, 766-775.	0.5	15

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109	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
110	Introduction to the Issue on Advanced Signal Processing in Microscopy and Cell Imaging. IEEE Journal on Selected Topics in Signal Processing, 2016, 10, 3-5.	10.8	3
111	System models for PET statistical iterative reconstruction: A review. Computerized Medical Imaging and Graphics, 2016, 48, 30-48.	5.8	35
112	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
113	Cryo-EM and the elucidation of new macromolecular structures: Random Conical Tilt revisited. Scientific Reports, 2015, 5, 14290.	3.3	16
114	Cost-Constrained Optimal Sampling for System Identification in Pharmacokinetics Applications with Population Priors and Nuisance Parameters. Journal of Pharmaceutical Sciences, 2015, 104, 2103-2109.	3.3	2
115	Iterative reconstruction for pet scanners with continuous scintillators. , 2015, 2015, 2259-62.		0
116	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
117	NF κ B 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
118	Alignment of direct detection device micrographs using a robust Optical Flow approach. Journal of Structural Biology, 2015, 189, 163-176.	2.8	59
119	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
120	Undergraduate Students Compete in the IEEE Signal Processing Cup: Part 1 [sp Education]. IEEE Signal Processing Magazine, 2015, 32, 123-125.	5.6	9
121	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
122	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
123	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359.	2.8	34
124	Using neighborhood cohesiveness to infer interactions between protein domains. Bioinformatics, 2015, 31, 2545-2552.	4.1	15
125	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
126	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

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127	Undergraduate Students Compete in the IEEE Signal Processing Cup: Part 2 [sp Education]. IEEE Signal Processing Magazine, 2015, 32, 109-111.	5.6	0
128	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
129	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
130	A Chimeric HIV-1 gp120 Fused with Vaccinia Virus 14K (A27) Protein as an HIV Immunogen. PLoS ONE, 2015, 10, e0133595.	2.5	8
131	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
132	Fast and accurate conversion of atomic models into electron density maps. AIMS Biophysics, 2015, 2, 8-20.	0.6	42
133	Elastic image registration to fully explore macromolecular dynamics by electron microscopy. , 2014, , .		0
134	An image processing approach to the simulation of electron microscopy volumes of atomic structures. , 2014, , .		0
135	Vaccinia Virus with Selective Deletions Enhances T Cell Response to HIV Antigens by Specific Neutrophil Recruitment. AIDS Research and Human Retroviruses, 2014, 30, A241-A241.	1.1	0
136	Bivalent NYVAC-based Vaccine Candidates against HIV/AIDS Expressing Clade C Trimeric Soluble gp140(ZM96) and Gag(ZM96)-Pol-Nef(CN54) as VLPs. AIDS Research and Human Retroviruses, 2014, 30, A119-A119.	1.1	0
137	Efficient initial volume determination from electron microscopy images of single particles. Bioinformatics, 2014, 30, 2891-2898.	4.1	63
138	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
139	Error analysis of the principal component analysis demodulation algorithm. Applied Physics B: Lasers and Optics, 2014, 115, 355-364.	2.2	16
140	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
141	Hybrid Electron Microscopy Normal Mode Analysis graphical interface and protocol. Journal of Structural Biology, 2014, 188, 134-141.	2.8	18
142	Comparing scientific performance among equals. Scientometrics, 2014, 101, 1731-1745.	3.0	12
143	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
144	Autofocused 3D Classification of Cryoelectron Subtomograms. Structure, 2014, 22, 1528-1537.	3.3	43

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145	Iterative Elastic 3D-to-2D Alignment Method Using Normal Modes for Studying Structural Dynamics of Large Macromolecular Complexes. <i>Structure</i> , 2014, 22, 496-506.	3.3	90
146	3D Cryo-Electron Reconstruction of BmrA, a Bacterial Multidrug ABC Transporter in an Inward-Facing Conformation and in a Lipidic Environment. <i>Journal of Molecular Biology</i> , 2014, 426, 2059-2069.	4.2	30
147	Improving miRNA-mRNA interaction predictions. <i>BMC Genomics</i> , 2014, 15, S2.	2.8	26
148	Interchanging Geometry Conventions in 3DEM: Mathematical Context for the Development of Standards. <i>Applied and Numerical Harmonic Analysis</i> , 2014, , 7-42.	0.3	8
149	Soft X-Ray Tomography Imaging for Biological Samples. <i>Applied and Numerical Harmonic Analysis</i> , 2014, , 187-220.	0.3	2
150	Quadrature Component Analysis for interferometry. <i>Optics and Lasers in Engineering</i> , 2013, 51, 637-641.	3.8	40
151	New vaccinia virus promoter as a potential candidate for future vaccines. <i>Journal of General Virology</i> , 2013, 94, 2771-2776.	2.9	22
152	Variable Internal Flexibility Characterizes the Helical Capsid Formed by <i>Agrobacterium</i> VirE2 Protein on Single-Stranded DNA. <i>Structure</i> , 2013, 21, 1158-1167.	3.3	8
153	FASTDEF: Fast defocus and astigmatism estimation for high-throughput transmission electron microscopy. <i>Journal of Structural Biology</i> , 2013, 181, 136-148.	2.8	31
154	Particle quality assessment and sorting for automatic and semiautomatic particle-picking techniques. <i>Journal of Structural Biology</i> , 2013, 183, 342-353.	2.8	31
155	Fringe pattern denoising by image dimensionality reduction. <i>Optics and Lasers in Engineering</i> , 2013, 51, 921-928.	3.8	25
156	Xmipp 3.0: An improved software suite for image processing in electron microscopy. <i>Journal of Structural Biology</i> , 2013, 184, 321-328.	2.8	261
157	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.	0.9	25
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159	Chromothripsis: Breakage-fusion-bridge over and over again. <i>Cell Cycle</i> , 2013, 12, 2016-2023.	2.6	46
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