Javier Vargas

List of Publications by Year
in descending order

103 papers	5,524 citations	218677 26 h-index	133252 59 g-index
114 all docs	114 docs citations	114 times ranked	6678 citing authors

#	Article	IF	Citations
1	Enhancement of Cryo-EM maps by a multiscale tubular filter. Optics Express, 2022, 30, 4515.	3.4	4
2	Incremental PCA algorithm for fringe pattern demodulation. Optics Express, 2022, 30, 12278.	3.4	4
3	Multivalent interactions essential for lentiviral integrase function. Nature Communications, 2022, 13, 2416.	12.8	12
4	Local computational methods to improve the interpretability and analysis of cryo-EM maps. Nature Communications, 2021, 12, 1240.	12.8	36
5	Robust weighted principal components analysis demodulation algorithm for phase-shifting interferometry. Optics Express, 2021, 29, 16534.	3.4	6
6	Facial morphology analysis in osteogenesis imperfecta types I, III and IV using computer vision. Orthodontics and Craniofacial Research, 2021, 24, 92-99.	2.8	1
7	DeepEMhancer: a deep learning solution for cryo-EM volume post-processing. Communications Biology, 2021, 4, 874.	4.4	561
8	ENRICH: A fast method to improve the quality of flexible macromolecular reconstructions. Progress in Biophysics and Molecular Biology, 2021, 164, 92-100.	2.9	2
9	A two steps phase-shifting demodulation method using the VU factorization. Optics and Lasers in Engineering, 2021, 147, 106730.	3.8	2
10	Advances in Xmipp for Cryo–Electron Microscopy: From Xmipp to Scipion. Molecules, 2021, 26, 6224.	3.8	22
11	Automatic local resolution-based sharpening of cryo-EM maps. Bioinformatics, 2020, 36, 765-772.	4.1	110
12	Phase-shifting VU factorization for interferometry. Optics and Lasers in Engineering, 2020, 124, 105797.	3.8	22
13	Rapid quantitative interferometric microscopy using fast Fourier transform and differential–integral based phase retrieval algorithm (FFT-DI-PRA). Optics Communications, 2020, 456, 124613.	2.1	3
14	Measuring local-directional resolution and local anisotropy in cryo-EM maps. Nature Communications, 2020, 11, 55.	12.8	28
15	High strength brushite bioceramics obtained by selective regulation of crystal growth with chiral biomolecules. Acta Biomaterialia, 2020, 106, 351-359.	8.3	24
16	Alternative conformations and motions adopted by 30S ribosomal subunits visualized by cryo-electron microscopy. Rna, 2020, 26, 2017-2030.	3.5	21
17	The inner junction complex of the cilia is an interaction hub that involves tubulin post-translational modifications. ELife, 2020, 9, .	6.0	1,191
18	A comprehensive review of the principal component analysis applied to the demodulation of phase-shifting interferograms. , 2020, , .		1

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19	Deep Learning for Validating and Estimating Resolution of Cryo-Electron Microscopy Density Maps â€. Molecules, 2019, 24, 1181.	3.8	25
20	Role of Era in assembly and homeostasis of the ribosomal small subunit. Nucleic Acids Research, 2019, 47, 8301-8317.	14.5	34
21	Computational Methods to Process Highly Heterogeneous Cryo-EM Samples. Microscopy and Microanalysis, 2019, 25, 1292-1293.	0.4	0
22	Tubulin lattice in cilia is in a stressed form regulated by microtubule inner proteins. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19930-19938.	7.1	61
23	A robust approach to ab initio cryo-electron microscopy initial volume determination. Journal of Structural Biology, 2019, 208, 107397.	2.8	10
24	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
25	Principal component analysis-based quantitative differential interference contrast microscopy. Optics Letters, 2019, 44, 45.	3.3	11
26	Linear algebra approach to phase shifting interferometry: numerical methods. , 2019, , .		0
27	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
28	MonoRes: Automatic and Accurate Estimation of Local Resolution for Electron Microscopy Maps. Structure, 2018, 26, 337-344.e4.	3.3	179
29	Blind estimation of DED camera gain in Electron Microscopy. Journal of Structural Biology, 2018, 203, 90-93.	2.8	7
30	Scipion web tools: Easy to use cryoâ€EM image processing over the web. Protein Science, 2018, 27, 269-275.	7.6	18
31	A new algorithm for high-resolution reconstruction of single particles by electron microscopy. Journal of Structural Biology, 2018, 204, 329-337.	2.8	28
32	Improving 3D reconstructions of macromolecular conformations. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a155-a155.	0.1	0
33	XTEND: Extending the depth of field in cryo soft X-ray tomography. Scientific Reports, 2017, 7, 45808.	3.3	24
34	Single-particle electron microscopy structure of UDP-glucose:glycoprotein glucosyltransferase suggests a selectivity mechanism for misfolded proteins. Journal of Biological Chemistry, 2017, 292, 11499-11507.	3.4	26
35	Pea PSII-LHCII supercomplexes form pairs by making connections across the stromal gap. Scientific Reports, 2017, 7, 10067.	3.3	30
36	Quantitative analysis of 3D alignment quality: its impact on soft-validation, particle pruning and homogeneity analysis. Scientific Reports, 2017, 7, 6307.	3.3	15

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37	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
38	A Survey of the Use of Iterative Reconstruction Algorithms in Electron Microscopy. BioMed Research International, 2017, 2017, 1-17.	1.9	29
39	Fast and automatic identification of particle tilt pairs based on Delaunay triangulation. Journal of Structural Biology, 2016, 196, 525-533.	2.8	4
40	Digital image compression for a 2f multiplexing optical setup. Journal of Optics (United Kingdom), 2016, 18, 075701.	2.2	2
41	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
42	Local analysis of strains and rotations for macromolecular electron microscopy maps. Journal of Structural Biology, 2016, 195, 123-128.	2.8	9
43	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
44	Asymmetric cryo-EM reconstruction of phage MS2 reveals genome structure in situ. Nature Communications, 2016, 7, 12524.	12.8	114
45	Precise phase retrieval under harsh conditions by constructing new connected interferograms. Scientific Reports, 2016, 6, 24416.	3.3	8
46	Particle alignment reliability in single particle electron cryomicroscopy: a general approach. Scientific Reports, 2016, 6, 21626.	3.3	21
47	Scipion: A software framework toward integration, reproducibility and validation in 3D electron microscopy. Journal of Structural Biology, 2016, 195, 93-99.	2.8	474
48	Cryo-EM and the elucidation of new macromolecular structures: Random Conical Tilt revisited. Scientific Reports, 2015, 5, 14290.	3.3	16
49	Alignment of direct detection device micrographs using a robust Optical Flow approach. Journal of Structural Biology, 2015, 189, 163-176.	2.8	59
50	Principal component analysis based simultaneous dual-wavelength phase-shifting interferometry. Optics Communications, 2015, 341, 276-283.	2.1	24
51	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
52	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
53	CTF Challenge: Result summary. Journal of Structural Biology, 2015, 190, 348-359.	2.8	34
54	Quantitative interferometric microscopy cytometer based on regularized optical flow algorithm. Optics Communications, 2015, 350, 222-229.	2.1	16

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55	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
56	Fast and accurate conversion of atomic models into electron density maps. AIMS Biophysics, 2015, 2, 8-20.	0.6	42
57	An image processing approach to the simulation of electron microscopy volumes of atomic structures. , 2014, , .		0
58	Shack-Hartmann spot dislocation map determination using an optical flow method. Optics Express, 2014, 22, 1319.	3.4	15
59	Efficient initial volume determination from electron microscopy images of single particles. Bioinformatics, 2014, 30, 2891-2898.	4.1	63
60	Error analysis of the principal component analysis demodulation algorithm. Applied Physics B: Lasers and Optics, 2014, 115, 355-364.	2.2	16
61	Comparing scientific performance among equals. Scientometrics, 2014, 101, 1731-1745.	3.0	12
62	Interchanging Geometry Conventions in 3DEM: Mathematical Context for the Development of Standards. Applied and Numerical Harmonic Analysis, 2014, , 7-42.	0.3	8
63	Quadrature Component Analysis for interferometry. Optics and Lasers in Engineering, 2013, 51, 637-641.	3.8	40
64	FASTDEF: Fast defocus and astigmatism estimation for high-throughput transmission electron microscopy. Journal of Structural Biology, 2013, 181, 136-148.	2.8	31
65	Particle quality assessment and sorting for automatic and semiautomatic particle-picking techniques. Journal of Structural Biology, 2013, 183, 342-353.	2.8	31
66	Fringe pattern denoising by image dimensionality reduction. Optics and Lasers in Engineering, 2013, 51, 921-928.	3.8	25
67	Xmipp 3.0: An improved software suite for image processing in electron microscopy. Journal of Structural Biology, 2013, 184, 321-328.	2.8	261
68	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
69	Generalization of the Principal Component Analysis algorithm for interferometry. Optics Communications, 2013, 286, 130-134.	2.1	63
70	A pattern matching approach to the automatic selection of particles from low-contrast electron micrographs. Bioinformatics, 2013, 29, 2460-2468.	4.1	73
71	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
72	Circular common-path point diffraction interferometer. Optics Letters, 2012, 37, 3927.	3.3	16

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73	Windowed phase unwrapping using a first-order dynamic system following iso-phase contours. Applied Optics, 2012, 51, 7549.	1.8	13
74	Fast two-dimensional simultaneous phase unwrapping and low-pass filtering. Optics Express, 2012, 20, 2556.	3.4	55
75	Multiplicative phase-shifting interferometry using optical flow. Applied Optics, 2012, 51, 5903.	1.8	8
76	Two-step demodulation based on the Gramâ€"Schmidt orthonormalization method. Optics Letters, 2012, 37, 443.	3.3	169
77	Shackâ€"Hartmann centroid detection using the spiral phase transform. Applied Optics, 2012, 51, 7362.	1.8	17
78	Spatial carrier phase-shifting algorithm based on principal component analysis method. Optics Express, 2012, 20, 16471.	3.4	64
79	2D simultaneous phase unwrapping and filtering: A review and comparison. Optics and Lasers in Engineering, 2012, 50, 1026-1029.	3.8	38
80	Effect of Aberrations on the Self-Imaging Phenomenon. Journal of Lightwave Technology, 2011, 29, 1051-1057.	4.6	7
81	Phase-shifting interferometry based on induced vibrations. Optics Express, 2011, 19, 584.	3.4	24
82	Two-step self-tuning phase-shifting interferometry. Optics Express, 2011, 19, 638.	3.4	68
83	Regularized least squares phase sampling interferometry. Optics Express, 2011, 19, 5002.	3.4	3
84	Role of the filter phase in phase sampling interferometry. Optics Express, 2011, 19, 19987.	3.4	2
85	Local fringe density determination by adaptive filtering. Optics Letters, 2011, 36, 70.	3.3	14
86	Phase-shifting interferometry based on principal component analysis. Optics Letters, 2011, 36, 1326.	3.3	189
87	Analysis of the principal component algorithm in phase-shifting interferometry. Optics Letters, 2011, 36, 2215.	3.3	96
88	Two-step interferometry by a regularized optical flow algorithm. Optics Letters, 2011, 36, 3485.	3.3	124
89	Space-qualified liquid-crystal variable retarders for wide-field-of-view coronagraphs. , 2011, , .		8
90	High dynamic range imaging method for interferometry. Optics Communications, 2011, 284, 4141-4145.	2.1	13

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91	Imaging polarimeters based on liquid crystal variable retarders: an emergent technology for space instrumentation. Proceedings of SPIE, 2011, , .	0.8	21
92	Optical inspection of liquid crystal variable retarder inhomogeneities. Applied Optics, 2010, 49, 568.	2.1	20
93	Shackâ€"Hartmann centroid detection method based on high dynamic range imaging and normalization techniques. Applied Optics, 2010, 49, 2409.	2.1	20
94	Deflectometric method for the measurement of user power for ophthalmic lenses. Applied Optics, 2010, 49, 5125.	2.1	38
95	Calibration of a Shackâ€"Hartmann wavefront sensor as an orthographic camera. Optics Letters, 2010, 35, 1762.	3.3	11
96	Direct demodulation of closed-fringe interferograms based on active contours. Optics Letters, 2010, 35, 3550.	3.3	6
97	Multiresolution approach based on projection matrices. Applied Optics, 2009, 48, 1295.	2.1	3
98	Three-dimensional measurement of microchips using structured light techniques. Optical Engineering, 2008, 47, 053602.	1.0	8
99	Novel multiresolution approach for an adaptive structured light system. Optical Engineering, 2008, 47, 023601.	1.0	9
100	Defect inspection by an active 3D multiresolution technique. , 2008, , .		1
101	Flexible calibration procedure for fringe projection profilometry. Optical Engineering, 2007, 46, 023601.	1.0	25
102	Adaptive spatiotemporal structured light method for fast three-dimensional measurement. Optical Engineering, 2006, 45, 107203.	1.0	6
103	Non-uniformly polarized beams across their transverse profiles: an introductory study for undergraduate optics courses. European Journal of Physics, 2004, 25, 793-800.	0.6	19