Chandrajit Bajaj

List of Publications by Year
in descending order

52 papers	1,720 citations	331670 21 h-index	302126 39 g-index
52 all docs	52 docs citations	52 times ranked	1582 citing authors

#	ARTICLE	IF	CITATIONS
1	Adaptive and quality quadrilateral/hexahedral meshing from volumetric data. Computer Methods in Applied Mechanics and Engineering, 2006, 195, 942-960.	6.6	182
2	3D finite element meshing from imaging data. Computer Methods in Applied Mechanics and Engineering, 2005, 194, 5083-5106.	6.6	155
3	High-resolution cryo-electron microscopy structure of the Trypanosoma brucei ribosome. Nature, 2013, 494, 385-389.	27.8	122
4	Quality meshing of implicit solvation models of biomolecular structures. Computer Aided Geometric Design, 2006, 23, 510-530.	1.2	100
5	Surface smoothing and quality improvement of quadrilateral/hexahedral meshes with geometric flow. Communications in Numerical Methods in Engineering, 2009, 25, 1-18.	1.3	90
6	The Capsid Proteins of a Large, Icosahedral dsDNA Virus. Journal of Molecular Biology, 2009, 385, 1287-1299.	4.2	64
7	Quadratic serendipity finite elements on polygons using generalized barycentric coordinates. Mathematics of Computation, 2014, 83, 2691-2716.	2.1	62
8	Computational Approaches for Automatic Structural Analysis of Large Biomolecular Complexes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 568-582.	3.0	61
9	Volumetric feature extraction and visualization of tomographic molecular imaging. Journal of Structural Biology, 2003, 144, 132-143.	2.8	56
10	Error estimates for generalized barycentric interpolation. Advances in Computational Mathematics, 2012, 37, 417-439.	1.6	56
11	A subdivision scheme for hexahedral meshes. Visual Computer, 2002, 18, 343-356.	3.5	53
12	An Efficient Higher-Order Fast Multipole Boundary Element Solution for Poisson–Boltzmann-Based Molecular Electrostatics. SIAM Journal of Scientific Computing, 2011, 33, 826-848.	2.8	52
13	Detecting circular and rectangular particles based on geometric feature detection in electron micrographs. Journal of Structural Biology, 2004, 145, 168-180.	2.8	50
14	Automated segmentation of molecular subunits in electron cryomicroscopy density maps. Journal of Structural Biology, 2006, 156, 432-441.	2.8	47
15	F^2Dock: Fast Fourier Protein-Protein Docking. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 45-58.	3.0	47
16	A fast and adaptive method for image contrast enhancement. , 0, , .		39
17	Automatic ultrastructure segmentation of reconstructed CryoEM maps of icosahedral viruses. IEEE Transactions on Image Processing, 2005, 14, 1324-1337.	9.8	37
18	Protein-Protein Docking with F2Dock 2.0 and GB-Rerank. PLoS ONE, 2013, 8, e51307.	2.5	33

#	Article	IF	Citations
19	Tetrameric Mouse Acetylcholinesterase: Continuum Diffusion Rate Calculations by Solving the Steady-State Smoluchowski Equation Using Finite Element Methods. Biophysical Journal, 2005, 88, 1659-1665.	0.5	31
20	Interpolation error estimates for mean value coordinates over convex polygons. Advances in Computational Mathematics, 2013, 39, 327-347.	1.6	30
21	Construction of Scalar and Vector Finite Element Families on Polygonal and Polyhedral Meshes. Computational Methods in Applied Mathematics, 2016, 16, 667-683.	0.8	30
22	Surface Smoothing and Quality Improvement of Quadrilateral/Hexahedral Meshes with Geometric Flow. , 2005, , 449-468.		30
23	Adaptive and quality 3D meshing from imaging data. , 2003, , .		28
24	Dual formulations of mixed finite element methods with applications. CAD Computer Aided Design, 2011, 43, 1213-1221.	2.7	26
25	Computational Refinement and Validation Protocol for Proteins with Large Variable Regions Applied to Model HIV Env Spike in CD4 and 17b Bound State. Structure, 2015, 23, 1138-1149.	3.3	25
26	VolRoverN: Enhancing Surface and Volumetric Reconstruction for Realistic Dynamical Simulation of Cellular and Subcellular Function. Neuroinformatics, 2014, 12, 277-289.	2.8	23
27	Electron Tomography of Cryo-Immobilized Plant Tissue: A Novel Approach to Studying 3D Macromolecular Architecture of Mature Plant Cell Walls In Situ. PLoS ONE, 2014, 9, e106928.	2.5	22
28	Macromolecular structure modeling from 3D EM using VolRover 2.0. Biopolymers, 2012, 97, 709-731.	2.4	16
29	Topology Based Selection and Curation of Level Sets. Mathematics and Visualization, 2009, 2009, 45-58.	0.6	15
30	Fast Molecular Solvation Energetics and Forces Computation. SIAM Journal of Scientific Computing, 2010, 31, 4524-4552.	2.8	14
31	An algebraic spline model of molecular surfaces. , 2007, , .		13
32	A Structure Tensor Approach for 3D Image Skeletonization: Applications in Protein Secondary Structure Analysis. , 2006, , .		11
33	Detection of secondary and supersecondary structures of proteins from cryo-electron microscopy. Journal of Structural Biology, 2012, 177, 367-381.	2.8	11
34	Shape-Based Regularization of Electron Tomographic Reconstruction. IEEE Transactions on Medical Imaging, 2012, 31, 2241-2252.	8.9	10
35	Progressive Conversion from B-rep to BSP for Streaming Geometric Modeling. Computer-Aided Design and Applications, 2006, 3, 577-586.	0.6	9
36	A dynamic data structure for flexible molecular maintenance and informatics. Bioinformatics, 2011, 27, 55-62.	4.1	8

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37	Nonuniform Fourier Transforms for Rigid-Body and Multidimensional Rotational Correlations. SIAM Journal of Scientific Computing, 2013, 35, B821-B845.	2.8	8
38	Secondary and Tertiary Structural Fold Elucidation from 3D EM Maps of Macromolecules. Lecture Notes in Computer Science, 2006, , 264-275.	1.3	7
39	Functional data approximation on bounded domains using polygonal finite elements. Computer Aided Geometric Design, 2018, 63, 149-163.	1.2	6
40	Proto-Plasm : parallel language for adaptive and scalable modelling of biosystems. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3045-3065.	3.4	5
41	PF2 fit: Polar Fast Fourier Matched Alignment of Atomistic Structures with 3D Electron Microscopy Maps. PLoS Computational Biology, 2015, 11, e1004289.	3.2	5
42	A generalization for stable mixed finite elements. , 2010, , .		5
43	A Laguerre Voronoi based scheme for meshing particle systems. Japan Journal of Industrial and Applied Mathematics, 2005, 22, 167-177.	0.9	4
44	On the construction of general cubature formula by flat extensions. Linear Algebra and Its Applications, 2016, 502, 104-125.	0.9	4
45	Multi-level grid algorithms for faster molecular energetics. , 2010, , .		4
46	An Algebraic Spline Model of Molecular Surfaces for Energetic Computations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1458-1467.	3.0	3
47	Statistical Framework for Uncertainty Quantification in Computational Molecular Modeling. , 2016, 2016, 146-155.		3
48	Modeling Cardiovascular Anatomy from Patient-Specific Imaging. , 2009, 13, 1-28.		2
49	Quality Partitioned Meshing of Multi-material Objects. Procedia Engineering, 2015, 124, 187-199.	1.2	2
50	High-resolution Cryo-EM Structure of the Trypanosoma brucei Ribosome: A Case Study. Applied and Numerical Harmonic Analysis, 2014, , 97-132.	0.3	2
51	AUTOMATIC STRUCTURE INTERPRETATION OF SINGLE PARTICLE CRYO-ELECTRON MICROSCOPY: FROM IMAGES TO PSUEDO-ATOMIC MODELS. , 2007, 2007, 236-239.		1
52	X-ray, Cryo-EM, and computationally predicted protein structures used in integrative modeling of HIV Env glycoprotein gp120 in complex with CD4 and 17b. Data in Brief, 2016, 6, 833-839.	1.0	1