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	Functional data approximation on bounded domains using polygonal finite elements. Computer Aided Geometric Design, 2018, 63, 149-163.	1.2	6
2	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
3	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
4	Statistical Framework for Uncertainty Quantification in Computational Molecular Modeling. , 2016, 2016, 146-155.		3
5	On the construction of general cubature formula by flat extensions. Linear Algebra and Its Applications, 2016, 502, 104-125.	0.9	4
6	Quality Partitioned Meshing of Multi-material Objects. Procedia Engineering, 2015, 124, 187-199.	1.2	2
7	PF2 fit: Polar Fast Fourier Matched Alignment of Atomistic Structures with 3D Electron Microscopy Maps. PLoS Computational Biology, 2015, 11, e1004289.	3.2	5
8	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
9	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
10	Quadratic serendipity finite elements on polygons using generalized barycentric coordinates. Mathematics of Computation, 2014, 83, 2691-2716.	2.1	62
11	VolRoverN: Enhancing Surface and Volumetric Reconstruction for Realistic Dynamical Simulation of Cellular and Subcellular Function. Neuroinformatics, 2014, 12, 277-289.	2.8	23
12	High-resolution Cryo-EM Structure of the Trypanosoma brucei Ribosome: A Case Study. Applied and Numerical Harmonic Analysis, 2014, , 97-132.	0.3	2
13	Interpolation error estimates for mean value coordinates over convex polygons. Advances in Computational Mathematics, 2013, 39, 327-347.	1.6	30
14	Nonuniform Fourier Transforms for Rigid-Body and Multidimensional Rotational Correlations. SIAM Journal of Scientific Computing, 2013, 35, B821-B845.	2.8	8
15	High-resolution cryo-electron microscopy structure of the Trypanosoma brucei ribosome. Nature, 2013, 494, 385-389.	27.8	122
16	Protein-Protein Docking with F2Dock 2.0 and GB-Rerank. PLoS ONE, 2013, 8, e51307.	2.5	33
17	Error estimates for generalized barycentric interpolation. Advances in Computational Mathematics, 2012, 37, 417-439.	1.6	56
18	Shape-Based Regularization of Electron Tomographic Reconstruction. IEEE Transactions on Medical Imaging, 2012, 31, 2241-2252.	8.9	10

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19	Detection of secondary and supersecondary structures of proteins from cryo-electron microscopy. Journal of Structural Biology, 2012, 177, 367-381.	2.8	11
20	Macromolecular structure modeling from 3D EM using VolRover 2.0. Biopolymers, 2012, 97, 709-731.	2.4	16
21	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
22	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
23	Dual formulations of mixed finite element methods with applications. CAD Computer Aided Design, 2011, 43, 1213-1221.	2.7	26
24	F^2Dock: Fast Fourier Protein-Protein Docking. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 45-58.	3.0	47
25	A dynamic data structure for flexible molecular maintenance and informatics. Bioinformatics, 2011, 27, 55-62.	4.1	8
26	Fast Molecular Solvation Energetics and Forces Computation. SIAM Journal of Scientific Computing, 2010, 31, 4524-4552.	2.8	14
27	A generalization for stable mixed finite elements. , 2010, , .		5
28	Multi-level grid algorithms for faster molecular energetics. , 2010, , .		4
29	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
30	The Capsid Proteins of a Large, Icosahedral dsDNA Virus. Journal of Molecular Biology, 2009, 385, 1287-1299.	4.2	64
31	Modeling Cardiovascular Anatomy from Patient-Specific Imaging. , 2009, 13, 1-28.		2
32	Topology Based Selection and Curation of Level Sets. Mathematics and Visualization, 2009, 2009, 45-58.	0.6	15
33	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
34	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
35	An algebraic spline model of molecular surfaces. , 2007, , .		13
36	AUTOMATIC STRUCTURE INTERPRETATION OF SINGLE PARTICLE CRYO-ELECTRON MICROSCOPY: FROM IMAGES TO PSUEDO-ATOMIC MODELS. , 2007, 2007, 236-239.		1

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37	Progressive Conversion from B-rep to BSP for Streaming Geometric Modeling. Computer-Aided Design and Applications, 2006, 3, 577-586.	0.6	9
38	Automated segmentation of molecular subunits in electron cryomicroscopy density maps. Journal of Structural Biology, 2006, 156, 432-441.	2.8	47
39	Quality meshing of implicit solvation models of biomolecular structures. Computer Aided Geometric Design, 2006, 23, 510-530.	1.2	100
40	Adaptive and quality quadrilateral/hexahedral meshing from volumetric data. Computer Methods in Applied Mechanics and Engineering, 2006, 195, 942-960.	6.6	182
41	A Structure Tensor Approach for 3D Image Skeletonization: Applications in Protein Secondary Structure Analysis. , 2006, , .		11
42	Secondary and Tertiary Structural Fold Elucidation from 3D EM Maps of Macromolecules. Lecture Notes in Computer Science, 2006, , 264-275.	1.3	7
43	3D finite element meshing from imaging data. Computer Methods in Applied Mechanics and Engineering, 2005, 194, 5083-5106.	6.6	155
44	A Laguerre Voronoi based scheme for meshing particle systems. Japan Journal of Industrial and Applied Mathematics, 2005, 22, 167-177.	0.9	4
45	Automatic ultrastructure segmentation of reconstructed CryoEM maps of icosahedral viruses. IEEE Transactions on Image Processing, 2005, 14, 1324-1337.	9.8	37
46	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
47	Surface Smoothing and Quality Improvement of Quadrilateral/Hexahedral Meshes with Geometric Flow. , 2005, , 449-468.		30
48	Detecting circular and rectangular particles based on geometric feature detection in electron micrographs. Journal of Structural Biology, 2004, 145, 168-180.	2.8	50
49	Volumetric feature extraction and visualization of tomographic molecular imaging. Journal of Structural Biology, 2003, 144, 132-143.	2.8	56
50	Adaptive and quality 3D meshing from imaging data. , 2003, , .		28
51	A subdivision scheme for hexahedral meshes. Visual Computer, 2002, 18, 343-356.	3.5	53
52	A fast and adaptive method for image contrast enhancement. , 0, , .		39