

Florence Tama

List of Publications by Year in descending order

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76
papers

5,208
citations

126708

33
h-index

88477

70
g-index

79
all docs

79
docs citations

79
times ranked

4268
citing authors

#	ARTICLE	IF	CITATIONS
1	Structures of human pannexin-1 in nanodiscs reveal gating mediated by dynamic movement of the N terminus and phospholipids. <i>Science Signaling</i> , 2022, 15, eabg6941.	1.6	34
2	Light-Control over Casein Kinase 1 γ Activity with Photopharmacology: A Clear Case for Arylazopyrazole-Based Inhibitors. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5326.	1.8	5
3	Photopharmacological Manipulation of Mammalian CRY1 for Regulation of the Circadian Clock. <i>Journal of the American Chemical Society</i> , 2021, 143, 2078-2087.	6.6	31
4	Reversible modulation of circadian time with chronophotopharmacology. <i>Nature Communications</i> , 2021, 12, 3164.	5.8	35
5	Structural differences in the FAD-binding pockets and lid loops of mammalian CRY1 and CRY2 for isoform-selective regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
6	Protocol for Retrieving Three-Dimensional Biological Shapes for a Few XFEL Single-Particle Diffraction Patterns. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 4108-4119.	2.5	1
7	Reconstruction of Three-Dimensional Conformations of Bacterial ClpB from High-Speed Atomic-Force-Microscopy Images. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 704274.	1.6	10
8	Conformational ensemble of an intrinsically flexible loop in mitochondrial import protein Tim21 studied by modeling and molecular dynamics simulations. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129417.	1.1	4
9	Crystal contact-free conformation of an intrinsically flexible loop in protein crystal: Tim21 as the case study. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129418.	1.1	3
10	Reconstruction of low-resolution molecular structures from simulated atomic force microscopy images. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129420.	1.1	21
11	Isoform-selective regulation of mammalian cryptochromes. <i>Nature Chemical Biology</i> , 2020, 16, 676-685.	3.9	61
12	Integrative/Hybrid Modeling Approaches for Studying Biomolecules. <i>Journal of Molecular Biology</i> , 2020, 432, 2846-2860.	2.0	25
13	Computational Protocol for Assessing the Optimal Pixel Size to Improve the Accuracy of Single-particle Cryo-electron Microscopy Maps. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2570-2580.	2.5	3
14	Dynamics at the serine loop underlie differential affinity of cryptochromes for CLOCK:BMAL1 to control circadian timing. <i>ELife</i> , 2020, 9, .	2.8	50
15	Controlling the Circadian Clock with High Temporal Resolution through Photodosing. <i>Journal of the American Chemical Society</i> , 2019, 141, 15784-15791.	6.6	37
16	Cell-based screen identifies a new potent and highly selective CK2 inhibitor for modulation of circadian rhythms and cancer cell growth. <i>Science Advances</i> , 2019, 5, eaau9060.	4.7	93
17	Bipartite anchoring of SCREAM enforces stomatal initiation by coupling MAP kinases to SPEECHLESS. <i>Nature Plants</i> , 2019, 5, 742-754.	4.7	55
18	Computational investigation of the conformational dynamics in Tom20 α mitochondrial presequence tethered complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 81-90.	1.5	4

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19	Cryo-Cooling Effect on DHFR Crystal Studied by Replica-Exchange Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2019, 116, 395-405.	0.2	3
20	Acceleration of cryo-EM Flexible Fitting for Large Biomolecular Systems by Efficient Space Partitioning. <i>Structure</i> , 2019, 27, 161-174.e3.	1.6	16
21	Parameter optimization for 3D-reconstruction from XFEL diffraction patterns based on Fourier slice matching. <i>Biophysics and Physicobiology</i> , 2019, 16, 367-376.	0.5	2
22	Conformational dynamics of human protein kinase CK2 β and its effect on function and inhibition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 344-353.	1.5	8
23	Hybrid Methods for Macromolecular Modeling by Molecular Mechanics Simulations with Experimental Data. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1105, 199-217.	0.8	8
24	Poisson image denoising by piecewise principal component analysis and its application in single-particle X-ray diffraction imaging. <i>IET Image Processing</i> , 2018, 12, 2264-2274.	1.4	5
25	Role of Computational Methods in Going beyond X-ray Crystallography to Explore Protein Structure and Dynamics. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3401.	1.8	52
26	Searching for 3D structural models from a library of biological shapes using a few 2D experimental images. <i>BMC Bioinformatics</i> , 2018, 19, 320.	1.2	4
27	Single-particle XFEL 3D reconstruction of ribosome-size particles based on Fourier slice matching: requirements to reach subnanometer resolution. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 1010-1021.	1.0	16
28	Gaussian mixture model for coarse-grained modeling from XFEL. <i>Optics Express</i> , 2018, 26, 26734.	1.7	8
29	Flexible fitting to cryo-EM density map using ensemble molecular dynamics simulations. <i>Journal of Computational Chemistry</i> , 2017, 38, 1447-1461.	1.5	46
30	Editorial overview: Macromolecular assemblies. <i>Current Opinion in Structural Biology</i> , 2017, 43, vii-ix.	2.6	0
31	Three-dimensional reconstruction for coherent diffraction patterns obtained by XFEL. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 727-737.	1.0	13
32	Local thermodynamics of the water molecules around single- and double-stranded DNA studied by grid inhomogeneous solvation theory. <i>Chemical Physics Letters</i> , 2016, 660, 250-255.	1.2	12
33	Hybrid approach for structural modeling of biological systems from X-ray free electron laser diffraction patterns. <i>Journal of Structural Biology</i> , 2016, 194, 325-336.	1.3	18
34	Thermodynamic properties of water molecules in the presence of cosolute depend on DNA structure: a study using grid inhomogeneous solvation theory. <i>Nucleic Acids Research</i> , 2015, 43, gkv1133.	6.5	29
35	Elastic image registration to fully explore macromolecular dynamics by electron microscopy. , 2014, , .		0
36	Macromolecular structures probed by combining single-shot free-electron laser diffraction with synchrotron coherent X-ray imaging. <i>Nature Communications</i> , 2014, 5, 3798.	5.8	61

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37	Hybrid Electron Microscopy Normal Mode Analysis graphical interface and protocol. Journal of Structural Biology, 2014, 188, 134-141.	1.3	18
38	Replica Exchange Molecular Dynamics Simulations Provide Insight into Substrate Recognition by Small Heat Shock Proteins. Biophysical Journal, 2014, 106, 2644-2655.	0.2	32
39	Iterative Elastic 3D-to-2D Alignment Method Using Normal Modes for Studying Structural Dynamics of Large Macromolecular Complexes. Structure, 2014, 22, 496-506.	1.6	90
40	Macromolecular Dynamics by Hybrid Electron Microscopy Normal Mode Analysis. Microscopy and Microanalysis, 2014, 20, 1218-1219.	0.2	7
41	Consensus among multiple approaches as a reliability measure for flexible fitting into cryo-EM data. Journal of Structural Biology, 2013, 182, 67-77.	1.3	20
42	Allosteric Regulation of DNA Cleavage and Sequence-Specificity through Run-On Oligomerization. Structure, 2013, 21, 1848-1858.	1.6	23
43	Molecular Model of a Soluble Guanylyl Cyclase Fragment Determined by Small-Angle X-ray Scattering and Chemical Cross-Linking. Biochemistry, 2013, 52, 1568-1582.	1.2	56
44	Network visualization of conformational sampling during molecular dynamics simulation. Journal of Molecular Graphics and Modelling, 2013, 46, 140-149.	1.3	11
45	3DEM Loupe: analysis of macromolecular dynamics using structures from electron microscopy. Nucleic Acids Research, 2013, 41, W363-W367.	6.5	14
46	Steered Molecular Dynamics Simulations of a Type IV Pilus Probe Initial Stages of a Force-Induced Conformational Transition. PLoS Computational Biology, 2013, 9, e1003032.	1.5	22
47	Twelve Transmembrane Helices Form the Functional Core of Mammalian MATE1 (Multidrug and Toxin) Tj ETQq1 1 Q.784314 ggBT /Over	1.6	48
48	Phosphorylated Smooth Muscle Heavy Meromyosin Shows an Open Conformation Linked to Activation. Journal of Molecular Biology, 2012, 415, 274-287.	2.0	25
49	Consensus among flexible fitting approaches improves the interpretation of cryo-EM data. Journal of Structural Biology, 2012, 177, 561-570.	1.3	38
50	Simulations of substrate transport in the multidrug transporter EmrD. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1620-1632.	1.5	20
51	Structure modeling from small angle X-ray scattering data with elastic network normal mode analysis. Journal of Structural Biology, 2011, 173, 451-460.	1.3	16
52	Excited states of ribosome translocation revealed through integrative molecular modeling. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18943-18948.	3.3	89
53	Three-dimensional structure of the anthrax toxin pore inserted into lipid nanodiscs and lipid vesicles. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3453-3457.	3.3	102
54	Biased coarse-grained molecular dynamics simulation approach for flexible fitting of X-ray structure into cryo electron microscopy maps. Journal of Structural Biology, 2010, 169, 95-105.	1.3	47

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55	Normal-Mode Flexible Fitting of High-Resolution Structure of Biological Molecules toward One-Dimensional Low-Resolution Data. <i>Biophysical Journal</i> , 2008, 94, 1589-1599.	0.2	62
56	Flexible Fitting of High-Resolution X-Ray Structures into Cryoelectron Microscopy Maps Using Biased Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2008, 95, 5692-5705.	0.2	101
57	SYMMETRY, FORM, AND SHAPE: Guiding Principles for Robustness in Macromolecular Machines. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006, 35, 115-133.	18.3	251
58	Model of the toxic complex of anthrax: Responsive conformational changes in both the lethal factor and the protective antigen heptamer. <i>Protein Science</i> , 2006, 15, 2190-2200.	3.1	22
59	Electrostatic properties of cowpea chlorotic mottle virus and cucumber mosaic virus capsids. <i>Biopolymers</i> , 2006, 82, 106-120.	1.2	59
60	Removal of Divalent Cations Induces Structural Transitions in Red Clover Necrotic Mosaic Virus , Revealing a Potential Mechanism for RNA Release. <i>Journal of Virology</i> , 2006, 80, 10395-10406.	1.5	106
61	Structure of the E. coli protein-conducting channel bound to a translating ribosome. <i>Nature</i> , 2005, 438, 318-324.	13.7	243
62	Diversity and Identity of Mechanical Properties of Icosahedral Viral Capsids Studied with Elastic Network Normal Mode Analysis. <i>Journal of Molecular Biology</i> , 2005, 345, 299-314.	2.0	177
63	The Requirement for Mechanical Coupling Between Head and S2 Domains in Smooth Muscle Myosin ATPase Regulation and its Implications for Dimeric Motor Function. <i>Journal of Molecular Biology</i> , 2005, 345, 837-854.	2.0	47
64	The 13Å... Structure of a Chaperonin GroELâ€“Protein Substrate Complex by Cryo-electron Microscopy. <i>Journal of Molecular Biology</i> , 2005, 348, 219-230.	2.0	65
65	Topology representing neural networks reconcile biomolecular shape, structure, and dynamics. <i>Neurocomputing</i> , 2004, 56, 365-379.	3.5	19
66	Ribosome motions modulate electrostatic properties. <i>Biopolymers</i> , 2004, 74, 423-431.	1.2	44
67	Normal mode based flexible fitting of high-resolution structure into low-resolution experimental data from cryo-EM. <i>Journal of Structural Biology</i> , 2004, 147, 315-326.	1.3	230
68	Flexible Multi-scale Fitting of Atomic Structures into Low-resolution Electron Density Maps with Elastic Network Normal Mode Analysis. <i>Journal of Molecular Biology</i> , 2004, 337, 985-999.	2.0	217
69	Mega-Dalton Biomolecular Motion Captured from Electron Microscopy Reconstructions. <i>Journal of Molecular Biology</i> , 2003, 326, 485-492.	2.0	113
70	Dynamic reorganization of the functionally active ribosome explored by normal mode analysis and cryo-electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9319-9323.	3.3	332
71	Normal Mode Analysis With Simplified Models To Investigate The Global Dynamics Of Biological Systems. <i>Protein and Peptide Letters</i> , 2003, 10, 119-132.	0.4	49
72	The Mechanism and Pathway of pH Induced Swelling in Cowpea Chlorotic Mottle Virus. <i>Journal of Molecular Biology</i> , 2002, 318, 733-747.	2.0	190

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73	Exploring Global Distortions of Biological Macromolecules and Assemblies from Low-resolution Structural Information and Elastic Network Theory. <i>Journal of Molecular Biology</i> , 2002, 321, 297-305.	2.0	193
74	Conformational change of proteins arising from normal mode calculations. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 1-6.	1.0	796
75	Building-block approach for determining low-frequency normal modes of macromolecules. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 1-7.	1.5	421
76	Molecular dynamics simulation shows large volume fluctuations of proteins. <i>European Biophysics Journal</i> , 2000, 29, 472-480.	1.2	15