

# Florence Tama

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

74  
papers

4,372  
citations

30  
h-index

66  
g-index

79  
ext. papers

4,850  
ext. citations

6.5  
avg, IF

5.53  
L-index

#	Paper	IF	Citations
74	Conformational change of proteins arising from normal mode calculations. <i>Protein Engineering, Design and Selection</i> , <b>2001</b> , 14, 1-6	1.9	716
73	Building-block approach for determining low-frequency normal modes of macromolecules. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2000</b> , 41, 1-7	4.2	379
72	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> , <b>2003</b> , 100, 9319-23	11.5	299
71	Symmetry, form, and shape: guiding principles for robustness in macromolecular machines. <i>Annual Review of Biophysics and Biomolecular Structure</i> , <b>2006</b> , 35, 115-33		228
70	Structure of the E. coli protein-conducting channel bound to a translating ribosome. <i>Nature</i> , <b>2005</b> , 438, 318-24	50.4	226
69	Normal mode based flexible fitting of high-resolution structure into low-resolution experimental data from cryo-EM. <i>Journal of Structural Biology</i> , <b>2004</b> , 147, 315-26	3.4	202
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> , <b>2004</b> , 337, 985-99	6.5	193
67	Exploring global distortions of biological macromolecules and assemblies from low-resolution structural information and elastic network theory. <i>Journal of Molecular Biology</i> , <b>2002</b> , 321, 297-305	6.5	175
66	The mechanism and pathway of pH induced swelling in cowpea chlorotic mottle virus. <i>Journal of Molecular Biology</i> , <b>2002</b> , 318, 733-47	6.5	173
65	Diversity and identity of mechanical properties of icosahedral viral capsids studied with elastic network normal mode analysis. <i>Journal of Molecular Biology</i> , <b>2005</b> , 345, 299-314	6.5	157
64	Mega-Dalton biomolecular motion captured from electron microscopy reconstructions. <i>Journal of Molecular Biology</i> , <b>2003</b> , 326, 485-92	6.5	98
63	Three-dimensional structure of the anthrax toxin pore inserted into lipid nanodiscs and lipid vesicles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 3453-7	11.5	88
62	Flexible fitting of high-resolution x-ray structures into cryoelectron microscopy maps using biased molecular dynamics simulations. <i>Biophysical Journal</i> , <b>2008</b> , 95, 5692-705	2.9	83
61	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> , <b>2006</b> , 80, 10395-406	6.6	82
60	Excited states of ribosome translocation revealed through integrative molecular modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 18943-8	11.5	77
59	The 13 angstroms structure of a chaperonin GroEL-protein substrate complex by cryo-electron microscopy. <i>Journal of Molecular Biology</i> , <b>2005</b> , 348, 219-30	6.5	60
58	Iterative elastic 3D-to-2D alignment method using normal modes for studying structural dynamics of large macromolecular complexes. <i>Structure</i> , <b>2014</b> , 22, 496-506	5.2	59

57	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> , <b>2019</b> , 5, eaau9060	14.3	54
56	Macromolecular structures probed by combining single-shot free-electron laser diffraction with synchrotron coherent X-ray imaging. <i>Nature Communications</i> , <b>2014</b> , 5, 3798	17.4	52
55	Normal-mode flexible fitting of high-resolution structure of biological molecules toward one-dimensional low-resolution data. <i>Biophysical Journal</i> , <b>2008</b> , 94, 1589-99	2.9	52
54	Molecular model of a soluble guanylyl cyclase fragment determined by small-angle X-ray scattering and chemical cross-linking. <i>Biochemistry</i> , <b>2013</b> , 52, 1568-82	3.2	51
53	Electrostatic properties of cowpea chlorotic mottle virus and cucumber mosaic virus capsids. <i>Biopolymers</i> , <b>2006</b> , 82, 106-20	2.2	50
52	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> , <b>2005</b> , 345, 837-54	6.5	45
51	Biased coarse-grained molecular dynamics simulation approach for flexible fitting of X-ray structure into cryo electron microscopy maps. <i>Journal of Structural Biology</i> , <b>2010</b> , 169, 95-105	3.4	44
50	Normal mode analysis with simplified models to investigate the global dynamics of biological systems. <i>Protein and Peptide Letters</i> , <b>2003</b> , 10, 119-32	1.9	44
49	Ribosome motions modulate electrostatic properties. <i>Biopolymers</i> , <b>2004</b> , 74, 423-31	2.2	40
48	Twelve transmembrane helices form the functional core of mammalian MATE1 (multidrug and toxin extruder 1) protein. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 27971-82	5.4	34
47	Bipartite anchoring of SCREAM enforces stomatal initiation by coupling MAP kinases to SPEECHLESS. <i>Nature Plants</i> , <b>2019</b> , 5, 742-754	11.5	33
46	Role of Computational Methods in Going beyond X-ray Crystallography to Explore Protein Structure and Dynamics. <i>International Journal of Molecular Sciences</i> , <b>2018</b> , 19,	6.3	33
45	Isoform-selective regulation of mammalian cryptochromes. <i>Nature Chemical Biology</i> , <b>2020</b> , 16, 676-685	11.7	30
44	Consensus among flexible fitting approaches improves the interpretation of cryo-EM data. <i>Journal of Structural Biology</i> , <b>2012</b> , 177, 561-70	3.4	30
43	Flexible fitting to cryo-EM density map using ensemble molecular dynamics simulations. <i>Journal of Computational Chemistry</i> , <b>2017</b> , 38, 1447-1461	3.5	29
42	Replica exchange molecular dynamics simulations provide insight into substrate recognition by small heat shock proteins. <i>Biophysical Journal</i> , <b>2014</b> , 106, 2644-55	2.9	28
41	Dynamics at the serine loop underlie differential affinity of cryptochromes for CLOCK:BMAL1 to control circadian timing. <i>ELife</i> , <b>2020</b> , 9,	8.9	27
40	Phosphorylated smooth muscle heavy meromyosin shows an open conformation linked to activation. <i>Journal of Molecular Biology</i> , <b>2012</b> , 415, 274-87	6.5	24

39	Controlling the Circadian Clock with High Temporal Resolution through Photodosing. <i>Journal of the American Chemical Society</i> , <b>2019</b> , 141, 15784-15791	16.4	23
38	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> , <b>2015</b> , 43, 10114-25 <sup>20.1</sup>	20.1	22
37	Model of the toxic complex of anthrax: responsive conformational changes in both the lethal factor and the protective antigen heptamer. <i>Protein Science</i> , <b>2006</b> , 15, 2190-200	6.3	21
36	Allosteric regulation of DNA cleavage and sequence-specificity through run-on oligomerization. <i>Structure</i> , <b>2013</b> , 21, 1848-58	5.2	20
35	Topology representing neural networks reconcile biomolecular shape, structure, and dynamics. <i>Neurocomputing</i> , <b>2004</b> , 56, 365-379	5.4	19
34	Consensus among multiple approaches as a reliability measure for flexible fitting into cryo-EM data. <i>Journal of Structural Biology</i> , <b>2013</b> , 182, 67-77	3.4	18
33	Simulations of substrate transport in the multidrug transporter EmrD. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2012</b> , 80, 1620-32	4.2	18
32	Hybrid Electron Microscopy Normal Mode Analysis graphical interface and protocol. <i>Journal of Structural Biology</i> , <b>2014</b> , 188, 134-41	3.4	17
31	Steered molecular dynamics simulations of a type IV pilus probe initial stages of a force-induced conformational transition. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003032	5	17
30	Structure modeling from small angle X-ray scattering data with elastic network normal mode analysis. <i>Journal of Structural Biology</i> , <b>2011</b> , 173, 451-60	3.4	16
29	Molecular dynamics simulation shows large volume fluctuations of proteins. <i>European Biophysics Journal</i> , <b>2000</b> , 29, 472-80	1.9	15
28	Hybrid approach for structural modeling of biological systems from X-ray free electron laser diffraction patterns. <i>Journal of Structural Biology</i> , <b>2016</b> , 194, 325-36	3.4	14
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> , <b>2018</b> , 25, 1010-1021	2.4	13
26	3DEM Loupe: Analysis of macromolecular dynamics using structures from electron microscopy. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, W363-7	20.1	12
25	Integrative/Hybrid Modeling Approaches for Studying Biomolecules. <i>Journal of Molecular Biology</i> , <b>2020</b> , 432, 2846-2860	6.5	11
24	Photopharmacological Manipulation of Mammalian CRY1 for Regulation of the Circadian Clock. <i>Journal of the American Chemical Society</i> , <b>2021</b> , 143, 2078-2087	16.4	11
23	Acceleration of cryo-EM Flexible Fitting for Large Biomolecular Systems by Efficient Space Partitioning. <i>Structure</i> , <b>2019</b> , 27, 161-174.e3	5.2	10
22	Local thermodynamics of the water molecules around single- and double-stranded DNA studied by grid inhomogeneous solvation theory. <i>Chemical Physics Letters</i> , <b>2016</b> , 660, 250-255	2.5	9

21	Three-dimensional reconstruction for coherent diffraction patterns obtained by XFEL. <i>Journal of Synchrotron Radiation</i> , <b>2017</b> , 24, 727-737	2.4	9
20	Reversible modulation of circadian time with chronopharmacology. <i>Nature Communications</i> , <b>2021</b> , 12, 3164	17.4	9
19	Reconstruction of low-resolution molecular structures from simulated atomic force microscopy images. <i>Biochimica Et Biophysica Acta - General Subjects</i> , <b>2020</b> , 1864, 129420	4	9
18	Network visualization of conformational sampling during molecular dynamics simulation. <i>Journal of Molecular Graphics and Modelling</i> , <b>2013</b> , 46, 140-9	2.8	8
17	Conformational dynamics of human protein kinase CK2 and its effect on function and inhibition. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2018</b> , 86, 344-353	4.2	8
16	Macromolecular Dynamics by Hybrid Electron Microscopy Normal Mode Analysis. <i>Microscopy and Microanalysis</i> , <b>2014</b> , 20, 1218-1219	0.5	7
15	Gaussian mixture model for coarse-grained modeling from XFEL. <i>Optics Express</i> , <b>2018</b> , 26, 26734-26749	3.3	7
14	Structures of human pannexin-1 in nanodiscs reveal gating mediated by dynamic movement of the N terminus and phospholipids.. <i>Science Signaling</i> , <b>2022</b> , 15, eabg6941	8.8	6
13	Hybrid Methods for Macromolecular Modeling by Molecular Mechanics Simulations with Experimental Data. <i>Advances in Experimental Medicine and Biology</i> , <b>2018</b> , 1105, 199-217	3.6	5
12	Computational investigation of the conformational dynamics in Tom20-mitochondrial presequence tethered complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2019</b> , 87, 81-90	4.2	4
11	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> , <b>2020</b> , 1864, 129417	4	4
10	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> , <b>2021</b> , 118,	11.5	3
9	Poisson image denoising by piecewise principal component analysis and its application in single-particle X-ray diffraction imaging. <i>IET Image Processing</i> , <b>2018</b> , 12, 2264-2274	1.7	3
8	Searching for 3D structural models from a library of biological shapes using a few 2D experimental images. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 320	3.6	3
7	Cryo-Cooling Effect on DHFR Crystal Studied by Replica-Exchange Molecular Dynamics Simulations. <i>Biophysical Journal</i> , <b>2019</b> , 116, 395-405	2.9	2
6	Reconstruction of Three-Dimensional Conformations of Bacterial ClpB from High-Speed Atomic-Force-Microscopy Images. <i>Frontiers in Molecular Biosciences</i> , <b>2021</b> , 8, 704274	5.6	2
5	Parameter optimization for 3D-reconstruction from XFEL diffraction patterns based on Fourier slice matching. <i>Biophysics and Physicobiology</i> , <b>2019</b> , 16, 367-376	1.4	1
4	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> , <b>2020</b> , 1864, 129418	4	1

- 3 Computational Protocol for Assessing the Optimal Pixel Size to Improve the Accuracy of Single-particle Cryo-electron Microscopy Maps. *Journal of Chemical Information and Modeling*, **2020**, 60, 2570-2580 6.1 ○
- 2 Protocol for Retrieving Three-Dimensional Biological Shapes for a Few XFEL Single-Particle Diffraction Patterns. *Journal of Chemical Information and Modeling*, **2021**, 61, 4108-4119 6.1 ○
- 1 Light-Control over Casein Kinase 1 Activity with Photopharmacology: A Clear Case for Arylazopyrazole-Based Inhibitors. *International Journal of Molecular Sciences*, **2022**, 23, 5326 6.3 ○