Florence Tama

List of Publications by Year in Descending Order

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	Structures of human pannexin-1 in nanodiscs reveal gating mediated by dynamic movement of the N terminus and phospholipids.. *Science Signaling*, **2022**, 15, eabg6941	8.8	6
73	Light-Control over Casein Kinase 1δ Activity with Photopharmacology: A Clear Case for Arylazopyrazole-Based Inhibitors. *International Journal of Molecular Sciences*, **2022**, 23, 5326	6.3	0
72	Reversible modulation of circadian time with chronophotopharmacology. *Nature Communications*, **2021**, 12, 3164	17.4	9
71	Structural differences in the FAD-binding pockets and lid loops of mammalian CRY1 and CRY2 for isoform-selective regulation. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	3
70	Photopharmacological Manipulation of Mammalian CRY1 for Regulation of the Circadian Clock. *Journal of the American Chemical Society*, **2021**, 143, 2078-2087	16.4	11
69	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	0
68	Reconstruction of Three-Dimensional Conformations of Bacterial ClpB from High-Speed Atomic-Force-Microscopy Images. *Frontiers in Molecular Biosciences*, **2021**, 8, 704274	5.6	2
67	Isoform-selective regulation of mammalian cryptochromes. *Nature Chemical Biology*, **2020**, 16, 676-685	11.7	30
66	Integrative/Hybrid Modeling Approaches for Studying Biomolecules. *Journal of Molecular Biology*, **2020**, 432, 2846-2860	6.5	11
65	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	0
64	Dynamics at the serine loop underlie differential affinity of cryptochromes for CLOCK:BMAL1 to control circadian timing. *ELife*, **2020**, 9,	8.9	27
63	Conformational ensemble of an intrinsically flexible loop in mitochondrial import protein Tim21 studied by modeling and molecular dynamics simulations. *Biochimica Et Biophysica Acta - General Subjects*, **2020**, 1864, 129417	4	4
62	Crystal contact-free conformation of an intrinsically flexible loop in protein crystal: Tim21 as the case study. *Biochimica Et Biophysica Acta - General Subjects*, **2020**, 1864, 129418	4	1
61	Reconstruction of low-resolution molecular structures from simulated atomic force microscopy images. *Biochimica Et Biophysica Acta - General Subjects*, **2020**, 1864, 129420	4	9
60	Controlling the Circadian Clock with High Temporal Resolution through Photodosing. *Journal of the American Chemical Society*, **2019**, 141, 15784-15791	16.4	23
59	Cell-based screen identifies a new potent and highly selective CK2 inhibitor for modulation of circadian rhythms and cancer cell growth. *Science Advances*, **2019**, 5, eaau9060	14.3	54
58	Bipartite anchoring of SCREAM enforces stomatal initiation by coupling MAP kinases to SPEECHLESS. *Nature Plants*, **2019**, 5, 742-754	11.5	33

57	Parameter optimization for 3D-reconstruction from XFEL diffraction patterns based on Fourier slice matching. *Biophysics and Physicobiology*, **2019**, 16, 367-376	1.4	1
56	Computational investigation of the conformational dynamics in Tom20-mitochondrial presequence tethered complexes. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 81-90	4.2	4
55	Cryo-Cooling Effect on DHFR Crystal Studied by Replica-Exchange Molecular Dynamics Simulations. *Biophysical Journal*, **2019**, 116, 395-405	2.9	2
54	Acceleration of cryo-EM Flexible Fitting for Large Biomolecular Systems by Efficient Space Partitioning. *Structure*, **2019**, 27, 161-174.e3	5.2	10
53	Gaussian mixture model for coarse-grained modeling from XFEL. *Optics Express*, **2018**, 26, 26734-26749	3.3	7
52	Conformational dynamics of human protein kinase CK2 and its effect on function and inhibition. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86, 344-353	4.2	8
51	Hybrid Methods for Macromolecular Modeling by Molecular Mechanics Simulations with Experimental Data. *Advances in Experimental Medicine and Biology*, **2018**, 1105, 199-217	3.6	5
50	Poisson image denoising by piecewise principal component analysis and its application in single-particle X-ray diffraction imaging. *IET Image Processing*, **2018**, 12, 2264-2274	1.7	3
49	Role of Computational Methods in Going beyond X-ray Crystallography to Explore Protein Structure and Dynamics. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	33
48	Searching for 3D structural models from a library of biological shapes using a few 2D experimental images. *BMC Bioinformatics*, **2018**, 19, 320	3.6	3
47	Single-particle XFEL 3D reconstruction of ribosome-size particles based on Fourier slice matching: requirements to reach subnanometer resolution. *Journal of Synchrotron Radiation*, **2018**, 25, 1010-1021	2.4	13
46	Flexible fitting to cryo-EM density map using ensemble molecular dynamics simulations. *Journal of Computational Chemistry*, **2017**, 38, 1447-1461	3.5	29
45	Three-dimensional reconstruction for coherent diffraction patterns obtained by XFEL. *Journal of Synchrotron Radiation*, **2017**, 24, 727-737	2.4	9
44	Local thermodynamics of the water molecules around single- and double-stranded DNA studied by grid inhomogeneous solvation theory. *Chemical Physics Letters*, **2016**, 660, 250-255	2.5	9
43	Hybrid approach for structural modeling of biological systems from X-ray free electron laser diffraction patterns. *Journal of Structural Biology*, **2016**, 194, 325-36	3.4	14
42	Thermodynamic properties of water molecules in the presence of cosolute depend on DNA structure: a study using grid inhomogeneous solvation theory. *Nucleic Acids Research*, **2015**, 43, 10114-25	20.1	22
41	Hybrid Electron Microscopy Normal Mode Analysis graphical interface and protocol. *Journal of Structural Biology*, **2014**, 188, 134-41	3.4	17
40	Replica exchange molecular dynamics simulations provide insight into substrate recognition by small heat shock proteins. *Biophysical Journal*, **2014**, 106, 2644-55	2.9	28

39	Iterative elastic 3D-to-2D alignment method using normal modes for studying structural dynamics of large macromolecular complexes. *Structure*, **2014**, 22, 496-506	5.2	59
38	Macromolecular Dynamics by Hybrid Electron Microscopy Normal Mode Analysis. *Microscopy and Microanalysis*, **2014**, 20, 1218-1219	0.5	7
37	Macromolecular structures probed by combining single-shot free-electron laser diffraction with synchrotron coherent X-ray imaging. *Nature Communications*, **2014**, 5, 3798	17.4	52
36	Consensus among multiple approaches as a reliability measure for flexible fitting into cryo-EM data. *Journal of Structural Biology*, **2013**, 182, 67-77	3.4	18
35	Allosteric regulation of DNA cleavage and sequence-specificity through run-on oligomerization. *Structure*, **2013**, 21, 1848-58	5.2	20
34	Molecular model of a soluble guanylyl cyclase fragment determined by small-angle X-ray scattering and chemical cross-linking. *Biochemistry*, **2013**, 52, 1568-82	3.2	51
33	Network visualization of conformational sampling during molecular dynamics simulation. *Journal of Molecular Graphics and Modelling*, **2013**, 46, 140-9	2.8	8
32	3DEM Loupe: Analysis of macromolecular dynamics using structures from electron microscopy. *Nucleic Acids Research*, **2013**, 41, W363-7	20.1	12
31	Steered molecular dynamics simulations of a type IV pilus probe initial stages of a force-induced conformational transition. *PLoS Computational Biology*, **2013**, 9, e1003032	5	17
30	Phosphorylated smooth muscle heavy meromyosin shows an open conformation linked to activation. *Journal of Molecular Biology*, **2012**, 415, 274-87	6.5	24
29	Consensus among flexible fitting approaches improves the interpretation of cryo-EM data. *Journal of Structural Biology*, **2012**, 177, 561-70	3.4	30
28	Simulations of substrate transport in the multidrug transporter EmrD. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1620-32	4.2	18
27	Twelve transmembrane helices form the functional core of mammalian MATE1 (multidrug and toxin extruder 1) protein. *Journal of Biological Chemistry*, **2012**, 287, 27971-82	5.4	34
26	Structure modeling from small angle X-ray scattering data with elastic network normal mode analysis. *Journal of Structural Biology*, **2011**, 173, 451-60	3.4	16
25	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, 18943-8	11.5	77
24	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, 3453-7	11.5	88
23	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	3.4	44
22	Normal-mode flexible fitting of high-resolution structure of biological molecules toward one-dimensional low-resolution data. *Biophysical Journal*, **2008**, 94, 1589-99	2.9	52

21	Flexible fitting of high-resolution x-ray structures into cryoelectron microscopy maps using biased molecular dynamics simulations. *Biophysical Journal*, **2008**, 95, 5692-705	2.9	83
20	Electrostatic properties of cowpea chlorotic mottle virus and cucumber mosaic virus capsids. *Biopolymers*, **2006**, 82, 106-20	2.2	50
19	Removal of divalent cations induces structural transitions in red clover necrotic mosaic virus, revealing a potential mechanism for RNA release. *Journal of Virology*, **2006**, 80, 10395-406	6.6	82
18	Symmetry, form, and shape: guiding principles for robustness in macromolecular machines. *Annual Review of Biophysics and Biomolecular Structure*, **2006**, 35, 115-33		228
17	Model of the toxic complex of anthrax: responsive conformational changes in both the lethal factor and the protective antigen heptamer. *Protein Science*, **2006**, 15, 2190-200	6.3	21
16	Structure of the E. coli protein-conducting channel bound to a translating ribosome. *Nature*, **2005**, 438, 318-24	50.4	226
15	Diversity and identity of mechanical properties of icosahedral viral capsids studied with elastic network normal mode analysis. *Journal of Molecular Biology*, **2005**, 345, 299-314	6.5	157
14	The requirement for mechanical coupling between head and S2 domains in smooth muscle myosin ATPase regulation and its implications for dimeric motor function. *Journal of Molecular Biology*, **2005**, 345, 837-54	6.5	45
13	The 13 angstroms structure of a chaperonin GroEL-protein substrate complex by cryo-electron microscopy. *Journal of Molecular Biology*, **2005**, 348, 219-30	6.5	60
12	Topology representing neural networks reconcile biomolecular shape, structure, and dynamics. *Neurocomputing*, **2004**, 56, 365-379	5.4	19
11	Ribosome motions modulate electrostatic properties. *Biopolymers*, **2004**, 74, 423-31	2.2	40
10	Normal mode based flexible fitting of high-resolution structure into low-resolution experimental data from cryo-EM. *Journal of Structural Biology*, **2004**, 147, 315-26	3.4	202
9	Flexible multi-scale fitting of atomic structures into low-resolution electron density maps with elastic network normal mode analysis. *Journal of Molecular Biology*, **2004**, 337, 985-99	6.5	193
8	Mega-Dalton biomolecular motion captured from electron microscopy reconstructions. *Journal of Molecular Biology*, **2003**, 326, 485-92	6.5	98
7	Dynamic reorganization of the functionally active ribosome explored by normal mode analysis and cryo-electron microscopy. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 9319-23	11.5	299
6	Normal mode analysis with simplified models to investigate the global dynamics of biological systems. *Protein and Peptide Letters*, **2003**, 10, 119-32	1.9	44
5	The mechanism and pathway of pH induced swelling in cowpea chlorotic mottle virus. *Journal of Molecular Biology*, **2002**, 318, 733-47	6.5	173
4	Exploring global distortions of biological macromolecules and assemblies from low-resolution structural information and elastic network theory. *Journal of Molecular Biology*, **2002**, 321, 297-305	6.5	175

3	Conformational change of proteins arising from normal mode calculations. *Protein Engineering, Design and Selection*, **2001**, 14, 1-6	1.9	716
2	Building-block approach for determining low-frequency normal modes of macromolecules. *Proteins: Structure, Function and Bioinformatics*, **2000**, 41, 1-7	4.2	379
1	Molecular dynamics simulation shows large volume fluctuations of proteins. *European Biophysics Journal*, **2000**, 29, 472-80	1.9	15