

# Ivet Bahar

## List of Publications by Year in descending order

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196  
papers

18,285  
citations

23500

58  
h-index

15218

126  
g-index

217  
all docs

217  
docs citations

217  
times ranked

17609  
citing authors

#	ARTICLE	IF	CITATIONS
1	Inactivation of RIP3 kinase sensitizes to 15LOX/PEBP1-mediated ferroptotic death. <i>Redox Biology</i> , 2022, 50, 102232.	3.9	15
2	Mapping transcriptomic vector fields of single cells. <i>Cell</i> , 2022, 185, 690-711.e45.	13.5	167
3	Sampling of Protein Conformational Space Using Hybrid Simulations: A Critical Assessment of Recent Methods. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 832847.	1.6	14
4	Editorial: Targeting Membrane Proteins: Structure-Function-Dynamics Relationships. <i>Frontiers in Chemistry</i> , 2022, 10, 862802.	1.8	0
5	Impact of new variants on SARS-CoV-2 infectivity and neutralization: A molecular assessment of the alterations in the spike-host protein interactions. <i>IScience</i> , 2022, 25, 103939.	1.9	32
6	Protein dynamics developments for the large scale and cryoEM: case study of <i>ProDy</i> 2.0. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 399-409.	1.1	7
7	Allosteric Modulator KM822 Attenuates Behavioral Actions of Amphetamine in <i>Caenorhabditis elegans</i> through Interactions with the Dopamine Transporter DAT-1. <i>Molecular Pharmacology</i> , 2022, 101, 123-131.	1.0	4
8	Precise druggability of the PTH type 1 receptor. <i>Nature Chemical Biology</i> , 2022, 18, 272-280.	3.9	11
9	Elastic network modeling of cellular networks unveils sensor and effector genes that control information flow. <i>PLoS Computational Biology</i> , 2022, 18, e1010181.	1.5	0
10	Activation and Speciation Mechanisms in Class A GPCRs. <i>Journal of Molecular Biology</i> , 2022, 434, 167690.	2.0	4
11	A Quantitative Systems Pharmacology Platform Reveals NAFLD Pathophysiological States and Targeting Strategies. <i>Metabolites</i> , 2022, 12, 528.	1.3	3
12	A network of phosphatidylinositol (4,5)-bisphosphate (PIP2) binding sites on the dopamine transporter regulates amphetamine behavior in <i>Drosophila Melanogaster</i> . <i>Molecular Psychiatry</i> , 2021, 26, 4417-4430.	4.1	26
13	State-dependent sequential allostery exhibited by chaperonin TRiC/CCT revealed by network analysis of Cryo-EM maps. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 160, 104-120.	1.4	12
14	COVID-19-associated multisystem inflammatory syndrome in children (MIS-C): A novel disease that mimics toxic shock syndrome—the superantigen hypothesis. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 57-59.	1.5	87
15	Resolving the paradox of ferroptotic cell death: Ferrostatin-1 binds to 15LOX/PEBP1 complex, suppresses generation of peroxidized ETE-PE, and protects against ferroptosis. <i>Redox Biology</i> , 2021, 38, 101744.	3.9	67
16	Adaptability and specificity: how do proteins balance opposing needs to achieve function?. <i>Current Opinion in Structural Biology</i> , 2021, 67, 25-32.	2.6	11
17	Direct coupling of oligomerization and oligomerization-driven endocytosis of the dopamine transporter to its conformational mechanics and activity. <i>Journal of Biological Chemistry</i> , 2021, 296, 100430.	1.6	9
18	Phospholipase iPLA2 $\beta$ averts ferroptosis by eliminating a redox lipid death signal. <i>Nature Chemical Biology</i> , 2021, 17, 465-476.	3.9	168

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19	Harold A. Scheraga (10/18/1921–8/1/2020): A pioneering scientist who laid the foundations of protein science in the 20th century. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2026796118.	3.3	0
20	Coupled mixed model for joint genetic analysis of complex disorders with two independently collected data sets. BMC Bioinformatics, 2021, 22, 50.	1.2	2
21	HLA class II-associated expansion of TRBV11-2 T cells in multisystem inflammatory syndrome in children. Journal of Clinical Investigation, 2021, 131, .	3.9	130
22	Predicting Protein-Protein Interactions Using Symmetric Logistic Matrix Factorization. Journal of Chemical Information and Modeling, 2021, 61, 1670-1682.	2.5	8
23	<i>ProDy</i> 2.0: increased scale and scope after 10 years of protein dynamics modelling with Python. Bioinformatics, 2021, 37, 3657-3659.	1.8	93
24	NO $\rightarrow$ Represses the Oxygenation of Arachidonoyl PE by 15LOX/PEBP1: Mechanism and Role in Ferroptosis. International Journal of Molecular Sciences, 2021, 22, 5253.	1.8	19
25	Normal mode analysis of membrane protein dynamics using the vibrational subsystem analysis. Journal of Chemical Physics, 2021, 154, 195102.	1.2	5
26	Psychomotor impairments and therapeutic implications revealed by a mutation associated with infantile Parkinsonism-Dystonia. ELife, 2021, 10, .	2.8	13
27	Functional Characterization of the Dopaminergic Psychostimulant Sydnocarb as an Allosteric Modulator of the Human Dopamine Transporter. Biomedicines, 2021, 9, 634.	1.4	9
28	ClustENMD: efficient sampling of biomolecular conformational space at atomic resolution. Bioinformatics, 2021, 37, 3956-3958.	1.8	11
29	A systems-level study reveals host-targeted repurposable drugs against SARS-CoV-2 infection. Molecular Systems Biology, 2021, 17, e10239.	3.2	22
30	A monoclonal antibody against staphylococcal enterotoxin B superantigen inhibits SARS-CoV-2 entry in vitro. Structure, 2021, 29, 951-962.e3.	1.6	28
31	HiDeF: identifying persistent structures in multiscale omics data. Genome Biology, 2021, 22, 21.	3.8	29
32	Recruitment of pro-IL-1 $\beta$ to mitochondrial cardiolipin, via shared LC3 binding domain, inhibits mitophagy and drives maximal NLRP3 activation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
33	Approximating deformation fields for the analysis of continuous heterogeneity of biological macromolecules by 3D Zernike polynomials. IUCr, 2021, 8, 992-1005.	1.0	9
34	Spatial bias in cAMP generation determines biological responses to PTH type 1 receptor activation. Science Signaling, 2021, 14, eabc5944.	1.6	43
35	Bile Acids Gate Dopamine Transporter Mediated Currents. Frontiers in Chemistry, 2021, 9, 753990.	1.8	6
36	Regulation of CFTR Bicarbonate Channel Activity by WNK1: Implications for Pancreatitis and CFTR-Related Disorders. Cellular and Molecular Gastroenterology and Hepatology, 2020, 9, 79-103.	2.3	27

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37	Pharmmaker: Pharmacophore modeling and hit identification based on druggability simulations. <i>Protein Science</i> , 2020, 29, 76-86.	3.1	19
38	Differences in the intrinsic spatial dynamics of the chromatin contribute to cell differentiation. <i>Nucleic Acids Research</i> , 2020, 48, 1131-1145.	6.5	8
39	Intrinsic dynamics is evolutionarily optimized to enable allosteric behavior. <i>Current Opinion in Structural Biology</i> , 2020, 62, 14-21.	2.6	85
40	Superantigenic character of an insert unique to SARS-CoV-2 spike supported by skewed TCR repertoire in patients with hyperinflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25254-25262.	3.3	252
41	Towards gaining sight of multiscale events: utilizing network models and normal modes in hybrid methods. <i>Current Opinion in Structural Biology</i> , 2020, 64, 34-41.	2.6	32
42	Pharmacologic Suppression of B7-H4 Glycosylation Restores Antitumor Immunity in Immune-Cold Breast Cancers. <i>Cancer Discovery</i> , 2020, 10, 1872-1893.	7.7	66
43	Essential site scanning analysis: A new approach for detecting sites that modulate the dispersion of protein global motions. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1577-1586.	1.9	35
44	PEBP1 acts as a rheostat between prosurvival autophagy and ferroptotic death in asthmatic epithelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14376-14385.	3.3	57
45	Allosteric interactions in the parathyroid hormone GPCR-arrestin complex formation. <i>Nature Chemical Biology</i> , 2020, 16, 1096-1104.	3.9	38
46	Rhapsody: predicting the pathogenicity of human missense variants. <i>Bioinformatics</i> , 2020, 36, 3084-3092.	1.8	63
47	Modulation of Toroidal Proteins Dynamics in Favor of Functional Mechanisms upon Ligand Binding. <i>Biophysical Journal</i> , 2020, 118, 1782-1794.	0.2	9
48	Redox lipid reprogramming commands susceptibility of macrophages and microglia to ferroptotic death. <i>Nature Chemical Biology</i> , 2020, 16, 278-290.	3.9	299
49	Mechanisms of Action of Autophagy Modulators Dissected by Quantitative Systems Pharmacology Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2855.	1.8	17
50	QuartataWeb: Integrated Chemical-Protein-Pathway Mapping for Polypharmacology and Chemogenomics. <i>Bioinformatics</i> , 2020, 36, 3935-3937.	1.8	23
51	EIF3H Orchestrates Hippo Pathway-Mediated Oncogenesis via Catalytic Control of YAP Stability. <i>Cancer Research</i> , 2020, 80, 2550-2563.	0.4	24
52	Complementary computational and experimental evaluation of missense variants in the ROMK potassium channel. <i>PLoS Computational Biology</i> , 2020, 16, e1007749.	1.5	6
53	Anti-Ferroptosis Drug Enhances Total-Body Irradiation Mitigation by Drugs that Block Apoptosis and Necroptosis. <i>Radiation Research</i> , 2020, 193, 435.	0.7	36
54	Dynamic Regulation of Bicarbonate Permeability through CFTR Channel by WNK1. <i>Biophysical Journal</i> , 2020, 118, 416a.	0.2	0

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55	New insight into the significance of KLF4 PARylation in genome stability, carcinogenesis, and therapy. <i>EMBO Molecular Medicine</i> , 2020, 12, e12391.	3.3	14
56	Radioresistance of Serpinb3a <sup>+/+</sup> Mice and Derived Hematopoietic and Marrow Stromal Cell Lines. <i>Radiation Research</i> , 2019, 192, 267.	0.7	3
57	Monoamine transporters: structure, intrinsic dynamics and allosteric regulation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 545-556.	3.6	68
58	A novel strategy to block mitotic progression for targeted therapy. <i>EBioMedicine</i> , 2019, 49, 40-54.	2.7	33
59	Druggability Simulations and X-Ray Crystallography Reveal a Ligand-Binding Site in the GluA3 AMPA Receptor N-Terminal Domain. <i>Structure</i> , 2019, 27, 241-252.e3.	1.6	16
60	Trimerization of dopamine transporter triggered by AIM-100 binding: Molecular mechanism and effect of mutations. <i>Neuropharmacology</i> , 2019, 161, 107676.	2.0	9
61	Dynamics of AMPA Receptors from Simulations and Electron Microscopy. <i>Biophysical Journal</i> , 2019, 116, 344a.	0.2	0
62	Harnessing Human Microphysiology Systems as Key Experimental Models for Quantitative Systems Pharmacology. <i>Handbook of Experimental Pharmacology</i> , 2019, 260, 327-367.	0.9	14
63	A novel small-molecule antagonizes PRMT5-mediated KLF4 methylation for targeted therapy. <i>EBioMedicine</i> , 2019, 44, 98-111.	2.7	27
64	Shared Signature Dynamics Tempered by Local Fluctuations Enables Fold Adaptability and Specificity. <i>Molecular Biology and Evolution</i> , 2019, 36, 2053-2068.	3.5	45
65	Quantitative Systems Pharmacological Analysis of Drugs of Abuse Reveals the Pleiotropy of Their Targets and the Effector Role of mTORC1. <i>Frontiers in Pharmacology</i> , 2019, 10, 191.	1.6	10
66	An analog of glibenclamide selectively enhances autophagic degradation of misfolded $\alpha$ 1-antitrypsin Z. <i>PLoS ONE</i> , 2019, 14, e0209748.	1.1	19
67	A Ligand-Binding Site in the GluA3 AMPA Receptor N-Terminal Domain Observed in Druggability Simulations and X-Ray Crystallography. <i>Biophysical Journal</i> , 2019, 116, 489a.	0.2	0
68	Allostery in Its Many Disguises: From Theory to Applications. <i>Structure</i> , 2019, 27, 566-578.	1.6	285
69	Characterization of Differential Dynamics, Specificity, and Allostery of Lipoxygenase Family Members. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 2496-2508.	2.5	34
70	Activation and desensitization of ionotropic glutamate receptors by selectively triggering pre-existing motions. <i>Neuroscience Letters</i> , 2019, 700, 22-29.	1.0	11
71	Structural dynamics is a determinant of the functional significance of missense variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4164-4169.	3.3	76
72	“œOnly a Life Lived for Others Is Worth Living” Redox Signaling by Oxygenated Phospholipids in Cell Fate Decisions. <i>Antioxidants and Redox Signaling</i> , 2018, 29, 1333-1358.	2.5	33

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73	Quantitative Assessment of the Energetics of Dopamine Translocation by Human Dopamine Transporter. <i>Journal of Physical Chemistry B</i> , 2018, 122, 5336-5346.	1.2	25
74	PINK1 Interacts with VCP/p97 and Activates PKA to Promote NSFL1C/p47 Phosphorylation and Dendritic Arborization in Neurons. <i>ENeuro</i> , 2018, 5, ENEURO.0466-18.2018.	0.9	34
75	Structural Dynamics is a Determinant of the Functional Significance of Missense Variants. <i>Biophysical Journal</i> , 2018, 114, 232a.	0.2	0
76	Dynamic Modulation of Binding as a Mechanism for Regulating Interferon Signaling. <i>Biophysical Journal</i> , 2018, 114, 232a.	0.2	0
77	Empowerment of 15-Lipoxygenase Catalytic Competence in Selective Oxidation of Membrane ETE-PE to Ferroptotic Death Signals, HpETE-PE. <i>Journal of the American Chemical Society</i> , 2018, 140, 17835-17839.	6.6	63
78	Key residues controlling bidirectional ion movements in Na <sup>+</sup> /Ca <sup>2+</sup> exchanger. <i>Cell Calcium</i> , 2018, 76, 10-22.	1.1	20
79	<i>Pseudomonas aeruginosa</i> utilizes host polyunsaturated phosphatidylethanolamines to trigger theft-ferroptosis in bronchial epithelium. <i>Journal of Clinical Investigation</i> , 2018, 128, 4639-4653.	3.9	159
80	Shared dynamics of LeuT superfamily members and allosteric differentiation by structural irregularities and multimerization. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170177.	1.8	24
81	Molecular Basis for the Functionality of $\hat{\nu}^3$ -Secretase Inferred From Structure-Based Modeling and Druggability Simulations. <i>Biophysical Journal</i> , 2018, 114, 232a.	0.2	1
82	Heterogeneities in Axonal Structure and Transporter Distribution Lower Dopamine Reuptake Efficiency. <i>ENeuro</i> , 2018, 5, ENEURO.0298-17.2017.	0.9	10
83	Effect of Dimerization on the Dynamics of Neurotransmitter:Sodium Symporters. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3657-3666.	1.2	20
84	Chromosomal dynamics predicted by an elastic network model explains genome-wide accessibility and long-range couplings. <i>Nucleic Acids Research</i> , 2017, 45, 3663-3673.	6.5	24
85	Allosteric modulation of human dopamine transporter activity under conditions promoting its dimerization. <i>Journal of Biological Chemistry</i> , 2017, 292, 12471-12482.	1.6	23
86	Importance of Dimerization in Facilitating the Functional Dynamics of Neurotransmitter: Sodium Symporters. <i>Biophysical Journal</i> , 2017, 112, 506a.	0.2	0
87	MechStiff : A New Tool for Evaluating Stress-Induced Dynamics and Application to Cell Adhesion Proteins. <i>Biophysical Journal</i> , 2017, 112, 45a-46a.	0.2	1
88	Effect of Spatial Complexity on Dopaminergic Signaling Revealed from Multiscale Simulations. <i>Biophysical Journal</i> , 2017, 112, 135a.	0.2	0
89	Regulation of XIAP Turnover Reveals a Role for USP11 in Promotion of Tumorigenesis. <i>EBioMedicine</i> , 2017, 15, 48-61.	2.7	61
90	PEBP1 Wardens Ferroptosis by Enabling Lipoxygenase Generation of Lipid Death Signals. <i>Cell</i> , 2017, 171, 628-641.e26.	13.5	589

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91	Nanomechanics of multidomain neuronal cell adhesion protein contactin revealed by single molecule AFM and SMD. <i>Scientific Reports</i> , 2017, 7, 8852.	1.6	17
92	Targeting of dopamine transporter to filopodia requires an outward-facing conformation of the transporter. <i>Scientific Reports</i> , 2017, 7, 5399.	1.6	16
93	Quantitative assessment of cell fate decision between autophagy and apoptosis. <i>Scientific Reports</i> , 2017, 7, 17605.	1.6	42
94	Dynamic Modulation of Binding Affinity as a Mechanism for Regulating Interferon Signaling. <i>Journal of Molecular Biology</i> , 2017, 429, 2571-2589.	2.0	14
95	Oxidized arachidonic and adrenic PEs navigate cells to ferroptosis. <i>Nature Chemical Biology</i> , 2017, 13, 81-90.	3.9	1,589
96	Improved Total-Body Irradiation Survival by Delivery of Two Radiation Mitigators that Target Distinct Cell Death Pathways. <i>Radiation Research</i> , 2017, 189, 68.	0.7	27
97	Allosteric Modulation of Intact $\hat{I}^3$ -Secretase Structural Dynamics. <i>Biophysical Journal</i> , 2017, 113, 2634-2649.	0.2	55
98	Connecting Neuronal Cell Protective Pathways and Drug Combinations in a Huntington's Disease Model through the Application of Quantitative Systems Pharmacology. <i>Scientific Reports</i> , 2017, 7, 17803.	1.6	22
99	DynOmics: dynamics of structural proteome and beyond. <i>Nucleic Acids Research</i> , 2017, 45, W374-W380.	6.5	135
100	Substrate transport and anion permeation proceed through distinct pathways in glutamate transporters. <i>ELife</i> , 2017, 6, .	2.8	26
101	Multi-Scale Spatial Simulations Reveal the Effect of Dopamine Transporter Localization on Dopamine Neurotransmission. <i>Biophysical Journal</i> , 2016, 110, 632a.	0.2	2
102	Pore dilatation increases the bicarbonate permeability of CFTR, ANO1 and glycine receptor anion channels. <i>Journal of Physiology</i> , 2016, 594, 2929-2955.	1.3	30
103	ClustENM: ENM-Based Sampling of Essential Conformational Space at Full Atomic Resolution. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 4549-4562.	2.3	43
104	Innate immune memory and homeostasis may be conferred through crosstalk between the TLR3 and TLR7 pathways. <i>Science Signaling</i> , 2016, 9, ra70.	1.6	46
105	Global Dynamics of Intact AMPA and NMDA Receptors using Elastic Network Models. <i>Biophysical Journal</i> , 2016, 110, 382a.	0.2	0
106	A Perspective on Implementing a Quantitative Systems Pharmacology Platform for Drug Discovery and the Advancement of Personalized Medicine. <i>Journal of Biomolecular Screening</i> , 2016, 21, 521-534.	2.6	46
107	<i>i</i> GNM 2.0: the Gaussian network model database for biomolecular structural dynamics. <i>Nucleic Acids Research</i> , 2016, 44, D415-D422.	6.5	71
108	Visualization of Molecular Events from Dopamine-Binding to -Release by Human Dopamine Transporter. <i>Biophysical Journal</i> , 2015, 108, 462a.	0.2	0

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109	Unified Model of Synaptic Transmission. <i>Biophysical Journal</i> , 2015, 108, 155a.	0.2	0
110	Energy landscape of LeuT from molecular simulations. <i>Journal of Chemical Physics</i> , 2015, 143, 243134.	1.2	34
111	Insights into the Modulation of Dopamine Transporter Function by Amphetamine, Orphenadrine, and Cocaine Binding. <i>Frontiers in Neurology</i> , 2015, 6, 134.	1.1	64
112	Microseconds Simulations Reveal a New Sodium-binding Site and the Mechanism of Sodium-coupled Substrate Uptake by LeuT. <i>Journal of Biological Chemistry</i> , 2015, 290, 544-555.	1.6	48
113	Comparative study of the effectiveness and limitations of current methods for detecting sequence coevolution. <i>Bioinformatics</i> , 2015, 31, 1929-1937.	1.8	22
114	Structure, Dynamics, and Allosteric Potential of Ionotropic Glutamate Receptor N-Terminal Domains. <i>Biophysical Journal</i> , 2015, 109, 1136-1148.	0.2	27
115	Adaptability of protein structures to enable functional interactions and evolutionary implications. <i>Current Opinion in Structural Biology</i> , 2015, 35, 17-23.	2.6	104
116	Inhibition of Peroxidase Activity of Cytochrome <i>c</i> : De Novo Compound Discovery and Validation. <i>Molecular Pharmacology</i> , 2015, 88, 421-427.	1.0	19
117	The center for causal discovery of biomedical knowledge from big data. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1132-1136.	2.2	30
118	Structure-Encoded Global Motions and Their Role in Mediating Protein-Substrate Interactions. <i>Biophysical Journal</i> , 2015, 109, 1101-1109.	0.2	55
119	BalestraWeb: efficient online evaluation of drug-target interactions. <i>Bioinformatics</i> , 2015, 31, 131-133.	1.8	28
120	Molecular Mechanism of Dopamine Transport by Human Dopamine Transporter. <i>Structure</i> , 2015, 23, 2171-2181.	1.6	81
121	Interplay between arginine methylation and ubiquitylation regulates KLF4-mediated genome stability and carcinogenesis. <i>Nature Communications</i> , 2015, 6, 8419.	5.8	107
122	Cooperative Dynamics of Intact AMPA and NMDA Glutamate Receptors: Similarities and Subfamily-Specific Differences. <i>Structure</i> , 2015, 23, 1692-1704.	1.6	73
123	The anisotropic network model web server at 2015 (ANM 2.0). <i>Bioinformatics</i> , 2015, 31, 1487-1489.	1.8	158
124	Biomolecular Systems Interactions, Dynamics, and Allostery: Reflections and New Directions. <i>Biophysical Journal</i> , 2015, 109, E01-E02.	0.2	0
125	ATPase Subdomain IA Is a Mediator of Interdomain Allostery in Hsp70 Molecular Chaperones. <i>PLoS Computational Biology</i> , 2014, 10, e1003624.	1.5	98
126	Exploring the Conformational Transitions of Biomolecular Systems Using a Simple Two-State Anisotropic Network Model. <i>PLoS Computational Biology</i> , 2014, 10, e1003521.	1.5	112



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127	Complete Mapping of Substrate Translocation Highlights the Role of LeuT N-terminal Segment in Regulating Transport Cycle. <i>PLoS Computational Biology</i> , 2014, 10, e1003879.	1.5	71
128	Mechanisms of CFTR Functional Variants That Impair Regulated Bicarbonate Permeation and Increase Risk for Pancreatitis but Not for Cystic Fibrosis. <i>PLoS Genetics</i> , 2014, 10, e1004376.	1.5	146
129	Designing inhibitors of cytochrome <i>c</i> /cardiolipin peroxidase complexes: mitochondria-targeted imidazole-substituted fatty acids. <i>Free Radical Biology and Medicine</i> , 2014, 71, 221-230.	1.3	40
130	A genome-wide RNAi screen identifies potential drug targets in a <i>C. elegans</i> model of $\alpha_1$ -antitrypsin deficiency. <i>Human Molecular Genetics</i> , 2014, 23, 5123-5132.	1.4	41
131	Coupling between Neurotransmitter Translocation and Protonation State of a Titratable Residue during Na <sup>+</sup> -Coupled Transport. <i>Biophysical Journal</i> , 2014, 106, 2547-2548.	0.2	2
132	<i>EvoL</i> and <i>ProDy</i> for bridging protein sequence evolution and structural dynamics. <i>Bioinformatics</i> , 2014, 30, 2681-2683.	1.8	207
133	Significance of p53 dynamics in regulating apoptosis in response to ionizing radiation and polypharmacological strategies. <i>Scientific Reports</i> , 2014, 4, 6245.	1.6	41
134	Global Transitions of Proteins Explored by a Multiscale Hybrid Methodology: Application to Adenylate Kinase. <i>Biophysical Journal</i> , 2013, 105, 1643-1652.	0.2	63
135	Predicting Drug-Target Interactions Using Probabilistic Matrix Factorization. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 3399-3409.	2.5	152
136	Cardiolipin externalization to the outer mitochondrial membrane acts as an elimination signal for mitophagy in neuronal cells. <i>Nature Cell Biology</i> , 2013, 15, 1197-1205.	4.6	792
137	Coupled Global and Local Changes Direct Substrate Translocation by $\alpha$ -Neurotransmitter-Sodium Symporter Ortholog LeuT. <i>Biophysical Journal</i> , 2013, 105, 630-639.	0.2	65
138	Intracellular Gating in an Inward-facing State of Aspartate Transporter GltPh Is Regulated by the Movements of the Helical Hairpin HP2. <i>Journal of Biological Chemistry</i> , 2013, 288, 8231-8237.	1.6	39
139	Sequence Evolution Correlates with Structural Dynamics. <i>Molecular Biology and Evolution</i> , 2012, 29, 2253-2263.	3.5	132
140	A Conformational Switch in a Partially Unwound Helix Selectively Determines the Pathway for Substrate Release from the Carnitine/ <sup>3</sup> -Butyrobetaine Antiporter CaiT. <i>Journal of Biological Chemistry</i> , 2012, 287, 31823-31832.	1.6	17
141	Comparative Dynamics of NMDA- and AMPA-Glutamate Receptor N-Terminal Domains. <i>Structure</i> , 2012, 20, 1838-1849.	1.6	34
142	FlexE: Using Elastic Network Models to Compare Models of Protein Structure. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 3985-3991.	2.3	20
143	Druggability Assessment of Allosteric Proteins by Dynamics Simulations in the Presence of Probe Molecules. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 2435-2447.	2.3	138
144	Constraints Imposed by the Membrane Selectively Guide the Alternating Access Dynamics of the Glutamate Transporter GltPh. <i>Biophysical Journal</i> , 2012, 102, 1331-1340.	0.2	47

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145	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	3.1	188
146	The mechanism of substrate release by the aspartate transporter Glt<sub>Ph</sub>: insights from simulations. <i>Molecular BioSystems</i> , 2011, 7, 832-842.	2.9	44
147	Sodium-coupled Secondary Transporters: Insights from Structure-based Computations. , 2011, , 199-229.		2
148	<i>ProDy</i>: Protein Dynamics Inferred from Theory and Experiments. <i>Bioinformatics</i> , 2011, 27, 1575-1577.	1.8	907
149	Development of Small-Molecule PUMA Inhibitors for Mitigating Radiation-Induced Cell Death. <i>Current Topics in Medicinal Chemistry</i> , 2011, 11, 281-290.	1.0	57
150	Dynamics and allosteric potential of the AMPA receptor N-terminal domain. <i>EMBO Journal</i> , 2011, 30, 972-982.	3.5	53
151	Cooperative dynamics of proteins unraveled by network models. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2011, 1, 426-439.	6.2	24
152	Pre-existing soft modes of motion uniquely defined by native contact topology facilitate ligand binding to proteins. <i>Protein Science</i> , 2011, 20, 1645-1658.	3.1	84
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