Sefika Banu Ozkan

List of Publications by Year
in descending order

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49 papers	2,929 citations	257450 24 h-index	214800 47 g-index
55 all docs	55 docs citations	55 times ranked	2983 citing authors

#	Article	IF	Citations
1	Dynamic allostery highlights the evolutionary differences between the CoV-1 and CoV-2 main proteases. Biophysical Journal, 2022, 121, 1483-1492.	0.5	7
2	Dynamic coupling of residues within proteins as a mechanistic foundation of many enigmatic pathogenic missense variants. PLoS Computational Biology, 2022, 18, e1010006.	3.2	16
3	Substitutions at Nonconserved Rheostat Positions Modulate Function by Rewiring Long-Range, Dynamic Interactions. Molecular Biology and Evolution, 2021, 38, 201-214.	8.9	30
4	Protein folding stability and binding interactions through the lens of evolution: a dynamical perspective. Current Opinion in Structural Biology, 2021, 66, 207-215.	5.7	27
5	Local Interactions That Contribute Minimal Frustration Determine Foldability. Journal of Physical Chemistry B, 2021, 125, 2617-2626.	2.6	3
6	Hinge-shift mechanism as a protein design principle for the evolution of Î²-lactamases from substrate promiscuity to specificity. Nature Communications, 2021, 12, 1852.	12.8	43
7	The Role of Rigid Residues in Modulating TEM-1 Î²-Lactamase Function and Thermostability. International Journal of Molecular Sciences, 2021, 22, 2895.	4.1	7
8	Can sequence-specific and dynamics-based metrics allow us to decipher the function in IDP sequences?. Biophysical Journal, 2021, 120, 1857-1859.	0.5	1
9	Dynamic Allosteric Residue Coupling Reveals Disease Mechanism for Gaucher Disease and NSNVS Across the Proteome. Biophysical Journal, 2020, 118, 53a.	0.5	2
10	Asymmetry in Dynamic Allosteric Residue Coupling (DARC) Interactions Captures Evolutionary Landscape. Biophysical Journal, 2020, 118, 52a.	0.5	3
11	Allostery and Epistasis: Emergent Properties of Anisotropic Networks. Entropy, 2020, 22, 667.	2.2	15
12	The Role of Conformational Dynamics and Allostery in Modulating Protein Evolution. Annual Review of Biophysics, 2020, 49, 267-288.	10.0	101
13	Information propagation in time through allosteric signaling. Physical Review Research, 2020, 2, .	3.6	0
14	Biotechnological and protein-engineering implications of ancestral protein resurrection. Current Opinion in Structural Biology, 2018, 51, 106-115.	5.7	60
15	Hinge-Shift Mechanism Modulates Allosteric Regulations in Human Pin1. Journal of Physical Chemistry B, 2018, 122, 5623-5629.	2.6	30
16	Coevolving residues inform protein dynamics profiles and disease susceptibility of nSNVs. PLoS Computational Biology, 2018, 14, e1006626.	3.2	12
17	Mutations Utilize Dynamic Allostery to Confer Resistance in TEM-1 Î²-lactamase. International Journal of Molecular Sciences, 2018, 19, 3808.	4.1	33
18	Ancient thioredoxins evolved to modern-day stabilityâ€“function requirement by altering native state ensemble. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170184.	4.0	45

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19	Design of Novel Lectins by Computerâ€Guided Directed Evolution. FASEB Journal, 2018, 32, 673.24.	0.5	0
20	Plant-expressed cocaine hydrolase variants of butyrylcholinesterase exhibit altered allosteric effects of cholinesterase activity and increased inhibitor sensitivity. Scientific Reports, 2017, 7, 10419.	3.3	29
21	Adaptive BP-Dock: An Induced Fit Docking Approach for Full Receptor Flexibility. Journal of Chemical Information and Modeling, 2016, 56, 734-746.	5.4	25
22	Partial unfolding and refolding for structure refinement: A unified approach of geometric simulations and molecular dynamics. Proteins: Structure, Function and Bioinformatics, 2015, 83, 2279-2292.	2.6	4
23	Integration of structural dynamics and molecular evolution via protein interaction networks: a new era in genomic medicine. Current Opinion in Structural Biology, 2015, 35, 135-142.	5.7	29
24	A Rigid Hinge Region Is Necessary for High-Affinity Binding of Dimannose to Cyanovirin and Associated Constructs. Biochemistry, 2015, 54, 6951-6960.	2.5	15
25	Conformational dynamics of nonsynonymous variants at protein interfaces reveals disease association. Proteins: Structure, Function and Bioinformatics, 2015, 83, 428-435.	2.6	30
26	A Hinge Migration Mechanism Unlocks the Evolution of Green-to-Red Photoconversion in GFP-like Proteins. Structure, 2015, 23, 34-43.	3.3	58
27	The Role of Conformational Dynamics and Allostery in the Disease Development of Human Ferritin. Biophysical Journal, 2015, 109, 1273-1281.	0.5	57
28	Evolution of Conformational Dynamics Determines the Conversion of a Promiscuous Generalist into a Specialist Enzyme. Molecular Biology and Evolution, 2015, 32, 132-143.	8.9	125
29	Proteome Folding Kinetics Is Limited by Protein Halflife. PLoS ONE, 2014, 9, e112701.	2.5	18
30	A Flexible Docking Scheme Efficiently Captures the Energetics of Glycan-Cyanovirin Binding. Biophysical Journal, 2014, 106, 1142-1151.	0.5	12
31	BP-Dock: A Flexible Docking Scheme for Exploring Proteinâ€“Ligand Interactions Based on Unbound Structures. Journal of Chemical Information and Modeling, 2014, 54, 913-925.	5.4	35
32	Structural dynamics flexibility informs function and evolution at a proteome scale. Evolutionary Applications, 2013, 6, 423-433.	3.1	88
33	Electrostatic Effect of the Ribosomal Surface on Nascent Polypeptide Dynamics. ACS Chemical Biology, 2013, 8, 1195-1204.	3.4	74
34	The antiviral lectin cyanovirin-N: probing multivalency and glycan recognition through experimental and computational approaches. Biochemical Society Transactions, 2013, 41, 1170-1176.	3.4	12
35	Dissipative electro-elastic network model of protein electrostatics. Physical Biology, 2012, 9, 036004.	1.8	9
36	Collective Dynamics Differentiates Functional Divergence in Protein Evolution. PLoS Computational Biology, 2012, 8, e1002428.	3.2	28

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37	The binding affinities of proteins interacting with the PDZ domain of PICK1. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1393-1408.	2.6	21
38	Local and non-local native topologies reveal the underlying folding landscape of proteins. Physical Biology, 2011, 8, 066011.	1.8	21
39	Change in Allosteric Network Affects Binding Affinities of PDZ Domains: Analysis through Perturbation Response Scanning. PLoS Computational Biology, 2011, 7, e1002154.	3.2	156
40	A flexible docking scheme to explore the binding selectivity of PDZ domains. Protein Science, 2010, 19, 914-928.	7.6	49
41	Union of Geometric Constraint-Based Simulations with Molecular Dynamics for Protein Structure Prediction. Biophysical Journal, 2010, 98, 1046-1054.	0.5	7
42	Identification of specificity and promiscuity of PDZ domain interactions through their dynamic behavior. Proteins: Structure, Function and Bioinformatics, 2009, 77, 796-811.	2.6	60
43	Blind Test of Physics-Based Prediction of Protein Structures. Biophysical Journal, 2009, 96, 917-924.	0.5	46
44	Structure and dynamic regulation of Src-family kinases. Cellular and Molecular Life Sciences, 2008, 65, 3058-3073.	5.4	162
45	The Protein Folding Problem. Annual Review of Biophysics, 2008, 37, 289-316.	10.0	916
46	Protein folding by zipping and assembly. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11987-11992.	7.1	141
47	The Ultimate Speed Limit to Protein Folding Is Conformational Searching. Journal of the American Chemical Society, 2007, 129, 11920-11927.	13.7	69
48	Fast-folding protein kinetics, hidden intermediates, and the sequential stabilization model. Protein Science, 2002, 11, 1958-1970.	7.6	67
49	Transition states and the meaning of Phi-values in protein folding kinetics. Nature Structural Biology, 2001, 8, 765-769.	9.7	125