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	The Protein Folding Problem. Annual Review of Biophysics, 2008, 37, 289-316.	10.0	916
2	Structure and dynamic regulation of Src-family kinases. Cellular and Molecular Life Sciences, 2008, 65, 3058-3073.	5.4	162
3	Change in Allosteric Network Affects Binding Affinities of PDZ Domains: Analysis through Perturbation Response Scanning. PLoS Computational Biology, 2011, 7, e1002154.	3.2	156
4	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
5	Transition states and the meaning of Phi-values in protein folding kinetics. Nature Structural Biology, 2001, 8, 765-769.	9.7	125
6	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
7	The Role of Conformational Dynamics and Allostery in Modulating Protein Evolution. Annual Review of Biophysics, 2020, 49, 267-288.	10.0	101
8	Structural dynamics flexibility informs function and evolution at a proteome scale. Evolutionary Applications, 2013, 6, 423-433.	3.1	88
9	Electrostatic Effect of the Ribosomal Surface on Nascent Polypeptide Dynamics. ACS Chemical Biology, 2013, 8, 1195-1204.	3.4	74
10	The Ultimate Speed Limit to Protein Folding Is Conformational Searching. Journal of the American Chemical Society, 2007, 129, 11920-11927.	13.7	69
11	Fast-folding protein kinetics, hidden intermediates, and the sequential stabilization model. Protein Science, 2002, 11, 1958-1970.	7.6	67
12	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
13	Biotechnological and protein-engineering implications of ancestral protein resurrection. Current Opinion in Structural Biology, 2018, 51, 106-115.	5.7	60
14	A Hinge Migration Mechanism Unlocks the Evolution of Green-to-Red Photoconversion in GFP-like Proteins. Structure, 2015, 23, 34-43.	3.3	58
15	The Role of Conformational Dynamics and Allostery in the Disease Development of Human Ferritin. Biophysical Journal, 2015, 109, 1273-1281.	0.5	57
16	A flexible docking scheme to explore the binding selectivity of PDZ domains. Protein Science, 2010, 19, 914-928.	7.6	49
17	Blind Test of Physics-Based Prediction of Protein Structures. Biophysical Journal, 2009, 96, 917-924.	0.5	46
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	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
20	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
21	Mutations Utilize Dynamic Allostery to Confer Resistance in TEM-1 Î²-lactamase. International Journal of Molecular Sciences, 2018, 19, 3808.	4.1	33
22	Conformational dynamics of nonsynonymous variants at protein interfaces reveals disease association. Proteins: Structure, Function and Bioinformatics, 2015, 83, 428-435.	2.6	30
23	Hinge-Shift Mechanism Modulates Allosteric Regulations in Human Pin1. Journal of Physical Chemistry B, 2018, 122, 5623-5629.	2.6	30
24	Substitutions at Nonconserved Rheostat Positions Modulate Function by Rewiring Long-Range, Dynamic Interactions. Molecular Biology and Evolution, 2021, 38, 201-214.	8.9	30
25	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
26	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
27	Collective Dynamics Differentiates Functional Divergence in Protein Evolution. PLoS Computational Biology, 2012, 8, e1002428.	3.2	28
28	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
29	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
30	Local and non-local native topologies reveal the underlying folding landscape of proteins. Physical Biology, 2011, 8, 066011.	1.8	21
31	The binding affinities of proteins interacting with the PDZ domain of PICK1. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1393-1408.	2.6	21
32	Proteome Folding Kinetics Is Limited by Protein Halflife. PLoS ONE, 2014, 9, e112701.	2.5	18
33	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
34	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
35	Allostery and Epistasis: Emergent Properties of Anisotropic Networks. Entropy, 2020, 22, 667.	2.2	15
36	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

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37	A Flexible Docking Scheme Efficiently Captures the Energetics of Glycan-Cyanovirin Binding. Biophysical Journal, 2014, 106, 1142-1151.	0.5	12
38	Coevolving residues inform protein dynamics profiles and disease susceptibility of nSNVs. PLoS Computational Biology, 2018, 14, e1006626.	3.2	12
39	Dissipative electro-elastic network model of protein electrostatics. Physical Biology, 2012, 9, 036004.	1.8	9
40	Union of Geometric Constraint-Based Simulations with Molecular Dynamics for Protein Structure Prediction. Biophysical Journal, 2010, 98, 1046-1054.	0.5	7
41	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
42	Dynamic allostery highlights the evolutionary differences between the CoV-1 and CoV-2 main proteases. Biophysical Journal, 2022, 121, 1483-1492.	0.5	7
43	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
44	Asymmetry in Dynamic Allosteric Residue Coupling (DARC) Interactions Captures Evolutionary Landscape. Biophysical Journal, 2020, 118, 52a.	0.5	3
45	Local Interactions That Contribute Minimal Frustration Determine Foldability. Journal of Physical Chemistry B, 2021, 125, 2617-2626.	2.6	3
46	Dynamic Allosteric Residue Coupling Reveals Disease Mechanism for Gaucher Disease and NSNVS Across the Proteome. Biophysical Journal, 2020, 118, 53a.	0.5	2
47	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
48	Design of Novel Lectins by Computerâ€Guided Directed Evolution. FASEB Journal, 2018, 32, 673.24.	0.5	0
49	Information propagation in time through allosteric signaling. Physical Review Research, 2020, 2, .	3.6	0