David De Sancho

List of Publications by Year
in descending order

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51 papers	1,393 citations	331538 21 h-index	360920 35 g-index
60 all docs	60 docs citations	60 times ranked	1880 citing authors

#	Article	IF	Citations
1	Interplay between partner and ligand facilitates the folding and binding of an intrinsically disordered protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15420-15425.	3.3	144
2	Mechanism of O2 diffusion and reduction in FeFe hydrogenases. Nature Chemistry, 2017, 9, 88-95.	6.6	105
3	Molecular origins of internal friction effects on protein-folding rates. Nature Communications, 2014, 5, 4307.	5.8	98
4	Residue-Specific Î±-Helix Propensities from Molecular Simulation. Biophysical Journal, 2012, 102, 1462-1467.	0.2	97
5	Modulation of an IDP binding mechanism and rates by helix propensity and non-native interactions: association of HIF1Î± with CBP. Molecular BioSystems, 2012, 8, 256-267.	2.9	83
6	What Is the Time Scale for Î±-Helix Nucleation?. Journal of the American Chemical Society, 2011, 133, 6809-6816.	6.6	68
7	Protein Folding Rates and Stability: How Much Is There Beyond Size?. Journal of the American Chemical Society, 2009, 131, 2074-2075.	6.6	67
8	Integrated prediction of protein folding and unfolding rates from only size and structural class. Physical Chemistry Chemical Physics, 2011, 13, 17030.	1.3	58
9	Mechanical architecture and folding of E. coli type 1 pilus domains. Nature Communications, 2018, 9, 2758.	5.8	55
10	An Abl-FBP17 mechanosensing system couples local plasma membrane curvature and stress fiber remodeling during mechanoadaptation. Nature Communications, 2019, 10, 5828.	5.8	50
11	Dependence of Internal Friction on Folding Mechanism. Journal of the American Chemical Society, 2015, 137, 3283-3290.	6.6	41
12	Thermodynamics of GÅ•type models for protein folding. Journal of Chemical Physics, 2005, 123, 154903.	1.2	35
13	Folding Kinetics and Unfolded State Dynamics of the GB1 Hairpin from Molecular Simulation. Journal of Chemical Theory and Computation, 2013, 9, 1743-1753.	2.3	35
14	The influence of disulfide bonds on the mechanical stability of proteins is context dependent. Journal of Biological Chemistry, 2017, 292, 13374-13380.	1.6	34
15	Mechanochemical evolution of the giant muscle protein titin as inferred from resurrected proteins. Nature Structural and Molecular Biology, 2017, 24, 652-657.	3.6	30
16	The Power of Force: Insights into the Protein Folding Process Using Single-Molecule Force Spectroscopy. Journal of Molecular Biology, 2016, 428, 4245-4257.	2.0	27
17	Aerobic Damage to [FeFe]â€Hydrogenases: Activation Barriers for the Chemical Attachment of O₂. Angewandte Chemie - International Edition, 2014, 53, 4081-4084.	7.2	26
18	Markov state models of protein misfolding. Journal of Chemical Physics, 2016, 144, 075101.	1.2	26

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19	The life of proteins under mechanical force. Chemical Society Reviews, 2018, 47, 3558-3573.	18.7	26
20	Exploiting the downhill folding regime via experiment. HFSP Journal, 2008, 2, 342-353.	2.5	25
21	MSM/RD: Coupling Markov state models of molecular kinetics with reaction-diffusion simulations. Journal of Chemical Physics, 2018, 148, 214107.	1.2	25
22	Resurrection of efficient Precambrian endoglucanases for lignocellulosic biomass hydrolysis. Communications Chemistry, 2019, 2, .	2.0	21
23	Reversible two-state folding of the ultrafast protein gpW under mechanical force. Communications Chemistry, 2018, 1, .	2.0	16
24	Nanomechanical Phenotypes in Cardiac Myosin-Binding Protein C Mutants That Cause Hypertrophic Cardiomyopathy. ACS Nano, 2021, 15, 10203-10216.	7.3	16
25	Modulation of Folding Internal Friction by Local and Global Barrier Heights. Journal of Physical Chemistry Letters, 2016, 7, 1028-1034.	2.1	15
26	Instrumental Effects in the Dynamics of an Ultrafast Folding Protein under Mechanical Force. Journal of Physical Chemistry B, 2018, 122, 11147-11154.	1.2	15
27	Competitive binding of HIF-1Î± and CITED2 to the TAZ1 domain of CBP from molecular simulations. Physical Chemistry Chemical Physics, 2020, 22, 8118-8127.	1.3	15
28	Reconciling Intermediates in Mechanical Unfolding Experiments with Two-State Protein Folding in Bulk. Journal of Physical Chemistry Letters, 2016, 7, 3798-3803.	2.1	13
29	Multifrequency Force Microscopy of Helical Protein Assembly on a Virus. Scientific Reports, 2016, 6, 21899.	1.6	13
30	Mechanism of Hydrogen Sulfide-Dependent Inhibition of FeFe Hydrogenase. ACS Catalysis, 2021, 11, 15162-15176.	5.5	13
31	Identification of Mutational Hot Spots for Substrate Diffusion: Application to Myoglobin. Journal of Chemical Theory and Computation, 2015, 11, 1919-1927.	2.3	12
32	Evaluation of coarse grained models for hydrogen bonds in proteins. Journal of Computational Chemistry, 2007, 28, 1187-1199.	1.5	11
33	Engineering Folding Dynamics from Two-State to Downhill: Application to Î»-Repressor. Journal of Physical Chemistry B, 2013, 117, 13435-13443.	1.2	11
34	Interplay between the folding mechanism and binding modes in folding coupled to binding processes. Physical Chemistry Chemical Physics, 2017, 19, 28512-28516.	1.3	10
35	Energy minimizations with a combination of two knowledgeâ€based potentials for protein folding. Journal of Computational Chemistry, 2008, 29, 1684-1692.	1.5	7
36	Bridging Experiments and Native-Centric Simulations of a Downhill Folding Protein. Journal of Physical Chemistry B, 2015, 119, 14925-14933.	1.2	7

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37	Evolutionary method for the assembly of rigid protein fragments. Journal of Computational Chemistry, 2005, 26, 131-141.	1.5	6
38	The Response of Greek Key Proteins to Changes in Connectivity Depends on the Nature of Their Secondary Structure. Journal of Molecular Biology, 2015, 427, 2159-2165.	2.0	5
39	Computation of Rate Constants for Diffusion of Small Ligands to and from Buried Protein Active Sites. Methods in Enzymology, 2016, 578, 299-326.	0.4	5
40	MasterMSM: A Package for Constructing Master Equation Models of Molecular Dynamics. Journal of Chemical Information and Modeling, 2019, 59, 3625-3629.	2.5	5
41	Assessment of protein folding potentials with an evolutionary method. Journal of Chemical Physics, 2006, 125, 014904.	1.2	4
42	Evaluation of a mean field potential for protein folding with different interaction centers. Physica A: Statistical Mechanics and Its Applications, 2006, 371, 449-462.	1.2	3
43	Slow Folding of a Helical Protein: Large Barriers, Strong Internal Friction, or a Shallow, Bumpy Landscape?. Journal of Physical Chemistry B, 2020, 124, 8973-8983.	1.2	3
44	Complex Dynamics in Single Molecule Force Spectroscopy from Simple Simulation Models. Biophysical Journal, 2017, 112, 196a.	0.2	1
45	Theoretical characterization of Al(III) binding to KSPVPKSPVEEKG: Insights into the propensity of aluminum to interact with key sequences for neurofilament formation. Journal of Inorganic Biochemistry, 2020, 210, 111169.	1.5	1
46	Dependence of Internal Friction on Native Topology. Biophysical Journal, 2015, 108, 518a.	0.2	0
47	Mechanochemical Evolution of the Giant Muscle Protein Titin as Inferred from Ancient Proteins. Biophysical Journal, 2016, 110, 14a.	0.2	0
48	Independent Tuning of Viscous and Elastic Properties of Protein Biomaterials. Biophysical Journal, 2020, 118, 163a-164a.	0.2	0
49	Markov state models from hierarchical density-based assignment. Journal of Chemical Physics, 2021, 155, 054102.	1.2	0
50	Prediction of Folding and Unfolding Rates of Proteins with Simple Models. Methods in Molecular Biology, 2022, 2376, 365-372.	0.4	0
51	Influence of the Nonprotein Amino Acid Mimosine in Peptide Conformational Propensities from Novel Amber Force Field Parameters. Journal of Physical Chemistry B, 2022, , .	1.2	0