David De Sancho

List of Publications by Year
in descending order

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	Prediction of Folding and Unfolding Rates of Proteins with Simple Models. Methods in Molecular Biology, 2022, 2376, 365-372.	0.4	0
2	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
3	Nanomechanical Phenotypes in Cardiac Myosin-Binding Protein C Mutants That Cause Hypertrophic Cardiomyopathy. ACS Nano, 2021, 15, 10203-10216.	7.3	16
4	Markov state models from hierarchical density-based assignment. Journal of Chemical Physics, 2021, 155, 054102.	1.2	0
5	Mechanism of Hydrogen Sulfide-Dependent Inhibition of FeFe Hydrogenase. ACS Catalysis, 2021, 11, 15162-15176.	5.5	13
6	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
7	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
8	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
9	Independent Tuning of Viscous and Elastic Properties of Protein Biomaterials. Biophysical Journal, 2020, 118, 163a-164a.	0.2	0
10	MasterMSM: A Package for Constructing Master Equation Models of Molecular Dynamics. Journal of Chemical Information and Modeling, 2019, 59, 3625-3629.	2.5	5
11	Resurrection of efficient Precambrian endoglucanases for lignocellulosic biomass hydrolysis. Communications Chemistry, 2019, 2, .	2.0	21
12	An Abl-FBP17 mechanosensing system couples local plasma membrane curvature and stress fiber remodeling during mechanoadaptation. Nature Communications, 2019, 10, 5828.	5.8	50
13	The life of proteins under mechanical force. Chemical Society Reviews, 2018, 47, 3558-3573.	18.7	26
14	Reversible two-state folding of the ultrafast protein gpW under mechanical force. Communications Chemistry, 2018, 1, .	2.0	16
15	Mechanical architecture and folding of E. coli type 1 pilus domains. Nature Communications, 2018, 9, 2758.	5.8	55
16	MSM/RD: Coupling Markov state models of molecular kinetics with reaction-diffusion simulations. Journal of Chemical Physics, 2018, 148, 214107.	1.2	25
17	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
18	Complex Dynamics in Single Molecule Force Spectroscopy from Simple Simulation Models. Biophysical Journal, 2017, 112, 196a.	0.2	1

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19	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
20	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
21	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
22	Mechanism of O2 diffusion and reduction in FeFe hydrogenases. Nature Chemistry, 2017, 9, 88-95.	6.6	105
23	Markov state models of protein misfolding. Journal of Chemical Physics, 2016, 144, 075101.	1.2	26
24	Mechanochemical Evolution of the Giant Muscle Protein Titin as Inferred from Ancient Proteins. Biophysical Journal, 2016, 110, 14a.	0.2	0
25	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
26	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
27	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
28	Multifrequency Force Microscopy of Helical Protein Assembly on a Virus. Scientific Reports, 2016, 6, 21899.	1.6	13
29	Modulation of Folding Internal Friction by Local and Global Barrier Heights. Journal of Physical Chemistry Letters, 2016, 7, 1028-1034.	2.1	15
30	Dependence of Internal Friction on Native Topology. Biophysical Journal, 2015, 108, 518a.	0.2	0
31	Bridging Experiments and Native-Centric Simulations of a Downhill Folding Protein. Journal of Physical Chemistry B, 2015, 119, 14925-14933.	1.2	7
32	Dependence of Internal Friction on Folding Mechanism. Journal of the American Chemical Society, 2015, 137, 3283-3290.	6.6	41
33	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
34	Identification of Mutational Hot Spots for Substrate Diffusion: Application to Myoglobin. Journal of Chemical Theory and Computation, 2015, 11, 1919-1927.	2.3	12
35	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
36	Molecular origins of internal friction effects on protein-folding rates. Nature Communications, 2014, 5, 4307.	5.8	98

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37	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
38	Engineering Folding Dynamics from Two-State to Downhill: Application to Î»-Repressor. Journal of Physical Chemistry B, 2013, 117, 13435-13443.	1.2	11
39	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
40	Residue-Specific Î±-Helix Propensities from Molecular Simulation. Biophysical Journal, 2012, 102, 1462-1467.	0.2	97
41	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
42	Integrated prediction of protein folding and unfolding rates from only size and structural class. Physical Chemistry Chemical Physics, 2011, 13, 17030.	1.3	58
43	What Is the Time Scale for Î±-Helix Nucleation?. Journal of the American Chemical Society, 2011, 133, 6809-6816.	6.6	68
44	Protein Folding Rates and Stability: How Much Is There Beyond Size?. Journal of the American Chemical Society, 2009, 131, 2074-2075.	6.6	67
45	Energy minimizations with a combination of two knowledgeâ€based potentials for protein folding. Journal of Computational Chemistry, 2008, 29, 1684-1692.	1.5	7
46	Exploiting the downhill folding regime via experiment. HFSP Journal, 2008, 2, 342-353.	2.5	25
47	Evaluation of coarse grained models for hydrogen bonds in proteins. Journal of Computational Chemistry, 2007, 28, 1187-1199.	1.5	11
48	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
49	Assessment of protein folding potentials with an evolutionary method. Journal of Chemical Physics, 2006, 125, 014904.	1.2	4
50	Evolutionary method for the assembly of rigid protein fragments. Journal of Computational Chemistry, 2005, 26, 131-141.	1.5	6
51	Thermodynamics of GÅ•type models for protein folding. Journal of Chemical Physics, 2005, 123, 154903.	1.2	35