Guillaume Stirnemann

List of Publications by Year
in descending order

48 papers	2,818 citations	218677 26 h-index	206112 48 g-index
57 all docs	57 docs citations	57 times ranked	2810 citing authors

#	Article	IF	Citations
1	Recent Advances and Emerging Challenges in the Molecular Modeling of Mechanobiological Processes. Journal of Physical Chemistry B, 2022, 126, 1365-1374.	2.6	14
2	Mass effects for thermodiffusion in dilute aqueous solutions. European Physical Journal E, 2022, 45, 37.	1.6	4
3	A Single-Molecule Strategy to Capture Non-native Intramolecular and Intermolecular Protein Disulfide Bridges. Nano Letters, 2022, , .	9.1	4
4	Molecular interpretation of single-molecule force spectroscopy experiments with computational approaches. Chemical Communications, 2022, 58, 7110-7119.	4.1	5
5	Specific Interactions and Environment Flexibility Tune Protein Stability under Extreme Crowding. Journal of Physical Chemistry B, 2021, 125, 6103-6111.	2.6	7
6	In silico all-atom approach to thermodiffusion in dilute aqueous solutions. Journal of Chemical Physics, 2021, 155, 174503.	3.0	5
7	Structural transitions in the RNA 7SK 5â€² hairpin and their effect on HEXIM binding. Nucleic Acids Research, 2020, 48, 373-389.	14.5	15
8	Differences in thermal structural changes and melting between mesophilic and thermophilic dihydrofolate reductase enzymes. Physical Chemistry Chemical Physics, 2020, 22, 18361-18373.	2.8	18
9	Thermal Adaptation of Enzymes: Impacts of Conformational Shifts on Catalytic Activation Energy and Optimum Temperature. Chemistry - A European Journal, 2020, 26, 10045-10056.	3.3	19
10	Water dynamics at electrified graphene interfaces: a jump model perspective. Physical Chemistry Chemical Physics, 2020, 22, 10581-10591.	2.8	19
11	Effect of Ions on Water Dynamics in Dilute and Concentrated Aqueous Salt Solutions. Journal of Physical Chemistry B, 2019, 123, 3312-3324.	2.6	37
12	The force-dependent mechanism of DnaK-mediated mechanical folding. Science Advances, 2018, 4, eaaq0243.	10.3	37
13	Three Weaknesses for Three Perturbations: Comparing Protein Unfolding Under Shear, Force, and Thermal Stresses. Journal of Physical Chemistry B, 2018, 122, 11922-11930.	2.6	24
14	Conformational entropy of a single peptide controlled under force governs protease recognition and catalysis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11525-11530.	7.1	11
15	Segmentation and the Entropic Elasticity of Modular Proteins. Journal of Physical Chemistry Letters, 2018, 9, 4707-4713.	4.6	19
16	Water dynamics in concentrated electrolytes: Local ion effect on hydrogen-bond jumps rather than collective coupling to ion clusters. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4953-E4954.	7.1	9
17	Forcing the reversibility of a mechanochemical reaction. Nature Communications, 2018, 9, 3155.	12.8	50
18	DNA Binding Induces a Nanomechanical Switch in the RRM1 Domain of TDP-43. Journal of Physical Chemistry Letters, 2018, 9, 3800-3807.	4.6	8

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19	The major Î²-catenin/E-cadherin junctional binding site is a primary molecular mechano-transductor of differentiation in vivo. ELife, 2018, 7, .	6.0	62
20	Tailoring protein nanomechanics with chemical reactivity. Nature Communications, 2017, 8, 15658.	12.8	26
21	Critical structural fluctuations of proteins upon thermal unfolding challenge the Lindemann criterion. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9361-9366.	7.1	35
22	Ab Initio Simulations of Water Dynamics in Aqueous TMAO Solutions: Temperature and Concentration Effects. Journal of Physical Chemistry B, 2017, 121, 11189-11197.	2.6	24
23	Mechanics of Protein Adaptation to High Temperatures. Journal of Physical Chemistry Letters, 2017, 8, 5884-5890.	4.6	28
24	Orientational Dynamics of Water at an Extended Hydrophobic Interface. Journal of the American Chemical Society, 2016, 138, 5551-5560.	13.7	42
25	Stability and Function at High Temperature. What Makes a Thermophilic GTPase Different from Its Mesophilic Homologue. Journal of Physical Chemistry B, 2016, 120, 2721-2730.	2.6	20
26	Recovering Protein Thermal Stability Using All-Atom Hamiltonian Replica-Exchange Simulations in Explicit Solvent. Journal of Chemical Theory and Computation, 2015, 11, 5573-5577.	5.3	40
27	How osmolytes influence hydrophobic polymer conformations: A unified view from experiment and theory. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9270-9275.	7.1	98
28	The elastic free energy of a tandem modular protein under force. Biochemical and Biophysical Research Communications, 2015, 460, 434-438.	2.1	27
29	The mechanochemistry of copper reports on the directionality of unfolding in model cupredoxin proteins. Nature Communications, 2015, 6, 7894.	12.8	57
30	How force unfolding differs from chemical denaturation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3413-3418.	7.1	83
31	Mechanisms of Acceleration and Retardation of Water Dynamics by Ions. Journal of the American Chemical Society, 2013, 135, 11824-11831.	13.7	203
32	Elasticity, structure, and relaxation of extended proteins under force. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3847-3852.	7.1	81
33	When Does Trimethylamine N-Oxide Fold a Polymer Chain and Urea Unfold It?. Journal of Physical Chemistry B, 2013, 117, 8723-8732.	2.6	99
34	Rate limit of protein elastic response is tether dependent. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14416-14421.	7.1	59
35	Water Jump Reorientation: From Theoretical Prediction to Experimental Observation. Accounts of Chemical Research, 2012, 45, 53-62.	15.6	90
36	Communication: On the origin of the non-Arrhenius behavior in water reorientation dynamics. Journal of Chemical Physics, 2012, 137, 031101.	3.0	63

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37	Magnitude and Molecular Origin of Water Slowdown Next to a Protein. Journal of the American Chemical Society, 2012, 134, 4116-4119.	13.7	171
38	Water jump reorientation and ultrafast vibrational spectroscopy. Journal of Photochemistry and Photobiology A: Chemistry, 2012, 234, 75-82.	3.9	7
39	Non-monotonic dependence of water reorientation dynamics on surface hydrophilicity: competing effects of the hydration structure and hydrogen-bond strength. Physical Chemistry Chemical Physics, 2011, 13, 19911.	2.8	60
40	Water reorientation dynamics in the first hydration shells of Fâ˜ and Iâ˜. Physical Chemistry Chemical Physics, 2011, 13, 19895.	2.8	52
41	Dynamics of Water in Concentrated Solutions of Amphiphiles: Key Roles of Local Structure and Aggregation. Journal of Physical Chemistry B, 2011, 115, 3254-3262.	2.6	70
42	Reorientation and Allied Dynamics in Water and Aqueous Solutions. Annual Review of Physical Chemistry, 2011, 62, 395-416.	10.8	310
43	Water reorientation in the hydration shells of hydrophilic and hydrophobic solutes. Science China: Physics, Mechanics and Astronomy, 2010, 53, 1068-1072.	5.1	11
44	Direct Evidence of Angular Jumps During Water Reorientation Through Two-Dimensional Infrared Anisotropy. Journal of Physical Chemistry Letters, 2010, 1, 1511-1516.	4.6	40
45	Water Hydrogen-Bond Dynamics around Amino Acids: The Key Role of Hydrophilic Hydrogen-Bond Acceptor Groups. Journal of Physical Chemistry B, 2010, 114, 2083-2089.	2.6	113
46	Water reorientation, hydrogen-bond dynamics and 2D-IR spectroscopy next to an extended hydrophobic surface. Faraday Discussions, 2010, 146, 263.	3.2	98
47	Water Hydrogen Bond Dynamics in Aqueous Solutions of Amphiphiles. Journal of Physical Chemistry B, 2010, 114, 3052-3059.	2.6	106
48	Why Water Reorientation Slows without Iceberg Formation around Hydrophobic Solutes. Journal of Physical Chemistry B, 2009, 113, 2428-2435.	2.6	338