Martin Gruebele

List of Publications by Year
in descending order

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195	10,069	38742	40979
papers	citations	50 h-index	93 g-index

351	351	351	7527
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Absolute comparison of simulated and experimental protein-folding dynamics. Nature, 2002, 420, 102-106.	27.8	646
2	Folding at the speed limit. Nature, 2003, 423, 193-197.	27.8	393
3	Direct observation of fast protein folding: the initial collapse of apomyoglobin.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 5759-5764.	7.1	326
4	Ten-Microsecond Molecular Dynamics Simulation of a Fast-Folding WW Domain. Biophysical Journal, 2008, 94, L75-L77.	0.5	309
5	Observation of strange kinetics in protein folding. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 6031-6036.	7.1	299
6	The folding mechanism of a Î²-sheet: the WW domain. Journal of Molecular Biology, 2001, 311, 373-393.	4.2	297
7	Structure, function, and folding of phosphoglycerate kinase are strongly perturbed by macromolecular crowding. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17586-17591.	7.1	284
8	Context-dependent contributions of backbone hydrogen bonding to Î²-sheet folding energetics. Nature, 2004, 430, 101-105.	27.8	260
9	Phase separation of YAP reorganizes genome topology for long-term YAP target gene expression. Nature Cell Biology, 2019, 21, 1578-1589.	10.3	237
10	Femtosecond wave packet spectroscopy: Coherences, the potential, and structural determination. Journal of Chemical Physics, 1993, 98, 883-902.	3.0	233
11	Protein folding stability and dynamics imaged in a living cell. Nature Methods, 2010, 7, 319-323.	19.0	213
12	THEFASTPROTEINFOLDINGPROBLEM. Annual Review of Physical Chemistry, 1999, 50, 485-516.	10.8	203
13	Structure-function-folding relationship in a WW domain. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 10648-10653.	7.1	199
14	Optical Control of Metal Ion Probes in Cells and Zebrafish Using Highly Selective DNAzymes Conjugated to Upconversion Nanoparticles. Journal of the American Chemical Society, 2018, 140, 17656-17665.	13.7	196
15	Vibrational Energy Flow and Chemical Reactions. Accounts of Chemical Research, 2004, 37, 261-267.	15.6	190
16	Molecular vibrational energy flow: Beyond the Golden Rule. International Reviews in Physical Chemistry, 1998, 17, 91-145.	2.3	163
17	Unraveling the Fluorescence Mechanism of Carbon Dots with Sub-Single-Particle Resolution. ACS Nano, 2020, 14, 6127-6137.	14.6	152
18	Tuning the free-energy landscape of a WW domain by temperature, mutation, and truncation. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3948-3953.	7.1	141

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19	An experimental survey of the transition between two-state and downhill protein folding scenarios. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2369-2374.	7.1	137
20	Protein Stability and Folding Kinetics in the Nucleus and Endoplasmic Reticulum of Eucaryotic Cells. Biophysical Journal, 2011, 101, 421-430.	0.5	136
21	Femtosecond realâ€time probing of reactions. V. The reaction of IHgI. Journal of Chemical Physics, 1989, 91, 7437-7450.	3.0	132
22	Temperature dependence of protein folding kinetics in living cells. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17863-17867.	7.1	123
23	Downhill protein folding: evolution meets physics. Comptes Rendus - Biologies, 2005, 328, 701-712.	0.2	116
24	Quinary protein structure and the consequences of crowding in living cells: Leaving the testâ€tube behind. BioEssays, 2013, 35, 984-993.	2.5	116
25	Protein folding: the free energy surface. Current Opinion in Structural Biology, 2002, 12, 161-168.	5.7	113
26	Computational Design and Experimental Testing of the Fastest-Folding Î²-Sheet Protein. Journal of Molecular Biology, 2011, 405, 43-48.	4.2	106
27	Folding Î»-Repressor at Its Speed Limit. Biophysical Journal, 2004, 87, 596-608.	0.5	105
28	Weak Chemical Interactions That Drive Protein Evolution: Crowding, Sticking, and Quinary Structure in Folding and Function. Chemical Reviews, 2019, 119, 10691-10717.	47.7	103
29	Kinetics are probe-dependent during downhill folding of an engineered Â6-85 protein. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2283-2287.	7.1	97
30	The vibrational energy flow transition in organic molecules: Theory meets experiment. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 5960-5964.	7.1	89
31	Weak proteinâ€“protein interactions in live cells are quantified by cell-volume modulation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6776-6781.	7.1	89
32	Role of Pressure in the Growth of Hexagonal Boron Nitride Thin Films from Ammonia-Borane. Chemistry of Materials, 2016, 28, 4169-4179.	6.7	85
33	Detection-Dependent Kinetics as a Probe of Folding Landscape Microstructure. Journal of the American Chemical Society, 2004, 126, 7758-7759.	13.7	84
34	Polymeric â€œClickaseâ€•Accelerates the Copper Click Reaction of Small Molecules, Proteins, and Cells. Journal of the American Chemical Society, 2019, 141, 9693-9700.	13.7	84
35	Globular Protein Folding In Vitro and In Vivo. Annual Review of Biophysics, 2016, 45, 233-251.	10.0	82
36	Biomolecule large-amplitude motion and solvation dynamics: modelling and probes from THz to X-rays. International Reviews in Physical Chemistry, 2006, 25, 553-582.	2.3	80

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37	The Extracellular Protein VlsE Is Destabilized Inside Cells. Journal of Molecular Biology, 2014, 426, 11-20.	4.2	79
38	A singleâ€sweep, nanosecond time resolution laser temperatureâ€jump apparatus. Review of Scientific Instruments, 1996, 67, 3694-3699.	1.3	77
39	Fast protein folding kinetics. Quarterly Reviews of Biophysics, 2014, 47, 95-142.	5.7	77
40	A simple matrix model of intramolecular vibrational redistribution and its implications. Chemical Physics Letters, 1995, 235, 604-613.	2.6	72
41	Rateâ˜Temperature Relationships in Î»-Repressor Fragment Î»6-85Foldingâ€. Biochemistry, 2004, 43, 13018-13025.	2.5	67
42	Vibrational Energy Flow: A State Space Approach. Advances in Chemical Physics, 2007, , 193-261.	0.3	66
43	How Does Vibrational Energy Flow Fill the Molecular State Space?. Journal of Physical Chemistry A, 1999, 103, 10083-10092.	2.5	62
44	The transition state transit time of WW domain folding is controlled by energy landscape roughness. Journal of Chemical Physics, 2009, 131, 195101.	3.0	62
45	On the Extended Î²-Conformation Propensity of Polypeptides at High Temperature. Journal of the American Chemical Society, 2003, 125, 16220-16227.	13.7	61
46	Temporal Variation of a Protein Folding Energy Landscape in the Cell. Journal of the American Chemical Society, 2013, 135, 19215-19221.	13.7	56
47	Submicrosecond real-time fluorescence sampling: application to protein folding. Journal of Photochemistry and Photobiology B: Biology, 2000, 54, 1-15.	3.8	53
48	Intramolecular vibrational dephasing obeys a power law at intermediate times. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 5965-5970.	7.1	52
49	What Causes Hyperfluorescence: Folding Intermediates or Conformationally Flexible Native States?. Biophysical Journal, 2002, 83, 473-483.	0.5	52
50	A quantum model of restricted vibrational energy flow on the way to the transition state in unimolecular reactions. Molecular Physics, 2008, 106, 433-442.	1.7	51
51	Microsecond folding experiments and simulations: a match is made. Physical Chemistry Chemical Physics, 2013, 15, 3372.	2.8	51
52	How does solvation in the cell affect protein folding and binding?. Current Opinion in Structural Biology, 2018, 48, 23-29.	5.7	49
53	On the importance of higher order anharmonic molecular couplings. Journal of Chemical Physics, 1998, 108, 6561-6570.	3.0	47
54	Approximate factorization of molecular potential surfaces. I. Basic approach. Journal of Chemical Physics, 1997, 106, 5874-5893.	3.0	45

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55	Mechanism and control of molecular energy flow: a modeling perspective. Theoretical Chemistry Accounts, 2003, 109, 53-63.	1.4	45
56	Tuning the Heterogeneous Early Folding Dynamics of Phosphoglycerate Kinase. Journal of Molecular Biology, 2003, 333, 187-199.	4.2	45
57	Comparing Fast Pressure Jump and Temperature Jump Protein Folding Experiments and Simulations. Journal of the American Chemical Society, 2015, 137, 7152-7159.	13.7	45
58	Femtosecond realâ€time probing of reactions. VIII. The bimolecular reaction Br+I2. Journal of Chemical Physics, 1992, 97, 4127-4148.	3.0	44
59	Protein Folding Landscapes in the Living Cell. Journal of Physical Chemistry Letters, 2011, 2, 314-319.	4.6	43
60	Direct Visualization of Two-State Dynamics on Metallic Glass Surfaces Well Below T_g. Journal of Physical Chemistry Letters, 2010, 1, 1941-1945.	4.6	42
61	Quantifying protein dynamics and stability in a living organism. Nature Communications, 2019, 10, 1179.	12.8	42
62	Cold-Denatured Ensemble of Apomyoglobin:â€‰ Implications for the Early Steps of Folding. Journal of Physical Chemistry B, 1998, 102, 1806-1819.	2.6	41
63	Two Structural Scenarios for Protein Stabilization by PEG. Journal of Physical Chemistry B, 2014, 118, 8388-8395.	2.6	41
64	Bose Statistics Triangle Rule Model for Intramolecular Vibrational Energy Redistribution. The Journal of Physical Chemistry, 1996, 100, 12183-12192.	2.9	40
65	Vibrational dynamics of SCCl2 from the zero point to the first dissociation limitElectronic supplementary information (ESI) available: Potential constants (table) conversion matrix from normal coordinates to Cartesian coordinates (table) and correlation between two normal coordinate force fields (figure). See http://www.rsc.org/suppdata/cp/b4/b403114h/. Physical Chemistry Chemical Physics, 2004, 6, 3786.	2.8	40
66	In-Cell Proteinâ€“Protein Contacts: Transient Interactions in the Crowd. Journal of Physical Chemistry Letters, 2019, 10, 5667-5673.	4.6	40
67	The Behavioral Space of Zebrafish Locomotion and Its Neural Network Analog. PLoS ONE, 2015, 10, e0128668.	2.5	39
68	Structural Characterization of Î»-Repressor Folding from All-Atom Molecular Dynamics Simulations. Journal of Physical Chemistry Letters, 2012, 3, 1117-1123.	4.6	37
69	Quantum computation with vibrationally excited polyatomic molecules: effects of rotation, level structure, and field gradients. Molecular Physics, 2007, 105, 1999-2008.	1.7	36
70	Coupled Protein Diffusion and Folding in the Cell. PLoS ONE, 2014, 9, e113040.	2.5	36
71	Protein Folding Dynamics in the Cell. Journal of Physical Chemistry B, 2014, 118, 8459-8470.	2.6	36
72	Direct Imaging of Protein Stability and Folding Kinetics in Hydrogels. ACS Applied Materials & Interfaces, 2017, 9, 21606-21617.	8.0	36

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73	In-Cell Titration of Small Solutes Controls Protein Stability and Aggregation. Journal of the American Chemical Society, 2018, 140, 10497-10503.	13.7	36
74	Loop and stem dynamics during RNA hairpin folding and unfolding. Rna, 2010, 16, 2427-2434.	3.5	35
75	The Diffusion Coefficient for PGK Folding in Eukaryotic Cells. Biophysical Journal, 2010, 99, L69-L71.	0.5	35
76	Femtosecond probing of bimolecular reactions: The collision complex. Journal of Chemical Physics, 1991, 95, 7763-7766.	3.0	33
77	Laser Absorption Scanning Tunneling Microscopy of Carbon Nanotubes. Nano Letters, 2006, 6, 45-49.	9.1	32
78	A Survey of Î» Repressor Fragments from Two-State to Downhill Folding. Journal of Molecular Biology, 2010, 397, 789-798.	4.2	32
79	ReAsH as a Quantitative Probe of In-Cell Protein Dynamics. Biochemistry, 2016, 55, 1968-1976.	2.5	32
80	The Effect of Fluorescent Protein Tags on Phosphoglycerate Kinase Stability Is Nonadditive. Journal of Physical Chemistry B, 2016, 120, 2878-2885.	2.6	31
81	The Molecular Basis for Life in Extreme Environments. Annual Review of Biophysics, 2021, 50, 343-372.	10.0	31
82	Intramolecular vibrational relaxation in aromatic molecules. 2: An experimental and computational study of pyrrole and triazine near the IVR threshold. Molecular Physics, 2003, 101, 551-568.	1.7	29
83	Nonâ€Steric Interactions Predict the Trend and Steric Interactions the Offset of Protein Stability in Cells. ChemPhysChem, 2018, 19, 2290-2294.	2.1	28
84	Better biomolecule thermodynamics from kinetics. Journal of Chemical Physics, 2011, 135, 015102.	3.0	27
85	Disulfide Bridges: Bringing Together Frustrated Structure in a Bioactive Peptide. Biophysical Journal, 2016, 110, 1744-1752.	0.5	27
86	Shifted-update rotation: simple integration of the many-level SchrÃ¶dinger equation to long times. Chemical Physics Letters, 1995, 233, 383-391.	2.6	26
87	Molecules: What Kind of a Bag of Atoms?. Journal of Physical Chemistry A, 2009, 113, 13139-13143.	2.5	26
88	The Fast and the Slow: Folding and Trapping of Î»_{6â€“85}. Journal of the American Chemical Society, 2011, 133, 19338-19341.	13.7	24
89	Mapping fast protein folding with multiple-site fluorescent probes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7966-7971.	7.1	24
90	Perspective: Reaches of chemical physics in biology. Journal of Chemical Physics, 2013, 139, 121701.	3.0	23

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91	Optoelectronic Switching of a Carbon Nanotube Chiral Junction Imaged with Nanometer Spatial Resolution. ACS Nano, 2015, 9, 10563-10570.	14.6	23
92	Correlation of early orientational ordering of engineered Î»6â€“85 structure with kinetics and thermodynamics. Chemical Physics, 2006, 323, 45-53.	1.9	22
93	Crowding effects on the small, fast-folding protein Î»6â€“85. Faraday Discussions, 2012, 157, 451.	3.2	22
94	Rapid Perturbation of Freeâ€Energy Landscapes: From In Vitro to In Vivo. Chemistry - A European Journal, 2012, 18, 6420-6427.	3.3	22
95	Cell Volume Controls Protein Stability and Compactness of the Unfolded State. Journal of Physical Chemistry B, 2018, 122, 11762-11770.	2.6	22
96	Direct Imaging of Two-State Dynamics on the Amorphous Silicon Surface. Physical Review Letters, 2011, 106, 235501.	7.8	21
97	Temperature-Dependent Two-State Dynamics of Individual Cooperatively Rearranging Regions on a Glass Surface. Physical Review Letters, 2012, 109, 166103.	7.8	21
98	Soluble Zwitterionic Poly(sulfobetaine) Destabilizes Proteins. Biomacromolecules, 2018, 19, 3894-3901.	5.4	21
99	Frequency-Modulated, Single-Molecule Absorption Detected by Scanning Tunneling Microscopy. Journal of Physical Chemistry C, 2007, 111, 3314-3321.	3.1	20
100	Protein stability at negative pressure. Methods, 2010, 52, 51-56.	3.8	20
101	High-Resolution Mapping of the Folding Transition State of a WW Domain. Journal of Molecular Biology, 2016, 428, 1617-1636.	4.2	20
102	Role of Electrostatics in Proteinâ€“RNA Binding: The Global vs the Local Energy Landscape. Journal of Physical Chemistry B, 2017, 121, 8437-8446.	2.6	20
103	A quantitative connection of experimental and simulated folding landscapes by vibrational spectroscopy. Chemical Science, 2018, 9, 9002-9011.	7.4	20
104	Approximate Factorization of Molecular Potential Surfaces II. Internal Rotors. Zeitschrift Fur Physikalische Chemie, 2000, 214, .	2.8	19
105	Nonexponential dephasing in a local random matrix model. Physical Review A, 2001, 63, .	2.5	19
106	Size and Energy Scaling of Nonstatistical Vibrational Quantum States. Physical Review Letters, 2008, 101, 250603.	7.8	19
107	Dynamical spectroscopy and microscopy of proteins in cells. Current Opinion in Structural Biology, 2021, 70, 1-7.	5.7	19
108	Quantizing Ulamâ€™s Control Conjecture. Physical Review Letters, 2007, 99, 060201.	7.8	18

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109	Comment on probeâ€dependent and nonexponential relaxation kinetics: Unreliable signatures of downhill protein folding. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1099-1102.	2.6	18
110	Regular vibrational state progressions at the dissociation limit of SCCl2. Journal of Chemical Physics, 2009, 130, 024305.	3.0	18
111	Imaging Excited Orbitals of Quantum Dots: Experiment and Electronic Structure Theory. Journal of the American Chemical Society, 2015, 137, 14743-14750.	13.7	18
112	Crowding, Sticking, and Partial Folding of GTT WW Domain in a Small Cytoplasm Model. Journal of Physical Chemistry B, 2020, 124, 4732-4740.	2.6	18
113	An in vitro mimic of inâ€cell solvation for protein folding studies. Protein Science, 2020, 29, 1046-1054.	7.6	18
114	Imaging and Manipulating Energy Transfer Among Quantum Dots at Individual Dot Resolution. ACS Nano, 2017, 11, 6328-6335.	14.6	17
115	Multistep Kinetics of the U1Aâ€“SL2 RNA Complex Dissociation. Journal of Molecular Biology, 2011, 408, 896-908.	4.2	16
116	Communication: An obligatory glass surface. Journal of Chemical Physics, 2012, 137, 141102.	3.0	16
117	Pressureâ€and heatâ€induced protein unfolding in bacterial cells: crowding vs. sticking. FEBS Letters, 2018, 592, 1357-1365.	2.8	16
118	Critical Phenomena in the Temperature-Pressure-Crowding Phase Diagram of a Protein. Physical Review X, 2019, 9, .	8.9	16
119	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. PLoS Computational Biology, 2020, 16, e1007717.	3.2	16
120	Ultrafast nanometric imaging of energy flow within and between single carbon dots. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	16
121	Single-sweep detection of relaxation kinetics by submicrosecond midinfrared spectroscopy. Review of Scientific Instruments, 2004, 75, 486-491.	1.3	15
122	Periodic and stochastic thermal modulation of protein folding kinetics. Journal of Chemical Physics, 2014, 141, 035103.	3.0	15
123	Transparent Metal Films for Detection of Single-Molecule Optical Absorption by Scanning Tunneling Microscopy. Journal of Physical Chemistry C, 2014, 118, 13196-13202.	3.1	15
124	Subcellular modulation of protein VlsE stability and folding kinetics. FEBS Letters, 2016, 590, 1409-1416.	2.8	15
125	Blue Light Is a Universal Signal for Escherichia coli Chemoreceptors. Journal of Bacteriology, 2019, 201, .	2.2	15
126	Molecular mechanism of capsid disassembly in hepatitis B virus. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	15

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127	Direct Imaging of Room Temperature Optical Absorption with Subnanometer Spatial Resolution. Nano Letters, 2010, 10, 4897-4900.	9.1	14
128	Transient Helical Structure during PI3K and Fyn SH3 Domain Folding. Journal of Physical Chemistry B, 2013, 117, 4836-4843.	2.6	14
129	Plasmonic support-mediated activation of 1 nm platinum clusters for catalysis. Physical Chemistry Chemical Physics, 2017, 19, 30570-30577.	2.8	14
130	Numerical potential functions for diatomic molecules. Molecular Physics, 1990, 69, 475-496.	1.7	13
131	Kinetic equivalence of the heat and cold structural transitions of Î» 6â€“85. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2005, 363, 565-573.	3.4	13
132	Orientation-dependent imaging of electronically excited quantum dots. Journal of Chemical Physics, 2018, 148, 064701.	3.0	13
133	Proteins: â€œBoil â€™Em, Mash â€™Em, Stick â€™Em in a Stewâ€• Journal of Physical Chemistry B, 2019, 123, 8341-8350.	2.6	13
134	Chaperones Hsc70 and Hsp70 Bind to the Protein PGK Differently inside Living Cells. Journal of Physical Chemistry B, 2020, 124, 3629-3635.	2.6	13
135	Fast Relaxation Imaging in Living Cells. Current Protocols in Protein Science, 2011, 65, Unit28.1.	2.8	12
136	Mechanical approach to chemical transport. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11116-11121.	7.1	12
137	Can Local Probes Go Global? A Joint Experimentâ€“Simulation Analysis of Î»_{6â€“85} Folding. Journal of Physical Chemistry Letters, 2016, 7, 1960-1965.	4.6	12
138	Parallel folding pathways of Fip35 WW domain explained by infrared spectra and their computer simulation. FEBS Letters, 2017, 591, 3265-3275.	2.8	12
139	The Surface of Protein Î»_{6â€“85} Can Act as a Template for Recurring Poly(ethylene glycol) Structure. Biochemistry, 2017, 56, 5671-5678.	2.5	12
140	A thermodynamic derivation of the reciprocal relations. Journal of Chemical Physics, 2013, 138, 124502.	3.0	11
141	STM Imaging of Localized Surface Plasmons on Individual Gold Nanoislands. Journal of Physical Chemistry Letters, 2018, 9, 1970-1976.	4.6	11
142	Thermodiffusion: The physico-chemical mechanics view. Journal of Chemical Physics, 2021, 154, 024112.	3.0	11
143	Cellular Sticking Can Strongly Reduce Complex Binding by Speeding Dissociation. Journal of Physical Chemistry B, 2021, 125, 3815-3823.	2.6	11
144	The energy landscape of glassy dynamics on the amorphous hafnium diboride surface. Journal of Chemical Physics, 2014, 141, 204501.	3.0	10

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145	Native Conformational Dynamics of the Spliceosomal U1A Protein. Journal of Physical Chemistry B, 2015, 119, 3651-3661.	2.6	10
146	Fast pressure-jump all-atom simulations and experiments reveal site-specific protein dehydration-folding dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5356-5361.	7.1	10
147	Cytoskeletal Drugs Modulate Off-Target Protein Folding Landscapes Inside Cells. Biochemistry, 2020, 59, 2650-2659.	2.5	10
148	More Protected Vibrational States at the Dissociation Limit of SCCl₂. Journal of Physical Chemistry A, 2013, 117, 12082-12090.	2.5	9
149	Dodine as a Protein Denaturant: The Best of Two Worlds?. Journal of Physical Chemistry B, 2013, 117, 13090-13097.	2.6	9
150	Sub-nanometer glass surface dynamics induced by illumination. Journal of Chemical Physics, 2015, 142, 234505.	3.0	9
151	Environmental Fluctuations and Stochastic Resonance in Protein Folding. ChemPhysChem, 2016, 17, 1341-1348.	2.1	9
152	Composition-dependent metallic glass alloys correlate atomic mobility with collective glass surface dynamics. Physical Chemistry Chemical Physics, 2016, 18, 16856-16861.	2.8	9
153	Heat shock-induced chaperoning by Hsp70 is enabled in-cell. PLoS ONE, 2019, 14, e0222990.	2.5	9
154	In-cell protein landscapes: making the match between theory, simulation and experiment. Current Opinion in Structural Biology, 2021, 66, 163-169.	5.7	9
155	Direct Observation of Single-Protein Transition State Passage by Nanopore Ionic Current Jumps. Journal of Physical Chemistry Letters, 2022, 13, 5918-5924.	4.6	9
156	Binary and Ternary Aggregation within Tethered Protein Constructs. Biophysical Journal, 2006, 90, 2930-2937.	0.5	8
157	Mapping an Aggregation Nucleus One Protein at a Time. Journal of Physical Chemistry Letters, 2010, 1, 16-19.	4.6	8
158	On readout of vibrational qubits using quantum beats. Journal of Chemical Physics, 2014, 141, 224306.	3.0	8
159	Glass Dynamics Deep in the Energy Landscape. Journal of Physical Chemistry B, 2021, 125, 9052-9068.	2.6	8
160	Dodine as a Kosmo-Chaotropic Agent. Journal of Physical Chemistry Letters, 2019, 10, 2600-2605.	4.6	7
161	Competition of individual domain folding with inter-domain interaction in WW domain engineered repeat proteins. Physical Chemistry Chemical Physics, 2019, 21, 24393-24405.	2.8	7
162	Fast-folding proteins under stress. Cellular and Molecular Life Sciences, 2015, 72, 4273-4285.	5.4	6

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163	Dodine as a transparent protein denaturant for circular dichroism and infrared studies. Protein Science, 2016, 25, 1061-1068.	7.6	6
164	Stochastic Resonance in Protein Folding Dynamics. ChemPhysChem, 2016, 17, 1305-1313.	2.1	6
165	Labeling for Quantitative Comparison of Imaging Measurementsin Vitroand in Cells. Biochemistry, 2018, 57, 1929-1938.	2.5	6
166	Excited-State Imaging of Single Particles on the Subnanometer Scale. Annual Review of Physical Chemistry, 2020, 71, 415-433.	10.8	6
167	How to mark off paths on the protein energy landscape. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18879-18880.	7.1	5
168	The Gold Nanorod-Biology Interface: From Proteins to Cells to Tissue. Current Physical Chemistry, 2013, 3, 128-135.	0.2	5
169	Stabilization and Kinetics of an Adsorbed Protein Depends on the Poly(N-isopropylacrylamide) Grafting Density. Biomacromolecules, 2021, 22, 4470-4478.	5.4	5
170	Quantum information scrambling in molecules. Physical Review A, 2022, 105, .	2.5	5
171	Estimation of Relative Proteinâ€“RNA Binding Strengths from Fluctuations in the Bound State. Journal of Chemical Theory and Computation, 2016, 12, 4593-4599.	5.3	4
172	Coherent Atomic-Scale Ripples on Metallic Glasses Patterned by Low-Energy Ion Irradiation for Large-Area Surface Structuring. ACS Applied Nano Materials, 2020, 3, 12025-12033.	5.0	4
173	Protein folding and surface interaction phase diagrams in vitro and in cells. FEBS Letters, 2021, 595, 1267-1274.	2.8	4
174	Sonification-Enhanced Lattice Model Animations for Teaching the Protein Folding Reaction. Journal of Chemical Education, 2022, 99, 1220-1230.	2.3	4
175	Protein Dynamics: From Molecules, to Interactions, to Biology. International Journal of Molecular Sciences, 2009, 10, 1360-1368.	4.1	3
176	Imaging of Carbon Nanotube Electronic States Polarized by the Field of an Excited Quantum Dot. ACS Nano, 2019, 13, 1012-1018.	14.6	3
177	A phase diagram for energy flow-limited reactivity. Journal of Chemical Physics, 2021, 154, 104301.	3.0	3
178	Multi-scale dynamics at the glassy silica surface. Journal of Chemical Physics, 2019, 151, 174502.	3.0	2
179	Protein folding. Methods, 2010, 52, 1-2.	3.8	1
180	CARPe Diem. Biophysical Journal, 2014, 107, 3-4.	0.5	1

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181	Electrostatic Interaction Effects on the Binding of Spliceosomal U1A Protein-SL2 RNA Hairpin. Biophysical Journal, 2015, 108, 15a.	0.5	1
182	Building a Modern Chemistry Undergraduate Program at Hanoi University of Science-Vietnam National University: A Vietnamâ˜U.S. Partnership. ACS Symposium Series, 2017, , 15-32.	0.5	1
183	Response to â€œComment on â€˜Thermodiffusion: The physico-chemical mechanics viewâ€™â€•[J. Chem. Phys. 155, 087101 (2021)]. Journal of Chemical Physics, 2021, 155, 087102.	3.0	1
184	1P109 Solvent-tuning collapse and helix formation time scales of Î»^*_6-85(3. Protein folding and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2006, 46, S174.	0.1	0
185	The THz dance of the protein with the water. , 2008, , .		0
186	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
187	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
188	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
189	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
190	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
191	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
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