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	Sonification-Enhanced Lattice Model Animations for Teaching the Protein Folding Reaction. Journal of Chemical Education, 2022, 99, 1220-1230.	2.3	4
2	Quantum information scrambling in molecules. Physical Review A, 2022, 105, .	2.5	5
3	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
4	In-cell protein landscapes: making the match between theory, simulation and experiment. Current Opinion in Structural Biology, 2021, 66, 163-169.	5.7	9
5	Thermodiffusion: The physico-chemical mechanics view. Journal of Chemical Physics, 2021, 154, 024112.	3.0	11
6	Protein folding and surface interaction phase diagrams in vitro and in cells. FEBS Letters, 2021, 595, 1267-1274.	2.8	4
7	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
8	A phase diagram for energy flow-limited reactivity. Journal of Chemical Physics, 2021, 154, 104301.	3.0	3
9	Cellular Sticking Can Strongly Reduce Complex Binding by Speeding Dissociation. Journal of Physical Chemistry B, 2021, 125, 3815-3823.	2.6	11
10	The Molecular Basis for Life in Extreme Environments. Annual Review of Biophysics, 2021, 50, 343-372.	10.0	31
11	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
12	Glass Dynamics Deep in the Energy Landscape. Journal of Physical Chemistry B, 2021, 125, 9052-9068.	2.6	8
13	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
14	Dynamical spectroscopy and microscopy of proteins in cells. Current Opinion in Structural Biology, 2021, 70, 1-7.	5.7	19
15	Stabilization and Kinetics of an Adsorbed Protein Depends on the Poly(N-isopropylacrylamide) Grafting Density. Biomacromolecules, 2021, 22, 4470-4478.	5.4	5
16	Excited-State Imaging of Single Particles on the Subnanometer Scale. Annual Review of Physical Chemistry, 2020, 71, 415-433.	10.8	6
17	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
18	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

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19	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. PLoS Computational Biology, 2020, 16, e1007717.	3.2	16
20	Cytoskeletal Drugs Modulate Off-Target Protein Folding Landscapes Inside Cells. Biochemistry, 2020, 59, 2650-2659.	2.5	10
21	An in vitro mimic of inâ€cell solvation for protein folding studies. Protein Science, 2020, 29, 1046-1054.	7.6	18
22	Unraveling the Fluorescence Mechanism of Carbon Dots with Sub-Single-Particle Resolution. ACS Nano, 2020, 14, 6127-6137.	14.6	152
23	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
24	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
25	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
26	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
27	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
28	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
29	An in-silico human cell model reveals the influence of spatial organization on RNA splicing. , 2020, 16, e1007717.		0
30	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
31	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
32	Multi-scale dynamics at the glassy silica surface. Journal of Chemical Physics, 2019, 151, 174502.	3.0	2
33	In-Cell Proteinâ€“Protein Contacts: Transient Interactions in the Crowd. Journal of Physical Chemistry Letters, 2019, 10, 5667-5673.	4.6	40
34	Heat shock-induced chaperoning by Hsp70 is enabled in-cell. PLoS ONE, 2019, 14, e0222990.	2.5	9
35	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
36	Dodine as a Kosmo-Chaotropic Agent. Journal of Physical Chemistry Letters, 2019, 10, 2600-2605.	4.6	7

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37	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
38	Blue Light Is a Universal Signal for Escherichia coli Chemoreceptors. Journal of Bacteriology, 2019, 201, .	2.2	15
39	Quantifying protein dynamics and stability in a living organism. Nature Communications, 2019, 10, 1179.	12.8	42
40	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
41	Phase separation of YAP reorganizes genome topology for long-term YAP target gene expression. Nature Cell Biology, 2019, 21, 1578-1589.	10.3	237
42	Critical Phenomena in the Temperature-Pressure-Crowding Phase Diagram of a Protein. Physical Review X, 2019, 9, .	8.9	16
43	Imaging of Carbon Nanotube Electronic States Polarized by the Field of an Excited Quantum Dot. ACS Nano, 2019, 13, 1012-1018.	14.6	3
44	Heat shock-induced chaperoning by Hsp70 is enabled in-cell. , 2019, 14, e0222990.		0
45	Heat shock-induced chaperoning by Hsp70 is enabled in-cell. , 2019, 14, e0222990.		0
46	Heat shock-induced chaperoning by Hsp70 is enabled in-cell. , 2019, 14, e0222990.		0
47	Heat shock-induced chaperoning by Hsp70 is enabled in-cell. , 2019, 14, e0222990.		0
48	Orientation-dependent imaging of electronically excited quantum dots. Journal of Chemical Physics, 2018, 148, 064701.	3.0	13
49	Pressureâ€•and heatâ€•induced protein unfolding in bacterial cells: crowding vs. sticking. FEBS Letters, 2018, 592, 1357-1365.	2.8	16
50	STM Imaging of Localized Surface Plasmons on Individual Gold Nanoislands. Journal of Physical Chemistry Letters, 2018, 9, 1970-1976.	4.6	11
51	Labeling for Quantitative Comparison of Imaging Measurementsin Vitroand in Cells. Biochemistry, 2018, 57, 1929-1938.	2.5	6
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	A quantitative connection of experimental and simulated folding landscapes by vibrational spectroscopy. Chemical Science, 2018, 9, 9002-9011.	7.4	20
54	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

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55	Cell Volume Controls Protein Stability and Compactness of the Unfolded State. Journal of Physical Chemistry B, 2018, 122, 11762-11770.	2.6	22
56	Nonâ€Steric Interactions Predict the Trend and Steric Interactions the Offset of Protein Stability in Cells. ChemPhysChem, 2018, 19, 2290-2294.	2.1	28
57	Soluble Zwitterionic Poly(sulfobetaine) Destabilizes Proteins. Biomacromolecules, 2018, 19, 3894-3901.	5.4	21
58	In-Cell Titration of Small Solutes Controls Protein Stability and Aggregation. Journal of the American Chemical Society, 2018, 140, 10497-10503.	13.7	36
59	Imaging and Manipulating Energy Transfer Among Quantum Dots at Individual Dot Resolution. ACS Nano, 2017, 11, 6328-6335.	14.6	17
60	Direct Imaging of Protein Stability and Folding Kinetics in Hydrogels. ACS Applied Materials & Interfaces, 2017, 9, 21606-21617.	8.0	36
61	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
62	Parallel folding pathways of Fip35 WW domain explained by infrared spectra and their computer simulation. FEBS Letters, 2017, 591, 3265-3275.	2.8	12
63	The Surface of Protein Î»‹sub›6â€“85‹/sub› Can Act as a Template for Recurring Poly(ethylene glycol) Structure. Biochemistry, 2017, 56, 5671-5678.	2.5	12
64	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
65	Plasmonic support-mediated activation of 1 nm platinum clusters for catalysis. Physical Chemistry Chemical Physics, 2017, 19, 30570-30577.	2.8	14
66	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
67	Environmental Fluctuations and Stochastic Resonance in Protein Folding. ChemPhysChem, 2016, 17, 1341-1348.	2.1	9
68	Globular Protein Folding In Vitro and In Vivo. Annual Review of Biophysics, 2016, 45, 233-251.	10.0	82
69	Disulfide Bridges: Bringing Together Frustrated Structure in a Bioactive Peptide. Biophysical Journal, 2016, 110, 1744-1752.	0.5	27
70	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
71	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
72	Dodine as a transparent protein denaturant for circular dichroism and infrared studies. Protein Science, 2016, 25, 1061-1068.	7.6	6

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73	Subcellular modulation of protein VlsE stability and folding kinetics. FEBS Letters, 2016, 590, 1409-1416.	2.8	15
74	Composition-dependent metallic glass alloys correlate atomic mobility with collective glass surface dynamics. Physical Chemistry Chemical Physics, 2016, 18, 16856-16861.	2.8	9
75	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
76	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
77	Stochastic Resonance in Protein Folding Dynamics. ChemPhysChem, 2016, 17, 1305-1313.	2.1	6
78	High-Resolution Mapping of the Folding Transition State of a WW Domain. Journal of Molecular Biology, 2016, 428, 1617-1636.	4.2	20
79	The Effect of Fluorescent Protein Tags on Phosphoglycerate Kinase Stability Is Nonadditive. Journal of Physical Chemistry B, 2016, 120, 2878-2885.	2.6	31
80	ReAsH as a Quantitative Probe of In-Cell Protein Dynamics. Biochemistry, 2016, 55, 1968-1976.	2.5	32
81	Sub-nanometer glass surface dynamics induced by illumination. Journal of Chemical Physics, 2015, 142, 234505.	3.0	9
82	Imaging Excited Orbitals of Quantum Dots: Experiment and Electronic Structure Theory. Journal of the American Chemical Society, 2015, 137, 14743-14750.	13.7	18
83	Electrostatic Interaction Effects on the Binding of Spliceosomal U1A Protein-SL2 RNA Hairpin. Biophysical Journal, 2015, 108, 15a.	0.5	1
84	Native Conformational Dynamics of the Spliceosomal U1A Protein. Journal of Physical Chemistry B, 2015, 119, 3651-3661.	2.6	10
85	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
86	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
87	Optoelectronic Switching of a Carbon Nanotube Chiral Junction Imaged with Nanometer Spatial Resolution. ACS Nano, 2015, 9, 10563-10570.	14.6	23
88	Fast-folding proteins under stress. Cellular and Molecular Life Sciences, 2015, 72, 4273-4285.	5.4	6
89	The Behavioral Space of Zebrafish Locomotion and Its Neural Network Analog. PLoS ONE, 2015, 10, e0128668.	2.5	39
90	Coupled Protein Diffusion and Folding in the Cell. PLoS ONE, 2014, 9, e113040.	2.5	36

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91	On readout of vibrational qubits using quantum beats. Journal of Chemical Physics, 2014, 141, 224306.	3.0	8
92	The energy landscape of glassy dynamics on the amorphous hafnium diboride surface. Journal of Chemical Physics, 2014, 141, 204501.	3.0	10
93	Periodic and stochastic thermal modulation of protein folding kinetics. Journal of Chemical Physics, 2014, 141, 035103.	3.0	15
94	Fast protein folding kinetics. Quarterly Reviews of Biophysics, 2014, 47, 95-142.	5.7	77
95	CARPe Diem. Biophysical Journal, 2014, 107, 3-4.	0.5	1
96	Protein Folding Dynamics in the Cell. Journal of Physical Chemistry B, 2014, 118, 8459-8470.	2.6	36
97	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
98	Two Structural Scenarios for Protein Stabilization by PEG. Journal of Physical Chemistry B, 2014, 118, 8388-8395.	2.6	41
99	The Extracellular Protein VlsE Is Destabilized Inside Cells. Journal of Molecular Biology, 2014, 426, 11-20.	4.2	79
100	Transient Helical Structure during PI3K and Fyn SH3 Domain Folding. Journal of Physical Chemistry B, 2013, 117, 4836-4843.	2.6	14
101	More Protected Vibrational States at the Dissociation Limit of SCCl₂. Journal of Physical Chemistry A, 2013, 117, 12082-12090.	2.5	9
102	Perspective: Reaches of chemical physics in biology. Journal of Chemical Physics, 2013, 139, 121701.	3.0	23
103	Microsecond folding experiments and simulations: a match is made. Physical Chemistry Chemical Physics, 2013, 15, 3372.	2.8	51
104	A thermodynamic derivation of the reciprocal relations. Journal of Chemical Physics, 2013, 138, 124502.	3.0	11
105	Temporal Variation of a Protein Folding Energy Landscape in the Cell. Journal of the American Chemical Society, 2013, 135, 19215-19221.	13.7	56
106	Dodine as a Protein Denaturant: The Best of Two Worlds?. Journal of Physical Chemistry B, 2013, 117, 13090-13097.	2.6	9
107	Quinary protein structure and the consequences of crowding in living cells: Leaving the testâ€tube behind. BioEssays, 2013, 35, 984-993.	2.5	116
108	The Gold Nanorod-Biology Interface: From Proteins to Cells to Tissue. Current Physical Chemistry, 2013, 3, 128-135.	0.2	5

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109	Communication: An obligatory glass surface. Journal of Chemical Physics, 2012, 137, 141102.	3.0	16
110	Temperature-Dependent Two-State Dynamics of Individual Cooperatively Rearranging Regions on a Glass Surface. Physical Review Letters, 2012, 109, 166103.	7.8	21
111	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
112	Crowding effects on the small, fast-folding protein Î»6â€“85. Faraday Discussions, 2012, 157, 451.	3.2	22
113	Structural Characterization of Î»-Repressor Folding from All-Atom Molecular Dynamics Simulations. Journal of Physical Chemistry Letters, 2012, 3, 1117-1123.	4.6	37
114	Rapid Perturbation of Freeâ€€Energy Landscapes: From In Vitro to In Vivo. Chemistry - A European Journal, 2012, 18, 6420-6427.	3.3	22
115	Protein Folding Landscapes in the Living Cell. Journal of Physical Chemistry Letters, 2011, 2, 314-319.	4.6	43
116	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
117	Protein Stability and Folding Kinetics in the Nucleus and Endoplasmic Reticulum of Eucaryotic Cells. Biophysical Journal, 2011, 101, 421-430.	0.5	136
118	Fast Relaxation Imaging in Living Cells. Current Protocols in Protein Science, 2011, 65, Unit28.1.	2.8	12
119	Computational Design and Experimental Testing of the Fastest-Folding Î²-Sheet Protein. Journal of Molecular Biology, 2011, 405, 43-48.	4.2	106
120	Multistep Kinetics of the U1Aâ€“SL2 RNA Complex Dissociation. Journal of Molecular Biology, 2011, 408, 896-908.	4.2	16
121	Better biomolecule thermodynamics from kinetics. Journal of Chemical Physics, 2011, 135, 015102.	3.0	27
122	Direct Imaging of Two-State Dynamics on the Amorphous Silicon Surface. Physical Review Letters, 2011, 106, 235501.	7.8	21
123	Protein folding stability and dynamics imaged in a living cell. Nature Methods, 2010, 7, 319-323.	19.0	213
124	Loop and stem dynamics during RNA hairpin folding and unfolding. Rna, 2010, 16, 2427-2434.	3.5	35
125	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
126	The Diffusion Coefficient for PGK Folding in Eukaryotic Cells. Biophysical Journal, 2010, 99, L69-L71.	0.5	35

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127	Mapping an Aggregation Nucleus One Protein at a Time. Journal of Physical Chemistry Letters, 2010, 1, 16-19.	4.6	8
128	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
129	A Survey of Î» Repressor Fragments from Two-State to Downhill Folding. Journal of Molecular Biology, 2010, 397, 789-798.	4.2	32
130	Protein stability at negative pressure. Methods, 2010, 52, 51-56.	3.8	20
131	Protein folding. Methods, 2010, 52, 1-2.	3.8	1
132	Direct Imaging of Room Temperature Optical Absorption with Subnanometer Spatial Resolution. Nano Letters, 2010, 10, 4897-4900.	9.1	14
133	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
134	Regular vibrational state progressions at the dissociation limit of SCCl2. Journal of Chemical Physics, 2009, 130, 024305.	3.0	18
135	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
136	Protein Dynamics: From Molecules, to Interactions, to Biology. International Journal of Molecular Sciences, 2009, 10, 1360-1368.	4.1	3
137	Molecules: What Kind of a Bag of Atoms?. Journal of Physical Chemistry A, 2009, 113, 13139-13143.	2.5	26
138	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
139	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
140	Ten-Microsecond Molecular Dynamics Simulation of a Fast-Folding WW Domain. Biophysical Journal, 2008, 94, L75-L77.	0.5	309
141	The THz dance of the protein with the water. , 2008, , .		0
142	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
143	Size and Energy Scaling of Nonstatistical Vibrational Quantum States. Physical Review Letters, 2008, 101, 250603.	7.8	19
144	Vibrational Energy Flow: A State Space Approach. Advances in Chemical Physics, 2007, , 193-261.	0.3	66

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145	Quantizing Ulamâ€™s Control Conjecture. Physical Review Letters, 2007, 99, 060201.	7.8	18
146	Quantum computation with vibrationally excited polyatomic molecules: effects of rotation, level structure, and field gradients. Molecular Physics, 2007, 105, 1999-2008.	1.7	36
147	Frequency-Modulated, Single-Molecule Absorption Detected by Scanning Tunneling Microscopy. Journal of Physical Chemistry C, 2007, 111, 3314-3321.	3.1	20
148	Binary and Ternary Aggregation within Tethered Protein Constructs. Biophysical Journal, 2006, 90, 2930-2937.	0.5	8
149	Laser Absorption Scanning Tunneling Microscopy of Carbon Nanotubes. Nano Letters, 2006, 6, 45-49.	9.1	32
150	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
151	Correlation of early orientational ordering of engineered Î»6â€“85 structure with kinetics and thermodynamics. Chemical Physics, 2006, 323, 45-53.	1.9	22
152	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
153	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
154	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
155	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
156	Downhill protein folding: evolution meets physics. Comptes Rendus - Biologies, 2005, 328, 701-712.	0.2	116
157	Single-sweep detection of relaxation kinetics by submicrosecond midinfrared spectroscopy. Review of Scientific Instruments, 2004, 75, 486-491.	1.3	15
158	Context-dependent contributions of backbone hydrogen bonding to Î²-sheet folding energetics. Nature, 2004, 430, 101-105.	27.8	260
159	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
160	Rateâ^'Temperature Relationships in Î»-Repressor Fragment Î»6-85Foldingâ€. Biochemistry, 2004, 43, 13018-13025.	2.5	67
161	Vibrational Energy Flow and Chemical Reactions. Accounts of Chemical Research, 2004, 37, 261-267.	15.6	190
162	Folding Î»-Repressor at Its Speed Limit. Biophysical Journal, 2004, 87, 596-608.	0.5	105

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163	Detection-Dependent Kinetics as a Probe of Folding Landscape Microstructure. Journal of the American Chemical Society, 2004, 126, 7758-7759.	13.7	84
164	Mechanism and control of molecular energy flow: a modeling perspective. Theoretical Chemistry Accounts, 2003, 109, 53-63.	1.4	45
165	Folding at the speed limit. Nature, 2003, 423, 193-197.	27.8	393
166	On the Extended Î²-Conformation Propensity of Polypeptides at High Temperature. Journal of the American Chemical Society, 2003, 125, 16220-16227.	13.7	61
167	Tuning the Heterogeneous Early Folding Dynamics of Phosphoglycerate Kinase. Journal of Molecular Biology, 2003, 333, 187-199.	4.2	45
168	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
169	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
170	What Causes Hyperfluorescence: Folding Intermediates or Conformationally Flexible Native States?. Biophysical Journal, 2002, 83, 473-483.	0.5	52
171	Protein folding: the free energy surface. Current Opinion in Structural Biology, 2002, 12, 161-168.	5.7	113
172	Absolute comparison of simulated and experimental protein-folding dynamics. Nature, 2002, 420, 102-106.	27.8	646
173	The folding mechanism of a Î²-sheet: the WW domain. Journal of Molecular Biology, 2001, 311, 373-393.	4.2	297
174	Nonexponential dephasing in a local random matrix model. Physical Review A, 2001, 63, .	2.5	19
175	Submicrosecond real-time fluorescence sampling: application to protein folding. Journal of Photochemistry and Photobiology B: Biology, 2000, 54, 1-15.	3.8	53
176	Approximate Factorization of Molecular Potential Surfaces II. Internal Rotors. Zeitschrift Fur Physikalische Chemie, 2000, 214, .	2.8	19
177	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
178	How Does Vibrational Energy Flow Fill the Molecular State Space?. Journal of Physical Chemistry A, 1999, 103, 10083-10092.	2.5	62
179	THEFASTPROTEINFOLDINGPROBLEM. Annual Review of Physical Chemistry, 1999, 50, 485-516.	10.8	203
180	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

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181	Molecular vibrational energy flow: Beyond the Golden Rule. International Reviews in Physical Chemistry, 1998, 17, 91-145.	2.3	163
182	On the importance of higher order anharmonic molecular couplings. Journal of Chemical Physics, 1998, 108, 6561-6570.	3.0	47
183	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
184	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
185	Approximate factorization of molecular potential surfaces. I. Basic approach. Journal of Chemical Physics, 1997, 106, 5874-5893.	3.0	45
186	A singleâ€sweep, nanosecond time resolution laser temperatureâ€jump apparatus. Review of Scientific Instruments, 1996, 67, 3694-3699.	1.3	77
187	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
188	Bose Statistics Triangle Rule Model for Intramolecular Vibrational Energy Redistribution. The Journal of Physical Chemistry, 1996, 100, 12183-12192.	2.9	40
189	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
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