Benjamin Schuler

List of Publications by Year
in descending order

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140 papers	11,553 citations	34105 52 h-index	30922 102 g-index
153 all docs	153 docs citations	153 times ranked	8083 citing authors

#	Article	IF	Citations
1	Labeling of Proteins for Single-Molecule Fluorescence Spectroscopy. Methods in Molecular Biology, 2022, 2376, 207-233.	0.9	5
2	Release of linker histone from the nucleosome driven by polyelectrolyte competition with a disordered protein. Nature Chemistry, 2022, 14, 224-231.	13.6	37
3	Structure, dynamics, and stability of the globular domain of human linker histone <scp>H1</scp>.0 and the role of positive charges. Protein Science, 2022, 31, 918-932.	7.6	7
4	Global Structure of the Intrinsically Disordered Protein Tau Emerges from Its Local Structure. Jacs Au, 2022, 2, 673-686.	7.9	48
5	Single-molecule Detection of Ultrafast Biomolecular Dynamics with Nanophotonics. Journal of the American Chemical Society, 2022, 144, 52-56.	13.7	18
6	Molecular Origins of Free Energies Associated with Complex Interactions of Biological Polyelectrolyte-Like Disordered Proteins. Biophysical Journal, 2021, 120, 286a.	0.5	0
7	FRET-based dynamic structural biology: Challenges, perspectives and an appeal for open-science practices. ELife, 2021, 10, .	6.0	152
8	Impact of Inâ€Cell and Inâ€Vitro Crowding on the Conformations and Dynamics of an Intrinsically Disordered Protein. Angewandte Chemie, 2021, 133, 10819-10824.	2.0	27
9	Impact of Inâ€Cell and Inâ€Vitro Crowding on the Conformations and Dynamics of an Intrinsically Disordered Protein. Angewandte Chemie - International Edition, 2021, 60, 10724-10729.	13.8	40
10	Combining Rapid Microfluidic Mixing and Three-Color Single-Molecule FRET for Probing the Kinetics of Protein Conformational Changes. Journal of Physical Chemistry B, 2021, 125, 6617-6628.	2.6	4
11	Apoptosis-inducing anti-HER2 agents operate through oligomerization-induced receptor immobilization. Communications Biology, 2021, 4, 762.	4.4	12
12	Slow Escape from a Helical Misfolded State of the Pore-Forming Toxin Cytolysin A. Jacs Au, 2021, 1, 1217-1230.	7.9	5
13	Resolving distance variations by single-molecule FRET and EPR spectroscopy using rotamer libraries. Biophysical Journal, 2021, 120, 4842-4858.	0.5	21
14	Binding without folding â€“ the biomolecular function of disordered polyelectrolyte complexes. Current Opinion in Structural Biology, 2020, 60, 66-76.	5.7	71
15	Transition Path Dynamics of a Dielectric Particle in a Bistable Optical Trap. Physical Review Letters, 2020, 125, 146001.	7.8	20
16	Polyelectrolyte interactions enable rapid association and dissociation in high-affinity disordered protein complexes. Nature Communications, 2020, 11, 5736.	12.8	74
17	Editorial overview: Molecular interactions that drive folding and binding: new challenges and opportunities. Current Opinion in Structural Biology, 2020, 60, iii-iv.	5.7	1
18	Depletion interactions modulate the binding between disordered proteins in crowded environments. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13480-13489.	7.1	97

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19	Thermodynamics of the Interaction between Biological Polyelectrolyte-Like Disordered Proteins: From Binary Complexes to Oligomers. Biophysical Journal, 2020, 118, 215a.	0.5	2
20	The Dynamic Association of an IDP with a Folded Protein Without Localized Binding Sites or Persistent Contacts. Biophysical Journal, 2020, 118, 371a.	0.5	0
21	Resolving the Dynamics of the Double Stranded RNA Binding Protein TRBP. Biophysical Journal, 2020, 118, 225a.	0.5	0
22	Structure-Guided Design of a Peptide Lock for Modular Peptide Binders. ACS Chemical Biology, 2020, 15, 457-468.	3.4	8
23	Conformational Ensembles and Dynamics of Single-Stranded Nucleic Acids using High-Resolution Single-Molecule Fluorescence Spectroscopy. Biophysical Journal, 2020, 118, 334a.	0.5	0
24	Disordered RNA chaperones can enhance nucleic acid folding via local charge screening. Nature Communications, 2019, 10, 2453.	12.8	59
25	Highly Disordered 10:1 Complex of Two Anti-Apoptotic, Chromatin-Remodelling Intrinsically Disordered Proteins. Biophysical Journal, 2019, 116, 453a.	0.5	0
26	Probing the Dynamics and Interactions of Disordered Proteins with Single-Molecule Spectroscopy. Biophysical Journal, 2019, 116, 12a.	0.5	2
27	A Proline Switch Explains Kinetic Heterogeneity in a Coupled Folding and Binding Reaction. Biophysical Journal, 2019, 116, 179a.	0.5	0
28	Disordered RNA Chaperones Enhance Nucleic Acid Folding via Local Charge Screening. Biophysical Journal, 2019, 116, 468a.	0.5	1
29	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
30	Efficient conversion of chemical energy into mechanical work by Hsp70 chaperones. ELife, 2019, 8, .	6.0	26
31	Extreme disorder in an ultrahigh-affinity protein complex. Nature, 2018, 555, 61-66.	27.8	538
32	Inferring Properties of Disordered Chains From FRET Transfer Efficiencies. Biophysical Journal, 2018, 114, 367a.	0.5	1
33	Structural basis of si <scp>RNA</scp> recognition by <scp>TRBP</scp> doubleâ€stranded <scp>RNA</scp> binding domains. EMBO Journal, 2018, 37, .	7.8	43
34	Inferring properties of disordered chains from FRET transfer efficiencies. Journal of Chemical Physics, 2018, 148, 123329.	3.0	84
35	The Three-Fold Axis of the HIV-1 Capsid Lattice Is the Species-Specific Binding Interface for TRIM5Î±. Journal of Virology, 2018, 92, .	3.4	22
36	Preface: Special Topic on Single-Molecule Biophysics. Journal of Chemical Physics, 2018, 148, 123001.	3.0	5

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37	Simulation of FRET dyes allows quantitative comparison against experimental data. Journal of Chemical Physics, 2018, 148, 123321.	3.0	39
38	Conformational Plasticity of Hepatitis C Virus Core Protein Enables RNA-Induced Formation of Nucleocapsid-like Particles. Journal of Molecular Biology, 2018, 430, 2453-2467.	4.2	22
39	Accurate Transfer Efficiencies, Distance Distributions, and Ensembles of Unfolded and Intrinsically Disordered Proteins From Single-Molecule FRET. Methods in Enzymology, 2018, 611, 287-325.	1.0	46
40	Transition path times of coupled folding and binding reveal the formation of an encounter complex. Nature Communications, 2018, 9, 4708.	12.8	79
41	Tribute to William A. Eaton. Journal of Physical Chemistry B, 2018, 122, 10971-10973.	2.6	1
42	Origin of Internal Friction in Disordered Proteins Depends on Solvent Quality. Journal of Physical Chemistry B, 2018, 122, 11478-11487.	2.6	19
43	Dispersion Correction Alleviates Dye Stacking of Single-Stranded DNA and RNA in Simulations of Single-Molecule Fluorescence Experiments. Journal of Physical Chemistry B, 2018, 122, 11626-11639.	2.6	21
44	Local and Global Dynamics in Intrinsically Disordered Synuclein. Angewandte Chemie - International Edition, 2018, 57, 15262-15266.	13.8	49
45	Lokale und globale Dynamik im ungeordneten Synukleinâ€Protein. Angewandte Chemie, 2018, 130, 15482-15486.	2.0	0
46	Charge Interactions Can Dominate Coupled Folding and Binding on the Ribosome. Biophysical Journal, 2018, 115, 996-1006.	0.5	20
47	Mapping an Equilibrium Folding Intermediate of the Cytolytic Pore Toxin ClyA with Single-Molecule FRET. Journal of Physical Chemistry B, 2018, 122, 11251-11261.	2.6	19
48	Precision and accuracy of single-molecule FRET measurementsâ€”a multi-laboratory benchmark study. Nature Methods, 2018, 15, 669-676.	19.0	350
49	Comment on â€œInnovative scattering analysis shows that hydrophobic disordered proteins are expanded in waterâ€. Science, 2018, 361, .	12.6	36
50	Perspective: Chain dynamics of unfolded and intrinsically disordered proteins from nanosecond fluorescence correlation spectroscopy combined with single-molecule FRET. Journal of Chemical Physics, 2018, 149, 010901.	3.0	40
51	A proline switch explains kinetic heterogeneity in a coupled folding and binding reaction. Nature Communications, 2018, 9, 3332.	12.8	81
52	Curvature of designed armadillo repeat proteins allows modular peptide binding. Journal of Structural Biology, 2018, 201, 108-117.	2.8	12
53	Quantifying kinetics from time series of single-molecule FÃ¶rster resonance energy transfer efficiency histograms. Nanotechnology, 2017, 28, 114002.	2.6	11
54	Integrated view of internal friction in unfolded proteins from single-molecule FRET, contact quenching, theory, and simulations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1833-E1839.	7.1	94

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55	Integrated View of Internal Friction in Unfolded Proteins from Single-Molecule FRET, Contact Quenching, Theory, and Simulations. Biophysical Journal, 2017, 112, 318a.	0.5	0
56	Rapid Microfluidic Double-Jump Mixing Device for Single-Molecule Spectroscopy. Journal of the American Chemical Society, 2017, 139, 6062-6065.	13.7	18
57	Rapid Microfluidic Dilution for Singleâ€Molecule Spectroscopy of Lowâ€Affinity Biomolecular Complexes. Angewandte Chemie - International Edition, 2017, 56, 7126-7129.	13.8	18
58	Rapid Microfluidic Dilution for Singleâ€Molecule Spectroscopy of Lowâ€Affinity Biomolecular Complexes. Angewandte Chemie, 2017, 129, 7232-7235.	2.0	6
59	Resolving the Controversy between SAXS and FRET Measurements on Unfolded Proteins. Biophysical Journal, 2017, 112, 315a.	0.5	0
60	Single-molecule electrometry. Nature Nanotechnology, 2017, 12, 488-495.	31.5	75
61	Combining short- and long-range fluorescence reporters with simulations to explore the intramolecular dynamics of an intrinsically disordered protein. Journal of Chemical Physics, 2017, 147, 152708.	3.0	21
62	Structural Biology outside the box â€" inside the cell. Current Opinion in Structural Biology, 2017, 46, 110-121.	5.7	72
63	Single-Molecule FRET Spectroscopy and the Polymer Physics of Unfolded and Intrinsically Disordered Proteins. Annual Review of Biophysics, 2016, 45, 207-231.	10.0	271
64	Probing the Action of Chemical Denaturant on an Intrinsically Disordered Protein by Simulation and Experiment. Journal of the American Chemical Society, 2016, 138, 11702-11713.	13.7	121
65	Consistent View of Polypeptide Chain Expansion in Chemical Denaturants from Multiple Experimental Methods. Journal of the American Chemical Society, 2016, 138, 11714-11726.	13.7	171
66	Comprehensive structural and dynamical view of an unfolded protein from the combination of single-molecule FRET, NMR, and SAXS. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5389-98.	7.1	134
67	Soluble Oligomers of the Pore-forming Toxin Cytolysin A from Escherichia coli Are Off-pathway Products of Pore Assembly. Journal of Biological Chemistry, 2016, 291, 5652-5663.	3.4	10
68	Surprising Abundance of Misfolding during Refolding of Multidomain Proteins. Biophysical Journal, 2015, 108, 501a.	0.5	0
69	Quantitative Interpretation of FRET Experiments via Molecular Simulation: Force Field and Validation. Biophysical Journal, 2015, 108, 2721-2731.	0.5	59
70	Editorial overview: Biophysical and molecular biological methods: Structure, dynamics, and single molecules. Current Opinion in Structural Biology, 2015, 34, iv-vi.	5.7	0
71	Empirical Optimization of Interactions between Proteins and Chemical Denaturants in Molecular Simulations. Journal of Chemical Theory and Computation, 2015, 11, 5543-5553.	5.3	23
72	Excited-state annihilation reduces power dependence of single-molecule FRET experiments. Physical Chemistry Chemical Physics, 2015, 17, 32304-32315.	2.8	21

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73	Temperature-cycle microscopy reveals single-molecule conformational heterogeneity. Physical Chemistry Chemical Physics, 2015, 17, 6532-6544.	2.8	6
74	Single-molecule spectroscopy of protein conformational dynamics in live eukaryotic cells. Nature Methods, 2015, 12, 773-779.	19.0	217
75	Gas-Phase FRET Efficiency Measurements To Probe the Conformation of Mass-Selected Proteins. Analytical Chemistry, 2015, 87, 7559-7565.	6.5	50
76	The assembly dynamics of the cytolytic pore toxin ClyA. Nature Communications, 2015, 6, 6198.	12.8	83
77	Transient misfolding dominates multidomain protein folding. Nature Communications, 2015, 6, 8861.	12.8	97
78	Single-molecule spectroscopy reveals chaperone-mediated expansion of substrate protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13355-13360.	7.1	103
79	Role of Denatured-State Properties in Chaperonin Action Probed by Single-Molecule Spectroscopy. Biophysical Journal, 2014, 107, 2891-2902.	0.5	3
80	Cryogenic Colocalization Microscopy for Nanometerâ€Distance Measurements. ChemPhysChem, 2014, 15, 763-770.	2.1	46
81	Temperature-dependent solvation modulates the dimensions of disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5213-5218.	7.1	161
82	Taylor dispersion and the position-to-time conversion in microfluidic mixing devices. Lab on A Chip, 2014, 14, 219-228.	6.0	23
83	Single-Molecule Studies of Intrinsically Disordered Proteins. Chemical Reviews, 2014, 114, 3281-3317.	47.7	121
84	Single-molecule spectroscopy reveals polymer effects of disordered proteins in crowded environments. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4874-4879.	7.1	212
85	Characterization of Variants of the Pore-Forming Toxin ClyA from Escherichia coli Controlled by a Redox Switch. Biochemistry, 2014, 53, 6357-6369.	2.5	13
86	Experimental and Computational Study of BODIPY Dye-Labeled Cavitand Dynamics. Journal of the American Chemical Society, 2014, 136, 2441-2449.	13.7	22
87	Microfluidic mixer designed for performing single-molecule kinetics with confocal detection on timescales from milliseconds to minutes. Nature Protocols, 2013, 8, 1459-1474.	12.0	76
88	Probing the Polymeric Properties of Unfolded and Disordered Proteins with Single-Molecule Spectroscopy. Biophysical Journal, 2013, 104, 5a.	0.5	0
89	Rough passage across a barrier. Nature, 2013, 502, 632-633.	27.8	10
90	Single-Molecule Spectroscopy of Cold Denaturation and the Temperature-Induced Collapse of Unfolded Proteins. Journal of the American Chemical Society, 2013, 135, 14040-14043.	13.7	65

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91	Single-molecule FRET of protein structure and dynamics - a primer. Journal of Nanobiotechnology, 2013, 11, S2.	9.1	68
92	Single-molecule spectroscopy of protein folding dynamicsâ€"expanding scope and timescales. Current Opinion in Structural Biology, 2013, 23, 36-47.	5.7	252
93	Intramolecular Distances and Dynamics from the Combined Photon Statistics of Single-Molecule FRET and Photoinduced Electron Transfer. Journal of Physical Chemistry B, 2013, 117, 13015-13028.	2.6	47
94	Correction for MÃ¼ller-SpÃth et al., Charge interactions can dominate the dimensions of intrinsically disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16693-16693.	7.1	1
95	Single-molecule spectroscopy of the unexpected collapse of an unfolded protein at low pH. Journal of Chemical Physics, 2013, 139, 121930.	3.0	20
96	Polymer scaling laws of unfolded and intrinsically disordered proteins quantified with single-molecule spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16155-16160.	7.1	393
97	Quantifying internal friction in unfolded and intrinsically disordered proteins with single-molecule spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17800-17806.	7.1	282
98	Application of Confocal Single-Molecule FRET to Intrinsically Disordered Proteins. , 2012, 896, 21-45.		33
99	3.6 Single-Molecule Spectroscopy of Protein Folding. , 2012, , 115-137.		0
100	Localizing internal friction along the reaction coordinate of protein folding by combining ensemble and single-molecule fluorescence spectroscopy. Nature Communications, 2012, 3, 1195.	12.8	112
101	Quantifying heterogeneity and conformational dynamics from single molecule FRET of diffusing molecules: recurrence analysis of single particles (RASP). Physical Chemistry Chemical Physics, 2011, 13, 1857.	2.8	106
102	Temperature-cycle single-molecule FRET microscopy on polyprolines. Physical Chemistry Chemical Physics, 2011, 13, 1762-1769.	2.8	17
103	Structure and Dynamics in Protein Folding from Single Molecule Fluorescence Spectroscopy. Biophysical Journal, 2011, 100, 373a.	0.5	0
104	Single-molecule fluorescence reveals sequence-specific misfolding in multidomain proteins. Nature, 2011, 474, 662-665.	27.8	158
105	Structural Heterogeneity and Quantitative FRET Efficiency Distributions of Polyprolines through a Hybrid Atomistic Simulation and Monte Carlo Approach. PLoS ONE, 2011, 6, e19791.	2.5	108
106	Charge interactions can dominate the dimensions of intrinsically disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14609-14614.	7.1	453
107	Single-molecule spectroscopy of protein folding in a chaperonin cage. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11793-11798.	7.1	107
108	Free Energy Surfaces from Single-Distance Information. Journal of Physical Chemistry B, 2010, 114, 15227-15235.	2.6	28

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109	Single-molecule spectroscopy of the temperature-induced collapse of unfolded proteins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20740-20745.	7.1	211
110	Protein dynamics from single-molecule fluorescence intensity correlation functions. Journal of Chemical Physics, 2009, 131, 095102.	3.0	71
111	Probing Proteinâ€“Chaperone Interactions with Singleâ€Molecule Fluorescence Spectroscopy. Angewandte Chemie - International Edition, 2008, 47, 6184-6188.	13.8	68
112	Protein folding studied by single-molecule FRET. Current Opinion in Structural Biology, 2008, 18, 16-26.	5.7	622
113	Protein Folding and Dynamics from Optical Single Molecule Spectroscopy. Springer Series in Biophysics, 2008, , 181-215.	0.4	3
114	Unfolded Protein and Peptide Dynamics Investigated with Single-Molecule FRET and Correlation Spectroscopy from Picoseconds to Seconds. Journal of Physical Chemistry B, 2008, 112, 6137-6146.	2.6	161
115	Scalable time-correlated photon counting system with multiple independent input channels. Review of Scientific Instruments, 2008, 79, 123113.	1.3	47
116	Microfluidic Mixers for the Investigation of Rapid Protein Folding Kinetics Using Synchrotron Radiation Circular Dichroism Spectroscopy. Analytical Chemistry, 2008, 80, 9534-9541.	6.5	47
117	Single Molecule Spectroscopy: Instrumentation and Multiparameter Detection. Springer Series on Fluorescence, 2008, , 199-212.	0.8	0
118	Chapter 7. Single Molecule Spectroscopy in Protein Folding: From Ensembles to Single Molecules. RSC Biomolecular Sciences, 2008, , 139-160.	0.4	0
119	Application of Single Molecule FÃ¶rster Resonance Energy Transfer to Protein Folding. , 2007, 350, 115-138.		51
120	Effect of flexibility and cis residues in single-molecule FRET studies of polyproline. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18964-18969.	7.1	201
121	Mapping protein collapse with single-molecule fluorescence and kinetic synchrotron radiation circular dichroism spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 105-110.	7.1	208
122	Ultrafast dynamics of protein collapse from single-molecule photon statistics. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2655-2660.	7.1	334
123	Subpopulation-Resolved Photon Statistics of Single-Molecule Energy Transfer Dynamics. IEEE Journal of Selected Topics in Quantum Electronics, 2007, 13, 990-995.	2.9	9
124	Detection and Analysis of Protein Aggregation with Confocal Single Molecule Fluorescence Spectroscopy. Journal of Fluorescence, 2007, 17, 759-765.	2.5	49
125	Recognition of helical kinks by xeroderma pigmentosum group A protein triggers DNA excision repair. Nature Structural and Molecular Biology, 2006, 13, 278-284.	8.2	102
126	Single-Molecule Fluorescence Spectroscopy of Protein Folding. ChemPhysChem, 2005, 6, 1206-1220.	2.1	159

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127	Polyproline and the "spectroscopic ruler" revisited with single-molecule fluorescence. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2754-2759.	7.1	422
128	Two-State Folding Observed in Individual Protein Molecules. Journal of the American Chemical Society, 2004, 126, 14686-14687.	13.7	169
129	Kinetics of Intramolecular Contact Formation in a Denatured Protein. Journal of Molecular Biology, 2003, 332, 9-12.	4.2	59
130	Single-Molecule Measurement of Protein Folding Kinetics. Science, 2003, 301, 1233-1235.	12.6	380
131	Thermodynamic Analysis of the Dissociation of the Aldolase Tetramer Substituted at One or Both of the Subunit Interfaces. Biological Chemistry, 2003, 384, 1463-71.	2.5	16
132	Specific Labeling of Polypeptides at Amino-Terminal Cysteine Residues Using Cy5-benzyl Thioester. Bioconjugate Chemistry, 2002, 13, 1039-1043.	3.6	45
133	Role of Entropy in Protein Thermostability:Â Folding Kinetics of a Hyperthermophilic Cold Shock Protein at High Temperatures Using19F NMRâ€. Biochemistry, 2002, 41, 11670-11680.	2.5	64
134	Probing the free-energy surface for protein folding with single-molecule fluorescence spectroscopy. Nature, 2002, 419, 743-747.	27.8	852
135	Solution NMR structure of the cold-shock protein from the hyperthermophilic bacterium Thermotoga maritima. FEBS Journal, 2001, 268, 2527-2539.	0.2	97
136	Plasticity and steric strain in a parallel ?-helix: Rational mutations in the P22 tailspike protein. Proteins: Structure, Function and Bioinformatics, 2000, 39, 89-101.	2.6	15
137	Formation of Fibrous Aggregates from a Non-native Intermediate: The Isolated P22 Tailspike Î²-Helix Domain. Journal of Biological Chemistry, 1999, 274, 18589-18596.	3.4	38
138	Phage P22 tailspike protein: Removal of headâ€binding domain unmasks effects of folding mutations on nativeâ€state thermal stability. Protein Science, 1998, 7, 2223-2232.	7.6	40
139	A Reversibly Unfolding Fragment of P22 Tailspike Protein with Native Structure:Â The Isolated Î²-Helix Domainâ€. Biochemistry, 1998, 37, 9160-9168.	2.5	31
140	P22 tailspike folding mutants revisited: effects on the thermodynamic stability of the isolated Î²-helix domain. Journal of Molecular Biology, 1998, 281, 227-234.	4.2	38