

# 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	Probing the free-energy surface for protein folding with single-molecule fluorescence spectroscopy. <i>Nature</i> , 2002, 419, 743-747.	27.8	852
2	Protein folding studied by single-molecule FRET. <i>Current Opinion in Structural Biology</i> , 2008, 18, 16-26.	5.7	622
3	Extreme disorder in an ultrahigh-affinity protein complex. <i>Nature</i> , 2018, 555, 61-66.	27.8	538
4	Charge interactions can dominate the dimensions of intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14609-14614.	7.1	453
5	Polyproline and the "spectroscopic ruler" revisited with single-molecule fluorescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2754-2759.	7.1	422
6	Polymer scaling laws of unfolded and intrinsically disordered proteins quantified with single-molecule spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16155-16160.	7.1	393
7	Single-Molecule Measurement of Protein Folding Kinetics. <i>Science</i> , 2003, 301, 1233-1235.	12.6	380
8	Precision and accuracy of single-molecule FRET measurements—a multi-laboratory benchmark study. <i>Nature Methods</i> , 2018, 15, 669-676.	19.0	350
9	Ultrafast dynamics of protein collapse from single-molecule photon statistics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2655-2660.	7.1	334
10	Quantifying internal friction in unfolded and intrinsically disordered proteins with single-molecule spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17800-17806.	7.1	282
11	Single-Molecule FRET Spectroscopy and the Polymer Physics of Unfolded and Intrinsically Disordered Proteins. <i>Annual Review of Biophysics</i> , 2016, 45, 207-231.	10.0	271
12	Single-molecule spectroscopy of protein folding dynamics—expanding scope and timescales. <i>Current Opinion in Structural Biology</i> , 2013, 23, 36-47.	5.7	252
13	Single-molecule spectroscopy of protein conformational dynamics in live eukaryotic cells. <i>Nature Methods</i> , 2015, 12, 773-779.	19.0	217
14	Single-molecule spectroscopy reveals polymer effects of disordered proteins in crowded environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4874-4879.	7.1	212
15	Single-molecule spectroscopy of the temperature-induced collapse of unfolded proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20740-20745.	7.1	211
16	Mapping protein collapse with single-molecule fluorescence and kinetic synchrotron radiation circular dichroism spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 105-110.	7.1	208
17	Effect of flexibility and <i>cis</i> residues in single-molecule FRET studies of polyproline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18964-18969.	7.1	201
18	Consistent View of Polypeptide Chain Expansion in Chemical Denaturants from Multiple Experimental Methods. <i>Journal of the American Chemical Society</i> , 2016, 138, 11714-11726.	13.7	171

#	ARTICLE	IF	CITATIONS
19	Two-State Folding Observed in Individual Protein Molecules. <i>Journal of the American Chemical Society</i> , 2004, 126, 14686-14687.	13.7	169
20	Unfolded Protein and Peptide Dynamics Investigated with Single-Molecule FRET and Correlation Spectroscopy from Picoseconds to Seconds. <i>Journal of Physical Chemistry B</i> , 2008, 112, 6137-6146.	2.6	161
21	Temperature-dependent solvation modulates the dimensions of disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5213-5218.	7.1	161
22	Single-Molecule Fluorescence Spectroscopy of Protein Folding. <i>ChemPhysChem</i> , 2005, 6, 1206-1220.	2.1	159
23	Single-molecule fluorescence reveals sequence-specific misfolding in multidomain proteins. <i>Nature</i> , 2011, 474, 662-665.	27.8	158
24	FRET-based dynamic structural biology: Challenges, perspectives and an appeal for open-science practices. <i>ELife</i> , 2021, 10, .	6.0	152
25	Comprehensive structural and dynamical view of an unfolded protein from the combination of single-molecule FRET, NMR, and SAXS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5389-98.	7.1	134
26	Single-Molecule Studies of Intrinsically Disordered Proteins. <i>Chemical Reviews</i> , 2014, 114, 3281-3317.	47.7	121
27	Probing the Action of Chemical Denaturant on an Intrinsically Disordered Protein by Simulation and Experiment. <i>Journal of the American Chemical Society</i> , 2016, 138, 11702-11713.	13.7	121
28	Localizing internal friction along the reaction coordinate of protein folding by combining ensemble and single-molecule fluorescence spectroscopy. <i>Nature Communications</i> , 2012, 3, 1195.	12.8	112
29	Structural Heterogeneity and Quantitative FRET Efficiency Distributions of Polyprolines through a Hybrid Atomistic Simulation and Monte Carlo Approach. <i>PLoS ONE</i> , 2011, 6, e19791.	2.5	108
30	Single-molecule spectroscopy of protein folding in a chaperonin cage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11793-11798.	7.1	107
31	Quantifying heterogeneity and conformational dynamics from single molecule FRET of diffusing molecules: recurrence analysis of single particles (RASP). <i>Physical Chemistry Chemical Physics</i> , 2011, 13, 1857.	2.8	106
32	Single-molecule spectroscopy reveals chaperone-mediated expansion of substrate protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13355-13360.	7.1	103
33	Recognition of helical kinks by xeroderma pigmentosum group A protein triggers DNA excision repair. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 278-284.	8.2	102
34	Solution NMR structure of the cold-shock protein from the hyperthermophilic bacterium <i>Thermotoga maritima</i> . <i>FEBS Journal</i> , 2001, 268, 2527-2539.	0.2	97
35	Transient misfolding dominates multidomain protein folding. <i>Nature Communications</i> , 2015, 6, 8861.	12.8	97
36	Depletion interactions modulate the binding between disordered proteins in crowded environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13480-13489.	7.1	97

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37	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
38	Inferring properties of disordered chains from FRET transfer efficiencies. Journal of Chemical Physics, 2018, 148, 123329.	3.0	84
39	The assembly dynamics of the cytolytic pore toxin ClyA. Nature Communications, 2015, 6, 6198.	12.8	83
40	A proline switch explains kinetic heterogeneity in a coupled folding and binding reaction. Nature Communications, 2018, 9, 3332.	12.8	81
41	Transition path times of coupled folding and binding reveal the formation of an encounter complex. Nature Communications, 2018, 9, 4708.	12.8	79
42	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
43	Single-molecule electrometry. Nature Nanotechnology, 2017, 12, 488-495.	31.5	75
44	Polyelectrolyte interactions enable rapid association and dissociation in high-affinity disordered protein complexes. Nature Communications, 2020, 11, 5736.	12.8	74
45	Structural Biology outside the box " inside the cell. Current Opinion in Structural Biology, 2017, 46, 110-121.	5.7	72
46	Protein dynamics from single-molecule fluorescence intensity correlation functions. Journal of Chemical Physics, 2009, 131, 095102.	3.0	71
47	Binding without folding " the biomolecular function of disordered polyelectrolyte complexes. Current Opinion in Structural Biology, 2020, 60, 66-76.	5.7	71
48	Probing Protein"Chaperone Interactions with Single-Molecule Fluorescence Spectroscopy. Angewandte Chemie - International Edition, 2008, 47, 6184-6188.	13.8	68
49	Single-molecule FRET of protein structure and dynamics - a primer. Journal of Nanobiotechnology, 2013, 11, S2.	9.1	68
50	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
51	Role of Entropy in Protein Thermostability: Folding Kinetics of a Hyperthermophilic Cold Shock Protein at High Temperatures Using <sup>19</sup> F NMR. Biochemistry, 2002, 41, 11670-11680.	2.5	64
52	Kinetics of Intramolecular Contact Formation in a Denatured Protein. Journal of Molecular Biology, 2003, 332, 9-12.	4.2	59
53	Quantitative Interpretation of FRET Experiments via Molecular Simulation: Force Field and Validation. Biophysical Journal, 2015, 108, 2721-2731.	0.5	59
54	Disordered RNA chaperones can enhance nucleic acid folding via local charge screening. Nature Communications, 2019, 10, 2453.	12.8	59

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55	Application of Single Molecule Förster Resonance Energy Transfer to Protein Folding. , 2007, 350, 115-138.		51
56	Gas-Phase FRET Efficiency Measurements To Probe the Conformation of Mass-Selected Proteins. Analytical Chemistry, 2015, 87, 7559-7565.	6.5	50
57	Detection and Analysis of Protein Aggregation with Confocal Single Molecule Fluorescence Spectroscopy. Journal of Fluorescence, 2007, 17, 759-765.	2.5	49
58	Local and Global Dynamics in Intrinsically Disordered Synuclein. Angewandte Chemie - International Edition, 2018, 57, 15262-15266.	13.8	49
59	Global Structure of the Intrinsically Disordered Protein Tau Emerges from Its Local Structure. JACS, 2022, 144, 673-686.	7.9	48
60	Scalable time-correlated photon counting system with multiple independent input channels. Review of Scientific Instruments, 2008, 79, 123113.	1.3	47
61	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
62	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
63	Cryogenic Colocalization Microscopy for Nanometer Distance Measurements. ChemPhysChem, 2014, 15, 763-770.	2.1	46
64	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
65	Specific Labeling of Polypeptides at Amino-Terminal Cysteine Residues Using Cy5-benzyl Thioester. Bioconjugate Chemistry, 2002, 13, 1039-1043.	3.6	45
66	Structural basis of siRNA recognition by TRBP double-stranded RNA binding domains. EMBO Journal, 2018, 37, .	7.8	43
67	Phage P22 tailspike protein: Removal of head-binding domain unmasks effects of folding mutations on native state thermal stability. Protein Science, 1998, 7, 2223-2232.	7.6	40
68	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
69	Impact of In-Cell and In-Vitro Crowding on the Conformations and Dynamics of an Intrinsically Disordered Protein. Angewandte Chemie - International Edition, 2021, 60, 10724-10729.	13.8	40
70	Simulation of FRET dyes allows quantitative comparison against experimental data. Journal of Chemical Physics, 2018, 148, 123321.	3.0	39
71	P22 tailspike folding mutants revisited: effects on the thermodynamic stability of the isolated $\beta^2$ -helix domain. Journal of Molecular Biology, 1998, 281, 227-234.	4.2	38
72	Formation of Fibrous Aggregates from a Non-native Intermediate: The Isolated P22 Tailspike $\beta^2$ -Helix Domain. Journal of Biological Chemistry, 1999, 274, 18589-18596.	3.4	38

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73	Release of linker histone from the nucleosome driven by polyelectrolyte competition with a disordered protein. <i>Nature Chemistry</i> , 2022, 14, 224-231.	13.6	37
74	Comment on "Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water". <i>Science</i> , 2018, 361, .	12.6	36
75	Application of Confocal Single-Molecule FRET to Intrinsically Disordered Proteins. , 2012, 896, 21-45.		33
76	A Reversibly Unfolding Fragment of P22 Tailspike Protein with Native Structure: The Isolated $\beta^2$ -Helix Domain". <i>Biochemistry</i> , 1998, 37, 9160-9168.	2.5	31
77	Free Energy Surfaces from Single-Distance Information. <i>Journal of Physical Chemistry B</i> , 2010, 114, 15227-15235.	2.6	28
78	Impact of In-Cell and In-Vitro Crowding on the Conformations and Dynamics of an Intrinsically Disordered Protein. <i>Angewandte Chemie</i> , 2021, 133, 10819-10824.	2.0	27
79	Efficient conversion of chemical energy into mechanical work by Hsp70 chaperones. <i>ELife</i> , 2019, 8, .	6.0	26
80	Taylor dispersion and the position-to-time conversion in microfluidic mixing devices. <i>Lab on A Chip</i> , 2014, 14, 219-228.	6.0	23
81	Empirical Optimization of Interactions between Proteins and Chemical Denaturants in Molecular Simulations. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 5543-5553.	5.3	23
82	Experimental and Computational Study of BODIPY Dye-Labeled Cavitand Dynamics. <i>Journal of the American Chemical Society</i> , 2014, 136, 2441-2449.	13.7	22
83	The Three-Fold Axis of the HIV-1 Capsid Lattice Is the Species-Specific Binding Interface for TRIM5 $\alpha$ . <i>Journal of Virology</i> , 2018, 92, .	3.4	22
84	Conformational Plasticity of Hepatitis C Virus Core Protein Enables RNA-Induced Formation of Nucleocapsid-like Particles. <i>Journal of Molecular Biology</i> , 2018, 430, 2453-2467.	4.2	22
85	Excited-state annihilation reduces power dependence of single-molecule FRET experiments. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 32304-32315.	2.8	21
86	Combining short- and long-range fluorescence reporters with simulations to explore the intramolecular dynamics of an intrinsically disordered protein. <i>Journal of Chemical Physics</i> , 2017, 147, 152708.	3.0	21
87	Dispersion Correction Alleviates Dye Stacking of Single-Stranded DNA and RNA in Simulations of Single-Molecule Fluorescence Experiments. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11626-11639.	2.6	21
88	Resolving distance variations by single-molecule FRET and EPR spectroscopy using rotamer libraries. <i>Biophysical Journal</i> , 2021, 120, 4842-4858.	0.5	21
89	Single-molecule spectroscopy of the unexpected collapse of an unfolded protein at low pH. <i>Journal of Chemical Physics</i> , 2013, 139, 121930.	3.0	20
90	Charge Interactions Can Dominate Coupled Folding and Binding on the Ribosome. <i>Biophysical Journal</i> , 2018, 115, 996-1006.	0.5	20

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91	Transition Path Dynamics of a Dielectric Particle in a Bistable Optical Trap. <i>Physical Review Letters</i> , 2020, 125, 146001.	7.8	20
92	Origin of Internal Friction in Disordered Proteins Depends on Solvent Quality. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11478-11487.	2.6	19
93	Mapping an Equilibrium Folding Intermediate of the Cytolytic Pore Toxin ClyA with Single-Molecule FRET. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11251-11261.	2.6	19
94	Rapid Microfluidic Double-Jump Mixing Device for Single-Molecule Spectroscopy. <i>Journal of the American Chemical Society</i> , 2017, 139, 6062-6065.	13.7	18
95	Rapid Microfluidic Dilution for Single-Molecule Spectroscopy of Low-Affinity Biomolecular Complexes. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 7126-7129.	13.8	18
96	Single-molecule Detection of Ultrafast Biomolecular Dynamics with Nanophotonics. <i>Journal of the American Chemical Society</i> , 2022, 144, 52-56.	13.7	18
97	Temperature-cycle single-molecule FRET microscopy on polyprolines. <i>Physical Chemistry Chemical Physics</i> , 2011, 13, 1762-1769.	2.8	17
98	Thermodynamic Analysis of the Dissociation of the Aldolase Tetramer Substituted at One or Both of the Subunit Interfaces. <i>Biological Chemistry</i> , 2003, 384, 1463-71.	2.5	16
99	Plasticity and steric strain in a parallel $\alpha$ -helix: Rational mutations in the P22 tailspike protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 39, 89-101.	2.6	15
100	Characterization of Variants of the Pore-Forming Toxin ClyA from <i>Escherichia coli</i> Controlled by a Redox Switch. <i>Biochemistry</i> , 2014, 53, 6357-6369.	2.5	13
101	Apoptosis-inducing anti-HER2 agents operate through oligomerization-induced receptor immobilization. <i>Communications Biology</i> , 2021, 4, 762.	4.4	12
102	Curvature of designed armadillo repeat proteins allows modular peptide binding. <i>Journal of Structural Biology</i> , 2018, 201, 108-117.	2.8	12
103	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	1.6	12
104	Quantifying kinetics from time series of single-molecule Förster resonance energy transfer efficiency histograms. <i>Nanotechnology</i> , 2017, 28, 114002.	2.6	11
105	Rough passage across a barrier. <i>Nature</i> , 2013, 502, 632-633.	27.8	10
106	Soluble Oligomers of the Pore-forming Toxin Cytolysin A from <i>Escherichia coli</i> Are Off-pathway Products of Pore Assembly. <i>Journal of Biological Chemistry</i> , 2016, 291, 5652-5663.	3.4	10
107	Subpopulation-Resolved Photon Statistics of Single-Molecule Energy Transfer Dynamics. <i>IEEE Journal of Selected Topics in Quantum Electronics</i> , 2007, 13, 990-995.	2.9	9
108	Structure-Guided Design of a Peptide Lock for Modular Peptide Binders. <i>ACS Chemical Biology</i> , 2020, 15, 457-468.	3.4	8

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109	Structure, dynamics, and stability of the globular domain of human linker histone H1 and the role of positive charges. <i>Protein Science</i> , 2022, 31, 918-932.	7.6	7
110	Temperature-cycle microscopy reveals single-molecule conformational heterogeneity. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 6532-6544.	2.8	6
111	Rapid Microfluidic Dilution for Single-Molecule Spectroscopy of Low-Affinity Biomolecular Complexes. <i>Angewandte Chemie</i> , 2017, 129, 7232-7235.	2.0	6
112	Preface: Special Topic on Single-Molecule Biophysics. <i>Journal of Chemical Physics</i> , 2018, 148, 123001.	3.0	5
113	Slow Escape from a Helical Misfolded State of the Pore-Forming Toxin Cytolysin A. <i>Jacs Au</i> , 2021, 1, 1217-1230.	7.9	5
114	Labeling of Proteins for Single-Molecule Fluorescence Spectroscopy. <i>Methods in Molecular Biology</i> , 2022, 2376, 207-233.	0.9	5
115	Combining Rapid Microfluidic Mixing and Three-Color Single-Molecule FRET for Probing the Kinetics of Protein Conformational Changes. <i>Journal of Physical Chemistry B</i> , 2021, 125, 6617-6628.	2.6	4
116	Protein Folding and Dynamics from Optical Single Molecule Spectroscopy. <i>Springer Series in Biophysics</i> , 2008, , 181-215.	0.4	3
117	Role of Denatured-State Properties in Chaperonin Action Probed by Single-Molecule Spectroscopy. <i>Biophysical Journal</i> , 2014, 107, 2891-2902.	0.5	3
118	Probing the Dynamics and Interactions of Disordered Proteins with Single-Molecule Spectroscopy. <i>Biophysical Journal</i> , 2019, 116, 12a.	0.5	2
119	Thermodynamics of the Interaction between Biological Polyelectrolyte-Like Disordered Proteins: From Binary Complexes to Oligomers. <i>Biophysical Journal</i> , 2020, 118, 215a.	0.5	2
120	Correction for Moller-Spath et al., Charge interactions can dominate the dimensions of intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16693-16693.	7.1	1
121	Inferring Properties of Disordered Chains From FRET Transfer Efficiencies. <i>Biophysical Journal</i> , 2018, 114, 367a.	0.5	1
122	Tribute to William A. Eaton. <i>Journal of Physical Chemistry B</i> , 2018, 122, 10971-10973.	2.6	1
123	Disordered RNA Chaperones Enhance Nucleic Acid Folding via Local Charge Screening. <i>Biophysical Journal</i> , 2019, 116, 468a.	0.5	1
124	Editorial overview: Molecular interactions that drive folding and binding: new challenges and opportunities. <i>Current Opinion in Structural Biology</i> , 2020, 60, iii-iv.	5.7	1
125	Single Molecule Spectroscopy: Instrumentation and Multiparameter Detection. <i>Springer Series on Fluorescence</i> , 2008, , 199-212.	0.8	0
126	Structure and Dynamics in Protein Folding from Single Molecule Fluorescence Spectroscopy. <i>Biophysical Journal</i> , 2011, 100, 373a.	0.5	0



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127	3.6 Single-Molecule Spectroscopy of Protein Folding. , 2012, , 115-137.		0
128	Probing the Polymeric Properties of Unfolded and Disordered Proteins with Single-Molecule Spectroscopy. Biophysical Journal, 2013, 104, 5a.	0.5	0
129	Surprising Abundance of Misfolding during Refolding of Multidomain Proteins. Biophysical Journal, 2015, 108, 501a.	0.5	0
130	Editorial overview: Biophysical and molecular biological methods: Structure, dynamics, and single molecules. Current Opinion in Structural Biology, 2015, 34, iv-vi.	5.7	0
131	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
132	Resolving the Controversy between SAXS and FRET Measurements on Unfolded Proteins. Biophysical Journal, 2017, 112, 315a.	0.5	0
133	Lokale und globale Dynamik im ungeordneten Synukleinâ€Protein. Angewandte Chemie, 2018, 130, 15482-15486.	2.0	0
134	Highly Disordered 10:1 Complex of Two Anti-Apoptotic, Chromatin-Remodelling Intrinsically Disordered Proteins. Biophysical Journal, 2019, 116, 453a.	0.5	0
135	A Proline Switch Explains Kinetic Heterogeneity in a Coupled Folding and Binding Reaction. Biophysical Journal, 2019, 116, 179a.	0.5	0
136	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
137	Resolving the Dynamics of the Double Stranded RNA Binding Protein TRBP. Biophysical Journal, 2020, 118, 225a.	0.5	0
138	Conformational Ensembles and Dynamics of Single-Stranded Nucleic Acids using High-Resolution Single-Molecule Fluorescence Spectroscopy. Biophysical Journal, 2020, 118, 334a.	0.5	0
139	Molecular Origins of Free Energies Associated with Complex Interactions of Biological Polyelectrolyte-Like Disordered Proteins. Biophysical Journal, 2021, 120, 286a.	0.5	0
140	Chapter 7. Single Molecule Spectroscopy in Protein Folding: From Ensembles to Single Molecules. RSC Biomolecular Sciences, 2008, , 139-160.	0.4	0