

Osman Bilsel

List of Publications by Year in descending order

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68
papers

2,727
citations

186265

28
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175258

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69
docs citations

69
times ranked

3396
citing authors

#	ARTICLE	IF	CITATIONS
1	Dye-Sensitized Core/Active Shell Upconversion Nanoparticles for Optogenetics and Bioimaging Applications. <i>ACS Nano</i> , 2016, 10, 1060-1066.	14.6	395
2	Engineering the Upconversion Nanoparticle Excitation Wavelength: Cascade Sensitization of Triâ€doped Upconversion Colloidal Nanoparticles at 800 nm. <i>Advanced Optical Materials</i> , 2013, 1, 644-650.	7.3	321
3	Probing the Folding Mechanism of a Leucine Zipper Peptide by Stopped-Flow Circular Dichroism Spectroscopy. <i>Biochemistry</i> , 1995, 34, 12812-12819.	2.5	204
4	Folding Mechanism of the Î±-Subunit of Tryptophan Synthase, an Î±/Î² Barrel Protein:â€ Global Analysis Highlights the Interconversion of Multiple Native, Intermediate, and Unfolded Forms through Parallel Channels. <i>Biochemistry</i> , 1999, 38, 1018-1029.	2.5	127
5	Tailoring dye-sensitized upconversion nanoparticle excitation bands towards excitation wavelength selective imaging. <i>Nanoscale</i> , 2015, 7, 18424-18428.	5.6	95
6	Fluorogenic probes for monitoring peptide binding to class II MHC proteins in living cells. <i>Nature Chemical Biology</i> , 2007, 3, 222-228.	8.0	85
7	Electronic states and optical properties of porphyrins in van der Waals contact: thorium(IV) sandwich complexes. <i>Journal of the American Chemical Society</i> , 1992, 114, 6528-6538.	13.7	81
8	The progressive development of structure and stability during the equilibrium folding of the Î± subunit of tryptophan synthase from <i>Escherichia coli</i> . <i>Protein Science</i> , 1999, 8, 1623-1635.	7.6	75
9	Microsecond Hydrophobic Collapse in the Folding of <i>Escherichia coli</i> Dihydrofolate Reductase, an Î±/Î²-Type Protein. <i>Journal of Molecular Biology</i> , 2007, 368, 219-229.	4.2	75
10	Picosecond relaxation of strongly coupled porphyrin dimers. <i>The Journal of Physical Chemistry</i> , 1990, 94, 3508-3512.	2.9	74
11	Barriers in protein folding reactions. <i>Advances in Protein Chemistry</i> , 2000, 53, 153-207.	4.4	64
12	Microsecond acquisition of heterogeneous structure in the folding of a TIM barrel protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13367-13372.	7.1	63
13	A microchannel solution mixer for studying microsecond protein folding reactions. <i>Review of Scientific Instruments</i> , 2005, 76, 014302.	1.3	62
14	Sub-millisecond time-resolved SAXS using a continuous-flow mixer and X-ray microbeam. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 820-825.	2.4	61
15	Metal Deficiency Increases Aberrant Hydrophobicity of Mutant Superoxide Dismutases That Cause Amyotrophic Lateral Sclerosis. <i>Journal of Biological Chemistry</i> , 2009, 284, 27746-27758.	3.4	60
16	Mapping the Folding Free Energy Surface for Metal-free Human Cu,Zn Superoxide Dismutase. <i>Journal of Molecular Biology</i> , 2006, 364, 1084-1102.	4.2	56
17	Observation of a new low-energy fluorescent 1(π,π^*) excited state in strongly coupled porphyrin dimers. <i>Journal of the American Chemical Society</i> , 1990, 112, 4075-4077.	13.7	55
18	Minireview: Structural insights into early folding events using continuousâ€flow timeâ€resolved smallâ€angle Xâ€ray scattering. <i>Biopolymers</i> , 2011, 95, 550-558.	2.4	50

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19	Unfolded states under folding conditions accommodate sequence-specific conformational preferences with random coil-like dimensions. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12301-12310.	7.1	50
20	Methods for analysis of size-exclusion chromatography–small-angle X-ray scattering and reconstruction of protein scattering. Journal of Applied Crystallography, 2015, 48, 1102-1113.	4.5	46
21	Metal-Free ALS Variants of Dimeric Human Cu,Zn-Superoxide Dismutase Have Enhanced Populations of Monomeric Species. PLoS ONE, 2010, 5, e10064.	2.5	45
22	Molecular dimensions and their distributions in early folding intermediates. Current Opinion in Structural Biology, 2006, 16, 86-93.	5.7	44
23	Microsecond Barrier-Limited Chain Collapse Observed by Time-Resolved FRET and SAXS. Journal of Molecular Biology, 2014, 426, 1980-1994.	4.2	43
24	Electronic states and (ϵ , ϵ^*) absorption and emission characteristics of strongly coupled porphyrin dimers: sandwich complexes of HfIV and ZrIV. Chemical Physics Letters, 1991, 182, 415-421.	2.6	41
25	Time-Resolved Fluorescence Anisotropy Study of the Refolding Reaction of the α -Subunit of Tryptophan Synthase Reveals Nonmonotonic Behavior of the Rotational Correlation Time. Biochemistry, 1999, 38, 4177-4187.	2.5	40
26	Ultrafast electronic deactivation and vibrational dynamics of photoexcited uranium(IV) porphyrin sandwich complexes. The Journal of Physical Chemistry, 1993, 97, 7216-7221.	2.9	37
27	Apparent Radii of the Native, Stable Intermediates and Unfolded Conformers of the α -Subunit of Tryptophan Synthase from <i>E. coli</i> , a TIM Barrel Protein. Biochemistry, 1999, 38, 13367-13378.	2.5	37
28	Microsecond Subdomain Folding in Dihydrofolate Reductase. Journal of Molecular Biology, 2011, 410, 329-342.	4.2	33
29	The Folding Free-Energy Surface of HIV-1 Protease: Insights into the Thermodynamic Basis for Resistance to Inhibitors. Journal of Molecular Biology, 2009, 387, 1002-1016.	4.2	26
30	Native State Conformational Heterogeneity of HP35 Revealed by Time-Resolved FRET. Journal of Physical Chemistry B, 2012, 116, 10631-10638.	2.6	26
31	Transient Kinetic Analysis of SWR1C-Catalyzed H2A.Z Deposition Unravels the Impact of Nucleosome Dynamics and the Asymmetry of Histone Exchange. Cell Reports, 2019, 27, 374-386.e4.	6.4	26
32	Modulation of frustration in folding by sequence permutation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10562-10567.	7.1	24
33	Topology and Sequence in the Folding of a TIM Barrel Protein: Global Analysis Highlights Partitioning between Transient Off-pathway and Stable On-pathway Folding Intermediates in the Complex Folding Mechanism of a $(\beta^2)_8$ Barrel of Unknown Function from <i>B. subtilis</i> . Journal of Molecular Biology, 2007, 372, 236-253.	4.2	22
34	Advances in turbulent mixing techniques to study microsecond protein folding reactions. Biopolymers, 2013, 99, 888-896.	2.4	22
35	ALS-linked PFN1 variants exhibit loss and gain of functions in the context of formin-induced actin polymerization. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
36	Frustration and folding of a TIM barrel protein. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16378-16383.	7.1	18

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37	SecA Folding Kinetics: A Large Dimeric Protein Rapidly Forms Multiple Native States. <i>Journal of Molecular Biology</i> , 2004, 341, 199-214.	4.2	15
38	Non-Native Structure Appears in Microseconds during the Folding of <i>E. coli</i> RNase H. <i>Journal of Molecular Biology</i> , 2015, 427, 443-453.	4.2	15
39	Structural Organization and Dynamics of Homodimeric Cytohesin Family Arf GTPase Exchange Factors in Solution and on Membranes. <i>Structure</i> , 2019, 27, 1782-1797.e7.	3.3	14
40	Structural Dynamics Control Allosteric Activation of Cytohesin Family Arf GTPase Exchange Factors. <i>Structure</i> , 2018, 26, 106-117.e6.	3.3	11
41	Atomistic structural ensemble refinement reveals non-native structure stabilizes a sub-millisecond folding intermediate of CheY. <i>Scientific Reports</i> , 2017, 7, 44116.	3.3	10
42	Sequential Closure of Loop Structures Forms the Folding Nucleus during the Refolding Transition of the <i>Escherichia coli</i> Adenylate Kinase Molecule. <i>Biochemistry</i> , 2016, 55, 79-91.	2.5	8
43	Selenomethionine, p-cyanophenylalanine pairs provide a convenient, sensitive, non-perturbing fluorescent probe of local helical structure. <i>Chemical Communications</i> , 2016, 52, 2055-2058.	4.1	8
44	In Situ Measurements of Polymer Micellization Kinetics with Millisecond Temporal Resolution. <i>Macromolecules</i> , 2019, 52, 3151-3157.	4.8	8
45	Computer design of microfluidic mixers for protein/RNA folding studies. <i>PLoS ONE</i> , 2018, 13, e0198534.	2.5	7
46	SAXS/SANS Probe of Intermolecular Interactions in Concentrated Protein Solutions. <i>Biophysical Journal</i> , 2014, 106, 771-773.	0.5	6
47	Nonnative structure in a peptide model of the unfolded state of superoxide dismutase 1 (SOD1): Implications for ALS-linked aggregation. <i>Journal of Biological Chemistry</i> , 2019, 294, 13708-13717.	3.4	6
48	Selenomethionine Quenching of Tryptophan Fluorescence Provides a Simple Probe of Protein Structure. <i>Biochemistry</i> , 2017, 56, 1085-1094.	2.5	4
49	Creating round focused micro-jets from rectangular nozzles. <i>Journal of Mechanical Science and Technology</i> , 2019, 33, 4281-4289.	1.5	3
50	High-speed velocimetry in microfluidic protein mixers using confocal fluorescence decay microscopy. <i>Experiments in Fluids</i> , 2018, 59, 1.	2.4	2
51	Friction-Limited Folding of Disulfide-Reduced Monomeric SOD1. <i>Biophysical Journal</i> , 2020, 118, 1992-2000.	0.5	2
52	Simulations and Experiments Provide a Convergent View of Protein Unfolded States under Folding Conditions. <i>Biophysical Journal</i> , 2017, 112, 315a.	0.5	1
53	Microfluidic Turbulent Mixers, Time Resolved SAXS and Folding Intermediates of CheY. <i>Biophysical Journal</i> , 2017, 112, 61a.	0.5	1
54	Probing Microsecond Reactions with Microfluidic Mixers and TCSPC. <i>Springer Series in Chemical Physics</i> , 2015, , 357-384.	0.2	1

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55	Time-resolved SAXS using continuous-flow microfluidic mixers. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a449-a449.	0.1	1
56	1P106 Submillisecond Folding of Escherichia coli Dihydrofolate Reductase Monitored by Time-Resolved Fluorescence Spectroscopy(3. Protein folding and misfolding (I),Poster Session,Abstract,Meeting) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
57	Merging microsecond mixing and time-correlated single-photon counting: using time-resolved FRET and time-resolved anisotropy to probe early events in protein folding. Proceedings of SPIE, 2007, , .	0.8	0
58	Observing and Characterizing Early Folding Intermediates of E.Coli Rnase H using Kinetic and Equilibrium Approaches. Biophysical Journal, 2014, 106, 246a.	0.5	0
59	Fast Closuer of Long Loops at the Initiation of a Protein Folding Pathway. Biophysical Journal, 2016, 110, 390a.	0.5	0
60	Examination of the Oligomerization Mechanism of SOD1 In Vitro and in Live Cells. Biophysical Journal, 2017, 112, 316a.	0.5	0
61	The Transient Collapsed Ensemble: TO of the Folding Pathway. Biophysical Journal, 2019, 116, 335a.	0.5	0
62	Protein Unfolded States are Characterized by the Duality of Sequence-Specific Conformational Preferences and Ensemble-Averaged Features of Canonical Random Coils. Biophysical Journal, 2019, 116, 199a-200a.	0.5	0
63	Heterogeneous folding and stretched kinetics. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18915-18917.	7.1	0
64	2H1536 Microsecond Subdomain Folding in Dihydrofolate Reductase(Protein: Property 3,The 48th) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
65	Sequence and Misfolding in the Ancient TIM Barrel Motif. FASEB Journal, 2015, 29, 882.12.	0.5	0
66	SAXS: a versatile tool to study biological macromolecules in solution. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a265-a265.	0.1	0
67	Nonâ€Native Structure Present in the Unfolded Ensemble May Initiate Aggregation of ALS variants of Superoxide Dismutase (SOD1). FASEB Journal, 2018, 32, .	0.5	0
68	Increasing Versatility of Small Angle Xâ€Ray Scattering. FASEB Journal, 2020, 34, 1-1.	0.5	0