

Osman Bilsel

List of Publications by Year in descending order

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68
papers

2,727
citations

186265

28
h-index

175258

52
g-index

69
all docs

69
docs citations

69
times ranked

3396
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Friction-Limited Folding of Disulfide-Reduced Monomeric SOD1. Biophysical Journal, 2020, 118, 1992-2000.	0.5	2
3	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
4	Increasing Versatility of Small Angle X-Ray Scattering. FASEB Journal, 2020, 34, 1-1.	0.5	0
5	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
6	Nonnative structure in a peptide model of the unfolded state of superoxide dismutase 1 (SOD1): Implications for ALS-linked aggregation. Journal of Biological Chemistry, 2019, 294, 13708-13717.	3.4	6
7	Structural Organization and Dynamics of Homodimeric Cytohesin Family Arf GTPase Exchange Factors in Solution and on Membranes. Structure, 2019, 27, 1782-1797.e7.	3.3	14
8	Creating round focused micro-jets from rectangular nozzles. Journal of Mechanical Science and Technology, 2019, 33, 4281-4289.	1.5	3
9	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
10	The Transient Collapsed Ensemble: TO of the Folding Pathway. Biophysical Journal, 2019, 116, 335a.	0.5	0
11	In Situ Measurements of Polymer Micellization Kinetics with Millisecond Temporal Resolution. Macromolecules, 2019, 52, 3151-3157.	4.8	8
12	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
13	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
14	Structural Dynamics Control Allosteric Activation of Cytohesin Family Arf GTPase Exchange Factors. Structure, 2018, 26, 106-117.e6.	3.3	11
15	High-speed velocimetry in microfluidic protein mixers using confocal fluorescence decay microscopy. Experiments in Fluids, 2018, 59, 1.	2.4	2
16	Computer design of microfluidic mixers for protein/RNA folding studies. PLoS ONE, 2018, 13, e0198534.	2.5	7
17	Non-Native Structure Present in the Unfolded Ensemble May Initiate Aggregation of ALS variants of Superoxide Dismutase (SOD1). FASEB Journal, 2018, 32, .	0.5	0
18	Time-resolved SAXS using continuous-flow microfluidic mixers. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a449-a449.	0.1	1

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19	Selenomethionine Quenching of Tryptophan Fluorescence Provides a Simple Probe of Protein Structure. <i>Biochemistry</i> , 2017, 56, 1085-1094.	2.5	4
20	Simulations and Experiments Provide a Convergent View of Protein Unfolded States under Folding Conditions. <i>Biophysical Journal</i> , 2017, 112, 315a.	0.5	1
21	Examination of the Oligomerization Mechanism of SOD1 In Vitro and in Live Cells. <i>Biophysical Journal</i> , 2017, 112, 316a.	0.5	0
22	Microfluidic Turbulent Mixers, Time Resolved SAXS and Folding Intermediates of CheY. <i>Biophysical Journal</i> , 2017, 112, 61a.	0.5	1
23	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
24	SAXS: a versatile tool to study biological macromolecules in solution. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a265-a265.	0.1	0
25	Fast Closures of Long Loops at the Initiation of a Protein Folding Pathway. <i>Biophysical Journal</i> , 2016, 110, 390a.	0.5	0
26	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
27	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
28	Dye-Sensitized Core/Active Shell Upconversion Nanoparticles for Optogenetics and Bioimaging Applications. <i>ACS Nano</i> , 2016, 10, 1060-1066.	14.6	395
29	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
30	Methods for analysis of size-exclusion chromatography–small-angle X-ray scattering and reconstruction of protein scattering. <i>Journal of Applied Crystallography</i> , 2015, 48, 1102-1113.	4.5	46
31	Tailoring dye-sensitized upconversion nanoparticle excitation bands towards excitation wavelength selective imaging. <i>Nanoscale</i> , 2015, 7, 18424-18428.	5.6	95
32	Probing Microsecond Reactions with Microfluidic Mixers and TCSPC. <i>Springer Series in Chemical Physics</i> , 2015, , 357-384.	0.2	1
33	Sequence and Misfolding in the Ancient TIM Barrel Motif. <i>FASEB Journal</i> , 2015, 29, 882.12.	0.5	0
34	Observing and Characterizing Early Folding Intermediates of <i>E. coli</i> RNase H using Kinetic and Equilibrium Approaches. <i>Biophysical Journal</i> , 2014, 106, 246a.	0.5	0
35	SAXS/SANS Probe of Intermolecular Interactions in Concentrated Protein Solutions. <i>Biophysical Journal</i> , 2014, 106, 771-773.	0.5	6
36	Modulation of frustration in folding by sequence permutation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10562-10567.	7.1	24

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37	Microsecond Barrier-Limited Chain Collapse Observed by Time-Resolved FRET and SAXS. <i>Journal of Molecular Biology</i> , 2014, 426, 1980-1994.	4.2	43
38	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
39	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
40	Advances in turbulent mixing techniques to study microsecond protein folding reactions. <i>Biopolymers</i> , 2013, 99, 888-896.	2.4	22
41	Native State Conformational Heterogeneity of HP35 Revealed by Time-Resolved FRET. <i>Journal of Physical Chemistry B</i> , 2012, 116, 10631-10638.	2.6	26
42	Microsecond Subdomain Folding in Dihydrofolate Reductase. <i>Journal of Molecular Biology</i> , 2011, 410, 329-342.	4.2	33
43	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
44	2H1536 Microsecond Subdomain Folding in Dihydrofolate Reductase(Protein: Property 3,The 48th) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	8.1	0
45	Metal-Free ALS Variants of Dimeric Human Cu,Zn-Superoxide Dismutase Have Enhanced Populations of Monomeric Species. <i>PLoS ONE</i> , 2010, 5, e10064.	2.5	45
46	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
47	The Folding Free-Energy Surface of HIV-1 Protease: Insights into the Thermodynamic Basis for Resistance to Inhibitors. <i>Journal of Molecular Biology</i> , 2009, 387, 1002-1016.	4.2	26
48	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
49	Merging microsecond mixing and time-correlated single-photon counting: using time-resolved FRET and time-resolved anisotropy to probe early events in protein folding. <i>Proceedings of SPIE</i> , 2007, , .	0.8	0
50	Microsecond Hydrophobic Collapse in the Folding of Escherichia coli Dihydrofolate Reductase, an Î±/Î²-Type Protein. <i>Journal of Molecular Biology</i> , 2007, 368, 219-229.	4.2	75
51	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 (Î±/Î²) ₈ Barrel of Unknown Function from <i>B. subtilis</i> . <i>Journal of Molecular Biology</i> , 2007, 372, 236-253.	4.2	22
52	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
53	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
54	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	8.1	0

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55	Molecular dimensions and their distributions in early folding intermediates. <i>Current Opinion in Structural Biology</i> , 2006, 16, 86-93.	5.7	44
56	A microchannel solution mixer for studying microsecond protein folding reactions. <i>Review of Scientific Instruments</i> , 2005, 76, 014302.	1.3	62
57	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
58	Barriers in protein folding reactions. <i>Advances in Protein Chemistry</i> , 2000, 53, 153-207.	4.4	64
59	The progressive development of structure and stability during the equilibrium folding of the $\hat{I}\pm$ subunit of tryptophan synthase from <i>Escherichia coli</i> . <i>Protein Science</i> , 1999, 8, 1623-1635.	7.6	75
60	Time-Resolved Fluorescence Anisotropy Study of the Refolding Reaction of the $\hat{I}\pm$ -Subunit of Tryptophan Synthase Reveals Nonmonotonic Behavior of the Rotational Correlation Time. <i>Biochemistry</i> , 1999, 38, 4177-4187.	2.5	40
61	Apparent Radii of the Native, Stable Intermediates and Unfolded Conformers of the $\hat{I}\pm$ -Subunit of Tryptophan Synthase from <i>E. coli</i> , a TIM Barrel Protein. <i>Biochemistry</i> , 1999, 38, 13367-13378.	2.5	37
62	Folding Mechanism of the $\hat{I}\pm$ -Subunit of Tryptophan Synthase, an $\hat{I}\pm/\hat{I}^2$ Barrel Protein: 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
63	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
64	Ultrafast electronic deactivation and vibrational dynamics of photoexcited uranium(IV) porphyrin sandwich complexes. <i>The Journal of Physical Chemistry</i> , 1993, 97, 7216-7221.	2.9	37
65	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
66	Electronic states and ($\hat{I}\epsilon$, $\hat{I}\epsilon^*$) absorption and emission characteristics of strongly coupled porphyrin dimers: sandwich complexes of HfIV and ZrIV. <i>Chemical Physics Letters</i> , 1991, 182, 415-421.	2.6	41
67	Observation of a new low-energy fluorescent $1(\pi, \pi^*)$ excited state in strongly coupled porphyrin dimers. <i>Journal of the American Chemical Society</i> , 1990, 112, 4075-4077.	13.7	55
68	Picosecond relaxation of strongly coupled porphyrin dimers. <i>The Journal of Physical Chemistry</i> , 1990, 94, 3508-3512.	2.9	74