Jayant B Udgaonkar

List of Publications by Year
in descending order

112 papers	4,846 citations	81743 39 h-index	114278 63 g-index
117 all docs	117 docs citations	117 times ranked	3276 citing authors

#	Article	IF	Citations
1	Heterogeneity in Protein Folding and Unfolding Reactions. Chemical Reviews, 2022, 122, 8911-8935.	23.0	25
2	Elongation of Fibrils Formed by a Tau Fragment is Inhibited by a Transient Dimeric Intermediate. Journal of Physical Chemistry B, 2022, 126, 3385-3397.	1.2	1
3	Mapping Distinct Sequences of Structure Formation Differentiating Multiple Folding Pathways of a Small Protein. Journal of the American Chemical Society, 2021, 143, 1447-1457.	6.6	9
4	The Lys 280â€‰â†’â€‰Gln mutation mimicking diseaseâ€linked acetylation of Lys 280 in tau extends the structural core of fibrils and modulates their catalytic properties. Protein Science, 2021, 30, 785-803.	3.1	4
5	Resolving Site-Specific Heterogeneity of the Unfolded State under Folding Conditions. Journal of Physical Chemistry Letters, 2021, 12, 3295-3302.	2.1	2
6	Structural Characterization of the Cooperativity of Unfolding of a Heterodimeric Protein using Hydrogen Exchange-Mass Spectrometry. Journal of Molecular Biology, 2021, 433, 167268.	2.0	2
7	Microsecond Dynamics During the Binding-induced Folding of an Intrinsically Disordered Protein. Journal of Molecular Biology, 2021, 433, 167254.	2.0	3
8	Destabilization of polar interactions in the prion protein triggers misfolding and oligomerization. Protein Science, 2021, 30, 2258-2271.	3.1	5
9	Observation of Continuous Contraction and a Metastable Misfolded State during the Collapse and Folding of a Small Protein. Journal of Molecular Biology, 2019, 431, 3814-3826.	2.0	11
10	Binding-induced folding under unfolding conditions: Switching between induced fit and conformational selection mechanisms. Journal of Biological Chemistry, 2019, 294, 16942-16952.	1.6	19
11	A five-residue motif for the design of domain swapping in proteins. Nature Communications, 2019, 10, 452.	5.8	37
12	Mechanistic approaches to understand the prion-like propagation of aggregates of the human tau protein. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 922-932.	1.1	8
13	Introducing the Mechanical Forces in Biochemistry Special Issue. Biochemistry, 2019, 58, 4655-4656.	1.2	0
14	Ruggedness in the Free Energy Landscape Dictates Misfolding of the Prion Protein. Journal of Molecular Biology, 2019, 431, 807-824.	2.0	16
15	Monitoring site-specific conformational changes in real-time reveals a misfolding mechanism of the prion protein. ELife, 2019, 8, .	2.8	18
16	Microsecond sub-domain motions and the folding and misfolding of the mouse prion protein. ELife, 2019, 8, .	2.8	16
17	Mechanism of aggregation and membrane interactions of mammalian prion protein. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 1927-1935.	1.4	37
18	Site-specific time-resolved FRET reveals local variations in the unfolding mechanism in an apparently two-state protein unfolding transition. Physical Chemistry Chemical Physics, 2018, 20, 3216-3232.	1.3	21

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19	Mechanistic and Structural Origins of the Asymmetric Barrier to Prion-like Cross-Seeding between Tau-3R and Tau-4R. Journal of Molecular Biology, 2018, 430, 5304-5312.	2.0	18
20	The Osmolyte TMAO Modulates Protein Folding Cooperativity by Altering Global Protein Stability. Biochemistry, 2018, 57, 5851-5863.	1.2	21
21	Structural mechanisms of oligomer and amyloid fibril formation by the prion protein. Chemical Communications, 2018, 54, 6230-6242.	2.2	20
22	Identification and Structural Characterization of the Precursor Conformation of the Prion Protein which Directly Initiates Misfolding and Oligomerization. Journal of Molecular Biology, 2017, 429, 886-899.	2.0	22
23	Salt-Mediated Oligomerization of the Mouse Prion Protein Monitored by Real-Time NMR. Journal of Molecular Biology, 2017, 429, 1852-1872.	2.0	26
24	The G126V Mutation in the Mouse Prion Protein Hinders Nucleation-Dependent Fibril Formation by Slowing Initial Fibril Growth and by Increasing the Critical Concentration. Biochemistry, 2017, 56, 5931-5942.	1.2	20
25	Chemical Denaturants Smoothen Ruggedness on the Free Energy Landscape of Protein Folding. Biochemistry, 2017, 56, 4053-4063.	1.2	6
26	Aminoâ€acid composition after loop deletion drives domain swapping. Protein Science, 2017, 26, 1994-2002.	3.1	13
27	Expression and purification of single cysteine-containing mutant variants of the mouse prion protein by oxidative refolding. Protein Expression and Purification, 2017, 140, 1-7.	0.6	3
28	Modulation of the extent of structural heterogeneity in Î±-synuclein fibrils by the small molecule thioflavin T. Journal of Biological Chemistry, 2017, 292, 16891-16903.	1.6	28
29	Modulation of the Extent of Cooperative Structural Change During Protein Folding by Chemical Denaturant. Journal of Physical Chemistry B, 2017, 121, 8263-8275.	1.2	10
30	Stepwise Assembly of Î²-Sheet Structure during the Folding of an SH3 Domain Revealed by a Pulsed Hydrogen Exchange Mass Spectrometry Study. Biochemistry, 2017, 56, 3754-3769.	1.2	11
31	A Dry Transition State More Compact Than the Native State Is Stabilized by Non-Native Interactions during the Unfolding of a Small Protein. Biochemistry, 2017, 56, 3699-3703.	1.2	5
32	Secondary Structural Change Can Occur Diffusely and Not Modularly during Protein Folding and Unfolding Reactions. Journal of the American Chemical Society, 2016, 138, 5866-5878.	6.6	18
33	Microsecond Rearrangements of Hydrophobic Clusters in an Initially Collapsed Globule Prime Structure Formation during the Folding of a Small Protein. Journal of Molecular Biology, 2016, 428, 3102-3117.	2.0	28
34	How cooperative are protein folding and unfolding transitions?. Protein Science, 2016, 25, 1924-1941.	3.1	70
35	Pathogenic Mutations within the Disordered Palindromic Region of the Prion Protein Induce Structure Therein and Accelerate the Formation of Misfolded Oligomers. Journal of Molecular Biology, 2016, 428, 3935-3947.	2.0	21
36	Unraveling the Molecular Mechanism of pH-Induced Misfolding and Oligomerization of the Prion Protein. Journal of Molecular Biology, 2016, 428, 1345-1355.	2.0	36

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37	The Pathogenic Mutation T182A Converts the Prion Protein into a Molten Globule-like Conformation Whose Misfolding to Oligomers but Not to Fibrils Is Drastically Accelerated. Biochemistry, 2016, 55, 459-469.	1.2	20
38	Tuning Cooperativity on the Free Energy Landscape of Protein Folding. Biochemistry, 2015, 54, 3431-3441.	1.2	26
39	Rise of the Helix from a Collapsed Globule during the Folding of Monellin. Biochemistry, 2015, 54, 5356-5365.	1.2	20
40	Molecular Mechanism of the Misfolding and Oligomerization of the Prion Protein: Current Understanding and Its Implications. Biochemistry, 2015, 54, 4431-4442.	1.2	53
41	Structural Effects of Multiple Pathogenic Mutations Suggest a Model for the Initiation of Misfolding of the Prion Protein. Angewandte Chemie - International Edition, 2015, 54, 7529-7533.	7.2	34
42	Partially Unfolded Forms of the Prion Protein Populated under Misfolding-promoting Conditions. Journal of Biological Chemistry, 2015, 290, 25227-25240.	1.6	42
43	Resonance Raman Spectroscopic Measurements Delineate the Structural Changes that Occur during Tau Fibril Formation. Biochemistry, 2014, 53, 6550-6565.	1.2	34
44	Rational Stabilization of Helix 2 of the Prion Protein Prevents Its Misfolding and Oligomerization. Journal of the American Chemical Society, 2014, 136, 16704-16707.	6.6	53
45	Thermodynamic Characterization of the Unfolding of the Prion Protein. Biophysical Journal, 2014, 106, 410-420.	0.2	26
46	High-Energy Intermediates in Protein Unfolding Characterized by Thiol Labeling under Nativelike Conditions. Biochemistry, 2014, 53, 3608-3620.	1.2	28
47	Multistage Unfolding of an SH3 Domain: An Initial Urea-Filled Dry Molten Globule Precedes a Wet Molten Globule with Non-Native Structure. Journal of Physical Chemistry B, 2014, 118, 6380-6392.	1.2	23
48	Amyloid Fibril Formation by the Chain B Subunit of Monellin Occurs by a Nucleation-Dependent Polymerization Mechanism. Biochemistry, 2014, 53, 1206-1217.	1.2	21
49	Unfolding of a Small Protein Proceeds via Dry and Wet Globules and a Solvated Transition State. Biophysical Journal, 2013, 105, 2392-2402.	0.2	39
50	Dissection of Conformational Conversion Events during Prion Amyloid Fibril Formation Using Hydrogen Exchange and Mass Spectrometry. Journal of Molecular Biology, 2013, 425, 3510-3521.	2.0	49
51	Polypeptide chain collapse and protein folding. Archives of Biochemistry and Biophysics, 2013, 531, 24-33.	1.4	52
52	Mechanistic Studies Unravel the Complexity Inherent in Tau Aggregation Leading to Alzheimerâ€™s Disease and the Tauopathies. Biochemistry, 2013, 52, 4107-4126.	1.2	51
53	The Utilization of Competing Unfolding Pathways of Monellin Is Dictated by Enthalpic Barriers. Biochemistry, 2013, 52, 5770-5779.	1.2	15
54	Difference in Fibril Core Stability between Two Tau Four-Repeat Domain Proteins: A Hydrogenâ€"Deuterium Exchange Coupled to Mass Spectrometry Study. Biochemistry, 2013, 52, 8787-8789.	1.2	11

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55	Critical Evaluation of the Two-State Model Describing the Equilibrium Unfolding of the PI3K SH3 Domain by Time-Resolved Fluorescence Resonance Energy Transfer. Biochemistry, 2013, 52, 9482-9496.	1.2	23
56	Transient Non-Native Burial of a Trp Residue Occurs Initially during the Unfolding of a SH3 Domain. Biochemistry, 2012, 51, 8226-8234.	1.2	16
57	Four-State Folding of a SH3 Domain: Salt-Induced Modulation of the Stabilities of the Intermediates and Native State. Biochemistry, 2012, 51, 4723-4734.	1.2	17
58	Evidence for the Existence of a Secondary Pathway for Fibril Growth during the Aggregation of Tau. Journal of Molecular Biology, 2012, 421, 296-314.	2.0	57
59	Kinetic Studies of the Folding of Heterodimeric Monellin: Evidence for Switching between Alternative Parallel Pathways. Journal of Molecular Biology, 2012, 420, 235-250.	2.0	18
60	Development of the Structural Core and of Conformational Heterogeneity during the Conversion of Oligomers of the Mouse Prion Protein to Worm-like Amyloid Fibrils. Journal of Molecular Biology, 2012, 423, 217-231.	2.0	54
61	Defining the Pathway of Worm-like Amyloid Fibril Formation by the Mouse Prion Protein by Delineation of the Productive and Unproductive Oligomerization Reactions. Biochemistry, 2011, 50, 1153-1161.	1.2	28
62	Equilibrium Unfolding Studies of Monellin: The Double-Chain Variant Appears To Be More Stable Than the Single-Chain Variant. Biochemistry, 2011, 50, 2434-2444.	1.2	20
63	Fluoroalcohol-Induced Modulation of the Pathway of Amyloid Protofibril Formation by Barstar. Biochemistry, 2011, 50, 805-819.	1.2	12
64	Identification of Multiple Folding Pathways of Monellin Using Pulsed Thiol Labeling and Mass Spectrometry. Biochemistry, 2011, 50, 3062-3074.	1.2	28
65	Heterologous expression, purification and characterization of heterodimeric monellin. Protein Expression and Purification, 2011, 76, 248-253.	0.6	17
66	Understanding the Kinetic Roles of the Inducer Heparin and of Rod-like Protofibrils during Amyloid Fibril Formation by Tau Protein. Journal of Biological Chemistry, 2011, 286, 38948-38959.	1.6	122
67	Salt-Induced Modulation of the Pathway of Amyloid Fibril Formation by the Mouse Prion Protein. Biochemistry, 2010, 49, 7615-7624.	1.2	101
68	Evidence for Initial Non-specific Polypeptide Chain Collapse During the Refolding of the SH3 Domain of PI3 Kinase. Journal of Molecular Biology, 2010, 403, 430-445.	2.0	42
69	Direct evidence for a dry molten globule intermediate during the unfolding of a small protein. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12289-12294.	3.3	121
70	Native state dynamics drive the unfolding of the SH3 domain of PI3 kinase at high denaturant concentration. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20711-20716.	3.3	36
71	Continuous dissolution of structure during the unfolding of a small protein. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11113-11118.	3.3	84
72	Conformational Conversion May Precede or Follow Aggregate Elongation on Alternative Pathways of Amyloid Protofibril Formation. Journal of Molecular Biology, 2009, 385, 1266-1276.	2.0	48

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73	Revealing a Concealed Intermediate that Forms after the Rate-limiting Step of Refolding of the SH3 Domain of PI3 Kinase. Journal of Molecular Biology, 2009, 387, 348-362.	2.0	24
74	GroEL Can Unfold Late Intermediates Populated on the Folding Pathways of Monellin. Journal of Molecular Biology, 2009, 389, 759-775.	2.0	6
75	Structurally Distinct Amyloid Protofibrils Form on Separate Pathways of Aggregation of a Small Protein. Biochemistry, 2009, 48, 6441-6449.	1.2	47
76	Native and nonnative conformational preferences in the urea-unfolded state of barstar. Protein Science, 2009, 13, 3085-3091.	3.1	28
77	Evidence for Stepwise Formation of Amyloid Fibrils by the Mouse Prion Protein. Journal of Molecular Biology, 2008, 382, 1228-1241.	2.0	75
78	Multiple Routes and Structural Heterogeneity in Protein Folding. Annual Review of Biophysics, 2008, 37, 489-510.	4.5	91
79	Barrierless evolution of structure during the submillisecond refolding reaction of a small protein. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7998-8003.	3.3	29
80	Exploring the Cooperativity of the Fast Folding Reaction of a Small Protein Using Pulsed Thiol Labeling and Mass Spectrometry. Journal of Biological Chemistry, 2007, 282, 37479-37491.	1.6	42
81	Diffusional Barrier in the Unfolding of a Small Protein. Journal of Molecular Biology, 2007, 366, 1016-1028.	2.0	37
82	Mechanism of Formation of Amyloid Protofibrils of Barstar from Soluble Oligomers: Evidence for Multiple Steps and Lateral Association Coupled to Conformational Conversion. Journal of Molecular Biology, 2007, 367, 1186-1204.	2.0	57
83	Dissecting the Non-specific and Specific Components of the Initial Folding Reaction of Barstar by Multi-site FRET Measurements. Journal of Molecular Biology, 2007, 370, 385-405.	2.0	51
84	Characterization of the Folding and Unfolding Reactions of Single-Chain Monellin:â€‰ Evidence for Multiple Intermediates and Competing Pathways. Biochemistry, 2007, 46, 11727-11743.	1.2	46
85	HX-ESI-MS and Optical Studies of the Unfolding of Thioredoxin Indicate Stabilization of a Partially Unfolded, Aggregation-Competent Intermediate at Low pHâ€. Biochemistry, 2006, 45, 11226-11238.	1.2	25
86	Characterization of Intra-molecular Distances and Site-specific Dynamics in Chemically Unfolded Barstar: Evidence for Denaturant-dependent Non-random Structure. Journal of Molecular Biology, 2006, 359, 174-189.	2.0	42
87	Protein dynamics control proton transfer from bulk solvent to protein interior: A case study with a green fluorescent protein. Protein Science, 2005, 14, 1787-1799.	3.1	29
88	Dependence of the Size of the Initially Collapsed Form During the Refolding of Barstar on Denaturant Concentration: Evidence for a Continuous Transition. Journal of Molecular Biology, 2005, 353, 704-718.	2.0	51
89	Osmolytes Induce Structure in an Early Intermediate on the Folding Pathway of Barstar. Journal of Biological Chemistry, 2004, 279, 40303-40313.	1.6	55
90	Effect of Salt on the Urea-Unfolded Form of Barstar Probed bymValue Measurementsâ€. Biochemistry, 2004, 43, 11393-11402.	1.2	23

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91	Increasing Stability Reduces Conformational Heterogeneity in a Protein Folding Intermediate Ensemble. Journal of Molecular Biology, 2004, 337, 699-711.	2.0	53
92	Folding subdomains of thioredoxin characterized by native-state hydrogen exchange. Protein Science, 2003, 12, 1719-1731.	3.1	29
93	Surface Expansion Is Independent of and Occurs Faster than Core Solvation during the Unfolding of Barstarâ€. Biochemistry, 2003, 42, 1551-1563.	1.2	37
94	Dynamics of the Core Tryptophan during the Formation of a Productive Molten Globule Intermediate of Barstar. Biochemistry, 2003, 42, 7986-8000.	1.2	41
95	Mechanism of Formation of a Productive Molten Globule Form of Barstarâ€. Biochemistry, 2002, 41, 1710-1716.	1.2	55
96	Characterization of the Unfolding of Ribonuclease A by a Pulsed Hydrogen Exchange Study:Â Evidence for Competing Pathways for Unfoldingâ€. Biochemistry, 2002, 41, 2641-2654.	1.2	52
97	Unfolding Rates of Barstar Determined in Native and Low Denaturant Conditions Indicate the Presence of Intermediates. Biochemistry, 2002, 41, 1568-1578.	1.2	48
98	Differential Salt-induced Stabilization of Structure in the Initial Folding Intermediate Ensemble of Barstar. Journal of Molecular Biology, 2002, 324, 331-347.	2.0	43
99	pH-Jump-Induced Folding and Unfolding Studies of Barstar:â€‰ Evidence for Multiple Folding and Unfolding Pathways. Biochemistry, 2001, 40, 15267-15279.	1.2	35
100	Structure is lost incrementally during the unfolding of barstar. Nature Structural Biology, 2001, 8, 799-804.	9.7	109
101	The slow folding reaction of barstar: the core tryptophan region attains tight packing before substantial secondary and tertiary structure formation and final compaction of the polypeptide chain 1 1Edited by C. R. Matthews. Journal of Molecular Biology, 2000, 302, 479-495.	2.0	46
102	Observation of Multistate Kinetics during the Slow Folding and Unfolding of Barstar. Biochemistry, 1999, 38, 9158-9168.	1.2	46
103	Two structural subdomains of barstar detected by rapid mixing NMR measurement of amide hydrogen exchange. , 1998, 30, 295-308.		34
104	Stopped-flow NMR measurement of hydrogen exchange rates in reduced horse cytochromec under strongly destabilizing conditions. Proteins: Structure, Function and Bioinformatics, 1998, 32, 241-247.	1.5	14
105	Multiple Kinetic Intermediates Accumulate during the Unfolding of Horse Cytochromecin the Oxidized Stateâ€. Biochemistry, 1998, 37, 9147-9155.	1.2	22
106	Folding of Tryptophan Mutants of Barstar:â€‰ Evidence for an Initial Hydrophobic Collapse on the Folding Pathway. Biochemistry, 1997, 36, 8602-8610.	1.2	39
107	Multiple intermediates and transition states during protein unfolding. Nature Structural Biology, 1997, 4, 1016-1024.	9.7	87
108	Initial hydrophobic collapse in the folding of barstar. Nature, 1995, 377, 754-757.	13.7	215

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109	The Folding Mechanism of Barstar: Evidence for Multiple Pathways and Multiple Intermediates. Journal of Molecular Biology, 1995, 247, 1013-1027.	2.0	107
110	Thermodynamics of Denaturation of Barstar: Evidence for Cold Denaturation and Evaluation of the Interaction with Guanidine Hydrochloride. Biochemistry, 1995, 34, 3286-3299.	1.2	221
111	Quantitative analysis of the kinetics of denaturation and renaturation of barstar in the folding transition zone. Protein Science, 1994, 3, 1409-1417.	3.1	48
112	NMR evidence for an early framework intermediate on the folding pathway of ribonuclease A. Nature, 1988, 335, 694-699.	13.7	633