Jayant B Udgaonkar

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112 papers 4,146 citations

38 h-index 60 g-index

117 ext. papers

4,557 ext. citations

6.7 avg, IF

5.99 L-index

#	Paper	IF	Citations
112	NMR evidence for an early framework intermediate on the folding pathway of ribonuclease A. <i>Nature</i> , 1988 , 335, 694-9	50.4	576
111	Thermodynamics of denaturation of barstar: evidence for cold denaturation and evaluation of the interaction with guanidine hydrochloride. <i>Biochemistry</i> , 1995 , 34, 3286-99	3.2	208
110	Initial hydrophobic collapse in the folding of barstar. <i>Nature</i> , 1995 , 377, 754-7	50.4	192
109	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, 12289-94	11.5	111
108	Structure is lost incrementally during the unfolding of barstar. <i>Nature Structural Biology</i> , 2001 , 8, 799-80	04	102
107	The folding mechanism of barstar: evidence for multiple pathways and multiple intermediates. Journal of Molecular Biology, 1995 , 247, 1013-27	6.5	99
106	Understanding the kinetic roles of the inducer heparin and of rod-like protofibrils during amyloid fibril formation by Tau protein. <i>Journal of Biological Chemistry</i> , 2011 , 286, 38948-59	5.4	95
105	Salt-induced modulation of the pathway of amyloid fibril formation by the mouse prion protein. <i>Biochemistry</i> , 2010 , 49, 7615-24	3.2	86
104	Multiple routes and structural heterogeneity in protein folding. <i>Annual Review of Biophysics</i> , 2008 , 37, 489-510	21.1	80
103	Multiple intermediates and transition states during protein unfolding. <i>Nature Structural Biology</i> , 1997 , 4, 1016-24		79
102	Continuous dissolution of structure during the unfolding of a small protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 11113-8	11.5	74
101	Evidence for stepwise formation of amyloid fibrils by the mouse prion protein. <i>Journal of Molecular Biology</i> , 2008 , 382, 1228-41	6.5	64
100	Mechanism of formation of a productive molten globule form of barstar. <i>Biochemistry</i> , 2002 , 41, 1710-6	3.2	50
99	Development of the structural core and of conformational heterogeneity during the conversion of oligomers of the mouse prion protein to worm-like amyloid fibrils. <i>Journal of Molecular Biology</i> , 2012 , 423, 217-31	6.5	49
98	Mechanism of formation of amyloid protofibrils of barstar from soluble oligomers: evidence for multiple steps and lateral association coupled to conformational conversion. <i>Journal of Molecular Biology</i> , 2007 , 367, 1186-204	6.5	48
97	Dependence of the size of the initially collapsed form during the refolding of barstar on denaturant concentration: evidence for a continuous transition. <i>Journal of Molecular Biology</i> , 2005 , 353, 704-18	6.5	48
96	Increasing stability reduces conformational heterogeneity in a protein folding intermediate ensemble. <i>Journal of Molecular Biology</i> , 2004 , 337, 699-711	6.5	48

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95	Structurally distinct amyloid protofibrils form on separate pathways of aggregation of a small protein. <i>Biochemistry</i> , 2009 , 48, 6441-9	3.2	47	
94	Dissecting the non-specific and specific components of the initial folding reaction of barstar by multi-site FRET measurements. <i>Journal of Molecular Biology</i> , 2007 , 370, 385-405	6.5	47	
93	Osmolytes induce structure in an early intermediate on the folding pathway of barstar. <i>Journal of Biological Chemistry</i> , 2004 , 279, 40303-13	5.4	47	
92	Characterization of the unfolding of ribonuclease a by a pulsed hydrogen exchange study: evidence for competing pathways for unfolding. <i>Biochemistry</i> , 2002 , 41, 2641-54	3.2	47	
91	Conformational conversion may precede or follow aggregate elongation on alternative pathways of amyloid protofibril formation. <i>Journal of Molecular Biology</i> , 2009 , 385, 1266-76	6.5	46	
90	Unfolding rates of barstar determined in native and low denaturant conditions indicate the presence of intermediates. <i>Biochemistry</i> , 2002 , 41, 1568-78	3.2	46	
89	Polypeptide chain collapse and protein folding. Archives of Biochemistry and Biophysics, 2013, 531, 24-33	4.1	45	
88	Evidence for the existence of a secondary pathway for fibril growth during the aggregation of tau. <i>Journal of Molecular Biology</i> , 2012 , 421, 296-314	6.5	45	
87	Mechanistic studies unravel the complexity inherent in tau aggregation leading to Alzheimer disease and the tauopathies. <i>Biochemistry</i> , 2013 , 52, 4107-26	3.2	45	
86	Rational stabilization of helix 2 of the prion protein prevents its misfolding and oligomerization. Journal of the American Chemical Society, 2014 , 136, 16704-7	16.4	44	
85	Quantitative analysis of the kinetics of denaturation and renaturation of barstar in the folding transition zone. <i>Protein Science</i> , 1994 , 3, 1409-17	6.3	44	
84	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. <i>Journal of Molecular Biology</i> , 2000 , 302, 479-95	6.5	43	
83	Observation of multistate kinetics during the slow folding and unfolding of barstar. <i>Biochemistry</i> , 1999 , 38, 9158-68	3.2	43	
82	How cooperative are protein folding and unfolding transitions?. <i>Protein Science</i> , 2016 , 25, 1924-1941	6.3	42	
81	Molecular Mechanism of the Misfolding and Oligomerization of the Prion Protein: Current Understanding and Its Implications. <i>Biochemistry</i> , 2015 , 54, 4431-42	3.2	41	
80	Characterization of the folding and unfolding reactions of single-chain monellin: evidence for multiple intermediates and competing pathways. <i>Biochemistry</i> , 2007 , 46, 11727-43	3.2	41	
79	Exploring the cooperativity of the fast folding reaction of a small protein using pulsed thiol labeling and mass spectrometry. <i>Journal of Biological Chemistry</i> , 2007 , 282, 37479-91	5.4	40	
78	Differential salt-induced stabilization of structure in the initial folding intermediate ensemble of barstar. <i>Journal of Molecular Biology</i> , 2002 , 324, 331-47	6.5	40	

77	Evidence for initial non-specific polypeptide chain collapse during the refolding of the SH3 domain of PI3 kinase. <i>Journal of Molecular Biology</i> , 2010 , 403, 430-45	6.5	39
76	Dissection of conformational conversion events during prion amyloid fibril formation using hydrogen exchange and mass spectrometry. <i>Journal of Molecular Biology</i> , 2013 , 425, 3510-21	6.5	38
75	Folding of tryptophan mutants of barstar: evidence for an initial hydrophobic collapse on the folding pathway. <i>Biochemistry</i> , 1997 , 36, 8602-10	3.2	38
74	Dynamics of the core tryptophan during the formation of a productive molten globule intermediate of barstar. <i>Biochemistry</i> , 2003 , 42, 7986-8000	3.2	38
73	Characterization of intra-molecular distances and site-specific dynamics in chemically unfolded barstar: evidence for denaturant-dependent non-random structure. <i>Journal of Molecular Biology</i> , 2006 , 359, 174-89	6.5	37
72	Surface expansion is independent of and occurs faster than core solvation during the unfolding of barstar. <i>Biochemistry</i> , 2003 , 42, 1551-63	3.2	35
71	Diffusional barrier in the unfolding of a small protein. <i>Journal of Molecular Biology</i> , 2007 , 366, 1016-28	6.5	34
70	pH-jump-induced folding and unfolding studies of barstar: evidence for multiple folding and unfolding pathways. <i>Biochemistry</i> , 2001 , 40, 15267-79	3.2	34
69	Unfolding of a small protein proceeds via dry and wet globules and a solvated transition state. <i>Biophysical Journal</i> , 2013 , 105, 2392-402	2.9	33
68	Partially Unfolded Forms of the Prion Protein Populated under Misfolding-promoting Conditions: CHARACTERIZATION BY HYDROGEN EXCHANGE MASS SPECTROMETRY AND NMR. <i>Journal of Biological Chemistry</i> , 2015 , 290, 25227-40	5.4	31
67	Native state dynamics drive the unfolding of the SH3 domain of PI3 kinase at high denaturant concentration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 20711-6	11.5	31
66	Two structural subdomains of barstar detected by rapid mixing NMR measurement of amide hydrogen exchange 1998 , 30, 295-308		28
65	Protein dynamics control proton transfer from bulk solvent to protein interior: a case study with a green fluorescent protein. <i>Protein Science</i> , 2005 , 14, 1787-99	6.3	28
64	Structural effects of multiple pathogenic mutations suggest a model for the initiation of misfolding of the prion protein. <i>Angewandte Chemie - International Edition</i> , 2015 , 54, 7529-33	16.4	27
63	Unraveling the Molecular Mechanism of pH-Induced Misfolding and Oligomerization of the Prion Protein. <i>Journal of Molecular Biology</i> , 2016 , 428, 1345-1355	6.5	27
62	Resonance Raman spectroscopic measurements delineate the structural changes that occur during tau fibril formation. <i>Biochemistry</i> , 2014 , 53, 6550-65	3.2	27
61	Folding subdomains of thioredoxin characterized by native-state hydrogen exchange. <i>Protein Science</i> , 2003 , 12, 1719-31	6.3	27
60	Defining the pathway of worm-like amyloid fibril formation by the mouse prion protein by delineation of the productive and unproductive oligomerization reactions. <i>Biochemistry</i> , 2011 , 50, 1153	- <u>87</u>	26

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59	Native and nonnative conformational preferences in the urea-unfolded state of barstar. <i>Protein Science</i> , 2004 , 13, 3085-91	6.3	26
58	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	11.5	26
57	High-energy intermediates in protein unfolding characterized by thiol labeling under nativelike conditions. <i>Biochemistry</i> , 2014 , 53, 3608-20	3.2	25
56	A five-residue motif for the design of domain swapping in proteins. <i>Nature Communications</i> , 2019 , 10, 452	17.4	24
55	Identification of multiple folding pathways of monellin using pulsed thiol labeling and mass spectrometry. <i>Biochemistry</i> , 2011 , 50, 3062-74	3.2	24
54	Tuning Cooperativity on the Free Energy Landscape of Protein Folding. <i>Biochemistry</i> , 2015 , 54, 3431-41	3.2	23
53	Mechanism of aggregation and membrane interactions of mammalian prion protein. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018 , 1860, 1927-1935	3.8	22
52	Multistage unfolding of an SH3 domain: an initial urea-filled dry molten globule precedes a wet molten globule with non-native structure. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 6380-92	3.4	22
51	Revealing a concealed intermediate that forms after the rate-limiting step of refolding of the SH3 domain of PI3 kinase. <i>Journal of Molecular Biology</i> , 2009 , 387, 348-62	6.5	22
50	HX-ESI-MS and optical studies of the unfolding of thioredoxin indicate stabilization of a partially unfolded, aggregation-competent intermediate at low pH. <i>Biochemistry</i> , 2006 , 45, 11226-38	3.2	22
49	Effect of salt on the urea-unfolded form of barstar probed by m value measurements. <i>Biochemistry</i> , 2004 , 43, 11393-402	3.2	22
48	Microsecond Rearrangements of Hydrophobic Clusters in an Initially Collapsed Globule Prime Structure Formation during the Folding of a Small Protein. <i>Journal of Molecular Biology</i> , 2016 , 428, 3102	2-9-5	22
47	Critical evaluation of the two-state model describing the equilibrium unfolding of the PI3K SH3 domain by time-resolved fluorescence resonance energy transfer. <i>Biochemistry</i> , 2013 , 52, 9482-96	3.2	20
46	Site-specific time-resolved FRET reveals local variations in the unfolding mechanism in an apparently two-state protein unfolding transition. <i>Physical Chemistry Chemical Physics</i> , 2018 , 20, 3216-3	232	19
45	Thermodynamic characterization of the unfolding of the prion protein. <i>Biophysical Journal</i> , 2014 , 106, 410-20	2.9	19
44	Modulation of the extent of structural heterogeneity in Esynuclein fibrils by the small molecule thioflavin T. <i>Journal of Biological Chemistry</i> , 2017 , 292, 16891-16903	5.4	19
43	Equilibrium unfolding studies of monellin: the double-chain variant appears to be more stable than the single-chain variant. <i>Biochemistry</i> , 2011 , 50, 2434-44	3.2	18
42	Multiple kinetic intermediates accumulate during the unfolding of horse cytochrome c in the oxidized state. <i>Biochemistry</i> , 1998 , 37, 9147-55	3.2	18

41	Salt-Mediated Oligomerization of the Mouse Prion Protein Monitored by Real-Time NMR. <i>Journal of Molecular Biology</i> , 2017 , 429, 1852-1872	6.5	17
40	Rise of the Helix from a Collapsed Globule during the Folding of Monellin. <i>Biochemistry</i> , 2015 , 54, 5356	-6552	17
39	Pathogenic Mutations within the Disordered Palindromic Region of the Prion Protein Induce Structure Therein and Accelerate the Formation of Misfolded Oligomers. <i>Journal of Molecular Biology</i> , 2016 , 428, 3935-3947	6.5	16
38	Four-state folding of a SH3 domain: salt-induced modulation of the stabilities of the intermediates and native state. <i>Biochemistry</i> , 2012 , 51, 4723-34	3.2	16
37	Kinetic studies of the folding of heterodimeric monellin: evidence for switching between alternative parallel pathways. <i>Journal of Molecular Biology</i> , 2012 , 420, 235-50	6.5	16
36	Amyloid fibril formation by the chain B subunit of monellin occurs by a nucleation-dependent polymerization mechanism. <i>Biochemistry</i> , 2014 , 53, 1206-17	3.2	15
35	Identification and Structural Characterization of the Precursor Conformation of the Prion Protein which Directly Initiates Misfolding and Oligomerization. <i>Journal of Molecular Biology</i> , 2017 , 429, 886-89	9 ^{6.5}	14
34	The G126V Mutation in the Mouse Prion Protein Hinders Nucleation-Dependent Fibril Formation by Slowing Initial Fibril Growth and by Increasing the Critical Concentration. <i>Biochemistry</i> , 2017 , 56, 5931-5	59 ³ 4 ² 2	14
33	Transient non-native burial of a Trp residue occurs initially during the unfolding of a SH3 domain. <i>Biochemistry</i> , 2012 , 51, 8226-34	3.2	14
32	Stopped-flow NMR measurement of hydrogen exchange rates in reduced horse cytochrome c under strongly destabilizing conditions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , 32, 241-2	472	14
31	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. <i>Biochemistry</i> , 2016 , 55, 459-69	3.2	13
30	Binding-induced folding under unfolding conditions: Switching between induced fit and conformational selection mechanisms. <i>Journal of Biological Chemistry</i> , 2019 , 294, 16942-16952	5.4	13
29	The utilization of competing unfolding pathways of monellin is dictated by enthalpic barriers. <i>Biochemistry</i> , 2013 , 52, 5770-9	3.2	13
28	Heterologous expression, purification and characterization of heterodimeric monellin. <i>Protein Expression and Purification</i> , 2011 , 76, 248-53	2	13
27	Secondary Structural Change Can Occur Diffusely and Not Modularly during Protein Folding and Unfolding Reactions. <i>Journal of the American Chemical Society</i> , 2016 , 138, 5866-78	16.4	13
26	Fluoroalcohol-induced modulation of the pathway of amyloid protofibril formation by barstar. <i>Biochemistry</i> , 2011 , 50, 805-19	3.2	12
25	Mechanistic and Structural Origins of the Asymmetric Barrier to Prion-like Cross-Seeding between Tau-3R and Tau-4R. <i>Journal of Molecular Biology</i> , 2018 , 430, 5304-5312	6.5	12
24	The Osmolyte TMAO Modulates Protein Folding Cooperativity by Altering Global Protein Stability. <i>Biochemistry</i> , 2018 , 57, 5851-5863	3.2	12

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23	Structural mechanisms of oligomer and amyloid fibril formation by the prion protein. <i>Chemical Communications</i> , 2018 , 54, 6230-6242	5.8	11
22	Amino-acid composition after loop deletion drives domain swapping. <i>Protein Science</i> , 2017 , 26, 1994-20	0023	10
21	Difference in fibril core stability between two tau four-repeat domain proteins: a hydrogen-deuterium exchange coupled to mass spectrometry study. <i>Biochemistry</i> , 2013 , 52, 8787-9	3.2	10
20	The Pathogenic A116V Mutation Enhances Ion-Selective Channel Formation by Prion Protein in Membranes. <i>Biophysical Journal</i> , 2016 , 110, 1766-1776	2.9	9
19	Mechanistic approaches to understand the prion-like propagation of aggregates of the human tau protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019 , 1867, 922-932	4	7
18	Modulation of the Extent of Cooperative Structural Change During Protein Folding by Chemical Denaturant. <i>Journal of Physical Chemistry B</i> , 2017 , 121, 8263-8275	3.4	7
17	Stepwise Assembly of Eheet Structure during the Folding of an SH3 Domain Revealed by a Pulsed Hydrogen Exchange Mass Spectrometry Study. <i>Biochemistry</i> , 2017 , 56, 3754-3769	3.2	7
16	Microsecond sub-domain motions and the folding and misfolding of the mouse prion protein. <i>ELife</i> , 2019 , 8,	8.9	7
15	Observation of Continuous Contraction and a Metastable Misfolded State during the Collapse and Folding of a Small Protein. <i>Journal of Molecular Biology</i> , 2019 , 431, 3814-3826	6.5	6
14	GroEL can unfold late intermediates populated on the folding pathways of monellin. <i>Journal of Molecular Biology</i> , 2009 , 389, 759-75	6.5	6
13	Ruggedness in the Free Energy Landscape Dictates Misfolding of the Prion Protein. <i>Journal of Molecular Biology</i> , 2019 , 431, 807-824	6.5	6
12	A Dry Transition State More Compact Than the Native State Is Stabilized by Non-Native Interactions during the Unfolding of a Small Protein. <i>Biochemistry</i> , 2017 , 56, 3699-3703	3.2	5
11	Structural Effects of Multiple Pathogenic Mutations Suggest a Model for the Initiation of Misfolding of the Prion Protein. <i>Angewandte Chemie</i> , 2015 , 127, 7639-7643	3.6	5
10	Monitoring site-specific conformational changes in real-time reveals a misfolding mechanism of the prion protein. <i>ELife</i> , 2019 , 8,	8.9	5
9	Chemical Denaturants Smoothen Ruggedness on the Free Energy Landscape of Protein Folding. <i>Biochemistry</i> , 2017 , 56, 4053-4063	3.2	4
8	Mapping Distinct Sequences of Structure Formation Differentiating Multiple Folding Pathways of a Small Protein. <i>Journal of the American Chemical Society</i> , 2021 , 143, 1447-1457	16.4	4
7	Expression and purification of single cysteine-containing mutant variants of the mouse prion protein by oxidative refolding. <i>Protein Expression and Purification</i> , 2017 , 140, 1-7	2	3
6	The Lys 280 -tGln mutation mimicking disease-linked acetylation of Lys 280 in tau extends the structural core of fibrils and modulates their catalytic properties. <i>Protein Science</i> , 2021 , 30, 785-803	6.3	3

5	Esynuclein aggregation intermediates form fibril polymorphs with distinct prion-like properties		1
4	Resolving Site-Specific Heterogeneity of the Unfolded State under Folding Conditions. <i>Journal of Physical Chemistry Letters</i> , 2021 , 12, 3295-3302	6.4	1
3	Destabilization of polar interactions in the prion protein triggers misfolding and oligomerization. <i>Protein Science</i> , 2021 , 30, 2258-2271	6.3	1
2	Structural Characterization of the Cooperativity of Unfolding of a Heterodimeric Protein using Hydrogen Exchange-Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2021 , 433, 167268	6.5	O
1	Microsecond Dynamics During the Binding-induced Folding of an Intrinsically Disordered Protein. Journal of Molecular Biology, 2021 , 433, 167254	6.5	О