Jayant B Udgaonkar

List of Publications by Year in Descending Order

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	Resolving Site-Specific Heterogeneity of the Unfolded State under Folding Conditions. *Journal of Physical Chemistry Letters*, **2021**, 12, 3295-3302	6.4	1
111	Mapping Distinct Sequences of Structure Formation Differentiating Multiple Folding Pathways of a Small Protein. *Journal of the American Chemical Society*, **2021**, 143, 1447-1457	16.4	4
110	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. *Protein Science*, **2021**, 30, 785-803	6.3	3
109	Structural Characterization of the Cooperativity of Unfolding of a Heterodimeric Protein using Hydrogen Exchange-Mass Spectrometry. *Journal of Molecular Biology*, **2021**, 433, 167268	6.5	0
108	Microsecond Dynamics During the Binding-induced Folding of an Intrinsically Disordered Protein. *Journal of Molecular Biology*, **2021**, 433, 167254	6.5	0
107	Destabilization of polar interactions in the prion protein triggers misfolding and oligomerization. *Protein Science*, **2021**, 30, 2258-2271	6.3	1
106	A five-residue motif for the design of domain swapping in proteins. *Nature Communications*, **2019**, 10, 452	17.4	24
105	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	4	7
104	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	6.5	6
103	Binding-induced folding under unfolding conditions: Switching between induced fit and conformational selection mechanisms. *Journal of Biological Chemistry*, **2019**, 294, 16942-16952	5.4	13
102	Monitoring site-specific conformational changes in real-time reveals a misfolding mechanism of the prion protein. *ELife*, **2019**, 8,	8.9	5
101	Microsecond sub-domain motions and the folding and misfolding of the mouse prion protein. *ELife*, **2019**, 8,	8.9	7
100	Ruggedness in the Free Energy Landscape Dictates Misfolding of the Prion Protein. *Journal of Molecular Biology*, **2019**, 431, 807-824	6.5	6
99	Mechanism of aggregation and membrane interactions of mammalian prion protein. *Biochimica Et Biophysica Acta - Biomembranes*, **2018**, 1860, 1927-1935	3.8	22
98	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	3.6	19
97	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	6.5	12
96	The Osmolyte TMAO Modulates Protein Folding Cooperativity by Altering Global Protein Stability. *Biochemistry*, **2018**, 57, 5851-5863	3.2	12

95	Structural mechanisms of oligomer and amyloid fibril formation by the prion protein. *Chemical Communications*, **2018**, 54, 6230-6242	5.8	11
94	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	6.5	14
93	Salt-Mediated Oligomerization of the Mouse Prion Protein Monitored by Real-Time NMR. *Journal of Molecular Biology*, **2017**, 429, 1852-1872	6.5	17
92	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	3.2	14
91	Chemical Denaturants Smoothen Ruggedness on the Free Energy Landscape of Protein Folding. *Biochemistry*, **2017**, 56, 4053-4063	3.2	4
90	Amino-acid composition after loop deletion drives domain swapping. *Protein Science*, **2017**, 26, 1994-2002	3	10
89	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	2	3
88	Modulation of the extent of structural heterogeneity in □synuclein fibrils by the small molecule thioflavin T. *Journal of Biological Chemistry*, **2017**, 292, 16891-16903	5.4	19
87	Modulation of the Extent of Cooperative Structural Change During Protein Folding by Chemical Denaturant. *Journal of Physical Chemistry B*, **2017**, 121, 8263-8275	3.4	7
86	Stepwise Assembly of □Sheet Structure during the Folding of an SH3 Domain Revealed by a Pulsed Hydrogen Exchange Mass Spectrometry Study. *Biochemistry*, **2017**, 56, 3754-3769	3.2	7
85	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	3.2	5
84	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	6.5	16
83	Unraveling the Molecular Mechanism of pH-Induced Misfolding and Oligomerization of the Prion Protein. *Journal of Molecular Biology*, **2016**, 428, 1345-1355	6.5	27
82	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, 459-69	3.2	13
81	Secondary Structural Change Can Occur Diffusely and Not Modularly during Protein Folding and Unfolding Reactions. *Journal of the American Chemical Society*, **2016**, 138, 5866-78	16.4	13
80	The Pathogenic A116V Mutation Enhances Ion-Selective Channel Formation by Prion Protein in Membranes. *Biophysical Journal*, **2016**, 110, 1766-1776	2.9	9
79	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, 3102-17	6.5	22
78	How cooperative are protein folding and unfolding transitions?. *Protein Science*, **2016**, 25, 1924-1941	6.3	42

77	Molecular Mechanism of the Misfolding and Oligomerization of the Prion Protein: Current Understanding and Its Implications. *Biochemistry*, **2015**, 54, 4431-42	3.2	41
76	Structural effects of multiple pathogenic mutations suggest a model for the initiation of misfolding of the prion protein. *Angewandte Chemie - International Edition*, **2015**, 54, 7529-33	16.4	27
75	Partially Unfolded Forms of the Prion Protein Populated under Misfolding-promoting Conditions: CHARACTERIZATION BY HYDROGEN EXCHANGE MASS SPECTROMETRY AND NMR. *Journal of Biological Chemistry*, **2015**, 290, 25227-40	5.4	31
74	Structural Effects of Multiple Pathogenic Mutations Suggest a Model for the Initiation of Misfolding of the Prion Protein. *Angewandte Chemie*, **2015**, 127, 7639-7643	3.6	5
73	Tuning Cooperativity on the Free Energy Landscape of Protein Folding. *Biochemistry*, **2015**, 54, 3431-41	3.2	23
72	Rise of the Helix from a Collapsed Globule during the Folding of Monellin. *Biochemistry*, **2015**, 54, 5356-65	3.2	17
71	Thermodynamic characterization of the unfolding of the prion protein. *Biophysical Journal*, **2014**, 106, 410-20	2.9	19
70	High-energy intermediates in protein unfolding characterized by thiol labeling under nativelike conditions. *Biochemistry*, **2014**, 53, 3608-20	3.2	25
69	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, 6380-92	3.4	22
68	Amyloid fibril formation by the chain B subunit of monellin occurs by a nucleation-dependent polymerization mechanism. *Biochemistry*, **2014**, 53, 1206-17	3.2	15
67	Resonance Raman spectroscopic measurements delineate the structural changes that occur during tau fibril formation. *Biochemistry*, **2014**, 53, 6550-65	3.2	27
66	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
65	Unfolding of a small protein proceeds via dry and wet globules and a solvated transition state. *Biophysical Journal*, **2013**, 105, 2392-402	2.9	33
64	Dissection of conformational conversion events during prion amyloid fibril formation using hydrogen exchange and mass spectrometry. *Journal of Molecular Biology*, **2013**, 425, 3510-21	6.5	38
63	Polypeptide chain collapse and protein folding. *Archives of Biochemistry and Biophysics*, **2013**, 531, 24-33	4.1	45
62	Mechanistic studies unravel the complexity inherent in tau aggregation leading to Alzheimer's disease and the tauopathies. *Biochemistry*, **2013**, 52, 4107-26	3.2	45
61	The utilization of competing unfolding pathways of monellin is dictated by enthalpic barriers. *Biochemistry*, **2013**, 52, 5770-9	3.2	13
60	Difference in fibril core stability between two tau four-repeat domain proteins: a hydrogen-deuterium exchange coupled to mass spectrometry study. *Biochemistry*, **2013**, 52, 8787-9	3.2	10

59	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, 9482-96	3.2	20
58	Transient non-native burial of a Trp residue occurs initially during the unfolding of a SH3 domain. *Biochemistry*, **2012**, 51, 8226-34	3.2	14
57	Four-state folding of a SH3 domain: salt-induced modulation of the stabilities of the intermediates and native state. *Biochemistry*, **2012**, 51, 4723-34	3.2	16
56	Evidence for the existence of a secondary pathway for fibril growth during the aggregation of tau. *Journal of Molecular Biology*, **2012**, 421, 296-314	6.5	45
55	Kinetic studies of the folding of heterodimeric monellin: evidence for switching between alternative parallel pathways. *Journal of Molecular Biology*, **2012**, 420, 235-50	6.5	16
54	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, 217-31	6.5	49
53	Heterologous expression, purification and characterization of heterodimeric monellin. *Protein Expression and Purification*, **2011**, 76, 248-53	2	13
52	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, 38948-59	5.4	95
51	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, 1153-61	3.2	26
50	Equilibrium unfolding studies of monellin: the double-chain variant appears to be more stable than the single-chain variant. *Biochemistry*, **2011**, 50, 2434-44	3.2	18
49	Fluoroalcohol-induced modulation of the pathway of amyloid protofibril formation by barstar. *Biochemistry*, **2011**, 50, 805-19	3.2	12
48	Identification of multiple folding pathways of monellin using pulsed thiol labeling and mass spectrometry. *Biochemistry*, **2011**, 50, 3062-74	3.2	24
47	Salt-induced modulation of the pathway of amyloid fibril formation by the mouse prion protein. *Biochemistry*, **2010**, 49, 7615-24	3.2	86
46	Evidence for initial non-specific polypeptide chain collapse during the refolding of the SH3 domain of PI3 kinase. *Journal of Molecular Biology*, **2010**, 403, 430-45	6.5	39
45	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
44	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, 20711-6	11.5	31
43	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, 11113-8	11.5	74
42	Conformational conversion may precede or follow aggregate elongation on alternative pathways of amyloid protofibril formation. *Journal of Molecular Biology*, **2009**, 385, 1266-76	6.5	46

41	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, 348-62	6.5	22
40	GroEL can unfold late intermediates populated on the folding pathways of monellin. *Journal of Molecular Biology*, **2009**, 389, 759-75	6.5	6
39	Structurally distinct amyloid protofibrils form on separate pathways of aggregation of a small protein. *Biochemistry*, **2009**, 48, 6441-9	3.2	47
38	Evidence for stepwise formation of amyloid fibrils by the mouse prion protein. *Journal of Molecular Biology*, **2008**, 382, 1228-41	6.5	64
37	Multiple routes and structural heterogeneity in protein folding. *Annual Review of Biophysics*, **2008**, 37, 489-510	21.1	80
36	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
35	Characterization of the folding and unfolding reactions of single-chain monellin: evidence for multiple intermediates and competing pathways. *Biochemistry*, **2007**, 46, 11727-43	3.2	41
34	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, 37479-91	5.4	40
33	Diffusional barrier in the unfolding of a small protein. *Journal of Molecular Biology*, **2007**, 366, 1016-28	6.5	34
32	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, 1186-204	6.5	48
31	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	6.5	47
30	HX-ESI-MS and optical studies of the unfolding of thioredoxin indicate stabilization of a partially unfolded, aggregation-competent intermediate at low pH. *Biochemistry*, **2006**, 45, 11226-38	3.2	22
29	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, 174-89	6.5	37
28	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, 704-18	6.5	48
27	Protein dynamics control proton transfer from bulk solvent to protein interior: a case study with a green fluorescent protein. *Protein Science*, **2005**, 14, 1787-99	6.3	28
26	Native and nonnative conformational preferences in the urea-unfolded state of barstar. *Protein Science*, **2004**, 13, 3085-91	6.3	26
25	Osmolytes induce structure in an early intermediate on the folding pathway of barstar. *Journal of Biological Chemistry*, **2004**, 279, 40303-13	5.4	47
24	Effect of salt on the urea-unfolded form of barstar probed by m value measurements. *Biochemistry*, **2004**, 43, 11393-402	3.2	22

23	Increasing stability reduces conformational heterogeneity in a protein folding intermediate ensemble. *Journal of Molecular Biology*, **2004**, 337, 699-711	6.5	48
22	Folding subdomains of thioredoxin characterized by native-state hydrogen exchange. *Protein Science*, **2003**, 12, 1719-31	6.3	27
21	Surface expansion is independent of and occurs faster than core solvation during the unfolding of barstar. *Biochemistry*, **2003**, 42, 1551-63	3.2	35
20	Dynamics of the core tryptophan during the formation of a productive molten globule intermediate of barstar. *Biochemistry*, **2003**, 42, 7986-8000	3.2	38
19	Mechanism of formation of a productive molten globule form of barstar. *Biochemistry*, **2002**, 41, 1710-6	3.2	50
18	Characterization of the unfolding of ribonuclease a by a pulsed hydrogen exchange study: evidence for competing pathways for unfolding. *Biochemistry*, **2002**, 41, 2641-54	3.2	47
17	Unfolding rates of barstar determined in native and low denaturant conditions indicate the presence of intermediates. *Biochemistry*, **2002**, 41, 1568-78	3.2	46
16	Differential salt-induced stabilization of structure in the initial folding intermediate ensemble of barstar. *Journal of Molecular Biology*, **2002**, 324, 331-47	6.5	40
15	Structure is lost incrementally during the unfolding of barstar. *Nature Structural Biology*, **2001**, 8, 799-804		102
14	pH-jump-induced folding and unfolding studies of barstar: evidence for multiple folding and unfolding pathways. *Biochemistry*, **2001**, 40, 15267-79	3.2	34
13	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. *Journal of Molecular Biology*, **2000**, 302, 479-95	6.5	43
12	Observation of multistate kinetics during the slow folding and unfolding of barstar. *Biochemistry*, **1999**, 38, 9158-68	3.2	43
11	Two structural subdomains of barstar detected by rapid mixing NMR measurement of amide hydrogen exchange **1998**, 30, 295-308		28
10	Stopped-flow NMR measurement of hydrogen exchange rates in reduced horse cytochrome c under strongly destabilizing conditions. *Proteins: Structure, Function and Bioinformatics*, **1998**, 32, 241-247	4.2	14
9	Multiple kinetic intermediates accumulate during the unfolding of horse cytochrome c in the oxidized state. *Biochemistry*, **1998**, 37, 9147-55	3.2	18
8	Folding of tryptophan mutants of barstar: evidence for an initial hydrophobic collapse on the folding pathway. *Biochemistry*, **1997**, 36, 8602-10	3.2	38
7	Multiple intermediates and transition states during protein unfolding. *Nature Structural Biology*, **1997**, 4, 1016-24		79
6	Initial hydrophobic collapse in the folding of barstar. *Nature*, **1995**, 377, 754-7	50.4	192

5	The folding mechanism of barstar: evidence for multiple pathways and multiple intermediates. *Journal of Molecular Biology*, **1995**, 247, 1013-27	6.5	99
4	Thermodynamics of denaturation of barstar: evidence for cold denaturation and evaluation of the interaction with guanidine hydrochloride. *Biochemistry*, **1995**, 34, 3286-99	3.2	208
3	Quantitative analysis of the kinetics of denaturation and renaturation of barstar in the folding transition zone. *Protein Science*, **1994**, 3, 1409-17	6.3	44
2	NMR evidence for an early framework intermediate on the folding pathway of ribonuclease A. *Nature*, **1988**, 335, 694-9	50.4	576
1	Synuclein aggregation intermediates form fibril polymorphs with distinct prion-like properties		1