

Stefano Gianni

List of Publications by Year in descending order

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150
papers

4,552
citations

87723

38
h-index

138251

58
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152
all docs

152
docs citations

152
times ranked

3881
citing authors

#	ARTICLE	IF	CITATIONS
1	Unveiling induced folding of intrinsically disordered proteins – Protein engineering, frustration and emerging themes. <i>Current Opinion in Structural Biology</i> , 2022, 72, 153-160.	2.6	15
2	On the Effects of Disordered Tails, Supertertiary Structure and Quinary Interactions on the Folding and Function of Protein Domains. <i>Biomolecules</i> , 2022, 12, 209.	1.8	5
3	Anticancer Activity of (S)-5-Chloro-3-((3,5-dimethylphenyl)sulfonyl)-N-(1-oxo-1-((pyridin-4-ylmethyl)amino)propan-2-yl)-1H-indole-2-carboxamide (RS4690), a New Dishevelled 1 Inhibitor. <i>Cancers</i> , 2022, 14, 1358.		4
4	Characterization of early and late transition states of the folding pathway of a <sc>SH2</sc> domain. <i>Protein Science</i> , 2022, 31, .	3.1	4
5	Double Mutant Cycles as a Tool to Address Folding, Binding, and Allostery. <i>International Journal of Molecular Sciences</i> , 2021, 22, 828.	1.8	17
6	Unveiling the Folding Mechanism of PDZ Domains. <i>Methods in Molecular Biology</i> , 2021, 2256, 149-156.	0.4	0
7	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. <i>Accounts of Chemical Research</i> , 2021, 54, 1251-1259.	7.6	88
8	Folding and Misfolding of a PDZ Tandem Repeat. <i>Journal of Molecular Biology</i> , 2021, 433, 166862.	2.0	8
9	Probing the Effects of Local Frustration in the Folding of a Multidomain Protein. <i>Journal of Molecular Biology</i> , 2021, 433, 167087.	2.0	6
10	Dissecting Inter-domain Cooperativity in the Folding of a Multi Domain Protein. <i>Journal of Molecular Biology</i> , 2021, 433, 167148.	2.0	10
11	Determining folding and binding properties of the C-terminal SH2 domain of SHP2. <i>Protein Science</i> , 2021, 30, 2385-2395.	3.1	6
12	Targeting PDZ domains as potential treatment for viral infections, neurodegeneration and cancer. <i>Biology Direct</i> , 2021, 16, 15.	1.9	12
13	Emerging Therapeutic Agents for Colorectal Cancer. <i>Molecules</i> , 2021, 26, 7463.	1.7	14
14	Experimental Characterization of the Interaction between the N-Terminal SH3 Domain of Crkl and C3G. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13174.	1.8	1
15	The Effect of Proline cis-trans Isomerization on the Folding of the C-Terminal SH2 Domain from p85. <i>International Journal of Molecular Sciences</i> , 2020, 21, 125.	1.8	3
16	Functional interplay between protein domains in a supramodular structure involving the postsynaptic density protein PSD-95. <i>Journal of Biological Chemistry</i> , 2020, 295, 1992-2000.	1.6	18
17	Direct Quantification of Protein Dimerization Preference Shed Light on SOD1-associated ALS. <i>Journal of Molecular Biology</i> , 2020, 432, 6003-6004.	2.0	0
18	Hidden kinetic traps in multidomain folding highlight the presence of a misfolded but functionally competent intermediate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19963-19969.	3.3	16

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19	Supertertiary protein structure affects an allosteric network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24294-24304.	3.3	27
20	Comparing the binding properties of peptides mimicking the Envelope protein of <scp>SARSâ€CoV</scp> and <scp>SARSâ€CoV</scp>â€2 to the <scp>PDZ</scp> domain of the tight junctionâ€associated <scp>PALS1</scp> protein. <i>Protein Science</i> , 2020, 29, 2038-2042.	3.1	48
21	Targeting the Interaction between the SH3 Domain of Grb2 and Gab2. <i>Cells</i> , 2020, 9, 2435.	1.8	7
22	Understanding the Binding Induced Folding of Intrinsically Disordered Proteins by Protein Engineering: Caveats and Pitfalls. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3484.	1.8	11
23	Unveiling the Molecular Basis of the Noonan Syndrome-Causing Mutation T42A of SHP2. <i>International Journal of Molecular Sciences</i> , 2020, 21, 461.	1.8	23
24	Templated folding of intrinsically disordered proteins. <i>Journal of Biological Chemistry</i> , 2020, 295, 6586-6593.	1.6	44
25	Demonstration of Binding Induced Structural Plasticity in a SH2 Domain. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 89.	1.6	5
26	Understanding Binding-Induced Folding by Temperature Jump. <i>Methods in Molecular Biology</i> , 2020, 2141, 651-661.	0.4	0
27	Affinity versus specificity in coupled binding and folding reactions. <i>Protein Engineering, Design and Selection</i> , 2019, 32, 355-357.	1.0	9
28	Structural characterization of an onâ€pathway intermediate and transition state in the folding of the Nâ€terminal SH2 domain from SHP2. <i>FEBS Journal</i> , 2019, 286, 4769-4777.	2.2	7
29	Binding induced folding: Lessons from the kinetics of interaction between NTAIL and XD. <i>Archives of Biochemistry and Biophysics</i> , 2019, 671, 255-261.	1.4	9
30	Investigating the Molecular Basis of the Aggregation Propensity of the Pathological D76N Mutant of Beta-2 Microglobulin: Role of the Denatured State. <i>International Journal of Molecular Sciences</i> , 2019, 20, 396.	1.8	5
31	A structurally heterogeneous transition state underlies coupled binding and folding of disordered proteins. <i>Journal of Biological Chemistry</i> , 2019, 294, 1230-1239.	1.6	39
32	Mapping the allosteric network within a SH3 domain. <i>Scientific Reports</i> , 2019, 9, 8279.	1.6	18
33	Characterization of human frataxin missense variants in cancer tissues. <i>Human Mutation</i> , 2019, 40, 1400-1413.	1.1	16
34	The kinetics of folding of the NSH2 domain from p85. <i>Scientific Reports</i> , 2019, 9, 4058.	1.6	9
35	Understanding Intramolecular Crosstalk in an Intrinsically Disordered Protein. <i>ACS Chemical Biology</i> , 2019, 14, 337-341.	1.6	18
36	Modulation of Measles Virus NTAIL Interactions through Fuzziness and Sequence Features of Disordered Binding Sites. <i>Biomolecules</i> , 2019, 9, 8.	1.8	17

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37	Drug Design and Synthesis of First in Class PDZ1 Targeting NHERF1 Inhibitors as Anticancer Agents. ACS Medicinal Chemistry Letters, 2019, 10, 499-503.	1.3	13
38	Folding mechanisms steer the amyloid fibril formation propensity of highly homologous proteins. Chemical Science, 2018, 9, 3290-3298.	3.7	18
39	Editorial overview: Folding and binding: In silico, in vitro and in cellula. Current Opinion in Structural Biology, 2018, 48, iv-vii.	2.6	0
40	How Robust Is the Mechanism of Folding-Upon-Binding for an Intrinsically Disordered Protein?. Biophysical Journal, 2018, 114, 1889-1894.	0.2	39
41	β -catenin knockdown promotes NHERF1-mediated survival of colorectal cancer cells: implications for a double-targeted therapy. Oncogene, 2018, 37, 3301-3316.	2.6	18
42	Partner-Mediated Polymorphism of an Intrinsically Disordered Protein. Journal of Molecular Biology, 2018, 430, 2493-2507.	2.0	18
43	Seeking allosteric networks in PDZ domains. Protein Engineering, Design and Selection, 2018, 31, 367-373.	1.0	25
44	Experimental Characterization of Fuzzy Protein Assemblies: Interactions of Paramyxoviral NTAIL Domains With Their Functional Partners. Methods in Enzymology, 2018, 611, 137-192.	0.4	8
45	Stability of an aggregation-prone partially folded state of human profilin-1 correlates with aggregation propensity. Journal of Biological Chemistry, 2018, 293, 10303-10313.	1.6	10
46	Mechanism of Folding and Binding of the N-Terminal SH2 Domain from SHP2. Journal of Physical Chemistry B, 2018, 122, 11108-11114.	1.2	19
47	InSiDDe: A Server for Designing Artificial Disordered Proteins. International Journal of Molecular Sciences, 2018, 19, 91.	1.8	10
48	A Carboxylate to Amide Substitution That Switches Protein Folds. Angewandte Chemie, 2018, 130, 12977-12980.	1.6	0
49	A Carboxylate to Amide Substitution That Switches Protein Folds. Angewandte Chemie - International Edition, 2018, 57, 12795-12798.	7.2	4
50	Folding Mechanism of the SH3 Domain from Grb2. Journal of Physical Chemistry B, 2018, 122, 11166-11173.	1.2	9
51	Understanding the role of phosphorylation in the binding mechanism of a PDZ domain. Protein Engineering, Design and Selection, 2017, 30, 1-5.	1.0	11
52	Structural Characterization of the Early Events in the Nucleation-Condensation Mechanism in a Protein Folding Process. Journal of the American Chemical Society, 2017, 139, 6899-6910.	6.6	18
53	The Folding Pathway of the KIX Domain. ACS Chemical Biology, 2017, 12, 1683-1690.	1.6	6
54	How order and disorder within paramyxoviral nucleoproteins and phosphoproteins orchestrate the molecular interplay of transcription and replication. Cellular and Molecular Life Sciences, 2017, 74, 3091-3118.	2.4	30

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55	Addressing the role of the α -helical extension in the folding of the third PDZ domain from PSD-95. <i>Scientific Reports</i> , 2017, 7, 12593.	1.6	13
56	How Fast Is Protein-Ligand Association?. <i>Trends in Biochemical Sciences</i> , 2017, 42, 847-849.	3.7	10
57	Regulation of the Human Phosphatase PTPN4 by the inter-domain linker connecting the PDZ and the phosphatase domains. <i>Scientific Reports</i> , 2017, 7, 7875.	1.6	12
58	Analyzing the Folding and Binding Steps of an Intrinsically Disordered Protein by Protein Engineering. <i>Biochemistry</i> , 2017, 56, 3780-3786.	1.2	28
59	Understanding the mechanism of binding between Gab2 and the C terminal SH3 domain from Grb2. <i>Oncotarget</i> , 2017, 8, 82344-82351.	0.8	10
60	Towards a structural biology of the hydrophobic effect in protein folding. <i>Scientific Reports</i> , 2016, 6, 28285.	1.6	91
61	Molecular medicine – To be or not to be. <i>Biophysical Chemistry</i> , 2016, 214-215, 33-46.	1.5	4
62	Identification and Structural Characterization of an Intermediate in the Folding of the Measles Virus X Domain. <i>Journal of Biological Chemistry</i> , 2016, 291, 10886-10892.	1.6	18
63	Ligand binding to the PDZ domains of postsynaptic density protein 95. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 169-175.	1.0	13
64	Activation Barrier-Limited Folding and Conformational Sampling of a Dynamic Protein Domain. <i>Biochemistry</i> , 2016, 55, 5289-5295.	1.2	14
65	Molecular Recognition by Templated Folding of an Intrinsically Disordered Protein. <i>Scientific Reports</i> , 2016, 6, 21994.	1.6	87
66	Mutational Analysis of the Binding-Induced Folding Reaction of the Mixed-Lineage Leukemia Protein to the KIX Domain. <i>Biochemistry</i> , 2016, 55, 3957-3962.	1.2	19
67	Coupled binding and folding of intrinsically disordered proteins: what can we learn from kinetics?. <i>Current Opinion in Structural Biology</i> , 2016, 36, 18-24.	2.6	78
68	Protein folding: Vexing debates on a fundamental problem. <i>Biophysical Chemistry</i> , 2016, 212, 17-21.	1.5	19
69	Fuzzy regions in an intrinsically disordered protein impair protein-protein interactions. <i>FEBS Journal</i> , 2016, 283, 576-594.	2.2	43
70	Understanding the effect of alternative splicing in the folding and function of the second PDZ from Protein Tyrosine Phosphatase-BL. <i>Scientific Reports</i> , 2015, 5, 9299.	1.6	4
71	Frustration Sculpts the Early Stages of Protein Folding. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 10867-10869.	7.2	11
72	Demonstration of a Folding after Binding Mechanism in the Recognition between the Measles Virus N-TAIL and X Domains. <i>ACS Chemical Biology</i> , 2015, 10, 795-802.	1.6	63

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73	The mechanism of binding of the second PDZ domain from the Protein Tyrosine Phosphatase-BL to the Adenomatous Polyposis Coli tumor suppressor. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 249-253.	1.0	3
74	Deciphering the mechanisms of binding induced folding at nearly atomic resolution: The $\hat{\rho}$ value analysis applied to IDPs. <i>Intrinsically Disordered Proteins</i> , 2014, 2, e970900.	1.9	9
75	Conserved nucleation sites reinforce the significance of Phi value analysis in protein folding studies. <i>IUBMB Life</i> , 2014, 66, 449-452.	1.5	15
76	The mechanism of binding of the KIX domain to the mixed lineage leukemia protein and its allosteric role in the recognition of c-Myb. <i>Protein Science</i> , 2014, 23, 962-969.	3.1	38
77	Structure of a Misfolded Intermediate of a PDZ Domain. , 2014, , 463-474.		0
78	Distinguishing induced fit from conformational selection. <i>Biophysical Chemistry</i> , 2014, 189, 33-39.	1.5	139
79	The kinetics of folding of frataxin. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 6391.	1.3	17
80	The binding mechanisms of intrinsically disordered proteins. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 6323-6331.	1.3	124
81	Understanding the frustration arising from the competition between function, misfolding, and aggregation in a globular protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14141-14146.	3.3	43
82	A Complex Equilibrium among Partially Unfolded Conformations in Monomeric Transthyretin. <i>Biochemistry</i> , 2014, 53, 4381-4392.	1.2	12
83	The folding pathway of a functionally competent C-terminal domain of nucleophosmin: Protein stability and denatured state residual structure. <i>Biochemical and Biophysical Research Communications</i> , 2013, 435, 64-68.	1.0	7
84	Energetic Pathway Sampling in a Protein Interaction Domain. <i>Structure</i> , 2013, 21, 1193-1202.	1.6	38
85	Probing the Role of Backbone Hydrogen Bonds in Protein-Peptide Interactions by Amide-to-Ester Mutations. <i>Journal of the American Chemical Society</i> , 2013, 135, 12998-13007.	6.6	45
86	Structure of the transition state for the binding of c-Myb and KIX highlights an unexpected order for a disordered system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14942-14947.	3.3	99
87	Functional role of transient conformations: Rediscovering "chronosteric effects" thirty years later. <i>IUBMB Life</i> , 2013, 65, 836-844.	1.5	17
88	GA/GB Fold switching may modulate fatty acid transfer from human serum albumin to bacteria. <i>IUBMB Life</i> , 2012, 64, 885-888.	1.5	10
89	Reassessing the folding of the KIX domain: Evidence for a two-state mechanism. <i>Protein Science</i> , 2012, 21, 1775-1779.	3.1	2
90	Interactions outside the Boundaries of the Canonical Binding Groove of a PDZ Domain Influence Ligand Binding. <i>Biochemistry</i> , 2012, 51, 8971-8979.	1.2	21

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91	Side-Chain Interactions Form Late and Cooperatively in the Binding Reaction between Disordered Peptides and PDZ Domains. <i>Journal of the American Chemical Society</i> , 2012, 134, 599-605.	6.6	41
92	An expanded view of the protein folding landscape of PDZ domains. <i>Biochemical and Biophysical Research Communications</i> , 2012, 421, 550-553.	1.0	12
93	Morphogenesis of a protein: folding pathways and the energy landscape ¹ . <i>Biochemical Society Transactions</i> , 2012, 40, 429-432.	1.6	10
94	A folding-after-binding mechanism describes the recognition between the transactivation domain of c-Myb and the KIX domain of the CREB-binding protein. <i>Biochemical and Biophysical Research Communications</i> , 2012, 428, 205-209.	1.0	71
95	Tolerance of Protein Folding to a Circular Permutation in a PDZ Domain. <i>PLoS ONE</i> , 2012, 7, e50055.	1.1	12
96	Folding pathways of proteins with increasing degree of sequence identities but different structure and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17772-17776.	3.3	25
97	Ligand binding by PDZ domains. <i>BioFactors</i> , 2012, 38, 338-348.	2.6	66
98	GB1 Is Not a Two-State Folder: Identification and Characterization of an On-Pathway Intermediate. <i>Biophysical Journal</i> , 2011, 101, 2053-2060.	0.2	29
99	The Denatured State Dictates the Topology of Two Proteins with Almost Identical Sequence but Different Native Structure and Function. <i>Journal of Biological Chemistry</i> , 2011, 286, 3863-3872.	1.6	37
100	Open conformation of human DOPA decarboxylase reveals the mechanism of PLP addition to Group II decarboxylases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20514-20519.	3.3	91
101	Sequence-specific Long Range Networks in PSD-95/Discs Large/ZO-1 (PDZ) Domains Tune Their Binding Selectivity. <i>Journal of Biological Chemistry</i> , 2011, 286, 27167-27175.	1.6	62
102	Structural and functional characterization of CcmG from <i>Pseudomonas aeruginosa</i> , a key component of the bacterial cytochrome c maturation apparatus. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2213-2221.	1.5	19
103	Structural characterization of a misfolded intermediate populated during the folding process of a PDZ domain. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1431-1437.	3.6	53
104	Deciphering the folding transition state structure and denatured state properties of Nucleophosmin C-terminal domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5447-5452.	3.3	33
105	Engineering a switchable toxin: the potential use of PDZ domains in the expression, targeting and activation of modified saporin variants. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 61-68.	1.0	13
106	The Plastic Energy Landscape of Protein Folding. <i>Journal of Biological Chemistry</i> , 2010, 285, 18051-18059.	1.6	20
107	Azole Drugs Trap Cytochrome P450 EryK in Alternative Conformational States. <i>Biochemistry</i> , 2010, 49, 9199-9206.	1.2	18
108	The Folding Mechanism of c-Type Cytochromes. , 2010, , 13-36.		0

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109	Folding mechanism of the C-terminal domain of nucleophosmin: residual structure in the denatured state and its pathophysiological significance. <i>FASEB Journal</i> , 2009, 23, 2360-2365.	0.2	31
110	Folding and stability of globular proteins and implications for function. <i>Current Opinion in Structural Biology</i> , 2009, 19, 3-7.	2.6	22
111	A Sequential Binding Mechanism in a PDZ Domain. <i>Biochemistry</i> , 2009, 48, 7089-7097.	1.2	46
112	Distinguishing between Smooth and Rough Free Energy Barriers in Protein Folding. <i>Biochemistry</i> , 2009, 48, 11825-11830.	1.2	10
113	A conserved hydrogen-bond network stabilizes the structure of Beta class glutathione S-transferases. <i>Biochemical and Biophysical Research Communications</i> , 2009, 382, 525-529.	1.0	9
114	Agitation and High Ionic Strength Induce Amyloidogenesis of a Folded PDZ Domain in Native Conditions. <i>Biophysical Journal</i> , 2009, 96, 2289-2298.	0.2	32
115	Engineered Symmetric Connectivity of Secondary Structure Elements Highlights Malleability of Protein Folding Pathways. <i>Journal of the American Chemical Society</i> , 2009, 131, 11727-11733.	6.6	25
116	Investigating the Structural Plasticity of a Cytochrome P450. <i>Journal of Biological Chemistry</i> , 2009, 284, 29170-29179.	1.6	66
117	Mechanisms of protein folding. <i>European Biophysics Journal</i> , 2008, 37, 721-728.	1.2	20
118	Fast folding kinetics and stabilization of apo-cytochrome c. <i>FEBS Letters</i> , 2008, 582, 1003-1007.	1.3	7
119	The Folding Process of Acylphosphatase from <i>Escherichia coli</i> is Remarkably Accelerated by the Presence of a Disulfide Bond. <i>Journal of Molecular Biology</i> , 2008, 379, 1107-1118.	2.0	14
120	Comparison of successive transition states for folding reveals alternative early folding pathways of two homologous proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 19241-19246.	3.3	59
121	Folding and Misfolding in a Naturally Occurring Circularly Permuted PDZ Domain. <i>Journal of Biological Chemistry</i> , 2008, 283, 8954-8960.	1.6	25
122	The folding pathway of an engineered circularly permuted PDZ domain. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 155-160.	1.0	20
123	Demonstration by burst-phase analysis of a robust folding intermediate in the FF domain. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 207-214.	1.0	9
124	An On-pathway Intermediate in the Folding of a PDZ Domain. <i>Journal of Biological Chemistry</i> , 2007, 282, 8568-8572.	1.6	42
125	PDZ Domains: Folding and Binding. <i>Biochemistry</i> , 2007, 46, 8701-8708.	1.2	154
126	A Strategic Protein in Cytochrome c Maturation. <i>Journal of Biological Chemistry</i> , 2007, 282, 27012-27019.	1.6	35

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127	Role of Ser11 in the stabilization of the structure of Ochrobactrum anthropi glutathione transferase. <i>Biochemical Journal</i> , 2007, 403, 267-274.	1.7	17
128	Plasticity of the protein folding landscape: Switching between on- and off-pathway intermediates. <i>Archives of Biochemistry and Biophysics</i> , 2007, 466, 172-176.	1.4	5
129	A conserved folding mechanism for PDZ domains. <i>FEBS Letters</i> , 2007, 581, 1109-1113.	1.3	45
130	A PDZ domain recapitulates a unifying mechanism for protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 128-133.	3.3	69
131	Identification and characterization of protein folding intermediates. <i>Biophysical Chemistry</i> , 2007, 128, 105-113.	1.5	69
132	Mechanism of Na ⁺ binding to thrombin resolved by ultra-rapid kinetics. <i>Biophysical Chemistry</i> , 2007, 131, 111-114.	1.5	26
133	Demonstration of Long-Range Interactions in a PDZ Domain by NMR, Kinetics, and Protein Engineering. <i>Structure</i> , 2006, 14, 1801-1809.	1.6	103
134	Two Conserved Residues Govern the Salt and pH Dependencies of the Binding Reaction of a PDZ Domain. <i>Journal of Biological Chemistry</i> , 2006, 281, 36811-36818.	1.6	46
135	The Kinetics of PDZ Domain-Ligand Interactions and Implications for the Binding Mechanism. <i>Journal of Biological Chemistry</i> , 2005, 280, 34805-34812.	1.6	87
136	An Obligatory Intermediate in the Folding Pathway of Cytochrome c552 from <i>Hydrogenobacter thermophilus</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 25729-25734.	1.6	68
137	Kinetic folding mechanism of PDZ2 from PTP-BL. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 389-395.	1.0	50
138	The Structure of the Major Transition State for Folding of an FF Domain from Experiment and Simulation. <i>Journal of Molecular Biology</i> , 2005, 350, 363-378.	2.0	68
139	Simulation and Experiment Conspire to Reveal Cryptic Intermediates and a Slide from the Nucleation-condensation to Framework Mechanism of Folding. <i>Journal of Molecular Biology</i> , 2005, 350, 757-775.	2.0	62
140	Demonstration of a low-energy on-pathway intermediate in a fast-folding protein by kinetics, protein engineering, and simulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6450-6455.	3.3	98
141	A common folding mechanism in the cytochrome family. <i>Trends in Biochemical Sciences</i> , 2004, 29, 535-541.	3.7	48
142	The Kinetic Pathway of Folding of Barnase. <i>Journal of Molecular Biology</i> , 2003, 333, 169-186.	2.0	78
143	Parallel Pathways in Cytochrome c551 Folding. <i>Journal of Molecular Biology</i> , 2003, 330, 1145-1152.	2.0	50
144	Unifying features in protein-folding mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13286-13291.	3.3	225

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145	Exploring the Cytochrome c Folding Mechanism. Journal of Biological Chemistry, 2003, 278, 41136-41140.	1.6	38
146	Cytochrome c551 as a model system for protein folding. Biophysical Chemistry, 2002, 100, 409-419.	1.5	7
147	Snapshots of protein folding. A study on the multiple transition state pathway of cytochrome c551 from Pseudomonas aeruginosa. Journal of Molecular Biology, 2001, 309, 1177-1187.	2.0	30
148	Refolding kinetics of cytochrome c551 reveals a mechanistic difference between urea and guanidine. Protein Science, 2001, 10, 1685-1688.	3.1	23
149	Fast Coordination Changes in Cytochrome c Do Not Necessarily Imply Folding. Journal of Biological Chemistry, 2001, 276, 41073-41078.	1.6	29
150	An Outlook on the Complexity of Protein Morphogenesis in Health and Disease. Frontiers in Molecular Biosciences, 0, 9, .	1.6	0