Stefano Gianni

List of Publications by Year
in descending order

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150	4,552	87888	138484
papers	citations	38 h-index	58 g-index

152	152	152	3881
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Unveiling induced folding of intrinsically disordered proteins â€“ Protein engineering, frustration and emerging themes. Current Opinion in Structural Biology, 2022, 72, 153-160.	5.7	15
2	On the Effects of Disordered Tails, Supertertiary Structure and Quinary Interactions on the Folding and Function of Protein Domains. Biomolecules, 2022, 12, 209.	4.0	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. Cancers, 2022, 14, 1358.	4.7	4
4	Characterization of early and late transition states of the folding pathway of a <scp>SH2</scp> domain. Protein Science, 2022, 31, .	7.6	4
5	Double Mutant Cycles as a Tool to Address Folding, Binding, and Allostery. International Journal of Molecular Sciences, 2021, 22, 828.	4.1	17
6	Unveiling the Folding Mechanism of PDZ Domains. Methods in Molecular Biology, 2021, 2256, 149-156.	0.9	0
7	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. Accounts of Chemical Research, 2021, 54, 1251-1259.	15.6	88
8	Folding and Misfolding of a PDZ Tandem Repeat. Journal of Molecular Biology, 2021, 433, 166862.	4.2	8
9	Probing the Effects of Local Frustration in the Folding of a Multidomain Protein. Journal of Molecular Biology, 2021, 433, 167087.	4.2	6
10	Dissecting Inter-domain Cooperativity in the Folding of a Multi Domain Protein. Journal of Molecular Biology, 2021, 433, 167148.	4.2	10
11	Determining folding and binding properties of the Câ€terminal SH2 domain of SHP2. Protein Science, 2021, 30, 2385-2395.	7.6	6
12	Targeting PDZ domains as potential treatment for viral infections, neurodegeneration and cancer. Biology Direct, 2021, 16, 15.	4.6	12
13	Emerging Therapeutic Agents for Colorectal Cancer. Molecules, 2021, 26, 7463.	3.8	14
14	Experimental Characterization of the Interaction between the N-Terminal SH3 Domain of Crkl and C3G. International Journal of Molecular Sciences, 2021, 22, 13174.	4.1	1
15	The Effect of Proline cis-trans Isomerization on the Folding of the C-Terminal SH2 Domain from p85. International Journal of Molecular Sciences, 2020, 21, 125.	4.1	3
16	Functional interplay between protein domains in a supramodular structure involving the postsynaptic density protein PSD-95. Journal of Biological Chemistry, 2020, 295, 1992-2000.	3.4	18
17	Direct Quantification of Protein Dimerization Preference Shed Light on SOD1-associated ALS. Journal of Molecular Biology, 2020, 432, 6003-6004.	4.2	0
18	Hidden kinetic traps in multidomain folding highlight the presence of a misfolded but functionally competent intermediate. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19963-19969.	7.1	16

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19	Supertertiary protein structure affects an allosteric network. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24294-24304.	7.1	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. Protein Science, 2020, 29, 2038-2042.	7.6	48
21	Targeting the Interaction between the SH3 Domain of Grb2 and Gab2. Cells, 2020, 9, 2435.	4.1	7
22	Understanding the Binding Induced Folding of Intrinsically Disordered Proteins by Protein Engineering: Caveats and Pitfalls. International Journal of Molecular Sciences, 2020, 21, 3484.	4.1	11
23	Unveiling the Molecular Basis of the Noonan Syndrome-Causing Mutation T42A of SHP2. International Journal of Molecular Sciences, 2020, 21, 461.	4.1	23
24	Templated folding of intrinsically disordered proteins. Journal of Biological Chemistry, 2020, 295, 6586-6593.	3.4	44
25	Demonstration of Binding Induced Structural Plasticity in a SH2 Domain. Frontiers in Molecular Biosciences, 2020, 7, 89.	3.5	5
26	Understanding Binding-Induced Folding by Temperature Jump. Methods in Molecular Biology, 2020, 2141, 651-661.	0.9	0
27	Affinity versus specificity in coupled binding and folding reactions. Protein Engineering, Design and Selection, 2019, 32, 355-357.	2.1	9
28	Structural characterization of an onâ€pathway intermediate and transition state in the folding of the Nâ€terminal SH2 domain from SHP2. FEBS Journal, 2019, 286, 4769-4777.	4.7	7
29	Binding induced folding: Lessons from the kinetics of interaction between NTAIL and XD. Archives of Biochemistry and Biophysics, 2019, 671, 255-261.	3.0	9
30	Investigating the Molecular Basis of the Aggregation Propensity of the Pathological D76N Mutant of Beta-2 Microglobulin: Role of the Denatured State. International Journal of Molecular Sciences, 2019, 20, 396.	4.1	5
31	A structurally heterogeneous transition state underlies coupled binding and folding of disordered proteins. Journal of Biological Chemistry, 2019, 294, 1230-1239.	3.4	39
32	Mapping the allosteric network within a SH3 domain. Scientific Reports, 2019, 9, 8279.	3.3	18
33	Characterization of human frataxin missense variants in cancer tissues. Human Mutation, 2019, 40, 1400-1413.	2.5	16
34	The kinetics of folding of the NSH2 domain from p85. Scientific Reports, 2019, 9, 4058.	3.3	9
35	Understanding Intramolecular Crosstalk in an Intrinsically Disordered Protein. ACS Chemical Biology, 2019, 14, 337-341.	3.4	18
36	Modulation of Measles Virus NTAIL Interactions through Fuzziness and Sequence Features of Disordered Binding Sites. Biomolecules, 2019, 9, 8.	4.0	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.	2.8	13
38	Folding mechanisms steer the amyloid fibril formation propensity of highly homologous proteins. Chemical Science, 2018, 9, 3290-3298.	7.4	18
39	Editorial overview: Folding and binding: In silico, in vitro and in cellula. Current Opinion in Structural Biology, 2018, 48, iv-vii.	5.7	0
40	How Robust Is the Mechanism of Folding-Upon-Binding for an Intrinsically Disordered Protein?. Biophysical Journal, 2018, 114, 1889-1894.	0.5	39
41	Î²-catenin knockdown promotes NHERF1-mediated survival of colorectal cancer cells: implications for a double-targeted therapy. Oncogene, 2018, 37, 3301-3316.	5.9	18
42	Partner-Mediated Polymorphism of an Intrinsically Disordered Protein. Journal of Molecular Biology, 2018, 430, 2493-2507.	4.2	18
43	Seeking allosteric networks in PDZ domains. Protein Engineering, Design and Selection, 2018, 31, 367-373.	2.1	25
44	Experimental Characterization of Fuzzy Protein Assemblies: Interactions of Paramyxoviral NTAIL Domains With Their Functional Partners. Methods in Enzymology, 2018, 611, 137-192.	1.0	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.	3.4	10
46	Mechanism of Folding and Binding of the N-Terminal SH2 Domain from SHP2. Journal of Physical Chemistry B, 2018, 122, 11108-11114.	2.6	19
47	InSiDDe: A Server for Designing Artificial Disordered Proteins. International Journal of Molecular Sciences, 2018, 19, 91.	4.1	10
48	A Carboxylate to Amide Substitution That Switches Protein Folds. Angewandte Chemie, 2018, 130, 12977-12980.	2.0	0
49	A Carboxylate to Amide Substitution That Switches Protein Folds. Angewandte Chemie - International Edition, 2018, 57, 12795-12798.	13.8	4
50	Folding Mechanism of the SH3 Domain from Grb2. Journal of Physical Chemistry B, 2018, 122, 11166-11173.	2.6	9
51	Understanding the role of phosphorylation in the binding mechanism of a PDZ domain. Protein Engineering, Design and Selection, 2017, 30, 1-5.	2.1	11
52	Structural Characterization of the Early Events in the Nucleationâ€“Condensation Mechanism in a Protein Folding Process. Journal of the American Chemical Society, 2017, 139, 6899-6910.	13.7	18
53	The Folding Pathway of the KIX Domain. ACS Chemical Biology, 2017, 12, 1683-1690.	3.4	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.	5.4	30

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55	Addressing the role of the Î±-helical extension in the folding of the third PDZ domain from PSD-95. Scientific Reports, 2017, 7, 12593.	3.3	13
56	How Fast Is Proteinâ€“Ligand Association?. Trends in Biochemical Sciences, 2017, 42, 847-849.	7.5	10
57	Regulation of the Human Phosphatase PTPN4 by the inter-domain linker connecting the PDZ and the phosphatase domains. Scientific Reports, 2017, 7, 7875.	3.3	12
58	Analyzing the Folding and Binding Steps of an Intrinsically Disordered Protein by Protein Engineering. Biochemistry, 2017, 56, 3780-3786.	2.5	28
59	Understanding the mechanism of binding between Gab2 and the C terminal SH3 domain from Grb2. Oncotarget, 2017, 8, 82344-82351.	1.8	10
60	Towards a structural biology of the hydrophobic effect in protein folding. Scientific Reports, 2016, 6, 28285.	3.3	91
61	Molecular medicine â€“ To be or not to be. Biophysical Chemistry, 2016, 214-215, 33-46.	2.8	4
62	Identification and Structural Characterization of an Intermediate in the Folding of the Measles Virus X Domain. Journal of Biological Chemistry, 2016, 291, 10886-10892.	3.4	18
63	Ligand binding to the PDZ domains of postsynaptic density protein 95. Protein Engineering, Design and Selection, 2016, 29, 169-175.	2.1	13
64	Activation Barrier-Limited Folding and Conformational Sampling of a Dynamic Protein Domain. Biochemistry, 2016, 55, 5289-5295.	2.5	14
65	Molecular Recognition by Templated Folding of an Intrinsically Disordered Protein. Scientific Reports, 2016, 6, 21994.	3.3	87
66	Mutational Analysis of the Binding-Induced Folding Reaction of the Mixed-Lineage Leukemia Protein to the KIX Domain. Biochemistry, 2016, 55, 3957-3962.	2.5	19
67	Coupled binding and folding of intrinsically disordered proteins: what can we learn from kinetics?. Current Opinion in Structural Biology, 2016, 36, 18-24.	5.7	78
68	Protein folding: Vexing debates on a fundamental problem. Biophysical Chemistry, 2016, 212, 17-21.	2.8	19
69	Fuzzy regions in an intrinsically disordered protein impair proteinâ€“protein interactions. FEBS Journal, 2016, 283, 576-594.	4.7	43
70	Understanding the effect of alternative splicing in the folding and function of the second PDZ from Protein Tyrosine Phosphatase-BL. Scientific Reports, 2015, 5, 9299.	3.3	4
71	Frustration Sculpts the Early Stages of Protein Folding. Angewandte Chemie - International Edition, 2015, 54, 10867-10869.	13.8	11
72	Demonstration of a Folding after Binding Mechanism in the Recognition between the Measles Virus N_{TAIL} and X Domains. ACS Chemical Biology, 2015, 10, 795-802.	3.4	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. Protein Engineering, Design and Selection, 2014, 27, 249-253.	2.1	3
74	Deciphering the mechanisms of binding induced folding at nearly atomic resolution: The Î¦ value analysis applied to IDPs. Intrinsically Disordered Proteins, 2014, 2, e970900.	1.9	9
75	Conserved nucleation sites reinforce the significance of Phi value analysis in proteinâ€folding studies. IUBMB Life, 2014, 66, 449-452.	3.4	15
76	The mechanism of binding of the KIX domain to the mixed lineage leukemia protein and its allosteric role in the recognition of câ€Myb. Protein Science, 2014, 23, 962-969.	7.6	38
77	Structure of a Misfolded Intermediate of a PDZ Domain. , 2014, , 463-474.		0
78	Distinguishing induced fit from conformational selection. Biophysical Chemistry, 2014, 189, 33-39.	2.8	139
79	The kinetics of folding of frataxin. Physical Chemistry Chemical Physics, 2014, 16, 6391.	2.8	17
80	The binding mechanisms of intrinsically disordered proteins. Physical Chemistry Chemical Physics, 2014, 16, 6323-6331.	2.8	124
81	Understanding the frustration arising from the competition between function, misfolding, and aggregation in a globular protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14141-14146.	7.1	43
82	A Complex Equilibrium among Partially Unfolded Conformations in Monomeric Transthyretin. Biochemistry, 2014, 53, 4381-4392.	2.5	12
83	The folding pathway of a functionally competent C-terminal domain of nucleophosmin: Protein stability and denatured state residual structure. Biochemical and Biophysical Research Communications, 2013, 435, 64-68.	2.1	7
84	Energetic Pathway Sampling in a Protein Interaction Domain. Structure, 2013, 21, 1193-1202.	3.3	38
85	Probing the Role of Backbone Hydrogen Bonds in Proteinâ€“Peptide Interactions by Amide-to-Ester Mutations. Journal of the American Chemical Society, 2013, 135, 12998-13007.	13.7	45
86	Structure of the transition state for the binding of c-Myb and KIX highlights an unexpected order for a disordered system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14942-14947.	7.1	99
87	Functional role of transient conformations: Rediscovering â€œchronosteric effectsâ€•thirty years later. IUBMB Life, 2013, 65, 836-844.	3.4	17
88	GA/GB Fold switching may modulate fatty acid transfer from human serum albumin to bacteria. IUBMB Life, 2012, 64, 885-888.	3.4	10
89	Reassessing the folding of the KIX domain: Evidence for a twoâ€state mechanism. Protein Science, 2012, 21, 1775-1779.	7.6	2
90	Interactions outside the Boundaries of the Canonical Binding Groove of a PDZ Domain Influence Ligand Binding. Biochemistry, 2012, 51, 8971-8979.	2.5	21

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91	Side-Chain Interactions Form Late and Cooperatively in the Binding Reaction between Disordered Peptides and PDZ Domains. Journal of the American Chemical Society, 2012, 134, 599-605.	13.7	41
92	An expanded view of the protein folding landscape of PDZ domains. Biochemical and Biophysical Research Communications, 2012, 421, 550-553.	2.1	12
93	Morphogenesis of a protein: folding pathways and the energy landscape1. Biochemical Society Transactions, 2012, 40, 429-432.	3.4	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. Biochemical and Biophysical Research Communications, 2012, 428, 205-209.	2.1	71
95	Tolerance of Protein Folding to a Circular Permutation in a PDZ Domain. PLoS ONE, 2012, 7, e50055.	2.5	12
96	Folding pathways of proteins with increasing degree of sequence identities but different structure and function. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17772-17776.	7.1	25
97	Ligand binding by PDZ domains. BioFactors, 2012, 38, 338-348.	5.4	66
98	GB1 Is Not a Two-State Folder: Identification and Characterization of an On-Pathway Intermediate. Biophysical Journal, 2011, 101, 2053-2060.	0.5	29
99	The Denatured State Dictates the Topology of Two Proteins with Almost Identical Sequence but Different Native Structure and Function. Journal of Biological Chemistry, 2011, 286, 3863-3872.	3.4	37
100	Open conformation of human DOPA decarboxylase reveals the mechanism of PLP addition to Group II decarboxylases. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20514-20519.	7.1	91
101	Sequence-specific Long Range Networks in PSD-95/Discs Large/ZO-1 (PDZ) Domains Tune Their Binding Selectivity. Journal of Biological Chemistry, 2011, 286, 27167-27175.	3.4	62
102	Structural and functional characterization of CcmG from Pseudomonas aeruginosa, a key component of the bacterial cytochrome c maturation apparatus. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2213-2221.	2.6	19
103	Structural characterization of a misfolded intermediate populated during the folding process of a PDZ domain. Nature Structural and Molecular Biology, 2010, 17, 1431-1437.	8.2	53
104	Deciphering the folding transition state structure and denatured state properties of Nucleophosmin C-terminal domain. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5447-5452.	7.1	33
105	Engineering a switchable toxin: the potential use of PDZ domains in the expression, targeting and activation of modified saporin variants. Protein Engineering, Design and Selection, 2010, 23, 61-68.	2.1	13
106	The Plastic Energy Landscape of Protein Folding. Journal of Biological Chemistry, 2010, 285, 18051-18059.	3.4	20
107	Azole Drugs Trap Cytochrome P450 EryK in Alternative Conformational States,. Biochemistry, 2010, 49, 9199-9206.	2.5	18
108	The Folding Mechanism of c-Type Cytochromes. , 2010, , 13-36.		0

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109	Folding mechanism of the Câ€terminal domain of nucleophosmin: residual structure in the denatured state and its pathophysiological significance. FASEB Journal, 2009, 23, 2360-2365.	0.5	31
110	Folding and stability of globular proteins and implications for function. Current Opinion in Structural Biology, 2009, 19, 3-7.	5.7	22
111	A Sequential Binding Mechanism in a PDZ Domain. Biochemistry, 2009, 48, 7089-7097.	2.5	46
112	Distinguishing between Smooth and Rough Free Energy Barriers in Protein Folding. Biochemistry, 2009, 48, 11825-11830.	2.5	10
113	A conserved hydrogen-bond network stabilizes the structure of Beta class glutathione S-transferases. Biochemical and Biophysical Research Communications, 2009, 382, 525-529.	2.1	9
114	Agitation and High Ionic Strength Induce Amyloidogenesis of a Folded PDZ Domain in Native Conditions. Biophysical Journal, 2009, 96, 2289-2298.	0.5	32
115	Engineered Symmetric Connectivity of Secondary Structure Elements Highlights Malleability of Protein Folding Pathways. Journal of the American Chemical Society, 2009, 131, 11727-11733.	13.7	25
116	Investigating the Structural Plasticity of a Cytochrome P450. Journal of Biological Chemistry, 2009, 284, 29170-29179.	3.4	66
117	Mechanisms of protein folding. European Biophysics Journal, 2008, 37, 721-728.	2.2	20
118	Fast folding kinetics and stabilization of apoâ€cytochrome c. FEBS Letters, 2008, 582, 1003-1007.	2.8	7
119	The Folding Process of Acylphosphatase from Escherichia coli is Remarkably Accelerated by the Presence of a Disulfide Bond. Journal of Molecular Biology, 2008, 379, 1107-1118.	4.2	14
120	Comparison of successive transition states for folding reveals alternative early folding pathways of two homologous proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19241-19246.	7.1	59
121	Folding and Misfolding in a Naturally Occurring Circularly Permuted PDZ Domain. Journal of Biological Chemistry, 2008, 283, 8954-8960.	3.4	25
122	The folding pathway of an engineered circularly permuted PDZ domain. Protein Engineering, Design and Selection, 2008, 21, 155-160.	2.1	20
123	Demonstration by burst-phase analysis of a robust folding intermediate in the FF domain. Protein Engineering, Design and Selection, 2008, 21, 207-214.	2.1	9
124	An On-pathway Intermediate in the Folding of a PDZ Domain. Journal of Biological Chemistry, 2007, 282, 8568-8572.	3.4	42
125	PDZ Domains:â€‰ Folding and Binding. Biochemistry, 2007, 46, 8701-8708.	2.5	154
126	A Strategic Protein in Cytochrome c Maturation. Journal of Biological Chemistry, 2007, 282, 27012-27019.	3.4	35

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127	Role of Ser11 in the stabilization of the structure of Ochrobactrum anthropi glutathione transferase. Biochemical Journal, 2007, 403, 267-274.	3.7	17
128	Plasticity of the protein folding landscape: Switching between on- and off-pathway intermediates. Archives of Biochemistry and Biophysics, 2007, 466, 172-176.	3.0	5
129	A conserved folding mechanism for PDZ domains. FEBS Letters, 2007, 581, 1109-1113.	2.8	45
130	A PDZ domain recapitulates a unifying mechanism for protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 128-133.	7.1	69
131	Identification and characterization of protein folding intermediates. Biophysical Chemistry, 2007, 128, 105-113.	2.8	69
132	Mechanism of Na+ binding to thrombin resolved by ultra-rapid kinetics. Biophysical Chemistry, 2007, 131, 111-114.	2.8	26
133	Demonstration of Long-Range Interactions in a PDZ Domain by NMR, Kinetics, and Protein Engineering. Structure, 2006, 14, 1801-1809.	3.3	103
134	Two Conserved Residues Govern the Salt and pH Dependencies of the Binding Reaction of a PDZ Domain. Journal of Biological Chemistry, 2006, 281, 36811-36818.	3.4	46
135	The Kinetics of PDZ Domain-Ligand Interactions and Implications for the Binding Mechanism. Journal of Biological Chemistry, 2005, 280, 34805-34812.	3.4	87
136	An Obligatory Intermediate in the Folding Pathway of Cytochromec552 from Hydrogenobacterthermophilus. Journal of Biological Chemistry, 2005, 280, 25729-25734.	3.4	68
137	Kinetic folding mechanism of PDZ2 from PTP-BL. Protein Engineering, Design and Selection, 2005, 18, 389-395.	2.1	50
138	The Structure of the Major Transition State for Folding of an FF Domain from Experiment and Simulation. Journal of Molecular Biology, 2005, 350, 363-378.	4.2	68
139	Simulation and Experiment Conspire to Reveal Cryptic Intermediates and a Slide from the Nucleation-condensation to Framework Mechanism of Folding. Journal of Molecular Biology, 2005, 350, 757-775.	4.2	62
140	Demonstration of a low-energy on-pathway intermediate in a fast-folding protein by kinetics, protein engineering, and simulation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6450-6455.	7.1	98
141	A common folding mechanism in the cytochrome family. Trends in Biochemical Sciences, 2004, 29, 535-541.	7.5	48
142	The Kinetic Pathway of Folding of Barnase. Journal of Molecular Biology, 2003, 333, 169-186.	4.2	78
143	Parallel Pathways in Cytochrome c551 Folding. Journal of Molecular Biology, 2003, 330, 1145-1152.	4.2	50
144	Unifying features in protein-folding mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13286-13291.	7.1	225

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145	Exploring the Cytochrome c Folding Mechanism. Journal of Biological Chemistry, 2003, 278, 41136-41140.	3.4	38
146	Cytochrome c551 as a model system for protein folding. Biophysical Chemistry, 2002, 100, 409-419.	2.8	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.	4.2	30
148	Refolding kinetics of cytochrome c551reveals a mechanistic difference between urea and guanidine. Protein Science, 2001, 10, 1685-1688.	7.6	23
149	Fast Coordination Changes in Cytochrome c Do Not Necessarily Imply Folding. Journal of Biological Chemistry, 2001, 276, 41073-41078.	3.4	29
150	An Outlook on the Complexity of Protein Morphogenesis in Health and Disease. Frontiers in Molecular Biosciences, 0, 9, .	3.5	0