

# Stefano Gianni

## List of Publications by Year in descending order

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150  
papers

4,552  
citations

87888

38  
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138484

58  
g-index

152  
all docs

152  
docs citations

152  
times ranked

3881  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	PDZ Domains: Folding and Binding. Biochemistry, 2007, 46, 8701-8708.	2.5	154
3	Distinguishing induced fit from conformational selection. Biophysical Chemistry, 2014, 189, 33-39.	2.8	139
4	The binding mechanisms of intrinsically disordered proteins. Physical Chemistry Chemical Physics, 2014, 16, 6323-6331.	2.8	124
5	Demonstration of Long-Range Interactions in a PDZ Domain by NMR, Kinetics, and Protein Engineering. Structure, 2006, 14, 1801-1809.	3.3	103
6	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
7	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
8	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
9	Towards a structural biology of the hydrophobic effect in protein folding. Scientific Reports, 2016, 6, 28285.	3.3	91
10	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. Accounts of Chemical Research, 2021, 54, 1251-1259.	15.6	88
11	The Kinetics of PDZ Domain-Ligand Interactions and Implications for the Binding Mechanism. Journal of Biological Chemistry, 2005, 280, 34805-34812.	3.4	87
12	Molecular Recognition by Templated Folding of an Intrinsically Disordered Protein. Scientific Reports, 2016, 6, 21994.	3.3	87
13	The Kinetic Pathway of Folding of Barnase. Journal of Molecular Biology, 2003, 333, 169-186.	4.2	78
14	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
15	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
16	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
17	Identification and characterization of protein folding intermediates. Biophysical Chemistry, 2007, 128, 105-113.	2.8	69
18	An Obligatory Intermediate in the Folding Pathway of Cytochrome c552 from Hydrogenobacter thermophilus. Journal of Biological Chemistry, 2005, 280, 25729-25734.	3.4	68

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19	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
20	Investigating the Structural Plasticity of a Cytochrome P450. Journal of Biological Chemistry, 2009, 284, 29170-29179.	3.4	66
21	Ligand binding by PDZ domains. BioFactors, 2012, 38, 338-348.	5.4	66
22	Demonstration of a Folding after Binding Mechanism in the Recognition between the Measles Virus N <sub>TAIL</sub> and X Domains. ACS Chemical Biology, 2015, 10, 795-802.	3.4	63
23	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
24	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
25	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
26	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
27	Parallel Pathways in Cytochrome c551 Folding. Journal of Molecular Biology, 2003, 330, 1145-1152.	4.2	50
28	Kinetic folding mechanism of PDZ2 from PTP-BL. Protein Engineering, Design and Selection, 2005, 18, 389-395.	2.1	50
29	A common folding mechanism in the cytochrome family. Trends in Biochemical Sciences, 2004, 29, 535-541.	7.5	48
30	Comparing the binding properties of peptides mimicking the Envelope protein of SARS-CoV and SARS-CoV-2 to the PDZ domain of the tight junction-associated PALS1 protein. Protein Science, 2020, 29, 2038-2042.	7.6	48
31	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
32	A Sequential Binding Mechanism in a PDZ Domain. Biochemistry, 2009, 48, 7089-7097.	2.5	46
33	A conserved folding mechanism for PDZ domains. FEBS Letters, 2007, 581, 1109-1113.	2.8	45
34	Probing the Role of Backbone Hydrogen Bonds in Protein-Peptide Interactions by Amide-to-Ester Mutations. Journal of the American Chemical Society, 2013, 135, 12998-13007.	13.7	45
35	Templated folding of intrinsically disordered proteins. Journal of Biological Chemistry, 2020, 295, 6586-6593.	3.4	44
36	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

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37	Fuzzy regions in an intrinsically disordered protein impair protein-protein interactions. FEBS Journal, 2016, 283, 576-594.	4.7	43
38	An On-pathway Intermediate in the Folding of a PDZ Domain. Journal of Biological Chemistry, 2007, 282, 8568-8572.	3.4	42
39	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
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	A structurally heterogeneous transition state underlies coupled binding and folding of disordered proteins. Journal of Biological Chemistry, 2019, 294, 1230-1239.	3.4	39
42	Exploring the Cytochrome c Folding Mechanism. Journal of Biological Chemistry, 2003, 278, 41136-41140.	3.4	38
43	Energetic Pathway Sampling in a Protein Interaction Domain. Structure, 2013, 21, 1193-1202.	3.3	38
44	The mechanism of binding of the KIX domain to the mixed lineage leukemia protein and its allosteric role in the recognition of c-Myc. Protein Science, 2014, 23, 962-969.	7.6	38
45	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
46	A Strategic Protein in Cytochrome c Maturation. Journal of Biological Chemistry, 2007, 282, 27012-27019.	3.4	35
47	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
48	Agitation and High Ionic Strength Induce Amyloidogenesis of a Folded PDZ Domain in Native Conditions. Biophysical Journal, 2009, 96, 2289-2298.	0.5	32
49	Folding mechanism of the C-terminal domain of nucleophosmin: residual structure in the denatured state and its pathophysiological significance. FASEB Journal, 2009, 23, 2360-2365.	0.5	31
50	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
51	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
52	Fast Coordination Changes in Cytochrome c Do Not Necessarily Imply Folding. Journal of Biological Chemistry, 2001, 276, 41073-41078.	3.4	29
53	GB1 Is Not a Two-State Folder: Identification and Characterization of an On-Pathway Intermediate. Biophysical Journal, 2011, 101, 2053-2060.	0.5	29
54	Analyzing the Folding and Binding Steps of an Intrinsically Disordered Protein by Protein Engineering. Biochemistry, 2017, 56, 3780-3786.	2.5	28

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55	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
56	Mechanism of Na <sup>+</sup> binding to thrombin resolved by ultra-rapid kinetics. Biophysical Chemistry, 2007, 131, 111-114.	2.8	26
57	Folding and Misfolding in a Naturally Occurring Circularly Permuted PDZ Domain. Journal of Biological Chemistry, 2008, 283, 8954-8960.	3.4	25
58	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
59	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
60	Seeking allosteric networks in PDZ domains. Protein Engineering, Design and Selection, 2018, 31, 367-373.	2.1	25
61	Refolding kinetics of cytochrome c551 reveals a mechanistic difference between urea and guanidine. Protein Science, 2001, 10, 1685-1688.	7.6	23
62	Unveiling the Molecular Basis of the Noonan Syndrome-Causing Mutation T42A of SHP2. International Journal of Molecular Sciences, 2020, 21, 461.	4.1	23
63	Folding and stability of globular proteins and implications for function. Current Opinion in Structural Biology, 2009, 19, 3-7.	5.7	22
64	Interactions outside the Boundaries of the Canonical Binding Groove of a PDZ Domain Influence Ligand Binding. Biochemistry, 2012, 51, 8971-8979.	2.5	21
65	Mechanisms of protein folding. European Biophysics Journal, 2008, 37, 721-728.	2.2	20
66	The folding pathway of an engineered circularly permuted PDZ domain. Protein Engineering, Design and Selection, 2008, 21, 155-160.	2.1	20
67	The Plastic Energy Landscape of Protein Folding. Journal of Biological Chemistry, 2010, 285, 18051-18059.	3.4	20
68	Structural and functional characterization of CcmG from <i>Pseudomonas aeruginosa</i> , a key component of the bacterial cytochrome c maturation apparatus. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2213-2221.	2.6	19
69	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
70	Protein folding: Vexing debates on a fundamental problem. Biophysical Chemistry, 2016, 212, 17-21.	2.8	19
71	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
72	Azole Drugs Trap Cytochrome P450 EryK in Alternative Conformational States,. Biochemistry, 2010, 49, 9199-9206.	2.5	18

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73	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.	3.4	18
74	Structural Characterization of the Early Events in the Nucleation–Condensation Mechanism in a Protein Folding Process. <i>Journal of the American Chemical Society</i> , 2017, 139, 6899-6910.	13.7	18
75	Folding mechanisms steer the amyloid fibril formation propensity of highly homologous proteins. <i>Chemical Science</i> , 2018, 9, 3290-3298.	7.4	18
76	Î2-catenin knockdown promotes NHERF1-mediated survival of colorectal cancer cells: implications for a double-targeted therapy. <i>Oncogene</i> , 2018, 37, 3301-3316.	5.9	18
77	Partner-Mediated Polymorphism of an Intrinsically Disordered Protein. <i>Journal of Molecular Biology</i> , 2018, 430, 2493-2507.	4.2	18
78	Mapping the allosteric network within a SH3 domain. <i>Scientific Reports</i> , 2019, 9, 8279.	3.3	18
79	Understanding Intramolecular Crosstalk in an Intrinsically Disordered Protein. <i>ACS Chemical Biology</i> , 2019, 14, 337-341.	3.4	18
80	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.	3.4	18
81	Role of Ser11 in the stabilization of the structure of <i>Ochrobactrum anthropi</i> glutathione transferase. <i>Biochemical Journal</i> , 2007, 403, 267-274.	3.7	17
82	Functional role of transient conformations: Rediscovering “allosteric effects” thirty years later. <i>IUBMB Life</i> , 2013, 65, 836-844.	3.4	17
83	The kinetics of folding of frataxin. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 6391.	2.8	17
84	Modulation of Measles Virus NTAIL Interactions through Fuzziness and Sequence Features of Disordered Binding Sites. <i>Biomolecules</i> , 2019, 9, 8.	4.0	17
85	Double Mutant Cycles as a Tool to Address Folding, Binding, and Allostery. <i>International Journal of Molecular Sciences</i> , 2021, 22, 828.	4.1	17
86	Characterization of human frataxin missense variants in cancer tissues. <i>Human Mutation</i> , 2019, 40, 1400-1413.	2.5	16
87	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.	7.1	16
88	Conserved nucleation sites reinforce the significance of Phi value analysis in protein folding studies. <i>IUBMB Life</i> , 2014, 66, 449-452.	3.4	15
89	Unveiling induced folding of intrinsically disordered proteins – Protein engineering, frustration and emerging themes. <i>Current Opinion in Structural Biology</i> , 2022, 72, 153-160.	5.7	15
90	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.	4.2	14

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91	Activation Barrier-Limited Folding and Conformational Sampling of a Dynamic Protein Domain. <i>Biochemistry</i> , 2016, 55, 5289-5295.	2.5	14
92	Emerging Therapeutic Agents for Colorectal Cancer. <i>Molecules</i> , 2021, 26, 7463.	3.8	14
93	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.	2.1	13
94	Ligand binding to the PDZ domains of postsynaptic density protein 95. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 169-175.	2.1	13
95	Addressing the role of the $\alpha$ -helical extension in the folding of the third PDZ domain from PSD-95. <i>Scientific Reports</i> , 2017, 7, 12593.	3.3	13
96	Drug Design and Synthesis of First in Class PDZ1 Targeting NHERF1 Inhibitors as Anticancer Agents. <i>ACS Medicinal Chemistry Letters</i> , 2019, 10, 499-503.	2.8	13
97	An expanded view of the protein folding landscape of PDZ domains. <i>Biochemical and Biophysical Research Communications</i> , 2012, 421, 550-553.	2.1	12
98	Tolerance of Protein Folding to a Circular Permutation in a PDZ Domain. <i>PLoS ONE</i> , 2012, 7, e50055.	2.5	12
99	A Complex Equilibrium among Partially Unfolded Conformations in Monomeric Transthyretin. <i>Biochemistry</i> , 2014, 53, 4381-4392.	2.5	12
100	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.	3.3	12
101	Targeting PDZ domains as potential treatment for viral infections, neurodegeneration and cancer. <i>Biology Direct</i> , 2021, 16, 15.	4.6	12
102	Frustration Sculpts the Early Stages of Protein Folding. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 10867-10869.	13.8	11
103	Understanding the role of phosphorylation in the binding mechanism of a PDZ domain. <i>Protein Engineering, Design and Selection</i> , 2017, 30, 1-5.	2.1	11
104	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.	4.1	11
105	Distinguishing between Smooth and Rough Free Energy Barriers in Protein Folding. <i>Biochemistry</i> , 2009, 48, 11825-11830.	2.5	10
106	GA/GB Fold switching may modulate fatty acid transfer from human serum albumin to bacteria. <i>IUBMB Life</i> , 2012, 64, 885-888.	3.4	10
107	Morphogenesis of a protein: folding pathways and the energy landscape <sup>1</sup> . <i>Biochemical Society Transactions</i> , 2012, 40, 429-432.	3.4	10
108	How Fast Is Protein-Ligand Association?. <i>Trends in Biochemical Sciences</i> , 2017, 42, 847-849.	7.5	10

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109	Stability of an aggregation-prone partially folded state of human profilin-1 correlates with aggregation propensity. <i>Journal of Biological Chemistry</i> , 2018, 293, 10303-10313.	3.4	10
110	InSiDDe: A Server for Designing Artificial Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2018, 19, 91.	4.1	10
111	Dissecting Inter-domain Cooperativity in the Folding of a Multi Domain Protein. <i>Journal of Molecular Biology</i> , 2021, 433, 167148.	4.2	10
112	Understanding the mechanism of binding between Gab2 and the C terminal SH3 domain from Grb2. <i>Oncotarget</i> , 2017, 8, 82344-82351.	1.8	10
113	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.	2.1	9
114	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.	2.1	9
115	Deciphering the mechanisms of binding induced folding at nearly atomic resolution: The $\hat{I}_I^{\dagger}$ value analysis applied to IDPs. <i>Intrinsically Disordered Proteins</i> , 2014, 2, e970900.	1.9	9
116	Folding Mechanism of the SH3 Domain from Grb2. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11166-11173.	2.6	9
117	Affinity versus specificity in coupled binding and folding reactions. <i>Protein Engineering, Design and Selection</i> , 2019, 32, 355-357.	2.1	9
118	Binding induced folding: Lessons from the kinetics of interaction between NTAIL and XD. <i>Archives of Biochemistry and Biophysics</i> , 2019, 671, 255-261.	3.0	9
119	The kinetics of folding of the NSH2 domain from p85. <i>Scientific Reports</i> , 2019, 9, 4058.	3.3	9
120	Experimental Characterization of Fuzzy Protein Assemblies: Interactions of Paramyxoviral NTAIL Domains With Their Functional Partners. <i>Methods in Enzymology</i> , 2018, 611, 137-192.	1.0	8
121	Folding and Misfolding of a PDZ Tandem Repeat. <i>Journal of Molecular Biology</i> , 2021, 433, 166862.	4.2	8
122	Cytochrome c551 as a model system for protein folding. <i>Biophysical Chemistry</i> , 2002, 100, 409-419.	2.8	7
123	Fast folding kinetics and stabilization of apo-cytochrome <i>c</i> . <i>FEBS Letters</i> , 2008, 582, 1003-1007.	2.8	7
124	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.	2.1	7
125	Structural characterization of an on-pathway intermediate and transition state in the folding of the N-terminal SH2 domain from SHP2. <i>FEBS Journal</i> , 2019, 286, 4769-4777.	4.7	7
126	Targeting the Interaction between the SH3 Domain of Grb2 and Gab2. <i>Cells</i> , 2020, 9, 2435.	4.1	7



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127	The Folding Pathway of the KIX Domain. ACS Chemical Biology, 2017, 12, 1683-1690.	3.4	6
128	Probing the Effects of Local Frustration in the Folding of a Multidomain Protein. Journal of Molecular Biology, 2021, 433, 167087.	4.2	6
129	Determining folding and binding properties of the C-terminal SH2 domain of SHP2. Protein Science, 2021, 30, 2385-2395.	7.6	6
130	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
131	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
132	Demonstration of Binding Induced Structural Plasticity in a SH2 Domain. Frontiers in Molecular Biosciences, 2020, 7, 89.	3.5	5
133	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
134	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
135	Molecular medicine “To be or not to be. Biophysical Chemistry, 2016, 214-215, 33-46.	2.8	4
136	A Carboxylate to Amide Substitution That Switches Protein Folds. Angewandte Chemie - International Edition, 2018, 57, 12795-12798.	13.8	4
137	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	4
138	Characterization of early and late transition states of the folding pathway of a <scp>SH2</scp> domain. Protein Science, 2022, 31, .	7.6	4
139	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
140	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
141	Reassessing the folding of the KIX domain: Evidence for a two-state mechanism. Protein Science, 2012, 21, 1775-1779.	7.6	2
142	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
143	Structure of a Misfolded Intermediate of a PDZ Domain. , 2014, , 463-474.		0
144	Editorial overview: Folding and binding: In silico, in vitro and in cellula. Current Opinion in Structural Biology, 2018, 48, iv-vii.	5.7	0

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145	A Carboxylate to Amide Substitution That Switches Protein Folds. Angewandte Chemie, 2018, 130, 12977-12980.	2.0	0
146	Direct Quantification of Protein Dimerization Preference Shed Light on SOD1-associated ALS. Journal of Molecular Biology, 2020, 432, 6003-6004.	4.2	0
147	Unveiling the Folding Mechanism of PDZ Domains. Methods in Molecular Biology, 2021, 2256, 149-156.	0.9	0
148	The Folding Mechanism of c-Type Cytochromes. , 2010, , 13-36.		0
149	Understanding Binding-Induced Folding by Temperature Jump. Methods in Molecular Biology, 2020, 2141, 651-661.	0.9	0
150	An Outlook on the Complexity of Protein Morphogenesis in Health and Disease. Frontiers in Molecular Biosciences, 0, 9, .	3.5	0