Angelo Toto

List of Publications by Year
in descending order

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46 papers	776 citations	623734 14 h-index	610901 24 g-index
46 all docs	46 docs citations	46 times ranked	865 citing authors

#	Article	IF	Citations
1	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
2	Molecular Recognition by Templated Folding of an Intrinsically Disordered Protein. Scientific Reports, 2016, 6, 21994.	3.3	87
3	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
4	Templated folding of intrinsically disordered proteins. Journal of Biological Chemistry, 2020, 295, 6586-6593.	3.4	44
5	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
6	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
7	Analyzing the Folding and Binding Steps of an Intrinsically Disordered Protein by Protein Engineering. Biochemistry, 2017, 56, 3780-3786.	2.5	28
8	Unveiling the Molecular Basis of the Noonan Syndrome-Causing Mutation T42A of SHP2. International Journal of Molecular Sciences, 2020, 21, 461.	4.1	23
9	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
10	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
11	Folding mechanisms steer the amyloid fibril formation propensity of highly homologous proteins. Chemical Science, 2018, 9, 3290-3298.	7.4	18
12	Mapping the allosteric network within a SH3 domain. Scientific Reports, 2019, 9, 8279.	3.3	18
13	The kinetics of folding of frataxin. Physical Chemistry Chemical Physics, 2014, 16, 6391.	2.8	17
14	Double Mutant Cycles as a Tool to Address Folding, Binding, and Allostery. International Journal of Molecular Sciences, 2021, 22, 828.	4.1	17
15	Characterization of human frataxin missense variants in cancer tissues. Human Mutation, 2019, 40, 1400-1413.	2.5	16
16	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
17	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
18	Activation Barrier-Limited Folding and Conformational Sampling of a Dynamic Protein Domain. Biochemistry, 2016, 55, 5289-5295.	2.5	14

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19	Ligand binding to the PDZ domains of postsynaptic density protein 95. Protein Engineering, Design and Selection, 2016, 29, 169-175.	2.1	13
20	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
21	Targeting PDZ domains as potential treatment for viral infections, neurodegeneration and cancer. Biology Direct, 2021, 16, 15.	4.6	12
22	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
23	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
24	Structural determinants driving the binding process between PDZ domain of wild type human PALS1 protein and SLiM sequences of SARS-CoV E proteins. Computational and Structural Biotechnology Journal, 2021, 19, 1838-1847.	4.1	11
25	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
26	Understanding the mechanism of binding between Gab2 and the C terminal SH3 domain from Grb2. Oncotarget, 2017, 8, 82344-82351.	1.8	10
27	Folding Mechanism of the SH3 Domain from Grb2. Journal of Physical Chemistry B, 2018, 122, 11166-11173.	2.6	9
28	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
29	The kinetics of folding of the NSH2 domain from p85. Scientific Reports, 2019, 9, 4058.	3.3	9
30	Folding and Misfolding of a PDZ Tandem Repeat. Journal of Molecular Biology, 2021, 433, 166862.	4.2	8
31	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
32	Targeting the Interaction between the SH3 Domain of Grb2 and Gab2. Cells, 2020, 9, 2435.	4.1	7
33	The Folding Pathway of the KIX Domain. ACS Chemical Biology, 2017, 12, 1683-1690.	3.4	6
34	Understanding the Mechanism of Recognition of Gab2 by the N-SH2 Domain of SHP2. Life, 2020, 10, 85.	2.4	6
35	Probing the Effects of Local Frustration in the Folding of a Multidomain Protein. Journal of Molecular Biology, 2021, 433, 167087.	4.2	6
36	Determining folding and binding properties of the Câ€terminal SH2 domain of SHP2. Protein Science, 2021, 30, 2385-2395.	7.6	6

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37	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
38	Demonstration of Binding Induced Structural Plasticity in a SH2 Domain. Frontiers in Molecular Biosciences, 2020, 7, 89.	3.5	5
39	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
40	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
41	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
42	Characterization of early and late transition states of the folding pathway of a <scp>SH2</scp> domain. Protein Science, 2022, 31, .	7.6	4
43	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
44	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
45	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
46	Understanding Binding-Induced Folding by Temperature Jump. Methods in Molecular Biology, 2020, 2141, 651-661.	0.9	0