Per Jemth

List of Publications by Year
in descending order

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89 papers	3,658 citations	126907 33 h-index	155660 55 g-index
103 all docs	103 docs citations	103 times ranked	3323 citing authors

#	Article	IF	Citations
1	A high-affinity, dimeric inhibitor of PSD-95 bivalently interacts with PDZ1-2 and protects against ischemic brain damage. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3317-3322.	7.1	162
2	Single molecule unfolding and stretching of protein domains inside a solid-state nanopore by electric field. Scientific Reports, 2013, 3, 1638.	3.3	157
3	PDZ Domains:â€‰ Folding and Binding. Biochemistry, 2007, 46, 8701-8708.	2.5	154
4	Helical Propensity in an Intrinsically Disordered Protein Accelerates Ligand Binding. Angewandte Chemie - International Edition, 2014, 53, 1548-1551.	13.8	146
5	Distinguishing induced fit from conformational selection. Biophysical Chemistry, 2014, 189, 33-39.	2.8	139
6	The binding mechanisms of intrinsically disordered proteins. Physical Chemistry Chemical Physics, 2014, 16, 6323-6331.	2.8	124
7	Demonstration of Long-Range Interactions in a PDZ Domain by NMR, Kinetics, and Protein Engineering. Structure, 2006, 14, 1801-1809.	3.3	103
8	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
9	Biosynthetic Oligosaccharide Libraries for Identification of Protein-binding Heparan Sulfate Motifs. Journal of Biological Chemistry, 2002, 277, 30567-30573.	3.4	90
10	Reassessing a sparse energetic network within a single protein domain. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4679-4684.	7.1	89
11	Affinity and specificity of motif-based proteinâ€“protein interactions. Current Opinion in Structural Biology, 2019, 54, 26-33.	5.7	88
12	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. Accounts of Chemical Research, 2021, 54, 1251-1259.	15.6	88
13	The Kinetics of PDZ Domain-Ligand Interactions and Implications for the Binding Mechanism. Journal of Biological Chemistry, 2005, 280, 34805-34812.	3.4	87
14	The transition state structure for coupled binding and folding of disordered protein domains. Scientific Reports, 2013, 3, 2076.	3.3	87
15	Fast Association and Slow Transitions in the Interaction between Two Intrinsically Disordered Protein Domains. Journal of Biological Chemistry, 2012, 287, 34316-34324.	3.4	82
16	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
17	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
18	Identification and characterization of protein folding intermediates. Biophysical Chemistry, 2007, 128, 105-113.	2.8	69

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19	Ligand binding by PDZ domains. BioFactors, 2012, 38, 338-348.	5.4	66
20	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
21	Modified Peptides as Potent Inhibitors of the Postsynaptic Density-95/N-Methyl-<scp>d</scp>-Aspartate Receptor Interaction. Journal of Medicinal Chemistry, 2008, 51, 6450-6459.	6.4	61
22	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
23	Design and Synthesis of Highly Potent and Plasmaâ€Stable Dimeric Inhibitors of the PSDâ€95â€“NMDA Receptor Interaction. Angewandte Chemie - International Edition, 2009, 48, 9685-9689.	13.8	55
24	Binding Rate Constants Reveal Distinct Features of Disordered Protein Domains. Biochemistry, 2015, 54, 4741-4750.	2.5	51
25	Large scale discovery of coronavirus-host factor protein interaction motifs reveals SARS-CoV-2 specific mechanisms and vulnerabilities. Nature Communications, 2021, 12, 6761.	12.8	47
26	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
27	A Sequential Binding Mechanism in a PDZ Domain. Biochemistry, 2009, 48, 7089-7097.	2.5	46
28	A conserved folding mechanism for PDZ domains. FEBS Letters, 2007, 581, 1109-1113.	2.8	45
29	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
30	Templated folding of intrinsically disordered proteins. Journal of Biological Chemistry, 2020, 295, 6586-6593.	3.4	44
31	An On-pathway Intermediate in the Folding of a PDZ Domain. Journal of Biological Chemistry, 2007, 282, 8568-8572.	3.4	42
32	Emergence and evolution of an interaction between intrinsically disordered proteins. ELife, 2017, 6, .	6.0	42
33	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
34	A Frustrated Binding Interface for Intrinsically Disordered Proteins. Journal of Biological Chemistry, 2014, 289, 5528-5533.	3.4	39
35	A structurally heterogeneous transition state underlies coupled binding and folding of disordered proteins. Journal of Biological Chemistry, 2019, 294, 1230-1239.	3.4	39
36	The Transition State of Coupled Folding and Binding for a Flexible Î²-Finger. Journal of Molecular Biology, 2012, 417, 253-261.	4.2	38

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37	Energetic Pathway Sampling in a Protein Interaction Domain. Structure, 2013, 21, 1193-1202.	3.3	38
38	Structure and dynamics conspire in the evolution of affinity between intrinsically disordered proteins. Science Advances, 2018, 4, eaau4130.	10.3	38
39	Oligosaccharide Library-based Assessment of Heparan Sulfate 6-O-Sulfotransferase Substrate Specificity. Journal of Biological Chemistry, 2003, 278, 24371-24376.	3.4	35
40	Probing backbone hydrogen bonding in PDZ/ligand interactions by protein amide-to-ester mutations. Nature Communications, 2014, 5, 3215.	12.8	33
41	Proteomeâ€scale mapping of binding sites in the unstructured regions of the human proteome. Molecular Systems Biology, 2022, 18, e10584.	7.2	33
42	Deciphering the Kinetic Binding Mechanism of Dimeric Ligands Using a Potent Plasma-stable Dimeric Inhibitor of Postsynaptic Density Protein-95 as an Example. Journal of Biological Chemistry, 2010, 285, 28252-28260.	3.4	29
43	The evolution of Sex-linked barring alleles in chickens involves both regulatory and coding changes in CDKN2A. PLoS Genetics, 2017, 13, e1006665.	3.5	29
44	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
45	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
46	Seeking allosteric networks in PDZ domains. Protein Engineering, Design and Selection, 2018, 31, 367-373.	2.1	25
47	Evolution of the p53-MDM2 pathway. BMC Evolutionary Biology, 2017, 17, 177.	3.2	23
48	Binding Kinetics of the Intrinsically Disordered p53 Family Transactivation Domains and MDM2. Journal of Physical Chemistry B, 2018, 122, 6899-6905.	2.6	23
49	Folding and stability of globular proteins and implications for function. Current Opinion in Structural Biology, 2009, 19, 3-7.	5.7	22
50	Interactions outside the Boundaries of the Canonical Binding Groove of a PDZ Domain Influence Ligand Binding. Biochemistry, 2012, 51, 8971-8979.	2.5	21
51	The Plastic Energy Landscape of Protein Folding. Journal of Biological Chemistry, 2010, 285, 18051-18059.	3.4	20
52	Disordered Regions Flanking the Binding Interface Modulate Affinity between CBP and NCOA. Journal of Molecular Biology, 2022, 434, 167643.	4.2	20
53	Protein folding: Vexing debates on a fundamental problem. Biophysical Chemistry, 2016, 212, 17-21.	2.8	19
54	Biophysical Characterization of the Complex between Human Papillomavirus E6 Protein and Synapse-associated Protein 97. Journal of Biological Chemistry, 2011, 286, 3597-3606.	3.4	18

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55	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
56	CRISPR/Cas9-based inactivation of human papillomavirus oncogenes E6 or E7 induces senescence in cervical cancer cells. Virology, 2021, 562, 92-102.	2.4	18
57	Double Mutant Cycles as a Tool to Address Folding, Binding, and Allostery. International Journal of Molecular Sciences, 2021, 22, 828.	4.1	17
58	Targeting Protein-Protein Interactions with Trimeric Ligands: High Affinity Inhibitors of the MAGUK Protein Family. PLoS ONE, 2015, 10, e0117668.	2.5	17
59	Design of a PDZbody, a bivalent binder of the E6 protein from human papillomavirus. Scientific Reports, 2015, 5, 9382.	3.3	16
60	An Early Association between the Î±-Helix of the TEAD Binding Domain of YAP and TEAD Drives the Formation of the YAP:TEAD Complex. Biochemistry, 2020, 59, 1804-1812.	2.5	16
61	Conserved nucleation sites reinforce the significance of Phi value analysis in proteinâ€folding studies. IUBMB Life, 2014, 66, 449-452.	3.4	15
62	Rigidified Clicked Dimeric Ligands for Studying the Dynamics of the PDZ1â€2 Supramodule of PSDâ€95. ChemBioChem, 2015, 16, 64-69.	2.6	15
63	Activation Barrier-Limited Folding and Conformational Sampling of a Dynamic Protein Domain. Biochemistry, 2016, 55, 5289-5295.	2.5	14
64	Improved affinity at the cost of decreased specificity: a recurring theme in PDZ-peptide interactions. Scientific Reports, 2016, 6, 34269.	3.3	14
65	Only Kinetics Can Prove Conformational Selection. Biophysical Journal, 2014, 107, 1997-1998.	0.5	13
66	Ligand binding to the PDZ domains of postsynaptic density protein 95. Protein Engineering, Design and Selection, 2016, 29, 169-175.	2.1	13
67	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
68	An expanded view of the protein folding landscape of PDZ domains. Biochemical and Biophysical Research Communications, 2012, 421, 550-553.	2.1	12
69	Tolerance of Protein Folding to a Circular Permutation in a PDZ Domain. PLoS ONE, 2012, 7, e50055.	2.5	12
70	Mapping the transition state for a binding reaction between ancient intrinsically disordered proteins. Journal of Biological Chemistry, 2020, 295, 17698-17712.	3.4	12
71	The Role of Backbone Hydrogen Bonds in the Transition State for Protein Folding of a PDZ Domain. PLoS ONE, 2014, 9, e95619.	2.5	11
72	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

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73	Probing Backbone Hydrogen Bonds in Proteins by Amideâ€toâ€Ester Mutations. ChemBioChem, 2018, 19, 2136-2145.	2.6	11
74	Deconvoluting Protein (Un)folding Structural Ensembles Using X-Ray Scattering, Nuclear Magnetic Resonance Spectroscopy and Molecular Dynamics Simulation. PLoS ONE, 2015, 10, e0125662.	2.5	10
75	How Fast Is Proteinâ€“Ligand Association?. Trends in Biochemical Sciences, 2017, 42, 847-849.	7.5	10
76	Dissecting Inter-domain Cooperativity in the Folding of a Multi Domain Protein. Journal of Molecular Biology, 2021, 433, 167148.	4.2	10
77	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
78	Affinity versus specificity in coupled binding and folding reactions. Protein Engineering, Design and Selection, 2019, 32, 355-357.	2.1	9
79	High affinity between CREBBP /p300 and NCOA evolved in vertebrates. Protein Science, 2020, 29, 1687-1691.	7.6	9
80	Coupled Binding and Helix Formation Monitored by Synchrotron-Radiation Circular Dichroism. Biophysical Journal, 2019, 117, 729-742.	0.5	8
81	Divergent Evolution of a Proteinâ€“Protein Interaction Revealed through Ancestral Sequence Reconstruction and Resurrection. Molecular Biology and Evolution, 2021, 38, 152-167.	8.9	8
82	Structure and Characterization of Phosphoglucomutase 5 from Atlantic and Baltic Herringâ€”An Inactive Enzyme with Intact Substrate Binding. Biomolecules, 2020, 10, 1631.	4.0	4
83	The dynamic properties of a nuclear coactivator binding domain are evolutionarily conserved. Communications Biology, 2022, 5, 286.	4.4	4
84	Development of Monoclonal Antibodies to Detect for SARS-CoV-2 Proteins. Journal of Molecular Biology, 2022, 434, 167583.	4.2	4
85	Molecular Details of a Coupled Binding and Folding Reaction between the Amyloid Precursor Protein and a Folded Domain. ACS Chemical Biology, 2021, 16, 1191-1200.	3.4	3
86	Characterization of the endopeptidase activity of tripeptidyl-peptidase II. Biochemical and Biophysical Research Communications, 2012, 424, 503-507.	2.1	2
87	Kinetic Methods of Deducing Binding Mechanisms Involving Intrinsically Disordered Proteins. Methods in Molecular Biology, 2021, 2263, 105-133.	0.9	1
88	Editorial overview: Folding and binding. Current Opinion in Structural Biology, 2019, 54, 139-140.	5.7	0
89	Direct Quantification of Protein Dimerization Preference Shed Light on SOD1-associated ALS. Journal of Molecular Biology, 2020, 432, 6003-6004.	4.2	0