Per Jemth

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7907081/publications.pdf

Version: 2024-02-01

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	Proteomeâ€scale mapping of binding sites in the unstructured regions of the human proteome. Molecular Systems Biology, 2022, 18, e10584.	7.2	33
2	The dynamic properties of a nuclear coactivator binding domain are evolutionarily conserved. Communications Biology, 2022, 5, 286.	4.4	4
3	Development of Monoclonal Antibodies to Detect for SARS-CoV-2 Proteins. Journal of Molecular Biology, 2022, 434, 167583.	4.2	4
4	Disordered Regions Flanking the Binding Interface Modulate Affinity between CBP and NCOA. Journal of Molecular Biology, 2022, 434, 167643.	4.2	20
5	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
6	Double Mutant Cycles as a Tool to Address Folding, Binding, and Allostery. International Journal of Molecular Sciences, 2021, 22, 828.	4.1	17
7	Kinetic Methods of Deducing Binding Mechanisms Involving Intrinsically Disordered Proteins. Methods in Molecular Biology, 2021, 2263, 105-133.	0.9	1
8	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. Accounts of Chemical Research, 2021, 54, 1251-1259.	15.6	88
9	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
10	Dissecting Inter-domain Cooperativity in the Folding of a Multi Domain Protein. Journal of Molecular Biology, 2021, 433, 167148.	4.2	10
11	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
12	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
13	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
14	Direct Quantification of Protein Dimerization Preference Shed Light on SOD1-associated ALS. Journal of Molecular Biology, 2020, 432, 6003-6004.	4.2	0
15	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
16	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
17	High affinity between CREBBP /p300 and NCOA evolved in vertebrates. Protein Science, 2020, 29, 1687-1691.	7.6	9
18	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

#	Article	IF	Citations
19	Templated folding of intrinsically disordered proteins. Journal of Biological Chemistry, 2020, 295, 6586-6593.	3.4	44
20	Mapping the transition state for a binding reaction between ancient intrinsically disordered proteins. Journal of Biological Chemistry, 2020, 295, 17698-17712.	3.4	12
21	Affinity versus specificity in coupled binding and folding reactions. Protein Engineering, Design and Selection, 2019, 32, 355-357.	2.1	9
22	Coupled Binding and Helix Formation Monitored by Synchrotron-Radiation Circular Dichroism. Biophysical Journal, 2019, 117, 729-742.	0.5	8
23	A structurally heterogeneous transition state underlies coupled binding and folding of disordered proteins. Journal of Biological Chemistry, 2019, 294, 1230-1239.	3.4	39
24	Editorial overview: Folding and binding. Current Opinion in Structural Biology, 2019, 54, 139-140.	5.7	0
25	Affinity and specificity of motif-based proteinâ€“protein interactions. Current Opinion in Structural Biology, 2019, 54, 26-33.	5.7	88
26	Seeking allosteric networks in PDZ domains. Protein Engineering, Design and Selection, 2018, 31, 367-373.	2.1	25
27	Structure and dynamics conspire in the evolution of affinity between intrinsically disordered proteins. Science Advances, 2018, 4, eaau4130.	10.3	38
28	Probing Backbone Hydrogen Bonds in Proteins by Amideâ€toâ€Ester Mutations. ChemBioChem, 2018, 19, 2136-2145.	2.6	11
29	Binding Kinetics of the Intrinsically Disordered p53 Family Transactivation Domains and MDM2. Journal of Physical Chemistry B, 2018, 122, 6899-6905.	2.6	23
30	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
31	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
32	How Fast Is Proteinâ€“Ligand Association?. Trends in Biochemical Sciences, 2017, 42, 847-849.	7.5	10
33	Evolution of the p53-MDM2 pathway. BMC Evolutionary Biology, 2017, 17, 177.	3.2	23
34	Emergence and evolution of an interaction between intrinsically disordered proteins. ELife, 2017, 6, .	6.0	42
35	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
36	Ligand binding to the PDZ domains of postsynaptic density protein 95. Protein Engineering, Design and Selection, 2016, 29, 169-175.	2.1	13

#	Article	IF	Citations
37	Activation Barrier-Limited Folding and Conformational Sampling of a Dynamic Protein Domain. Biochemistry, 2016, 55, 5289-5295.	2.5	14
38	Improved affinity at the cost of decreased specificity: a recurring theme in PDZ-peptide interactions. Scientific Reports, 2016, 6, 34269.	3.3	14
39	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
40	Protein folding: Vexing debates on a fundamental problem. Biophysical Chemistry, 2016, 212, 17-21.	2.8	19
41	Design of a PDZbody, a bivalent binder of the E6 protein from human papillomavirus. Scientific Reports, 2015, 5, 9382.	3.3	16
42	Rigidified Clicked Dimeric Ligands for Studying the Dynamics of the PDZ1â€2 Supramodule of PSDâ€95. ChemBioChem, 2015, 16, 64-69.	2.6	15
43	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
44	Binding Rate Constants Reveal Distinct Features of Disordered Protein Domains. Biochemistry, 2015, 54, 4741-4750.	2.5	51
45	Targeting Protein-Protein Interactions with Trimeric Ligands: High Affinity Inhibitors of the MAGUK Protein Family. PLoS ONE, 2015, 10, e0117668.	2.5	17
46	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
47	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
48	Conserved nucleation sites reinforce the significance of Phi value analysis in proteinâ€folding studies. IUBMB Life, 2014, 66, 449-452.	3.4	15
49	A Frustrated Binding Interface for Intrinsically Disordered Proteins. Journal of Biological Chemistry, 2014, 289, 5528-5533.	3.4	39
50	Distinguishing induced fit from conformational selection. Biophysical Chemistry, 2014, 189, 33-39.	2.8	139
51	The binding mechanisms of intrinsically disordered proteins. Physical Chemistry Chemical Physics, 2014, 16, 6323-6331.	2.8	124
52	Only Kinetics Can Prove Conformational Selection. Biophysical Journal, 2014, 107, 1997-1998.	0.5	13
53	Probing backbone hydrogen bonding in PDZ/ligand interactions by protein amide-to-ester mutations. Nature Communications, 2014, 5, 3215.	12.8	33
54	Helical Propensity in an Intrinsically Disordered Protein Accelerates Ligand Binding. Angewandte Chemie - International Edition, 2014, 53, 1548-1551.	13.8	146

#	Article	IF	Citations
55	Energetic Pathway Sampling in a Protein Interaction Domain. Structure, 2013, 21, 1193-1202.	3.3	38
56	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
57	Single molecule unfolding and stretching of protein domains inside a solid-state nanopore by electric field. Scientific Reports, 2013, 3, 1638.	3.3	157
58	The transition state structure for coupled binding and folding of disordered protein domains. Scientific Reports, 2013, 3, 2076.	3.3	87
59	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
60	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
61	Interactions outside the Boundaries of the Canonical Binding Groove of a PDZ Domain Influence Ligand Binding. Biochemistry, 2012, 51, 8971-8979.	2.5	21
62	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
63	The Transition State of Coupled Folding and Binding for a Flexible Î²-Finger. Journal of Molecular Biology, 2012, 417, 253-261.	4.2	38
64	An expanded view of the protein folding landscape of PDZ domains. Biochemical and Biophysical Research Communications, 2012, 421, 550-553.	2.1	12
65	Characterization of the endopeptidase activity of tripeptidyl-peptidase II. Biochemical and Biophysical Research Communications, 2012, 424, 503-507.	2.1	2
66	Tolerance of Protein Folding to a Circular Permutation in a PDZ Domain. PLoS ONE, 2012, 7, e50055.	2.5	12
67	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
68	Ligand binding by PDZ domains. BioFactors, 2012, 38, 338-348.	5.4	66
69	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
70	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
71	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
72	The Plastic Energy Landscape of Protein Folding. Journal of Biological Chemistry, 2010, 285, 18051-18059.	3.4	20

#	Article	IF	Citations
73	Folding and stability of globular proteins and implications for function. Current Opinion in Structural Biology, 2009, 19, 3-7.	5.7	22
74	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
75	A Sequential Binding Mechanism in a PDZ Domain. Biochemistry, 2009, 48, 7089-7097.	2.5	46
76	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
77	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
78	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
79	An On-pathway Intermediate in the Folding of a PDZ Domain. Journal of Biological Chemistry, 2007, 282, 8568-8572.	3.4	42
80	PDZ Domains:â€‰ Folding and Binding. Biochemistry, 2007, 46, 8701-8708.	2.5	154
81	A conserved folding mechanism for PDZ domains. FEBS Letters, 2007, 581, 1109-1113.	2.8	45
82	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
83	Identification and characterization of protein folding intermediates. Biophysical Chemistry, 2007, 128, 105-113.	2.8	69
84	Demonstration of Long-Range Interactions in a PDZ Domain by NMR, Kinetics, and Protein Engineering. Structure, 2006, 14, 1801-1809.	3.3	103
85	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
86	The Kinetics of PDZ Domain-Ligand Interactions and Implications for the Binding Mechanism. Journal of Biological Chemistry, 2005, 280, 34805-34812.	3.4	87
87	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
88	Oligosaccharide Library-based Assessment of Heparan Sulfate 6-O-Sulfotransferase Substrate Specificity. Journal of Biological Chemistry, 2003, 278, 24371-24376.	3.4	35
89	Biosynthetic Oligosaccharide Libraries for Identification of Protein-binding Heparan Sulfate Motifs. Journal of Biological Chemistry, 2002, 277, 30567-30573.	3.4	90