PÃ©tÃ©r S Tompa

List of Publications by Year
in descending order

187 papers	25,036 citations	16450 64 h-index	7744 150 g-index
194 all docs	194 docs citations	194 times ranked	21467 citing authors

#	Article	IF	Citations
1	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	14.5	117
2	F/YGG-motif is an intrinsically disordered nucleic-acid binding motif. RNA Biology, 2022, 19, 622-635.	3.1	7
3	Degron masking outlines degronons, co-degrading functional modules in the proteome. Communications Biology, 2022, 5, 445.	4.4	7
4	â€œProteinâ€• no longer means what it used to. Current Research in Structural Biology, 2021, 3, 146-152.	2.2	3
5	Integration of Data from Liquidâ€"Liquid Phase Separation Databases Highlights Concentration and Dosage Sensitivity of LLPS Drivers. International Journal of Molecular Sciences, 2021, 22, 3017.	4.1	29
6	Liquidâ€"Liquid Phase Separation Enhances TDP-43 LCD Aggregation but Delays Seeded Aggregation. Biomolecules, 2021, 11, 548.	4.0	18
7	DNAâ€binding domain as the minimal region driving RNAâ€dependent liquidâ€"liquid phase separation of androgen receptor. Protein Science, 2021, 30, 1380-1392.	7.6	21
8	Cellular Chaperone Function of Intrinsically Disordered Dehydrin ERD14. International Journal of Molecular Sciences, 2021, 22, 6190.	4.1	11
9	Exploring Curated Conformational Ensembles of Intrinsically Disordered Proteins in the Protein Ensemble Database. Current Protocols, 2021, 1, e192.	2.9	4
10	The role of ordered cooperative assembly in biomolecular condensates. Nature Reviews Molecular Cell Biology, 2021, 22, 647-648.	37.0	17
11	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. Nucleic Acids Research, 2021, 49, D404-D411.	14.5	95
12	A generic approach to study the kinetics of liquidâ€"liquid phase separation under near-native conditions. Communications Biology, 2021, 4, 77.	4.4	39
13	PhaSePro: the database of proteins driving liquidâ€"liquid phase separation. Nucleic Acids Research, 2020, 48, D360-D367.	14.5	100
14	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	14.5	141
15	Dehydrin ERD14 activates glutathione transferase Phi9 in Arabidopsis thaliana under osmotic stress. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129506.	2.4	28
16	Interplay of Structural Disorder and Short Binding Elements in the Cellular Chaperone Function of Plant Dehydrin ERD14. Cells, 2020, 9, 1856.	4.1	12
17	Chasing coevolutionary signals in intrinsically disordered proteins complexes. Scientific Reports, 2020, 10, 17962.	3.3	7
18	Specific Conformational Dynamics and Expansion Underpin a Multi-Step Mechanism for Specific Binding of p27 with Cdk2/Cyclin A. Journal of Molecular Biology, 2020, 432, 2998-3017.	4.2	26

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19	WT and A53T Î±-Synuclein Systems: Melting Diagram and Its New Interpretation. International Journal of Molecular Sciences, 2020, 21, 3997.	4.1	7
20	A guide to regulation of the formation of biomolecular condensates. FEBS Journal, 2020, 287, 1924-1935.	4.7	48
21	Interaction between the scaffold proteins CBP by IQGAP1 provides an interface between gene expression and cytoskeletal activity. Scientific Reports, 2020, 10, 5753.	3.3	6
22	Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. Biophysical Journal, 2020, 118, 2952-2965.	0.5	17
23	Learning of Signaling Networks: Molecular Mechanisms. Trends in Biochemical Sciences, 2020, 45, 284-294.	7.5	29
24	Targeting an Intrinsically Disordered Protein by Covalent Modification. Methods in Molecular Biology, 2020, 2141, 835-854.	0.9	1
25	Focusing of Microcrystals and Liquid Condensates in Acoustofluidics. Crystals, 2019, 9, 120.	2.2	7
26	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. Journal of Molecular Biology, 2019, 431, 1650-1670.	4.2	41
27	Emergent functions of proteins in non-stoichiometric supramolecular assemblies. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 970-979.	2.3	49
28	Dynamic anticipation by Cdk2/Cyclin A-bound p27 mediates signal integration in cell cycle regulation. Nature Communications, 2019, 10, 1676.	12.8	71
29	Spontaneous driving forces give rise to proteinâˆ’RNA condensates with coexisting phases and complex material properties. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7889-7898.	7.1	365
30	Misprediction of Structural Disorder in Halophiles. Molecules, 2019, 24, 479.	3.8	5
31	Does Intrinsic Disorder in Proteins Favor Their Interaction with Lipids?. Proteomics, 2019, 19, e1800098.	2.2	18
32	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
33	Calpain Purification Through Calpastatin and Calcium: Strategy and Procedures. Methods in Molecular Biology, 2019, 1929, 233-244.	0.9	1
34	Chemical shift assignments of the partially deuterated Fyn SH2â€“SH3 domain. Biomolecular NMR Assignments, 2018, 12, 117-122.	0.8	0
35	In vivo biotinylated calpastatin improves the affinity purification of human m-calpain. Protein Expression and Purification, 2018, 145, 77-84.	1.3	6
36	A comprehensive assessment of long intrinsic protein disorder from the DisProt database. Bioinformatics, 2018, 34, 445-452.	4.1	53

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37	Protein Phase Separation: A New Phase in Cell Biology. Trends in Cell Biology, 2018, 28, 420-435.	7.9	1,439
38	AmyPro: a database of proteins with validated amyloidogenic regions. Nucleic Acids Research, 2018, 46, D387-D392.	14.5	59
39	The Melting Diagram of Protein Solutions and Its Thermodynamic Interpretation. International Journal of Molecular Sciences, 2018, 19, 3571.	4.1	5
40	Co-Evolution of Intrinsically Disordered Proteins with Folded Partners Witnessed by Evolutionary Couplings. International Journal of Molecular Sciences, 2018, 19, 3315.	4.1	23
41	Challenges in the Structuralâ€"Functional Characterization of Multidomain, Partially Disordered Proteins CBP and p300: Preparing Native Proteins and Developing Nanobody Tools. Methods in Enzymology, 2018, 611, 607-675.	1.0	7
42	Unique Physicochemical Patterns of Residues in Proteinâ€"Protein Interfaces. Journal of Chemical Information and Modeling, 2018, 58, 2164-2173.	5.4	7
43	Disordered Substrates of the 20S Proteasome Link Degradation with Phase Separation. Proteomics, 2018, 18, e1800276.	2.2	3
44	Phasing in on the cell cycle. Cell Division, 2018, 13, 1.	2.4	33
45	Quantification of Intrinsically Disordered Proteins: A Problem Not Fully Appreciated. Frontiers in Molecular Biosciences, 2018, 5, 83.	3.5	26
46	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	14.5	190
47	Yeast and Cancer: Common Mechanism Underlying Activation of Ras by Glycolytic Flux. FASEB Journal, 2018, 32, lb143.	0.5	0
48	Hydrogen Mobility and Proteinâ€"Water Interactions in Proteins in the Solid State. ChemPhysChem, 2017, 18, 677-682.	2.1	11
49	1H, 15N, 13C resonance assignment of plant dehydrin early response to dehydration 10 (ERD10). Biomolecular NMR Assignments, 2017, 11, 127-131.	0.8	3
50	Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins. , 2017, , 167-203.		5
51	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	14.5	242
52	To be disordered or not to be disordered: is that still a question for proteins in the cell?. Cellular and Molecular Life Sciences, 2017, 74, 3185-3204.	5.4	33
53	Phase Separation of C9orf72 Dipeptide Repeats Perturbs Stress Granule Dynamics. Molecular Cell, 2017, 65, 1044-1055.e5.	9.7	437
54	Simultaneous quantification of protein order and disorder. Nature Chemical Biology, 2017, 13, 339-342.	8.0	113

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55	Linking functions: an additional role for an intrinsically disordered linker domain in the transcriptional coactivator CBP. Scientific Reports, 2017, 7, 4676.	3.3	39
56	Phosphorylation of MAP65-1 by Arabidopsis Aurora Kinases Is Required for Efficient Cell Cycle Progression. Plant Physiology, 2017, 173, 582-599.	4.8	44
57	Protein Delivery into Plant Cells: Toward In vivo Structural Biology. Frontiers in Plant Science, 2017, 8, 519.	3.6	14
58	Affinity purification of human m-calpain through an intrinsically disordered inhibitor, calpastatin. PLoS ONE, 2017, 12, e0174125.	2.5	6
59	Arginine-rich Peptides Can Actively Mediate Liquid-liquid Phase Separation. Bio-protocol, 2017, 7, e2525.	0.4	23
60	Editorial: Function and Flexibility: Friend or Foe?. Frontiers in Molecular Biosciences, 2016, 3, 31.	3.5	6
61	Numerous proteins with unique characteristics are degraded by the 26S proteasome following monoubiquitination. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4639-47.	7.1	127
62	Essential functions linked with structural disorder in organisms of minimal genome. Biology Direct, 2016, 11, 45.	4.6	4
63	Start2Fold: a database of hydrogen/deuterium exchange data on protein folding and stability. Nucleic Acids Research, 2016, 44, D429-D434.	14.5	28
64	Coding Regions of Intrinsic Disorder Accommodate Parallel Functions. Trends in Biochemical Sciences, 2016, 41, 898-906.	7.5	20
65	Computational analysis of translational readthrough proteins in Drosophila and yeast reveals parallels to alternative splicing. Scientific Reports, 2016, 6, 32142.	3.3	9
66	Three reasons protein disorder analysis makes more sense in the light of collagen. Protein Science, 2016, 25, 1030-1036.	7.6	7
67	The principle of conformational signaling. Chemical Society Reviews, 2016, 45, 4252-4284.	38.1	46
68	Just a Flexible Linker? The Structural and Dynamic Properties of CBP-ID4 Revealed by NMR Spectroscopy. Biophysical Journal, 2016, 110, 372-381.	0.5	29
69	Design Principles Involving Protein Disorder Facilitate Specific Substrate Selection and Degradation by the Ubiquitin-Proteasome System. Journal of Biological Chemistry, 2016, 291, 6723-6731.	3.4	47
70	Tripartite degrons confer diversity and specificity on regulated protein degradation in the ubiquitin-proteasome system. Nature Communications, 2016, 7, 10239.	12.8	110
71	A Novel Method for Assessing the Chaperone Activity of Proteins. PLoS ONE, 2016, 11, e0161970.	2.5	18
72	Wide-line NMR and DSC studies on intrinsically disordered p53 transactivation domain and its helically pre-structured segment. BMB Reports, 2016, 49, 497-501.	2.4	4

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73	Computational approaches for inferring the functions of intrinsically disordered proteins. Frontiers in Molecular Biosciences, 2015, 2, 45.	3.5	37
74	Functional Advantages of Conserved Intrinsic Disorder in RNA-Binding Proteins. PLoS ONE, 2015, 10, e0139731.	2.5	100
75	SnapShot: Intrinsic Structural Disorder. Cell, 2015, 161, 1230-1230.e1.	28.9	16
76	DisCons: a novel tool to quantify and classify evolutionary conservation of intrinsic protein disorder. BMC Bioinformatics, 2015, 16, 153.	2.6	23
77	The role of structural disorder in cell cycle regulation, related clinical proteomics, disease development and drug targeting. Expert Review of Proteomics, 2015, 12, 221-233.	3.0	14
78	Intrinsically disordered proteins: emerging interaction specialists. Current Opinion in Structural Biology, 2015, 35, 49-59.	5.7	177
79	Polymer physics of intracellular phase transitions. Nature Physics, 2015, 11, 899-904.	16.7	1,145
80	Post-Translational Modification of P27 Regulates Signal Transmission via a Dynamic Interaction with Cdk2/Cyclin. Biophysical Journal, 2015, 108, 193a.	0.5	1
81	The Protein Ensemble Database. Advances in Experimental Medicine and Biology, 2015, 870, 335-349.	1.6	23
82	Ensemble Methods Enable a New Definition for the Solution to Gas-Phase Transfer of Intrinsically Disordered Proteins. Journal of the American Chemical Society, 2015, 137, 13807-13817.	13.7	44
83	Disordered regions in transmembrane proteins. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 2839-2848.	2.6	28
84	Towards Understanding Protein Disorder In-Cell. Advances in Experimental Medicine and Biology, 2015, 870, 319-334.	1.6	3
85	Bioinformatics Approaches for Predicting Disordered Protein Motifs. Advances in Experimental Medicine and Biology, 2015, 870, 291-318.	1.6	23
86	Redefining the BH3 Death Domain as a â€˜Short Linear Motifâ€™. Trends in Biochemical Sciences, 2015, 40, 736-748.	7.5	57
87	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. Nucleic Acids Research, 2014, 42, D326-D335.	14.5	195
88	Synonymous Constraint Elements Show a Tendency to Encode Intrinsically Disordered Protein Segments. PLoS Computational Biology, 2014, 10, e1003607.	3.2	21
89	The DynaMine webserver: predicting protein dynamics from sequence. Nucleic Acids Research, 2014, 42, W264-W270.	14.5	125
90	Predicting the Predictive Power of IDP Ensembles. Structure, 2014, 22, 177-178.	3.3	21

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91	Introducing Protein Intrinsic Disorder. Chemical Reviews, 2014, 114, 6561-6588.	47.7	628
92	Multisteric Regulation by Structural Disorder in Modular Signaling Proteins: An Extension of the Concept of Allostery. Chemical Reviews, 2014, 114, 6715-6732.	47.7	96
93	Contribution of proline to the pre-structuring tendency of transient helical secondary structure elements in intrinsically disordered proteins. Biochimica Et Biophysica Acta - General Subjects, 2014, 1840, 993-1003.	2.4	26
94	A Million Peptide Motifs for the Molecular Biologist. Molecular Cell, 2014, 55, 161-169.	9.7	429
95	Classification of Intrinsically Disordered Regions and Proteins. Chemical Reviews, 2014, 114, 6589-6631.	47.7	1,618
96	Discrete Molecular Dynamics Can Predict Helical Prestructured Motifs in Disordered Proteins. PLoS ONE, 2014, 9, e95795.	2.5	19
97	From protein sequence to dynamics and disorder with DynaMine. Nature Communications, 2013, 4, 2741.	12.8	139
98	Molecular Mechanism of SSR128129E, an Extracellularly Acting, Small-Molecule, Allosteric Inhibitor of FGF Receptor Signaling. Cancer Cell, 2013, 23, 489-501.	16.8	125
99	New mâ€calpain substrateâ€based azapeptide inhibitors. Journal of Peptide Science, 2013, 19, 370-376.	1.4	6
100	Intrinsic Structural Disorder in Cytoskeletal Proteins. Cytoskeleton, 2013, 70, 550-571.	2.0	52
101	Multiple fuzzy interactions in the moonlighting function of thymosin-Î²4. Intrinsically Disordered Proteins, 2013, 1, e26204.	1.9	12
102	Hydrogel formation by multivalent IDPs: A reincarnation of the microtrabecular lattice?. Intrinsically Disordered Proteins, 2013, 1, e24068.	1.9	9
103	Polycation-Ï€ Interactions Are a Driving Force for Molecular Recognition by an Intrinsically Disordered Oncoprotein Family. PLoS Computational Biology, 2013, 9, e1003239.	3.2	57
104	Whatâ€™s in a name? Why these proteins are intrinsically disordered. Intrinsically Disordered Proteins, 2013, 1, e24157.	1.9	226
105	Structural Disorder Provides Increased Adaptability for Vesicle Trafficking Pathways. PLoS Computational Biology, 2013, 9, e1003144.	3.2	46
106	Hydrogen skeleton, mobility and protein architecture. Intrinsically Disordered Proteins, 2013, 1, e25767.	1.9	3
107	The alphabet of intrinsic disorder. Intrinsically Disordered Proteins, 2013, 1, e24360.	1.9	208
108	Exon-phase symmetry and intrinsic structural disorder promote modular evolution in the human genome. Nucleic Acids Research, 2013, 41, 4409-4422.	14.5	15

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109	Structural Characterization of Intrinsically Disordered Proteins by NMR Spectroscopy. Molecules, 2013, 18, 10802-10828.	3.8	146
110	Functional Diversity and Structural Disorder in the Human Ubiquitination Pathway. PLoS ONE, 2013, 8, e65443.	2.5	27
111	Diverse functional manifestations of intrinsic structural disorder in molecular chaperones. Biochemical Society Transactions, 2012, 40, 963-968.	3.4	34
112	Structural Disorder in Eukaryotes. PLoS ONE, 2012, 7, e34687.	2.5	157
113	Intrinsically disordered proteins: a 10-year recap. Trends in Biochemical Sciences, 2012, 37, 509-516.	7.5	543
114	Structural disorder in proteins brings order to crystal growth in biomineralization. Bone, 2012, 51, 528-534.	2.9	107
115	On the supertertiary structure of proteins. Nature Chemical Biology, 2012, 8, 597-600.	8.0	66
116	Fuzzy Complexes: A More Stochastic View of Protein Function. Advances in Experimental Medicine and Biology, 2012, 725, 1-14.	1.6	183
117	Long-Range Interactions in Nonsense-Mediated mRNA Decay Are Mediated by Intrinsically Disordered Protein Regions. Journal of Molecular Biology, 2012, 424, 125-131.	4.2	7
118	Increased structural disorder of proteins encoded on human sex chromosomes. Molecular BioSystems, 2012, 8, 229-236.	2.9	22
119	Intrinsic disorder in cell signaling and gene transcription. Molecular and Cellular Endocrinology, 2012, 348, 457-465.	3.2	101
120	Unstructural biology coming of age. Current Opinion in Structural Biology, 2011, 21, 419-425.	5.7	277
121	Full backbone assignment and dynamics of the intrinsically disordered dehydrin ERD14. Biomolecular NMR Assignments, 2011, 5, 189-193.	0.8	36
122	The Levinthal paradox of the interactome. Protein Science, 2011, 20, 2074-2079.	7.6	30
123	Structural Flexibility Allows the Functional Diversity of Potyvirus Genome-Linked Protein VPg. Journal of Virology, 2011, 85, 2449-2457.	3.4	67
124	Verification of alternative splicing variants based on domain integrity, truncation length and intrinsic protein disorder. Nucleic Acids Research, 2011, 39, 1208-1219.	14.5	46
125	Accessory proteins in signal transduction: scaffold proteins and beyond. FEBS Journal, 2010, 277, 4347-4347.	4.7	6
126	Functional classification of scaffold proteins and related molecules. FEBS Journal, 2010, 277, 4348-4355.	4.7	70

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127	Reduction in Structural Disorder and Functional Complexity in the Thermal Adaptation of Prokaryotes. PLoS ONE, 2010, 5, e12069.	2.5	69
128	Dual coding in alternative reading frames correlates with intrinsic protein disorder. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5429-5434.	7.1	92
129	Power Law Distribution Defines Structural Disorder as a Structural Element Directly Linked with Function. Journal of Molecular Biology, 2010, 403, 346-350.	4.2	29
130	Intrinsically disordered chaperones in plants and animalsThis paper is one of a selection of papers published in this special issue entitled â€œCanadian Society of Biochemistry, Molecular & Cellular Biology 52nd Annual Meeting â€” Protein Folding: Principles and Diseasesâ€•and has undergone the Journal's usual peer review process.. Biochemistry and Cell Biology, 2010, 88, 167-174.	2.0	125
131	Intrinsic Structural Disorder Confers Cellular Viability on Oncogenic Fusion Proteins. PLoS Computational Biology, 2009, 5, e1000552.	3.2	74
132	The androgen receptor gene polyglycine repeat polymorphism is associated with memory performance in healthy Chinese individuals. Psychoneuroendocrinology, 2009, 34, 947-952.	2.7	10
133	Fuzzy interactome: the limitations of models in molecular biology. Trends in Biochemical Sciences, 2009, 34, 3.	7.5	11
134	Janus chaperones: Assistance of both RNAâ€•and proteinâ€ƒolding by ribosomal proteins. FEBS Letters, 2009, 583, 88-92.	2.8	41
135	Cold stability of intrinsically disordered proteins. FEBS Letters, 2009, 583, 465-469.	2.8	50
136	Close encounters of the third kind: disordered domains and the interactions of proteins. BioEssays, 2009, 31, 328-335.	2.5	229
137	High levels of structural disorder in scaffold proteins as exemplified by a novel neuronal protein, CASKâ€interactive protein1. FEBS Journal, 2009, 276, 3744-3756.	4.7	65
138	Interfacial Water at Protein Surfaces: Wide-Line NMR and DSC Characterization of Hydration in Ubiquitin Solutions. Biophysical Journal, 2009, 96, 2789-2798.	0.5	42
139	Binding-induced folding transitions in calpastatin subdomains A and C. Protein Science, 2009, 12, 2327-2336.	7.6	32
140	Malleable machines take shape in eukaryotic transcriptional regulation. Nature Chemical Biology, 2008, 4, 728-737.	8.0	192
141	Calciumâ€induced tripartite binding of intrinsically disordered calpastatin to its cognate enzyme, calpain. FEBS Letters, 2008, 582, 2149-2154.	2.8	29
142	Fuzzy complexes: polymorphism and structural disorder in proteinâ€“protein interactions. Trends in Biochemical Sciences, 2008, 33, 2-8.	7.5	942
143	Structural and Dynamic Characterization of Intrinsically Disordered Human Securin by NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 16873-16879.	13.7	67
144	Intrinsic Structural Disorder of DF31, a <i>Drosophila</i> Protein of Chromatin Decondensation and Remodeling Activities. Journal of Proteome Research, 2008, 7, 2291-2299.	3.7	18

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145	Chaperone Activity of ERD10 and ERD14, Two Disordered Stress-Related Plant Proteins. Plant Physiology, 2008, 147, 381-390.	4.8	373
146	Disordered plant LEA proteins as molecular chaperones. Plant Signaling and Behavior, 2008, 3, 710-713.	2.4	65
147	Intrinsically Disordered Proteins Display No Preference for Chaperone Binding In Vivo. PLoS Computational Biology, 2008, 4, e1000017.	3.2	48
148	Prediction of Protein Disorder at the Domain Level. Current Protein and Peptide Science, 2007, 8, 161-171.	1.4	71
149	Towards Proteomic Approaches for the Identification of Structural Disorder. Current Protein and Peptide Science, 2007, 8, 173-179.	1.4	20
150	Local structural disorder imparts plasticity on linear motifs. Bioinformatics, 2007, 23, 950-956.	4.1	376
151	Molecular Principles of the Interactions of Disordered Proteins. Journal of Molecular Biology, 2007, 372, 549-561.	4.2	242
152	DisProt: the Database of Disordered Proteins. Nucleic Acids Research, 2007, 35, D786-D793.	14.5	711
153	Synthesis of Cell-Penetrating Conjugates of Calpain Activator Peptides. Bioconjugate Chemistry, 2007, 18, 130-137.	3.6	17
154	Structural disorder promotes assembly of protein complexes. BMC Structural Biology, 2007, 7, 65.	2.3	96
155	Disorder and Sequence Repeats in Hub Proteins and Their Implications for Network Evolution. Journal of Proteome Research, 2006, 5, 2985-2995.	3.7	312
156	Prevalent Structural Disorder inE.coliandS.cerevisiaeProteomes. Journal of Proteome Research, 2006, 5, 1996-2000.	3.7	119
157	CG15031/PPYR1 is an intrinsically unstructured protein that interacts with protein phosphatase Y. Archives of Biochemistry and Biophysics, 2006, 451, 59-67.	3.0	10
158	Phosphorylation-induced transient intrinsic structure in the kinase-inducible domain of CREB facilitates its recognition by the KIX domain of CBP. Proteins: Structure, Function and Bioinformatics, 2006, 64, 749-757.	2.6	31
159	A Novel Two-dimensional Electrophoresis Technique for the Identification of Intrinsically Unstructured Proteins. Molecular and Cellular Proteomics, 2006, 5, 265-273.	3.8	65
160	Structural disorder throws new light on moonlighting. Trends in Biochemical Sciences, 2005, 30, 484-489.	7.5	430
161	IUPred: web server for the prediction of intrinsically unstructured regions of proteins based on estimated energy content. Bioinformatics, 2005, 21, 3433-3434.	4.1	1,832
162	Primary Contact Sites in Intrinsically Unstructured Proteins:Â The Case of Calpastatin and Microtubule-Associated Protein 2â€. Biochemistry, 2005, 44, 3955-3964.	2.5	97

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163	The Pairwise Energy Content Estimated from Amino Acid Composition Discriminates between Folded and Intrinsically Unstructured Proteins. Journal of Molecular Biology, 2005, 347, 827-839.	4.2	911
164	The interplay between structure and function in intrinsically unstructured proteins. FEBS Letters, 2005, 579, 3346-3354.	2.8	634
165	NMR Relaxation Studies on the Hydrate Layer of Intrinsically Unstructured Proteins. Biophysical Journal, 2005, 88, 2030-2037.	0.5	89
166	The role of structural disorder in the function of RNA and protein chaperones. FASEB Journal, 2004, 18, 1169-1175.	0.5	496
167	On the Sequential Determinants of Calpain Cleavage. Journal of Biological Chemistry, 2004, 279, 20775-20785.	3.4	279
168	Contribution of Distinct Structural Elements to Activation of Calpain by Ca2+ Ions. Journal of Biological Chemistry, 2004, 279, 20118-20126.	3.4	24
169	Differential distribution of calpain small subunit 1 and 2 in rat brain. European Journal of Neuroscience, 2004, 19, 1819-1825.	2.6	10
170	Calpain as a multi-site regulator of cell cycle. Biochemical Pharmacology, 2004, 67, 1513-1521.	4.4	47
171	The calpain-system ofDrosophila melanogaster: coming of age. BioEssays, 2004, 26, 1088-1096.	2.5	32
172	Preformed Structural Elements Feature in Partner Recognition by Intrinsically Unstructured Proteins. Journal of Molecular Biology, 2004, 338, 1015-1026.	4.2	494
173	Intrinsically unstructured proteins evolve by repeat expansion. BioEssays, 2003, 25, 847-855.	2.5	247
174	Molecular cloning and RNA expression of a novel Drosophila calpain, Calpain C. Biochemical and Biophysical Research Communications, 2003, 303, 343-349.	2.1	15
175	Calpastatin Subdomains A and C Are Activators of Calpain. Journal of Biological Chemistry, 2002, 277, 9022-9026.	3.4	50
176	The Role of Dimerization in Prion Replication. Biophysical Journal, 2002, 82, 1711-1718.	0.5	51
177	Intrinsically unstructured proteins. Trends in Biochemical Sciences, 2002, 27, 527-533.	7.5	1,868
178	Domain III of Calpain Is a Ca2+-Regulated Phospholipid-Binding Domain. Biochemical and Biophysical Research Communications, 2001, 280, 1333-1339.	2.1	147
179	Synaptic metaplasticity and the local charge effect in postsynaptic densities. Trends in Neurosciences, 1998, 21, 97-102.	8.6	20
180	Phosphorylation and Dephosphorylation in the Proline-Rich C-Terminal Domain of Microtubule-Associated Protein 2. FEBS Journal, 1996, 241, 765-771.	0.2	51

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181	The Calpain Cascade. Journal of Biological Chemistry, 1996, 271, 33161-33164.	3.4	50
182	Interaction of rabbit muscle enolase and 3-phosphoglycerate mutase studied by ELISA and by batch gel filtration. Archives of Biochemistry and Biophysics, 1992, 296, 650-653.	3.0	12
183	A possible in vivo mechanism of intermediate transfer by glycolytic enzyme complexes: Steady state fluorescence anisotropy analysis of an enzyme complex formation. Archives of Biochemistry and Biophysics, 1992, 296, 654-659.	3.0	1
184	The mechanism of succinate or fumarate transfer in the tricarboxylic acid cycle allows molecular rotation of the intermediate. Archives of Biochemistry and Biophysics, 1990, 276, 191-198.	3.0	17
185	How to determine the efficiency of intermediate transfer in an interacting enzyme system?. FEBS Letters, 1987, 214, 244-248.	2.8	19
186	The phosphate group of 3-phosphoglycerate accounts for conformational changes occurring on binding to 3-phosphoglycerate kinase. Enzyme inhibition and thiol reactivity studies. FEBS Journal, 1986, 154, 643-649.	0.2	35
187	Interaction of enzymes involved in triosephosphate metabolism. Comparison of yeast and rabbit muscle cytoplasmic systems. FEBS Journal, 1986, 159, 117-124.	0.2	26