

Ptr S Tompa

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

187
papers

19,582
citations

58
h-index

139
g-index

194
ext. papers

22,885
ext. citations

8.6
avg, IF

7.33
L-index

#	Paper	IF	Citations
187	Intrinsically unstructured proteins. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 527-33	10.3	1663
186	IUPred: web server for the prediction of intrinsically unstructured regions of proteins based on estimated energy content. <i>Bioinformatics</i> , 2005 , 21, 3433-4	7.2	1571
185	Classification of intrinsically disordered regions and proteins. <i>Chemical Reviews</i> , 2014 , 114, 6589-631	68.1	1141
184	Protein Phase Separation: A New Phase in Cell Biology. <i>Trends in Cell Biology</i> , 2018 , 28, 420-435	18.3	869
183	Fuzzy complexes: polymorphism and structural disorder in protein-protein interactions. <i>Trends in Biochemical Sciences</i> , 2008 , 33, 2-8	10.3	788
182	The pairwise energy content estimated from amino acid composition discriminates between folded and intrinsically unstructured proteins. <i>Journal of Molecular Biology</i> , 2005 , 347, 827-39	6.5	767
181	Polymer physics of intracellular phase transitions. <i>Nature Physics</i> , 2015 , 11, 899-904	16.2	705
180	DisProt: the Database of Disordered Proteins. <i>Nucleic Acids Research</i> , 2007 , 35, D786-93	20.1	631
179	The interplay between structure and function in intrinsically unstructured proteins. <i>FEBS Letters</i> , 2005 , 579, 3346-54	3.8	563
178	Introducing protein intrinsic disorder. <i>Chemical Reviews</i> , 2014 , 114, 6561-88	68.1	487
177	The role of structural disorder in the function of RNA and protein chaperones. <i>FASEB Journal</i> , 2004 , 18, 1169-75	0.9	456
176	Intrinsically disordered proteins: a 10-year recap. <i>Trends in Biochemical Sciences</i> , 2012 , 37, 509-16	10.3	451
175	Preformed structural elements feature in partner recognition by intrinsically unstructured proteins. <i>Journal of Molecular Biology</i> , 2004 , 338, 1015-26	6.5	448
174	Structural disorder throws new light on moonlighting. <i>Trends in Biochemical Sciences</i> , 2005 , 30, 484-9	10.3	381
173	Local structural disorder imparts plasticity on linear motifs. <i>Bioinformatics</i> , 2007 , 23, 950-6	7.2	335
172	A million peptide motifs for the molecular biologist. <i>Molecular Cell</i> , 2014 , 55, 161-9	17.6	310
171	Chaperone activity of ERD10 and ERD14, two disordered stress-related plant proteins. <i>Plant Physiology</i> , 2008 , 147, 381-90	6.6	308

170	Phase Separation of C9orf72 Dipeptide Repeats Perturbs Stress Granule Dynamics. <i>Molecular Cell</i> , 2017 , 65, 1044-1055.e5	17.6	307
169	Disorder and sequence repeats in hub proteins and their implications for network evolution. <i>Journal of Proteome Research</i> , 2006 , 5, 2985-95	5.6	273
168	Unstructural biology coming of age. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 419-25	8.1	251
167	On the sequential determinants of calpain cleavage. <i>Journal of Biological Chemistry</i> , 2004 , 279, 20775-85	5.4	245
166	Intrinsically unstructured proteins evolve by repeat expansion. <i>BioEssays</i> , 2003 , 25, 847-55	4.1	222
165	Molecular principles of the interactions of disordered proteins. <i>Journal of Molecular Biology</i> , 2007 , 372, 549-61	6.5	220
164	Close encounters of the third kind: disordered domains and the interactions of proteins. <i>BioEssays</i> , 2009 , 31, 328-35	4.1	197
163	Spontaneous driving forces give rise to protein-RNA condensates with coexisting phases and complex material properties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 7889-7898	11.5	186
162	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017 , 45, D219-D227	20.1	182
161	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24157		171
160	Fuzzy complexes: a more stochastic view of protein function. <i>Advances in Experimental Medicine and Biology</i> , 2012 , 725, 1-14	3.6	162
159	Malleable machines take shape in eukaryotic transcriptional regulation. <i>Nature Chemical Biology</i> , 2008 , 4, 728-37	11.7	161
158	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014 , 42, D326-35	20.1	159
157	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018 , 46, D471-D476	20.1	143
156	The alphabet of intrinsic disorder: I. Act like a Pro: On the abundance and roles of proline residues in intrinsically disordered proteins. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24360		143
155	Structural disorder in eukaryotes. <i>PLoS ONE</i> , 2012 , 7, e34687	3.7	141
154	Intrinsically disordered proteins: emerging interaction specialists. <i>Current Opinion in Structural Biology</i> , 2015 , 35, 49-59	8.1	136
153	Domain III of calpain is a Ca^{2+} -regulated phospholipid-binding domain. <i>Biochemical and Biophysical Research Communications</i> , 2001 , 280, 1333-9	3.4	134

152	Structural characterization of intrinsically disordered proteins by NMR spectroscopy. <i>Molecules</i> , 2013 , 18, 10802-28	4.8	118
151	Intrinsically disordered chaperones in plants and animals. <i>Biochemistry and Cell Biology</i> , 2010 , 88, 167-74	3.6	112
150	From protein sequence to dynamics and disorder with DynaMine. <i>Nature Communications</i> , 2013 , 4, 2741	17.4	103
149	Prevalent structural disorder in E. coli and S. cerevisiae proteomes. <i>Journal of Proteome Research</i> , 2006 , 5, 1996-2000	5.6	102
148	Molecular mechanism of SSR128129E, an extracellularly acting, small-molecule, allosteric inhibitor of FGF receptor signaling. <i>Cancer Cell</i> , 2013 , 23, 489-501	24.3	99
147	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D269-D276	20.1	91
146	Structural disorder in proteins brings order to crystal growth in biomineralization. <i>Bone</i> , 2012 , 51, 528-34	4.7	91
145	Numerous proteins with unique characteristics are degraded by the 26S proteasome following monoubiquitination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E4639-47	11.5	91
144	The DynaMine webserver: predicting protein dynamics from sequence. <i>Nucleic Acids Research</i> , 2014 , 42, W264-70	20.1	89
143	Primary contact sites in intrinsically unstructured proteins: the case of calpastatin and microtubule-associated protein 2. <i>Biochemistry</i> , 2005 , 44, 3955-64	3.2	88
142	Intrinsic disorder in cell signaling and gene transcription. <i>Molecular and Cellular Endocrinology</i> , 2012 , 348, 457-65	4.4	87
141	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017 , 13, 339-342	11.7	83
140	Structural disorder promotes assembly of protein complexes. <i>BMC Structural Biology</i> , 2007 , 7, 65	2.7	78
139	Multiteric regulation by structural disorder in modular signaling proteins: an extension of the concept of allostery. <i>Chemical Reviews</i> , 2014 , 114, 6715-32	68.1	72
138	NMR relaxation studies on the hydrate layer of intrinsically unstructured proteins. <i>Biophysical Journal</i> , 2005 , 88, 2030-7	2.9	72
137	Tripartite degrons confer diversity and specificity on regulated protein degradation in the ubiquitin-proteasome system. <i>Nature Communications</i> , 2016 , 7, 10239	17.4	71
136	Functional Advantages of Conserved Intrinsic Disorder in RNA-Binding Proteins. <i>PLoS ONE</i> , 2015 , 10, e0139731	3.7	71
135	Prediction of protein disorder at the domain level. <i>Current Protein and Peptide Science</i> , 2007 , 8, 161-71	2.8	65

134	Intrinsic structural disorder confers cellular viability on oncogenic fusion proteins. <i>PLoS Computational Biology</i> , 2009 , 5, e1000552	5	63
133	Structural and dynamic characterization of intrinsically disordered human securin by NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2008 , 130, 16873-9	16.4	63
132	High levels of structural disorder in scaffold proteins as exemplified by a novel neuronal protein, CASK-interactive protein1. <i>FEBS Journal</i> , 2009 , 276, 3744-56	5.7	61
131	Dual coding in alternative reading frames correlates with intrinsic protein disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 5429-34	11.5	60
130	Functional classification of scaffold proteins and related molecules. <i>FEBS Journal</i> , 2010 , 277, 4348-55	5.7	59
129	Reduction in structural disorder and functional complexity in the thermal adaptation of prokaryotes. <i>PLoS ONE</i> , 2010 , 5, e12069	3.7	56
128	A novel two-dimensional electrophoresis technique for the identification of intrinsically unstructured proteins. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 265-73	7.6	56
127	On the supertertiary structure of proteins. <i>Nature Chemical Biology</i> , 2012 , 8, 597-600	11.7	53
126	Disordered plant LEA proteins as molecular chaperones. <i>Plant Signaling and Behavior</i> , 2008 , 3, 710-3	2.5	52
125	Polycation- π interactions are a driving force for molecular recognition by an intrinsically disordered oncoprotein family. <i>PLoS Computational Biology</i> , 2013 , 9, e1003239	5	50
124	The calpain cascade. Mu-calpain activates m-calpain. <i>Journal of Biological Chemistry</i> , 1996 , 271, 33161-4	5.4	46
123	Calpain as a multi-site regulator of cell cycle. <i>Biochemical Pharmacology</i> , 2004 , 67, 1513-21	6	44
122	The role of dimerization in prion replication. <i>Biophysical Journal</i> , 2002 , 82, 1711-8	2.9	44
121	Phosphorylation and dephosphorylation in the proline-rich C-terminal domain of microtubule-associated protein 2. <i>FEBS Journal</i> , 1996 , 241, 765-71		44
120	Dynamic anticipation by Cdk2/Cyclin A-bound p27 mediates signal integration in cell cycle regulation. <i>Nature Communications</i> , 2019 , 10, 1676	17.4	43
119	PhaSePro: the database of proteins driving liquid-liquid phase separation. <i>Nucleic Acids Research</i> , 2020 , 48, D360-D367	20.1	43
118	Intrinsic structural disorder in cytoskeletal proteins. <i>Cytoskeleton</i> , 2013 , 70, 550-71	2.4	43
117	Intrinsically disordered proteins display no preference for chaperone binding in vivo. <i>PLoS Computational Biology</i> , 2008 , 4, e1000017	5	43

116	Calpastatin subdomains A and C are activators of calpain. <i>Journal of Biological Chemistry</i> , 2002 , 277, 9023-6	5.4	43
115	A comprehensive assessment of long intrinsic protein disorder from the DisProt database. <i>Bioinformatics</i> , 2018 , 34, 445-452	7.2	42
114	Verification of alternative splicing variants based on domain integrity, truncation length and intrinsic protein disorder. <i>Nucleic Acids Research</i> , 2011 , 39, 1208-19	20.1	41
113	Redefining the BH3 Death Domain as a Short Linear Motif. <i>Trends in Biochemical Sciences</i> , 2015 , 40, 736-748	10.3	40
112	Structural flexibility allows the functional diversity of potyvirus genome-linked protein VPg. <i>Journal of Virology</i> , 2011 , 85, 2449-57	6.6	38
111	Ensemble Methods Enable a New Definition for the Solution to Gas-Phase Transfer of Intrinsically Disordered Proteins. <i>Journal of the American Chemical Society</i> , 2015 , 137, 13807-17	16.4	37
110	Cold stability of intrinsically disordered proteins. <i>FEBS Letters</i> , 2009 , 583, 465-9	3.8	37
109	Janus chaperones: assistance of both RNA- and protein-folding by ribosomal proteins. <i>FEBS Letters</i> , 2009 , 583, 88-92	3.8	36
108	Interfacial water at protein surfaces: wide-line NMR and DSC characterization of hydration in ubiquitin solutions. <i>Biophysical Journal</i> , 2009 , 96, 2789-98	2.9	36
107	The phosphate group of 3-phosphoglycerate accounts for conformational changes occurring on binding to 3-phosphoglycerate kinase. Enzyme inhibition and thiol reactivity studies. <i>FEBS Journal</i> , 1986 , 154, 643-9		34
106	Full backbone assignment and dynamics of the intrinsically disordered dehydrin ERD14. <i>Biomolecular NMR Assignments</i> , 2011 , 5, 189-93	0.7	33
105	Computational approaches for inferring the functions of intrinsically disordered proteins. <i>Frontiers in Molecular Biosciences</i> , 2015 , 2, 45	5.6	32
104	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021 , 49, D404-D411	20.1	31
103	AmyPro: a database of proteins with validated amyloidogenic regions. <i>Nucleic Acids Research</i> , 2018 , 46, D387-D392	20.1	30
102	The calpain-system of <i>Drosophila melanogaster</i> : coming of age. <i>BioEssays</i> , 2004 , 26, 1088-96	4.1	30
101	A guide to regulation of the formation of biomolecular condensates. <i>FEBS Journal</i> , 2020 , 287, 1924-1935	5.7	29
100	The principle of conformational signaling. <i>Chemical Society Reviews</i> , 2016 , 45, 4252-84	58.5	29
99	Design Principles Involving Protein Disorder Facilitate Specific Substrate Selection and Degradation by the Ubiquitin-Proteasome System. <i>Journal of Biological Chemistry</i> , 2016 , 291, 6723-31	5.4	29

98	Structural disorder provides increased adaptability for vesicle trafficking pathways. <i>PLoS Computational Biology</i> , 2013 , 9, e1003144	5	29
97	Linking functions: an additional role for an intrinsically disordered linker domain in the transcriptional coactivator CBP. <i>Scientific Reports</i> , 2017 , 7, 4676	4.9	28
96	Binding-induced folding transitions in calpastatin subdomains A and C. <i>Protein Science</i> , 2003 , 12, 2327-36.3	6.3	28
95	Emergent functions of proteins in non-stoichiometric supramolecular assemblies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019 , 1867, 970-979	4	27
94	Phosphorylation of MAP65-1 by Arabidopsis Aurora Kinases Is Required for Efficient Cell Cycle Progression. <i>Plant Physiology</i> , 2017 , 173, 582-599	6.6	27
93	Power law distribution defines structural disorder as a structural element directly linked with function. <i>Journal of Molecular Biology</i> , 2010 , 403, 346-50	6.5	27
92	Phosphorylation-induced transient intrinsic structure in the kinase-inducible domain of CREB facilitates its recognition by the KIX domain of CBP. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 749-57	4.2	27
91	Contribution of proline to the pre-structuring tendency of transient helical secondary structure elements in intrinsically disordered proteins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014 , 1840, 993-1003	4	26
90	Interaction of enzymes involved in triosephosphate metabolism. Comparison of yeast and rabbit muscle cytoplasmic systems. <i>FEBS Journal</i> , 1986 , 159, 117-24		26
89	Diverse functional manifestations of intrinsic structural disorder in molecular chaperones. <i>Biochemical Society Transactions</i> , 2012 , 40, 963-8	5.1	25
88	Calcium-induced tripartite binding of intrinsically disordered calpastatin to its cognate enzyme, calpain. <i>FEBS Letters</i> , 2008 , 582, 2149-54	3.8	25
87	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. <i>Journal of Molecular Biology</i> , 2019 , 431, 1650-1670	6.5	24
86	To be disordered or not to be disordered: is that still a question for proteins in the cell?. <i>Cellular and Molecular Life Sciences</i> , 2017 , 74, 3185-3204	10.3	23
85	Increased structural disorder of proteins encoded on human sex chromosomes. <i>Molecular BioSystems</i> , 2012 , 8, 229-36		22
84	Functional diversity and structural disorder in the human ubiquitination pathway. <i>PLoS ONE</i> , 2013 , 8, e65443	3.7	22
83	Contribution of distinct structural elements to activation of calpain by Ca ²⁺ ions. <i>Journal of Biological Chemistry</i> , 2004 , 279, 20118-26	5.4	22
82	Phasing in on the cell cycle. <i>Cell Division</i> , 2018 , 13, 1	2.8	21
81	DisCons: a novel tool to quantify and classify evolutionary conservation of intrinsic protein disorder. <i>BMC Bioinformatics</i> , 2015 , 16, 153	3.6	21

80	The Levinthal paradox of the interactome. <i>Protein Science</i> , 2011 , 20, 2074-9	6.3	21
79	Synaptic metaplasticity and the local charge effect in postsynaptic densities. <i>Trends in Neurosciences</i> , 1998 , 21, 97-102	13.3	20
78	The Protein Ensemble Database. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 870, 335-49	3.6	19
77	Predicting the predictive power of IDP ensembles. <i>Structure</i> , 2014 , 22, 177-8	5.2	19
76	How to determine the efficiency of intermediate transfer in an interacting enzyme system?. <i>FEBS Letters</i> , 1987 , 214, 244-8	3.8	19
75	Disordered regions in transmembrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 2839-48	3.8	18
74	Just a Flexible Linker? The Structural and Dynamic Properties of CBP-ID4 Revealed by NMR Spectroscopy. <i>Biophysical Journal</i> , 2016 , 110, 372-381	2.9	18
73	Synonymous constraint elements show a tendency to encode intrinsically disordered protein segments. <i>PLoS Computational Biology</i> , 2014 , 10, e1003607	5	18
72	Discrete molecular dynamics can predict helical prestructured motifs in disordered proteins. <i>PLoS ONE</i> , 2014 , 9, e95795	3.7	17
71	Start2Fold: a database of hydrogen/deuterium exchange data on protein folding and stability. <i>Nucleic Acids Research</i> , 2016 , 44, D429-34	20.1	17
70	Coding Regions of Intrinsic Disorder Accommodate Parallel Functions. <i>Trends in Biochemical Sciences</i> , 2016 , 41, 898-906	10.3	16
69	Intrinsic structural disorder of DF31, a Drosophila protein of chromatin decondensation and remodeling activities. <i>Journal of Proteome Research</i> , 2008 , 7, 2291-9	5.6	16
68	Towards proteomic approaches for the identification of structural disorder. <i>Current Protein and Peptide Science</i> , 2007 , 8, 173-9	2.8	16
67	Bioinformatics Approaches for Predicting Disordered Protein Motifs. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 870, 291-318	3.6	15
66	Quantification of Intrinsically Disordered Proteins: A Problem Not Fully Appreciated. <i>Frontiers in Molecular Biosciences</i> , 2018 , 5, 83	5.6	14
65	Molecular cloning and RNA expression of a novel Drosophila calpain, Calpain C. <i>Biochemical and Biophysical Research Communications</i> , 2003 , 303, 343-9	3.4	14
64	Arginine-rich Peptides Can Actively Mediate Liquid-liquid Phase Separation. <i>Bio-protocol</i> , 2017 , 7, e2525	0.9	14
63	Synthesis of cell-penetrating conjugates of calpain activator peptides. <i>Bioconjugate Chemistry</i> , 2007 , 18, 130-7	6.3	13

62	The mechanism of succinate or fumarate transfer in the tricarboxylic acid cycle allows molecular rotation of the intermediate. <i>Archives of Biochemistry and Biophysics</i> , 1990 , 276, 191-8	4.1	13
61	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2021 ,	20.1	13
60	Dehydrin ERD14 activates glutathione transferase Phi9 in Arabidopsis thaliana under osmotic stress. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020 , 1864, 129506	4	13
59	The role of structural disorder in cell cycle regulation, related clinical proteomics, disease development and drug targeting. <i>Expert Review of Proteomics</i> , 2015 , 12, 221-33	4.2	12
58	SnapShot: Intrinsic Structural Disorder. <i>Cell</i> , 2015 , 161, 1230-1230.e1	56.2	12
57	Co-Evolution of Intrinsically Disordered Proteins with Folded Partners Witnessed by Evolutionary Couplings. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	12
56	Exon-phase symmetry and intrinsic structural disorder promote modular evolution in the human genome. <i>Nucleic Acids Research</i> , 2013 , 41, 4409-22	20.1	11
55	Interaction of rabbit muscle enolase and 3-phosphoglycerate mutase studied by ELISA and by batch gel filtration. <i>Archives of Biochemistry and Biophysics</i> , 1992 , 296, 650-3	4.1	11
54	Learning of Signaling Networks: Molecular Mechanisms. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 284-294	10.3	11
53	Does Intrinsic Disorder in Proteins Favor Their Interaction with Lipids?. <i>Proteomics</i> , 2019 , 19, e1800098	4.8	11
52	Specific Conformational Dynamics and Expansion Underpin a Multi-Step Mechanism for Specific Binding of p27 with Cdk2/Cyclin A. <i>Journal of Molecular Biology</i> , 2020 , 432, 2998-3017	6.5	10
51	Fuzzy interactome: the limitations of models in molecular biology. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 3	10.3	10
50	CG15031/PPYR1 is an intrinsically unstructured protein that interacts with protein phosphatase Y. <i>Archives of Biochemistry and Biophysics</i> , 2006 , 451, 59-67	4.1	10
49	Differential distribution of calpain small subunit 1 and 2 in rat brain. <i>European Journal of Neuroscience</i> , 2004 , 19, 1819-25	3.5	10
48	A generic approach to study the kinetics of liquid-liquid phase separation under near-native conditions. <i>Communications Biology</i> , 2021 , 4, 77	6.7	10
47	The androgen receptor gene polyglycine repeat polymorphism is associated with memory performance in healthy Chinese individuals. <i>Psychoneuroendocrinology</i> , 2009 , 34, 947-52	5	9
46	A Novel Method for Assessing the Chaperone Activity of Proteins. <i>PLoS ONE</i> , 2016 , 11, e0161970	3.7	9
45	Liquid-Liquid Phase Separation Enhances TDP-43 LCD Aggregation but Delays Seeded Aggregation. <i>Biomolecules</i> , 2021 , 11,	5.9	9

44	Hydrogen Mobility and Protein-Water Interactions in Proteins in the Solid State. <i>ChemPhysChem</i> , 2017 , 18, 677-682	3.2	8
43	Protein Delivery into Plant Cells: Toward Structural Biology. <i>Frontiers in Plant Science</i> , 2017 , 8, 519	6.2	8
42	Multiple fuzzy interactions in the moonlighting function of thymosin- β . <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e26204		8
41	Hydrogel formation by multivalent IDPs: A reincarnation of the microtrabecular lattice?. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24068		8
40	Integration of Data from Liquid-Liquid Phase Separation Databases Highlights Concentration and Dosage Sensitivity of LLPS Drivers. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	8
39	Long-range interactions in nonsense-mediated mRNA decay are mediated by intrinsically disordered protein regions. <i>Journal of Molecular Biology</i> , 2012 , 424, 125-31	6.5	7
38	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019 , 8,	3.6	7
37	Three reasons protein disorder analysis makes more sense in the light of collagen. <i>Protein Science</i> , 2016 , 25, 1030-6	6.3	6
36	Accessory proteins in signal transduction: scaffold proteins and beyond. <i>FEBS Journal</i> , 2010 , 277, 4347	5.7	6
35	Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2020 , 118, 2952-2965	2.9	6
34	Interplay of Structural Disorder and Short Binding Elements in the Cellular Chaperone Function of Plant Dehydrin ERD14. <i>Cells</i> , 2020 , 9,	7.9	6
33	Focusing of Microcrystals and Liquid Condensates in Acoustofluidics. <i>Crystals</i> , 2019 , 9, 120	2.3	5
32	In vivo biotinylated calpastatin improves the affinity purification of human m-calpain. <i>Protein Expression and Purification</i> , 2018 , 145, 77-84	2	5
31	Intrinsically Disordered Proteins 2012 , 136-152		5
30	Unique Physicochemical Patterns of Residues in Protein-Protein Interfaces. <i>Journal of Chemical Information and Modeling</i> , 2018 , 58, 2164-2173	6.1	5
29	Misprediction of Structural Disorder in Halophiles. <i>Molecules</i> , 2019 , 24,	4.8	4
28	Computational analysis of translational readthrough proteins in Drosophila and yeast reveals parallels to alternative splicing. <i>Scientific Reports</i> , 2016 , 6, 32142	4.9	4
27	New m-calpain substrate-based azapeptide inhibitors. <i>Journal of Peptide Science</i> , 2013 , 19, 370-6	2.1	4

26	Wide-line NMR and DSC studies on intrinsically disordered p53 transactivation domain and its helically pre-structured segment. <i>BMB Reports</i> , 2016 , 49, 497-501	5.5	4
25	DNA-binding domain as the minimal region driving RNA-dependent liquid-liquid phase separation of androgen receptor. <i>Protein Science</i> , 2021 , 30, 1380-1392	6.3	4
24	Essential functions linked with structural disorder in organisms of minimal genome. <i>Biology Direct</i> , 2016 , 11, 45	7.2	4
23	Challenges in the Structural-Functional Characterization of Multidomain, Partially Disordered Proteins CBP and p300: Preparing Native Proteins and Developing Nanobody Tools. <i>Methods in Enzymology</i> , 2018 , 611, 607-675	1.7	4
22	H, N, C resonance assignment of plant dehydrin early response to dehydration 10 (ERD10). <i>Biomolecular NMR Assignments</i> , 2017 , 11, 127-131	0.7	3
21	Cellular Chaperone Function of Intrinsically Disordered Dehydrin ERD14. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
20	Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins 2017 , 167-203		2
19	Towards Understanding Protein Disorder In-Cell. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 870, 319-34	3.6	2
18	WT and A53T β synuclein Systems: Melting Diagram and Its New Interpretation. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	2
17	Affinity purification of human m-calpain through an intrinsically disordered inhibitor, calpastatin. <i>PLoS ONE</i> , 2017 , 12, e0174125	3.7	2
16	Molecular Motions and Interactions in Aqueous Solutions of Thymosin- β 4 Stabilin C-Terminal Domain (CTD) and Their 1:1 Complex Studied by H NMR Spectroscopy. <i>ChemPhysChem</i> , 2018 , 19, 848-856 ^{2,2}		2
15	Hydrogen skeleton, mobility and protein architecture. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e25767		2
14	Chasing coevolutionary signals in intrinsically disordered proteins complexes. <i>Scientific Reports</i> , 2020 , 10, 17962	4.9	2
13	The Melting Diagram of Protein Solutions and Its Thermodynamic Interpretation. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	2
12	Interaction between the scaffold proteins CBP by IQGAP1 provides an interface between gene expression and cytoskeletal activity. <i>Scientific Reports</i> , 2020 , 10, 5753	4.9	1
11	Disordered Substrates of the 20S Proteasome Link Degradation with Phase Separation. <i>Proteomics</i> , 2018 , 18, e1800276	4.8	1
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9	Targeting an Intrinsically Disordered Protein by Covalent Modification. <i>Methods in Molecular Biology</i> , 2020 , 2141, 835-854	1.4	1

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5	"Protein" no longer means what it used to. <i>Current Research in Structural Biology</i> , 2021 , 3, 146-152	2.8	0
4	F/YGG-motif is an intrinsically disordered nucleic-acid binding motif.. <i>RNA Biology</i> , 2022 , 19, 622-635	4.8	0
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1	Yeast and Cancer: Common Mechanism Underlying Activation of Ras by Glycolytic Flux. <i>FASEB Journal</i> , 2018 , 32, lb143	0.9	