

# Folding of an intrinsically disordered protein by phospho

Nature

519, 106-109

DOI: [10.1038/nature13999](https://doi.org/10.1038/nature13999)

Citation Report

#	ARTICLE	IF	CITATIONS
3	Signalling to eIF4E in cancer. Biochemical Society Transactions, 2015, 43, 763-772.	3.4	177
4	Mammalian Bcnt/Cfdp1, a potential epigenetic factor characterized by an acidic stretch in the disordered N-terminal and Ser250 phosphorylation in the conserved C-terminal regions. Bioscience Reports, 2015, 35, .	2.4	10
5	Effect of O-Linked Glycosylation on the Equilibrium Structural Ensemble of Intrinsically Disordered Polypeptides. Journal of Physical Chemistry B, 2015, 119, 15583-15592.	2.6	19
6	Structural Basis for Regulation of RNA-Binding Proteins by Phosphorylation. ACS Chemical Biology, 2015, 10, 652-666.	3.4	50
7	Phosphorylation regulates IDP folding. Nature Reviews Molecular Cell Biology, 2015, 16, 66-66.	37.0	2
8	Molecular Architecture of 4E-BP Translational Inhibitors Bound to eIF4E. Molecular Cell, 2015, 57, 1074-1087.	9.7	130
9	Quantitative studies of mRNA recruitment to the eukaryotic ribosome. Biochimie, 2015, 114, 58-71.	2.6	28
10	Folding upon phosphorylation: translational regulation by a disorder-to-order transition. Trends in Biochemical Sciences, 2015, 40, 243-244.	7.5	10
11	Differential Requirements for eIF4E Dose in Normal Development and Cancer. Cell, 2015, 162, 59-71.	28.9	283
12	Functional advantages of dynamic protein disorder. FEBS Letters, 2015, 589, 2433-2440.	2.8	162
13	Structure and Functional Characterization of the Conserved JAK Interaction Region in the Intrinsically Disordered N-Terminus of SOCS5. Biochemistry, 2015, 54, 4672-4682.	2.5	14
14	Molecular mechanism of the dual activity of 4EGI-1: Dissociating eIF4G from eIF4E but stabilizing the binding of unphosphorylated 4E-BP1. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4036-45.	7.1	90
15	A functional Bucky ball-GFP transgene visualizes germ plasm in living zebrafish. Gene Expression Patterns, 2015, 18, 44-52.	0.8	41
16	The Acetylation Landscape of the H4 Histone Tail: Disentangling the Interplay between the Specific and Cumulative Effects. Journal of the American Chemical Society, 2015, 137, 6245-6253.	13.7	64
17	Structural Biology Turned on Its Head. ChemBioChem, 2015, 16, 1033-1034.	2.6	4
18	High-resolution structural characterization of Noxa, an intrinsically disordered protein, by microsecond molecular dynamics simulations. Molecular BioSystems, 2015, 11, 1850-1856.	2.9	7
19	PKA Phosphorylates the ATPase Inhibitory Factor 1 and Inactivates Its Capacity to Bind and Inhibit the Mitochondrial H <sup>+</sup> -ATP Synthase. Cell Reports, 2015, 12, 2143-2155.	6.4	104
20	Intrinsically disordered proteins: emerging interaction specialists. Current Opinion in Structural Biology, 2015, 35, 49-59.	5.7	177

#	ARTICLE	IF	CITATIONS
21	Energetic and topological determinants of a phosphorylation-induced disorder-to-order protein conformational switch. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 27264-27269.	2.8	13
22	Emerging Roles of Disordered Sequences in RNA-Binding Proteins. <i>Trends in Biochemical Sciences</i> , 2015, 40, 662-672.	7.5	195
23	Protein Phosphorylation: A Major Switch Mechanism for Metabolic Regulation. <i>Trends in Endocrinology and Metabolism</i> , 2015, 26, 676-687.	7.1	402
24	Mextli proteins use both canonical bipartite and novel tripartite binding modes to form eIF4E complexes that display differential sensitivity to 4E-BP regulation. <i>Genes and Development</i> , 2015, 29, 1835-1849.	5.9	19
25	Phosphorylation-induced Conformational Ensemble Switching in an Intrinsically Disordered Cancer/Testis Antigen. <i>Journal of Biological Chemistry</i> , 2015, 290, 25090-25102.	3.4	55
26	Order, Disorder, and Everything in Between. <i>Molecules</i> , 2016, 21, 1090.	3.8	72
27	NMR Meets Tau: Insights into Its Function and Pathology. <i>Biomolecules</i> , 2016, 6, 28.	4.0	25
28	Finding Our Way in the Dark Proteome. <i>Journal of the American Chemical Society</i> , 2016, 138, 9730-9742.	13.7	111
29	Disorder, Promiscuous Interactions, and Stochasticity Regulate State Switching in the Unstable Prostate. <i>Journal of Cellular Biochemistry</i> , 2016, 117, 2235-2240.	2.6	5
30	Asymmetric Modulation of Protein Orderâ€“Disorder Transitions by Phosphorylation and Partner Binding. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 1675-1679.	13.8	28
31	Spatial proximity statistics suggest a regulatory role of protein phosphorylation on compound binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 565-579.	2.6	6
32	Hypertension: the missing WNKs. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 311, F16-F27.	2.7	20
33	Asymmetric Modulation of Protein Orderâ€“Disorder Transitions by Phosphorylation and Partner Binding. <i>Angewandte Chemie</i> , 2016, 128, 1707-1711.	2.0	5
34	A combined computational and structural model of the full-length human prolactin receptor. <i>Nature Communications</i> , 2016, 7, 11578.	12.8	52
35	Insights into Coupled Folding and Binding Mechanisms from Kinetic Studies. <i>Journal of Biological Chemistry</i> , 2016, 291, 6689-6695.	3.4	141
36	Protein dynamics and function from solution state NMR spectroscopy. <i>Quarterly Reviews of Biophysics</i> , 2016, 49, e6.	5.7	123
37	Phase Separation: Linking Cellular Compartmentalization to Disease. <i>Trends in Cell Biology</i> , 2016, 26, 547-558.	7.9	291
38	Conformations of a Metastable SH3 Domain Characterized by smFRET and an Excluded-Volume Polymer Model. <i>Biophysical Journal</i> , 2016, 110, 1510-1522.	0.5	23

#	ARTICLE	IF	CITATIONS
39	Structural characterization of the interaction of $\alpha$ -synuclein nascent chains with the ribosomal surface and trigger factor. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5012-5017.	7.1	54
40	Quantifying Protein Disorder through Measures of Excess Conformational Entropy. Journal of Physical Chemistry B, 2016, 120, 4341-4350.	2.6	36
41	New frontiers in translational control of the cancer genome. Nature Reviews Cancer, 2016, 16, 288-304.	28.4	282
42	Advances in NMR Methods To Map Allosteric Sites: From Models to Translation. Chemical Reviews, 2016, 116, 6267-6304.	47.7	76
43	Phosphorylation of Cysteine String Protein Triggers a Major Conformational Switch. Structure, 2016, 24, 1380-1386.	3.3	23
44	Knr4: a disordered hub protein at the heart of fungal cell wall signalling. Cellular Microbiology, 2016, 18, 1217-1227.	2.1	13
45	Electrostatics and Intrinsic Disorder Drive Translocon Binding of the SRP Receptor FtsY. Angewandte Chemie - International Edition, 2016, 55, 9544-9547.	13.8	16
46	Evaluating the influence of initial magnetization conditions on extracted exchange parameters in NMR relaxation experiments: applications to CPMG and CEST. Journal of Biomolecular NMR, 2016, 65, 143-156.	2.8	6
47	Absence of residual structure in the intrinsically disordered regulatory protein CP12 in its reduced state. Biochemical and Biophysical Research Communications, 2016, 477, 20-26.	2.1	14
48	Evolution of TOR and Translation Control. , 2016, , 327-411.		8
49	Molecular Determinants of Tubulin's C-Terminal Tail Conformational Ensemble. ACS Chemical Biology, 2016, 11, 2981-2990.	3.4	33
50	Structured States of Disordered Proteins from Genomic Sequences. Cell, 2016, 167, 158-170.e12.	28.9	127
51	Translational Control in Echinoderms: The Calm Before the Storm. , 2016, , 413-434.		5
52	Kinetics of the Interactions between Copper and Amyloid $\beta$ with FAD Mutations and Phosphorylation at the N-terminus. ChemBioChem, 2016, 17, 1732-1737.	2.6	15
53	Non-covalent forces tune the electron transfer complex between ferredoxin and sulfite reductase to optimize enzymatic activity. Biochemical Journal, 2016, 473, 3837-3854.	3.7	12
54	Oxidative Unfolding of the Rubredoxin Domain and the Natively Disordered N-terminal Region Regulate the Catalytic Activity of Mycobacterium tuberculosis Protein Kinase G. Journal of Biological Chemistry, 2016, 291, 27062-27072.	3.4	12
55	Rapid Brownian Motion Primes Ultrafast Reconstruction of Intrinsically Disordered Phe-Gly Repeats Inside the Nuclear Pore Complex. Scientific Reports, 2016, 6, 29991.	3.3	28
56	Whi5 phosphorylation embedded in the G1/S network dynamically controls critical cell size and cell fate. Nature Communications, 2016, 7, 11372.	12.8	35

#	ARTICLE	IF	CITATIONS
58	Fimbrin phosphorylation by metaphase Cdk1 regulates actin cable dynamics in budding yeast. <i>Nature Communications</i> , 2016, 7, 11265.	12.8	32
59	Ligand-Receptor Interaction Modulates the Energy Landscape of Enzyme-Instructed Self-Assembly of Small Molecules. <i>Journal of the American Chemical Society</i> , 2016, 138, 15397-15404.	13.7	42
60	Sequence Determinants of the Conformational Properties of an Intrinsically Disordered Protein Prior to and upon Multisite Phosphorylation. <i>Journal of the American Chemical Society</i> , 2016, 138, 15323-15335.	13.7	217
61	Destabilizing an interacting motif strengthens the association of a designed ankyrin repeat protein with tubulin. <i>Scientific Reports</i> , 2016, 6, 28922.	3.3	27
62	The contribution of intrinsically disordered regions to protein function, cellular complexity, and human disease. <i>Biochemical Society Transactions</i> , 2016, 44, 1185-1200.	3.4	323
63	Foldamer-mediated manipulation of a pre-amyloid toxin. <i>Nature Communications</i> , 2016, 7, 11412.	12.8	56
64	Electrostatics and Intrinsic Disorder Drive Translocon Binding of the SRP Receptor FtsY. <i>Angewandte Chemie</i> , 2016, 128, 9696-9699.	2.0	2
65	Low potency toxins reveal dense interaction networks in metabolism. <i>BMC Systems Biology</i> , 2016, 10, 19.	3.0	2
66	Using a second-order differential model to fit data without baselines in protein isothermal chemical denaturation. <i>Protein Science</i> , 2016, 25, 898-904.	7.6	4
67	Targeting intrinsically disordered proteins in rational drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2016, 11, 65-77.	5.0	74
68	Examining the Influence of Phosphorylation on Peptide Ion Structure by Ion Mobility Spectrometry-Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 786-794.	2.8	28
69	Enhanced translation initiation factor 4G levels correlate with production levels of monoclonal antibodies in recombinant CHO cell lines. <i>Biochemical Journal</i> , 2016, 473, e11-e13.	3.7	0
70	Expanding the Range of Protein Function at the Far End of the Order-Structure Continuum. <i>Journal of Biological Chemistry</i> , 2016, 291, 6706-6713.	3.4	14
71	Deubiquitination and the regulation of stress granule assembly. <i>Current Genetics</i> , 2016, 62, 503-506.	1.7	19
72	Modulation of Intrinsically Disordered Protein Function by Post-translational Modifications. <i>Journal of Biological Chemistry</i> , 2016, 291, 6696-6705.	3.4	402
73	Phosphorylation and calcium antagonistically tune myosin-binding protein C <sup>TM</sup> s structure and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3239-3244.	7.1	84
74	Dynamic Protein Interaction Networks and New Structural Paradigms in Signaling. <i>Chemical Reviews</i> , 2016, 116, 6424-6462.	47.7	161
75	The ATPase Inhibitory Factor 1 (IF1): A master regulator of energy metabolism and of cell survival. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1167-1182.	1.0	101

#	ARTICLE	IF	CITATIONS
76	Intracellular and extracellular microtubule associated protein tau as a therapeutic target in Alzheimer disease and other tauopathies. Expert Opinion on Therapeutic Targets, 2016, 20, 653-661.	3.4	24
77	Retention and splicing complex (RES) – the importance of cooperativity. RNA Biology, 2016, 13, 128-133.	3.1	12
78	Cytoplasmic stress granules: Dynamic modulators of cell signaling and disease. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2017, 1863, 884-895.	3.8	203
79	Structural Basis for the Interaction of a Human Small Heat Shock Protein with the 14-3-3 Universal Signaling Regulator. Structure, 2017, 25, 305-316.	3.3	101
81	Phosphorylation at Ser8 as an Intrinsic Regulatory Switch to Regulate the Morphologies and Structures of Alzheimer's 40-residue Î²-Amyloid (AÎ²40) Fibrils. Journal of Biological Chemistry, 2017, 292, 2611-2623.	3.4	29
82	Dynein Binding of Competitive Regulators Dynactin and NudE Involves Novel Interplay between Phosphorylation Site and Disordered Spliced Linkers. Structure, 2017, 25, 421-433.	3.3	25
83	Application of NMR to studies of intrinsically disordered proteins. Archives of Biochemistry and Biophysics, 2017, 628, 57-70.	3.0	82
84	Phosphorylation induces sequence-specific conformational switches in the RNA polymerase II C-terminal domain. Nature Communications, 2017, 8, 15233.	12.8	70
85	Effect of Phosphorylation on a Human-like Osteopontin Peptide. Biophysical Journal, 2017, 112, 1586-1596.	0.5	25
86	Insights into the conformations and dynamics of intrinsically disordered proteins using single-molecule fluorescence. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1696-1706.	2.3	37
87	A pH Switch for Î²-Sheet Protein Folding. Angewandte Chemie - International Edition, 2017, 56, 7074-7077.	13.8	9
88	A pH Switch for Î²-Sheet Protein Folding. Angewandte Chemie, 2017, 129, 7180-7183.	2.0	0
89	Structure of eIF4E in Complex with an eIF4G Peptide Supports a Universal Bipartite Binding Mode for Protein Translation. Plant Physiology, 2017, 174, 1476-1491.	4.8	32
90	Conditionally disordered proteins: bringing the environment back into the fold. Cellular and Molecular Life Sciences, 2017, 74, 3149-3162.	5.4	12
91	A simple model for electrical charge in globular macromolecules and linear polyelectrolytes in solution. Journal of Chemical Physics, 2017, 146, 205101.	3.0	28
92	Intrinsically Disordered Proteins as Important Players during Desiccation Stress of Soybean Radicles. Journal of Proteome Research, 2017, 16, 2393-2409.	3.7	13
93	A phosphorylation-motif for tuneable helix stabilisation in intrinsically disordered proteins – Lessons from the sodium proton exchanger 1 (NHE1). Cellular Signalling, 2017, 37, 40-51.	3.6	34
94	Functions of intrinsic disorder in transmembrane proteins. Cellular and Molecular Life Sciences, 2017, 74, 3205-3224.	5.4	63

#	ARTICLE	IF	CITATIONS
95	Whatâ€™s in an Average? An Ensemble View of Phosphorylation Effects. <i>Structure</i> , 2017, 25, 573-575.	3.3	0
96	Understanding CARD Tricks in Apoptosomes. <i>Structure</i> , 2017, 25, 575-577.	3.3	8
97	Biochemical alterations in duckweed and algae induced by carrier solvents: Selection of an appropriate solvent in toxicity testing. <i>Environmental Toxicology and Chemistry</i> , 2017, 36, 2631-2639.	4.3	13
98	Single-molecule electrometry. <i>Nature Nanotechnology</i> , 2017, 12, 488-495.	31.5	75
99	Functional analysis of TOEFAZ1 uncovers protein domains essential for cytokinesis in <i>Trypanosoma brucei</i> . <i>Journal of Cell Science</i> , 2017, 130, 3918-3932.	2.0	18
100	Arc Requires PSD95 for Assembly into Postsynaptic Complexes Involved with Neural Dysfunction and Intelligence. <i>Cell Reports</i> , 2017, 21, 679-691.	6.4	79
101	Stereoselective Postassembly CH Oxidation of Self-Assembled Metalâ€“Ligand Cage Complexes. <i>Inorganic Chemistry</i> , 2017, 56, 11435-11442.	4.0	25
102	The effect of phosphorylation on the salt-tolerance-related functions of the soybean protein PM18, a member of the group-3 LEA protein family. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1291-1303.	2.3	16
103	Exploring the Sequence-based Prediction of Folding Initiation Sites in Proteins. <i>Scientific Reports</i> , 2017, 7, 8826.	3.3	39
104	Phosphorylation of the type II transmembrane serine protease, TMPRSS13, in hepatocyte growth factor activator inhibitor-1 and -2â€“mediated cell-surface localization. <i>Journal of Biological Chemistry</i> , 2017, 292, 14867-14884.	3.4	24
105	Exploring the dark foldable proteome by considering hydrophobic amino acids topology. <i>Scientific Reports</i> , 2017, 7, 41425.	3.3	22
106	Predictions of Backbone Dynamics in Intrinsically Disordered Proteins Using De Novo Fragment-Based Protein Structure Predictions. <i>Scientific Reports</i> , 2017, 7, 6999.	3.3	11
107	Fuzziness enables context dependence of protein interactions. <i>FEBS Letters</i> , 2017, 591, 2682-2695.	2.8	60
108	MeCP2 and CTCF: enhancing the cross-talk of silencers. <i>Biochemistry and Cell Biology</i> , 2017, 95, 593-608.	2.0	7
109	Translation regulator ballet in meiotic spindle. <i>Cell Cycle</i> , 2017, 16, 733-734.	2.6	3
110	Identification of the Tau phosphorylation pattern that drives its aggregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9080-9085.	7.1	168
111	An Efficient Method for Estimating the Hydrodynamic Radius of Disordered Protein Conformations. <i>Biophysical Journal</i> , 2017, 113, 550-557.	0.5	110
112	Site-specific phosphorylation regulates the structure and function of an intrinsically disordered domain of the glucocorticoid receptor. <i>Scientific Reports</i> , 2017, 7, 15440.	3.3	23

#	ARTICLE	IF	CITATIONS
113	High-Throughput Chemical Probing of Full-Length Protein-Protein Interactions. ACS Combinatorial Science, 2017, 19, 763-769.	3.8	14
114	Molecular Dynamics Analysis of 4E-BP2 Protein Fold Stabilization Induced by Phosphorylation. Journal of Physical Chemistry B, 2017, 121, 3387-3393.	2.6	11
115	Phosphorylation regulates the secondary structure and function of dentin phosphoprotein peptides. Bone, 2017, 95, 65-75.	2.9	18
116	Random-phase-approximation theory for sequence-dependent, biologically functional liquid-liquid phase separation of intrinsically disordered proteins. Journal of Molecular Liquids, 2017, 228, 176-193.	4.9	103
117	Mechanism of Phosphorylation-Induced Folding of 4E-BP2 Revealed by Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2017, 13, 320-328.	5.3	16
118	Phosphorylation of the IDP KID Modulates Affinity for KIX by Increasing the Lifetime of the Complex. Biophysical Journal, 2017, 113, 2706-2712.	0.5	22
120	The complexity of glycoprotein-derived glycans. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 2017, 93, 64-86.	3.8	18
121	It Pays To Be in Phase. Biochemistry, 2018, 57, 2520-2529.	2.5	32
122	Fuzziness in Protein Interactions-A Historical Perspective. Journal of Molecular Biology, 2018, 430, 2278-2287.	4.2	118
123	Structural characterization of the intrinsically disordered domain of Mycobacterium tuberculosis protein tyrosine kinase A. FEBS Letters, 2018, 592, 1233-1245.	2.8	5
124	Phosphorylation induced cochaperone unfolding promotes kinase recruitment and client class-specific Hsp90 phosphorylation. Nature Communications, 2018, 9, 265.	12.8	39
125	Structural Impact of Phosphorylation and Dielectric Constant Variation on Synaptotagmin's IDR. Biophysical Journal, 2018, 114, 550-561.	0.5	13
126	Collapse Transitions of Proteins and the Interplay Among Backbone, Sidechain, and Solvent Interactions. Annual Review of Biophysics, 2018, 47, 19-39.	10.0	98
127	Spectrally resolved single-molecule electrometry. Journal of Chemical Physics, 2018, 148, 123307.	3.0	8
128	IDPs in macromolecular complexes: the roles of multivalent interactions in diverse assemblies. Current Opinion in Structural Biology, 2018, 49, 36-43.	5.7	98
129	Solution NMR Structure and Backbone Dynamics of Partially Disordered <i>Arabidopsis thaliana</i> Phloem Protein 16-1, a Putative mRNA Transporter. Biochemistry, 2018, 57, 912-924.	2.5	8
130	Electrostatic Interactions in Protein Structure, Folding, Binding, and Condensation. Chemical Reviews, 2018, 118, 1691-1741.	47.7	577
131	Pervasive Protein Thermal Stability Variation during the Cell Cycle. Cell, 2018, 173, 1495-1507.e18.	28.9	183



#	ARTICLE	IF	CITATIONS
132	Modeling the Early Stages of Phase Separation in Disordered Elastin-like Proteins. Biophysical Journal, 2018, 114, 1563-1578.	0.5	16
133	Structural Regulation of a Neurofilament-Inspired Intrinsically Disordered Protein Brush by Multisite Phosphorylation. Biochemistry, 2018, 57, 4019-4028.	2.5	12
134	Protein plasticity driven by disorder and collapse governs the heterogeneous binding of CytR to DNA. Nucleic Acids Research, 2018, 46, 4044-4053.	14.5	19
135	High-Resolution 2D NMR of Disordered Proteins Enhanced by Hyperpolarized Water. Analytical Chemistry, 2018, 90, 6169-6177.	6.5	36
136	Spatial features of proteins related to their phosphorylation and associated structural changes. Proteins: Structure, Function and Bioinformatics, 2018, 86, 13-20.	2.6	7
137	Sequence charge decoration dictates coil-globule transition in intrinsically disordered proteins. Journal of Chemical Physics, 2018, 148, 123305.	3.0	73
138	Regulation of Androgen Receptor Activity by Transient Interactions of Its Transactivation Domain with General Transcription Regulators. Structure, 2018, 26, 145-152.e3.	3.3	45
139	Dynamic control of <sc>RSK</sc> complexes by phosphoswitchâ€based regulation. FEBS Journal, 2018, 285, 46-71.	4.7	26
140	Force field development and simulations of intrinsically disordered proteins. Current Opinion in Structural Biology, 2018, 48, 40-48.	5.7	139
141	Concerted millisecond timescale dynamics in the intrinsically disordered carboxyl terminus of Î³-tubulin induced by mutation of a conserved tyrosine residue. Protein Science, 2018, 27, 531-545.	7.6	3
142	Complex regulatory mechanisms mediated by the interplay of multiple post-translational modifications. Current Opinion in Structural Biology, 2018, 48, 58-67.	5.7	90
143	REM1.3's phospho-status defines its plasma membrane nanodomain organization and activity in restricting PVX cell-to-cell movement. PLoS Pathogens, 2018, 14, e1007378.	4.7	73
144	Computational modeling suggests impaired interactions between NKX2.5 and GATA4 in individuals carrying a novel pathogenic D16N NKX2.5 mutation. Oncotarget, 2018, 9, 13713-13732.	1.8	27
145	Single Molecule FRET: A Powerful Tool to Study Intrinsically Disordered Proteins. Biomolecules, 2018, 8, 140.	4.0	50
146	Spider silk proteome provides insight into the structural characterization of Nephila clavipes flagelliform spidroin. Scientific Reports, 2018, 8, 14674.	3.3	28
147	15N transverse relaxation measurements for the characterization of Âµs dynamics are deteriorated by the deuterium isotope effect on 15N resulting from solvent exchange. Journal of Biomolecular NMR, 2018, 72, 125-137.	2.8	8
148	Characterization of Dynamic IDP Complexes by NMR Spectroscopy. Methods in Enzymology, 2018, 611, 193-226.	1.0	29
149	Bioinspired structural transition of synthetic polymers through biomolecular ligand binding. Chemical Communications, 2018, 54, 12006-12009.	4.1	8

#	ARTICLE	IF	CITATIONS
150	GhCPK33 Negatively Regulates Defense against <i>Verticillium dahliae</i> by Phosphorylating GhOPR3. <i>Plant Physiology</i> , 2018, 178, 876-889.	4.8	76
151	<i>Arabidopsis</i> downy mildew effector HaRxL106 suppresses plant immunity by binding to RADICAL-INDUCED CELL DEATH1. <i>New Phytologist</i> , 2018, 220, 232-248.	7.3	51
152	Discrimination and highly selective adsorption of phosphoproteins and glycoproteins with arginine-functionalized polyhedral oligomeric silsesquioxane frameworks. <i>Journal of Materials Chemistry B</i> , 2018, 6, 4116-4123.	5.8	17
153	Characterization of intrinsically disordered proteins and their dynamic complexes: From in vitro to cell-like environments. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2018, 109, 79-100.	7.5	67
154	The Disordered Landscape of the 20S Proteasome Substrates Reveals Tight Association with Phase Separated Granules. <i>Proteomics</i> , 2018, 18, e1800076.	2.2	32
155	Comparative analysis of human and mouse transcriptional cofactors (TcoFs) with special emphasis on intrinsically disordered regions and their associated regulating post-translational modifications. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 8531-8546.	2.6	1
156	Phenotypic Plasticity, Bet-Hedging, and Androgen Independence in Prostate Cancer: Role of Non-Genetic Heterogeneity. <i>Frontiers in Oncology</i> , 2018, 8, 50.	2.8	122
157	Sequence Reversal Prevents Chain Collapse and Yields Heat-Sensitive Intrinsic Disorder. <i>Biophysical Journal</i> , 2018, 115, 328-340.	0.5	7
158	Phosphorylation of human TRM9L integrates multiple stress-signaling pathways for tumor growth suppression. <i>Science Advances</i> , 2018, 4, eaas9184.	10.3	22
159	Protein Synthesis Initiation in Eukaryotic Cells. <i>Cold Spring Harbor Perspectives in Biology</i> , 2018, 10, a033092.	5.5	230
160	Structural metamorphism and polymorphism in proteins on the brink of thermodynamic stability. <i>Protein Science</i> , 2018, 27, 1557-1567.	7.6	34
161	Modulating charge patterning and ionic strength as a strategy to induce conformational changes in intrinsically disordered proteins. <i>Journal of Chemical Physics</i> , 2018, 149, 085101.	3.0	36
162	Multiple Modes of Protein-Protein Interactions Promote RNP Granule Assembly. <i>Journal of Molecular Biology</i> , 2018, 430, 4636-4649.	4.2	179
163	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018, 46, D471-D476.	14.5	190
164	A disordered acidic domain in GPIHBP1 harboring a sulfated tyrosine regulates lipoprotein lipase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6020-E6029.	7.1	51
165	A Conditionally Fluorescent Peptide Reporter of Secondary Structure Modulation. <i>ChemBioChem</i> , 2019, 20, 40-45.	2.6	4
166	Specificity of MYB interactions relies on motifs in ordered and disordered contexts. <i>Nucleic Acids Research</i> , 2019, 47, 9592-9608.	14.5	30
167	The Intrinsically Disordered C-Terminal Domain Triggers Nucleolar Localization and Function Switch of PARN in Response to DNA Damage. <i>Cells</i> , 2019, 8, 836.	4.1	9

#	ARTICLE	IF	CITATIONS
168	q-Canonical Monte Carlo Sampling for Modeling the Linkage between Charge Regulation and Conformational Equilibria of Peptides. <i>Journal of Physical Chemistry B</i> , 2019, 123, 6952-6967.	2.6	29
169	AMPK and AKT protein kinases hierarchically phosphorylate the N-terminus of the FOXO1 transcription factor, modulating interactions with 14-3-3 proteins. <i>Journal of Biological Chemistry</i> , 2019, 294, 13106-13116.	3.4	71
170	Random coil shifts of posttranslationally modified amino acids. <i>Journal of Biomolecular NMR</i> , 2019, 73, 587-599.	2.8	24
171	Entropy and Information within Intrinsically Disordered Protein Regions. <i>Entropy</i> , 2019, 21, 662.	2.2	41
172	Ubiquitin is double-phosphorylated by PINK1 for enhanced pH-sensitivity of conformational switch. <i>Protein and Cell</i> , 2019, 10, 908-913.	11.0	6
173	Smart polymers driven by multiple and tunable hydrogen bonds for intact phosphoprotein enrichment. <i>Science and Technology of Advanced Materials</i> , 2019, 20, 858-869.	6.1	6
174	R2R3 MYB Transcription Factors “ Functions outside the DNA-Binding Domain. <i>Trends in Plant Science</i> , 2019, 24, 934-946.	8.8	109
175	Experimental studies of binding of intrinsically disordered proteins to their partners. , 2019, , 139-187.		3
176	Random coil chemical shifts for serine, threonine and tyrosine phosphorylation over a broad pH range. <i>Journal of Biomolecular NMR</i> , 2019, 73, 713-725.	2.8	24
177	Features of molecular recognition of intrinsically disordered proteins via coupled folding and binding. <i>Protein Science</i> , 2019, 28, 1952-1965.	7.6	55
178	Insights into the sediment toxicity of personal care products to freshwater oligochaete worms using Fourier transform infrared spectroscopy. <i>Ecotoxicology and Environmental Safety</i> , 2019, 172, 296-302.	6.0	12
179	Mitosis-related phosphorylation of the eukaryotic translation suppressor 4E-BP1 and its interaction with eukaryotic translation initiation factor 4E (eIF4E). <i>Journal of Biological Chemistry</i> , 2019, 294, 11840-11852.	3.4	23
180	The Organizing Principles of Eukaryotic Ribosome Recruitment. <i>Annual Review of Biochemistry</i> , 2019, 88, 307-335.	11.1	196
181	The Structural and Functional Diversity of Intrinsically Disordered Regions in Transmembrane Proteins. <i>Journal of Membrane Biology</i> , 2019, 252, 273-292.	2.1	14
182	Membrane interactions of intrinsically disordered proteins: The example of alpha-synuclein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 879-889.	2.3	35
183	The functional importance of structure in unstructured protein regions. <i>Current Opinion in Structural Biology</i> , 2019, 56, 155-163.	5.7	77
184	Single-molecule fluorescence studies of intrinsically disordered proteins and liquid phase separation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 980-987.	2.3	33
185	Recent Advances in Computational Protocols Addressing Intrinsically Disordered Proteins. <i>Biomolecules</i> , 2019, 9, 146.	4.0	50

#	ARTICLE	IF	CITATIONS
186	Quo Vadis Biomolecular NMR Spectroscopy?. International Journal of Molecular Sciences, 2019, 20, 1278.	4.1	16
187	A Yeast System for Discovering Optogenetic Inhibitors of Eukaryotic Translation Initiation. ACS Synthetic Biology, 2019, 8, 744-757.	3.8	16
188	p53 Phosphomimetics Preserve Transient Secondary Structure but Reduce Binding to Mdm2 and MdmX. Biomolecules, 2019, 9, 83.	4.0	4
189	Role of Phosphorylation in the Modulation of the Glucocorticoid Receptor's Intrinsically Disordered Domain. Biomolecules, 2019, 9, 95.	4.0	22
190	Spontaneous Switching among Conformational Ensembles in Intrinsically Disordered Proteins. Biomolecules, 2019, 9, 114.	4.0	41
191	Intrinsic disorder associated with 14-3-3 proteins and their partners. Progress in Molecular Biology and Translational Science, 2019, 166, 19-61.	1.7	47
193	Dynamic anticipation by Cdk2/Cyclin A-bound p27 mediates signal integration in cell cycle regulation. Nature Communications, 2019, 10, 1676.	12.8	71
194	Disordered domains in chromatin-binding proteins. Essays in Biochemistry, 2019, 63, 147-156.	4.7	36
195	Translational Control of Canonical and Non-Canonical Translation Initiation Factors at the Sea Urchin Egg to Embryo Transition. International Journal of Molecular Sciences, 2019, 20, 626.	4.1	5
196	Role of Backbone Dynamics in Modulating the Interactions of Disordered Ligands with the TAZ1 Domain of the CREB-Binding Protein. Biochemistry, 2019, 58, 1354-1362.	2.5	33
197	Polymer effects modulate binding affinities in disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19506-19512.	7.1	63
198	Multimics-Based Signaling Pathway Network Alterations in Human Non-functional Pituitary Adenomas. Frontiers in Endocrinology, 2019, 10, 835.	3.5	40
199	Raptor-Mediated Proteasomal Degradation of Deamidated 4E-BP2 Regulates Postnatal Neuronal Translation and NF- $\kappa$ B Activity. Cell Reports, 2019, 29, 3620-3635.e7.	6.4	8
200	AWESOME: a database of SNPs that affect protein post-translational modifications. Nucleic Acids Research, 2019, 47, D874-D880.	14.5	53
201	FBP21's C-Terminal Domain Remains Dynamic When Wrapped around the c-Sec63 Unit of Brr2 Helicase. Biophysical Journal, 2019, 116, 406-418.	0.5	2
202	AMBER and CHARMM Force Fields Inconsistently Portray the Microscopic Details of Phosphorylation. Journal of Chemical Theory and Computation, 2019, 15, 665-679.	5.3	18
203	Preparation of Phosphorylated Proteins for NMR Spectroscopy. Methods in Enzymology, 2019, 614, 187-205.	1.0	2
204	Fold or not to fold upon binding " does it really matter?. Current Opinion in Structural Biology, 2019, 54, 19-25.	5.7	73

#	ARTICLE	IF	CITATIONS
205	Elucidating binding mechanisms and dynamics of intrinsically disordered protein complexes using NMR spectroscopy. <i>Current Opinion in Structural Biology</i> , 2019, 54, 10-18.	5.7	78
206	IDDomainSpotter: Compositional bias reveals domains in long disordered protein regionsâ€”Insights from transcription factors. <i>Protein Science</i> , 2020, 29, 169-183.	7.6	14
207	Subnanometer resolution cryo-EM structure of <i>Arabidopsis thaliana</i> ATG9. <i>Autophagy</i> , 2020, 16, 575-583.	9.1	36
208	Modulation of p53 N-terminal transactivation domain 2 conformation ensemble and kinetics by phosphorylation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 2613-2623.	3.5	9
209	Temperature dependence of NMR chemical shifts: Tracking and statistical analysis. <i>Protein Science</i> , 2020, 29, 306-314.	7.6	23
210	Quantitative proteomics indicate a strong correlation of mitotic phospho-/dephosphorylation with non-structured regions of substrates. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140295.	2.3	5
211	Characterizing Post-Translational Modifications and Their Effects on Protein Conformation Using NMR Spectroscopy. <i>Biochemistry</i> , 2020, 59, 57-73.	2.5	29
212	The regulation mechanism of phosphorylation and mutations in intrinsically disordered protein 4E-BP2. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 2938-2948.	2.8	5
213	NMR-based investigation into protein phosphorylation. <i>International Journal of Biological Macromolecules</i> , 2020, 145, 53-63.	7.5	15
214	Crosstalk of Phosphorylation and Arginine Methylation in Disordered SRGG Repeats of <i>Saccharomyces cerevisiae</i> Fibrillarin and Its Association with Nucleolar Localization. <i>Journal of Molecular Biology</i> , 2020, 432, 448-466.	4.2	22
215	Structural preferences of cysteine sulfinic acid: The sulfinate engages in multiple local interactions with the peptide backbone. <i>Free Radical Biology and Medicine</i> , 2020, 148, 96-107.	2.9	5
216	Unveiling invisible protein states with NMR spectroscopy. <i>Current Opinion in Structural Biology</i> , 2020, 60, 39-49.	5.7	73
217	Multifunnel Energy Landscapes for Phosphorylated Translation Repressor 4E-BP2 and Its Mutants. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 800-810.	5.3	3
218	Computational Disorder Analysis in Ethylene Response Factors Uncovers Binding Motifs Critical to Their Diverse Functions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 74.	4.1	7
219	A variant in the RP1L1 gene in a family with occult macular dystrophy in a predicted intrinsically disordered region. <i>Ophthalmic Genetics</i> , 2020, 41, 599-605.	1.2	5
220	Exploring protein phosphorylation by combining computational approaches and biochemical methods. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1852-1863.	4.1	29
221	Phenotypic switching and prostate diseases: a model proposing a causal link between benign prostatic hyperplasia and prostate cancer. , 2020, , 569-589.		0
222	Short Disordered Epitope of CRTAM Ig-Like V Domain as a Potential Target for Blocking Antibodies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8798.	4.1	0

#	ARTICLE	IF	CITATIONS
223	Classifying the Binding Modes of Disordered Proteins. International Journal of Molecular Sciences, 2020, 21, 8615.	4.1	49
224	Revealing the functional roles of tyrosine sulfation using synthetic sulfopeptides and sulfoproteins. Current Opinion in Chemical Biology, 2020, 58, 72-85.	6.1	24
225	Adaptor proteins: Flexible and dynamic modulators of immune cell signalling. Scandinavian Journal of Immunology, 2020, 92, e12951.	2.7	10
226	Evolving Role of Conformational Dynamics in Understanding Fundamental Biomolecular Behavior. ACS Symposium Series, 2020, , 57-81.	0.5	1
227	Identification of synthetic inhibitors for the DNA binding of intrinsically disordered circadian clock transcription factors. Chemical Communications, 2020, 56, 11203-11206.	4.1	5
228	A Phosphorylation-Induced Switch in the Nuclear Localization Sequence of the Intrinsically Disordered NUPR1 Hampers Binding to Importin. Biomolecules, 2020, 10, 1313.	4.0	13
229	Phosphorylation regulates the binding of intrinsically disordered proteins via a flexible conformation selection mechanism. Communications Chemistry, 2020, 3, .	4.5	25
230	Solution structure of Gaussia Luciferase with five disulfide bonds and identification of a putative coelenterazine binding cavity by heteronuclear NMR. Scientific Reports, 2020, 10, 20069.	3.3	34
231	Aromatic Interactions Drive the Coupled Folding and Binding of the Intrinsically Disordered <i>Sesbania mosaic</i> Virus VPg Protein. Biochemistry, 2020, 59, 4663-4680.	2.5	4
232	Expansion of Intrinsically Disordered Proteins Increases the Range of Stability of Liquid-Liquid Phase Separation. Molecules, 2020, 25, 4705.	3.8	42
233	Identifying sequence perturbations to an intrinsically disordered protein that determine its phase-separation behavior. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11421-11431.	7.1	202
234	Depletion interactions modulate the binding between disordered proteins in crowded environments. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13480-13489.	7.1	97
235	The C-terminal domains of the NMDA receptor: How intrinsically disordered tails affect signalling, plasticity and disease. European Journal of Neuroscience, 2021, 54, 6713-6739.	2.6	31
236	Sequence-based prediction of protein binding mode landscapes. PLoS Computational Biology, 2020, 16, e1007864.	3.2	41
237	Molecular Structure, Binding Affinity, and Biological Activity in the Epigenome. International Journal of Molecular Sciences, 2020, 21, 4134.	4.1	9
238	Interactions by Disorder – A Matter of Context. Frontiers in Molecular Biosciences, 2020, 7, 110.	3.5	124
239	C1188D mutation abolishes specific recognition between MLL1 CXXC domain and CpG site by inducing conformational switch of flexible N-terminal. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1401-1412.	2.6	1
240	The diversity, plasticity, and adaptability of cap-dependent translation initiation and the associated machinery. RNA Biology, 2020, 17, 1239-1251.	3.1	34

#	ARTICLE	IF	CITATIONS
241	Coupling hydrophilic interaction chromatography materials with immobilized Fe <sup>3+</sup> for phosphopeptide and glycopeptide enrichment and separation. RSC Advances, 2020, 10, 22176-22182.	3.6	8
242	Non-cooperative 4E-BP2 folding with exchange between eIF4E-binding and binding-incompatible states tunes cap-dependent translation inhibition. Nature Communications, 2020, 11, 3146.	12.8	17
243	Phosphorylation of multiple proteins involved in ciliogenesis by Tau Tubulin kinase 2. Molecular Biology of the Cell, 2020, 31, 1032-1046.	2.1	29
244	Mass-spectrometry-based draft of the Arabidopsis proteome. Nature, 2020, 579, 409-414.	27.8	328
245	Protein folding: how, why, and beyond. , 2020, , 3-22.		0
246	Competitive binding of HIF-1 $\alpha$ and CITED2 to the TAZ1 domain of CBP from molecular simulations. Physical Chemistry Chemical Physics, 2020, 22, 8118-8127.	2.8	15
247	Spotlight on the Ballet of Proteins: The Structural Dynamic Properties of Proteins Illuminated by Solution NMR. International Journal of Molecular Sciences, 2020, 21, 1829.	4.1	7
248	Probing Surfaces in Dynamic Protein Interactions. Journal of Molecular Biology, 2020, 432, 2949-2972.	4.2	17
249	Analytical Theory for Sequence-Specific Binary Fuzzy Complexes of Charged Intrinsically Disordered Proteins. Journal of Physical Chemistry B, 2020, 124, 6709-6720.	2.6	38
250	IDPs and their complexes in GPCR and nuclear receptor signaling. Progress in Molecular Biology and Translational Science, 2020, 174, 105-155.	1.7	6
251	Single-Molecule FRET of Intrinsically Disordered Proteins. Annual Review of Physical Chemistry, 2020, 71, 391-414.	10.8	48
252	A Prion Epigenetic Switch Establishes an Active Chromatin State. Cell, 2020, 180, 928-940.e14.	28.9	54
253	Copper-Free Huisgen Cycloaddition for the 14 $\beta$ -3 $\alpha$ -Templated Synthesis of Fusicoccinâ€Peptide Conjugates. Chemistry - an Asian Journal, 2020, 15, 742-747.	3.3	9
254	Biomolecular Phase Separation: From Molecular Driving Forces to Macroscopic Properties. Annual Review of Physical Chemistry, 2020, 71, 53-75.	10.8	368
255	Translational Control Through the EIF4E Binding Proteins in the Brain. , 0, , 23-42.		2
256	In-situ fingerprinting phosphorylated proteins via surface-enhanced Raman spectroscopy: Single-site discrimination of Tau biomarkers in Alzheimer's disease. Biosensors and Bioelectronics, 2021, 171, 112748.	10.1	22
257	Intrinsically disordered protein domain of human ameloblastin in synthetic fusion with calmodulin increases calmodulin stability and modulates its function. International Journal of Biological Macromolecules, 2021, 168, 1-12.	7.5	3
258	MobiDB: intrinsically disordered proteins in 2021. Nucleic Acids Research, 2021, 49, D361-D367.	14.5	183



#	ARTICLE	IF	CITATIONS
259	Functional and Regulatory Roles of Fold-Switching Proteins. <i>Structure</i> , 2021, 29, 6-14.	3.3	43
260	Drug design targeting active posttranslational modification protein isoforms. <i>Medicinal Research Reviews</i> , 2021, 41, 1701-1750.	10.5	33
261	mTORC1/2 signaling is downregulated by amino acid-free culture of mouse preimplantation embryos and is only partially restored by amino acid readdition. <i>American Journal of Physiology - Cell Physiology</i> , 2021, 320, C30-C44.	4.6	7
262	Selective Affimers Recognise the BCL-2 Family Proteins BCL-X <sub>L</sub> and MCL1 through Noncanonical Structural Motifs**. <i>ChemBioChem</i> , 2021, 22, 232-240.	2.6	9
263	Peptide-based inhibitors of protein-protein interactions: biophysical, structural and cellular consequences of introducing a constraint. <i>Chemical Science</i> , 2021, 12, 5977-5993.	7.4	56
264	Chemical Approach Toward Controlling of Transient Protein Interactions. , 2021, , 77-96.		0
265	Intrinsic Disorder in the T Cell Receptor Creates Cooperativity and Controls ZAP70 Binding. <i>Biophysical Journal</i> , 2021, 120, 379-392.	0.5	8
268	&lt;i>In Situ &lt;/i>Photopolymerization of Functionalized Polyacrylamide-Based Preconcentrators for Highly Sensitive Specific Detection of Various Analytes by Microchip Electrophoresis. <i>Chromatography</i> , 2021, 42, 29-36.	1.7	5
269	Chain Entropy Beats Hydrogen Bonds to Unfold and Thread Dialcohol Phosphates inside Cyanostar Macrocycles To Form [3]Pseudorotaxanes. <i>Journal of Organic Chemistry</i> , 2021, 86, 4532-4546.	3.2	10
270	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. <i>Accounts of Chemical Research</i> , 2021, 54, 1251-1259.	15.6	88
271	NMR spectroscopy captures the essential role of dynamics in regulating biomolecular function. <i>Cell</i> , 2021, 184, 577-595.	28.9	103
272	Facile synthesis of titanium(IV) ion-immobilized arsenate-modified poly(glycidyl methacrylate) microparticles and the application to the specific enrichment of phosphoproteins. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 2893-2901.	3.7	4
274	Intrinsically Disordered Proteins as Regulators of Transient Biological Processes and as Untapped Drug Targets. <i>Molecules</i> , 2021, 26, 2118.	3.8	13
275	Investigation of Phosphorylation-Induced Folding of an Intrinsically Disordered Protein by Coarse-Grained Molecular Dynamics. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 3203-3220.	5.3	11
276	Mechanisms and regulation underlying membraneless organelle plasticity control. <i>Journal of Molecular Cell Biology</i> , 2021, 13, 239-258.	3.3	14
277	Hyperphosphorylation of Human Osteopontin and Its Impact on Structural Dynamics and Molecular Recognition. <i>Biochemistry</i> , 2021, 60, 1347-1355.	2.5	15
278	RLIP76: A Structural and Functional Triumvirate. <i>Cancers</i> , 2021, 13, 2206.	3.7	4
279	Phosphorylation-regulated HMGA1a-P53 interaction unveils the function of HMGA1a acidic tail phosphorylations via synthetic proteins. <i>Cell Chemical Biology</i> , 2021, 28, 722-732.e8.	5.2	10



#	ARTICLE	IF	CITATIONS
280	Overlapping regions of Caf20 mediate its interactions with the mRNA-5' cap-binding protein eIF4E and with ribosomes. <i>Scientific Reports</i> , 2021, 11, 13467.	3.3	4
281	Progressive Phosphorylation Modulates the Self-Association of a Variably Modified Histone H3 Peptide. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 698182.	3.5	6
282	The Boscombe Valley mystery: A lesson in the perils of dogmatism in science. <i>Journal of Biosciences</i> , 2021, 46, 1.	1.1	1
283	Combinatorial phosphorylation modulates the structure and function of the G protein $\beta^3$ subunit in yeast. <i>Science Signaling</i> , 2021, 14, .	3.6	4
284	The dynamic mechanism of 4E-BP1 recognition and phosphorylation by mTORC1. <i>Molecular Cell</i> , 2021, 81, 2403-2416.e5.	9.7	32
285	A Tale of Loops and Tails: The Role of Intrinsically Disordered Protein Regions in R-Loop Recognition and Phase Separation. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 691694.	3.5	21
286	Intrinsically disordered proteins and biomolecular condensates as drug targets. <i>Current Opinion in Chemical Biology</i> , 2021, 62, 90-100.	6.1	57
287	Preorganization boosts the artificial esterase activity of a self-assembling peptide. <i>Science China Chemistry</i> , 2021, 64, 1554-1559.	8.2	15
288	A biphenyl inhibitor of eIF4E targeting an internal binding site enables the design of cell-permeable PROTAC-degraders. <i>European Journal of Medicinal Chemistry</i> , 2021, 219, 113435.	5.5	15
289	Cancer-Associated Mutations Perturb the Disordered Ensemble and Interactions of the Intrinsically Disordered p53 Transactivation Domain. <i>Journal of Molecular Biology</i> , 2021, 433, 167048.	4.2	14
290	Poly amidoamine functionalized poly (styrene-divinylbenzene-glycidylmethacrylate) composites for the rapid enrichment and determination of N-phosphoryl peptides. <i>Microchemical Journal</i> , 2021, 166, 106213.	4.5	3
291	The Protein Folding Problem: The Role of Theory. <i>Journal of Molecular Biology</i> , 2021, 433, 167126.	4.2	52
292	Intracellular wetting mediates contacts between liquid compartments and membrane-bound organelles. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	30
293	The plasticity of mRNA translation during cancer progression and therapy resistance. <i>Nature Reviews Cancer</i> , 2021, 21, 558-577.	28.4	100
294	The sequence-ensemble relationship in fuzzy protein complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	12
295	Control of the eIF4E activity: structural insights and pharmacological implications. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 6869-6885.	5.4	28
296	Theory and Practice of Coarse-Grained Molecular Dynamics of Biologically Important Systems. <i>Biomolecules</i> , 2021, 11, 1347.	4.0	29
297	Structural Insights into Protein Regulation by Phosphorylation and Substrate Recognition of Protein Kinases/Phosphatases. <i>Life</i> , 2021, 11, 957.	2.4	23

#	ARTICLE	IF	CITATIONS
298	Liquidâ€“liquid phase separation underpins the formation of replication factories in rotaviruses. EMBO Journal, 2021, 40, e107711.	7.8	65
300	Phosphorylated Osteopontin Secreted from Cancer Cells Induces Cancer Cell Motility. Biomolecules, 2021, 11, 1323.	4.0	8
301	Regulation of the NMDA receptor by its cytoplasmic domains: (How) is the tail wagging the dog?. Neuropharmacology, 2021, 195, 108634.	4.1	10
302	Post-translational modification analysis of Saccharomyces cerevisiae histone methylation enzymes reveals phosphorylation sites of regulatory potential. Journal of Biological Chemistry, 2021, 296, 100192.	3.4	10
303	Quantitative Phosphoproteomic Analysis of Legume Using TiO2-Based Enrichment Coupled with Isobaric Labeling. Methods in Molecular Biology, 2020, 2107, 395-406.	0.9	1
304	Toward Multiscale Modeling of Molecular and Biochemical Events Occurring at Fertilization Time in Sea Urchins. Results and Problems in Cell Differentiation, 2018, 65, 69-89.	0.7	2
305	Allostery in Drug Development. Advances in Experimental Medicine and Biology, 2019, 1163, 1-23.	1.6	15
306	Recent advances in measuring the kinetics of biomolecules by NMR relaxation dispersion spectroscopy. Archives of Biochemistry and Biophysics, 2017, 628, 81-91.	3.0	30
307	Dynamic Nuclear Polarization Nuclear Magnetic Resonance in Human Cells Using Fluorescent Polarizing Agents. Biochemistry, 2018, 57, 4741-4746.	2.5	58
308	Fuzzy protein theory for disordered proteins. Biochemical Society Transactions, 2020, 48, 2557-2564.	3.4	16
309	Intrinsically disordered proteins and membranes: a marriage of convenience for cell signalling?. Biochemical Society Transactions, 2020, 48, 2669-2689.	3.4	36
310	Connecting the dots: from nanodomains to physiological functions of REMORINs. Plant Physiology, 2021, 185, 632-649.	4.8	22
313	Identification of a Novel Regulatory Mechanism of Nutrient Transport Controlled by TORC1-Npr1-Amu1/Par32. PLoS Genetics, 2015, 11, e1005382.	3.5	30
314	IRBIT Interacts with the Catalytic Core of Phosphatidylinositol Phosphate Kinase Type II $\alpha$ and II $\beta$ through Conserved Catalytic Aspartate Residues. PLoS ONE, 2015, 10, e0141569.	2.5	11
315	Cyclin B Translation Depends on mTOR Activity after Fertilization in Sea Urchin Embryos. PLoS ONE, 2016, 11, e0150318.	2.5	18
316	Intrinsic Disorder in Transmembrane Proteins: Roles in Signaling and Topology Prediction. PLoS ONE, 2016, 11, e0158594.	2.5	59
317	Regulation of Androgen Receptor Activity by Transient Interactions of Its Transactivation Domain with General Transcription Regulators. SSRN Electronic Journal, 0, , .	0.4	1
318	From Levinthalâ€™s Paradox to the Effects of Cell Environmental Perturbation on Protein Folding. Current Medicinal Chemistry, 2020, 26, 7537-7554.	2.4	6

#	ARTICLE	IF	CITATIONS
319	Cancer/testis antigens and obligate participation in multiple hallmarks of cancer: an update. Asian Journal of Andrology, 2016, 18, 711.	1.6	4
320	Phenotypic plasticity in prostate cancer: role of intrinsically disordered proteins. Asian Journal of Andrology, 2016, 18, 704.	1.6	68
321	Chemical perturbation of an intrinsically disordered region of TFIID distinguishes two modes of transcription initiation. ELife, 2015, 4, .	6.0	35
322	CPEB4 is regulated during cell cycle by ERK2/Cdk1-mediated phosphorylation and its assembly into liquid-like droplets. ELife, 2016, 5, .	6.0	45
323	An order-to-disorder structural switch activates the FoxM1 transcription factor. ELife, 2019, 8, .	6.0	34
324	Multi-state recognition pathway of the intrinsically disordered protein kinase inhibitor by protein kinase A. ELife, 2020, 9, .	6.0	16
325	Disorder-to-order transition of the amyloid-Î² peptide upon lipid binding. Biophysical Chemistry, 2022, 280, 106700.	2.8	58
326	Evolution of eIF4E-Interacting Proteins. , 2016, , 207-234.		3
327	A QUESTION OF PERSPECTIVE?. , 2017, , .		0
328	Protein Misfolding. , 2017, , 1-16.		0
331	Protein Misfolding. , 2018, , 2253-2268.		0
332	Raptor-Mediated Proteasomal Degradation of Deamidated 4E-BP2 Regulates Postnatal Neuronal Translation and NF-Kappa B Activity. SSRN Electronic Journal, 0, , .	0.4	0
333	Posttranslational Modifications (PTMs): Alteration of the Three-Dimensional Structure of Proteins. , 2019, , 151-179.		1
337	Study of dielectric parameters of protein solution. , 2019, , .		2
343	Determination of pKa Values in Intrinsically Disordered Proteins. Methods in Molecular Biology, 2020, 2141, 319-336.	0.9	1
344	NMR Lineshape Analysis of Intrinsically Disordered Protein Interactions. Methods in Molecular Biology, 2020, 2141, 477-504.	0.9	8
345	FuzDB: a new phase in understanding fuzzy interactions. Nucleic Acids Research, 2022, 50, D509-D517.	14.5	25
347	Quantifying Protein Electrostatic Interactions in Cells by Nuclear Magnetic Resonance Spectroscopy. Journal of the American Chemical Society, 2021, 143, 19606-19613.	13.7	9

#	ARTICLE	IF	CITATIONS
348	Tyrosine 136 phosphorylation of $\alpha$ -synuclein aggregates in the Lewy body dementia brain: involvement of serine 129 phosphorylation by casein kinase 2. <i>Acta Neuropathologica Communications</i> , 2021, 9, 182.	5.2	17
349	Quantifying charge state heterogeneity for proteins with multiple ionizable residues. <i>Biophysical Journal</i> , 2021, 120, 5438-5453.	0.5	21
350	An engineered construct of cFLIP provides insight into DED1 structure and interactions. <i>Structure</i> , 2021, , .	3.3	4
352	Expanding the Disorder-Function Paradigm in the C-Terminal Tails of Erbbs. <i>Biomolecules</i> , 2021, 11, 1690.	4.0	2
353	eIF4E homologous protein (4EHP): a multifarious cap-binding protein. <i>FEBS Journal</i> , 2023, 290, 266-285.	4.7	15
354	Carbodiimide-fueled catalytic reaction cycles to regulate supramolecular processes. <i>Chemical Communications</i> , 2022, 58, 1284-1297.	4.1	25
355	Analysis of a crucial interaction between the coronavirus nucleocapsid protein and the major membrane-bound subunit of the viral replicase-transcriptase complex. <i>Virology</i> , 2022, 567, 1-14.	2.4	19
356	Macromolecular Crowding Induces a Binding Competent Transient Structure in Intrinsically Disordered Gab1. <i>Journal of Molecular Biology</i> , 2022, 434, 167407.	4.2	6
358	Matrin3: Disorder and ALS Pathogenesis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 794646.	3.5	10
359	The Energy Landscape Perspective: Encoding Structure and Function for Biomolecules. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 820792.	3.5	11
361	Direct measurement of protein electrostatic interactions in cells. <i>Magnetic Resonance Letters</i> , 2022, 2, 59-60.	1.3	0
362	Identification and Characterization of the Interaction Between the Methyl-7-Guanosine Cap Maturation Enzyme RNMT and the Cap-Binding Protein eIF4E. <i>Journal of Molecular Biology</i> , 2022, 434, 167451.	4.2	14
363	The auto-inhibition mechanism of transcription factor Ets-1 induced by phosphorylation on the intrinsically disordered region. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1132-1141.	4.1	3
364	Challenges in Protein Sequencing Using 2-D MoS <sub>2</sub> Nanopores. <i>Nanostructure Science and Technology</i> , 2022, , 343-366.	0.1	1
367	In-Cell Structural Biology by NMR: The Benefits of the Atomic Scale. <i>Chemical Reviews</i> , 2022, 122, 9497-9570.	47.7	55
368	PRP4KA phosphorylates SERRATE for degradation via 20 S proteasome to fine-tune miRNA production in <i>Arabidopsis</i> . <i>Science Advances</i> , 2022, 8, eabm8435.	10.3	16
369	Thermal Proteome Profiling Reveals the O-GlcNAc-Dependent Meltome. <i>Journal of the American Chemical Society</i> , 2022, 144, 3833-3842.	13.7	19
370	The X-ray crystallography phase problem solved thanks to <i>AlphaFold</i> and <i>RoseTTAFold</i> models: a case-study report. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 517-531.	2.3	22

#	ARTICLE	IF	CITATIONS
371	Î±-Helix stabilization by co-operative side chain charge-reinforced interactions to phosphoserine in a basic kinase-substrate motif. <i>Biochemical Journal</i> , 2022, 479, 687-700.	3.7	2
372	Advances in the adsorption/enrichment of proteins/peptides by metal-organic frameworks-affinity adsorbents. <i>TrAC - Trends in Analytical Chemistry</i> , 2022, 153, 116627.	11.4	18
373	Cancer: More than a geneticist's Pandora's box. <i>Journal of Biosciences</i> , 2022, 47, .	1.1	2
375	In Situ Pinpoint Photopolymerization of Phos-Tag Polyacrylamide Gel in Poly(dimethylsiloxane)/Glass Microchip for Specific Entrapment, Derivatization, and Separation of Phosphorylated Compounds. <i>Gels</i> , 2021, 7, 268.	4.5	1
376	Phase Separation of Intrinsically Disordered Nucleolar Proteins Relate to Localization and Function. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13095.	4.1	11
377	Preconcentration of Hemoglobin by a Nickel-Based Metal-Organic Framework (MOF) with Biphenyl Ligands. <i>Analytical Letters</i> , 0, , 1-12.	1.8	0
383	Structural Insights into the Intrinsically Disordered GPCR C-Terminal Region, Major Actor in Arrestin-GPCR Interaction. <i>Biomolecules</i> , 2022, 12, 617.	4.0	7
384	Î²-Arrestin2 Is Critically Involved in the Differential Regulation of Phosphosignaling Pathways by Thyrotropin-Releasing Hormone and Taltirelin. <i>Cells</i> , 2022, 11, 1473.	4.1	2
385	The metaphorical swiss army knife: The multitude and diverse roles of HEAT domains in eukaryotic translation initiation. <i>Nucleic Acids Research</i> , 2022, 50, 5424-5442.	14.5	8
386	Herpesvirus Replication Compartments: Dynamic Biomolecular Condensates?. <i>Viruses</i> , 2022, 14, 960.	3.3	9
387	mTOR substrate phosphorylation in growth control. <i>Cell</i> , 2022, 185, 1814-1836.	28.9	120
389	Additional principles that govern the release of pre-ribosomes from the nucleolus into the nucleoplasm in yeast. <i>Nucleic Acids Research</i> , 0, , .	14.5	5
392	A Mechanistic Model for Cell Cycle Control in Which CDKs Act as Switches of Disordered Protein Phase Separation. <i>Cells</i> , 2022, 11, 2189.	4.1	4
393	Multisite phosphorylation and binding alter conformational dynamics of the 4E-BP2 protein. <i>Biophysical Journal</i> , 2022, 121, 3049-3060.	0.5	4
394	ERK2 MAP kinase regulates SUFU binding by multisite phosphorylation of GLI1. <i>Life Science Alliance</i> , 2022, 5, e202101353.	2.8	8
395	Highly selective titanium (IV)-immobilized O-phospho-L-tyrosine modified magnetic nanoparticles for the enrichment of intact phosphoproteins. <i>Journal of Separation Science</i> , 0, , .	2.5	0
396	Extended disordered regions of ribosome-associated NAC proteins paralogs belong only to the germline in <i>Drosophila melanogaster</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	1
397	Zinc controls PML nuclear body formation through regulation of a paralog specific auto-inhibition in SUMO1. <i>Nucleic Acids Research</i> , 2022, 50, 8331-8348.	14.5	3

#	ARTICLE	IF	CITATIONS
398	Systematic discovery of biomolecular condensate-specific protein phosphorylation. <i>Nature Chemical Biology</i> , 2022, 18, 1104-1114.	8.0	39
400	Characterising Intrinsically Disordered Proteins Using NMR Spectroscopy and MD Simulations. <i>New Developments in NMR</i> , 2022, , 383-410.	0.1	2
401	The role of structural dynamics in the thermal adaptation of hyperthermophilic enzymes. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	3
402	Balanced Force Field ff03CMAP Improving the Dynamics Conformation Sampling of Phosphorylation Site. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11285.	4.1	3
404	Phosphorylation of the DNA repair scaffold SLX4 drives folding of the SAP domain and activation of the MUS81-EME1 endonuclease. <i>Cell Reports</i> , 2022, 41, 111537.	6.4	10
405	Major structural features of membrane-less organelles. , 2023, , 83-99.		0
406	How phosphorylation impacts intrinsically disordered proteins and their function. <i>Essays in Biochemistry</i> , 2022, 66, 901-913.	4.7	21
407	Excessive Protein Accumulation and Impaired Autophagy in the Hippocampus of Angelman Syndrome Modeled in Mice. <i>Biological Psychiatry</i> , 2023, 94, 68-83.	1.3	2
408	Phosphorylation of Thr9 Affects the Folding Landscape of the N-Terminal Segment of Human AGT Enhancing Protein Aggregation of Disease-Causing Mutants. <i>Molecules</i> , 2022, 27, 8762.	3.8	1
409	NMR insights into dynamic, multivalent interactions of intrinsically disordered regions: from discrete complexes to condensates. <i>Essays in Biochemistry</i> , 2022, 66, 863-873.	4.7	12
410	Protein-protein interactions in plant antioxidant defense. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
411	Control of protein stability by post-translational modifications. <i>Nature Communications</i> , 2023, 14, .	12.8	63
412	Structural determinants of REMORIN nanodomain formation in anionic membranes. <i>Biophysical Journal</i> , 2023, 122, 2192-2202.	0.5	4
413	Phosphorylation alters the mechanical stiffness of a model fragment of the dystrophin homologue utrophin. <i>Journal of Biological Chemistry</i> , 2023, 299, 102847.	3.4	1
414	The enzyme activity of sortase A is regulated by phosphorylation in <i>Staphylococcus aureus</i> . <i>Virulence</i> , 2023, 14, .	4.4	3
415	Electronegative clusters modulate folding status and RNA binding of unstructured RNA-binding proteins. <i>Protein Science</i> , 2023, 32, .	7.6	2
416	The Conserved Yeast Protein Knr4 Involved in Cell Wall Integrity Is a Multi-domain Intrinsically Disordered Protein. <i>Journal of Molecular Biology</i> , 2023, 435, 168048.	4.2	0
417	Intrinsic Disorder of the Neuronal SNARE Protein SNAP25a in its Pre-fusion Conformation. <i>Journal of Molecular Biology</i> , 2023, 435, 168069.	4.2	2

#	ARTICLE	IF	CITATIONS
418	Protocol for inÂvitro phosphorylation of the MUS81-binding region of SLX4 using CDK1-cyclin B. STAR Protocols, 2023, 4, 102152.	1.2	0
419	Distinguishing features of foldâ€switching proteins. Protein Science, 2023, 32, .	7.6	8
422	In silico analysis of the possible crosstalk between O-linked Î²-GlcNAcylation and phosphorylation sites of Disabled 1 adaptor protein in vertebrates. Amino Acids, 0, , .	2.7	0
423	Largeâ€scale phosphomimetic screening identifies phosphoâ€modulated motifâ€based protein interactions. Molecular Systems Biology, 2023, 19, .	7.2	3
424	Crosslink-Induced Conformation Change of Intrinsically Disordered Proteins Have a Nontrivial Effect on Phase Separation Dynamics and Thermodynamics. Journal of Physical Chemistry B, 2023, 127, 5018-5026.	2.6	1
425	Simultaneous Adsorption of Intact Glycoproteins and Phosphoproteins Using Hydrophilic Titanium (IV) Ion-Immobilized Cotton Fiber Functionalized by Phytic Acid Assembly. Journal of Chemistry, 2023, 2023, 1-10.	1.9	0
426	How to evict HP1 from H3: Using a complex salt bridge. Biophysical Chemistry, 2023, 300, 107062.	2.8	0
427	Structural basis of protein condensation on microtubules underlying branching microtubule nucleation. Nature Communications, 2023, 14, .	12.8	1
429	Conformational Plasticity in Î±-Synuclein and How Crowded Environment Modulates It. Journal of Physical Chemistry B, 2023, 127, 4032-4049.	2.6	5
430	From Immunogenic Peptides to Intrinsically Disordered Proteins. Israel Journal of Chemistry, 0, , .	2.3	0
431	Conformation and Affinity Modulations by Multiple Phosphorylation Occurring in the BIN1 SH3 Domain Binding Site of the Tau Protein Proline-Rich Region. Biochemistry, 2023, 62, 1631-1642.	2.5	0
432	Proteomic tools to study phosphorylation of intrinsically disordered proteins. Expert Review of Proteomics, 2023, 20, 93-107.	3.0	0
433	Non-uniform sampling of similar NMR spectra and its application to studies of the interaction between alpha-synuclein and liposomes. Journal of Biomolecular NMR, 2023, 77, 149-163.	2.8	2
435	N-terminal intrinsic disorder is an ancestral feature of GÎ³ subunits that influences the balance between different GÎ²Î³ signaling axes in yeast. Journal of Biological Chemistry, 2023, 299, 104947.	3.4	0
436	Functional regulation of an intrinsically disordered protein via a conformationally excited state. Science Advances, 2023, 9, .	10.3	8
437	Minimum information guidelines for experiments structurally characterizing intrinsically disordered protein regions. Nature Methods, 2023, 20, 1291-1303.	19.0	5
438	Fluid protein fold space and its implications. BioEssays, 2023, 45, .	2.5	2
439	Comparative proteomic and phosphoproteomic analysis reveals differential heat response mechanism in two congeneric oyster species. Ecotoxicology and Environmental Safety, 2023, 263, 115197.	6.0	3



443	Mechanosensitive ion channels MSL8, MSL9, and MSL10 have environmentally sensitive intrinsically disordered regions with distinct biophysical characteristics in vitro. <i>Plant Direct</i> , 2023, 7, .	1.9	2
-----	--	-----	---



#	ARTICLE	IF	CITATIONS
461	Functional evaluation of an electrophilic focused library to identify a covalent inhibitor against intrinsically disordered circadian clock transcription factors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2024, 98, 129588.	2.2	0
462	Dynamics and interactions of intrinsically disordered proteins. <i>Current Opinion in Structural Biology</i> , 2024, 84, 102734.	5.7	0
464	A cyclin D1 intrinsically disordered domain accesses modified histone motifs to govern gene transcription. <i>Oncogenesis</i> , 2024, 13, .	4.9	0
465	Sensitivity-enhanced NMR 15N R1 and R1ρ-relaxation experiments for the investigation of intrinsically disordered proteins at high magnetic fields. <i>Methods</i> , 2024, 223, 1-15.	3.8	0
466	Interplay between posttranslational modifications and liquidâ€”liquid phase separation in tumors. <i>Cancer Letters</i> , 2024, 584, 216614.	7.2	1
468	An evolutionarily conserved phosphoserine-arginine salt bridge in the interface between ribosomal proteins uS4 and uS5 regulates translational accuracy in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2024, 52, 3989-4001.	14.5	0
470	The prefoldinâ€”like protein <scp>AtURI</scp> exhibits characteristics of intrinsically disordered proteins. <i>FEBS Letters</i> , 2024, 598, 556-570.	2.8	0