

Vladimir N Uversky

List of Publications by Year in descending order

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990
papers

81,516
citations

419

132
h-index

693

253
g-index

1452
all docs

1452
docs citations

1452
times ranked

54637
citing authors

#	ARTICLE	IF	CITATIONS
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	9.1	4,701
2	Why are ?natively unfolded? proteins unstructured under physiologic conditions?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 415-427.	2.6	1,931
3	Natively unfolded proteins: A point where biology waits for physics. <i>Protein Science</i> , 2002, 11, 739-756.	7.6	1,650
4	Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631.	47.7	1,618
5	Study of the ?molten globule? intermediate state in protein folding by a hydrophobic fluorescent probe. <i>Biopolymers</i> , 1991, 31, 119-128.	2.4	1,264
6	Intrinsically Disordered Proteins in Human Diseases: Introducing the D ² Concept. <i>Annual Review of Biophysics</i> , 2008, 37, 215-246.	10.0	1,222
7	Effect of Environmental Factors on the Kinetics of Insulin Fibril Formation: Elucidation of the Molecular Mechanism. <i>Biochemistry</i> , 2001, 40, 6036-6046.	2.5	1,077
8	Flexible nets. The roles of intrinsic disorder in protein interaction networks. <i>FEBS Journal</i> , 2005, 272, 5129-5148.	4.7	1,052
9	Understanding protein non-folding. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1231-1264.	2.3	1,030
10	PONDR-FIT: A meta-predictor of intrinsically disordered amino acids. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 996-1010.	2.3	993
11	Evidence for a Partially Folded Intermediate in Î±-Synuclein Fibril Formation. <i>Journal of Biological Chemistry</i> , 2001, 276, 10737-10744.	3.4	955
12	Metal-triggered Structural Transformations, Aggregation, and Fibrillation of Human Î±-Synuclein. <i>Journal of Biological Chemistry</i> , 2001, 276, 44284-44296.	3.4	953
13	Conformational constraints for amyloid fibrillation: the importance of being unfolded. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1698, 131-153.	2.3	887
14	What does it mean to be natively unfolded?. <i>FEBS Journal</i> , 2002, 269, 2-12.	0.2	865
15	Function and structure of inherently disordered proteins. <i>Current Opinion in Structural Biology</i> , 2008, 18, 756-764.	5.7	864
16	Showing your ID: intrinsic disorder as an ID for recognition, regulation and cell signaling. <i>Journal of Molecular Recognition</i> , 2005, 18, 343-384.	2.1	762
17	DisProt: the Database of Disordered Proteins. <i>Nucleic Acids Research</i> , 2007, 35, D786-D793.	14.5	711
18	Analysis of Molecular Recognition Features (MoRFs). <i>Journal of Molecular Biology</i> , 2006, 362, 1043-1059.	4.2	672

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19	Intrinsic Disorder in Transcription Factors. <i>Biochemistry</i> , 2006, 45, 6873-6888.	2.5	654
20	Intrinsic Disorder and Functional Proteomics. <i>Biophysical Journal</i> , 2007, 92, 1439-1456.	0.5	643
21	Introducing Protein Intrinsic Disorder. <i>Chemical Reviews</i> , 2014, 114, 6561-6588.	47.7	628
22	Coupled Folding and Binding with α -Helix-Forming Molecular Recognition Elements. <i>Biochemistry</i> , 2005, 44, 12454-12470.	2.5	593
23	D2P2: database of disordered protein predictions. <i>Nucleic Acids Research</i> , 2012, 41, D508-D516.	14.5	570
24	The Herbicide Paraquat Causes Up-regulation and Aggregation of α -Synuclein in Mice. <i>Journal of Biological Chemistry</i> , 2002, 277, 1641-1644.	3.4	566
25	α -Synuclein misfolding and Parkinson's disease. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2012, 1822, 261-285.	3.8	526
26	Functional Anthology of Intrinsic Disorder. 1. Biological Processes and Functions of Proteins with Long Disordered Regions. <i>Journal of Proteome Research</i> , 2007, 6, 1882-1898.	3.7	525
27	Intrinsically disordered proteins in overcrowded milieu: Membrane-less organelles, phase separation, and intrinsic disorder. <i>Current Opinion in Structural Biology</i> , 2017, 44, 18-30.	5.7	515
28	Intrinsic Disorder Is a Common Feature of Hub Proteins from Four Eukaryotic Interactomes. <i>PLoS Computational Biology</i> , 2006, 2, e100.	3.2	512
29	Comparing and Combining Predictors of Mostly Disordered Proteins. <i>Biochemistry</i> , 2005, 44, 1989-2000.	2.5	485
30	The unfoldomics decade: an update on intrinsically disordered proteins. <i>BMC Genomics</i> , 2008, 9, S1.	2.8	485
31	Effect of Familial Parkinson's Disease Point Mutations A30P and A53T on the Structural Properties, Aggregation, and Fibrillation of Human α -Synuclein. <i>Biochemistry</i> , 2001, 40, 11604-11613.	2.5	482
32	Flexible nets: disorder and induced fit in the associations of p53 and 14-3-3 with their partners. <i>BMC Genomics</i> , 2008, 9, S1.	2.8	482
33	Neuropathology, biochemistry, and biophysics of α -synuclein aggregation. <i>Journal of Neurochemistry</i> , 2007, 103, 17-37.	3.9	471
34	Orderly order in protein intrinsic disorder distribution: disorder in 3500 proteomes from viruses and the three domains of life. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 30, 137-149.	3.5	465
35	Use of fast protein size-exclusion liquid chromatography to study the unfolding of proteins which denature through the molten globule. <i>Biochemistry</i> , 1993, 32, 13288-13298.	2.5	462
36	Unusual biophysics of intrinsically disordered proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 932-951.	2.3	459

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37	A Protein-Chameleon: Conformational Plasticity of α -Synuclein, a Disordered Protein Involved in Neurodegenerative Disorders. <i>Journal of Biomolecular Structure and Dynamics</i> , 2003, 21, 211-234.	3.5	450
38	Disorder in the nuclear pore complex: The FG repeat regions of nucleoporins are natively unfolded. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2450-2455.	7.1	444
39	Characterization of Molecular Recognition Features, MoRFs, and Their Binding Partners. <i>Journal of Proteome Research</i> , 2007, 6, 2351-2366.	3.7	433
40	Alternative splicing in concert with protein intrinsic disorder enables increased functional diversity in multicellular organisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8390-8395.	7.1	428
41	What Macromolecular Crowding Can Do to a Protein. <i>International Journal of Molecular Sciences</i> , 2014, 15, 23090-23140.	4.1	425
42	A decade and a half of protein intrinsic disorder: Biology still waits for physics. <i>Protein Science</i> , 2013, 22, 693-724.	7.6	415
43	Biophysical Properties of the Synucleins and Their Propensities to Fibrillate. <i>Journal of Biological Chemistry</i> , 2002, 277, 11970-11978.	3.4	413
44	Predicting intrinsic disorder in proteins: an overview. <i>Cell Research</i> , 2009, 19, 929-949.	12.0	389
45	Assessing protein disorder and induced folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 24-45.	2.6	388
46	Intrinsically disordered proteins from A to Z. <i>International Journal of Biochemistry and Cell Biology</i> , 2011, 43, 1090-1103.	2.8	372
47	Functional Anthology of Intrinsic Disorder. 3. Ligands, Post-Translational Modifications, and Diseases Associated with Intrinsically Disordered Proteins. <i>Journal of Proteome Research</i> , 2007, 6, 1917-1932.	3.7	369
48	TOP-IDP-Scale: A New Amino Acid Scale Measuring Propensity for Intrinsic Disorder. <i>Protein and Peptide Letters</i> , 2008, 15, 956-963.	0.9	361
49	Intrinsically Disordered Proteins and Their "Mysterious" (Meta)Physics. <i>Frontiers in Physics</i> , 2019, 7, .	2.1	352
50	Composition Profiler: a tool for discovery and visualization of amino acid composition differences. <i>BMC Bioinformatics</i> , 2007, 8, 211.	2.6	350
51	Heparin and Other Glycosaminoglycans Stimulate the Formation of Amyloid Fibrils from α -Synuclein in Vitro. <i>Biochemistry</i> , 2002, 41, 1502-1511.	2.5	322
52	Pesticides directly accelerate the rate of α -synuclein fibril formation: a possible factor in Parkinson's disease. <i>FEBS Letters</i> , 2001, 500, 105-108.	2.8	314
53	Exceptionally abundant exceptions: comprehensive characterization of intrinsic disorder in all domains of life. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 137-151.	5.4	314
54	Probing the Mechanism of Insulin Fibril Formation with Insulin Mutants. <i>Biochemistry</i> , 2001, 40, 8397-8409.	2.5	313

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55	MoRFpred, a computational tool for sequence-based prediction and characterization of short disorder-to-order transitioning binding regions in proteins. <i>Bioinformatics</i> , 2012, 28, i75-i83.	4.1	311
56	Intrinsically Disordered Proteins and Their Environment: Effects of Strong Denaturants, Temperature, pH, Counter Ions, Membranes, Binding Partners, Osmolytes, and Macromolecular Crowding. <i>Protein Journal</i> , 2009, 28, 305-325.	1.6	303
57	Mining α -Helix-Forming Molecular Recognition Features with Cross Species Sequence Alignments. <i>Biochemistry</i> , 2007, 46, 13468-13477.	2.5	300
58	Thioflavin T as a Molecular Rotor: Fluorescent Properties of Thioflavin T in Solvents with Different Viscosity. <i>Journal of Physical Chemistry B</i> , 2008, 112, 15893-15902.	2.6	300
59	Nuclear Localization of α -Synuclein and Its Interaction with Histones. <i>Biochemistry</i> , 2003, 42, 8465-8471.	2.5	299
60	Protein folding revisited. A polypeptide chain at the folding ? misfolding ? nonfolding cross-roads: which way to go?. <i>Cellular and Molecular Life Sciences</i> , 2003, 60, 1852-1871.	5.4	296
61	Biophysics of Parkinsons Disease: Structure and Aggregation of α -Synuclein. <i>Current Protein and Peptide Science</i> , 2009, 10, 483-499.	1.4	292
62	A Bimodal Distribution of Two Distinct Categories of Intrinsically Disordered Structures with Separate Functions in FG Nucleoporins. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2205-2224.	3.8	289
63	The structural and functional signatures of proteins that undergo multiple events of post-translational modification. <i>Protein Science</i> , 2014, 23, 1077-1093.	7.6	287
64	The effect of macromolecular crowding on protein aggregation and amyloid fibril formation. <i>Journal of Molecular Recognition</i> , 2004, 17, 456-464.	2.1	286
65	Is Congo Red an Amyloid-specific Dye?. <i>Journal of Biological Chemistry</i> , 2001, 276, 22715-22721.	3.4	280
66	"Domain" Coil-Globule Transition in Homopolymers. <i>Macromolecules</i> , 1995, 28, 7519-7524.	4.8	278
67	Neurotoxicant-induced animal models of Parkinson's disease: understanding the role of rotenone, maneb and paraquat in neurodegeneration. <i>Cell and Tissue Research</i> , 2004, 318, 225-241.	2.9	266
68	Intrinsic disorder in scaffold proteins: Getting more from less. <i>Progress in Biophysics and Molecular Biology</i> , 2008, 98, 85-106.	2.9	259
69	Accelerated α -synuclein fibrillation in crowded milieu. <i>FEBS Letters</i> , 2002, 515, 99-103.	2.8	255
70	Accelerated neurodegeneration through chaperone-mediated oligomerization of tau. <i>Journal of Clinical Investigation</i> , 2013, 123, 4158-4169.	8.2	246
71	Conformational Behavior and Aggregation of α -Synuclein in Organic Solvents: Modeling the Effects of Membranes. <i>Biochemistry</i> , 2003, 42, 2720-2730.	2.5	244
72	Functional Anthology of Intrinsic Disorder. 2. Cellular Components, Domains, Technical Terms, Developmental Processes, and Coding Sequence Diversities Correlated with Long Disordered Regions. <i>Journal of Proteome Research</i> , 2007, 6, 1899-1916.	3.7	244

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73	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	14.5	242
74	Early Events in the Fibrillation of Monomeric Insulin. <i>Journal of Biological Chemistry</i> , 2005, 280, 42669-42675.	3.4	237
75	Unfoldomics of human diseases: linking protein intrinsic disorder with diseases. <i>BMC Genomics</i> , 2009, 10, S7.	2.8	236
76	Intrinsic Disorder-based Protein Interactions and their Modulators. <i>Current Pharmaceutical Design</i> , 2013, 19, 4191-4213.	1.9	231
77	Pathological Unfoldomics of Uncontrolled Chaos: Intrinsically Disordered Proteins and Human Diseases. <i>Chemical Reviews</i> , 2014, 114, 6844-6879.	47.7	231
78	Do viral proteins possess unique biophysical features?. <i>Trends in Biochemical Sciences</i> , 2009, 34, 53-59.	7.5	229
79	Close encounters of the third kind: disordered domains and the interactions of proteins. <i>BioEssays</i> , 2009, 31, 328-335.	2.5	229
80	Multitude of binding modes attainable by intrinsically disordered proteins: a portrait gallery of disorder-based complexes. <i>Chemical Society Reviews</i> , 2011, 40, 1623-1634.	38.1	226
81	Whatâ€™s in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157.	1.9	226
82	Rational drug design via intrinsically disordered protein. <i>Trends in Biotechnology</i> , 2006, 24, 435-442.	9.3	225
83	Molten Globule-Like State of Cytochrome c under Conditions Simulating Those Near the Membrane Surface. <i>Biochemistry</i> , 1996, 35, 6058-6063.	2.5	217
84	Methionine oxidation inhibits fibrillation of human Î±-synuclein in vitro. <i>FEBS Letters</i> , 2002, 517, 239-244.	2.8	213
85	Conformational Prerequisites for Î±-Lactalbumin Fibrillation. <i>Biochemistry</i> , 2002, 41, 12546-12551.	2.5	211
86	Distinct Î²-Sheet Structure in Protein Aggregates Determined by ATR-FTIR Spectroscopy. <i>Biochemistry</i> , 2013, 52, 5176-5183.	2.5	210
87	The alphabet of intrinsic disorder. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24360.	1.9	208
88	Further Evidence on the Equilibrium Pre-molten Globule State: Four-state Guanidinium Chloride-induced Unfolding of Carbonic Anhydrase B at Low Temperature. <i>Journal of Molecular Biology</i> , 1996, 255, 215-228.	4.2	206
89	Partially Folded Intermediates in Insulin Fibrillation. <i>Biochemistry</i> , 2003, 42, 11404-11416.	2.5	206
90	The Mysterious Unfoldome: Structureless, Underappreciated, Yet Vital Part of Any Given Proteome. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-14.	3.0	206

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91	Role of Protein-Water Interactions and Electrostatics in α -Synuclein Fibril Formation. <i>Biochemistry</i> , 2004, 43, 3289-3300.	2.5	204
92	Intrinsically disordered proteins as crucial constituents of cellular aqueous two phase systems and coacervates. <i>FEBS Letters</i> , 2015, 589, 15-22.	2.8	203
93	Rifampicin Inhibits α -Synuclein Fibrillation and Disaggregates Fibrils. <i>Chemistry and Biology</i> , 2004, 11, 1513-1521.	6.0	202
94	Intrinsic disorder in proteins associated with neurodegenerative diseases. <i>Frontiers in Bioscience - Landmark</i> , 2009, 14, 5188.	3.0	201
95	"Partly Folded" State, a New Equilibrium State of Protein Molecules: Four-State Guanidinium Chloride-Induced Unfolding of β -Lactamase at Low Temperature. <i>Biochemistry</i> , 1994, 33, 2782-2791.	2.5	196
96	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014, 42, D326-D335.	14.5	195
97	Malleable machines take shape in eukaryotic transcriptional regulation. <i>Nature Chemical Biology</i> , 2008, 4, 728-737.	8.0	192
98	Intrinsic Disorder and Posttranslational Modifications: The Darker Side of the Biological Dark Matter. <i>Frontiers in Genetics</i> , 2018, 9, 158.	2.3	190
99	Spectral Properties of Thioflavin T in Solvents with Different Dielectric Properties and in a Fibril-Incorporated Form. <i>Journal of Proteome Research</i> , 2007, 6, 1392-1401.	3.7	187
100	Synergistic Effects of Pesticides and Metals on the Fibrillation of α -Synuclein: Implications for Parkinson's Disease. <i>NeuroToxicology</i> , 2002, 23, 527-536.	3.0	183
101	The protein kingdom extended: Ordered and intrinsically disordered proteins, their folding, supramolecular complex formation, and aggregation. <i>Progress in Biophysics and Molecular Biology</i> , 2010, 102, 73-84.	2.9	181
102	Structural Disorder in Viral Proteins. <i>Chemical Reviews</i> , 2014, 114, 6880-6911.	47.7	181
103	Abundance of Intrinsic Disorder in Protein Associated with Cardiovascular Disease. <i>Biochemistry</i> , 2006, 45, 10448-10460.	2.5	179
104	Mysterious oligomerization of the amyloidogenic proteins. <i>FEBS Journal</i> , 2010, 277, 2940-2953.	4.7	178
105	Structural Characteristics of α -Synuclein Oligomers Stabilized by the Flavonoid Baicalein. <i>Journal of Molecular Biology</i> , 2008, 383, 214-223.	4.2	177
106	α -Synuclein Misfolding and Neurodegenerative Diseases. <i>Current Protein and Peptide Science</i> , 2008, 9, 507-540.	1.4	177
107	Trimethylamine-N-oxide-induced folding of α -synuclein. <i>FEBS Letters</i> , 2001, 509, 31-35.	2.8	175
108	Protein intrinsic disorder-based liquid-liquid phase transitions in biological systems: Complex coacervates and membrane-less organelles. <i>Advances in Colloid and Interface Science</i> , 2017, 239, 97-114.	14.7	174

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109	Certain Metals Trigger Fibrillation of Methionine-oxidized α -Synuclein. <i>Journal of Biological Chemistry</i> , 2003, 278, 27630-27635.	3.4	171
110	Conformational transitions provoked by organic solvents in β -lactoglobulin: can a molten globule like intermediate be induced by the decrease in dielectric constant?. <i>Folding & Design</i> , 1997, 2, 163-172.	4.5	169
111	Amyloidogenesis of Natively Unfolded Proteins. <i>Current Alzheimer Research</i> , 2008, 5, 260-287.	1.4	167
112	Guiding Protein Aggregation with Macromolecular Crowding. <i>Biochemistry</i> , 2008, 47, 8993-9006.	2.5	165
113	Conditionally and Transiently Disordered Proteins: Awakening Cryptic Disorder To Regulate Protein Function. <i>Chemical Reviews</i> , 2014, 114, 6779-6805.	47.7	165
114	Functional roles of transiently and intrinsically disordered regions within proteins. <i>FEBS Journal</i> , 2015, 282, 1182-1189.	4.7	165
115	Stabilization of Partially Folded Conformation during α -Synuclein Oligomerization in Both Purified and Cytosolic Preparations. <i>Journal of Biological Chemistry</i> , 2001, 276, 43495-43498.	3.4	164
116	Dancing Protein Clouds: The Strange Biology and Chaotic Physics of Intrinsically Disordered Proteins. <i>Journal of Biological Chemistry</i> , 2016, 291, 6681-6688.	3.4	164
117	The molten globule is a third thermodynamical state of protein molecules. <i>FEBS Letters</i> , 1994, 341, 15-18.	2.8	160
118	Beyond the Excluded Volume Effects: Mechanistic Complexity of the Crowded Milieu. <i>Molecules</i> , 2015, 20, 1377-1409.	3.8	157
119	Structural and Functional Adaptations to Extreme Temperatures in Psychrophilic, Mesophilic, and Thermophilic DNA Ligases. <i>Journal of Biological Chemistry</i> , 2003, 278, 37015-37023.	3.4	155
120	Exploring the binding diversity of intrinsically disordered proteins involved in one-to-many binding. <i>Protein Science</i> , 2013, 22, 258-273.	7.6	155
121	Comprehensive review of methods for prediction of intrinsic disorder and its molecular functions. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3069-3090.	5.4	153
122	Nitration inhibits fibrillation of human α -synuclein in vitro by formation of soluble oligomers. <i>FEBS Letters</i> , 2003, 542, 147-152.	2.8	152
123	Fluorescence Quantum Yield of Thioflavin T in Rigid Isotropic Solution and Incorporated into the Amyloid Fibrils. <i>PLoS ONE</i> , 2010, 5, e15385.	2.5	152
124	Intrinsically disordered proteins and their (disordered) proteomes in neurodegenerative disorders. <i>Frontiers in Aging Neuroscience</i> , 2015, 7, 18.	3.4	152
125	Drugs for "protein clouds": targeting intrinsically disordered transcription factors. <i>Current Opinion in Pharmacology</i> , 2010, 10, 782-788.	3.5	151
126	Nickel impact on human health: An intrinsic disorder perspective. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1714-1731.	2.3	151

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127	Intrinsically Disordered Proteome of Human Membraneâ€Less Organelles. <i>Proteomics</i> , 2018, 18, e1700193.	2.2	151
128	Methionine oxidation, Î±-synuclein and Parkinson's disease. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1703, 157-169.	2.3	150
129	SPINE-D: Accurate Prediction of Short and Long Disordered Regions by a Single Neural-Network Based Method. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 29, 799-813.	3.5	150
130	Structural, morphological, and functional diversity of amyloid oligomers. <i>FEBS Letters</i> , 2015, 589, 2640-2648.	2.8	150
131	Conformational Behavior of Human Î±-Synuclein is Modulated by Familial Parkinsonâ€™s Disease Point Mutations A30P and A53T. <i>NeuroToxicology</i> , 2002, 23, 553-567.	3.0	147
132	Natively Unfolded Human Prothymosin Î± Adopts Partially Folded Collapsed Conformation at Acidic pH. <i>Biochemistry</i> , 1999, 38, 15009-15016.	2.5	145
133	Effects of nitration on the structure and aggregation of Î±-synuclein. <i>Molecular Brain Research</i> , 2005, 134, 84-102.	2.3	144
134	Molecular recognition features (MoRFs) in three domains of life. <i>Molecular BioSystems</i> , 2016, 12, 697-710.	2.9	141
135	Intrinsic Disorder in the Protein Data Bank. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007, 24, 325-341.	3.5	140
136	Multifarious Roles of Intrinsic Disorder in Proteins Illustrate Its Broad Impact on Plant Biology. <i>Plant Cell</i> , 2013, 25, 38-55.	6.6	138
137	Fluorescent Proteins as Biomarkers and Biosensors: Throwing Color Lights on Molecular and Cellular Processes. <i>Current Protein and Peptide Science</i> , 2008, 9, 338-369.	1.4	136
138	A functionally required unfoldome from the plant kingdom: intrinsically disordered N-terminal domains of GRAS proteins are involved in molecular recognition during plant development. <i>Plant Molecular Biology</i> , 2011, 77, 205-223.	3.9	135
139	Signal transduction via unstructured protein conduits. <i>Nature Chemical Biology</i> , 2008, 4, 229-230.	8.0	134
140	Carbon-Based Nanomaterials: Promising Antiviral Agents to Combat COVID-19 in the Microbial-Resistant Era. <i>ACS Nano</i> , 2021, 15, 8069-8086.	14.6	134
141	Bioactive Peptides: Synthesis, Sources, Applications, and Proposed Mechanisms of Action. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1445.	4.1	133
142	p53 Proteoforms and Intrinsic Disorder: An Illustration of the Protein Structureâ€Function Continuum Concept. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1874.	4.1	131
143	Use of the Phase Diagram Method to Analyze the Protein Unfolding-Refolding Reactions:â€ Fishing Out the â€Invisibleâ€ Intermediates. <i>Journal of Proteome Research</i> , 2004, 3, 485-494.	3.7	130
144	The structural basis of accelerated host cell entry by SARSâ€CoVâ€2â€. <i>FEBS Journal</i> , 2021, 288, 5010-5020.	4.7	129

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145	Oncogenic Partnerships: EWS-FLI1 Protein Interactions Initiate Key Pathways of Ewing's Sarcoma. <i>Clinical Cancer Research</i> , 2010, 16, 4077-4083.	7.0	128
146	Intrinsic disorder in pathogenic and non-pathogenic microbes: discovering and analyzing the unfoldomes of early-branching eukaryotes. <i>Molecular BioSystems</i> , 2008, 4, 328.	2.9	127
147	Protein Intrinsic Disorder and Human Papillomaviruses: An Increased Amount of Disorder in E6 and E7 Oncoproteins from High Risk HPVs. <i>Journal of Proteome Research</i> , 2006, 5, 1829-1842.	3.7	126
148	Conservation of Intrinsic Disorder in Protein Domains and Families: An II. Functions of Conserved Disorder. <i>Journal of Proteome Research</i> , 2006, 5, 888-898.	3.7	126
149	Protein disorder in the human diseasesome: unfoldomics of human genetic diseases. <i>BMC Genomics</i> , 2009, 10, S12.	2.8	126
150	Molecular Mechanisms Underlying the Flavonoid-Induced Inhibition of α -Synuclein Fibrillation. <i>Biochemistry</i> , 2009, 48, 8206-8224.	2.5	126
151	Conservation of Intrinsic Disorder in Protein Domains and Families: An I. A Database of Conserved Predicted Disordered Regions. <i>Journal of Proteome Research</i> , 2006, 5, 879-887.	3.7	124
152	Use of fluorescence decay times of 8-ANS-protein complexes to study the conformational transitions in proteins which unfold through the molten globule state. <i>Biophysical Chemistry</i> , 1996, 60, 79-88.	2.8	123
153	CDF it all: Consensus prediction of intrinsically disordered proteins based on various cumulative distribution functions. <i>FEBS Letters</i> , 2009, 583, 1469-1474.	2.8	123
154	Disease-Associated Mutations Disrupt Functionally Important Regions of Intrinsic Protein Disorder. <i>PLoS Computational Biology</i> , 2012, 8, e1002709.	3.2	123
155	Polycation-induced oligomerization and accelerated fibrillation of human alpha-synuclein in vitro. <i>Protein Science</i> , 2003, 12, 702-707.	7.6	122
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157	Protein Interactions and Misfolding Analyzed by AFM Force Spectroscopy. <i>Journal of Molecular Biology</i> , 2005, 354, 1028-1042.	4.2	121
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