

A Keith Dunker

List of Publications by Year in descending order

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166
papers

36,808
citations

5782

84
h-index

6872

160
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193
all docs

193
docs citations

193
times ranked

23233
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational, Experimental, and Clinical Evidence of a Specific but Peculiar Evolutionary Nature of (COVID-19) SARS-CoV-2. <i>Journal of Proteome Research</i> , 2022, 21, 874-890.	1.8	18
2	Intrinsically disordered proteins play diverse roles in cell signaling. <i>Cell Communication and Signaling</i> , 2022, 20, 20.	2.7	68
3	Characterization of intrinsically disordered regions in proteins informed by human genetic diversity. <i>PLoS Computational Biology</i> , 2022, 18, e1009911.	1.5	13
4	Shell Disorder Models Detect That Omicron Has Harder Shells with Attenuation but Is Not a Descendant of the Wuhan-Hu-1 SARS-CoV-2. <i>Biomolecules</i> , 2022, 12, 631.	1.8	4
5	DescribePROT: database of amino acid-level protein structure and function predictions. <i>Nucleic Acids Research</i> , 2021, 49, D298-D308.	6.5	46
6	Enzyme catalysis prior to aromatic residues: Reverse engineering of a dephospho-CoA kinase. <i>Protein Science</i> , 2021, 30, 1022-1034.	3.1	15
7	On the roles of intrinsically disordered proteins and regions in cell communication and signaling. <i>Cell Communication and Signaling</i> , 2021, 19, 88.	2.7	57
8	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
9	A Novel Strategy for the Development of Vaccines for SARS-CoV-2 (COVID-19) and Other Viruses Using AI and Viral Shell Disorder. <i>Journal of Proteome Research</i> , 2020, 19, 4355-4363.	1.8	14
10	Identification of Intrinsic Disorder in Complexes from the Protein Data Bank. <i>ACS Omega</i> , 2020, 5, 17883-17891.	1.6	17
11	Shell Disorder Analysis Suggests That Pangolins Offered a Window for a Silent Spread of an Attenuated SARS-CoV-2 Precursor among Humans. <i>Journal of Proteome Research</i> , 2020, 19, 4543-4552.	1.8	23
12	Shell disorder analysis predicts greater resilience of the SARS-CoV-2 (COVID-19) outside the body and in body fluids. <i>Microbial Pathogenesis</i> , 2020, 144, 104177.	1.3	71
13	Rigidity of the Outer Shell Predicted by a Protein Intrinsic Disorder Model Sheds Light on the COVID-19 (Wuhan-2019-nCoV) Infectivity. <i>Biomolecules</i> , 2020, 10, 331.	1.8	54
14	Nipah shell disorder, modes of infection, and virulence. <i>Microbial Pathogenesis</i> , 2020, 141, 103976.	1.3	16
15	Computational Prediction of Intrinsic Disorder in Protein Sequences with the disCoP Meta-predictor. <i>Methods in Molecular Biology</i> , 2020, 2141, 21-35.	0.4	4
16	Feasibility of the vaccine development for SARS-CoV-2 and other viruses using the shell disorder analysis. , 2020, , .		3
17	Intrinsically disordered domains: Sequence " disorder " function relationships. <i>Protein Science</i> , 2019, 28, 1652-1663.	3.1	31
18	Introduction to intrinsically disordered proteins and regions. , 2019, , 1-34.		17

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19	Zika and Flavivirus Shell Disorder: Virulence and Fetal Morbidity. <i>Biomolecules</i> , 2019, 9, 710.	1.8	22
20	Entropy, Fluctuations, and Disordered Proteins. <i>Entropy</i> , 2019, 21, 764.	1.1	5
21	HIV Vaccine Mystery and Viral Shell Disorder. <i>Biomolecules</i> , 2019, 9, 178.	1.8	36
22	On the Importance of Computational Biology and Bioinformatics to the Origins and Rapid Progression of the Intrinsically Disordered Proteins Field. , 2019, , .		0
23	Intrinsically Disordered Proteins Link Alternative Splicing and Post-translational Modifications to Complex Cell Signaling and Regulation. <i>Journal of Molecular Biology</i> , 2018, 430, 2342-2359.	2.0	79
24	The evolutionary origins of cell type diversification and the role of intrinsically disordered proteins. <i>Journal of Experimental Botany</i> , 2018, 69, 1437-1446.	2.4	52
25	Regulating Protein Function by Delayed Folding. <i>Structure</i> , 2018, 26, 679-681.	1.6	9
26	Comparing NMR and X-ray protein structure: Lindemann-like parameters and NMR disorder. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 2331-2341.	2.0	13
27	Sequence fingerprints distinguish erroneous from correct predictions of intrinsically disordered protein regions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 4338-4351.	2.0	9
28	Identification of intrinsic disorder in complexes from Protein Data Bank. , 2018, , .		0
29	Evolution of Protein Ductility in Duplicated Genes of Plants. <i>Frontiers in Plant Science</i> , 2018, 9, 1216.	1.7	9
30	Time, space, and disorder in the expanding proteome universe. <i>Proteomics</i> , 2017, 17, 1600399.	1.3	19
31	Evidence for a Strong Correlation Between Transcription Factor Protein Disorder and Organismic Complexity. <i>Genome Biology and Evolution</i> , 2017, 9, 1248-1265.	1.1	49
32	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	6.5	242
33	Correlating Flavivirus virulence and levels of intrinsic disorder in shell proteins: protective roles vs. immune evasion. <i>Molecular BioSystems</i> , 2016, 12, 1881-1891.	2.9	37
34	Lipopolysaccharide treatment induces genome-wide pre-mRNA splicing pattern changes in mouse bone marrow stromal stem cells. <i>BMC Genomics</i> , 2016, 17, 509.	1.2	7
35	Molecular recognition features (MoRFs) in three domains of life. <i>Molecular BioSystems</i> , 2016, 12, 697-710.	2.9	141
36	Prostate-associated gene 4 (PAGE4), an intrinsically disordered cancer/testis antigen, is a novel therapeutic target for prostate cancer. <i>Asian Journal of Andrology</i> , 2016, 18, 695.	0.8	19

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37	Rethinking gene regulatory networks in light of alternative splicing, intrinsically disordered protein domains, and post-translational modifications. <i>Frontiers in Cell and Developmental Biology</i> , 2015, 3, 8.	1.8	96
38	Shell disorder, immune evasion and transmission behaviors among human and animal retroviruses. <i>Molecular BioSystems</i> , 2015, 11, 2312-2323.	2.9	21
39	Detection of links between Ebola nucleocapsid and virulence using disorder analysis. <i>Molecular BioSystems</i> , 2015, 11, 2337-2344.	2.9	19
40	Back to the Future: Nuclear Magnetic Resonance and Bioinformatics Studies on Intrinsically Disordered Proteins. <i>Advances in Experimental Medicine and Biology</i> , 2015, 870, 1-34.	0.8	18
41	Intrinsic disorder mediates hepatitis C virus core-host cell protein interactions. <i>Protein Science</i> , 2015, 24, 221-235.	3.1	47
42	Intrinsically disordered proteins and multicellular organisms. <i>Seminars in Cell and Developmental Biology</i> , 2015, 37, 44-55.	2.3	128
43	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014, 42, D326-D335.	6.5	195
44	A creature with a hundred waggly tails: intrinsically disordered proteins in the ribosome. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 1477-1504.	2.4	119
45	Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631.	23.0	1,618
46	Intrinsically Disordered Proteins and Intrinsically Disordered Protein Regions. <i>Annual Review of Biochemistry</i> , 2014, 83, 553-584.	5.0	850
47	The structural and functional signatures of proteins that undergo multiple events of post-translational modification. <i>Protein Science</i> , 2014, 23, 1077-1093.	3.1	287
48	Intrinsically disordered regions of p53 family are highly diversified in evolution. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 725-738.	1.1	68
49	An assignment of intrinsically disordered regions of proteins based on NMR structures. <i>Journal of Structural Biology</i> , 2013, 181, 29-36.	1.3	26
50	Utilization of protein intrinsic disorder knowledge in structural proteomics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 487-498.	1.1	58
51	Exploring the binding diversity of intrinsically disordered proteins involved in one-to-many binding. <i>Protein Science</i> , 2013, 22, 258-273.	3.1	155
52	Stochastic machines as a colocalization mechanism for scaffold protein function. <i>FEBS Letters</i> , 2013, 587, 1587-1591.	1.3	40
53	Another Disordered Chameleon: The Micro-Exon Gene 14 Protein from Schistosomiasis. <i>Biophysical Journal</i> , 2013, 104, 2326-2328.	0.2	2
54	Alternative splicing of intrinsically disordered regions and rewiring of protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 443-450.	2.6	166

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55	Distribution and cluster analysis of predicted intrinsically disordered protein Pfam domains. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e25724.	1.9	12
56	Functional fragments of disorder in outer membrane β^2 barrel proteins. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24848.	1.9	4
57	Whatâ€™s in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157.	1.9	226
58	The alphabet of intrinsic disorder. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24360.	1.9	208
59	Prediction of Intrinsic Disorder in MERS-CoV/HCoV-EMC Supports a High Oral-Fecal Transmission. <i>PLOS Currents</i> , 2013, 5, .	1.4	60
60	Proline Rich Motifs as Drug Targets in Immune Mediated Disorders. <i>International Journal of Peptides</i> , 2012, 2012, 1-14.	0.7	26
61	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.	1.8	311
62	Understanding Viral Transmission Behavior via Protein Intrinsic Disorder Prediction: Coronaviruses. <i>Journal of Pathogens</i> , 2012, 2012, 1-13.	0.9	40
63	High-throughput characterization of intrinsic disorder in proteins from the Protein Structure Initiative. <i>Journal of Structural Biology</i> , 2012, 180, 201-215.	1.3	34
64	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.	2.0	150
65	The Roles of Intrinsic Disorder in Orchestrating the Wnt-Pathway. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 29, 843-861.	2.0	44
66	Sweeping Away Protein Aggregation with Entropic Bristles: Intrinsically Disordered Protein Fusions Enhance Soluble Expression. <i>Biochemistry</i> , 2012, 51, 7250-7262.	1.2	100
67	Disorder to Order, Nonlife to Life: In the Beginning There Was a Mistake. <i>Cellular Origin and Life in Extreme Habitats</i> , 2012, , 415-435.	0.3	7
68	Structural Basis for Activation of Calcineurin by Calmodulin. <i>Journal of Molecular Biology</i> , 2012, 415, 307-317.	2.0	83
69	Protein intrinsic disorder and induced pluripotent stem cells. <i>Molecular BioSystems</i> , 2012, 8, 134-150.	2.9	45
70	Multiparametric Analysis of Intrinsically Disordered Proteins: Looking at Intrinsic Disorder through Compound Eyes. <i>Analytical Chemistry</i> , 2012, 84, 2096-2104.	3.2	77
71	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.	2.0	465
72	Intrinsic protein disorder and protein-protein interactions. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 116-27.	0.7	42

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73	Subclassifying disordered proteins by the CH-CDF plot method. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 128-39.	0.7	30
74	The Orderly Chaos of Proteins. Scientific American, 2011, 304, 68-73.	1.0	18
75	Regions of intrinsic disorder help identify a novel nuclear localization signal in <i>Toxoplasma gondii</i> histone acetyltransferase TgGCN5-B. Molecular and Biochemical Parasitology, 2011, 175, 192-195.	0.5	20
76	Evolution and disorder. Current Opinion in Structural Biology, 2011, 21, 441-446.	2.6	243
77	Sequences and topology: intrinsic disorder in the evolving universe of protein structure. Current Opinion in Structural Biology, 2011, 21, 379-381.	2.6	21
78	A functionally required unfoldome from the plant kingdom: intrinsically disordered N-terminal domains of GRAS proteins are involved in molecular recognition during plant development. Plant Molecular Biology, 2011, 77, 205-223.	2.0	135
79	In-silico prediction of disorder content using hybrid sequence representation. BMC Bioinformatics, 2011, 12, 245.	1.2	45
80	Abundance and functional roles of intrinsic disorder in allergenic proteins and allergen representative peptides. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2595-2606.	1.5	6
81	INTRINSICALLY DISORDERED PROTEINS: ANALYSIS, PREDICTION, SIMULATION, AND BIOLOGY. , 2011, , ,		0
82	PONDR-FIT: A meta-predictor of intrinsically disordered amino acids. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 996-1010.	1.1	993
83	Understanding protein non-folding. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 1231-1264.	1.1	1,030
84	Archaic chaos: intrinsically disordered proteins in Archaea. BMC Systems Biology, 2010, 4, S1.	3.0	111
85	SPA: Short peptide analyzer of intrinsic disorder status of short peptides. Genes To Cells, 2010, 15, 635-646.	0.5	8
86	Musite, a Tool for Global Prediction of General and Kinase-specific Phosphorylation Sites. Molecular and Cellular Proteomics, 2010, 9, 2586-2600.	2.5	233
87	N-terminal Domains of DELLA Proteins Are Intrinsically Unstructured in the Absence of Interaction with GID1/Gibberellic Acid Receptors. Journal of Biological Chemistry, 2010, 285, 11557-11571.	1.6	67
88	Retro-MoRFs: Identifying Protein Binding Sites by Normal and Reverse Alignment and Intrinsic Disorder Prediction. International Journal of Molecular Sciences, 2010, 11, 3725-3747.	1.8	42
89	Viral Disorder or Disordered Viruses: Do Viral Proteins Possess Unique Features?. Protein and Peptide Letters, 2010, 17, 932-951.	0.4	109
90	Drugs for "protein clouds": targeting intrinsically disordered transcription factors. Current Opinion in Pharmacology, 2010, 10, 782-788.	1.7	151

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91	Replacement of aromatic amino acids based on their consensus temporal order suggests that ancient proteins tend to be intrinsically disordered. <i>FASEB Journal</i> , 2010, 24, 901.2.	0.2	0
92	Overlapping Genes Produce Proteins with Unusual Sequence Properties and Offer Insight into De Novo Protein Creation. <i>Journal of Virology</i> , 2009, 83, 10719-10736.	1.5	161
93	Protein disorder in the human diseasome: unfoldomics of human genetic diseases. <i>BMC Genomics</i> , 2009, 10, S12.	1.2	126
94	Unfoldomics of human diseases: linking protein intrinsic disorder with diseases. <i>BMC Genomics</i> , 2009, 10, S7.	1.2	236
95	CDF it all: Consensus prediction of intrinsically disordered proteins based on various cumulative distribution functions. <i>FEBS Letters</i> , 2009, 583, 1469-1474.	1.3	123
96	Close encounters of the third kind: disordered domains and the interactions of proteins. <i>BioEssays</i> , 2009, 31, 328-335.	1.2	229
97	Protein intrinsic disorder and influenza virulence: the 1918 H1N1 and H5N1 viruses. <i>Virology Journal</i> , 2009, 6, 69.	1.4	71
98	Analysis of structured and intrinsically disordered regions of transmembrane proteins. <i>Molecular BioSystems</i> , 2009, 5, 1688.	2.9	59
99	Predicting intrinsic disorder in proteins: an overview. <i>Cell Research</i> , 2009, 19, 929-949.	5.7	389
100	A New Machine Learning Approach for Protein Phosphorylation Site Prediction in Plants. <i>Lecture Notes in Computer Science</i> , 2009, , 18-29.	1.0	15
101	Signal transduction via unstructured protein conduits. <i>Nature Chemical Biology</i> , 2008, 4, 229-230.	3.9	134
102	Potato virus A genome-linked protein VPg is an intrinsically disordered molten globule-like protein with a hydrophobic core. <i>Virology</i> , 2008, 377, 280-288.	1.1	65
103	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.	1.2	482
104	Investigation of transmembrane proteins using a computational approach. <i>BMC Genomics</i> , 2008, 9, S7.	1.2	22
105	The unfoldomics decade: an update on intrinsically disordered proteins. <i>BMC Genomics</i> , 2008, 9, S1.	1.2	485
106	Short Linear Motifs recognized by SH2, SH3 and Ser/Thr Kinase domains are conserved in disordered protein regions. <i>BMC Genomics</i> , 2008, 9, S26.	1.2	67
107	Protein intrinsic disorder toolbox for comparative analysis of viral proteins. <i>BMC Genomics</i> , 2008, 9, S4.	1.2	61
108	Function and structure of inherently disordered proteins. <i>Current Opinion in Structural Biology</i> , 2008, 18, 756-764.	2.6	864

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109	Intrinsic disorder in scaffold proteins: Getting more from less. <i>Progress in Biophysics and Molecular Biology</i> , 2008, 98, 85-106.	1.4	259
110	Intrinsically Disordered Proteins in Human Diseases: Introducing the D ² Concept. <i>Annual Review of Biophysics</i> , 2008, 37, 215-246.	4.5	1,222
111	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
112	A comparative analysis of viral matrix proteins using disorder predictors. <i>Virology Journal</i> , 2008, 5, 126.	1.4	60
113	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2008, 134, 534-545.	13.5	196
114	Protein Disorder Is Positively Correlated with Gene Expression in <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2008, 7, 2234-2245.	1.8	32
115	Malleable Machines in Transcription Regulation: The Mediator Complex. <i>PLoS Computational Biology</i> , 2008, 4, e1000243.	1.5	109
116	TOP-IDP-Scale: A New Amino Acid Scale Measuring Propensity for Intrinsic Disorder. <i>Protein and Peptide Letters</i> , 2008, 15, 956-963.	0.4	361
117	Structural Basis for Regulation of Protein Phosphatase 1 by Inhibitor-2. <i>Journal of Biological Chemistry</i> , 2007, 282, 28874-28883.	1.6	175
118	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.	1.8	525
119	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.	1.8	369
120	Intrinsically Disordered Proteins: An Update. , 2007, , .		1
121	Mining \pm -Helix-Forming Molecular Recognition Features with Cross Species Sequence Alignments. <i>Biochemistry</i> , 2007, 46, 13468-13477.	1.2	300
122	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.	1.8	244
123	DisProt: the Database of Disordered Proteins. <i>Nucleic Acids Research</i> , 2007, 35, D786-D793.	6.5	711
124	Characterization of Molecular Recognition Features, MoRFs, and Their Binding Partners. <i>Journal of Proteome Research</i> , 2007, 6, 2351-2366.	1.8	433
125	Intrinsic Disorder and Functional Proteomics. <i>Biophysical Journal</i> , 2007, 92, 1439-1456.	0.2	643
126	Intrinsic Disorder in the Protein Data Bank. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007, 24, 325-341.	2.0	140

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127	Composition Profiler: a tool for discovery and visualization of amino acid composition differences. BMC Bioinformatics, 2007, 8, 211.	1.2	350
128	Another Window into Disordered Protein Function. Structure, 2007, 15, 1026-1028.	1.6	14
129	Engineering productive enzyme confinement. Trends in Biotechnology, 2007, 25, 189-190.	4.9	26
130	Prediction of Intrinsic Disorder and Its Use in Functional Proteomics. Methods in Molecular Biology, 2007, 408, 69-92.	0.4	37
131	Disorder and Sequence Repeats in Hub Proteins and Their Implications for Network Evolution. Journal of Proteome Research, 2006, 5, 2985-2995.	1.8	312
132	Abundance of Intrinsic Disorder in Protein Associated with Cardiovascular Disease. Biochemistry, 2006, 45, 10448-10460.	1.2	179
133	Intrinsic Disorder in Transcription Factors. Biochemistry, 2006, 45, 6873-6888.	1.2	654
134	Protein Intrinsic Disorder and Human Papillomaviruses: Increased Amount of Disorder in E6 and E7 Oncoproteins from High Risk HPVs. Journal of Proteome Research, 2006, 5, 1829-1842.	1.8	126
135	Conservation of Intrinsic Disorder in Protein Domains and Families: II. Functions of Conserved Disorder. Journal of Proteome Research, 2006, 5, 888-898.	1.8	126
136	Conservation of Intrinsic Disorder in Protein Domains and Families: I. A Database of Conserved Predicted Disordered Regions. Journal of Proteome Research, 2006, 5, 879-887.	1.8	124
137	Analysis of Molecular Recognition Features (MoRFs). Journal of Molecular Biology, 2006, 362, 1043-1059.	2.0	672
138	Calmodulin signaling: Analysis and prediction of a disorder-dependent molecular recognition. Proteins: Structure, Function and Bioinformatics, 2006, 63, 398-410.	1.5	93
139	Rational drug design via intrinsically disordered protein. Trends in Biotechnology, 2006, 24, 435-442.	4.9	225
140	Length-dependent prediction of protein intrinsic disorder. BMC Bioinformatics, 2006, 7, 208.	1.2	780
141	Alternative splicing in concert with protein intrinsic disorder enables increased functional diversity in multicellular organisms. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8390-8395.	3.3	428
142	Flexible nets. The roles of intrinsic disorder in protein interaction networks. FEBS Journal, 2005, 272, 5129-5148.	2.2	1,052
143	Showing your ID: intrinsic disorder as an ID for recognition, regulation and cell signaling. Journal of Molecular Recognition, 2005, 18, 343-384.	1.1	762
144	Exploiting heterogeneous sequence properties improves prediction of protein disorder. Proteins: Structure, Function and Bioinformatics, 2005, 61, 176-182.	1.5	511

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145	OPTIMIZING LONG INTRINSIC DISORDER PREDICTORS WITH PROTEIN EVOLUTIONARY INFORMATION. <i>Journal of Bioinformatics and Computational Biology</i> , 2005, 03, 35-60.	0.3	428
146	DisProt: a database of protein disorder. <i>Bioinformatics</i> , 2005, 21, 137-140.	1.8	231
147	Comparing and Combining Predictors of Mostly Disordered Proteins. <i>Biochemistry</i> , 2005, 44, 1989-2000.	1.2	485
148	Coupled Folding and Binding with α -Helix-Forming Molecular Recognition Elements. <i>Biochemistry</i> , 2005, 44, 12454-12470.	1.2	593
149	Combining prediction, computation and experiment for the characterization of protein disorder. <i>Current Opinion in Structural Biology</i> , 2004, 14, 570-576.	2.6	125
150	Classification and knowledge discovery in protein databases. <i>Journal of Biomedical Informatics</i> , 2004, 37, 224-239.	2.5	75
151	Protein flexibility and intrinsic disorder. <i>Protein Science</i> , 2004, 13, 71-80.	3.1	306
152	The importance of intrinsic disorder for protein phosphorylation. <i>Nucleic Acids Research</i> , 2004, 32, 1037-1049.	6.5	1,230
153	Improved amino acid flexibility parameters. <i>Protein Science</i> , 2003, 12, 1060-1072.	3.1	158
154	Flavors of protein disorder. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 573-584.	1.5	340
155	Predicting intrinsic disorder from amino acid sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 566-572.	1.5	415
156	Intrinsic Disorder and Protein Function. <i>Biochemistry</i> , 2002, 41, 6573-6582.	1.2	1,605
157	Identification and functions of usefully disordered proteins. <i>Advances in Protein Chemistry</i> , 2002, 62, 25-49.	4.4	352
158	Intrinsic Disorder in Cell-signaling and Cancer-associated Proteins. <i>Journal of Molecular Biology</i> , 2002, 323, 573-584.	2.0	1,077
159	Evolutionary Rate Heterogeneity in Proteins with Long Disordered Regions. <i>Journal of Molecular Evolution</i> , 2002, 55, 104-110.	0.8	398
160	Improving sequence alignments for intrinsically disordered proteins. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2002, , 589-600.	0.7	13
161	Clusterin, a Binding Protein with a Molten Globule-like Region. <i>Biochemistry</i> , 2001, 40, 11828-11840.	1.2	115
162	Sequence complexity of disordered protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 42, 38-48.	1.5	1,547

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163	Identification of intrinsic order and disorder in the DNA repair protein XPA. <i>Protein Science</i> , 2001, 10, 560-571.	3.1	108
164	The protein trinity—linking function and disorder. <i>Nature Biotechnology</i> , 2001, 19, 805-806.	9.4	545
165	Aberrant mobility phenomena of the DNA repair protein XPA. <i>Protein Science</i> , 2001, 10, 1353-1362.	3.1	67
166	Proposed Knobs-Into-Holes Packing for Several Membrane Proteins. <i>Membrane Biochemistry</i> , 1978, 2, 1-16.	0.6	23