

# Bin Xue

## List of Publications by Year in descending order

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Version: 2024-02-01

97  
papers

7,111  
citations

71061

41  
h-index

60583

81  
g-index

110  
all docs

110  
docs citations

110  
times ranked

8604  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analyzing aggregation propensities of clinically relevant PTEN mutants: a new culprit in pathogenesis of cancer and other PTENopathies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 2253-2266.	2.0	6
2	The dark side of Alzheimer's disease: unstructured biology of proteins from the amyloid cascade signaling pathway. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 4163-4208.	2.4	23
3	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.	1.8	7
4	Intrinsic Disorder in Tetratricopeptide Repeat Proteins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3709.	1.8	9
5	Recent Advances in Machine Learning Based Prediction of RNA-protein Interactions. <i>Protein and Peptide Letters</i> , 2019, 26, 601-619.	0.4	7
6	Significant improvement of miRNA target prediction accuracy in large datasets using meta-strategy based on comprehensive voting and artificial neural networks. <i>BMC Genomics</i> , 2019, 20, 158.	1.2	6
7	How many differentially expressed genes: A perspective from the comparison of genotypic and phenotypic distances. <i>Genomics</i> , 2018, 110, 67-73.	1.3	57
8	Decision-Tree Based Meta-Strategy Improved Accuracy of Disorder Prediction and Identified Novel Disordered Residues Inside Binding Motifs. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3052.	1.8	12
9	Data on evolution of intrinsically disordered regions of the human kinome and contribution of FAK1 IDRs to cytoskeletal remodeling. <i>Data in Brief</i> , 2017, 10, 315-324.	0.5	1
10	Improving prediction accuracy using decision-tree-based meta-strategy and multi-threshold sequential-voting exemplified by miRNA target prediction. <i>Genomics</i> , 2017, 109, 227-232.	1.3	7
11	Consensus datasets of mouse miRNA-mRNA interactions from multiple online resources. <i>Data in Brief</i> , 2017, 14, 143-147.	0.5	2
12	Structural pliability adjacent to the kinase domain highlights contribution of FAK1 IDRs to cytoskeletal remodeling. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 43-54.	1.1	2
13	Measuring the inter-sample heterogeneity by dynamic PCA biplot. , 2017, , ,		1
14	Self-regulation of functional pathways by motifs inside the disordered tails of beta-catenin. <i>BMC Genomics</i> , 2016, 17, 484.	1.2	10
15	Intrinsic Disorder in Transmembrane Proteins: Roles in Signaling and Topology Prediction. <i>PLoS ONE</i> , 2016, 11, e0158594.	1.1	59
16	Integrated Strategy Improves the Prediction Accuracy of miRNA in Large Dataset. <i>PLoS ONE</i> , 2016, 11, e0168392.	1.1	9
17	Unfoldomes and Unfoldomics: Introducing Intrinsically Disordered Proteins. , 2016, , 125-150.		2
18	Superdomains in the protein structure hierarchy: The case of PTP-C2. <i>Protein Science</i> , 2015, 24, 874-882.	3.1	9

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19	Identifying Similar Patterns of Structural Flexibility in Proteins by Disorder Prediction and Dynamic Programming. <i>International Journal of Molecular Sciences</i> , 2015, 16, 13829-13849.	1.8	7
20	Improving MiRNA prediction accuracy by deep learning strategies. , 2015, , .		0
21	Role of structural flexibility in the evolution of emerin. <i>Journal of Theoretical Biology</i> , 2015, 385, 102-111.	0.8	7
22	Intrinsic disorder mediates hepatitis C virus coreâ€‘host cell protein interactions. <i>Protein Science</i> , 2015, 24, 221-235.	3.1	47
23	Exceptionally abundant exceptions: comprehensive characterization of intrinsic disorder in all domains of life. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 137-151.	2.4	314
24	Disorder in Milk Proteins: Caseins, Intrinsically Disordered Colloids. <i>Current Protein and Peptide Science</i> , 2015, 16, 228-242.	0.7	35
25	DBC1/CCAR2 and CCAR1 Are Largely Disordered Proteins that Have Evolved from One Common Ancestor. <i>BioMed Research International</i> , 2014, 2014, 1-13.	0.9	24
26	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
27	A putative role of the Sup35p C-terminal domain in the cytoskeleton organization during yeast mitosis. <i>Molecular BioSystems</i> , 2014, 10, 925-940.	2.9	5
28	Disordered Proteinaceous Machines. <i>Chemical Reviews</i> , 2014, 114, 6806-6843.	23.0	109
29	Structural Disorder in Viral Proteins. <i>Chemical Reviews</i> , 2014, 114, 6880-6911.	23.0	181
30	Contribution of proline to the pre-structuring tendency of transient helical secondary structure elements in intrinsically disordered proteins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 993-1003.	1.1	26
31	The intrinsically disordered structural platform of the plant defence hub protein <scp>RPM</scp>â€™interacting protein 4 provides insights into its mode of action in the hostâ€™pathogen interface and evolution of the nitrateâ€™induced domain protein family. <i>FEBS Journal</i> , 2014, 281, 3955-3979.	2.2	50
32	The intrinsic disorder status of the human hepatitis C virus proteome. <i>Molecular BioSystems</i> , 2014, 10, 1345-1363.	2.9	57
33	Presence and utility of intrinsically disordered regions in kinases. <i>Molecular BioSystems</i> , 2014, 10, 2876-2888.	2.9	26
34	Intrinsic Disorder in Proteins Involved in the Innate Antiviral Immunity: Another Flexible Side of a Molecular Arms Race. <i>Journal of Molecular Biology</i> , 2014, 426, 1322-1350.	2.0	37
35	Improving protein order-disorder classification using charge-hydropathy plots. <i>BMC Bioinformatics</i> , 2014, 15, S4.	1.2	63
36	Identifying Novel Cell Cycle Proteins in Apicomplexa Parasites through Co-Expression Decision Analysis. <i>PLoS ONE</i> , 2014, 9, e97625.	1.1	16

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37	Disordered Interactome of Human Papillomavirus. <i>Current Pharmaceutical Design</i> , 2014, 20, 1274-1292.	0.9	22
38	Accurate prediction of protein dihedral angles through conditional random field. <i>Frontiers in Biology</i> , 2013, 8, 353-361.	0.7	5
39	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
40	Protein intrinsic disorder in the acetylome of intracellular and extracellular <i>Toxoplasma gondii</i> . <i>Molecular BioSystems</i> , 2013, 9, 645.	2.9	57
41	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
42	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
43	Stochastic machines as a colocalization mechanism for scaffold protein function. <i>FEBS Letters</i> , 2013, 587, 1587-1591.	1.3	40
44	Distribution and cluster analysis of predicted intrinsically disordered protein Pfam domains. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e25724.	1.9	12
45	Structural characterizations of phosphorylatable residues in transmembrane proteins from <i>Arabidopsis thaliana</i> . <i>Intrinsically Disordered Proteins</i> , 2013, 1, e25713.	1.9	5
46	Intrinsic Disorder in PTEN and its Interactome Confers Structural Plasticity and Functional Versatility. <i>Scientific Reports</i> , 2013, 3, 2035.	1.6	69
47	Ordered Disorder of the Astrocytic Dystrophin-Associated Protein Complex in the Norm and Pathology. <i>PLoS ONE</i> , 2013, 8, e73476.	1.1	12
48	On the intrinsic disorder status of the major players in programmed cell death pathways. <i>F1000Research</i> , 2013, 2, 190.	0.8	20
49	Actinidia DRM1 - An Intrinsically Disordered Protein Whose mRNA Expression Is Inversely Correlated with Spring Budbreak in Kiwifruit. <i>PLoS ONE</i> , 2013, 8, e57354.	1.1	25
50	Malleable ribonucleoprotein machine: protein intrinsic disorder in the <i>Saccharomyces cerevisiae</i> spliceosome. <i>PeerJ</i> , 2013, 1, e2.	0.9	32
51	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
52	HSF Transcription Factor Family, Heat Shock Response, and Protein Intrinsic Disorder. <i>Current Protein and Peptide Science</i> , 2012, 13, 86-103.	0.7	100
53	Accurate prediction of protein structural classes using functional domains and predicted secondary structure sequences. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 29, 1127-1137.	2.0	17
54	D2P2: database of disordered protein predictions. <i>Nucleic Acids Research</i> , 2012, 41, D508-D516.	6.5	570

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55	NOT THAT RIGID MIDGETS AND NOT SO FLEXIBLE GIANTS: ON THE ABUNDANCE AND ROLES OF INTRINSIC DISORDER IN SHORT AND LONG PROTEINS. <i>Journal of Biological Systems</i> , 2012, 20, 471-511.	0.5	19
56	Local Flexibility Facilitates Oxidization of Buried Methionine Residues. <i>Protein and Peptide Letters</i> , 2012, 19, 688-697.	0.4	26
57	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
58	More than just tails: intrinsic disorder in histone proteins. <i>Molecular BioSystems</i> , 2012, 8, 1886.	2.9	99
59	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
60	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
61	Protein intrinsic disorder and induced pluripotent stem cells. <i>Molecular BioSystems</i> , 2012, 8, 134-150.	2.9	45
62	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
63	Protein intrinsic disorder as a flexible armor and a weapon of HIV-1. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 1211-1259.	2.4	94
64	Interactions between the C-terminus of Kv1.5 and Kv1 <sup>2</sup> regulate pyridine nucleotide-dependent changes in channel gating. <i>Pflugers Archiv European Journal of Physiology</i> , 2012, 463, 799-818.	1.3	37
65	Intrinsic protein disorder and protein-protein interactions. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 116-27.	0.7	42
66	Subclassifying disordered proteins by the CH-CDF plot method. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 128-39.	0.7	30
67	SUBCLASSIFYING DISORDERED PROTEINS BY THE CH-CDF PLOT METHOD. , 2011, , .		36
68	Intrinsic disorder of the extracellular matrix. <i>Molecular BioSystems</i> , 2011, 7, 3353.	2.9	54
69	Intrinsic disorder in S100 proteins. <i>Molecular BioSystems</i> , 2011, 7, 2164.	2.9	28
70	INTRINSIC PROTEIN DISORDER AND PROTEIN-PROTEIN INTERACTIONS. , 2011, , .		32
71	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.	2.0	135
72	In-silico prediction of disorder content using hybrid sequence representation. <i>BMC Bioinformatics</i> , 2011, 12, 245.	1.2	45

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73	Abundance and functional roles of intrinsic disorder in allergenic proteins and allergen representative peptides. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2595-2606.	1.5	6
74	In silico functional profiling of human disease-associated and polymorphic amino acid substitutions. <i>Human Mutation</i> , 2010, 31, 335-346.	1.1	57
75	PONDR-FIT: A meta-predictor of intrinsically disordered amino acids. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 996-1010.	1.1	993
76	Archaic chaos: intrinsically disordered proteins in Archaea. <i>BMC Systems Biology</i> , 2010, 4, S1.	3.0	111
77	Protein tandem repeats – the more perfect, the less structured. <i>FEBS Journal</i> , 2010, 277, 2673-2682.	2.2	119
78	SPA: Short peptide analyzer of intrinsic disorder status of short peptides. <i>Genes To Cells</i> , 2010, 15, 635-646.	0.5	8
79	Effect of solvation-related interaction on the low-temperature dynamics of proteins. <i>Physical Review E</i> , 2010, 81, 031917.	0.8	5
80	N-terminal Domains of DELLA Proteins Are Intrinsically Unstructured in the Absence of Interaction with GID1/Gibberellic Acid Receptors. <i>Journal of Biological Chemistry</i> , 2010, 285, 11557-11571.	1.6	67
81	Retro-MoRFs: Identifying Protein Binding Sites by Normal and Reverse Alignment and Intrinsic Disorder Prediction. <i>International Journal of Molecular Sciences</i> , 2010, 11, 3725-3747.	1.8	42
82	Viral Disorder or Disordered Viruses: Do Viral Proteins Possess Unique Features?. <i>Protein and Peptide Letters</i> , 2010, 17, 932-951.	0.4	109
83	Protein tandem repeats - the more perfect, the less structured. <i>FEBS Journal</i> , 2010, 277, 2673-2682.	2.2	85
84	Unfoldomics of human diseases: linking protein intrinsic disorder with diseases. <i>BMC Genomics</i> , 2009, 10, S7.	1.2	236
85	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
86	Improving the prediction accuracy of residue solvent accessibility and real-value backbone torsion angles of proteins by guided-learning through a two-layer neural network. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 847-856.	1.5	125
87	Predicting residue-residue contact maps by a two-layer, integrated neural network method. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 176-183.	1.5	38
88	Analysis of structured and intrinsically disordered regions of transmembrane proteins. <i>Molecular BioSystems</i> , 2009, 5, 1688.	2.9	59
89	Predicting intrinsic disorder in proteins: an overview. <i>Cell Research</i> , 2009, 19, 929-949.	5.7	389
90	Real-value prediction of backbone torsion angles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 427-433.	1.5	66

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91	Effect of Methionine Oxidation on the Structural Properties, Conformational Stability, and Aggregation of Immunoglobulin Light Chain LEN. <i>Biochemistry</i> , 2008, 47, 8665-8677.	1.2	34
92	DDOMAIN: Dividing structures into domains using a normalized domain-domain interaction profile. <i>Protein Science</i> , 2007, 16, 947-955.	3.1	67
93	The orientational preferences of backbones of proteins. <i>Science Bulletin</i> , 2006, 51, 2559-2565.	1.7	0
94	Permeation of particle through a four-helix-bundle model channel. <i>Journal of Chemical Physics</i> , 2005, 122, 104703.	1.2	0
95	Influence of external vibration on tether chain in ligand-receptor binding. <i>Journal of Chemical Physics</i> , 2005, 122, 194912.	1.2	10
96	THE "FOLDING" BEHAVIORS OF HOMOPOLYMERS WITH ONE END FIXED. <i>International Journal of Modern Physics B</i> , 2004, 18, 2123-2139.	1.0	5
97	Collapse of homopolymer chains with two fixed terminals. <i>Journal of Chemical Physics</i> , 2003, 119, 7534-7542.	1.2	7