Lukasz A Kurgan

List of Publications by Year
in descending order

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Version: 2024-02-01

240 papers	11,990 citations	25423 59 h-index	40945 97 g-index
256 all docs	256 docs citations	256 times ranked	11884 citing authors

#	Article	IF	Citations
1	DeepDISOBind: accurate prediction of RNA-, DNA- and protein-binding intrinsically disordered residues with deep multi-task learning. Briefings in Bioinformatics, 2022, 23, .	3.2	28
2	Deep learning in prediction of intrinsic disorder in proteins. Computational and Structural Biotechnology Journal, 2022, 20, 1286-1294.	1.9	24
3	Resources for computational prediction of intrinsic disorder in proteins. Methods, 2022, 204, 132-141.	1.9	17
4	Complementarity of the residue-level protein function and structure predictions in human proteins. Computational and Structural Biotechnology Journal, 2022, 20, 2223-2234.	1.9	1
5	iFeatureOmega:an integrative platform for engineering, visualization and analysis of features from molecular sequences, structural and ligand data sets. Nucleic Acids Research, 2022, 50, W434-W447.	6.5	24
6	Compositional Bias of Intrinsically Disordered Proteins and Regions and Their Predictions. Biomolecules, 2022, 12, 888.	1.8	11
7	Systematic evaluation of machine learning methods for identifying humanâ€“pathogen proteinâ€“protein interactions. Briefings in Bioinformatics, 2021, 22, .	3.2	23
8	IDPology of the living cell: intrinsic disorder in the subcellular compartments of the human cell. Cellular and Molecular Life Sciences, 2021, 78, 2371-2385.	2.4	15
9	DescribePROT: database of amino acid-level protein structure and function predictions. Nucleic Acids Research, 2021, 49, D298-D308.	6.5	46
10	The Methods and Tools for Intrinsic Disorder Prediction and their Application to Systems Medicine. , 2021, , 159-169.		3
11	iLearnPlus:a comprehensive and automated machine-learning platform for nucleic acid and protein sequence analysis, prediction and visualization. Nucleic Acids Research, 2021, 49, e60-e60.	6.5	124
12	Structures of <scp>MERSâ€CoV</scp> macro domain in aqueous solution with dynamics: Impacts of parallel tempering simulation techniques and <scp>CHARMM36m</scp> and <scp>AMBER99SB</scp> force field parameters. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1289-1299.	1.5	2
13	XRRpred: accurate predictor of crystal structure quality from protein sequence. Bioinformatics, 2021, 37, 4366-4374.	1.8	3
14	flDPnn: Accurate intrinsic disorder prediction with putative propensities of disorder functions. Nature Communications, 2021, 12, 4438.	5.8	141
15	DNAgenie: accurate prediction of DNA-type-specific binding residues in protein sequences. Briefings in Bioinformatics, 2021, 22, .	3.2	11
16	DisoLipPred: accurate prediction of disordered lipid-binding residues in protein sequences with deep recurrent networks and transfer learning. Bioinformatics, 2021, 38, 115-124.	1.8	31
17	Accurate Sequence-Based Prediction of Deleterious nsSNPs with Multiple Sequence Profiles and Putative Binding Residues. Biomolecules, 2021, 11, 1337.	1.8	1
18	Intrinsic Disorder in Human RNA-Binding Proteins. Journal of Molecular Biology, 2021, 433, 167229.	2.0	23

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19	QUARTERplus: Accurate disorder predictions integrated with interpretable residue-level quality assessment scores. Computational and Structural Biotechnology Journal, 2021, 19, 2597-2606.	1.9	4
20	Surveying over 100 predictors of intrinsic disorder in proteins. Expert Review of Proteomics, 2021, 18, 1019-1029.	1.3	18
21	Codon selection reduces GC content bias in nucleic acids encoding for intrinsically disordered proteins. Cellular and Molecular Life Sciences, 2020, 77, 149-160.	2.4	8
22	Structural and functional analysis of â€œnon-smellyâ€•proteins. Cellular and Molecular Life Sciences, 2020, 77, 2423-2440.	2.4	16
23	DISOselect: Disorder predictor selection at the protein level. Protein Science, 2020, 29, 184-200.	3.1	10
24	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. Bioinformatics, 2020, 36, 1057-1065.	1.8	102
25	Accuracy of protein-level disorder predictions. Briefings in Bioinformatics, 2020, 21, 1509-1522.	3.2	36
26	DEPICTER: Intrinsic Disorder and Disorder Function Prediction Server. Journal of Molecular Biology, 2020, 432, 3379-3387.	2.0	46
27	Attention convolutional neural network for accurate segmentation and quantification of lesions in ischemic stroke disease. Medical Image Analysis, 2020, 65, 101791.	7.0	63
28	Comprehensive Survey and Comparative Assessment of RNA-Binding Residue Predictions with Analysis by RNA Type. International Journal of Molecular Sciences, 2020, 21, 6879.	1.8	13
29	Comparative Assessment of Intrinsic Disorder Predictions with a Focus on Protein and Nucleic Acid-Binding Proteins. Biomolecules, 2020, 10, 1636.	1.8	24
30	Prediction of protein-binding residues: dichotomy of sequence-based methods developed using structured complexes versus disordered proteins. Bioinformatics, 2020, 36, 4729-4738.	1.8	16
31	PSIONplusm Server for Accurate Multi-Label Prediction of Ion Channels and Their Types. Biomolecules, 2020, 10, 876.	1.8	7
32	NetEPD: A network-based essential protein discovery platform. Tsinghua Science and Technology, 2020, 25, 542-552.	4.1	15
33	Disordered RNA-Binding Region Prediction with DisoRDPbind. Methods in Molecular Biology, 2020, 2106, 225-239.	0.4	16
34	Prediction of Intrinsic Disorder with Quality Assessment Using QUARTER. Methods in Molecular Biology, 2020, 2165, 83-101.	0.4	3
35	PROBselect: accurate prediction of protein-binding residues from proteins sequences via dynamic predictorÂselection. Bioinformatics, 2020, 36, i735-i744.	1.8	19
36	A comprehensive overview of sequence-based protein-binding residue predictions for structured and disordered regions. , 2020, , 33-58.		4

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37	Survey of Similarity-Based Prediction of Drug-Protein Interactions. Current Medicinal Chemistry, 2020, 27, 5856-5886.	1.2	32
38	OUP accepted manuscript. Bioinformatics, 2020, 36, i754-i761.	1.8	6
39	Computational Prediction of Intrinsic Disorder in Protein Sequences with the disCoP Meta-predictor. Methods in Molecular Biology, 2020, 2141, 21-35.	0.4	4
40	Review and comparative assessment of similarity-based methods for prediction of drugâ€“protein interactions in the druggable human proteome. Briefings in Bioinformatics, 2019, 20, 2066-2087.	3.2	19
41	Sequence Similarity Searching. Current Protocols in Protein Science, 2019, 95, e71.	2.8	50
42	SCRIBER: accurate and partner type-specific prediction of protein-binding residues from proteins sequences. Bioinformatics, 2019, 35, i343-i353.	1.8	90
43	Introduction to intrinsically disordered proteins and regions. , 2019, , 1-34.		17
44	Endoplasmic reticulum and the microRNA environment in the cardiovascular system. Canadian Journal of Physiology and Pharmacology, 2019, 97, 515-527.	0.7	3
45	Computational prediction of functions of intrinsically disordered regions. Progress in Molecular Biology and Translational Science, 2019, 166, 341-369.	0.9	27
46	Computational Prediction of MoRFs, Short Disorder-to-order Transitioning Protein Binding Regions. Computational and Structural Biotechnology Journal, 2019, 17, 454-462.	1.9	50
47	PDID: Database of Experimental and Putative Drug Targets in Human Proteome. , 2019, , 827-847.		2
48	DeepFunc: A Deep Learning Framework for Accurate Prediction of Protein Functions from Protein Sequences and Interactions. Proteomics, 2019, 19, e1900019.	1.3	72
49	Computational Prediction of Secondary and Supersecondary Structures from Protein Sequences. Methods in Molecular Biology, 2019, 1958, 73-100.	0.4	11
50	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	15
51	Sequence-Derived Markers of Drug Targets and Potentially Druggable Human Proteins. Frontiers in Genetics, 2019, 10, 1075.	1.1	14
52	Quality assessment for the putative intrinsic disorder in proteins. Bioinformatics, 2019, 35, 1692-1700.	1.8	20
53	Predicting Functions of Disordered Proteins with MoRFpred. Methods in Molecular Biology, 2019, 1851, 337-352.	0.4	14
54	Comprehensive review and empirical analysis of hallmarks of DNA-, RNA- and protein-binding residues in protein chains. Briefings in Bioinformatics, 2019, 20, 1250-1268.	3.2	84

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55	Prediction of Ion Channels and their Types from Protein Sequences: Comprehensive Review and Comparative Assessment. Current Drug Targets, 2019, 20, 579-592.	1.0	6
56	Disordered Function Conjunction: On the in-silico function annotation of intrinsically disordered regions. , 2019, , .		1
57	On the Importance of Computational Biology and Bioinformatics to the Origins and Rapid Progression of the Intrinsically Disordered Proteins Field. , 2019, , .		0
58	Functional and structural characterization of osteocytic MLO-Y4 cell proteins encoded by genes differentially expressed in response to mechanical signals in vitro. Scientific Reports, 2018, 8, 6716.	1.6	11
59	Review and comparative assessment of sequence-based predictors of protein-binding residues. Briefings in Bioinformatics, 2018, 19, 821-837.	3.2	78
60	Critical evaluation of bioinformatics tools for the prediction of protein crystallization propensity. Briefings in Bioinformatics, 2018, 19, 838-852.	3.2	22
61	Cyclosporine A binding to COX-2 reveals a novel signaling pathway that activates the IRE1Î± unfolded protein response sensor. Scientific Reports, 2018, 8, 16678.	1.6	16
62	Prediction of DNA-binding residues in local segments of protein sequences with Fuzzy Cognitive Maps. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	1.9	15
63	Taxonomic Landscape of the Dark Proteomes: Wholeâ€Proteome Scale Interplay Between Structural Darkness, Intrinsic Disorder, and Crystallization Propensity. Proteomics, 2018, 18, 1800243.	1.3	27
64	In Silico Prediction and Validation of Novel RNA Binding Proteins and Residues in the Human Proteome. Proteomics, 2018, 18, e1800064.	1.3	19
65	Highâ€throughput prediction of disordered moonlighting regions in protein sequences. Proteins: Structure, Function and Bioinformatics, 2018, 86, 1097-1110.	1.5	29
66	Survey of Similarity-based Prediction of Drug-protein Interactions.. Current Medicinal Chemistry, 2018, 25, .	1.2	10
67	Comprehensive review of methods for prediction of intrinsic disorder and its molecular functions. Cellular and Molecular Life Sciences, 2017, 74, 3069-3090.	2.4	153
68	DRNApred, fast sequence-based method that accurately predicts and discriminates DNA- and RNA-binding residues. Nucleic Acids Research, 2017, 45, gkx059.	6.5	114
69	Computational Prediction of Intrinsic Disorder in Proteins. Current Protocols in Protein Science, 2017, 88, 2.16.1-2.16.14.	2.8	49
70	How to manipulate partition behavior of proteins in aqueous two-phase systems: Effect of trimethylamine N-oxide (TMAO). Fluid Phase Equilibria, 2017, 449, 217-224.	1.4	5
71	Prediction of Disordered RNA, DNA, and Protein Binding Regions Using DisoRDPbind. Methods in Molecular Biology, 2017, 1484, 187-203.	0.4	59
72	What are the structural features that drive partitioning of proteins in aqueous two-phase systems?. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 113-120.	1.1	16

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73	fDETECT webserver: fast predictor of propensity for protein production, purification, and crystallization. BMC Bioinformatics, 2017, 18, 580.	1.2	22
74	Functional Analysis of Human Hub Proteins and Their Interactors Involved in the Intrinsic Disorder-Enriched Interactions. International Journal of Molecular Sciences, 2017, 18, 2761.	1.8	85
75	Exploratory Analysis of Quality Assessment of Putative Intrinsic Disorder in Proteins. Lecture Notes in Computer Science, 2017, , 722-732.	1.0	4
76	Survey of Predictors of Propensity for Protein Production and Crystallization with Application to Predict Resolution of Crystal Structures. Current Protein and Peptide Science, 2017, 19, 200-210.	0.7	7
77	Compartmentalization and Functionality of Nuclear Disorder: Intrinsic Disorder and Protein-Protein Interactions in Intra-Nuclear Compartments. International Journal of Molecular Sciences, 2016, 17, 24.	1.8	94
78	PSIONplus: Accurate Sequence-Based Predictor of Ion Channels and Their Types. PLoS ONE, 2016, 11, e0152964.	1.1	12
79	Autophagy-related intrinsically disordered proteins in intra-nuclear compartments. Molecular BioSystems, 2016, 12, 2798-2817.	2.9	27
80	DFLpred: High-throughput prediction of disordered flexible linker regions in protein sequences. Bioinformatics, 2016, 32, i341-i350.	1.8	72
81	How disordered is my protein and what is its disorder for? A guide through the â€œdark sideâ€•of the protein universe. Intrinsically Disordered Proteins, 2016, 4, e1259708.	1.9	87
82	Genes encoding intrinsic disorder in Eukaryota have high GC content. Intrinsically Disordered Proteins, 2016, 4, e1262225.	1.9	25
83	Computational Prediction of Protein Secondary Structure from Sequence. Current Protocols in Protein Science, 2016, 86, 2.3.1-2.3.10.	2.8	10
84	Disordered nucleiome: Abundance of intrinsic disorder in the DNAâ€•and RNAâ€•binding proteins in 1121 species from Eukaryota, Bacteria and Archaea. Proteomics, 2016, 16, 1486-1498.	1.3	92
85	Molecular recognition features (MoRFs) in three domains of life. Molecular BioSystems, 2016, 12, 697-710.	2.9	141
86	PDID: database of molecular-level putative proteinâ€“drug interactions in the structural human proteome. Bioinformatics, 2016, 32, 579-586.	1.8	38
87	A comprehensive comparative review of sequence-based predictors of DNA- and RNA-binding residues. Briefings in Bioinformatics, 2016, 17, 88-105.	3.2	88
88	Untapped Potential of Disordered Proteins in Current Druggable Human Proteome. Current Drug Targets, 2016, 17, 1198-1205.	1.0	52
89	Unstructural biology of the dengue virus proteins. FEBS Journal, 2015, 282, 3368-3394.	2.2	58
90	In various protein complexes, disordered protomers have large perâ€•residue surface areas and area of proteinâ€“DNAâ€•and RNAâ€•binding interfaces. FEBS Letters, 2015, 589, 2561-2569.	1.3	42

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91	Analyzing the effects of protecting osmolytes on soluteâ€“water interactions by solvatochromic comparison method: II. Globular proteins. RSC Advances, 2015, 5, 59780-59791.	1.7	22
92	Systematic investigation of sequence and structural motifs that recognize ATP. Computational Biology and Chemistry, 2015, 56, 131-141.	1.1	3
93	High-throughput prediction of RNA, DNA and protein binding regions mediated by intrinsic disorder. Nucleic Acids Research, 2015, 43, e121-e121.	6.5	131
94	Comprehensive overview and assessment of computational prediction of microRNA targets in animals. Briefings in Bioinformatics, 2015, 16, 780-794.	3.2	71
95	Exceptionally abundant exceptions: comprehensive characterization of intrinsic disorder in all domains of life. Cellular and Molecular Life Sciences, 2015, 72, 137-151.	2.4	314
96	Consensus-Based Prediction of RNA and DNA Binding Residues from Protein Sequences. Lecture Notes in Computer Science, 2015, , 501-511.	1.0	1
97	Intrinsic Disorder in the BK Channel and Its Interactome. PLoS ONE, 2014, 9, e94331.	1.1	16
98	Genome-wide analysis of thapsigargin-induced microRNAs and their targets in NIH3T3 cells. Genomics Data, 2014, 2, 325-327.	1.3	3
99	Covering complete proteomes with X-ray structures: a current snapshot. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2781-2793.	2.5	30
100	Genome-scale prediction of proteins with long intrinsically disordered regions. Proteins: Structure, Function and Bioinformatics, 2014, 82, 145-158.	1.5	104
101	Improved prediction of residue flexibility by embedding optimized amino acid grouping into RSA-based linear models. Amino Acids, 2014, 46, 2665-2680.	1.2	10
102	A creature with a hundred waggly tails: intrinsically disordered proteins in the ribosome. Cellular and Molecular Life Sciences, 2014, 71, 1477-1504.	2.4	119
103	Prediction and characterization of cyclic proteins from sequences in three domains of life. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 181-190.	1.1	19
104	Structural features important for differences in protein partitioning in aqueous dextranâ€“polyethylene glycol two-phase systems of different ionic compositions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 694-704.	1.1	21
105	Disordered Proteinaceous Machines. Chemical Reviews, 2014, 114, 6806-6843.	23.0	109
106	Structural Disorder in Viral Proteins. Chemical Reviews, 2014, 114, 6880-6911.	23.0	181
107	Sequence-based Gaussian network model for protein dynamics. Bioinformatics, 2014, 30, 497-505.	1.8	24
108	The intrinsic disorder status of the human hepatitis C virus proteome. Molecular BioSystems, 2014, 10, 1345-1363.	2.9	57

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109	Human structural proteome-wide characterization of Cyclosporine A targets. Bioinformatics, 2014, 30, 3561-3566.	1.8	38
110	Accurate prediction of disorder in protein chains with a comprehensive and empirically designed consensus. Journal of Biomolecular Structure and Dynamics, 2014, 32, 448-464.	2.0	146
111	Interplay Between the Oxidoreductase PDIA6 and microRNA-322 Controls the Response to Disrupted Endoplasmic Reticulum Calcium Homeostasis. Science Signaling, 2014, 7, ra54.	1.6	92
112	Comprehensively designed consensus of standalone secondary structure predictors improvesQ3by over 3%. Journal of Biomolecular Structure and Dynamics, 2014, 32, 36-51.	2.0	11
113	P125Endoplasmic reticulum stress responses to disrupted endoplasmic reticulum ca2+ homeostasis. Cardiovascular Research, 2014, 103, S22.1-S22.	1.8	0
114	Prediction of Intrinsic Disorder in Proteins Using MFDp2. Methods in Molecular Biology, 2014, 1137, 147-162.	0.4	37
115	Computational Prediction of B Cell Epitopes from Antigen Sequences. Methods in Molecular Biology, 2014, 1184, 197-215.	0.4	24
116	mi-DS: Multiple-Instance Learning Algorithm. IEEE Transactions on Cybernetics, 2013, 43, 143-154.	6.2	15
117	Monocytes from patients with osteoarthritis display increased osteoclastogenesis and bone resorption: The In Vitro Osteoclast Differentiation in Arthritis study. Arthritis and Rheumatism, 2013, 65, 148-158.	6.7	41
118	RAPID: Fast and accurate sequence-based prediction of intrinsic disorder content on proteomic scale. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1671-1680.	1.1	49
119	Stochastic machines as a colocalization mechanism for scaffold protein function. FEBS Letters, 2013, 587, 1587-1591.	1.3	40
120	Resilience of death: intrinsic disorder in proteins involved in the programmed cell death. Cell Death and Differentiation, 2013, 20, 1257-1267.	5.0	71
121	MFDp2. Intrinsically Disordered Proteins, 2013, 1, e24428.	1.9	92
122	On the intrinsic disorder status of the major players in programmed cell death pathways. F1000Research, 2013, 2, 190.	0.8	20
123	MoRFpred, a computational tool for sequence-based prediction and characterization of short disorder-to-order transitioning binding regions in proteins. Bioinformatics, 2012, 28, i75-i83.	1.8	311
124	D2P2: database of disordered protein predictions. Nucleic Acids Research, 2012, 41, D508-D516.	6.5	570
125	NOT THAT RIGID MIDGETS AND NOT SO FLEXIBLE GIANTS: ON THE ABUNDANCE AND ROLES OF INTRINSIC DISORDER IN SHORT AND LONG PROTEINS. Journal of Biological Systems, 2012, 20, 471-511.	0.5	19
126	Prediction and analysis of nucleotide-binding residues using sequence and sequence-derived structural descriptors. Bioinformatics, 2012, 28, 331-341.	1.8	106

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127	Comprehensive Comparative Assessment of In-Silico Predictors of Disordered Regions. Current Protein and Peptide Science, 2012, 13, 6-18.	0.7	170
128	Learning of Fuzzy Cognitive Maps Using Density Estimate. IEEE Transactions on Systems, Man, and Cybernetics, 2012, 42, 900-912.	5.5	65
129	More than just tails: intrinsic disorder in histone proteins. Molecular BioSystems, 2012, 8, 1886.	2.9	99
130	Neural Networks in Bioinformatics. , 2012, , 565-583.		8
131	Computational Prediction of Secondary and Supersecondary Structures. Methods in Molecular Biology, 2012, 932, 63-86.	0.4	13
132	Finding Protein Targets for Small Biologically Relevant Ligands across Fold Space Using Inverse Ligand Binding Predictions. Structure, 2012, 20, 1815-1822.	1.6	19
133	BEST: Improved Prediction of B-Cell Epitopes from Antigen Sequences. PLoS ONE, 2012, 7, e40104.	1.1	79
134	CRYSpred: Accurate Sequence-Based Protein Crystallization Propensity Prediction Using Sequence-Derived Structural Characteristics. Protein and Peptide Letters, 2012, 19, 40-49.	0.4	19
135	Protein intrinsic disorder as a flexible armor and a weapon of HIV-1. Cellular and Molecular Life Sciences, 2012, 69, 1211-1259.	2.4	94
136	SPINE X: Improving protein secondary structure prediction by multistep learning coupled with prediction of solvent accessible surface area and backbone torsion angles. Journal of Computational Chemistry, 2012, 33, 259-267.	1.5	209
137	Determination of protein folding kinetic types using sequence and predicted secondary structure and solvent accessibility. Amino Acids, 2012, 42, 271-283.	1.2	18
138	On the complementarity of the consensus-based disorder prediction. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 176-87.	0.7	35
139	The increased in vitro osteoclastogenesis in patients with rheumatoid arthritis is due to increased percentage of precursors and decreased apoptosis â€" The In Vitro Osteoclast Differentiation in Arthritis (IODA) study. Bone, 2011, 48, 588-596.	1.4	37
140	Editorial [Hot Topic: Machine Learning Models in Protein Bioinformatics (Guest Editors: Lukasz) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	0.7	7
141	Structural Protein Descriptors in 1-Dimension and their Sequence-Based Predictions. Current Protein and Peptide Science, 2011, 12, 470-489.	0.7	28
142	ON THE COMPLEMENTARITY OF THE CONSENSUS-BASED DISORDER PREDICTION. , 2011, , .		33
143	A Critical Comparative Assessment of Predictions of Protein-Binding Sites for Biologically Relevant Organic Compounds. Structure, 2011, 19, 613-621.	1.6	59
144	iFC2: an integrated web-server for improved prediction of protein structural class, fold type, and secondary structure content. Amino Acids, 2011, 40, 963-973.	1.2	13

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145	ATPsite: sequence-based prediction of ATP-binding residues. Proteome Science, 2011, 9, S4.	0.7	57
146	In-silico prediction of disorder content using hybrid sequence representation. BMC Bioinformatics, 2011, 12, 245.	1.2	45
147	Improved identification of outer membrane beta barrel proteins using primary sequence, predicted secondary structure, and evolutionary information. Proteins: Structure, Function and Bioinformatics, 2011, 79, 294-303.	1.5	12
148	Sequence-based prediction of protein crystallization, purification and production propensity. Bioinformatics, 2011, 27, i24-i33.	1.8	69
149	IMPROVED SEQUENCE-BASED PREDICTION OF STRAND RESIDUES. Journal of Bioinformatics and Computational Biology, 2011, 09, 67-89.	0.3	5
150	Critical assessment of high-throughput standalone methods for secondary structure prediction. Briefings in Bioinformatics, 2011, 12, 672-688.	3.2	53
151	Analysis and Prediction of RNA-Binding Residues Using Sequence, Evolutionary Conservation, and Predicted Secondary Structure and Solvent Accessibility. Current Protein and Peptide Science, 2010, 11, 609-628.	0.7	50
152	Discovery of factors influencing patent value based on machine learning in patents in the field of nanotechnology. Scientometrics, 2010, 82, 217-241.	1.6	45
153	A divide and conquer method for learning large Fuzzy Cognitive Maps. Fuzzy Sets and Systems, 2010, 161, 2515-2532.	1.6	89
154	Accurate prediction of protein folding rates from sequence and sequence-derived residue flexibility and solvent accessibility. Proteins: Structure, Function and Bioinformatics, 2010, 78, NA-NA.	1.5	25
155	Discretization as the enabling technique for the NaÃ¯ve Bayes and semi-NaÃ¯ve Bayes-based classification. Knowledge Engineering Review, 2010, 25, 421-449.	2.1	21
156	Improved sequence-based prediction of disordered regions with multilayer fusion of multiple information sources. Bioinformatics, 2010, 26, i489-i496.	1.8	154
157	Expert-Based and Computational Methods for Developing Fuzzy Cognitive Maps. Studies in Fuzziness and Soft Computing, 2010, , 23-41.	0.6	45
158	Accurate prediction of ATP-binding residues using sequence and sequence-derived structural descriptors. , 2010, , .		0
159	Recognition of Partially Occluded and Rotated Images With a Network of Spiking Neurons. IEEE Transactions on Neural Networks, 2010, 21, 1697-1709.	4.8	32
160	Machine Learning Algorithms Inspired by the Work of Ryszard Spencer Michalski. Studies in Computational Intelligence, 2010, , 49-74.	0.7	1
161	Modular prediction of protein structural classes from sequences of twilight-zone identity with predicting sequences. BMC Bioinformatics, 2009, 10, 414.	1.2	85
162	Prediction of integral membrane protein type by collocated hydrophobic amino acid pairs. Journal of Computational Chemistry, 2009, 30, 163-172.	1.5	66

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163	Prediction of protein folding rates from primary sequences using hybrid sequence representation. Journal of Computational Chemistry, 2009, 30, 772-783.	1.5	33
164	On the relation between residue flexibility and local solvent accessibility in proteins. Proteins: Structure, Function and Bioinformatics, 2009, 76, 617-636.	1.5	76
165	CRYSTALP2: sequence-based protein crystallization propensity prediction. BMC Structural Biology, 2009, 9, 50.	2.3	70
166	Meta prediction of protein crystallization propensity. Biochemical and Biophysical Research Communications, 2009, 390, 10-15.	1.0	29
167	Investigation of Atomic Level Patterns in Proteinâ€"Small Ligand Interactions. PLoS ONE, 2009, 4, e4473.	1.1	55
168	Sequence-Based Protein Crystallization Propensity Prediction for Structural Genomics: Review and Comparative Analysis. Natural Science, 2009, 01, 93-106.	0.2	11
169	On the Relation Between the Predicted Secondary Structure and the Protein Size. Protein Journal, 2008, 27, 234-239.	0.7	3
170	Secondary structure-based assignment of the protein structural classes. Amino Acids, 2008, 35, 551-564.	1.2	54
171	Prediction of protein structural class using novel evolutionary collocationâ€based sequence representation. Journal of Computational Chemistry, 2008, 29, 1596-1604.	1.5	148
172	Impact of imputation of missing values on classification error for discrete data. Pattern Recognition, 2008, 41, 3692-3705.	5.1	267
173	Identification of tubulin drug binding sites and prediction of relative differences in binding affinities to tubulin isotypes using digital signal processing. Journal of Molecular Graphics and Modelling, 2008, 27, 497-505.	1.3	15
174	A tree-projection-based algorithm for multi-label recurrent-item associative-classification rule generation. Data and Knowledge Engineering, 2008, 64, 171-197.	2.1	29
175	SCPRED: Accurate prediction of protein structural class for sequences of twilight-zone similarity with predicting sequences. BMC Bioinformatics, 2008, 9, 226.	1.2	129
176	Sequence based residue depth prediction using evolutionary information and predicted secondary structure. BMC Bioinformatics, 2008, 9, 388.	1.2	35
177	Prediction of beta-turns at over 80% accuracy based on an ensemble of predicted secondary structures and multiple alignments. BMC Bioinformatics, 2008, 9, 430.	1.2	41
178	Improved machine learning method for analysis of gas phase chemistry of peptides. BMC Bioinformatics, 2008, 9, 515.	1.2	1
179	Numerical and Linguistic Prediction of Time Series With the Use of Fuzzy Cognitive Maps. IEEE Transactions on Fuzzy Systems, 2008, 16, 61-72.	6.5	158
180	HuMiTar: A sequence-based method for prediction of human microRNA targets. Algorithms for Molecular Biology, 2008, 3, 16.	0.3	21

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181	Data-driven Nonlinear Hebbian Learning method for Fuzzy Cognitive Maps. , 2008, , .		73
182	Accurate sequence-based prediction of catalytic residues. Bioinformatics, 2008, 24, 2329-2338.	1.8	75
183	Comparative Analysis of the Impact of Discretization on the Classification with Naïve Bayes and Semi-Naïve Bayes Classifiers. , 2008, , .		17
184	Searching for Factors that Distinguish Disease-Prone and Disease-Resistant Prions via Sequence Analysis. Bioinformatics and Biology Insights, 2008, 2, BBI.S550.	1.0	2
185	Sequence-Based Methods for Real Value Predictions of Protein Structure. Current Bioinformatics, 2008, 3, 183-196.	0.7	10
186	Sequence-Only Based Prediction of Î² -Turn Location and Type Using Collocation of Amino Acid Pairs. Open Bioinformatics Journal, 2008, 2, 37-49.	1.0	5
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