Lukasz A Kurgan

List of Publications by Year
in descending order

240 papers	11,990 citations	22099 59 h-index	35952 97 g-index
256 all docs	256 docs citations	256 times ranked	10615 citing authors

#	Article	IF	Citations
1	D2P2: database of disordered protein predictions. Nucleic Acids Research, 2012, 41, D508-D516.	6.5	570
2	Genetic learning of fuzzy cognitive maps. Fuzzy Sets and Systems, 2005, 153, 371-401.	1.6	416
3	CAIM discretization algorithm. IEEE Transactions on Knowledge and Data Engineering, 2004, 16, 145-153.	4.0	352
4	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
5	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
6	A survey of Knowledge Discovery and Data Mining process models. Knowledge Engineering Review, 2006, 21, 1-24.	2.1	293
7	Impact of imputation of missing values on classification error for discrete data. Pattern Recognition, 2008, 41, 3692-3705.	5.1	267
8	Knowledge discovery approach to automated cardiac SPECT diagnosis. Artificial Intelligence in Medicine, 2001, 23, 149-169.	3.8	209
9	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
10	Structural Disorder in Viral Proteins. Chemical Reviews, 2014, 114, 6880-6911.	23.0	181
11	Comprehensive Comparative Assessment of In-Silico Predictors of Disordered Regions. Current Protein and Peptide Science, 2012, 13, 6-18.	0.7	170
12	A Novel Framework for Imputation of Missing Values in Databases. IEEE Transactions on Systems, Man and Cybernetics, Part A: Systems and Humans, 2007, 37, 692-709.	3.4	169
13	Classifier ensembles for protein structural class prediction with varying homology. Biochemical and Biophysical Research Communications, 2006, 348, 981-988.	1.0	168
14	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
15	Improved sequence-based prediction of disordered regions with multilayer fusion of multiple information sources. Bioinformatics, 2010, 26, i489-i496.	1.8	154
16	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
17	Prediction of structural classes for protein sequences and domains€"Impact of prediction algorithms, sequence representation and homology, and test procedures on accuracy. Pattern Recognition, 2006, 39, 2323-2343.	5.1	151
18	Prediction of protein structural class using novel evolutionary collocation€based sequence representation. Journal of Computational Chemistry, 2008, 29, 1596-1604.	1.5	148

#	Article	IF	Citations
19	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
20	Molecular recognition features (MoRFs) in three domains of life. Molecular BioSystems, 2016, 12, 697-710.	2.9	141
21	flDPnn: Accurate intrinsic disorder prediction with putative propensities of disorder functions. Nature Communications, 2021, 12, 4438.	5.8	141
22	High-throughput prediction of RNA, DNA and protein binding regions mediated by intrinsic disorder. Nucleic Acids Research, 2015, 43, e121-e121.	6.5	131
23	SCPRED: Accurate prediction of protein structural class for sequences of twilight-zone similarity with predicting sequences. BMC Bioinformatics, 2008, 9, 226.	1.2	129
24	*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
25	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
26	DRNApred, fast sequence-based method that accurately predicts and discriminates DNA- and RNA-binding residues. Nucleic Acids Research, 2017, 45, gkx059.	6.5	114
27	Disordered Proteinaceous Machines. Chemical Reviews, 2014, 114, 6806-6843.	23.0	109
28	PFRES: protein fold classification by using evolutionary information and predicted secondary structure. Bioinformatics, 2007, 23, 2843-2850.	1.8	108
29	Prediction and analysis of nucleotide-binding residues using sequence and sequence-derived structural descriptors. Bioinformatics, 2012, 28, 331-341.	1.8	106
30	Genome-scale prediction of proteins with long intrinsically disordered regions. Proteins: Structure, Function and Bioinformatics, 2014, 82, 145-158.	1.5	104
31	Prediction of protein crystallization using collocation of amino acid pairs. Biochemical and Biophysical Research Communications, 2007, 355, 764-769.	1.0	102
32	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. Bioinformatics, 2020, 36, 1057-1065.	1.8	102
33	Prediction of flexible/rigid regions from protein sequences using k-spaced amino acid pairs. BMC Structural Biology, 2007, 7, 25.	2.3	100
34	More than just tails: intrinsic disorder in histone proteins. Molecular BioSystems, 2012, 8, 1886.	2.9	99
35	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
36	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

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37	MFDp2. Intrinsically Disordered Proteins, 2013, 1, e24428.	1.9	92
38	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
39	Disordered nucleiome: Abundance of intrinsic disorder in the DNA–and RNA–binding proteins in 1121 species from Eukaryota, Bacteria and Archaea. Proteomics, 2016, 16, 1486-1498.	1.3	92
40	SCRIBER: accurate and partner type-specific prediction of protein-binding residues from proteins sequences. Bioinformatics, 2019, 35, i343-i353.	1.8	90
41	A divide and conquer method for learning large Fuzzy Cognitive Maps. Fuzzy Sets and Systems, 2010, 161, 2515-2532.	1.6	89
42	A comprehensive comparative review of sequence-based predictors of DNA- and RNA-binding residues. Briefings in Bioinformatics, 2016, 17, 88-105.	3.2	88
43	How disordered is my protein and what is its disorder for? A guide through the "dark side" of the protein universe. Intrinsically Disordered Proteins, 2016, 4, e1259708.	1.9	87
44	Modular prediction of protein structural classes from sequences of twilight-zone identity with predicting sequences. BMC Bioinformatics, 2009, 10, 414.	1.2	85
45	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
46	Prediction of protein structural class for the twilight zone sequences. Biochemical and Biophysical Research Communications, 2007, 357, 453-460.	1.0	84
47	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
48	BEST: Improved Prediction of B-Cell Epitopes from Antigen Sequences. PLoS ONE, 2012, 7, e40104.	1.1	79
49	Review and comparative assessment of sequence-based predictors of protein-binding residues. Briefings in Bioinformatics, 2018, 19, 821-837.	3.2	78
50	On the relation between residue flexibility and local solvent accessibility in proteins. Proteins: Structure, Function and Bioinformatics, 2009, 76, 617-636.	1.5	76
51	Accurate sequence-based prediction of catalytic residues. Bioinformatics, 2008, 24, 2329-2338.	1.8	75
52	Data-driven Nonlinear Hebbian Learning method for Fuzzy Cognitive Maps. , 2008, , .		73
53	DFLpred: High-throughput prediction of disordered flexible linker regions in protein sequences. Bioinformatics, 2016, 32, i341-i350.	1.8	72
54	DeepFunc: A Deep Learning Framework for Accurate Prediction of Protein Functions from Protein Sequences and Interactions. Proteomics, 2019, 19, e1900019.	1.3	72

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55	Resilience of death: intrinsic disorder in proteins involved in the programmed cell death. Cell Death and Differentiation, 2013, 20, 1257-1267.	5.0	71
56	Comprehensive overview and assessment of computational prediction of microRNA targets in animals. Briefings in Bioinformatics, 2015, 16, 780-794.	3.2	71
57	CRYSTALP2: sequence-based protein crystallization propensity prediction. BMC Structural Biology, 2009, 9, 50.	2.3	70
58	Sequence-based prediction of protein crystallization, purification and production propensity. Bioinformatics, 2011, 27, i24-i33.	1.8	69
59	Prediction of integral membrane protein type by collocated hydrophobic amino acid pairs. Journal of Computational Chemistry, 2009, 30, 163-172.	1.5	66
60	Learning of Fuzzy Cognitive Maps Using Density Estimate. IEEE Transactions on Systems, Man, and Cybernetics, 2012, 42, 900-912.	5.5	65
61	Attention convolutional neural network for accurate segmentation and quantification of lesions in ischemic stroke disease. Medical Image Analysis, 2020, 65, 101791.	7.0	63
62	A Critical Comparative Assessment of Predictions of Protein-Binding Sites for Biologically Relevant Organic Compounds. Structure, 2011, 19, 613-621.	1.6	59
63	Prediction of Disordered RNA, DNA, and Protein Binding Regions Using DisoRDPbind. Methods in Molecular Biology, 2017, 1484, 187-203.	0.4	59
64	Unstructural biology of the dengue virus proteins. FEBS Journal, 2015, 282, 3368-3394.	2.2	58
65	ATPsite: sequence-based prediction of ATP-binding residues. Proteome Science, 2011, 9, S4.	0.7	57
66	The intrinsic disorder status of the human hepatitis C virus proteome. Molecular BioSystems, 2014, 10, 1345-1363.	2.9	57
67	Trends in Data Mining and Knowledge Discovery. , 2005, , 1-26.		55
68	Investigation of Atomic Level Patterns in Protein–Small Ligand Interactions. PLoS ONE, 2009, 4, e4473.	1.1	55
69	The Roles of β-Tubulin Mutations and Isotype Expression in Acquired Drug Resistance. Cancer Informatics, 2007, 3, 117693510700300.	0.9	54
70	Secondary structure-based assignment of the protein structural classes. Amino Acids, 2008, 35, 551-564.	1.2	54
71	Critical assessment of high-throughput standalone methods for secondary structure prediction. Briefings in Bioinformatics, 2011, 12, 672-688.	3.2	53
72	Untapped Potential of Disordered Proteins in Current Druggable Human Proteome. Current Drug Targets, 2016, 17, 1198-1205.	1.0	52

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73	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
74	Sequence Similarity Searching. Current Protocols in Protein Science, 2019, 95, e71.	2.8	50
75	Computational Prediction of MoRFs, Short Disorder-to-order Transitioning Protein Binding Regions. Computational and Structural Biotechnology Journal, 2019, 17, 454-462.	1.9	50
76	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
77	Computational Prediction of Intrinsic Disorder in Proteins. Current Protocols in Protein Science, 2017, 88, 2.16.1-2.16.14.	2.8	49
78	DEPICTER: Intrinsic Disorder and Disorder Function Prediction Server. Journal of Molecular Biology, 2020, 432, 3379-3387.	2.0	46
79	DescribePROT: database of amino acid-level protein structure and function predictions. Nucleic Acids Research, 2021, 49, D298-D308.	6.5	46
80	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
81	Expert-Based and Computational Methods for Developing Fuzzy Cognitive Maps. Studies in Fuzziness and Soft Computing, 2010, , 23-41.	0.6	45
82	In-silico prediction of disorder content using hybrid sequence representation. BMC Bioinformatics, 2011, 12, 245.	1.2	45
83	Novel scales based on hydrophobicity indices for secondary protein structure. Journal of Theoretical Biology, 2007, 248, 354-366.	0.8	42
84	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
85	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
86	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
87	Stochastic machines as a colocalization mechanism for scaffold protein function. FEBS Letters, 2013, 587, 1587-1591.	1.3	40
88	CLIP4: Hybrid inductive machine learning algorithm that generates inequality rules. Information Sciences, 2004, 163, 37-83.	4.0	39
89	Human structural proteome-wide characterization of Cyclosporine A targets. Bioinformatics, 2014, 30, 3561-3566.	1.8	38
90	PDID: database of molecular-level putative proteinâ€"drug interactions in the structural human proteome. Bioinformatics, 2016, 32, 579-586.	1.8	38

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91	Highly scalable and robust rule learner: performance evaluation and comparison. IEEE Transactions on Systems, Man, and Cybernetics, 2006, 36, 32-53.	5.5	37
92	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
93	Prediction of Intrinsic Disorder in Proteins Using MFDp2. Methods in Molecular Biology, 2014, 1137, 147-162.	0.4	37
94	Accuracy of protein-level disorder predictions. Briefings in Bioinformatics, 2020, 21, 1509-1522.	3.2	36
95	Parallel Learning of Large Fuzzy Cognitive Maps. Neural Networks (IJCNN), International Joint Conference on, 2007, , .	0.0	35
96	Sequence based residue depth prediction using evolutionary information and predicted secondary structure. BMC Bioinformatics, 2008, 9, 388.	1.2	35
97	On the complementarity of the consensus-based disorder prediction. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 176-87.	0.7	35
98	Prediction of protein folding rates from primary sequences using hybrid sequence representation. Journal of Computational Chemistry, 2009, 30, 772-783.	1.5	33
99	ON THE COMPLEMENTARITY OF THE CONSENSUS-BASED DISORDER PREDICTION. , 2011, , .		33
100	Prediction of protein secondary structure content for the twilight zone sequences. Proteins: Structure, Function and Bioinformatics, 2007, 69, 486-498.	1.5	32
101	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
102	Survey of Similarity-Based Prediction of Drug-Protein Interactions. Current Medicinal Chemistry, 2020, 27, 5856-5886.	1.2	32
103	Learning fuzzy cognitive maps with required precision using genetic algorithm approach. Electronics Letters, 2004, 40, 1519.	0.5	31
104	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
105	Covering complete proteomes with X-ray structures: a current snapshot. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2781-2793.	2.5	30
106	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
107	Meta prediction of protein crystallization propensity. Biochemical and Biophysical Research Communications, 2009, 390, 10-15.	1.0	29
108	Highâ€throughput prediction of disordered moonlighting regions in protein sequences. Proteins: Structure, Function and Bioinformatics, 2018, 86, 1097-1110.	1.5	29

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109	Structural Protein Descriptors in 1-Dimension and their Sequence-Based Predictions. Current Protein and Peptide Science, 2011, 12, 470-489.	0.7	28
110	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
111	Highly accurate and consistent method for prediction of helix and strand content from primary protein sequences. Artificial Intelligence in Medicine, 2005, 35, 19-35.	3.8	27
112	Autophagy-related intrinsically disordered proteins in intra-nuclear compartments. Molecular BioSystems, 2016, 12, 2798-2817.	2.9	27
113	Taxonomic Landscape of the Dark Proteomes: Whole‐Proteome Scale Interplay Between Structural Darkness, Intrinsic Disorder, and Crystallization Propensity. Proteomics, 2018, 18, 1800243.	1.3	27
114	Computational prediction of functions of intrinsically disordered regions. Progress in Molecular Biology and Translational Science, 2019, 166, 341-369.	0.9	27
115	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
116	Genes encoding intrinsic disorder in Eukaryota have high GC content. Intrinsically Disordered Proteins, 2016, 4, e1262225.	1.9	25
117	Sequence-based Gaussian network model for protein dynamics. Bioinformatics, 2014, 30, 497-505.	1.8	24
118	Comparative Assessment of Intrinsic Disorder Predictions with a Focus on Protein and Nucleic Acid-Binding Proteins. Biomolecules, 2020, 10, 1636.	1.8	24
119	Computational Prediction of B Cell Epitopes from Antigen Sequences. Methods in Molecular Biology, 2014, 1184, 197-215.	0.4	24
120	Deep learning in prediction of intrinsic disorder in proteins. Computational and Structural Biotechnology Journal, 2022, 20, 1286-1294.	1.9	24
121	<i>iFeatureOmega:</i> 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
122	Systematic evaluation of machine learning methods for identifying human–pathogen protein–protein interactions. Briefings in Bioinformatics, 2021, 22, .	3.2	23
123	Intrinsic Disorder in Human RNA-Binding Proteins. Journal of Molecular Biology, 2021, 433, 167229.	2.0	23
124	A New Synaptic Plasticity Rule for Networks of Spiking Neurons. IEEE Transactions on Neural Networks, 2006, 17, 94-105.	4.8	22
125	Analyzing the effects of protecting osmolytes on solute–water interactions by solvatochromic comparison method: II. Globular proteins. RSC Advances, 2015, 5, 59780-59791.	1.7	22
126	fDETECT webserver: fast predictor of propensity for protein production, purification, and crystallization. BMC Bioinformatics, 2017, 18, 580.	1.2	22

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127	Critical evaluation of bioinformatics tools for the prediction of protein crystallization propensity. Briefings in Bioinformatics, 2018, 19, 838-852.	3.2	22
128	Experimental analysis of methods for imputation of missing values in databases. , 2004, , .		21
129	Evolutionary Development of Fuzzy Cognitive Maps. , 0, , .		21
130	The Knowledge Discovery Process. , 2007, , 9-24.		21
131	HuMiTar: A sequence-based method for prediction of human microRNA targets. Algorithms for Molecular Biology, 2008, 3, 16.	0.3	21
132	Discretization as the enabling technique for the Naïve Bayes and semi-Naïve Bayes-based classification. Knowledge Engineering Review, 2010, 25, 421-449.	2.1	21
133	Structural features important for differences in protein partitioning in aqueous dextran–polyethylene glycol two-phase systems of different ionic compositions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 694-704.	1.1	21
134	Quality assessment for the putative intrinsic disorder in proteins. Bioinformatics, 2019, 35, 1692-1700.	1.8	20
135	On the intrinsic disorder status of the major players in programmed cell death pathways. F1000Research, 2013, 2, 190.	0.8	20
136	Higher-order Fuzzy Cognitive Maps. , 2006, , .		19
137	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
138	Finding Protein Targets for Small Biologically Relevant Ligands across Fold Space Using Inverse Ligand Binding Predictions. Structure, 2012, 20, 1815-1822.	1.6	19
139	CRYSpred: Accurate Sequence-Based Protein Crystallization Propensity Prediction Using Sequence-Derived Structural Characteristics. Protein and Peptide Letters, 2012, 19, 40-49.	0.4	19
140	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
141	In Silico Prediction and Validation of Novel RNA Binding Proteins and Residues in the Human Proteome. Proteomics, 2018, 18, e1800064.	1.3	19
142	Review and comparative assessment of similarity-based methods for prediction of drug–protein interactions in the druggable human proteome. Briefings in Bioinformatics, 2019, 20, 2066-2087.	3.2	19
143	PROBselect: accurate prediction of protein-binding residues from proteins sequences via dynamic predictorÂselection. Bioinformatics, 2020, 36, i735-i744.	1.8	19
144	Optimization of the Sliding Window Size for Protein Structure Prediction. , 2006, , .		18

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145	Multilabel associative classification categorization of MEDLINE aticles into MeSH keywords. IEEE Engineering in Medicine and Biology Magazine, 2007, 26, 47-55.	1.1	18
146	Determination of protein folding kinetic types using sequence and predicted secondary structure and solvent accessibility. Amino Acids, 2012, 42, 271-283.	1.2	18
147	Surveying over 100 predictors of intrinsic disorder in proteins. Expert Review of Proteomics, 2021, 18, 1019-1029.	1.3	18
148	A comment on â€œPrediction of protein structural classes by a new measure of information discrepancyâ€• Computational Biology and Chemistry, 2006, 30, 393-394.	1.1	17
149	Comparative Analysis of the Impact of Discretization on the Classification with Na&#x0EF;ve Bayes and Semi-Na&#x0EF;ve Bayes Classifiers. , 2008, , .		17
150	Introduction to intrinsically disordered proteins and regions. , 2019, , 1-34.		17
151	Resources for computational prediction of intrinsic disorder in proteins. Methods, 2022, 204, 132-141.	1.9	17
152	Intrinsic Disorder in the BK Channel and Its Interactome. PLoS ONE, 2014, 9, e94331.	1.1	16
153	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
154	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
155	Structural and functional analysis of â€œnon-smellyâ€•proteins. Cellular and Molecular Life Sciences, 2020, 77, 2423-2440.	2.4	16
156	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
157	Disordered RNA-Binding Region Prediction with DisoRDPbind. Methods in Molecular Biology, 2020, 2106, 225-239.	0.4	16
158	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
159	mi-DS: Multiple-Instance Learning Algorithm. IEEE Transactions on Cybernetics, 2013, 43, 143-154.	6.2	15
160	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
161	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
162	NetEPD: A network-based essential protein discovery platform. Tsinghua Science and Technology, 2020, 25, 542-552.	4.1	15

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163	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
164	Hybrid Inductive Machine Learning: An Overview of CLIP Algorithms. Studies in Fuzziness and Soft Computing, 2002, , 276-322.	0.6	15
165	Multi-label Associative Classification of Medical Documents from MEDLINE. , 0, , .		14
166	Sequence-Derived Markers of Drug Targets and Potentially Druggable Human Proteins. Frontiers in Genetics, 2019, 10, 1075.	1.1	14
167	Predicting Functions of Disordered Proteins with MoRFpred. Methods in Molecular Biology, 2019, 1851, 337-352.	0.4	14
168	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
169	Computational Prediction of Secondary and Supersecondary Structures. Methods in Molecular Biology, 2012, 932, 63-86.	0.4	13
170	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
171	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
172	PSIONplus: Accurate Sequence-Based Predictor of Ion Channels and Their Types. PLoS ONE, 2016, 11, e0152964.	1.1	12
173	Sequence based prediction of relative solvent accessibility using two-stage support vector regression with confidence values. Journal of Biomedical Science and Engineering, 2008, 01, 1-9.	0.2	12
174	Prediction of Secondary Protein Structure Content from Primary Sequence Alone â€" A Feature Selection Based Approach. Lecture Notes in Computer Science, 2005, , 334-345.	1.0	11
175	Classification of Cell Membrane Proteins. , 2007, , .		11
176	Comprehensively designed consensus of standalone secondary structure predictors improvesQ3by over 3%. Journal of Biomolecular Structure and Dynamics, 2014, 32, 36-51.	2.0	11
177	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
178	Computational Prediction of Secondary and Supersecondary Structures from Protein Sequences. Methods in Molecular Biology, 2019, 1958, 73-100.	0.4	11
179	DNAgenie: accurate prediction of DNA-type-specific binding residues in protein sequences. Briefings in Bioinformatics, 2021, 22, .	3.2	11
180	Sequence-Based Protein Crystallization Propensity Prediction for Structural Genomics: Review and Comparative Analysis. Natural Science, 2009, 01, 93-106.	0.2	11

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181	Compositional Bias of Intrinsically Disordered Proteins and Regions and Their Predictions. Biomolecules, 2022, 12, 888.	1.8	11
182	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
183	Computational Prediction of Protein Secondary Structure from Sequence. Current Protocols in Protein Science, 2016, 86, 2.3.1-2.3.10.	2.8	10
184	DISOselect: Disorder predictor selection at the protein level. Protein Science, 2020, 29, 184-200.	3.1	10
185	Survey of Similarity-based Prediction of Drug-protein Interactions.. Current Medicinal Chemistry, 2018, 25, .	1.2	10
186	Sequence-Based Methods for Real Value Predictions of Protein Structure. Current Bioinformatics, 2008, 3, 183-196.	0.7	10
187	<title>Ensemble of classifiers to improve accuracy of the CLIP4 machine-learning algorithm</title>. , 2002, 4731, 22.		8
188	Prediction of Three Dimensional Structure of Calmodulin. Protein Journal, 2006, 25, 57-70.	0.7	8
189	Machine learning in the life sciences. IEEE Engineering in Medicine and Biology Magazine, 2007, 26, 14-16.	1.1	8
190	Neural Networks in Bioinformatics. , 2012, , 565-583.		8
191	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
192	Editorial [Hot Topic: Machine Learning Models in Protein Bioinformatics (Guest Editors: Lukasz) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30	0.7	7
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