

# Lukasz A Kurgan

## List of Publications by Year in descending order

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240  
papers

11,990  
citations

22153

59  
h-index

36028

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. <i>Nucleic Acids Research</i> , 2012, 41, D508-D516.	14.5	570
2	Genetic learning of fuzzy cognitive maps. <i>Fuzzy Sets and Systems</i> , 2005, 153, 371-401.	2.7	416
3	CAIM discretization algorithm. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2004, 16, 145-153.	5.7	352
4	Exceptionally abundant exceptions: comprehensive characterization of intrinsic disorder in all domains of life. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 137-151.	5.4	314
5	MoRFPred, a computational tool for sequence-based prediction and characterization of short disorder-to-order transitioning binding regions in proteins. <i>Bioinformatics</i> , 2012, 28, i75-i83.	4.1	311
6	A survey of Knowledge Discovery and Data Mining process models. <i>Knowledge Engineering Review</i> , 2006, 21, 1-24.	2.6	293
7	Impact of imputation of missing values on classification error for discrete data. <i>Pattern Recognition</i> , 2008, 41, 3692-3705.	8.1	267
8	Knowledge discovery approach to automated cardiac SPECT diagnosis. <i>Artificial Intelligence in Medicine</i> , 2001, 23, 149-169.	6.5	209
9	SPINE X: Improving protein secondary structure prediction by multistep learning coupled with prediction of solvent accessible surface area and backbone torsion angles. <i>Journal of Computational Chemistry</i> , 2012, 33, 259-267.	3.3	209
10	Structural Disorder in Viral Proteins. <i>Chemical Reviews</i> , 2014, 114, 6880-6911.	47.7	181
11	Comprehensive Comparative Assessment of In-Silico Predictors of Disordered Regions. <i>Current Protein and Peptide Science</i> , 2012, 13, 6-18.	1.4	170
12	A Novel Framework for Imputation of Missing Values in Databases. <i>IEEE Transactions on Systems, Man and Cybernetics, Part A: Systems and Humans</i> , 2007, 37, 692-709.	2.9	169
13	Classifier ensembles for protein structural class prediction with varying homology. <i>Biochemical and Biophysical Research Communications</i> , 2006, 348, 981-988.	2.1	168
14	Numerical and Linguistic Prediction of Time Series With the Use of Fuzzy Cognitive Maps. <i>IEEE Transactions on Fuzzy Systems</i> , 2008, 16, 61-72.	9.8	158
15	Improved sequence-based prediction of disordered regions with multilayer fusion of multiple information sources. <i>Bioinformatics</i> , 2010, 26, i489-i496.	4.1	154
16	Comprehensive review of methods for prediction of intrinsic disorder and its molecular functions. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3069-3090.	5.4	153
17	Prediction of structural classes for protein sequences and domains—Impact of prediction algorithms, sequence representation and homology, and test procedures on accuracy. <i>Pattern Recognition</i> , 2006, 39, 2323-2343.	8.1	151
18	Prediction of protein structural class using novel evolutionary collocation-based sequence representation. <i>Journal of Computational Chemistry</i> , 2008, 29, 1596-1604.	3.3	148

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19	Accurate prediction of disorder in protein chains with a comprehensive and empirically designed consensus. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 448-464.	3.5	146
20	Molecular recognition features (MoRFs) in three domains of life. <i>Molecular BioSystems</i> , 2016, 12, 697-710.	2.9	141
21	fDPnn: Accurate intrinsic disorder prediction with putative propensities of disorder functions. <i>Nature Communications</i> , 2021, 12, 4438.	12.8	141
22	High-throughput prediction of RNA, DNA and protein binding regions mediated by intrinsic disorder. <i>Nucleic Acids Research</i> , 2015, 43, e121-e121.	14.5	131
23	SCPPRED: Accurate prediction of protein structural class for sequences of twilight-zone similarity with predicting sequences. <i>BMC Bioinformatics</i> , 2008, 9, 226.	2.6	129
24	iLearnPlus: a comprehensive and automated machine-learning platform for nucleic acid and protein sequence analysis, prediction and visualization. <i>Nucleic Acids Research</i> , 2021, 49, e60-e60.	14.5	124
25	A creature with a hundred waggly tails: intrinsically disordered proteins in the ribosome. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 1477-1504.	5.4	119
26	DRNAPred, fast sequence-based method that accurately predicts and discriminates DNA- and RNA-binding residues. <i>Nucleic Acids Research</i> , 2017, 45, gkx059.	14.5	114
27	Disordered Proteinaceous Machines. <i>Chemical Reviews</i> , 2014, 114, 6806-6843.	47.7	109
28	PFRES: protein fold classification by using evolutionary information and predicted secondary structure. <i>Bioinformatics</i> , 2007, 23, 2843-2850.	4.1	108
29	Prediction and analysis of nucleotide-binding residues using sequence and sequence-derived structural descriptors. <i>Bioinformatics</i> , 2012, 28, 331-341.	4.1	106
30	Genome-scale prediction of proteins with long intrinsically disordered regions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 145-158.	2.6	104
31	Prediction of protein crystallization using collocation of amino acid pairs. <i>Biochemical and Biophysical Research Communications</i> , 2007, 355, 764-769.	2.1	102
32	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. <i>Bioinformatics</i> , 2020, 36, 1057-1065.	4.1	102
33	Prediction of flexible/rigid regions from protein sequences using k-spaced amino acid pairs. <i>BMC Structural Biology</i> , 2007, 7, 25.	2.3	100
34	More than just tails: intrinsic disorder in histone proteins. <i>Molecular BioSystems</i> , 2012, 8, 1886.	2.9	99
35	Protein intrinsic disorder as a flexible armor and a weapon of HIV-1. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 1211-1259.	5.4	94
36	Compartmentalization and Functionality of Nuclear Disorder: Intrinsic Disorder and Protein-Protein Interactions in Intra-Nuclear Compartments. <i>International Journal of Molecular Sciences</i> , 2016, 17, 24.	4.1	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.	3.6	92
39	Disordered nucleome: Abundance of intrinsic disorder in the DNA- and RNA-binding proteins in 1121 species from Eukaryota, Bacteria and Archaea. Proteomics, 2016, 16, 1486-1498.	2.2	92
40	SCRIBER: accurate and partner type-specific prediction of protein-binding residues from proteins sequences. Bioinformatics, 2019, 35, i343-i353.	4.1	90
41	A divide and conquer method for learning large Fuzzy Cognitive Maps. Fuzzy Sets and Systems, 2010, 161, 2515-2532.	2.7	89
42	A comprehensive comparative review of sequence-based predictors of DNA- and RNA-binding residues. Briefings in Bioinformatics, 2016, 17, 88-105.	6.5	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.	2.6	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.	4.1	85
46	Prediction of protein structural class for the twilight zone sequences. Biochemical and Biophysical Research Communications, 2007, 357, 453-460.	2.1	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.	6.5	84
48	BEST: Improved Prediction of B-Cell Epitopes from Antigen Sequences. PLoS ONE, 2012, 7, e40104.	2.5	79
49	Review and comparative assessment of sequence-based predictors of protein-binding residues. Briefings in Bioinformatics, 2018, 19, 821-837.	6.5	78
50	On the relation between residue flexibility and local solvent accessibility in proteins. Proteins: Structure, Function and Bioinformatics, 2009, 76, 617-636.	2.6	76
51	Accurate sequence-based prediction of catalytic residues. Bioinformatics, 2008, 24, 2329-2338.	4.1	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.	4.1	72
54	DeepFunc: A Deep Learning Framework for Accurate Prediction of Protein Functions from Protein Sequences and Interactions. Proteomics, 2019, 19, e1900019.	2.2	72

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55	Resilience of death: intrinsic disorder in proteins involved in the programmed cell death. <i>Cell Death and Differentiation</i> , 2013, 20, 1257-1267.	11.2	71
56	Comprehensive overview and assessment of computational prediction of microRNA targets in animals. <i>Briefings in Bioinformatics</i> , 2015, 16, 780-794.	6.5	71
57	CRYSTALP2: sequence-based protein crystallization propensity prediction. <i>BMC Structural Biology</i> , 2009, 9, 50.	2.3	70
58	Sequence-based prediction of protein crystallization, purification and production propensity. <i>Bioinformatics</i> , 2011, 27, i24-i33.	4.1	69
59	Prediction of integral membrane protein type by collocated hydrophobic amino acid pairs. <i>Journal of Computational Chemistry</i> , 2009, 30, 163-172.	3.3	66
60	Learning of Fuzzy Cognitive Maps Using Density Estimate. <i>IEEE Transactions on Systems, Man, and Cybernetics</i> , 2012, 42, 900-912.	5.0	65
61	Attention convolutional neural network for accurate segmentation and quantification of lesions in ischemic stroke disease. <i>Medical Image Analysis</i> , 2020, 65, 101791.	11.6	63
62	A Critical Comparative Assessment of Predictions of Protein-Binding Sites for Biologically Relevant Organic Compounds. <i>Structure</i> , 2011, 19, 613-621.	3.3	59
63	Prediction of Disordered RNA, DNA, and Protein Binding Regions Using DisoRDPbind. <i>Methods in Molecular Biology</i> , 2017, 1484, 187-203.	0.9	59
64	Unstructural biology of the dengue virus proteins. <i>FEBS Journal</i> , 2015, 282, 3368-3394.	4.7	58
65	ATPsite: sequence-based prediction of ATP-binding residues. <i>Proteome Science</i> , 2011, 9, S4.	1.7	57
66	The intrinsic disorder status of the human hepatitis C virus proteome. <i>Molecular BioSystems</i> , 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. <i>PLoS ONE</i> , 2009, 4, e4473.	2.5	55
69	The Roles of $\beta$ -Tubulin Mutations and Isozyme Expression in Acquired Drug Resistance. <i>Cancer Informatics</i> , 2007, 3, 117693510700300.	1.9	54
70	Secondary structure-based assignment of the protein structural classes. <i>Amino Acids</i> , 2008, 35, 551-564.	2.7	54
71	Critical assessment of high-throughput standalone methods for secondary structure prediction. <i>Briefings in Bioinformatics</i> , 2011, 12, 672-688.	6.5	53
72	Untapped Potential of Disordered Proteins in Current Druggable Human Proteome. <i>Current Drug Targets</i> , 2016, 17, 1198-1205.	2.1	52

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73	Analysis and Prediction of RNA-Binding Residues Using Sequence, Evolutionary Conservation, and Predicted Secondary Structure and Solvent Accessibility. <i>Current Protein and Peptide Science</i> , 2010, 11, 609-628.	1.4	50
74	Sequence Similarity Searching. <i>Current Protocols in Protein Science</i> , 2019, 95, e71.	2.8	50
75	Computational Prediction of MoRFs, Short Disorder-to-order Transitioning Protein Binding Regions. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 454-462.	4.1	50
76	RAPID: Fast and accurate sequence-based prediction of intrinsic disorder content on proteomic scale. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1671-1680.	2.3	49
77	Computational Prediction of Intrinsic Disorder in Proteins. <i>Current Protocols in Protein Science</i> , 2017, 88, 2.16.1-2.16.14.	2.8	49
78	DEPICTER: Intrinsic Disorder and Disorder Function Prediction Server. <i>Journal of Molecular Biology</i> , 2020, 432, 3379-3387.	4.2	46
79	DescribePROT: database of amino acid-level protein structure and function predictions. <i>Nucleic Acids Research</i> , 2021, 49, D298-D308.	14.5	46
80	Discovery of factors influencing patent value based on machine learning in patents in the field of nanotechnology. <i>Scientometrics</i> , 2010, 82, 217-241.	3.0	45
81	Expert-Based and Computational Methods for Developing Fuzzy Cognitive Maps. <i>Studies in Fuzziness and Soft Computing</i> , 2010, , 23-41.	0.8	45
82	In-silico prediction of disorder content using hybrid sequence representation. <i>BMC Bioinformatics</i> , 2011, 12, 245.	2.6	45
83	Novel scales based on hydrophobicity indices for secondary protein structure. <i>Journal of Theoretical Biology</i> , 2007, 248, 354-366.	1.7	42
84	In various protein complexes, disordered protomers have large perâ€residue surface areas and area of proteinâ€™s DNAâ€™and RNAâ€™binding interfaces. <i>FEBS Letters</i> , 2015, 589, 2561-2569.	2.8	42
85	Prediction of beta-turns at over 80% accuracy based on an ensemble of predicted secondary structures and multiple alignments. <i>BMC Bioinformatics</i> , 2008, 9, 430.	2.6	41
86	Monocytes from patients with osteoarthritis display increased osteoclastogenesis and bone resorption: The In Vitro Osteoclast Differentiation in Arthritis study. <i>Arthritis and Rheumatism</i> , 2013, 65, 148-158.	6.7	41
87	Stochastic machines as a colocalization mechanism for scaffold protein function. <i>FEBS Letters</i> , 2013, 587, 1587-1591.	2.8	40
88	CLIP4: Hybrid inductive machine learning algorithm that generates inequality rules. <i>Information Sciences</i> , 2004, 163, 37-83.	6.9	39
89	Human structural proteome-wide characterization of Cyclosporine A targets. <i>Bioinformatics</i> , 2014, 30, 3561-3566.	4.1	38
90	PDID: database of molecular-level putative proteinâ€™drug interactions in the structural human proteome. <i>Bioinformatics</i> , 2016, 32, 579-586.	4.1	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.	5.0	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.	2.9	37
93	Prediction of Intrinsic Disorder in Proteins Using MFDp2. Methods in Molecular Biology, 2014, 1137, 147-162.	0.9	37
94	Accuracy of protein-level disorder predictions. Briefings in Bioinformatics, 2020, 21, 1509-1522.	6.5	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.	2.6	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.	3.3	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.	2.6	32
101	Recognition of Partially Occluded and Rotated Images With a Network of Spiking Neurons. IEEE Transactions on Neural Networks, 2010, 21, 1697-1709.	4.2	32
102	Survey of Similarity-Based Prediction of Drug-Protein Interactions. Current Medicinal Chemistry, 2020, 27, 5856-5886.	2.4	32
103	Learning fuzzy cognitive maps with required precision using genetic algorithm approach. Electronics Letters, 2004, 40, 1519.	1.0	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.	4.1	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.	3.4	29
107	Meta prediction of protein crystallization propensity. Biochemical and Biophysical Research Communications, 2009, 390, 10-15.	2.1	29
108	High-throughput prediction of disordered moonlighting regions in protein sequences. Proteins: Structure, Function and Bioinformatics, 2018, 86, 1097-1110.	2.6	29

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109	Structural Protein Descriptors in 1-Dimension and their Sequence-Based Predictions. <i>Current Protein and Peptide Science</i> , 2011, 12, 470-489.	1.4	28
110	DeepDISOBind: accurate prediction of RNA-, DNA- and protein-binding intrinsically disordered residues with deep multi-task learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	28
111	Highly accurate and consistent method for prediction of helix and strand content from primary protein sequences. <i>Artificial Intelligence in Medicine</i> , 2005, 35, 19-35.	6.5	27
112	Autophagy-related intrinsically disordered proteins in intra-nuclear compartments. <i>Molecular BioSystems</i> , 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. <i>Proteomics</i> , 2018, 18, 1800243.	2.2	27
114	Computational prediction of functions of intrinsically disordered regions. <i>Progress in Molecular Biology and Translational Science</i> , 2019, 166, 341-369.	1.7	27
115	Accurate prediction of protein folding rates from sequence and sequence-derived residue flexibility and solvent accessibility. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, NA-NA.	2.6	25
116	Genes encoding intrinsic disorder in Eukaryota have high GC content. <i>Intrinsically Disordered Proteins</i> , 2016, 4, e1262225.	1.9	25
117	Sequence-based Gaussian network model for protein dynamics. <i>Bioinformatics</i> , 2014, 30, 497-505.	4.1	24
118	Comparative Assessment of Intrinsic Disorder Predictions with a Focus on Protein and Nucleic Acid-Binding Proteins. <i>Biomolecules</i> , 2020, 10, 1636.	4.0	24
119	Computational Prediction of B Cell Epitopes from Antigen Sequences. <i>Methods in Molecular Biology</i> , 2014, 1184, 197-215.	0.9	24
120	Deep learning in prediction of intrinsic disorder in proteins. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1286-1294.	4.1	24
121	<i>FeatureOmega</i> : an integrative platform for engineering, visualization and analysis of features from molecular sequences, structural and ligand data sets. <i>Nucleic Acids Research</i> , 2022, 50, W434-W447.	14.5	24
122	Systematic evaluation of machine learning methods for identifying human-pathogen protein-protein interactions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	23
123	Intrinsic Disorder in Human RNA-Binding Proteins. <i>Journal of Molecular Biology</i> , 2021, 433, 167229.	4.2	23
124	A New Synaptic Plasticity Rule for Networks of Spiking Neurons. <i>IEEE Transactions on Neural Networks</i> , 2006, 17, 94-105.	4.2	22
125	Analyzing the effects of protecting osmolytes on solute-water interactions by solvatochromic comparison method: II. Globular proteins. <i>RSC Advances</i> , 2015, 5, 59780-59791.	3.6	22
126	fDETECT webserver: fast predictor of propensity for protein production, purification, and crystallization. <i>BMC Bioinformatics</i> , 2017, 18, 580.	2.6	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.	6.5	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.	1.2	21
132	Discretization as the enabling technique for the Naïve Bayes and semi-Naïve Bayes-based classification. Knowledge Engineering Review, 2010, 25, 421-449.	2.6	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.	2.3	21
134	Quality assessment for the putative intrinsic disorder in proteins. Bioinformatics, 2019, 35, 1692-1700.	4.1	20
135	On the intrinsic disorder status of the major players in programmed cell death pathways. F1000Research, 2013, 2, 190.	1.6	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.	1.4	19
138	Finding Protein Targets for Small Biologically Relevant Ligands across Fold Space Using Inverse Ligand Binding Predictions. Structure, 2012, 20, 1815-1822.	3.3	19
139	CRYSpred: Accurate Sequence-Based Protein Crystallization Propensity Prediction Using Sequence-Derived Structural Characteristics. Protein and Peptide Letters, 2012, 19, 40-49.	0.9	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.	2.3	19
141	In Silico Prediction and Validation of Novel RNA Binding Proteins and Residues in the Human Proteome. Proteomics, 2018, 18, e1800064.	2.2	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.	6.5	19
143	PROBselect: accurate prediction of protein-binding residues from proteins sequences via dynamic predictor selection. Bioinformatics, 2020, 36, i735-i744.	4.1	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.	0.8	18
146	Determination of protein folding kinetic types using sequence and predicted secondary structure and solvent accessibility. Amino Acids, 2012, 42, 271-283.	2.7	18
147	Surveying over 100 predictors of intrinsic disorder in proteins. Expert Review of Proteomics, 2021, 18, 1019-1029.	3.0	18
148	A comment on "Prediction of protein structural classes by a new measure of information discrepancy". Computational Biology and Chemistry, 2006, 30, 393-394.	2.3	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.	3.8	17
152	Intrinsic Disorder in the BK Channel and Its Interactome. PLoS ONE, 2014, 9, e94331.	2.5	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.	2.3	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.	3.3	16
155	Structural and functional analysis of "non-smelly" proteins. Cellular and Molecular Life Sciences, 2020, 77, 2423-2440.	5.4	16
156	Prediction of protein-binding residues: dichotomy of sequence-based methods developed using structured complexes versus disordered proteins. Bioinformatics, 2020, 36, 4729-4738.	4.1	16
157	Disordered RNA-Binding Region Prediction with DisoRDPbind. Methods in Molecular Biology, 2020, 2106, 225-239.	0.9	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.	2.4	15
159	mi-DS: Multiple-Instance Learning Algorithm. IEEE Transactions on Cybernetics, 2013, 43, 143-154.	9.5	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.	3.0	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, .	3.0	15
162	NetEPD: A network-based essential protein discovery platform. Tsinghua Science and Technology, 2020, 25, 542-552.	6.1	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.	5.4	15
164	Hybrid Inductive Machine Learning: An Overview of CLIP Algorithms. Studies in Fuzziness and Soft Computing, 2002, , 276-322.	0.8	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.	2.3	14
167	Predicting Functions of Disordered Proteins with MoRFPred. Methods in Molecular Biology, 2019, 1851, 337-352.	0.9	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.	2.7	13
169	Computational Prediction of Secondary and Supersecondary Structures. Methods in Molecular Biology, 2012, 932, 63-86.	0.9	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.	4.1	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.	2.6	12
172	PSIONplus: Accurate Sequence-Based Predictor of Ion Channels and Their Types. PLoS ONE, 2016, 11, e0152964.	2.5	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.	0.4	12
174	Prediction of Secondary Protein Structure Content from Primary Sequence Alone – A Feature Selection Based Approach. Lecture Notes in Computer Science, 2005, , 334-345.	1.3	11
175	Classification of Cell Membrane Proteins. , 2007, , .		11
176	Comprehensively designed consensus of standalone secondary structure predictors improves Q3 by over 3%. Journal of Biomolecular Structure and Dynamics, 2014, 32, 36-51.	3.5	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.	3.3	11
178	Computational Prediction of Secondary and Supersecondary Structures from Protein Sequences. Methods in Molecular Biology, 2019, 1958, 73-100.	0.9	11
179	DNAgenie: accurate prediction of DNA-type-specific binding residues in protein sequences. Briefings in Bioinformatics, 2021, 22, .	6.5	11
180	Sequence-Based Protein Crystallization Propensity Prediction for Structural Genomics: Review and Comparative Analysis. Natural Science, 2009, 01, 93-106.	0.4	11

#	ARTICLE	IF	CITATIONS
181	Compositional Bias of Intrinsically Disordered Proteins and Regions and Their Predictions. <i>Biomolecules</i> , 2022, 12, 888.	4.0	11
182	Improved prediction of residue flexibility by embedding optimized amino acid grouping into RSA-based linear models. <i>Amino Acids</i> , 2014, 46, 2665-2680.	2.7	10
183	Computational Prediction of Protein Secondary Structure from Sequence. <i>Current Protocols in Protein Science</i> , 2016, 86, 2.3.1-2.3.10.	2.8	10
184	DISOselect: Disorder predictor selection at the protein level. <i>Protein Science</i> , 2020, 29, 184-200.	7.6	10
185	Survey of Similarity-based Prediction of Drug-protein Interactions.. <i>Current Medicinal Chemistry</i> , 2018, 25, .	2.4	10
186	Sequence-Based Methods for Real Value Predictions of Protein Structure. <i>Current Bioinformatics</i> , 2008, 3, 183-196.	1.5	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. <i>Protein Journal</i> , 2006, 25, 57-70.	1.6	8
189	Machine learning in the life sciences. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2007, 26, 14-16.	0.8	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. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 149-160.	5.4	8
192	Editorial [Hot Topic: Machine Learning Models in Protein Bioinformatics (Guest Editors: Lukasz Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30	1.4	7
193	PSIONplum Server for Accurate Multi-Label Prediction of Ion Channels and Their Types. <i>Biomolecules</i> , 2020, 10, 876.	4.0	7
194	Survey of Predictors of Propensity for Protein Production and Crystallization with Application to Predict Resolution of Crystal Structures. <i>Current Protein and Peptide Science</i> , 2017, 19, 200-210.	1.4	7
195	Quantitative Analysis of the Conservation of the Tertiary Structure of Protein Segments. <i>Protein Journal</i> , 2006, 25, 301-315.	1.6	6
196	Prediction of Ion Channels and their Types from Protein Sequences: Comprehensive Review and Comparative Assessment. <i>Current Drug Targets</i> , 2019, 20, 579-592.	2.1	6
197	OUP accepted manuscript. <i>Bioinformatics</i> , 2020, 36, i754-i761.	4.1	6
198	Reducing complexity of rule based models via meta mining. , 0, , .		5

#	ARTICLE	IF	CITATIONS
199	IMPROVED SEQUENCE-BASED PREDICTION OF STRAND RESIDUES. Journal of Bioinformatics and Computational Biology, 2011, 09, 67-89.	0.8	5
200	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.	2.5	5
201	Sequence-Only Based Prediction of $\hat{\beta}^2$ -Turn Location and Type Using Collocation of Amino Acid Pairs. Open Bioinformatics Journal, 2008, 2, 37-49.	1.0	5
202	QUARTERplus: Accurate disorder predictions integrated with interpretable residue-level quality assessment scores. Computational and Structural Biotechnology Journal, 2021, 19, 2597-2606.	4.1	4
203	Unsupervised Learning: Association Rules. , 2007, , 289-306.		4
204	Exploratory Analysis of Quality Assessment of Putative Intrinsic Disorder in Proteins. Lecture Notes in Computer Science, 2017, , 722-732.	1.3	4
205	A comprehensive overview of sequence-based protein-binding residue predictions for structured and disordered regions. , 2020, , 33-58.		4
206	Computational Prediction of Intrinsic Disorder in Protein Sequences with the disCoP Meta-predictor. Methods in Molecular Biology, 2020, 2141, 21-35.	0.9	4
207	Sequence Representation and Prediction of Protein Secondary Structure for Structural Motifs in Twilight Zone Proteins. Protein Journal, 2006, 25, 463-474.	1.6	3
208	On the Relation Between the Predicted Secondary Structure and the Protein Size. Protein Journal, 2008, 27, 234-239.	1.6	3
209	Genome-wide analysis of thapsigargin-induced microRNAs and their targets in NIH3T3 cells. Genomics Data, 2014, 2, 325-327.	1.3	3
210	Systematic investigation of sequence and structural motifs that recognize ATP. Computational Biology and Chemistry, 2015, 56, 131-141.	2.3	3
211	Endoplasmic reticulum and the microRNA environment in the cardiovascular system. Canadian Journal of Physiology and Pharmacology, 2019, 97, 515-527.	1.4	3
212	The Methods and Tools for Intrinsic Disorder Prediction and their Application to Systems Medicine. , 2021, , 159-169.		3
213	XRRpred: accurate predictor of crystal structure quality from protein sequence. Bioinformatics, 2021, 37, 4366-4374.	4.1	3
214	Prediction of Intrinsic Disorder with Quality Assessment Using QUARTER. Methods in Molecular Biology, 2020, 2165, 83-101.	0.9	3
215	xGENIA: A comprehensive OWL ontology based on the GENIA corpus. Bioinformatics, 2007, 1, 360-362.	0.5	3
216	Impact of the Predicted Protein Structural Content on Prediction of Structural Classes for the Twilight Zone Proteins. , 2006, , .		2

#	ARTICLE	IF	CITATIONS
217	Searching for Factors that Distinguish Disease-Prone and Disease-Resistant Prions via Sequence Analysis. <i>Bioinformatics and Biology Insights</i> , 2008, 2, BBI.S550.	2.0	2
218	PDID: Database of Experimental and Putative Drug Targets in Human Proteome. , 2019, , 827-847.		2
219	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. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1289-1299.	2.6	2
220	The WWW Based Data Mining Toolbox Architecture. , 2003, , 855-860.		2
221	Supervised Learning: Decision Trees, Rule Algorithms, and Their Hybrids. , 0, , 381-417.		2
222	Prediction of Protein Structural Class Using PSI-BLAST Profile Based Collocation of Amino Acid Pairs. , 2007, , .		1
223	Text Mining. , 2007, , 453-465.		1
224	Improved machine learning method for analysis of gas phase chemistry of peptides. <i>BMC Bioinformatics</i> , 2008, 9, 515.	2.6	1
225	Accurate Sequence-Based Prediction of Deleterious nsSNPs with Multiple Sequence Profiles and Putative Binding Residues. <i>Biomolecules</i> , 2021, 11, 1337.	4.0	1
226	Machine Learning Algorithms Inspired by the Work of Ryszard Spencer Michalski. <i>Studies in Computational Intelligence</i> , 2010, , 49-74.	0.9	1
227	Consensus-Based Prediction of RNA and DNA Binding Residues from Protein Sequences. <i>Lecture Notes in Computer Science</i> , 2015, , 501-511.	1.3	1
228	Disordered Function Conjunction: On the in-silico function annotation of intrinsically disordered regions. , 2019, , .		1
229	Complementarity of the residue-level protein function and structure predictions in human proteins. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2223-2234.	4.1	1
230	Prediction of the Number of Helices for the Twilight Zone Proteins. , 2006, , .		0
231	Improved Prediction of Relative Solvent Accessibility Using Two-stage Support Vector Regression. , 2007, , .		0
232	Society News - membership development data. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2007, 26, 8-9.	0.8	0
233	Accurate prediction of ATP-binding residues using sequence and sequence-derived structural descriptors. , 2010, , .		0
234	P125Endoplasmic reticulum stress responses to disrupted endoplasmic reticulum ca2+ homeostasis. <i>Cardiovascular Research</i> , 2014, 103, S22.1-S22.	3.8	0

#	ARTICLE	IF	CITATIONS
235	iFC2: an integrated web-server for the improved prediction of protein fold type, structural class, and secondary structure content. Protocol Exchange, 0, , .	0.3	0
236	On the Importance of Computational Biology and Bioinformatics to the Origins and Rapid Progression of the Intrinsically Disordered Proteins Field. , 2019, , .		0
237	Supervised Learning: Neural Networks. , 0, , 419-451.		0
238	Assessment of Data Models. , 0, , 469-486.		0
239	Databases, Data Warehouses, and OLAP. , 0, , 95-131.		0
240	Discretization Methods. , 0, , 235-254.		0