Predrag Radivojac

List of Publications by Year
in descending order

117	13,795	70961	25716
papers	citations	41	108
		h-index	g-index

125	125	125	19771
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants. American Journal of Human Genetics, 2016, 99, 877-885.	2.6	1,555
2	The importance of intrinsic disorder for protein phosphorylation. Nucleic Acids Research, 2004, 32, 1037-1049.	6.5	1,230
3	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
4	Length-dependent prediction of protein intrinsic disorder. BMC Bioinformatics, 2006, 7, 208.	1.2	780
5	Automated inference of molecular mechanisms of disease from amino acid substitutions. Bioinformatics, 2009, 25, 2744-2750.	1.8	691
6	Analysis of Molecular Recognition Features (MoRFs). Journal of Molecular Biology, 2006, 362, 1043-1059.	2.0	672
7	Intrinsic Disorder and Functional Proteomics. Biophysical Journal, 2007, 92, 1439-1456.	0.2	643
8	Identification, analysis, and prediction of protein ubiquitination sites. Proteins: Structure, Function and Bioinformatics, 2010, 78, 365-380.	1.5	513
9	Intrinsic Disorder Is a Common Feature of Hub Proteins from Four Eukaryotic Interactomes. PLoS Computational Biology, 2006, 2, e100.	1.5	512
10	Characterization of Molecular Recognition Features, MoRFs, and Their Binding Partners. Journal of Proteome Research, 2007, 6, 2351-2366.	1.8	433
11	OPTIMIZING LONG INTRINSIC DISORDER PREDICTORS WITH PROTEIN EVOLUTIONARY INFORMATION. Journal of Bioinformatics and Computational Biology, 2005, 03, 35-60.	0.3	428
12	Alternative splicing in concert with protein intrinsic disorder enables increased functional diversity in multicellular organisms. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8390-8395.	3.3	428
13	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
14	Protein flexibility and intrinsic disorder. Protein Science, 2004, 13, 71-80.	3.1	306
15	Inferring the molecular and phenotypic impact of amino acid variants with MutPred2. Nature Communications, 2020, 11, 5918.	5.8	305
16	The structural and functional signatures of proteins that undergo multiple events of post‐translational modification. Protein Science, 2014, 23, 1077-1093.	3.1	287
17	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	3.8	261
18	Testing the Ortholog Conjecture with Comparative Functional Genomic Data from Mammals. PLoS Computational Biology, 2011, 7, e1002073.	1.5	185

#	Article	IF	Citations
19	Allosteric post-translational modification codes. Trends in Biochemical Sciences, 2012, 37, 447-455.	3.7	172
20	Improved amino acid flexibility parameters. Protein Science, 2003, 12, 1060-1072.	3.1	158
21	An integrated approach to inferring gene–disease associations in humans. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1030-1037.	1.5	153
22	MutPred Splice: machine learning-based prediction of exonic variants that disrupt splicing. Genome Biology, 2014, 15, R19.	13.9	135
23	Intrinsic disorder in pathogenic and non-pathogenic microbes: discovering and analyzing the unfoldomes of early-branching eukaryotes. Molecular BioSystems, 2008, 4, 328.	2.9	127
24	Analysis of protein function and its prediction from amino acid sequence. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2086-2096.	1.5	124
25	Comparing Phylogeny and the Predicted Pathogenicity of Protein Variations Reveals Equal Purifying Selection across the Global Human mtDNA Diversity. American Journal of Human Genetics, 2011, 88, 433-439.	2.6	103
26	Bioinformatics Curriculum Guidelines: Toward a Definition of Core Competencies. PLoS Computational Biology, 2014, 10, e1003496.	1.5	102
27	Information-theoretic evaluation of predicted ontological annotations. Bioinformatics, 2013, 29, i53-i61.	1.8	97
28	Gain and loss of phosphorylation sites in human cancer. Bioinformatics, 2008, 24, i241-i247.	1.8	94
29	Reproductive Longevity Predicts Mutation Rates in Primates. Current Biology, 2018, 28, 3193-3197.e5.	1.8	94
30	Calmodulin signaling: Analysis and prediction of a disorder-dependent molecular recognition. Proteins: Structure, Function and Bioinformatics, 2006, 63, 398-410.	1.5	93
31	Calibration of Multiple In Silico Tools for Predicting Pathogenicity of Mismatch Repair Gene Missense Substitutions. Human Mutation, 2013, 34, 255-265.	1.1	80
32	Classification and knowledge discovery in protein databases. Journal of Biomedical Informatics, 2004, 37, 224-239.	2.5	75
33	A Bayesian Approach to Protein Inference Problem in Shotgun Proteomics. Journal of Computational Biology, 2009, 16, 1183-1193.	0.8	72
34	Quantitative Measurement of Phosphoproteome Response to Osmotic Stress in Arabidopsis Based on Library-Assisted eXtracted Ion Chromatogram (LAXIC). Molecular and Cellular Proteomics, 2013, 12, 2354-2369.	2.5	62
35	Evaluation of features for catalytic residue prediction in novel folds. Protein Science, 2006, 16, 216-226.	3.1	61
36	In silico functional profiling of human disease-associated and polymorphic amino acid substitutions. Human Mutation, 2010, 31, 335-346.	1.1	57

#	Article	IF	Citations
37	LOSS OF POST-TRANSLATIONAL MODIFICATION SITES IN DISEASE. , 2009, , 337-347.		56
38	When loss-of-function is loss of function: assessing mutational signatures and impact of loss-of-function genetic variants. Bioinformatics, 2017, 33, i389-i398.	1.8	53
39	Ultra High-Dimensional Nonlinear Feature Selection for Big Biological Data. IEEE Transactions on Knowledge and Data Engineering, 2018, 30, 1352-1365.	4.0	48
40	Paternal age in rhesus macaques is positively associated with germline mutation accumulation but not with measures of offspring sociability. Genome Research, 2020, 30, 826-834.	2.4	48
41	Fast and accurate identification of semi-tryptic peptides in shotgun proteomics. Bioinformatics, 2008, 24, 102-109.	1.8	47
42	Influence of Sequence Changes and Environment on Intrinsically Disordered Proteins. PLoS Computational Biology, 2009, 5, e1000497.	1.5	47
43	The ortholog conjecture revisited: the value of orthologs and paralogs in function prediction. Bioinformatics, 2020, 36, i219-i226.	1.8	47
44	On the Accuracy and Limits of Peptide Fragmentation Spectrum Prediction. Analytical Chemistry, 2011, 83, 790-796.	3.2	45
45	Graphlet Kernels for Prediction of Functional Residues in Protein Structures. Journal of Computational Biology, 2010, 17, 55-72.	0.8	44
46	Computational approaches to protein inference in shotgun proteomics. BMC Bioinformatics, 2012, 13, S4.	1.2	44
47	The impact of incomplete knowledge on the evaluation of protein function prediction: a structured-output learning perspective. Bioinformatics, 2014, 30, i609-i616.	1.8	43
48	Protein function in precision medicine: deep understanding with machine learning. FEBS Letters, 2016, 590, 2327-2341.	1.3	43
49	The Importance of Peptide Detectability for Protein Identification, Quantification, and Experiment Design in MS/MS Proteomics. Journal of Proteome Research, 2010, 9, 6288-6297.	1.8	41
50	Missense variant pathogenicity predictors generalize well across a range of function€specific prediction challenges. Human Mutation, 2017, 38, 1092-1108.	1.1	39
51	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	1.1	39
52	Evaluating Purifying Selection in the Mitochondrial DNA of Various Mammalian Species. PLoS ONE, 2013, 8, e58993.	1.1	39
53	Prediction of Intrinsic Disorder and Its Use in Functional Proteomics. Methods in Molecular Biology, 2007, 408, 69-92.	0.4	37
54	MutDB: update on development of tools for the biochemical analysis of genetic variation. Nucleic Acids Research, 2007, 36, D815-D819.	6.5	34

#	ARTICLE	IF	CITATIONS
55	Pathogenicity and functional impact of non-frameshifting insertion/deletion variation in the human genome. PLoS Computational Biology, 2019, 15, e1007112.	1.5	34
56	HIP2: An online database of human plasma proteins from healthy individuals. BMC Medical Genomics, 2008, 1, 12.	0.7	28
57	Examining the Influence of Phosphorylation on Peptide Ion Structure by Ion Mobility Spectrometry-Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2016, 27, 786-794.	1.2	28
58	Prediction of boundaries between intrinsically ordered and disordered protein regions. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2003, , 216-27.	0.7	27
59	Target site specificity and in vivo complexity of the mammalian arginylome. Scientific Reports, 2018, 8, 16177.	1.6	25
60	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.5	24
61	Computational Methods for Identification of Functional Residues in Protein Structures. Current Protein and Peptide Science, 2011, 12, 456-469.	0.7	24
62	Prediction of functional regulatory SNPs in monogenic and complex disease. Human Mutation, 2011, 32, 1183-1190.	1.1	21
63	PREDICTION OF BOUNDARIES BETWEEN INTRINSICALLY ORDERED AND DISORDERED PROTEIN REGIONS. , 2002, , .		20
64	Assessment of blind predictions of the clinical significance of <i>BRCA1</i> and <i>BRCA2</i> variants. Human Mutation, 2019, 40, 1546-1556.	1.1	19
65	Community-Wide Evaluation of Computational Function Prediction. Methods in Molecular Biology, 2017, 1446, 133-146.	0.4	17
66	Combinatorial Libraries of Synthetic Peptides as a Model for Shotgun Proteomics. Analytical Chemistry, 2010, 82, 6559-6568.	3.2	16
67	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	1.1	16
68	The Loss and Gain of Functional Amino Acid Residues Is a Common Mechanism Causing Human Inherited Disease. PLoS Computational Biology, 2016, 12, e1005091.	1.5	16
69	XLSearch: a Probabilistic Database Search Algorithm for Identifying Cross-Linked Peptides. Journal of Proteome Research, 2016, 15, 1830-1841.	1.8	15
70	Physicochemical sequence characteristics that influence <i>S</i>-palmitoylation propensity. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2337-2350.	2.0	15
71	New<i>Drosophila</i>Long-Term Memory Genes Revealed by Assessing Computational Function Prediction Methods. G3: Genes, Genomes, Genetics, 2019, 9, 251-267.	0.8	15
72	An Integrated Regulatory Network Reveals Pervasive Cross-Regulation among Transcription and Splicing Factors. PLoS Computational Biology, 2012, 8, e1002603.	1.5	14

#	Article	IF	Citations
73	Penultimate Proline in Neuropeptides. Analytical Chemistry, 2015, 87, 8466-8472.	3.2	14
74	Intrinsic size parameters for palmitoylated and carboxyamidomethylated peptides. International Journal of Mass Spectrometry, 2014, 368, 6-14.	0.7	13
75	Regulatory Single-Nucleotide Variant Predictor Increases Predictive Performance of Functional Regulatory Variants. Human Mutation, 2016, 37, 1137-1143.	1.1	13
76	Improving sequence alignments for intrinsically disordered proteins. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2002, , 589-600.	0.7	13
77	Unraveling the nature of the segmentation clock: Intrinsic disorder of clock proteins and their interaction map. Computational Biology and Chemistry, 2006, 30, 241-248.	1.1	12
78	On the Split Personality of Penultimate Proline. Journal of the American Society for Mass Spectrometry, 2015, 26, 444-452.	1.2	12
79	IMPROVING SEQUENCE ALIGNMENTS FOR INTRINSICALLY DISORDERED PROTEINS. , 2001, , .		12
80	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGIâ€5 intellectual disability challenge. Human Mutation, 2019, 40, 1330-1345.	1.1	11
81	Generalized graphlet kernels for probabilistic inference in sparse graphs. Network Science, 2014, 2, 254-276.	0.8	10
82	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. Human Mutation, 2019, 40, 1373-1391.	1.1	10
83	Assessment of predicted enzymatic activity of Î±â€‹<i>N</i> â€‹acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	1.1	10
84	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	1.1	10
85	Extending the coverage of spectral libraries: A neighbor-based approach to predicting intensities of peptide fragmentation spectra. Proteomics, 2013, 13, 756-765.	1.3	9
86	Ten Simple Rules for a Community Computational Challenge. PLoS Computational Biology, 2015, 11, e1004150.	1.5	9
87	Classification in biological networks with hypergraphlet kernels. Bioinformatics, 2021, 37, 1000-1007.	1.8	9
88	ISCB Computational Biology Wikipedia Competition. PLoS Computational Biology, 2013, 9, e1003242.	1.5	8
89	Global human frequencies of predicted nuclear pathogenic variants and the role played by protein hydrophobicity in pathogenicity potential. Scientific Reports, 2014, 4, 7155.	1.6	8
90	Impact of Amidation on Peptide Fragmentation and Identification in Shotgun Proteomics. Journal of Proteome Research, 2016, 15, 3656-3665.	1.8	8

#	Article	IF	Citations
91	Assessing the performance of in silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. Human Mutation, 2019, 40, 1612-1622.	1.1	8
92	Distinct error rates for reference and nonreference genotypes estimated by pedigree analysis. Genetics, 2021, 217, 1-10.	1.2	8
93	Protein identification problem from a Bayesian point of view. Statistics and Its Interface, 2012, 5, 21-37.	0.2	8
94	New mixture models for decoy-free false discovery rate estimation in mass spectrometry proteomics. Bioinformatics, 2020, 36, i745-i753.	1.8	8
95	Enumerating consistent sub-graphs of directed acyclic graphs: an insight into biomedical ontologies. Bioinformatics, 2018, 34, i313-i322.	1.8	7
96	A new class of metrics for learning on real-valued and structured data. Data Mining and Knowledge Discovery, 2019, 33, 995-1016.	2.4	7
97	Investigation of VUV photodissociation propensities using peptide libraries. International Journal of Mass Spectrometry, 2011, 308, 142-154.	0.7	6
98	Assessing computational predictions of the phenotypic effect of cystathionine‐beta‐synthase variants. Human Mutation, 2019, 40, 1530-1545.	1.1	5
99	Estimating classification accuracy in positive-unlabeled learning: characterization and correction strategies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 124-135.	0.7	5
100	Position of Proline Mediates the Reactivity of S-Palmitoylation. ACS Chemical Biology, 2015, 10, 2529-2536.	1.6	4
101	Fast Nonparametric Estimation of Class Proportions in the Positive-Unlabeled Classification Setting. Proceedings of the AAAI Conference on Artificial Intelligence, 2020, 34, 6729-6736.	3.6	4
102	Advancing remote homology detection: A step toward understanding and accurately predicting protein function. Cell Systems, 2022, 13, 435-437.	2.9	4
103	Analysis of Features from Protein-protein Hetero-complex Structures to Predict Protein Interaction Interfaces Using Machine Learning. Procedia Technology, 2013, 10, 62-66.	1.1	3
104	Improving phosphopeptide identification in shotgun proteomics by supervised filtering of peptide-spectrum matches. , 2013, , .		3
105	A link graph-based approach to identify forum spam. Security and Communication Networks, 2015, 8, 176-188.	1.0	3
106	Proteomic Evidence for In-Frame and Out-of-Frame Alternatively Spliced Isoforms in Human and Mouse. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1284-1289.	1.9	3
107	The sequencing and interpretation of the genome obtained from a Serbian individual. PLoS ONE, 2018, 13, e0208901.	1.1	3
108	Identifiability of two‐component skew normal mixtures with one known component. Scandinavian Journal of Statistics, 2019, 46, 955-986.	0.9	3

#	Article	IF	Citations
109	TRAINING THE NEXT GENERATION OF QUANTITATIVE BIOLOGISTS IN THE ERA OF BIG DATA. , 2014, , .		3
110	Identification of N–terminal protein processing sites by chemical labeling mass spectrometry. Rapid Communications in Mass Spectrometry, 2019, 33, 1015-1023.	0.7	2
111	VECTOR QUANTIZATION KERNELS FOR THE CLASSIFICATION OF PROTEIN SEQUENCES AND STRUCTURES. , 2013, , .		2
112	Protein Structure Prediction: Bioinformatics Approach. Briefings in Bioinformatics, 2004, 5, 207-209.	3.2	1
113	ISMB/ECCB 2019 Proceedings. Bioinformatics, 2019, 35, i1-i2.	1.8	1
114	Prioritizing de novo autism risk variants with calibrated gene- and variant-scoring models. Human Genetics, 2021, , 1.	1.8	1
115	ISMB 2018 proceedings. Bioinformatics, 2018, 34, i2-i3.	1.8	0
116	An examination of citation-based impact of the computational biology conferences. Bioinformatics, 2020, 36, 2958-2962.	1.8	0
117	On the Importance of Computational Biology and Bioinformatics to the Origins and Rapid Progression of the Intrinsically Disordered Proteins Field. , 2019, , .		0