

Predrag Radivojac

List of Publications by Year in Descending Order

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Version: 2024-04-25

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

114
papers

10,313
citations

40
h-index

101
g-index

125
ext. papers

12,215
ext. citations

5.8
avg. IF

5.79
L-index

#	Paper	IF	Citations
114	Distinct error rates for reference and nonreference genotypes estimated by pedigree analysis. <i>Genetics</i> , 2021 , 217, 1-10	4	3
113	Classification in biological networks with hypergraphlet kernels. <i>Bioinformatics</i> , 2021 , 37, 1000-1007	7.2	1
112	Prioritizing de novo autism risk variants with calibrated gene- and variant-scoring models. <i>Human Genetics</i> , 2021 , 1	6.3	0
111	Paternal age in rhesus macaques is positively associated with germline mutation accumulation but not with measures of offspring sociability. <i>Genome Research</i> , 2020 , 30, 826-834	9.7	19
110	An examination of citation-based impact of the computational biology conferences. <i>Bioinformatics</i> , 2020 , 36, 2958-2962	7.2	
109	Fast Nonparametric Estimation of Class Proportions in the Positive-Unlabeled Classification Setting. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2020 , 34, 6729-6736	5	2
108	New mixture models for decoy-free false discovery rate estimation in mass spectrometry proteomics. <i>Bioinformatics</i> , 2020 , 36, i745-i753	7.2	2
107	The ortholog conjecture revisited: the value of orthologs and paralogs in function prediction. <i>Bioinformatics</i> , 2020 , 36, i219-i226	7.2	15
106	Inferring the molecular and phenotypic impact of amino acid variants with MutPred2. <i>Nature Communications</i> , 2020 , 11, 5918	17.4	84
105	Assessing the performance of in silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. <i>Human Mutation</i> , 2019 , 40, 1612-1622	4.7	4
104	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. <i>Human Mutation</i> , 2019 , 40, 1495-1506	4.7	10
103	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2019 , 40, 1314-1320	4.7	5
102	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGI-5 intellectual disability challenge. <i>Human Mutation</i> , 2019 , 40, 1330-1345	4.7	4
101	Pathogenicity and functional impact of non-frameshifting insertion/deletion variation in the human genome. <i>PLoS Computational Biology</i> , 2019 , 15, e1007112	5	15
100	Identification of N-terminal protein processing sites by chemical labeling mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2019 , 33, 1015-1023	2.2	2
99	A new class of metrics for learning on real-valued and structured data. <i>Data Mining and Knowledge Discovery</i> , 2019 , 33, 995-1016	5.6	5
98	Identifiability of two-component skew normal mixtures with one known component. <i>Scandinavian Journal of Statistics</i> , 2019 , 46, 955-986	0.8	3

97	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. <i>Human Mutation</i> , 2019 , 40, 1373-1391	4.7	5
96	ISMB/ECCB 2019 Proceedings. <i>Bioinformatics</i> , 2019 , 35, i1-i2	7.2	1
95	Assessment of blind predictions of the clinical significance of BRCA1 and BRCA2 variants. <i>Human Mutation</i> , 2019 , 40, 1546-1556	4.7	13
94	Assessing computational predictions of the phenotypic effect of cystathionine-beta-synthase variants. <i>Human Mutation</i> , 2019 , 40, 1530-1545	4.7	3
93	Assessment of predicted enzymatic activity of N-acetylglucosaminidase variants of unknown significance for CAGI 2016. <i>Human Mutation</i> , 2019 , 40, 1519-1529	4.7	4
92	Estimating classification accuracy in positive-unlabeled learning: characterization and correction strategies. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019 , 24, 124-135	1.3	4
91	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019 , 20, 244	18.3	111
90	New Long-Term Memory Genes Revealed by Assessing Computational Function Prediction Methods. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 251-267	3.2	11
89	Proteomic Evidence for In-Frame and Out-of-Frame Alternatively Spliced Isoforms in Human and Mouse. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 1284-1289	3	2
88	Ultra High-Dimensional Nonlinear Feature Selection for Big Biological Data. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2018 , 30, 1352-1365	4.2	24
87	ISMB 2018 proceedings. <i>Bioinformatics</i> , 2018 , 34, i2-i3	7.2	
86	Target site specificity and in vivo complexity of the mammalian arginylome. <i>Scientific Reports</i> , 2018 , 8, 16177	4.9	16
85	The sequencing and interpretation of the genome obtained from a Serbian individual. <i>PLoS ONE</i> , 2018 , 13, e0208901	3.7	2
84	Reproductive Longevity Predicts Mutation Rates in Primates. <i>Current Biology</i> , 2018 , 28, 3193-3197.e5	6.3	48
83	Enumerating consistent sub-graphs of directed acyclic graphs: an insight into biomedical ontologies. <i>Bioinformatics</i> , 2018 , 34, i313-i322	7.2	4
82	Missense variant pathogenicity predictors generalize well across a range of function-specific prediction challenges. <i>Human Mutation</i> , 2017 , 38, 1092-1108	4.7	30
81	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017 , 38, 1182-1192	4.7	28
80	Community-Wide Evaluation of Computational Function Prediction. <i>Methods in Molecular Biology</i> , 2017 , 1446, 133-146	1.4	15

79	Physicochemical sequence characteristics that influence S-palmitoylation propensity. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 2337-2350	3.6	13
78	When loss-of-function is loss of function: assessing mutational signatures and impact of loss-of-function genetic variants. <i>Bioinformatics</i> , 2017 , 33, i389-i398	7.2	23
77	Impact of Amidination on Peptide Fragmentation and Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2016 , 15, 3656-3665	5.6	7
76	Protein function in precision medicine: deep understanding with machine learning. <i>FEBS Letters</i> , 2016 , 590, 2327-41	3.8	31
75	Regulatory Single-Nucleotide Variant Predictor Increases Predictive Performance of Functional Regulatory Variants. <i>Human Mutation</i> , 2016 , 37, 1137-1143	4.7	12
74	Examining the Influence of Phosphorylation on Peptide Ion Structure by Ion Mobility Spectrometry-Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 786-94 ⁵	3.5	17
73	The Loss and Gain of Functional Amino Acid Residues Is a Common Mechanism Causing Human Inherited Disease. <i>PLoS Computational Biology</i> , 2016 , 12, e1005091	5	11
72	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum Task Force of ISCB ^U Education Committee). <i>PLoS Computational Biology</i> , 2016 , 12, e1004943 ⁵	4.5	15
71	XLSearch: a Probabilistic Database Search Algorithm for Identifying Cross-Linked Peptides. <i>Journal of Proteome Research</i> , 2016 , 15, 1830-41	5.6	14
70	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016 , 17, 184	18.3	218
69	REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants. <i>American Journal of Human Genetics</i> , 2016 , 99, 877-885	11	722
68	Penultimate proline in neuropeptides. <i>Analytical Chemistry</i> , 2015 , 87, 8466-72	7.8	13
67	Position of Proline Mediates the Reactivity of S-Palmitoylation. <i>ACS Chemical Biology</i> , 2015 , 10, 2529-36	4.9	3
66	A link graph-based approach to identify forum spam. <i>Security and Communication Networks</i> , 2015 , 8, 176-188	1.9	2
65	On the split personality of penultimate proline. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 444-52	3.5	11
64	Intrinsic Size Parameters for Palmitoylated and Carboxyamidomethylated Peptides. <i>International Journal of Mass Spectrometry</i> , 2014 , 368, 6-14	1.9	9
63	The structural and functional signatures of proteins that undergo multiple events of post-translational modification. <i>Protein Science</i> , 2014 , 23, 1077-93	6.3	226
62	Global human frequencies of predicted nuclear pathogenic variants and the role played by protein hydrophobicity in pathogenicity potential. <i>Scientific Reports</i> , 2014 , 4, 7155	4.9	5

61	Bioinformatics curriculum guidelines: toward a definition of core competencies. <i>PLoS Computational Biology</i> , 2014 , 10, e1003496	5	75
60	The impact of incomplete knowledge on the evaluation of protein function prediction: a structured-output learning perspective. <i>Bioinformatics</i> , 2014 , 30, i609-16	7.2	33
59	Generalized graphlet kernels for probabilistic inference in sparse graphs. <i>Network Science</i> , 2014 , 2, 254-276	7	
58	MutPred Splice: machine learning-based prediction of exonic variants that disrupt splicing. <i>Genome Biology</i> , 2014 , 15, R19	18.3	102
57	Analysis of Features from Protein-protein Hetero-complex Structures to Predict Protein Interaction Interfaces Using Machine Learning. <i>Procedia Technology</i> , 2013 , 10, 62-66		3
56	Calibration of multiple in silico tools for predicting pathogenicity of mismatch repair gene missense substitutions. <i>Human Mutation</i> , 2013 , 34, 255-65	4.7	70
55	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013 , 10, 221-7	21.6	587
54	Improving phosphopeptide identification in shotgun proteomics by supervised filtering of peptide-spectrum matches 2013 ,		2
53	ISCB computational biology Wikipedia competition. <i>PLoS Computational Biology</i> , 2013 , 9, e1003242	5	3
52	Information-theoretic evaluation of predicted ontological annotations. <i>Bioinformatics</i> , 2013 , 29, i53-61	7.2	66
51	Extending the coverage of spectral libraries: a neighbor-based approach to predicting intensities of peptide fragmentation spectra. <i>Proteomics</i> , 2013 , 13, 756-65	4.8	9
50	Quantitative measurement of phosphoproteome response to osmotic stress in arabidopsis based on Library-Assisted eXtracted Ion Chromatogram (LAXIC). <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2354-69	7.6	55
49	Evaluating purifying selection in the mitochondrial DNA of various mammalian species. <i>PLoS ONE</i> , 2013 , 8, e58993	3.7	33
48	Allosteric post-translational modification codes. <i>Trends in Biochemical Sciences</i> , 2012 , 37, 447-55	10.3	152
47	Computational approaches to protein inference in shotgun proteomics. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 16, S4	3.6	36
46	An integrated regulatory network reveals pervasive cross-regulation among transcription and splicing factors. <i>PLoS Computational Biology</i> , 2012 , 8, e1002603	5	13
45	Protein identification problem from a Bayesian point of view. <i>Statistics and Its Interface</i> , 2012 , 5, 21-37	0.4	8
44	Investigation of VUV Photodissociation Propensities Using Peptide Libraries. <i>International Journal of Mass Spectrometry</i> , 2011 , 308, 142-154	1.9	5

43	Comparing phylogeny and the predicted pathogenicity of protein variations reveals equal purifying selection across the global human mtDNA diversity. <i>American Journal of Human Genetics</i> , 2011 , 88, 433-9 ¹¹		85
42	Analysis of protein function and its prediction from amino acid sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2086-96	4.2	92
41	Prediction of functional regulatory SNPs in monogenic and complex disease. <i>Human Mutation</i> , 2011 , 32, 1183-90	4.7	20
40	On the accuracy and limits of peptide fragmentation spectrum prediction. <i>Analytical Chemistry</i> , 2011 , 83, 790-6	7.8	40
39	Testing the ortholog conjecture with comparative functional genomic data from mammals. <i>PLoS Computational Biology</i> , 2011 , 7, e1002073	5	117
38	Computational methods for identification of functional residues in protein structures. <i>Current Protein and Peptide Science</i> , 2011 , 12, 456-69	2.8	21
37	The importance of peptide detectability for protein identification, quantification, and experiment design in MS/MS proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 6288-97	5.6	31
36	Combinatorial libraries of synthetic peptides as a model for shotgun proteomics. <i>Analytical Chemistry</i> , 2010 , 82, 6559-68	7.8	14
35	Graphlet kernels for prediction of functional residues in protein structures. <i>Journal of Computational Biology</i> , 2010 , 17, 55-72	1.7	36
34	Loss of post-translational modification sites in disease. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2010 , 337-47	1.3	47
33	In silico functional profiling of human disease-associated and polymorphic amino acid substitutions. <i>Human Mutation</i> , 2010 , 31, 335-46	4.7	55
32	Identification, analysis, and prediction of protein ubiquitination sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 365-80	4.2	424
31	A bayesian approach to protein inference problem in shotgun proteomics. <i>Journal of Computational Biology</i> , 2009 , 16, 1183-93	1.7	55
30	Influence of sequence changes and environment on intrinsically disordered proteins. <i>PLoS Computational Biology</i> , 2009 , 5, e1000497	5	37
29	Automated inference of molecular mechanisms of disease from amino acid substitutions. <i>Bioinformatics</i> , 2009 , 25, 2744-50	7.2	580
28	Intrinsic disorder in pathogenic and non-pathogenic microbes: discovering and analyzing the unfoldomes of early-branching eukaryotes. <i>Molecular BioSystems</i> , 2008 , 4, 328-40		101
27	Gain and loss of phosphorylation sites in human cancer. <i>Bioinformatics</i> , 2008 , 24, i241-7	7.2	81
26	Fast and accurate identification of semi-tryptic peptides in shotgun proteomics. <i>Bioinformatics</i> , 2008 , 24, 102-9	7.2	40

25	HIP2: an online database of human plasma proteins from healthy individuals. <i>BMC Medical Genomics</i> , 2008 , 1, 12	3.7	25
24	An integrated approach to inferring gene-disease associations in humans. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 72, 1030-7	4.2	127
23	MutDB: update on development of tools for the biochemical analysis of genetic variation. <i>Nucleic Acids Research</i> , 2008 , 36, D815-9	20.1	28
22	Characterization of molecular recognition features, MoRFs, and their binding partners. <i>Journal of Proteome Research</i> , 2007 , 6, 2351-66	5.6	386
21	Intrinsic disorder and functional proteomics. <i>Biophysical Journal</i> , 2007 , 92, 1439-56	2.9	571
20	Evaluation of features for catalytic residue prediction in novel folds. <i>Protein Science</i> , 2007 , 16, 216-26	6.3	53
19	Prediction of intrinsic disorder and its use in functional proteomics. <i>Methods in Molecular Biology</i> , 2007 , 408, 69-92	1.4	32
18	Length-dependent prediction of protein intrinsic disorder. <i>BMC Bioinformatics</i> , 2006 , 7, 208	3.6	630
17	Intrinsic disorder is a common feature of hub proteins from four eukaryotic interactomes. <i>PLoS Computational Biology</i> , 2006 , 2, e100	5	435
16	Alternative splicing in concert with protein intrinsic disorder enables increased functional diversity in multicellular organisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 8390-5	11.5	358
15	Analysis of molecular recognition features (MoRFs). <i>Journal of Molecular Biology</i> , 2006 , 362, 1043-59	6.5	579
14	Calmodulin signaling: analysis and prediction of a disorder-dependent molecular recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 398-410	4.2	86
13	Unraveling the nature of the segmentation clock: Intrinsic disorder of clock proteins and their interaction map. <i>Computational Biology and Chemistry</i> , 2006 , 30, 241-8	3.6	12
12	Optimizing long intrinsic disorder predictors with protein evolutionary information. <i>Journal of Bioinformatics and Computational Biology</i> , 2005 , 3, 35-60	1	346
11	Protein Structure Prediction: Bioinformatics Approach. <i>Briefings in Bioinformatics</i> , 2004 , 5, 207-209	13.4	
10	Classification and knowledge discovery in protein databases. <i>Journal of Biomedical Informatics</i> , 2004 , 37, 224-39	10.2	64
9	Protein flexibility and intrinsic disorder. <i>Protein Science</i> , 2004 , 13, 71-80	6.3	269
8	The importance of intrinsic disorder for protein phosphorylation. <i>Nucleic Acids Research</i> , 2004 , 32, 1037-40	40.1	1043

7	Improved amino acid flexibility parameters. <i>Protein Science</i> , 2003 , 12, 1060-72	6.3	137
6	Prediction of boundaries between intrinsically ordered and disordered protein regions. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2003 , 216-27	1.3	26
5	Improving sequence alignments for intrinsically disordered proteins. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2002 , 589-600	1.3	12
4	IMPROVING SEQUENCE ALIGNMENTS FOR INTRINSICALLY DISORDERED PROTEINS 2001 ,		3
3	New <i>Drosophila</i> long-term memory genes revealed by assessing computational function prediction methods		3
2	MutPred2: inferring the molecular and phenotypic impact of amino acid variants		79
1	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7