

Petri Toronen

List of Publications by Year in descending order

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38
papers

3,497
citations

394421

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345221

36
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43
all docs

43
docs citations

43
times ranked

4766
citing authors

#	ARTICLE	IF	CITATIONS
1	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
2	Analysis of gene expression data using self-organizing maps. <i>FEBS Letters</i> , 1999, 451, 142-146.	2.8	454
3	PANNZER2: a rapid functional annotation web server. <i>Nucleic Acids Research</i> , 2018, 46, W84-W88.	14.5	328
4	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
5	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.	8.8	261
6	Defense-related transcription factors <i>WRKY70</i> and <i>WRKY54</i> modulate osmotic stress tolerance by regulating stomatal aperture in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2013, 200, 457-472.	7.3	223
7	Analysis and visualization of gene expression data using Self-Organizing Maps. <i>Neural Networks</i> , 2002, 15, 953-966.	5.9	139
8	PANNZER: high-throughput functional annotation of uncharacterized proteins in an error-prone environment. <i>Bioinformatics</i> , 2015, 31, 1544-1552.	4.1	123
9	AAI-profiler: fast proteome-wide exploratory analysis reveals taxonomic identity, misclassification and contamination. <i>Nucleic Acids Research</i> , 2018, 46, W479-W485.	14.5	119
10	Trustworthiness and metrics in visualizing similarity of gene expression. <i>BMC Bioinformatics</i> , 2003, 4, 48.	2.6	97
11	Revised Phylogeny and Novel Horizontally Acquired Virulence Determinants of the Model Soft Rot Phytopathogen <i>Pectobacterium wasabiae</i> SCC3193. <i>PLoS Pathogens</i> , 2012, 8, e1003013.	4.7	93
12	Changes in gene expression in atherosclerotic plaques analyzed using DNA array. <i>Atherosclerosis</i> , 2002, 165, 23-32.	0.8	81
13	Antipsychotic drug treatment induces differential gene expression in the rat cortex. <i>Journal of Neurochemistry</i> , 2002, 83, 1043-1053.	3.9	71
14	PANNZER: A practical tool for protein function prediction. <i>Protein Science</i> , 2022, 31, 118-128.	7.6	55
15	Theme discovery from gene lists for identification and viewing of multiple functional groups. <i>BMC Bioinformatics</i> , 2005, 6, 162.	2.6	46
16	Bayesian search of functionally divergent protein subgroups and their function specific residues. <i>Bioinformatics</i> , 2006, 22, 2466-2474.	4.1	40
17	Selection of informative clusters from hierarchical cluster tree with gene classes. <i>BMC Bioinformatics</i> , 2004, 5, 32.	2.6	37
18	Robust extraction of functional signals from gene set analysis using a generalized threshold free scoring function. <i>BMC Bioinformatics</i> , 2009, 10, 307.	2.6	35

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19	Brain-derived neurotrophic factor signaling modifies hippocampal gene expression during epileptogenesis in transgenic mice. <i>European Journal of Neuroscience</i> , 2004, 19, 3245-3254.	2.6	29
20	Effects of Antidepressant Drug Imipramine on Gene Expression in Rat Prefrontal Cortex. <i>Neurochemical Research</i> , 2004, 29, 1235-1244.	3.3	21
21	Mlh1 deficiency in normal mouse colon mucosa associates with chromosomally unstable colon cancer. <i>Carcinogenesis</i> , 2018, 39, 788-797.	2.8	18
22	Gene set analysis: limitations in popular existing methods and proposed improvements. <i>Bioinformatics</i> , 2014, 30, 2747-2756.	4.1	15
23	Identifying functional gene sets from hierarchically clustered expression data: map of abiotic stress regulated genes in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2006, 34, e124-e124.	14.5	13
24	Novel comparison of evaluation metrics for gene ontology classifiers reveals drastic performance differences. <i>PLoS Computational Biology</i> , 2019, 15, e1007419.	3.2	12
25	Molecular Fingerprint and Developmental Regulation of the Tegmental GABAergic and Glutamatergic Neurons Derived from the Anterior Hindbrain. <i>Cell Reports</i> , 2020, 33, 108268.	6.4	11
26	POXO: a web-enabled tool series to discover transcription factor binding sites. <i>Nucleic Acids Research</i> , 2006, 34, W534-W540.	14.5	10
27	Expression profiling to understand actions of NMDA/glutamate receptor antagonists in rat brain. <i>Neurochemical Research</i> , 2002, 27, 1209-1220.	3.3	9
28	Oxidative Stress Components Explored in Anoxic and Hypoxic Global Gene Expression Data. <i>Plant Cell Monographs</i> , 2014, , 19-39.	0.4	8
29	Epigenome-450K-wide methylation signatures of active cigarette smoking: The Young Finns Study. <i>Bioscience Reports</i> , 2020, 40, .	2.4	8
30	Synexpression analysis of ESTs in the rat brain reveals distinct patterns and potential drug targets. <i>Molecular Brain Research</i> , 2002, 104, 176-183.	2.3	6
31	Generation of Gene Ontology benchmark datasets with various types of positive signal. <i>BMC Bioinformatics</i> , 2009, 10, 319.	2.6	5
32	GOParGenPy: a high throughput method to generate Gene Ontology data matrices. <i>BMC Bioinformatics</i> , 2013, 14, 242.	2.6	5
33	Interspaced transcription chimeras: Neglected pathological mechanism infiltrating gene accession queries?. <i>Journal of Biomedical Informatics</i> , 2009, 42, 382-389.	4.3	4
34	Robust multi-group gene set analysis with few replicates. <i>BMC Bioinformatics</i> , 2016, 17, 526.	2.6	4
35	Exploratory Clustering of Gene Expression Profiles of Mutated Yeast Strains. , 2006, , 61-74.		2
36	Novel split quality measures for stratified multilabel cross validation with application to large and sparse gene ontology datasets. , 2022, 2, 49-62.		2

#	ARTICLE	IF	CITATIONS
37	Heuristic Bayesian Segmentation for Discovery of Coexpressed Genes within Genomic Regions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 37-49.	3.0	1
38	Methods for Quantitation and Clustering of Gene Expression Data. Current Genomics, 2003, 4, 445-463.	1.6	1