

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	<sc>PANNZER</sc> – A practical tool for protein function prediction. Protein Science, 2022, 31, 118-128.	7.6	55
2	Novel split quality measures for stratified multilabel cross validation with application to large and sparse gene ontology datasets. , 2022, 2, 49-62.		2
3	Molecular Fingerprint and Developmental Regulation of the Tegmental GABAergic and Glutamatergic Neurons Derived from the Anterior Hindbrain. Cell Reports, 2020, 33, 108268.	6.4	11
4	Epigenome-450K-wide methylation signatures of active cigarette smoking: The Young Finns Study. Bioscience Reports, 2020, 40, .	2.4	8
5	Novel comparison of evaluation metrics for gene ontology classifiers reveals drastic performance differences. PLoS Computational Biology, 2019, 15, e1007419.	3.2	12
6	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
7	Mlh1 deficiency in normal mouse colon mucosa associates with chromosomally unstable colon cancer. Carcinogenesis, 2018, 39, 788-797.	2.8	18
8	AAI-profiler: fast proteome-wide exploratory analysis reveals taxonomic identity, misclassification and contamination. Nucleic Acids Research, 2018, 46, W479-W485.	14.5	119
9	PANNZER2: a rapid functional annotation web server. Nucleic Acids Research, 2018, 46, W84-W88.	14.5	328
10	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
11	Robust multi-group gene set analysis with few replicates. BMC Bioinformatics, 2016, 17, 526.	2.6	4
12	PANNZER: high-throughput functional annotation of uncharacterized proteins in an error-prone environment. Bioinformatics, 2015, 31, 1544-1552.	4.1	123
13	Oxidative Stress Components Explored in Anoxic and Hypoxic Global Gene Expression Data. Plant Cell Monographs, 2014, , 19-39.	0.4	8
14	Gene set analysis: limitations in popular existing methods and proposed improvements. Bioinformatics, 2014, 30, 2747-2756.	4.1	15
15	GOParGenPy: a high throughput method to generate Gene Ontology data matrices. BMC Bioinformatics, 2013, 14, 242.	2.6	5
16	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789
17	Defense-related transcription factors <sc>WRKY</sc>70 and <sc>WRKY</sc>54 modulate osmotic stress tolerance by regulating stomatal aperture in <i><sc>Arabidopsis</sc></i>. New Phytologist, 2013, 200, 457-472.	7.3	223
18	Revised Phylogeny and Novel Horizontally Acquired Virulence Determinants of the Model Soft Rot Phytopathogen Pectobacterium wasabiae SCC3193. PLoS Pathogens, 2012, 8, e1003013.	4.7	93

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19	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
20	Robust extraction of functional signals from gene set analysis using a generalized threshold free scoring function. BMC Bioinformatics, 2009, 10, 307.	2.6	35
21	Interspaced transcription chimeras: Neglected pathological mechanism infiltrating gene accession queries?. Journal of Biomedical Informatics, 2009, 42, 382-389.	4.3	4
22	Generation of Gene Ontology benchmark datasets with various types of positive signal. BMC Bioinformatics, 2009, 10, 319.	2.6	5
23	Identifying functional gene sets from hierarchically clustered expression data: map of abiotic stress regulated genes in Arabidopsis thaliana. Nucleic Acids Research, 2006, 34, e124-e124.	14.5	13
24	POXO: a web-enabled tool series to discover transcription factor binding sites. Nucleic Acids Research, 2006, 34, W534-W540.	14.5	10
25	Bayesian search of functionally divergent protein subgroups and their function specific residues. Bioinformatics, 2006, 22, 2466-2474.	4.1	40
26	Exploratory Clustering of Gene Expression Profiles of Mutated Yeast Strains. , 2006, , 61-74.		2
27	Theme discovery from gene lists for identification and viewing of multiple functional groups. BMC Bioinformatics, 2005, 6, 162.	2.6	46
28	Brain-derived neurotrophic factor signaling modifies hippocampal gene expression during epileptogenesis in transgenic mice. European Journal of Neuroscience, 2004, 19, 3245-3254.	2.6	29
29	Selection of informative clusters from hierarchical cluster tree with gene classes. BMC Bioinformatics, 2004, 5, 32.	2.6	37
30	Effects of Antidepressant Drug Imipramine on Gene Expression in Rat Prefrontal Cortex. Neurochemical Research, 2004, 29, 1235-1244.	3.3	21
31	Trustworthiness and metrics in visualizing similarity of gene expression. BMC Bioinformatics, 2003, 4, 48.	2.6	97
32	Methods for Quantitation and Clustering of Gene Expression Data. Current Genomics, 2003, 4, 445-463.	1.6	1
33	Changes in gene expression in atherosclerotic plaques analyzed using DNA array. Atherosclerosis, 2002, 165, 23-32.	0.8	81
34	Synexpression analysis of ESTs in the rat brain reveals distinct patterns and potential drug targets. Molecular Brain Research, 2002, 104, 176-183.	2.3	6
35	Antipsychotic drug treatment induces differential gene expression in the rat cortex. Journal of Neurochemistry, 2002, 83, 1043-1053.	3.9	71
36	Analysis and visualization of gene expression data using Self-Organizing Maps. Neural Networks, 2002, 15, 953-966.	5.9	139

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37	Expression profiling to understand actions of NMDA/glutamate receptor antagonists in rat brain. <i>Neurochemical Research</i> , 2002, 27, 1209-1220.	3.3	9
38	Analysis of gene expression data using self-organizing maps. <i>FEBS Letters</i> , 1999, 451, 142-146.	2.8	454