

Claude Pasquier

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

685
citations

840776

11
h-index

580821

25
g-index

30
all docs

30
docs citations

30
times ranked

907
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel method for predicting transmembrane segments in proteins based on a statistical analysis of the SwissProt database: the PRED-TMR algorithm. Protein Engineering, Design and Selection, 1999, 12, 381-385.	2.1	152
2	Prediction of miRNA-disease associations with a vector space model. Scientific Reports, 2016, 6, 27036.	3.3	105
3	An hierarchical artificial neural network system for the classification of transmembrane proteins. Protein Engineering, Design and Selection, 1999, 12, 631-634.	2.1	65
4	Evaluation of annotation strategies using an entire genome sequence. Bioinformatics, 2003, 19, 717-726.	4.1	65
5	GenMiner: mining non-redundant association rules from integrated gene expression data and annotations. Bioinformatics, 2008, 24, 2643-2644.	4.1	56
6	Biological data integration using Semantic Web technologies. Biochimie, 2008, 90, 584-594.	2.6	40
7	PRED-CLASS: Cascading neural networks for generalized protein classification and genome-wide applications. Proteins: Structure, Function and Bioinformatics, 2001, 44, 361-369.	2.6	37
8	THEA: ontology-driven analysis of microarray data. Bioinformatics, 2004, 20, 2636-2643.	4.1	28
9	A novel tool for the prediction of transmembrane protein topology based on a statistical analysis of the SwissProt database: the OrientTM algorithm. Protein Engineering, Design and Selection, 2001, 14, 387-390.	2.1	22
10	Environmentally Selected Aphid Variants in Clonality Context Display Differential Patterns of Methylation in the Genome. PLoS ONE, 2014, 9, e115022.	2.5	15
11	GenMiner: Mining Informative Association Rules from Genomic Data. , 2007, , .		13
12	Frequent pattern mining in attributed trees: algorithms and applications. Knowledge and Information Systems, 2016, 46, 491-514.	3.2	13
13	Prediction of miRNA-disease Associations using an Evolutionary Tuned Latent Semantic Analysis. Scientific Reports, 2017, 7, 10548.	3.3	12
14	Computational search of hybrid human/SARS-CoV-2 dsRNA reveals unique viral sequences that diverge from those of other coronavirus strains. Heliyon, 2021, 7, e07284.	3.2	10
15	Aspect and XML-oriented Semantic Framework Generator. Electronic Notes in Theoretical Computer Science, 2002, 65, 97-116.	0.9	9
16	The Mapping of Predicted Triplex DNA:RNA in the Drosophila Genome Reveals a Prominent Location in Development- and Morphogenesis-Related Genes. G3: Genes, Genomes, Genetics, 2017, 7, 2295-2304.	1.8	8
17	SmartTools: A Generator of Interactive Environments Tools. Lecture Notes in Computer Science, 2001, , 355-360.	1.3	5
18	Attributed graph mining in the presence of automorphism. Knowledge and Information Systems, 2017, 50, 569-584.	3.2	4

#	ARTICLE	IF	CITATIONS
19	Temporal and sequential order of nonoverlapping gene networks unraveled in mated female <i>Drosophila</i> . <i>Life Science Alliance</i> , 2022, 5, e202101119.	2.8	4
20	Computational prediction of miRNA/mRNA duplexomes at the whole human genome scale reveals functional subnetworks of interacting genes with embedded miRNA annealing motifs. <i>Computational Biology and Chemistry</i> , 2020, 88, 107366.	2.3	3
21	Co-expressed gene groups analysis (CGGA): An automatic tool for the interpretation of microarray experiments. <i>Journal of Integrative Bioinformatics</i> , 2006, 3, 188-198.	1.5	2
22	Transcriptome-wide-scale-predicted dsRNAs potentially involved in RNA homeostasis are remarkably excluded from genes with no/very low expression in all developmental stages. <i>RNA Biology</i> , 2020, 17, 554-570.	3.1	2
23	Frequent Pattern Mining in Attributed Trees. <i>Lecture Notes in Computer Science</i> , 2013, , 26-37.	1.3	2
24	Population-based meta-heuristic for active modules identification. , 2019, , .		2
25	Persistent Properties of a Subpopulation of Cancer Cells Overexpressing the Hedgehog Receptor Patched. <i>Pharmaceutics</i> , 2022, 14, 988.	4.5	2
26	Mining evolutions of complex spatial objects using a single-attributed Directed Acyclic Graph. <i>Knowledge and Information Systems</i> , 2020, 62, 3931-3971.	3.2	1
27	Mining Association Rule Bases from Integrated Genomic Data and Annotations. <i>Lecture Notes in Computer Science</i> , 2009, , 78-90.	1.3	1
28	Interpreting Microarray Experiments Via Co-expressed Gene Groups Analysis (CGGA). <i>Lecture Notes in Computer Science</i> , 2006, , 316-320.	1.3	0