

# Claude Pasquier

## List of Publications by Year in descending order

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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	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
2	Persistent Properties of a Subpopulation of Cancer Cells Overexpressing the Hedgehog Receptor Patched. <i>Pharmaceutics</i> , 2022, 14, 988.	4.5	2
3	Computational search of hybrid human/SARS-CoV-2 dsRNA reveals unique viral sequences that diverge from those of other coronavirus strains. <i>Heliyon</i> , 2021, 7, e07284.	3.2	10
4	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
5	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
6	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
7	Population-based meta-heuristic for active modules identification. , 2019, , .		2
8	Attributed graph mining in the presence of automorphism. <i>Knowledge and Information Systems</i> , 2017, 50, 569-584.	3.2	4
9	The Mapping of Predicted Triplex DNA:RNA in the <i>Drosophila</i> Genome Reveals a Prominent Location in Development- and Morphogenesis-Related Genes. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2295-2304.	1.8	8
10	Prediction of miRNA-disease Associations using an Evolutionary Tuned Latent Semantic Analysis. <i>Scientific Reports</i> , 2017, 7, 10548.	3.3	12
11	Prediction of miRNA-disease associations with a vector space model. <i>Scientific Reports</i> , 2016, 6, 27036.	3.3	105
12	Frequent pattern mining in attributed trees: algorithms and applications. <i>Knowledge and Information Systems</i> , 2016, 46, 491-514.	3.2	13
13	Environmentally Selected Aphid Variants in Clonality Context Display Differential Patterns of Methylation in the Genome. <i>PLoS ONE</i> , 2014, 9, e115022.	2.5	15
14	Frequent Pattern Mining in Attributed Trees. <i>Lecture Notes in Computer Science</i> , 2013, , 26-37.	1.3	2
15	Mining Association Rule Bases from Integrated Genomic Data and Annotations. <i>Lecture Notes in Computer Science</i> , 2009, , 78-90.	1.3	1
16	Biological data integration using Semantic Web technologies. <i>Biochimie</i> , 2008, 90, 584-594.	2.6	40
17	GenMiner: mining non-redundant association rules from integrated gene expression data and annotations. <i>Bioinformatics</i> , 2008, 24, 2643-2644.	4.1	56
18	GenMiner: Mining Informative Association Rules from Genomic Data. , 2007, , .		13

#	ARTICLE	IF	CITATIONS
19	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
20	Interpreting Microarray Experiments Via Co-expressed Gene Groups Analysis (CGGA). <i>Lecture Notes in Computer Science</i> , 2006, , 316-320.	1.3	0
21	THEA: ontology-driven analysis of microarray data. <i>Bioinformatics</i> , 2004, 20, 2636-2643.	4.1	28
22	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	4.1	65
23	Aspect and XML-oriented Semantic Framework Generator. <i>Electronic Notes in Theoretical Computer Science</i> , 2002, 65, 97-116.	0.9	9
24	PRED-CLASS: Cascading neural networks for generalized protein classification and genome-wide applications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 44, 361-369.	2.6	37
25	A novel tool for the prediction of transmembrane protein topology based on a statistical analysis of the SwissProt database: the OrientTM algorithm. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 387-390.	2.1	22
26	SmartTools: A Generator of Interactive Environments Tools. <i>Lecture Notes in Computer Science</i> , 2001, , 355-360.	1.3	5
27	An hierarchical artificial neural network system for the classification of transmembrane proteins. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 631-634.	2.1	65
28	A novel method for predicting transmembrane segments in proteins based on a statistical analysis of the SwissProt database: the PRED-TMR algorithm. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 381-385.	2.1	152