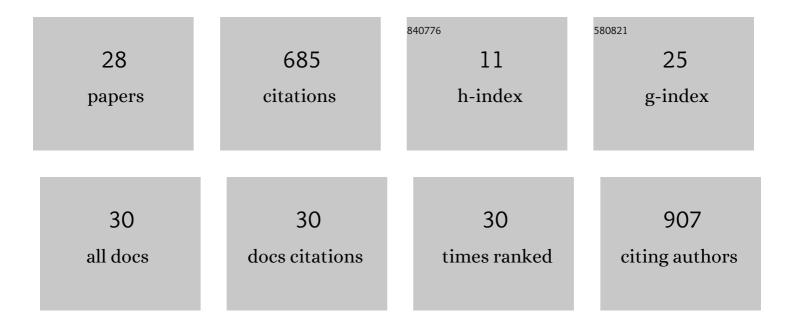
Claude Pasquier

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Temporal and sequential order of nonoverlapping gene networks unraveled in mated female Drosophila. Life Science Alliance, 2022, 5, e202101119.	2.8	4
2	Persistent Properties of a Subpopulation of Cancer Cells Overexpressing the Hedgehog Receptor Patched. Pharmaceutics, 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. Heliyon, 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. Computational Biology and Chemistry, 2020, 88, 107366.	2.3	3
5	Mining evolutions of complex spatial objects using a single-attributed Directed Acyclic Graph. Knowledge and Information Systems, 2020, 62, 3931-3971.	3.2	1
6	Transcriptome-wide-scale-predicted dsRNAs potentially involved in RNA homoeostasis are remarkably excluded from genes with no/very low expression in all developmental stages. RNA Biology, 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. Knowledge and Information Systems, 2017, 50, 569-584.	3.2	4
9	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
10	Prediction of miRNA-disease Associations using an Evolutionary Tuned Latent Semantic Analysis. Scientific Reports, 2017, 7, 10548.	3.3	12
11	Prediction of miRNA-disease associations with a vector space model. Scientific Reports, 2016, 6, 27036.	3.3	105
12	Frequent pattern mining in attributed trees: algorithms and applications. Knowledge and Information Systems, 2016, 46, 491-514.	3.2	13
13	Environmentally Selected Aphid Variants in Clonality Context Display Differential Patterns of Methylation in the Genome. PLoS ONE, 2014, 9, e115022.	2.5	15
14	Frequent Pattern Mining in Attributed Trees. Lecture Notes in Computer Science, 2013, , 26-37.	1.3	2
15	Mining Association Rule Bases from Integrated Genomic Data and Annotations. Lecture Notes in Computer Science, 2009, , 78-90.	1.3	1
16	Biological data integration using Semantic Web technologies. Biochimie, 2008, 90, 584-594.	2.6	40
17	GenMiner: mining non-redundant association rules from integrated gene expression data and annotations. Bioinformatics, 2008, 24, 2643-2644.	4.1	56
18	GenMiner: Mining Informative Association Rules from Genomic Data. , 2007, , .		13

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#	Article	IF	CITATIONS
19	Co-expressed gene groups analysis (CGGA): An automatic tool for the interpretation of microarray experiments. Journal of Integrative Bioinformatics, 2006, 3, 188-198.	1.5	2
20	Interpreting Microarray Experiments Via Co-expressed Gene Groups Analysis (CGGA). Lecture Notes in Computer Science, 2006, , 316-320.	1.3	0
21	THEA: ontology-driven analysis of microarray data. Bioinformatics, 2004, 20, 2636-2643.	4.1	28
22	Evaluation of annotation strategies using an entire genome sequence. Bioinformatics, 2003, 19, 717-726.	4.1	65
23	Aspect and XML-oriented Semantic Framework Generator. Electronic Notes in Theoretical Computer Science, 2002, 65, 97-116.	0.9	9
24	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
25	A novel tool for the prediction of transmembrane protein topology based on a statistical analysis of the SwissProt database: the OrienTM algorithm. Protein Engineering, Design and Selection, 2001, 14, 387-390.	2.1	22
26	SmartTools: A Generator of Interactive Environments Tools. Lecture Notes in Computer Science, 2001, , 355-360.	1.3	5
27	An hierarchical artificial neural network system for the classification of transmembrane proteins. Protein Engineering, Design and Selection, 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. Protein Engineering, Design and Selection, 1999, 12, 381-385.	2.1	152