Vincent Lacroix

List of Publications by Year
in descending order

37 papers	1,915 citations	331670 21 h-index	315739 38 g-index
41 all docs	41 docs citations	41 times ranked	3185 citing authors

#	Article	IF	Citations
1	Clinical interpretation of variants identified in RNU4ATAC, a non-coding spliceosomal gene. PLoS ONE, 2020, 15, e0235655.	2.5	8
2	Influenza virus infection induces widespread alterations of host cell splicing. NAR Genomics and Bioinformatics, 2020, 2, lqaa095.	3.2	6
3	Transcriptome profiling of mouse samples using nanopore sequencing of cDNA and RNA molecules. Scientific Reports, 2019, 9, 14908.	3.3	90
4	New insights into minor splicing—a transcriptomic analysis of cells derived from TALS patients. Rna, 2019, 25, 1130-1149.	3.5	27
5	Advances in Analyzing Virus-Induced Alterations of Host Cell Splicing. Trends in Microbiology, 2019, 27, 268-281.	7.7	49
6	Complementarity of assembly-first and mapping-first approaches for alternative splicing annotation and differential analysis from RNAseq data. Scientific Reports, 2018, 8, 4307.	3.3	31
7	A fast and agnostic method for bacterial genome-wide association studies: Bridging the gap between k-mers and genetic events. PLoS Genetics, 2018, 14, e1007758.	3.5	144
8	Identification of misexpressed genetic elements in hybrids between Drosophila-related species. Scientific Reports, 2017, 7, 40618.	3.3	49
9	Playing hide and seek with repeats in local and global de novo transcriptome assembly of short RNA-seq reads. Algorithms for Molecular Biology, 2017, 12, 2.	1.2	18
10	SNP calling from RNA-seq data without a reference genome: identification, quantification, differential analysis and impact on the protein sequence. Nucleic Acids Research, 2016, 44, gkw655.	14.5	66
11	Splicing misregulation of SCN5A contributes to cardiac-conduction delay and heart arrhythmia in myotonic dystrophy. Nature Communications, 2016, 7, 11067.	12.8	155
12	Colib'read on galaxy: a tools suite dedicated to biological information extraction from raw NGS reads. GigaScience, 2016, 5, 9.	6.4	2
13	A polynomial delay algorithm for the enumeration of bubbles with length constraints in directed graphs. Algorithms for Molecular Biology, 2015, 10, 20.	1.2	2
14	Reference-free detection of isolated SNPs. Nucleic Acids Research, 2015, 43, e11-e11.	14.5	75
15	Telling metabolic stories to explore metabolomics data: a case study on the yeast response to cadmium exposure. Bioinformatics, 2014, 30, 61-70.	4.1	13
16	Navigating in a Sea of Repeats in RNA-seq without Drowning. Lecture Notes in Computer Science, 2014, , 82-96.	1.3	2
17	Short and long-term genome stability analysis of prokaryotic genomes. BMC Genomics, 2013, 14, 309.	2.8	9
18	A Polynomial Delay Algorithm for the Enumeration of Bubbles with Length Constraints in Directed Graphs and Its Application to the Detection of Alternative Splicing in RNA-seq Data. Lecture Notes in Computer Science, 2013, , 99-111.	1.3	6

#	Article	IF	Citations
19	ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. Nucleic Acids Research, 2012, 41, D142-D151.	14.5	47
20	Modelling and simulating generic RNA-Seq experiments with the flux simulator. Nucleic Acids Research, 2012, 40, 10073-10083.	14.5	264
21	Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. Genome Research, 2012, 22, 1231-1242.	5.5	143
22	Exploration of the core metabolism of symbiotic bacteria. BMC Genomics, 2012, 13, 438.	2.8	11
23	Telling stories: Enumerating maximal directed acyclic graphs with a constrained set of sources and targets. Theoretical Computer Science, 2012, 457, 1-9.	0.9	8
24	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. PLoS ONE, 2012, 7, e28213.	2.5	61
25	KIS SPLICE: de-novo calling alternative splicing events from RNA-seq data. BMC Bioinformatics, 2012, 13, S5.	2.6	85
26	Efficient Bubble Enumeration in Directed Graphs. Lecture Notes in Computer Science, 2012, , 118-129.	1.3	13
27	Close 3D proximity of evolutionary breakpoints argues for the notion of spatial synteny. BMC Genomics, 2011, 12, 303.	2.8	42
28	Identifying SNPs without a Reference Genome by Comparing Raw Reads. Lecture Notes in Computer Science, 2010, , 147-158.	1.3	35
29	Enumerating Chemical Organisations in Consistent Metabolic Networks: Complexity and Algorithms. Lecture Notes in Computer Science, 2010, , 226-237.	1.3	1
30	Assessing the Exceptionality of Coloured Motifs in Networks. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 1-9.	1.4	11
31	Modes and cuts in metabolic networks: Complexity and algorithms. BioSystems, 2009, 95, 51-60.	2.0	88
32	Assessing the Exceptionality of Coloured Motifs in Networks. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 616234.	1.4	15
33	An Introduction to Metabolic Networks and Their Structural Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 594-617.	3.0	103
34	Exact Transcriptome Reconstruction from Short Sequence Reads. Lecture Notes in Computer Science, 2008, , 50-63.	1.3	40
35	Metabolic network visualization eliminating node redundance and preserving metabolic pathways. BMC Systems Biology, 2007, 1, 29.	3.0	35
36	Motif Search in Graphs: Application to Metabolic Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 360-368.	3.0	146

#	ARTICLE	IF	CITATIONS
37	Reaction Motifs in Metabolic Networks. Lecture Notes in Computer Science, 2005, , 178-191.	1.3	7