

Vincent Lacroix

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4423980/publications.pdf>

Version: 2024-02-01

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	Modelling and simulating generic RNA-Seq experiments with the flux simulator. <i>Nucleic Acids Research</i> , 2012, 40, 10073-10083.	14.5	264
2	Splicing misregulation of SCN5A contributes to cardiac-conduction delay and heart arrhythmia in myotonic dystrophy. <i>Nature Communications</i> , 2016, 7, 11067.	12.8	155
3	Motif Search in Graphs: Application to Metabolic Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 360-368.	3.0	146
4	A fast and agnostic method for bacterial genome-wide association studies: Bridging the gap between k-mers and genetic events. <i>PLoS Genetics</i> , 2018, 14, e1007758.	3.5	144
5	Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. <i>Genome Research</i> , 2012, 22, 1231-1242.	5.5	143
6	An Introduction to Metabolic Networks and Their Structural Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 594-617.	3.0	103
7	Transcriptome profiling of mouse samples using nanopore sequencing of cDNA and RNA molecules. <i>Scientific Reports</i> , 2019, 9, 14908.	3.3	90
8	Modes and cuts in metabolic networks: Complexity and algorithms. <i>BioSystems</i> , 2009, 95, 51-60.	2.0	88
9	KIS SPLICE: de-novo calling alternative splicing events from RNA-seq data. <i>BMC Bioinformatics</i> , 2012, 13, S5.	2.6	85
10	Reference-free detection of isolated SNPs. <i>Nucleic Acids Research</i> , 2015, 43, e11-e11.	14.5	75
11	SNP calling from RNA-seq data without a reference genome: identification, quantification, differential analysis and impact on the protein sequence. <i>Nucleic Acids Research</i> , 2016, 44, gkw655.	14.5	66
12	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. <i>PLoS ONE</i> , 2012, 7, e28213.	2.5	61
13	Identification of misexpressed genetic elements in hybrids between <i>Drosophila</i> -related species. <i>Scientific Reports</i> , 2017, 7, 40618.	3.3	49
14	Advances in Analyzing Virus-Induced Alterations of Host Cell Splicing. <i>Trends in Microbiology</i> , 2019, 27, 268-281.	7.7	49
15	ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. <i>Nucleic Acids Research</i> , 2012, 41, D142-D151.	14.5	47
16	Close 3D proximity of evolutionary breakpoints argues for the notion of spatial synteny. <i>BMC Genomics</i> , 2011, 12, 303.	2.8	42
17	Exact Transcriptome Reconstruction from Short Sequence Reads. <i>Lecture Notes in Computer Science</i> , 2008, , 50-63.	1.3	40
18	Metabolic network visualization eliminating node redundancy and preserving metabolic pathways. <i>BMC Systems Biology</i> , 2007, 1, 29.	3.0	35

#	ARTICLE	IF	CITATIONS
19	Identifying SNPs without a Reference Genome by Comparing Raw Reads. Lecture Notes in Computer Science, 2010, , 147-158.	1.3	35
20	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
21	New insights into minor splicingâ€™a transcriptomic analysis of cells derived from TALS patients. Rna, 2019, 25, 1130-1149.	3.5	27
22	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
23	Assessing the Exceptionality of Coloured Motifs in Networks. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 616234.	1.4	15
24	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
25	Efficient Bubble Enumeration in Directed Graphs. Lecture Notes in Computer Science, 2012, , 118-129.	1.3	13
26	Assessing the Exceptionality of Coloured Motifs in Networks. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 1-9.	1.4	11
27	Exploration of the core metabolism of symbiotic bacteria. BMC Genomics, 2012, 13, 438.	2.8	11
28	Short and long-term genome stability analysis of prokaryotic genomes. BMC Genomics, 2013, 14, 309.	2.8	9
29	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
30	Clinical interpretation of variants identified in RNU4ATAC, a non-coding spliceosomal gene. PLoS ONE, 2020, 15, e0235655.	2.5	8
31	Reaction Motifs in Metabolic Networks. Lecture Notes in Computer Science, 2005, , 178-191.	1.3	7
32	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
33	Influenza virus infection induces widespread alterations of host cell splicing. NAR Genomics and Bioinformatics, 2020, 2, lqaa095.	3.2	6
34	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
35	Colibâ€™read on galaxy: a tools suite dedicated to biological information extraction from raw NGS reads. GigaScience, 2016, 5, 9.	6.4	2
36	Navigating in a Sea of Repeats in RNA-seq without Drowning. Lecture Notes in Computer Science, 2014, , 82-96.	1.3	2

#	ARTICLE	IF	CITATIONS
37	Enumerating Chemical Organisations in Consistent Metabolic Networks: Complexity and Algorithms. Lecture Notes in Computer Science, 2010, , 226-237.	1.3	1