

Guillaume Marçais

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4829454/publications.pdf>

Version: 2024-02-01

24
papers

5,225
citations

471509

17
h-index

642732

23
g-index

29
all docs

29
docs citations

29
times ranked

9068
citing authors

#	ARTICLE	IF	CITATIONS
1	Harvestman: a framework for hierarchical feature learning and selection from whole genome sequencing data. BMC Bioinformatics, 2021, 22, 174.	2.6	1
2	Lower Density Selection Schemes via Small Universal Hitting Sets with Short Remaining Path Length. Journal of Computational Biology, 2021, 28, 395-409.	1.6	5
3	Sequence-specific minimizers via polar sets. Bioinformatics, 2021, 37, i187-i195.	4.1	14
4	Improved design and analysis of practical minimizers. Bioinformatics, 2020, 36, i119-i127.	4.1	31
5	Lower Density Selection Schemes via Small Universal Hitting Sets with Short Remaining Path Length. Lecture Notes in Computer Science, 2020, , 202-217.	1.3	6
6	Locality-sensitive hashing for the edit distance. Bioinformatics, 2019, 35, i127-i135.	4.1	40
7	Practical Universal k-mer Sets for Minimizer Schemes. , 2019, , .		18
8	Sketching and Sublinear Data Structures in Genomics. Annual Review of Biomedical Data Science, 2019, 2, 93-118.	6.5	37
9	Asymptotically optimal minimizers schemes. Bioinformatics, 2018, 34, i13-i22.	4.1	44
10	MUMmer4: A fast and versatile genome alignment system. PLoS Computational Biology, 2018, 14, e1005944.	3.2	1,412
11	Hybrid assembly of the large and highly repetitive genome of <i>Aegilops tauschii</i> , a progenitor of bread wheat, with the MaSuRCA mega-reads algorithm. Genome Research, 2017, 27, 787-792.	5.5	382
12	Improving the performance of minimizers and winnowing schemes. Bioinformatics, 2017, 33, i110-i117.	4.1	62
13	Designing small universal k-mer hitting sets for improved analysis of high-throughput sequencing. PLoS Computational Biology, 2017, 13, e1005777.	3.2	42
14	Compact Universal k-mer Hitting Sets. Lecture Notes in Computer Science, 2016, , 257-268.	1.3	24
15	Sequence of the Sugar Pine Megagenome. Genetics, 2016, 204, 1613-1626.	2.9	169
16	Quorum: An Error Corrector for Illumina Reads. PLoS ONE, 2015, 10, e0130821.	2.5	71
17	A new rhesus macaque assembly and annotation for next-generation sequencing analyses. Biology Direct, 2014, 9, 20.	4.6	165
18	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. Genetics, 2014, 196, 875-890.	2.9	286

#	ARTICLE	IF	CITATIONS
19	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014, 15, R59.	9.6	424
20	Parsimonious reconstruction of network evolution. <i>Algorithms for Molecular Biology</i> , 2012, 7, 25.	1.2	13
21	GAGE: A critical evaluation of genome assemblies and assembly algorithms. <i>Genome Research</i> , 2012, 22, 557-567.	5.5	597
22	Mis-Assembled "Segmental Duplications" in Two Versions of the <i>Bos taurus</i> Genome. <i>PLoS ONE</i> , 2012, 7, e42680.	2.5	22
23	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (<i>Meleagris gallopavo</i>): Genome Assembly and Analysis. <i>PLoS Biology</i> , 2010, 8, e1000475.	5.6	348
24	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . <i>Genome Biology</i> , 2009, 10, R42.	9.6	1,005