Guillaume MarÃ§ais

List of Publications by Year
in descending order

24 papers	5,225 citations	471371 17 h-index	642610 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.	1.2	1
2	Lower Density Selection Schemes via Small Universal Hitting Sets with Short Remaining Path Length. Journal of Computational Biology, 2021, 28, 395-409.	0.8	5
3	Sequence-specific minimizers via polar sets. Bioinformatics, 2021, 37, i187-i195.	1.8	14
4	Improved design and analysis of practical minimizers. Bioinformatics, 2020, 36, i119-i127.	1.8	31
5	Lower Density Selection Schemes viaÂSmall Universal Hitting Sets withÂShort Remaining Path Length. Lecture Notes in Computer Science, 2020, , 202-217.	1.0	6
6	Locality-sensitive hashing for the edit distance. Bioinformatics, 2019, 35, i127-i135.	1.8	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.	2.8	37
9	Asymptotically optimal minimizers schemes. Bioinformatics, 2018, 34, i13-i22.	1.8	44
10	MUMmer4: A fast and versatile genome alignment system. PLoS Computational Biology, 2018, 14, e1005944.	1.5	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.	2.4	382
12	Improving the performance of minimizers and winnowing schemes. Bioinformatics, 2017, 33, i110-i117.	1.8	62
13	Designing small universal k-mer hitting sets for improved analysis of high-throughput sequencing. PLoS Computational Biology, 2017, 13, e1005777.	1.5	42
14	Compact Universal k-mer Hitting Sets. Lecture Notes in Computer Science, 2016, , 257-268.	1.0	24
15	Sequence of the Sugar Pine Megagenome. Genetics, 2016, 204, 1613-1626.	1.2	169
16	QuorUM: An Error Corrector for Illumina Reads. PLoS ONE, 2015, 10, e0130821.	1.1	71
17	A new rhesus macaque assembly and annotation for next-generation sequencing analyses. Biology Direct, 2014, 9, 20.	1.9	165
18	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. Genetics, 2014, 196, 875-890.	1.2	286

#	Article	IF	Citations
19	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. Genome Biology, 2014, 15, R59.	13.9	424
20	Parsimonious reconstruction of network evolution. Algorithms for Molecular Biology, 2012, 7, 25.	0.3	13
21	GAGE: A critical evaluation of genome assemblies and assembly algorithms. Genome Research, 2012, 22, 557-567.	2.4	597
22	Mis-Assembled â€œSegmental Duplicationsâ€•in Two Versions of the Bos taurus Genome. PLoS ONE, 2012, 7, e42680.	1.1	22
23	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	2.6	348
24	A whole-genome assembly of the domestic cow, Bos taurus. Genome Biology, 2009, 10, R42.	13.9	1,005