Guillaume MarÃ§ais

List of Publications by Year
in descending order

		471061	642321
24 papers	5,225 citations	17 h-index	23 g-index
29 all docs	29 docs citations	29 times ranked	9068 citing authors

#	Article	IF	Citations
1	MUMmer4: A fast and versatile genome alignment system. PLoS Computational Biology, 2018, 14, e1005944.	1.5	1,412
2	A whole-genome assembly of the domestic cow, Bos taurus. Genome Biology, 2009, 10, R42.	13.9	1,005
3	GAGE: A critical evaluation of genome assemblies and assembly algorithms. Genome Research, 2012, 22, 557-567.	2.4	597
4	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. Genome Biology, 2014, 15, R59.	13.9	424
5	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
6	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	2.6	348
7	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. Genetics, 2014, 196, 875-890.	1.2	286
8	Sequence of the Sugar Pine Megagenome. Genetics, 2016, 204, 1613-1626.	1.2	169
9	A new rhesus macaque assembly and annotation for next-generation sequencing analyses. Biology Direct, 2014, 9, 20.	1.9	165
10	QuorUM: An Error Corrector for Illumina Reads. PLoS ONE, 2015, 10, e0130821.	1.1	71
11	Improving the performance of minimizers and winnowing schemes. Bioinformatics, 2017, 33, i110-i117.	1.8	62
12	Asymptotically optimal minimizers schemes. Bioinformatics, 2018, 34, i13-i22.	1.8	44
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	Locality-sensitive hashing for the edit distance. Bioinformatics, 2019, 35, i127-i135.	1.8	40
15	Sketching and Sublinear Data Structures in Genomics. Annual Review of Biomedical Data Science, 2019, 2, 93-118.	2.8	37
16	Improved design and analysis of practical minimizers. Bioinformatics, 2020, 36, i119-i127.	1.8	31
17	Compact Universal k-mer Hitting Sets. Lecture Notes in Computer Science, 2016, , 257-268.	1.0	24
18	Mis-Assembled "Segmental Duplications" in Two Versions of the Bos taurus Genome. PLoS ONE, 2012, 7, e42680.	1.1	22

#	Article	IF	Citations
19	Practical Universal k-mer Sets for Minimizer Schemes. , 2019, , .		18
20	Sequence-specific minimizers via polar sets. Bioinformatics, 2021, 37, i187-i195.	1.8	14
21	Parsimonious reconstruction of network evolution. Algorithms for Molecular Biology, 2012, 7, 25.	0.3	13
22	Lower Density Selection Schemes viaÂSmall Universal Hitting Sets withÂShort Remaining Path Length. Lecture Notes in Computer Science, 2020, , 202-217.	1.0	6
23	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
24	Harvestman: a framework for hierarchical feature learning and selection from whole genome sequencing data. BMC Bioinformatics, 2021, 22, 174.	1.2	1