Xian F Mallory

List of Publications by Year
in descending order

20 papers	4,876 citations	567281 15 h-index	752698 20 g-index
22 all docs	22 docs citations	22 times ranked	11483 citing authors

#	Article	IF	Citations
1	SimSCSnTree: a simulator of single-cell DNA sequencing data. Bioinformatics, 2022, 38, 2912-2914.	4.1	7
2	Theoretical Analysis Reveals the Cost and Benefit of Proofreading in Coronavirus Genome Replication. Journal of Physical Chemistry Letters, 2021, 12, 2691-2698.	4.6	4
3	Assessing the performance of methods for copy number aberration detection from single-cell DNA sequencing data. PLoS Computational Biology, 2020, 16, e1008012.	3.2	33
4	Methods for copy number aberration detection from single-cell DNA-sequencing data. Genome Biology, 2020, 21, 208.	8.8	72
5	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
6	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
7	HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. Genome Research, 2017, 27, 793-800.	5.5	32
8	novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2017, 14, 65-67.	19.0	93
9	BreakPoint Surveyor: a pipeline for structural variant visualization. Bioinformatics, 2017, 33, 3121-3122.	4.1	5
10	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
11	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
12	Towards accurate characterization of clonal heterogeneity based on structural variation. BMC Bioinformatics, 2014, 15, 299.	2.6	10
13	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. Genome Research, 2014, 24, 310-317.	5.5	81
14	BreakDancer: Identification of Genomic Structural Variation from Pairedâ€End Read Mapping. Current Protocols in Bioinformatics, 2014, 45, 15.6.1-11.	25.8	135
15	BreakTrans: uncovering the genomic architecture of gene fusions. Genome Biology, 2013, 14, R87.	9.6	25
16	Integrated genotyping of structural variation. , 2013, , .		0
17	Background Mutations in Parental Cells Account for Most of the Genetic Heterogeneity of Induced Pluripotent Stem Cells. Cell Stem Cell, 2012, 10, 570-582.	11.1	199
18	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	27.0	688

#	Article	IF	Citations
19	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	19.0	451
20	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. Journal of Clinical Investigation, 2011, 121, 1445-1455.	8.2	91