Ashley D Sanders

List of Publications by Year
in descending order

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Version: 2024-02-01

23 papers	2,425 citations	430442 18 h-index	642321 23 g-index
35 all docs	35 docs citations	35 times ranked	3162 citing authors

#	Article	IF	Citations
1	Familial long-read sequencing increases yield of de novo mutations. American Journal of Human Genetics, 2022, 109, 631-646.	2.6	32
2	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	13.5	67
3	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. Nature Biotechnology, 2021, 39, 302-308.	9.4	127
4	Construction of Whole Genomes from Scaffolds Using Single Cell Strand-Seq Data. International Journal of Molecular Sciences, 2021, 22, 3617.	1.8	5
5	ASHLEYS: automated quality control for single-cell Strand-seq data. Bioinformatics, 2021, 37, 3356-3357.	1.8	9
6	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
7	breakpointR: an R/Bioconductor package to localize strand state changes in Strand-seq data. Bioinformatics, 2020, 36, 1260-1261.	1.8	32
8	Improved assembly and variant detection of a haploid human genome using singleâ€molecule, highâ€fidelity long reads. Annals of Human Genetics, 2020, 84, 125-140.	0.3	100
9	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. Nature Biotechnology, 2020, 38, 343-354.	9.4	59
10	Single-cell strand sequencing of a macaque genome reveals multiple nested inversions and breakpoint reuse during primate evolution. Genome Research, 2020, 30, 1680-1693.	2.4	16
11	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, .	6.0	105
12	Recurrent inversion toggling and great ape genome evolution. Nature Genetics, 2020, 52, 849-858.	9.4	40
13	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
14	Genomic inversions and GOLGA core duplicons underlie disease instability at the 15q25 locus. PLoS Genetics, 2019, 15, e1008075.	1.5	17
15	Strand-seq enables reliable separation of long reads by chromosome via expectation maximization. Bioinformatics, 2018, 34, i115-i123.	1.8	24
16	Single-cell template strand sequencing by Strand-seq enables the characterization of individual homologs. Nature Protocols, 2017, 12, 1151-1176.	5.5	89
17	Dense and accurate whole-chromosome haplotyping of individual genomes. Nature Communications, 2017, 8, 1293.	5.8	83
18	Characterizing polymorphic inversions in human genomes by single-cell sequencing. Genome Research, 2016, 26, 1575-1587.	2.4	67

#	Article	IF	Citations
19	Direct chromosome-length haplotyping by single-cell sequencing. Genome Research, 2016, 26, 1565-1574.	2.4	52
20	The Prognostic Impact of CD163-Positive Macrophages in Follicular Lymphoma: A Study from the BC Cancer Agency and the Lymphoma Study Association. Clinical Cancer Research, 2015, 21, 3428-3435.	3.2	101
21	DNA template strand sequencing of single-cells maps genomic rearrangements at high resolution. Nature Methods, 2012, 9, 1107-1112.	9.0	160
22	Adult Spinal Cord Radial Glia Display a Unique Progenitor Phenotype. PLoS ONE, 2011, 6, e24538.	1.1	40
23	Essential role for Ptpn11 in survival of hematopoietic stem and progenitor cells. Blood, 2011, 117, 4253-4261.	0.6	82