Ashley D Sanders

List of Publications by Year
in descending order

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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	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
2	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
3	DNA template strand sequencing of single-cells maps genomic rearrangements at high resolution. Nature Methods, 2012, 9, 1107-1112.	9.0	160
4	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
5	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, .	6.0	105
6	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
7	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
8	Single-cell template strand sequencing by Strand-seq enables the characterization of individual homologs. Nature Protocols, 2017, 12, 1151-1176.	5.5	89
9	Dense and accurate whole-chromosome haplotyping of individual genomes. Nature Communications, 2017, 8, 1293.	5.8	83
10	Essential role for Ptpn11 in survival of hematopoietic stem and progenitor cells. Blood, 2011, 117, 4253-4261.	0.6	82
11	Characterizing polymorphic inversions in human genomes by single-cell sequencing. Genome Research, 2016, 26, 1575-1587.	2.4	67
12	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	13.5	67
13	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. Nature Biotechnology, 2020, 38, 343-354.	9.4	59
14	Direct chromosome-length haplotyping by single-cell sequencing. Genome Research, 2016, 26, 1565-1574.	2.4	52
15	Adult Spinal Cord Radial Glia Display a Unique Progenitor Phenotype. PLoS ONE, 2011, 6, e24538.	1.1	40
16	Recurrent inversion toggling and great ape genome evolution. Nature Genetics, 2020, 52, 849-858.	9.4	40
17	breakpointR: an R/Bioconductor package to localize strand state changes in Strand-seq data. Bioinformatics, 2020, 36, 1260-1261.	1.8	32
18	Familial long-read sequencing increases yield of de novo mutations. American Journal of Human Genetics, 2022, 109, 631-646.	2.6	32

#	Article	IF	Citations
19	Strand-seq enables reliable separation of long reads by chromosome via expectation maximization. Bioinformatics, 2018, 34, i115-i123.	1.8	24
20	Genomic inversions and GOLGA core duplicons underlie disease instability at the 15q25 locus. PLoS Genetics, 2019, 15, e1008075.	1.5	17
21	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
22	ASHLEYS: automated quality control for single-cell Strand-seq data. Bioinformatics, 2021, 37, 3356-3357.	1.8	9
23	Construction of Whole Genomes from Scaffolds Using Single Cell Strand-Seq Data. International Journal of Molecular Sciences, 2021, 22, 3617.	1.8	5