Andrew Carroll

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4705451/publications.pdf

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19	2,287	933447	996975
papers	citations	10 h-index	15 g-index

32	32	32	3141
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. Nature Biotechnology, 2019, 37, 1155-1162.	17.5	1,010
2	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
3	Assessing structural variation in a personal genomeâ€"towards a human reference diploid genome. BMC Genomics, 2015, 16, 286.	2.8	153
4	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. Nature Methods, 2021, 18, 1322-1332.	19.0	139
5	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	12.6	132
6	Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting. New England Journal of Medicine, 2022, 386, 700-702.	27.0	116
7	Accurate, scalable cohort variant calls using DeepVariant and GLnexus. Bioinformatics, 2021, 36, 5582-5589.	4.1	86
8	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	12.8	56
9	Accelerated identification of disease-causing variants with ultra-rapid nanopore genome sequencing. Nature Biotechnology, 2022, 40, 1035-1041.	17.5	45
10	Large-scale machine-learning-based phenotyping significantly improves genomic discovery for optic nerve head morphology. American Journal of Human Genetics, 2021, 108, 1217-1230.	6.2	35
11	DeepNull models non-linear covariate effects to improve phenotypic prediction and association power. Nature Communications, 2022, 13, 241.	12.8	17
12	A population-specific reference panel for improved genotype imputation in African Americans. Communications Biology, 2021, 4, 1269.	4.4	15
13	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
14	Ultra-Rapid Nanopore Whole Genome Genetic Diagnosis of Dilated Cardiomyopathy in an Adolescent With Cardiogenic Shock. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003591.	3.6	3
15	A complete pedigree-based graph workflow for rare candidate variant analysis. Genome Research, 2022, , .	5.5	1
16	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
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