Andrew Carroll

List of Publications by Year
in descending order

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

Version: 2024-02-01

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	DeepNull models non-linear covariate effects to improve phenotypic prediction and association power. Nature Communications, 2022, 13, 241.	12.8	17
2	Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting. New England Journal of Medicine, 2022, 386, 700-702.	27.0	116
3	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
4	Accelerated identification of disease-causing variants with ultra-rapid nanopore genome sequencing. Nature Biotechnology, 2022, 40, 1035-1041.	17.5	45
5	A complete pedigree-based graph workflow for rare candidate variant analysis. Genome Research, 2022, , .	5.5	1
6	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
7	Accurate, scalable cohort variant calls using DeepVariant and GLnexus. Bioinformatics, 2021, 36, 5582-5589.	4.1	86
8	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. Nature Methods, 2021, 18, 1322-1332.	19.0	139
9	A population-specific reference panel for improved genotype imputation in African Americans. Communications Biology, 2021, 4, 1269.	4.4	15
10	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	12.6	132
11	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	12.8	56
12	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
13	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
14	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
15	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
16	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
17	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
18	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

#	Article	IF	Citations
19	Assessing structural variation in a personal genomeâ€”towards a human reference diploid genome. BMC Genomics, 2015, 16, 286.	2.8	153