Chunlin Xiao

List of Publications by Year
in descending order

21	15,676	759055 12	839398 18
papers	citations	h-index	g-index

28	28	28	15624
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome Biology, 2022, 23, 2.	3.8	18
2	Achieving robust somatic mutation detection with deep learning models derived from reference data sets of a cancer sample. Genome Biology, 2022, 23, 12.	3.8	11
3	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	9.4	90
4	A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533.	6.0	144
5	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
6	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	3.0	77
7	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	3.8	20
8	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	9.4	66
9	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. Nature Biotechnology, 2021, 39, 1151-1160.	9.4	39
10	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. Scientific Data, 2021, 8, 296.	2.4	15
11	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	5.8	56
12	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	9.4	233
13	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	1.5	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	High-coverage, long-read sequencing of Han Chinese trio reference samples. Scientific Data, 2019, 6, 91.	2.4	13

#	Article	IF	Citations
19	An open resource for accurately benchmarking small variant and reference calls. Nature Biotechnology, 2019, 37, 561-566.	9.4	277
20	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	2.4	575
21	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623