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List of Publications by Year
in descending order

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Version: 2024-02-01

22 papers	2,606 citations	759233 12 h-index	794594 19 g-index
30 all docs	30 docs citations	30 times ranked	6633 citing authors

#	Article	IF	Citations
1	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	17.5	90
2	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
3	Somatic variant analysis of linked-reads sequencing data with Lancet. Bioinformatics, 2021, 37, 1918-1919.	4.1	1
4	Feather Gene Expression Elucidates the Developmental Basis of Plumage Iridescence in African Starlings. Journal of Heredity, 2021, 112, 417-429.	2.4	15
5	The genomic basis of evolutionary differentiation among honey bees. Genome Research, 2021, 31, 1203-1215.	5.5	17
6	Coding and noncoding variants in EBF3 are involved in HADDS and simplex autism. Human Genomics, 2021, 15, 44.	2.9	16
7	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. Nature Biotechnology, 2021, 39, 1129-1140.	17.5	69
8	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
9	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
10	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
11	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
12	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
13	ExpansionHunter: a sequence-graph-based tool to analyze variation in short tandem repeat regions. Bioinformatics, 2019, 35, 4754-4756.	4.1	183
14	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
15	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
16	Genome-wide somatic variant calling using localized colored de Bruijn graphs. Communications Biology, 2018, 1, 20.	4.4	85
17	YES1 amplification is a mechanism of acquired resistance to EGFR inhibitors identified by transposon mutagenesis and clinical genomics. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6030-E6038.	7.1	44
18	Indel variant analysis of short-read sequencing data with Scalpel. Nature Protocols, 2016, 11, 2529-2548.	12.0	99

#	Article	IF	Citations
19	The Challenge of Small-Scale Repeats for Indel Discovery. Frontiers in Bioengineering and Biotechnology, 2015, 3, 8.	4.1	41
20	Reducing INDEL calling errors in whole genome and exome sequencing data. Genome Medicine, 2014, 6, 89.	8.2	144
21	Accurate de novo and transmitted indel detection in exome-capture data using microassembly. Nature Methods, 2014, 11, 1033-1036.	19.0	194
22	De Novo Gene Disruptions in Children on the Autistic Spectrum. Neuron, 2012, 74, 285-299.	8.1	1,311