Giuseppe Narzisi

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7716561/publications.pdf

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	De Novo Gene Disruptions in Children on the Autistic Spectrum. Neuron, 2012, 74, 285-299.	8.1	1,311
2	Accurate de novo and transmitted indel detection in exome-capture data using microassembly. Nature Methods, 2014, 11, 1033-1036.	19.0	194
3	ExpansionHunter: a sequence-graph-based tool to analyze variation in short tandem repeat regions. Bioinformatics, 2019, 35, 4754-4756.	4.1	183
4	Reducing INDEL calling errors in whole genome and exome sequencing data. Genome Medicine, 2014, 6, 89.	8.2	144
5	Indel variant analysis of short-read sequencing data with Scalpel. Nature Protocols, 2016, 11, 2529-2548.	12.0	99
6	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	17.5	90
7	Genome-wide somatic variant calling using localized colored de Bruijn graphs. Communications Biology, 2018, 1, 20.	4.4	85
8	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
9	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. Nature Biotechnology, 2021, 39, 1129-1140.	17.5	69
10	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
11	The Challenge of Small-Scale Repeats for Indel Discovery. Frontiers in Bioengineering and Biotechnology, 2015, 3, 8.	4.1	41
12	The genomic basis of evolutionary differentiation among honey bees. Genome Research, 2021, 31, 1203-1215.	5.5	17
13	Coding and noncoding variants in EBF3 are involved in HADDS and simplex autism. Human Genomics, 2021, 15, 44.	2.9	16
14	Feather Gene Expression Elucidates the Developmental Basis of Plumage Iridescence in African Starlings. Journal of Heredity, 2021, 112, 417-429.	2.4	15
15	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
16	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
17	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
18	Somatic variant analysis of linked-reads sequencing data with Lancet. Bioinformatics, 2021, 37, 1918-1919.	4.1	1

#	Article	IF	Citations
19	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
20	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
21	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
22	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0