Noah Spies

List of Publications by Year in descending order

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1163117 1281871 1,217 14 8 11 citations h-index g-index papers 20 20 20 2481 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	5.3	575
2	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
3	Genome-wide reconstruction of complex structural variants using read clouds. Nature Methods, 2017, 14, 915-920.	19.0	96
4	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562. Genome Research, 2019, 29, 472-484.	5 . 5	78
5	Concepts in solid tumor evolution. Trends in Genetics, 2015, 31, 208-214.	6.7	51
6	svviz: a read viewer for validating structural variants. Bioinformatics, 2015, 31, 3994-3996.	4.1	46
7	Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2. Nucleic Acids Research, 2019, 47, 3846-3861.	14.5	45
8	Cell-lineage heterogeneity and driver mutation recurrence in pre-invasive breast neoplasia. Genome Medicine, 2015, 7, 28.	8.2	17
9	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
10	Constraint and divergence of global gene expression in the mammalian embryo. ELife, 2015, 4, e05538.	6.0	3
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	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
14	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0