Xian Fan

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11162411/publications.pdf

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16	4,847	687363 13	940533 16
papers	citations	h-index	g-index

20	20	20	11433
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
2	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
3	Detecting Large Indels Using Optical Map Data. Lecture Notes in Computer Science, 2018, , 108-127.	1.3	3
4	HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. Genome Research, 2017, 27, 793-800.	5.5	32
5	novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2017, 14, 65-67.	19.0	93
6	BreakPoint Surveyor: a pipeline for structural variant visualization. Bioinformatics, 2017, 33, 3121-3122.	4.1	5
7	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
8	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
9	Towards accurate characterization of clonal heterogeneity based on structural variation. BMC Bioinformatics, 2014, 15, 299.	2.6	10
10	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. Genome Research, 2014, 24, 310-317.	5.5	81
11	BreakDancer: Identification of Genomic Structural Variation from Pairedâ€End Read Mapping. Current Protocols in Bioinformatics, 2014, 45, 15.6.1-11.	25.8	135
12	BreakTrans: uncovering the genomic architecture of gene fusions. Genome Biology, 2013, 14, R87.	9.6	25
13	Background Mutations in Parental Cells Account for Most of the Genetic Heterogeneity of Induced Pluripotent Stem Cells. Cell Stem Cell, 2012, 10, 570-582.	11.1	199
14	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	27.0	688
15	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	19.0	451
16	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. Journal of Clinical Investigation, 2011, 121, 1445-1455.	8.2	91