Byunggil Yoo

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6181897/publications.pdf

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17	732	933447 10	1281871 11
papers	citations	h-index	g-index

19	19	19	1710
all docs	docs citations	times ranked	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	Factors Affecting Migration to GRCh38 in Laboratories Performing Clinical Next-Generation Sequencing. Journal of Molecular Diagnostics, 2021, 23, 651-657.	2.8	13
4	Single-Cell Genomic Analysis Identifies Prognostically Significant Gene Expression Programs in Infant Acute Lymphoblastic Leukemia. Blood, 2021, 138, 3480-3480.	1.4	0
5	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	12.8	56
6	Decitabine and Vorinostat with Chemotherapy in Relapsed Pediatric Acute Lymphoblastic Leukemia: A TACL Pilot Study. Clinical Cancer Research, 2020, 26, 2297-2307.	7.0	28
7	Germline Variants Associated with Cancer Predisposition and Bone Marrow Failure Are Common in KMT2A-r Infant Acute Lymphoblastic Leukemia Patients. Blood, 2020, 136, 41-41.	1.4	0
8	Single Cell Sequencing Reveals Heterogeneity of Gene Expression in KMT2A Rearranged Infant ALL at Relapse Compared to Diagnosis. Blood, 2019, 134, 2756-2756.	1.4	0
9	POLR3A variants in hereditary spastic paraplegia and ataxia. Brain, 2018, 141, e1-e1.	7.6	17
10	Whole Genome Bisulfite Sequencing (WGBS) Robustly Measures the Pharmacodynamic Effect of Decitabine/Vorinostat Epigenetic Treatment in Relapsed Pediatric ALL Demonstrating Potent Hypomethylation Associated with Upregulation of PRC2 and TP53 Targets. Blood, 2018, 132, 918-918.	1.4	0
11	The CMH Warehouse. , 2016, , .		0
12	Clinical detection of deletion structural variants in whole-genome sequences. Npj Genomic Medicine, 2016, 1, 16026.	3.8	29
13	Landscape of Somatic Mutations and Gene Expression Changes in Relapsed Infant MLL-Rearranged Acute Lymphoblastic Leukemia. Blood, 2016, 128, 1735-1735.	1.4	22
14	Deciphering the Developmental Dynamics of the Mouse Liver Transcriptome. PLoS ONE, 2015, 10, e0141220.	2.5	35
15	A 26-hour system of highly sensitive whole genome sequencing for emergency management of genetic diseases. Genome Medicine, 2015, 7, 100.	8.2	237
16	An integrated transcriptome and expressed variant analysis of sepsis survival and death. Genome Medicine, 2014, 6, 111.	8.2	70
17	Use of Dried Blood Spots for High through-Put, Rapid Turnaround Mutational Analysis in Patients with Hemophilia. Blood, 2014, 124, 5034-5034.	1.4	0