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	A 26-hour system of highly sensitive whole genome sequencing for emergency management of genetic diseases. Genome Medicine, 2015, 7, 100.	8.2	237
2	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	17.5	90
3	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
4	An integrated transcriptome and expressed variant analysis of sepsis survival and death. Genome Medicine, 2014, 6, 111.	8.2	70
5	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	12.8	56
6	Deciphering the Developmental Dynamics of the Mouse Liver Transcriptome. PLoS ONE, 2015, 10, e0141220.	2.5	35
7	Clinical detection of deletion structural variants in whole-genome sequences. Npj Genomic Medicine, 2016, 1, 16026.	3.8	29
8	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
9	Landscape of Somatic Mutations and Gene Expression Changes in Relapsed Infant MLL-Rearranged Acute Lymphoblastic Leukemia. Blood, 2016, 128, 1735-1735.	1.4	22
10	POLR3A variants in hereditary spastic paraplegia and ataxia. Brain, 2018, 141, e1-e1.	7.6	17
11	Factors Affecting Migration to GRCh38 in Laboratories Performing Clinical Next-Generation Sequencing. Journal of Molecular Diagnostics, 2021, 23, 651-657.	2.8	13
12	The CMH Warehouse. , 2016, , .		0
13	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
14	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
15	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
16	Single-Cell Genomic Analysis Identifies Prognostically Significant Gene Expression Programs in Infant Acute Lymphoblastic Leukemia. Blood, 2021, 138, 3480-3480.	1.4	0
17	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