Liqing Tian

List of Publications by Year
in descending order

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26 papers	1,381 citations	623699 14 h-index	752679 20 g-index
27 all docs	27 docs citations	27 times ranked	2678 citing authors

#	Article	IF	Citations
1	LncRNA profile study reveals a three-lncRNA signature associated with the survival of patients with oesophageal squamous cell carcinoma. Gut, 2014, 63, 1700-1710.	12.1	385
2	Analysis of error profiles in deep next-generation sequencing data. Genome Biology, 2019, 20, 50.	8.8	196
3	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. Blood, 2020, 135, 41-55.	1.4	171
4	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. Cancer Discovery, 2021, 11, 1082-1099.	9.4	109
5	Acute depletion of CTCF directly affects MYC regulation through loss of enhancerâ€“promoter looping. Nucleic Acids Research, 2019, 47, 6699-6713.	14.5	98
6	CICERO: a versatile method for detecting complex and diverse driver fusions using cancer RNA sequencing data. Genome Biology, 2020, 21, 126.	8.8	74
7	Improved side-chain modeling by coupling clash-detection guided iterative search with rotamer relaxation. Bioinformatics, 2011, 27, 785-790.	4.1	52
8	MiRâ€23a in amplified 19p13.13 loci targets metallothionein 2A and promotes growth in gastric cancer cells. Journal of Cellular Biochemistry, 2013, 114, 2160-2169.	2.6	49
9	Discovery of regulatory noncoding variants in individual cancer genomes by using cis-X. Nature Genetics, 2020, 52, 811-818.	21.4	47
10	MiRNA expression profile reveals a prognostic signature for esophageal squamous cell carcinoma. Cancer Letters, 2014, 350, 34-42.	7.2	43
11	Transcriptome profiling of esophageal squamous cell carcinoma reveals a long noncoding RNA acting as a tumor suppressor. Oncotarget, 2015, 6, 17065-17080.	1.8	39
12	Integrated Genomic Analysis Identifies UBTF Tandem Duplications as a Recurrent Lesion in Pediatric Acute Myeloid Leukemia. Blood Cancer Discovery, 2022, 3, 194-207.	5.0	38
13	Exploration of Coding and Non-coding Variants in Cancer Using GenomePaint. Cancer Cell, 2021, 39, 83-95.e4.	16.8	18
14	Long-read sequencing unveils IGH-DUX4 translocation into the silenced IGH allele in B-cell acute lymphoblastic leukemia. Nature Communications, 2019, 10, 2789.	12.8	14
15	Incorporation of Local Structural Preference Potential Improves Fold Recognition. PLoS ONE, 2011, 6, e17215.	2.5	13
16	Integrative network analysis reveals USP7 haploinsufficiency inhibits E-protein activity in pediatric T-lineage acute lymphoblastic leukemia (T-ALL). Scientific Reports, 2021, 11, 5154.	3.3	10
17	The landscape of coding RNA editing events in pediatric cancer. BMC Cancer, 2021, 21, 1233.	2.6	7
18	NCACO-score: An effective main-chain dependent scoring function for structure modeling. BMC Bioinformatics, 2011, 12, 208.	2.6	4

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19	A point mutation in the DNA-binding domain of HPV-2 E2 protein increases its DNA-binding capacity and reverses its transcriptional regulatory activity on the viral early promoter. BMC Molecular Biology, 2012, 13, 5.	3.0	4
20	Editorial: Big Data and Machine Learning in Cancer Genomics. Frontiers in Genetics, 2021, 12, 749584.	2.3	2
21	Abstract 1485: Allelic specificity of immunoglobulin heavy chain (IGH) translocation in B-cell acute lymphoblastic leukemia (B-ALL) unveiled by long-read sequencing. , 2018, , .		2
22	Abstract 1543: Mining cancer-specific isoforms as CAR T-cell therapy targets for pediatric solid and brain tumors. , 2021, , .		1
23	Mutational Landscape and Temporal Evolution during Treatment of Relapsed Acute Lymphoblastic Leukemia. Blood, 2018, 132, 917-917.	1.4	0
24	Abstract 2872: Acquisition of drug resistance mutations during chemotherapy treatment in pediatric acute lymphoblastic leukemia. , 2019, , .		0
25	Abstract 5478: CICERO: An accurate method for detecting complex and diverse driver fusions using cancer transcriptome sequencing (RNA-seq) data. , 2020, , .		0
26	Integrated Genomic Analysis Identifies UBTF Tandem Duplications As a Subtype-Defining Lesion in Pediatric Acute Myeloid Leukemia. Blood, 2021, 138, LBA-4-LBA-4.	1.4	0