

Qiang Gong

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

1,602
citations

623574

14
h-index

526166

27
g-index

31
all docs

31
docs citations

31
times ranked

2940
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic characterization and drug sensitivity study of newly derived HGBL double/triple-hit lymphoma cell lines. <i>Blood Advances</i> , 2022, 6, 5067-5071.	2.5	2
2	Genomic profiling identifies distinct genetic subtypes in extra-nodal natural killer/T-cell lymphoma. <i>Leukemia</i> , 2022, 36, 2064-2075.	3.3	15
3	Double-hit Signature with <i>TP53</i> Abnormalities Predicts Poor Survival in Patients with Germinal Center Type Diffuse Large B-cell Lymphoma Treated with R-CHOP. <i>Clinical Cancer Research</i> , 2021, 27, 1671-1680.	3.2	24
4	Genetic manipulation of primary human natural killer cells to investigate the functional and oncogenic roles of PRDM1. <i>Haematologica</i> , 2020, 106, haematol.2020.254276.	1.7	5
5	Genomic characterization of diffuse large B-cell lymphoma transformation of nodular lymphocyte-predominant Hodgkin lymphoma. <i>Leukemia</i> , 2020, 34, 2238-2242.	3.3	6
6	Double-Hit Signature with <i>TP53</i> Abnormalities Predicts Poor Survival in Patients with Germinal Center Type Diffuse Large B-Cell Lymphoma Treated with R-CHOP. <i>Blood</i> , 2020, 136, 25-26.	0.6	1
7	A Unique Histone H3K4me3 Genome Binding Pattern Identified in a Cancer Pedigree with an MLL3 Germline Mutation. <i>Blood</i> , 2020, 136, 35-36.	0.6	0
8	Genetic drivers of oncogenic pathways in molecular subgroups of peripheral T-cell lymphoma. <i>Blood</i> , 2019, 133, 1664-1676.	0.6	184
9	Multi-omics Analysis of Primary Cell Culture Models Reveals Genetic and Epigenetic Basis of Intratumoral Phenotypic Diversity. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 576-589.	3.0	10
10	PRDM1 Binds an Extensive Network of Genes to Regulate Human Natural Killer Cell Homeostasis. <i>Blood</i> , 2019, 134, 2536-2536.	0.6	0
11	Genomic Characterization of Diffuse Large B-Cell Lymphoma Transformation from Nodular Lymphocyte Predominant Hodgkin Lymphoma. <i>Blood</i> , 2019, 134, 1486-1486.	0.6	0
12	Multi-Kinase Inhibitor with Anti-p38 $\hat{1}$ 3 Activity in Cutaneous T-Cell Lymphoma. <i>Journal of Investigative Dermatology</i> , 2018, 138, 2377-2387.	0.3	16
13	New Genomic Model Integrating Clinical Factors and Gene Mutations to Predict Overall Survival in Patients with Diffuse Large B-Cell Lymphoma Treated with R-CHOP. <i>Blood</i> , 2018, 132, 346-346.	0.6	6
14	Combined copy number and mutation analysis identifies oncogenic pathways associated with transformation of follicular lymphoma. <i>Leukemia</i> , 2017, 31, 83-91.	3.3	87
15	Whole transcriptome analysis reveals dysregulated oncogenic lncRNAs in natural killer/T-cell lymphoma and establishes MIR155HG as a target of PRDM1. <i>Tumor Biology</i> , 2017, 39, 101042831770164.	0.8	30
16	Assessment of T-cell receptor repertoire and clonal expansion in peripheral T-cell lymphoma using RNA-seq data. <i>Scientific Reports</i> , 2017, 7, 11301.	1.6	27
17	Flow cytometric sorting coupled with exon capture sequencing identifies somatic mutations in archival lymphoma tissues. <i>Laboratory Investigation</i> , 2017, 97, 1364-1374.	1.7	1
18	Diagnostic and Biological Significance of KIR Expression Profile Determined by RNA-Seq in Natural Killer/T-Cell Lymphoma. <i>American Journal of Pathology</i> , 2016, 186, 1435-1441.	1.9	16

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19	Comment on: Frequent CTLA4-CD28 gene fusion in diverse types of T-cell lymphoma, by Yoo et al.. Haematologica, 2016, 101, e269-e270.	1.7	14
20	Recurrent activating mutations of CD28 in peripheral T-cell lymphomas. Leukemia, 2016, 30, 1062-1070.	3.3	107
21	Driver Mutations Affecting Natural Killer/T Cell Lymphoma. Blood, 2016, 128, 4109-4109.	0.6	1
22	IDH2 R172 mutations define a unique subgroup of patients with angioimmunoblastic T-cell lymphoma. Blood, 2015, 126, 1741-1752.	0.6	184
23	Activating mutations of STAT5B and STAT3 in lymphomas derived from $\alpha\beta$ -T or NK cells. Nature Communications, 2015, 6, 6025.	5.8	334
24	Global Promoter Methylation Analysis Reveals Novel Candidate Tumor Suppressor Genes in Natural Killer Cell Lymphoma. Clinical Cancer Research, 2015, 21, 1699-1711.	3.2	78
25	Extremely high genetic diversity in a single tumor points to prevalence of non-Darwinian cell evolution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6496-505.	3.3	313
26	Assessment of T-Cell Receptor Repertoire and Clonal Expansion in Peripheral T-Cell Lymphoma Using RNA-Seq Data. Blood, 2015, 126, 1451-1451.	0.6	0
27	Identification of medium-sized genomic deletions with low coverage, mate-paired restricted tags. BMC Genomics, 2013, 14, 51.	1.2	1
28	The Evolution of Small Insertions and Deletions in the Coding Genes of Drosophila melanogaster. Molecular Biology and Evolution, 2013, 30, 2699-2708.	3.5	6
29	Pseudo-Sanger sequencing: massively parallel production of long and near error-free reads using NGS technology. BMC Genomics, 2013, 14, 711.	1.2	12
30	Rapid growth of a hepatocellular carcinoma and the driving mutations revealed by cell-population genetic analysis of whole-genome data. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12042-12047.	3.3	117
31	Nucleotide polymorphism of the TNF gene cluster in six Chinese populations. Journal of Human Genetics, 2010, 55, 350-357.	1.1	5