

Guangwu Guo

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

6,724
citations

394421

19
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642732

23
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26
all docs

26
docs citations

26
times ranked

13736
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell-free DNA for the detection of emerging treatment failure in relapsed/ refractory multiple myeloma. <i>Leukemia</i> , 2022, 36, 1078-1087.	7.2	13
2	Single-cell RNA-seq reveals developmental plasticity with coexisting oncogenic states and immune evasion programs in ETP-ALL. <i>Blood</i> , 2021, 137, 2463-2480.	1.4	35
3	Single-Cell Profiling Reveals Metabolic Reprogramming as a Resistance Mechanism in <i>BRAF</i> -Mutated Multiple Myeloma. <i>Clinical Cancer Research</i> , 2021, 27, 6432-6444.	7.0	18
4	CD4 ⁺ TSCMs in the Bone Marrow Assist in Maturation of Antibodies against Influenza in Mice. <i>Mediators of Inflammation</i> , 2019, 2019, 1-10.	3.0	4
5	Defining the Differentiation States of Multiple Myeloma at Single Cell Resolution Reveals Opportunities for Immunotherapy. <i>Blood</i> , 2019, 134, 3091-3091.	1.4	0
6	Genomic discovery and clonal tracking in multiple myeloma by cell-free DNA sequencing. <i>Leukemia</i> , 2018, 32, 1838-1841.	7.2	42
7	Insertions and Deletions Target Lineage-Defining Genes in Human Cancers. <i>Cell</i> , 2017, 168, 460-472.e14.	28.9	106
8	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	28.9	1,742
9	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	21.4	933
10	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. <i>Science Translational Medicine</i> , 2016, 8, 363ra147.	12.4	126
11	Peptidomimetic Blockade of MYB in Acute Myeloid Leukemia. <i>Blood</i> , 2016, 128, 3945-3945.	1.4	0
12	Comprehensive Genetic Interrogation of Circulating Multiple Myeloma Cells at Single Cell Resolution. <i>Blood</i> , 2016, 128, 800-800.	1.4	0
13	Whole Exome Sequencing Identifies Frequent Somatic Mutations in Cell-Cell Adhesion Genes in Chinese Patients with Lung Squamous Cell Carcinoma. <i>Scientific Reports</i> , 2015, 5, 14237.	3.3	51
14	Whole-Exome Sequencing Reveals Frequent Genetic Alterations in <i>BAP1</i> , <i>NF2</i> , <i>CDKN2A</i> , and <i>CUL1</i> in Malignant Pleural Mesothelioma. <i>Cancer Research</i> , 2015, 75, 264-269.	0.9	289
15	Multilayered molecular profiling supported the monoclonal origin of metastatic renal cell carcinoma. <i>International Journal of Cancer</i> , 2014, 135, 78-87.	5.1	30
16	Concurrent Alterations in <i>TERT</i> , <i>KDM6A</i> , and the BRCA Pathway in Bladder Cancer. <i>Clinical Cancer Research</i> , 2014, 20, 4935-4948.	7.0	101
17	SOAPfuse: an algorithm for identifying fusion transcripts from paired-end RNA-Seq data. <i>Genome Biology</i> , 2013, 14, R12.	9.6	197
18	Whole-genome and whole-exome sequencing of bladder cancer identifies frequent alterations in genes involved in sister chromatid cohesion and segregation. <i>Nature Genetics</i> , 2013, 45, 1459-1463.	21.4	400

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19	Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor. <i>Cell</i> , 2012, 148, 886-895.	28.9	622
20	Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. <i>GigaScience</i> , 2012, 1, 12.	6.4	99
21	Frequent mutations of genes encoding ubiquitin-mediated proteolysis pathway components in clear cell renal cell carcinoma. <i>Nature Genetics</i> , 2012, 44, 17-19.	21.4	295
22	Frequent mutations of chromatin remodeling genes in transitional cell carcinoma of the bladder. <i>Nature Genetics</i> , 2011, 43, 875-878.	21.4	638
23	Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. <i>Nature Biotechnology</i> , 2010, 28, 516-520.	17.5	349
24	Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. <i>Genome Research</i> , 2010, 20, 646-654.	5.5	435
25	Survey of the transcriptome of <i>Aspergillus oryzae</i> via massively parallel mRNA sequencing. <i>Nucleic Acids Research</i> , 2010, 38, 5075-5087.	14.5	189