

Hongyi Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

607
citations

840776

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834
citing authors

#	ARTICLE	IF	CITATIONS
1	AXL targeting restores PD-1 blockade sensitivity of STK11/LKB1 mutant NSCLC through expansion of TCF1+ CD8 T cells. <i>Cell Reports Medicine</i> , 2022, 3, 100554.	6.5	29
2	Concurrent delivery of immune checkpoint blockade modulates T cell dynamics to enhance neoantigen vaccine-generated antitumor immunity. <i>Nature Cancer</i> , 2022, 3, 437-452.	13.2	19
3	DNA Sensing in Mismatch Repair-Deficient Tumor Cells Is Essential for Anti-tumor Immunity. <i>Cancer Cell</i> , 2021, 39, 96-108.e6.	16.8	153
4	GIANA allows computationally-efficient TCR clustering and multi-disease repertoire classification by isometric transformation. <i>Nature Communications</i> , 2021, 12, 4699.	12.8	30
5	602...AXL targeting with bemcentinib restores PD-1 blockade sensitivity of STK11/LKB1 mutant NSCLC through innate immune cell mediated expansion of TCF1+ CD8 T cells. , 2021, 9, A632-A632.		0
6	Investigation of Antigen-Specific T-Cell Receptor Clusters in Human Cancers. <i>Clinical Cancer Research</i> , 2020, 26, 1359-1371.	7.0	90
7	Breast cancer prognosis signature: linking risk stratification to disease subtypes. <i>Briefings in Bioinformatics</i> , 2019, 20, 2130-2140.	6.5	81
8	Sex difference of mutation clonality in diffuse glioma evolution. <i>Neuro-Oncology</i> , 2019, 21, 201-213.	1.2	32
9	Identifying mutual exclusivity across cancer genomes: computational approaches to discover genetic interaction and reveal tumor vulnerability. <i>Briefings in Bioinformatics</i> , 2019, 20, 254-266.	6.5	46
10	Abstract LB-145: Investigation of T cell dynamic changes in tumor progression by using single-cell data. , 2019, , .		0
11	SEECancer: a resource for somatic events in evolution of cancer genome. <i>Nucleic Acids Research</i> , 2018, 46, D1018-D1026.	14.5	9
12	Transcriptome analysis reveals a long non-coding RNA signature to improve biochemical recurrence prediction in prostate cancer. <i>Oncotarget</i> , 2018, 9, 24936-24949.	1.8	9
13	Cooperative genomic alteration network reveals molecular classification across 12 major cancer types. <i>Nucleic Acids Research</i> , 2017, 45, 567-582.	14.5	32
14	MeSiC: A Model-Based Method for Estimating 5mC Levels at Single-CpG Resolution from MeDIP-seq. <i>Scientific Reports</i> , 2015, 5, 14699.	3.3	12
15	Identifying core gene modules in glioblastoma based on multilayer factor-mediated dysfunctional regulatory networks through integrating multi-dimensional genomic data. <i>Nucleic Acids Research</i> , 2015, 43, 1997-2007.	14.5	31
16	Integrating Multi-Omics for Uncovering the Architecture of Cross-Talking Pathways in Breast Cancer. <i>PLoS ONE</i> , 2014, 9, e104282.	2.5	21
17	IndividualizedPath: identifying genetic alterations contributing to the dysfunctional pathways in glioblastoma individuals. <i>Molecular BioSystems</i> , 2014, 10, 2031-2042.	2.9	10