Liam F Spurr

List of Publications by Year in descending order

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Version: 2024-02-01

		759233	794594
18	1,130	12	19
papers	citations	h-index	g-index
24	24	24	2048
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Mechanisms and therapeutic implications of hypermutation in gliomas. Nature, 2020, 580, 517-523.	27.8	374
2	Microenvironment drives cell state, plasticity, and drug response in pancreatic cancer. Cell, 2021, 184, 6119-6137.e26.	28.9	201
3	Molecular Mechanisms of Acquired Resistance to MET Tyrosine Kinase Inhibitors in Patients with MET Exon 14–Mutant NSCLC. Clinical Cancer Research, 2020, 26, 2615-2625.	7.0	129
4	Impact of DNA Damage Response and Repair (DDR) Gene Mutations on Efficacy of PD-(L)1 Immune Checkpoint Inhibition in Non–Small Cell Lung Cancer. Clinical Cancer Research, 2020, 26, 4135-4142.	7.0	95
5	CDKN2A loss-of-function predicts immunotherapy resistance in non-small cell lung cancer. Scientific Reports, 2021, 11, 20059.	3.3	53
6	SMARCA4 and Other SWItch/Sucrose NonFermentable Family Genomic Alterations in NSCLC: Clinicopathologic Characteristics and Outcomes to Immune Checkpoint Inhibition. Journal of Thoracic Oncology, 2021, 16, 1176-1187.	1.1	49
7	Mammalian SWI/SNF Complex Genomic Alterations and Immune Checkpoint Blockade in Solid Tumors. Cancer Immunology Research, 2020, 8, 1075-1084.	3.4	47
8	Synthetic Lethal Interaction between the ESCRT Paralog Enzymes VPS4A and VPS4B in Cancers Harboring Loss of Chromosome 18q or 16q. Cell Reports, 2020, 33, 108493.	6.4	28
9	Genomic Characterization of <i>de novo</i> Metastatic Breast Cancer. Clinical Cancer Research, 2021, 27, 1105-1118.	7.0	24
10	Systematic pan-cancer analysis of somatic allele frequency. Scientific Reports, 2018, 8, 7735.	3.3	21
11	Quantification of aneuploidy in targeted sequencing data using ASCETS. Bioinformatics, 2021, 37, 2461-2463.	4.1	21
12	Molecular Characterization and Therapeutic Targeting of Colorectal Cancers Harboring Receptor Tyrosine Kinase Fusions. Clinical Cancer Research, 2021, 27, 1695-1705.	7.0	19
13	Estimating the Allele-Specific Expression of SNVs From 10× Genomics Single-Cell RNA-Sequencing Data. Genes, 2020, 11, 240.	2.4	14
14	ReQTL: identifying correlations between expressed SNVs and gene expression using RNA-sequencing data. Bioinformatics, 2020, 36, 1351-1359.	4.1	13
15	scReQTL: an approach to correlate SNVs to gene expression from individual scRNA-seq datasets. BMC Genomics, 2021, 22, 40.	2.8	11
16	Transcriptional dysregulation in developing trigeminal sensory neurons in the LgDel mouse model of DiGeorge 22q11.2 deletion syndrome. Human Molecular Genetics, 2020, 29, 1002-1017.	2.9	8
17	Overexpressed somatic alleles are enriched in functional elements in Breast Cancer. Scientific Reports, 2017, 7, 8287.	3.3	3
18	GeTallele: A Method for Analysis of DNA and RNA Allele Frequency Distributions. Frontiers in Bioengineering and Biotechnology, 2020, 8, 1021.	4.1	2