Qingsong Gao

List of Publications by Year
in descending order

26 papers	6,598 citations	516710 16 h-index	610901 24 g-index
27 all docs	27 docs citations	27 times ranked	13324 citing authors

#	Article	IF	Citations
1	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
2	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
3	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
4	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430
5	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
6	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	28.9	296
7	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
8	Co-evolution of tumor and immune cells during progression of multiple myeloma. Nature Communications, 2021, 12, 2559.	12.8	68
9	Phase Separation Mediates NUP98 Fusion Oncoprotein Leukemic Transformation. Cancer Discovery, 2022, 12, 1152-1169.	9.4	68
10	CharGer: clinical Characterization of Germline variants. Bioinformatics, 2019, 35, 865-867.	4.1	39
11	Predominant contribution of cisâ€‹ regulatory divergence in the evolution of mouse alternative splicing. Molecular Systems Biology, 2015, 11, 816.	7.2	34
12	Evolution and structure of clinically relevant gene fusions in multiple myeloma. Nature Communications, 2020, 11, 2666.	12.8	31
13	Discovery of driver non-coding splice-site-creating mutations in cancer. Nature Communications, 2020, 11, 5573.	12.8	26
14	Global analysis of regulatory divergence in the evolution of mouse alternative polyadenylation. Molecular Systems Biology, 2016, 12, 890.	7.2	23
15	Detection for gene-gene co-association via kernel canonical correlation analysis. BMC Genetics, 2012, 13, 83.	2.7	22
16	Enhancer retargeting of CDX2 and UBTF::ATXN7L3 define a subtype of high-risk B-progenitor acute lymphoblastic leukemia. Blood, 2022, 139, 3519-3531.	1.4	20
17	Discriminating a common somatic ASXL1 mutation (c.1934dup; p.G646Wfs*12) from artifact in myeloid malignancies using NGS. Leukemia, 2018, 32, 1874-1878.	7.2	18
18	Gene- or region-based association study via kernel principal component analysis. BMC Genetics, 2011, 12, 75.	2.7	14

#	Article	IF	Citations
19	FAM46B is a prokaryotic-like cytoplasmic poly(A) polymerase essential in human embryonic stem cells. Nucleic Acids Research, 2020, 48, 2733-2748.	14.5	13
20	ZNF384 Fusion Oncoproteins Drive Lineage Aberrancy in Acute Leukemia. Blood Cancer Discovery, 2022, 3, 240-263.	5.0	11
21	Pervasive allele-specific regulation on RNA decay in hybrid mice. Life Science Alliance, 2018, 1, e201800052.	2.8	10
22	A systematic evaluation of hybridization-based mouse exome capture system. BMC Genomics, 2013, 14, 492.	2.8	5
23	Mammalian splicing divergence is shaped by drift, buffering in trans, and a scaling law. Life Science Alliance, 2022, 5, e202101333.	2.8	3
24	MEDB-78. Unified rhombic lip origins of Group 3 and Group 4 medulloblastoma. Neuro-Oncology, 2022, 24, i124-i125.	1.2	1
25	Characterization of Germline Variants in Multiple Myeloma. Blood, 2018, 132, 4499-4499.	1.4	0
26	EPCO-26. INTEGRATIVE MULTI-OMICS IDENTIFIES CONVERGING DEVELOPMENTAL ORIGINS OF DISTINCT MEDULLOBLASTOMA SUBGROUPS. Neuro-Oncology, 2021, 23, vi7-vi7.	1.2	0