

Qingsong Gao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7148091/publications.pdf>

Version: 2024-02-01

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	Phase Separation Mediates NUP98 Fusion Oncoprotein Leukemic Transformation. <i>Cancer Discovery</i> , 2022, 12, 1152-1169.	9.4	68
2	Enhancer retargeting of <i>CDX2</i> and <i>UBTF::ATXN7L3</i> define a subtype of high-risk B-progenitor acute lymphoblastic leukemia. <i>Blood</i> , 2022, 139, 3519-3531.	1.4	20
3	ZNF384 Fusion Oncoproteins Drive Lineage Aberrancy in Acute Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 240-263.	5.0	11
4	Mammalian splicing divergence is shaped by drift, buffering in <i>trans</i> , and a scaling law. <i>Life Science Alliance</i> , 2022, 5, e202101333.	2.8	3
5	MEDB-78. Unified rhombic lip origins of Group 3 and Group 4 medulloblastoma. <i>Neuro-Oncology</i> , 2022, 24, i124-i125.	1.2	1
6	Co-evolution of tumor and immune cells during progression of multiple myeloma. <i>Nature Communications</i> , 2021, 12, 2559.	12.8	68
7	EPCO-26. INTEGRATIVE MULTI-OMICS IDENTIFIES CONVERGING DEVELOPMENTAL ORIGINS OF DISTINCT MEDULLOBLASTOMA SUBGROUPS. <i>Neuro-Oncology</i> , 2021, 23, vi7-vi7.	1.2	0
8	Discovery of driver non-coding splice-site-creating mutations in cancer. <i>Nature Communications</i> , 2020, 11, 5573.	12.8	26
9	Evolution and structure of clinically relevant gene fusions in multiple myeloma. <i>Nature Communications</i> , 2020, 11, 2666.	12.8	31
10	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
11	FAM46B is a prokaryotic-like cytoplasmic poly(A) polymerase essential in human embryonic stem cells. <i>Nucleic Acids Research</i> , 2020, 48, 2733-2748.	14.5	13
12	CharGer: clinical Characterization of Germline variants. <i>Bioinformatics</i> , 2019, 35, 865-867.	4.1	39
13	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
14	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	28.9	1,670
15	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	28.9	2,111
16	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.4	407
17	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	6.4	177
18	Discriminating a common somatic ASXL1 mutation (c.1934dup; p.G646Wfs*12) from artifact in myeloid malignancies using NGS. <i>Leukemia</i> , 2018, 32, 1874-1878.	7.2	18

#	ARTICLE	IF	CITATIONS
19	Pervasive allele-specific regulation on RNA decay in hybrid mice. <i>Life Science Alliance</i> , 2018, 1, e201800052.	2.8	10
20	Characterization of Germline Variants in Multiple Myeloma. <i>Blood</i> , 2018, 132, 4499-4499.	1.4	0
21	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	28.9	738
22	Global analysis of regulatory divergence in the evolution of mouse alternative polyadenylation. <i>Molecular Systems Biology</i> , 2016, 12, 890.	7.2	23
23	Predominant contribution of <i>cis</i> regulatory divergence in the evolution of mouse alternative splicing. <i>Molecular Systems Biology</i> , 2015, 11, 816.	7.2	34
24	A systematic evaluation of hybridization-based mouse exome capture system. <i>BMC Genomics</i> , 2013, 14, 492.	2.8	5
25	Detection for gene-gene co-association via kernel canonical correlation analysis. <i>BMC Genetics</i> , 2012, 13, 83.	2.7	22
26	Gene- or region-based association study via kernel principal component analysis. <i>BMC Genetics</i> , 2011, 12, 75.	2.7	14