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List of Publications by Year
in descending order

69 papers	5,593 citations	126907 33 h-index	98798 67 g-index
77 all docs	77 docs citations	77 times ranked	10136 citing authors

#	Article	IF	Citations
1	Genomic and Transcriptomic Landscape of Triple-Negative Breast Cancers: Subtypes and Treatment Strategies. Cancer Cell, 2019, 35, 428-440.e5.	16.8	571
2	Telomerase activation by genomic rearrangements in high-risk neuroblastoma. Nature, 2015, 526, 700-704.	27.8	478
3	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. Nature Biotechnology, 2014, 32, 926-932.	17.5	420
4	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
5	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. Nature Communications, 2014, 5, 3230.	12.8	316
6	The Risk-Associated Long Noncoding RNA NBAT-1 Controls Neuroblastoma Progression by Regulating Cell Proliferation and Neuronal Differentiation. Cancer Cell, 2014, 26, 722-737.	16.8	287
7	Multi-Omics Profiling Reveals Distinct Microenvironment Characterization and Suggests Immune Escape Mechanisms of Triple-Negative Breast Cancer. Clinical Cancer Research, 2019, 25, 5002-5014.	7.0	269
8	Detecting and correcting systematic variation in large-scale RNA sequencing data. Nature Biotechnology, 2014, 32, 888-895.	17.5	174
9	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
10	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	28.9	164
11	Optimized CRISPR guide RNA design for two high-fidelity Cas9 variants by deep learning. Nature Communications, 2019, 10, 4284.	12.8	163
12	A Comprehensive Mouse Transcriptomic BodyMap across 17 Tissues by RNA-seq. Scientific Reports, 2017, 7, 4200.	3.3	139
13	Genomic and immune profiling of pre-invasive lung adenocarcinoma. Nature Communications, 2019, 10, 5472.	12.8	127
14	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	17.5	126
15	Blood molecular markers associated with COVIDâ€19 immunopathology and multiâ€organ damage. EMBO Journal, 2020, 39, e105896.	7.8	123
16	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
17	Single-cell analyses of X Chromosome inactivation dynamics and pluripotency during differentiation. Genome Research, 2016, 26, 1342-1354.	5.5	93
18	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. Cancer Research, 2014, 74, 4016-4023.	0.9	90

#	ARTICLE	IF	CITATIONS
19	Advances in single-cell RNA sequencing and its applications in cancer research. Oncotarget, 2017, 8, 53763-53779.	1.8	76
20	Dynamic transcriptomes identify biogenic amines and insect-like hormonal regulation for mediating reproduction in Schistosoma japonicum. Nature Communications, 2017, 8, 14693.	12.8	75
21	Machine Learning Methods for Predicting HLA-Peptide Binding Activity. Bioinformatics and Biology Insights, 2015, 9s3, BBI.S29466.	2.0	68
22	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. Nature Communications, 2019, 10, 5026.	12.8	67
23	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	17.5	66
24	DDI-CPI, a server that predicts drugâ€“drug interactions through implementing the chemicalâ€“protein interactome. Nucleic Acids Research, 2014, 42, W46-W52.	14.5	63
25	Identification of Tissue-Specific Protein-Coding and Noncoding Transcripts across 14 Human Tissues Using RNA-seq. Scientific Reports, 2016, 6, 28400.	3.3	57
26	Somatic mutations in ZFHX4 gene are associated with poor overall survival of Chinese esophageal squamous cell carcinoma patients. Scientific Reports, 2017, 7, 4951.	3.3	46
27	PreMedKB: an integrated precision medicine knowledgebase for interpreting relationships between diseases, genes, variants and drugs. Nucleic Acids Research, 2019, 47, D1090-D1101.	14.5	45
28	Endoplasmic reticulum stress and MAPK signaling pathway activation underlie leflunomide-induced toxicity in HepG2 Cells. Toxicology, 2017, 392, 11-21.	4.2	44
29	Multiple microRNAs function as self-protective modules in acetaminophen-induced hepatotoxicity in humans. Archives of Toxicology, 2018, 92, 845-858.	4.2	42
30	Exploring functions of long noncoding RNAs across multiple cancers through co-expression network. Scientific Reports, 2017, 7, 754.	3.3	41
31	A genomic characterization of the influence of silver nanoparticles on bone differentiation in MC3T3â€E1 cells. Journal of Applied Toxicology, 2018, 38, 172-179.	2.8	39
32	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. Nature Biotechnology, 2021, 39, 1151-1160.	17.5	39
33	Mitochondrial dysfunction induced by leflunomide and its active metabolite. Toxicology, 2018, 396-397, 33-45.	4.2	38
34	Activation of the Nrf2 signaling pathway in usnic acid-induced toxicity in HepG2 cells. Archives of Toxicology, 2017, 91, 1293-1307.	4.2	37
35	Alcohol Intake Interacts with Functional Genetic Polymorphisms of Aldehyde Dehydrogenase (ALDH2) and Alcohol Dehydrogenase (ADH) to Increase Esophageal Squamous Cell Cancer Risk. Journal of Thoracic Oncology, 2019, 14, 712-725.	1.1	37
36	mRNA enrichment protocols determine the quantification characteristics of external RNA spike-in controls in RNA-Seq studies. Science China Life Sciences, 2013, 56, 134-142.	4.9	36

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37	Characterizing and annotating the genome using RNA-seq data. Science China Life Sciences, 2017, 60, 116-125.	4.9	35
38	Assessment of pharmacogenomic agreement. F1000Research, 2016, 5, 825.	1.6	34
39	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. Nature Biotechnology, 2017, 35, 1127-1128.	17.5	32
40	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. Scientific Data, 2014, 1, 140021.	5.3	30
41	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. Genome Biology, 2021, 22, 111.	8.8	29
42	DPDR-CPI, a server that predicts Drug Positioning and Drug Repositioning via Chemical-Protein Interactome. Scientific Reports, 2016, 6, 35996.	3.3	27
43	Accumulation of potential driver genes with genomic alterations predicts survival of high-risk neuroblastoma patients. Biology Direct, 2018, 13, 14.	4.6	27
44	Overcoming chemoresistance in prostate cancer with Chinese medicine Tripterygium wilfordii via multiple mechanisms. Oncotarget, 2016, 7, 61246-61261.	1.8	23
45	Comprehensive RNA-Seq transcriptomic profiling across 11 organs, 4 ages, and 2 sexes of Fischer 344 rats. Scientific Data, 2014, 1, 140013.	5.3	22
46	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. Scientific Data, 2014, 1, 140020.	5.3	21
47	MicroRNA-302d promotes the proliferation of human pluripotent stem cell-derived cardiomyocytes by inhibiting LATS2 in the Hippo pathway. Clinical Science, 2019, 133, 1387-1399.	4.3	20
48	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	8.8	20
49	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. Nucleic Acids Research, 2020, 48, 8320-8331.	14.5	19
50	Hidden biases in germline structural variant detection. Genome Biology, 2021, 22, 347.	8.8	19
51	A seven-gene prognostic signature predicts overall survival of patients with lung adenocarcinoma (LUAD). Cancer Cell International, 2021, 21, 294.	4.1	18
52	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome Biology, 2022, 23, 2.	8.8	18
53	Identifying and annotating human bifunctional RNAs reveals their versatile functions. Science China Life Sciences, 2016, 59, 981-992.	4.9	16
54	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. Scientific Data, 2021, 8, 296.	5.3	15

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55	Integrative Analysis of Somatic Mutations in Non-coding Regions Altering RNA Secondary Structures in Cancer Genomes. Scientific Reports, 2019, 9, 8205.	3.3	14
56	Significant variations in alternative splicing patterns and expression profiles between human-mouse orthologs in early embryos. Science China Life Sciences, 2017, 60, 178-188.	4.9	11
57	Genomic features of rapid versus late relapse in triple negative breast cancer. BMC Cancer, 2021, 21, 568.	2.6	10
58	Standardization efforts enabling next-generation sequencing and microarray based biomarkers for precision medicine. Biomarkers in Medicine, 2015, 9, 1265-1272.	1.4	9
59	Clinical Significance of Variants in the TTN Gene in a Large Cohort of Patients With Sporadic Dilated Cardiomyopathy. Frontiers in Cardiovascular Medicine, 2021, 8, 657689.	2.4	8
60	Deep oncopanel sequencing reveals within block position-dependent quality degradation in FFPE processed samples. Genome Biology, 2022, 23, .	8.8	8
61	HLADR: a database system for enhancing the discovery of biomarkers for predicting human leukocyte antigen-mediated idiosyncratic adverse drug reactions. Biomarkers in Medicine, 2015, 9, 1079-1093.	1.4	7
62	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. Science China Life Sciences, 2019, 62, 895-904.	4.9	5
63	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. Scientific Reports, 2016, 6, 38575.	3.3	4
64	Functional consequences of a rare missense BARD1 c.403G>A germline mutation identified in a triple-negative breast cancer patient. Breast Cancer Research, 2021, 23, 53.	5.0	4
65	Allele frequency deviation (AFD) as a new prognostic model to predict overall survival in lung adenocarcinoma (LUAD). Cancer Cell International, 2021, 21, 451.	4.1	3
66	ECCDIA: an interactive web tool for the comprehensive analysis of clinical and survival data of esophageal cancer patients. BMC Cancer, 2020, 20, 985.	2.6	2
67	Comprehensive microRNA-seq transcriptomic profiling across 11 organs, 4 ages, and 2 sexes of Fischer 344 rats. Scientific Data, 2022, 9, 201.	5.3	2
68	Fortyâ€three key gene expressions involved in the effect of indoleamine 2,3â€dioxygenase 1 expression on cancer prognosis may be a potential indoleamine 2,3â€dioxygenase 1 inhibitor biomarker. Clinical and Translational Medicine, 2021, 11, e330.	4.0	0
69	A Comprehensive Analysis of Gene Expression of Xenobiotic and Endogenous Metabolizing Enzymes and Transporters in Rat Multiple Organs. Current Pharmaceutical Biotechnology, 2018, 19, 240-249.	1.6	0