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List of Publications by Year in descending order

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69
papers

5,593
citations

126907

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docs citations

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times ranked

10136
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. <i>Genome Biology</i> , 2022, 23, 2.	8.8	18
2	Comprehensive microRNA-seq transcriptomic profiling across 11 organs, 4 ages, and 2 sexes of Fischer 344 rats. <i>Scientific Data</i> , 2022, 9, 201.	5.3	2
3	Deep oncopanel sequencing reveals within block position-dependent quality degradation in FFPE processed samples. <i>Genome Biology</i> , 2022, 23, .	8.8	8
4	Forty-three key gene expressions involved in the effect of indoleamine 2,3-dioxygenase 1 expression on cancer prognosis may be a potential indoleamine 2,3-dioxygenase 1 inhibitor biomarker. <i>Clinical and Translational Medicine</i> , 2021, 11, e330.	4.0	0
5	Clinical Significance of Variants in the TTN Gene in a Large Cohort of Patients With Sporadic Dilated Cardiomyopathy. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 657689.	2.4	8
6	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	17.5	126
7	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	8.8	20
8	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , 2021, 22, 111.	8.8	29
9	Functional consequences of a rare missense BARD1 c.403G>A germline mutation identified in a triple-negative breast cancer patient. <i>Breast Cancer Research</i> , 2021, 23, 53.	5.0	4
10	Genomic features of rapid versus late relapse in triple negative breast cancer. <i>BMC Cancer</i> , 2021, 21, 568.	2.6	10
11	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
12	A seven-gene prognostic signature predicts overall survival of patients with lung adenocarcinoma (LUAD). <i>Cancer Cell International</i> , 2021, 21, 294.	4.1	18
13	Allele frequency deviation (AFD) as a new prognostic model to predict overall survival in lung adenocarcinoma (LUAD). <i>Cancer Cell International</i> , 2021, 21, 451.	4.1	3
14	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1141-1150.	17.5	66
15	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1151-1160.	17.5	39
16	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. <i>Scientific Data</i> , 2021, 8, 296.	5.3	15
17	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170
18	Hidden biases in germline structural variant detection. <i>Genome Biology</i> , 2021, 22, 347.	8.8	19

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19	ECCDIA: an interactive web tool for the comprehensive analysis of clinical and survival data of esophageal cancer patients. <i>BMC Cancer</i> , 2020, 20, 985.	2.6	2
20	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. <i>Nucleic Acids Research</i> , 2020, 48, 8320-8331.	14.5	19
21	Blood molecular markers associated with COVID-19 immunopathology and multi-organ damage. <i>EMBO Journal</i> , 2020, 39, e105896.	7.8	123
22	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. <i>Nature Communications</i> , 2019, 10, 5026.	12.8	67
23	Optimized CRISPR guide RNA design for two high-fidelity Cas9 variants by deep learning. <i>Nature Communications</i> , 2019, 10, 4284.	12.8	163
24	MicroRNA-302d promotes the proliferation of human pluripotent stem cell-derived cardiomyocytes by inhibiting <i>LATS2</i> in the Hippo pathway. <i>Clinical Science</i> , 2019, 133, 1387-1399.	4.3	20
25	Integrative Analysis of Somatic Mutations in Non-coding Regions Altering RNA Secondary Structures in Cancer Genomes. <i>Scientific Reports</i> , 2019, 9, 8205.	3.3	14
26	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. <i>Science China Life Sciences</i> , 2019, 62, 895-904.	4.9	5
27	Multi-Omics Profiling Reveals Distinct Microenvironment Characterization and Suggests Immune Escape Mechanisms of Triple-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 5002-5014.	7.0	269
28	Genomic and Transcriptomic Landscape of Triple-Negative Breast Cancers: Subtypes and Treatment Strategies. <i>Cancer Cell</i> , 2019, 35, 428-440.e5.	16.8	571
29	Alcohol Intake Interacts with Functional Genetic Polymorphisms of Aldehyde Dehydrogenase (ALDH2) and Alcohol Dehydrogenase (ADH) to Increase Esophageal Squamous Cell Cancer Risk. <i>Journal of Thoracic Oncology</i> , 2019, 14, 712-725.	1.1	37
30	Genomic and immune profiling of pre-invasive lung adenocarcinoma. <i>Nature Communications</i> , 2019, 10, 5472.	12.8	127
31	PreMedKB: an integrated precision medicine knowledgebase for interpreting relationships between diseases, genes, variants and drugs. <i>Nucleic Acids Research</i> , 2019, 47, D1090-D1101.	14.5	45
32	Mitochondrial dysfunction induced by leflunomide and its active metabolite. <i>Toxicology</i> , 2018, 396-397, 33-45.	4.2	38
33	Multiple microRNAs function as self-protective modules in acetaminophen-induced hepatotoxicity in humans. <i>Archives of Toxicology</i> , 2018, 92, 845-858.	4.2	42
34	A genomic characterization of the influence of silver nanoparticles on bone differentiation in MC3T3-E1 cells. <i>Journal of Applied Toxicology</i> , 2018, 38, 172-179.	2.8	39
35	Accumulation of potential driver genes with genomic alterations predicts survival of high-risk neuroblastoma patients. <i>Biology Direct</i> , 2018, 13, 14.	4.6	27
36	A Comprehensive Analysis of Gene Expression of Xenobiotic and Endogenous Metabolizing Enzymes and Transporters in Rat Multiple Organs. <i>Current Pharmaceutical Biotechnology</i> , 2018, 19, 240-249.	1.6	0

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37	Characterizing and annotating the genome using RNA-seq data. <i>Science China Life Sciences</i> , 2017, 60, 116-125.	4.9	35
38	Significant variations in alternative splicing patterns and expression profiles between human-mouse orthologs in early embryos. <i>Science China Life Sciences</i> , 2017, 60, 178-188.	4.9	11
39	Activation of the Nrf2 signaling pathway in usnic acid-induced toxicity in HepG2 cells. <i>Archives of Toxicology</i> , 2017, 91, 1293-1307.	4.2	37
40	Exploring functions of long noncoding RNAs across multiple cancers through co-expression network. <i>Scientific Reports</i> , 2017, 7, 754.	3.3	41
41	Dynamic transcriptomes identify biogenic amines and insect-like hormonal regulation for mediating reproduction in <i>Schistosoma japonicum</i> . <i>Nature Communications</i> , 2017, 8, 14693.	12.8	75
42	Endoplasmic reticulum stress and MAPK signaling pathway activation underlie leflunomide-induced toxicity in HepG2 Cells. <i>Toxicology</i> , 2017, 392, 11-21.	4.2	44
43	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. <i>Nature Biotechnology</i> , 2017, 35, 1127-1128.	17.5	32
44	A Comprehensive Mouse Transcriptomic BodyMap across 17 Tissues by RNA-seq. <i>Scientific Reports</i> , 2017, 7, 4200.	3.3	139
45	Somatic mutations in ZFH4 gene are associated with poor overall survival of Chinese esophageal squamous cell carcinoma patients. <i>Scientific Reports</i> , 2017, 7, 4951.	3.3	46
46	Advances in single-cell RNA sequencing and its applications in cancer research. <i>Oncotarget</i> , 2017, 8, 53763-53779.	1.8	76
47	Overcoming chemoresistance in prostate cancer with Chinese medicine <i>Tripterygium wilfordii</i> via multiple mechanisms. <i>Oncotarget</i> , 2016, 7, 61246-61261.	1.8	23
48	Identifying and annotating human bifunctional RNAs reveals their versatile functions. <i>Science China Life Sciences</i> , 2016, 59, 981-992.	4.9	16
49	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. <i>Scientific Reports</i> , 2016, 6, 38575.	3.3	4
50	Identification of Tissue-Specific Protein-Coding and Noncoding Transcripts across 14 Human Tissues Using RNA-seq. <i>Scientific Reports</i> , 2016, 6, 28400.	3.3	57
51	Single-cell analyses of X Chromosome inactivation dynamics and pluripotency during differentiation. <i>Genome Research</i> , 2016, 26, 1342-1354.	5.5	93
52	DPDR-CPI, a server that predicts Drug Positioning and Drug Repositioning via Chemical-Protein Interactome. <i>Scientific Reports</i> , 2016, 6, 35996.	3.3	27
53	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , 2016, 5, 825.	1.6	34
54	Machine Learning Methods for Predicting HLA-Peptide Binding Activity. <i>Bioinformatics and Biology Insights</i> , 2015, 9s3, BBI.S29466.	2.0	68

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55	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133.	8.8	325
56	Standardization efforts enabling next-generation sequencing and microarray based biomarkers for precision medicine. <i>Biomarkers in Medicine</i> , 2015, 9, 1265-1272.	1.4	9
57	Telomerase activation by genomic rearrangements in high-risk neuroblastoma. <i>Nature</i> , 2015, 526, 700-704.	27.8	478
58	HLADR: a database system for enhancing the discovery of biomarkers for predicting human leukocyte antigen-mediated idiosyncratic adverse drug reactions. <i>Biomarkers in Medicine</i> , 2015, 9, 1079-1093.	1.4	7
59	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140021.	5.3	30
60	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. <i>Nature Communications</i> , 2014, 5, 3230.	12.8	316
61	The Risk-Associated Long Noncoding RNA NBAT-1 Controls Neuroblastoma Progression by Regulating Cell Proliferation and Neuronal Differentiation. <i>Cancer Cell</i> , 2014, 26, 722-737.	16.8	287
62	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014, 5, 5125.	12.8	122
63	Detecting and correcting systematic variation in large-scale RNA sequencing data. <i>Nature Biotechnology</i> , 2014, 32, 888-895.	17.5	174
64	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. <i>Nature Biotechnology</i> , 2014, 32, 926-932.	17.5	420
65	DDI-CPI, a server that predicts drug-drug interactions through implementing the chemical-protein interactome. <i>Nucleic Acids Research</i> , 2014, 42, W46-W52.	14.5	63
66	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. <i>Cancer Research</i> , 2014, 74, 4016-4023.	0.9	90
67	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140020.	5.3	21
68	Comprehensive RNA-Seq transcriptomic profiling across 11 organs, 4 ages, and 2 sexes of Fischer 344 rats. <i>Scientific Data</i> , 2014, 1, 140013.	5.3	22
69	mRNA enrichment protocols determine the quantification characteristics of external RNA spike-in controls in RNA-Seq studies. <i>Science China Life Sciences</i> , 2013, 56, 134-142.	4.9	36