

Geng Chen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46
papers

1,207
citations

18
h-index

34
g-index

53
ext. papers

1,880
ext. citations

9.2
avg, IF

5.09
L-index

#	Paper	IF	Citations
46	RSPO2/RANKL-LGR4 signaling regulates osteoclastic pre-metastatic niche formation and bone metastasis. <i>Journal of Clinical Investigation</i> , 2021 ,	15.9	1
45	Advances in bulk and single-cell multi-omics approaches for systems biology and precision medicine. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3
44	Comparative Transcriptome Profiling of Cold Exposure and β -AR Agonist CL316,243-Induced Browning of White Fat. <i>Frontiers in Physiology</i> , 2021 , 12, 667698	4.6	1
43	Single-cell transcriptomic analysis reveals dynamic alternative splicing and gene regulatory networks among pancreatic islets. <i>Science China Life Sciences</i> , 2021 , 64, 174-176	8.5	2
42	GRNdb: decoding the gene regulatory networks in diverse human and mouse conditions. <i>Nucleic Acids Research</i> , 2021 , 49, D97-D103	20.1	13
41	Fatty acid sensing GPCR (GPR84) signaling safeguards cartilage homeostasis and protects against osteoarthritis. <i>Pharmacological Research</i> , 2021 , 164, 105406	10.2	10
40	Dual base editor catalyzes both cytosine and adenine base conversions in human cells. <i>Nature Biotechnology</i> , 2020 , 38, 856-860	44.5	69
39	Systematic profiling of ACE2 expression in diverse physiological and pathological conditions for COVID-19/SARS-CoV-2. <i>Journal of Cellular and Molecular Medicine</i> , 2020 , 24, 9478-9482	5.6	24
38	Co-occurrence and Mutual Exclusivity Analysis of DNA Methylation Reveals Distinct Subtypes in Multiple Cancers. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 20	5.7	6
37	Proteasome-dependent degradation of Smad7 is critical for lung cancer metastasis. <i>Cell Death and Differentiation</i> , 2020 , 27, 1795-1806	12.7	19
36	Exploring Additional Valuable Information From Single-Cell RNA-Seq Data. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 593007	5.7	4
35	The REG1 inhibitor NIP30 increases sensitivity to chemotherapy in p53-deficient tumor cells. <i>Nature Communications</i> , 2020 , 11, 3904	17.4	5
34	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. <i>Nucleic Acids Research</i> , 2020 , 48, 8320-8331	20.1	10
33	DNMIVD: DNA methylation interactive visualization database. <i>Nucleic Acids Research</i> , 2020 , 48, D856-D862.	20.1	38
32	REG1 ablation impedes dedifferentiation of anaplastic thyroid carcinoma and accentuates radio-therapeutic response by regulating the Smad7-TGF- β pathway. <i>Cell Death and Differentiation</i> , 2020 , 27, 497-508	12.7	11
31	Integrative analysis identifies potential DNA methylation biomarkers for pan-cancer diagnosis and prognosis. <i>Epigenetics</i> , 2019 , 14, 67-80	5.7	44
30	LncRNA-mRNA competing endogenous RNA network depicts transcriptional regulation in ischaemia reperfusion injury. <i>Journal of Cellular and Molecular Medicine</i> , 2019 , 23, 2272-2276	5.6	16

29	QuaPra: Efficient transcript assembly and quantification using quadratic programming with Apriori algorithm. <i>Science China Life Sciences</i> , 2019 , 62, 937-946	8.5	6
28	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. <i>Science China Life Sciences</i> , 2019 , 62, 895-904	8.5	5
27	Systematic expression analysis of ligand-receptor pairs reveals important cell-to-cell interactions inside glioma. <i>Cell Communication and Signaling</i> , 2019 , 17, 48	7.5	17
26	Single-Cell RNA-Seq Technologies and Related Computational Data Analysis. <i>Frontiers in Genetics</i> , 2019 , 10, 317	4.5	277
25	Comprehensive Identification and Characterization of Human Secretome Based on Integrative Proteomic and Transcriptomic Data. <i>Frontiers in Cell and Developmental Biology</i> , 2019 , 7, 299	5.7	8
24	REG β Controls Hippo Signaling and Reciprocal NF- κ B-YAP Regulation to Promote Colon Cancer. <i>Clinical Cancer Research</i> , 2018 , 24, 2015-2025	12.9	31
23	eRAM: encyclopedia of rare disease annotations for precision medicine. <i>Nucleic Acids Research</i> , 2018 , 46, D937-D943	20.1	21
22	Lack of correlation between aristolochic acid exposure and hepatocellular carcinoma. <i>Science China Life Sciences</i> , 2018 , 61, 727-728	8.5	3
21	SPC24 Regulates breast cancer progression by PI3K/AKT signaling. <i>Gene</i> , 2018 , 675, 272-277	3.8	12
20	PedAM: a database for Pediatric Disease Annotation and Medicine. <i>Nucleic Acids Research</i> , 2018 , 46, D977-D983	20.1	21
19	Characterizing and annotating the genome using RNA-seq data. <i>Science China Life Sciences</i> , 2017 , 60, 116-125	8.5	24
18	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	8.5	5
17	REG β accelerates melanoma formation by regulating Wnt/ β -catenin signalling pathway. <i>Experimental Dermatology</i> , 2017 , 26, 1118-1124	4	13
16	dbSAP: single amino-acid polymorphism database for protein variation detection. <i>Nucleic Acids Research</i> , 2017 , 45, D827-D832	20.1	19
15	Identifying and Characterizing the Circular RNAs during the Lifespan of Arabidopsis Leaves. <i>Frontiers in Plant Science</i> , 2017 , 8, 1278	6.2	34
14	miR-195-5p is critical in REG β -mediated regulation of wnt/ β -catenin pathway in renal cell carcinoma. <i>Oncotarget</i> , 2017 , 8, 63986-64000	3.3	23
13	Laser capture microscopy coupled with Smart-seq2 for precise spatial transcriptomic profiling. <i>Nature Communications</i> , 2016 , 7, 12139	17.4	164
12	Identifying and annotating human bifunctional RNAs reveals their versatile functions. <i>Science China Life Sciences</i> , 2016 , 59, 981-992	8.5	8

11	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. <i>Scientific Reports</i> , 2016 , 6, 38575	4.9	4
10	Identification of Tissue-Specific Protein-Coding and Noncoding Transcripts across 14 Human Tissues Using RNA-seq. <i>Scientific Reports</i> , 2016 , 6, 28400	4.9	28
9	Single-cell analyses of X Chromosome inactivation dynamics and pluripotency during differentiation. <i>Genome Research</i> , 2016 , 26, 1342-1354	9.7	64
8	Re-annotation of presumed noncoding disease/trait-associated genetic variants by integrative analyses. <i>Scientific Reports</i> , 2015 , 5, 9453	4.9	12
7	Comprehensively identifying and characterizing the missing gene sequences in human reference genome with integrated analytic approaches. <i>Human Genetics</i> , 2013 , 132, 899-911	6.3	10
6	Incorporating the human gene annotations in different databases significantly improved transcriptomic and genetic analyses. <i>Rna</i> , 2013 , 19, 479-89	5.8	16
5	Dissecting the Characteristics and Dynamics of Human Protein Complexes at Transcriptome Cascade Using RNA-Seq Data. <i>PLoS ONE</i> , 2013 , 8, e66521	3.7	3
4	Revealing the missing expressed genes beyond the human reference genome by RNA-Seq. <i>BMC Genomics</i> , 2011 , 12, 590	4.5	23
3	Overview of available methods for diverse RNA-Seq data analyses. <i>Science China Life Sciences</i> , 2011 , 54, 1121-8	8.5	49
2	De novo transcriptome assembly of RNA-Seq reads with different strategies. <i>Science China Life Sciences</i> , 2011 , 54, 1129-33	8.5	14
1	Comparative analysis of human protein-coding and noncoding RNAs between brain and 10 mixed cell lines by RNA-Seq. <i>PLoS ONE</i> , 2011 , 6, e28318	3.7	24