Geng Chen

List of Publications by Year
in descending order

51 papers	2,303 citations	279487 23 h-index	243296 44 g-index
53 all docs	53 docs citations	53 times ranked	3838 citing authors

#	Article	IF	Citations
1	Single-Cell RNA-Seq Technologies and Related Computational Data Analysis. Frontiers in Genetics, 2019, 10, 317.	1.1	611
2	Laser capture microscopy coupled with Smart-seq2 for precise spatial transcriptomic profiling. Nature Communications, 2016, 7, 12139.	5.8	246
3	Dual base editor catalyzes both cytosine and adenine base conversions in human cells. Nature Biotechnology, 2020, 38, 856-860.	9.4	165
4	Single-cell analyses of X Chromosome inactivation dynamics and pluripotency during differentiation. Genome Research, 2016, 26, 1342-1354.	2.4	93
5	Integrative analysis identifies potential DNA methylation biomarkers for pan-cancer diagnosis and prognosis. Epigenetics, 2019, 14, 67-80.	1.3	91
6	DNMIVD: DNA methylation interactive visualization database. Nucleic Acids Research, 2020, 48, D856-D862.	6.5	86
7	GRNdb: decoding the gene regulatory networks in diverse human and mouse conditions. Nucleic Acids Research, 2021, 49, D97-D103.	6.5	58
8	Identification of Tissue-Specific Protein-Coding and Noncoding Transcripts across 14 Human Tissues Using RNA-seq. Scientific Reports, 2016, 6, 28400.	1.6	57
9	eRAM: encyclopedia of rare disease annotations for precision medicine. Nucleic Acids Research, 2018, 46, D937-D943.	6.5	56
10	Identifying and Characterizing the Circular RNAs during the Lifespan of Arabidopsis Leaves. Frontiers in Plant Science, 2017, 8, 1278.	1.7	55
11	Overview of available methods for diverse RNA-Seq data analyses. Science China Life Sciences, 2011, 54, 1121-1128.	2.3	54
12	Systematic profiling of ACE2 expression in diverse physiological and pathological conditions for COVIDâ€19/SARSâ€CoVâ€2. Journal of Cellular and Molecular Medicine, 2020, 24, 9478-9482.	1.6	42
13	REGÎ³ Controls Hippo Signaling and Reciprocal NF-ÎºBâ€"YAP Regulation to Promote Colon Cancer. Clinical Cancer Research, 2018, 24, 2015-2025.	3.2	41
14	Characterizing and annotating the genome using RNA-seq data. Science China Life Sciences, 2017, 60, 116-125.	2.3	35
15	miR-195-5p is critical in REGÎ³-mediated regulation of wnt/Î²-catenin pathway in renal cell carcinoma. Oncotarget, 2017, 8, 63986-64000.	0.8	35
16	Revealing the missing expressed genes beyond the human reference genome by RNA-Seq. BMC Genomics, 2011, 12, 590.	1.2	34
17	Systematic expression analysis of ligand-receptor pairs reveals important cell-to-cell interactions inside glioma. Cell Communication and Signaling, 2019, 17, 48.	2.7	31
18	Proteasome-dependent degradation of Smad7 is critical for lung cancer metastasis. Cell Death and Differentiation, 2020, 27, 1795-1806.	5.0	31

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19	Advances in bulk and single-cell multi-omics approaches for systems biology and precision medicine. Briefings in Bioinformatics, 2021, 22, .	3.2	31
20	RSPO2 and RANKL signal through LGR4 to regulate osteoclastic premetastatic niche formation and bone metastasis. Journal of Clinical Investigation, 2022, 132, .	3.9	30
21	Incorporating the human gene annotations in different databases significantly improved transcriptomic and genetic analyses. Rna, 2013, 19, 479-489.	1.6	29
22	dbSAP: single amino-acid polymorphism database for protein variation detection. Nucleic Acids Research, 2017, 45, D827-D832.	6.5	27
23	PedAM: a database for Pediatric Disease Annotation and Medicine. Nucleic Acids Research, 2018, 46, D977-D983.	6.5	27
24	Comparative Analysis of Human Protein-Coding and Noncoding RNAs between Brain and 10 Mixed Cell Lines by RNA-Seq. PLoS ONE, 2011, 6, e28318.	1.1	27
25	LncRNAâ€mRNA competing endogenous RNA network depicts transcriptional regulation in ischaemia reperfusion injury. Journal of Cellular and Molecular Medicine, 2019, 23, 2272-2276.	1.6	25
26	Comprehensive Identification and Characterization of Human Secretome Based on Integrative Proteomic and Transcriptomic Data. Frontiers in Cell and Developmental Biology, 2019, 7, 299.	1.8	25
27	REGÎ³ ablation impedes dedifferentiation of anaplastic thyroid carcinoma and accentuates radio-therapeutic response by regulating the Smad7-TGF-Î² pathway. Cell Death and Differentiation, 2020, 27, 497-508.	5.0	21
28	Fatty acid sensing GPCR (GPR84) signaling safeguards cartilage homeostasis and protects against osteoarthritis. Pharmacological Research, 2021, 164, 105406.	3.1	21
29	SPC24 Regulates breast cancer progression by PI3K/AKT signaling. Gene, 2018, 675, 272-277.	1.0	20
30	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. Nucleic Acids Research, 2020, 48, 8320-8331.	6.5	19
31	De novo transcriptome assembly of RNA-Seq reads with different strategies. Science China Life Sciences, 2011, 54, 1129-1133.	2.3	16
32	Identifying and annotating human bifunctional RNAs reveals their versatile functions. Science China Life Sciences, 2016, 59, 981-992.	2.3	16
33	<scp>REG</scp>Î³ accelerates melanoma formation by regulating Wnt/Î²â€catenin signalling pathway. Experimental Dermatology, 2017, 26, 1118-1124.	1.4	16
34	Co-occurrence and Mutual Exclusivity Analysis of DNA Methylation Reveals Distinct Subtypes in Multiple Cancers. Frontiers in Cell and Developmental Biology, 2020, 8, 20.	1.8	15
35	QuaPra: Efficient transcript assembly and quantification using quadratic programming with Apriori algorithm. Science China Life Sciences, 2019, 62, 937-946.	2.3	14
36	Comprehensively identifying and characterizing the missing gene sequences in human reference genome with integrated analytic approaches. Human Genetics, 2013, 132, 899-911.	1.8	13

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37	Re-annotation of presumed noncoding disease/trait-associated genetic variants by integrative analyses. Scientific Reports, 2015, 5, 9453.	1.6	13
38	Exploring Additional Valuable Information From Single-Cell RNA-Seq Data. Frontiers in Cell and Developmental Biology, 2020, 8, 593007.	1.8	12
39	Significant variations in alternative splicing patterns and expression profiles between human-mouse orthologs in early embryos. Science China Life Sciences, 2017, 60, 178-188.	2.3	11
40	The REGÎ³ inhibitor NIP30 increases sensitivity to chemotherapy in p53-deficient tumor cells. Nature Communications, 2020, 11, 3904.	5.8	10
41	Single-cell transcriptomic analysis reveals dynamic alternative splicing and gene regulatory networks among pancreatic islets. Science China Life Sciences, 2021, 64, 174-176.	2.3	8
42	Comparative Transcriptome Profiling of Cold Exposure and Î²3-AR Agonist CL316,243-Induced Browning of White Fat. Frontiers in Physiology, 2021, 12, 667698.	1.3	8
43	Lack of correlation between aristolochic acid exposure and hepatocellular carcinoma. Science China Life Sciences, 2018, 61, 727-728.	2.3	6
44	Next-generation sequencing technologies for personalized medicine: promising but challenging. Science China Life Sciences, 2013, 56, 101-103.	2.3	5
45	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. Science China Life Sciences, 2019, 62, 895-904.	2.3	5
46	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. Scientific Reports, 2016, 6, 38575.	1.6	4
47	Dissecting the Characteristics and Dynamics of Human Protein Complexes at Transcriptome Cascade Using RNA-Seq Data. PLoS ONE, 2013, 8, e66521.	1.1	4
48	Low Quality Cells Should Be Removed from Single-Cell RNA-Seq Data Analysis. SSRN Electronic Journal, 0, , .	0.4	1
49	A multi-omics annotation platform for rare disease to benefit precision medicine. Scientia Sinica Vitae, 2018, 48, 1026-1032.	0.1	1
50	Editorial: Multimodal and Integrative Analysis of Single-Cell or Bulk Sequencing Data. Frontiers in Genetics, 2021, 12, 658185.	1.1	0
51	Integrative Analysis Identifies Potential DNA Methylation Biomarkers for Pan-Cancer Diagnosis and Prognosis. SSRN Electronic Journal, 0, , .	0.4	0