

A scaling normalization method for differential express

Genome Biology

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A survey of statistical software for analysing RNA-seq data. <i>Human Genomics</i> , 2010, 5, 56.	1.4	24
2	Processing and analyzing ChIP-seq data: from short reads to regulatory interactions. <i>Briefings in Functional Genomics</i> , 2010, 9, 466-476.	1.3	15
3	Normalization strategies for microRNA profiling experiments: a "normal" way to a hidden layer of complexity?. <i>Biotechnology Letters</i> , 2010, 32, 1777-1788.	1.1	190
4	The transcriptomics of sympatric dwarf and normal lake whitefish (<i>Coregonus clupeaformis</i> spp.,) Tj ETQq1 1 0.784314 rgBT /Overl... 5389-5403.	2.0	93
5	The Lkb1 metabolic sensor maintains haematopoietic stem cell survival. <i>Nature</i> , 2010, 468, 659-663.	13.7	346
6	A two-parameter generalized Poisson model to improve the analysis of RNA-seq data. <i>Nucleic Acids Research</i> , 2010, 38, e170-e170.	6.5	131
7	Microarray analysis of gene expression during early development: a cautionary overview. <i>Reproduction</i> , 2010, 140, 787-801.	1.1	29
8	Exploring molecular signaling in plant-fungal symbioses using high throughput RNA sequencing. <i>Plant Signaling and Behavior</i> , 2010, 5, 1353-1358.	1.2	8
9	Differential expression analysis for sequence count data. <i>Genome Biology</i> , 2010, 11, R106.	3.8	13,707
10	From RNA-seq reads to differential expression results. <i>Genome Biology</i> , 2010, 11, 220.	13.9	603
11	Studying bacterial transcriptomes using RNA-seq. <i>Current Opinion in Microbiology</i> , 2010, 13, 619-624.	2.3	238
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14	Gene ontology analysis for RNA-seq: accounting for selection bias. <i>Genome Biology</i> , 2010, 11, R14.	13.9	5,824
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16	Differential expression in RNA-seq: A matter of depth. <i>Genome Research</i> , 2011, 21, 2213-2223.	2.4	1,456
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18	On Differential Gene expression Using RNA-Seq Data. <i>Cancer Informatics</i> , 2011, 10, CIN.S7473.	0.9	18

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20	GC-Content Normalization for RNA-Seq Data. <i>BMC Bioinformatics</i> , 2011, 12, 480.	1.2	712
21	ExpressionPlot: a web-based framework for analysis of RNA-Seq and microarray gene expression data. <i>Genome Biology</i> , 2011, 12, R69.	3.8	32
22	RNA-Seq for Plant Pathogenic Bacteria. <i>Genes</i> , 2011, 2, 689-705.	1.0	9
23	Review Application of RNA-seq to reveal the transcript profile in bacteria. <i>Genetics and Molecular Research</i> , 2011, 10, 1707-1718.	0.3	58
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28	Quantitative analysis of a deeply sequenced marine microbial metatranscriptome. <i>ISME Journal</i> , 2011, 5, 461-472.	4.4	195
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31	Expression divergence measured by transcriptome sequencing of four yeast species. <i>BMC Genomics</i> , 2011, 12, 635.	1.2	26
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33	Dynamics of transcriptional start site selection during nitrogen stress-induced cell differentiation in <i>Anabaena</i> sp. PCC7120. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20130-20135.	3.3	241
34	Transcriptomic analysis of avian digits reveals conserved and derived digit identities in birds. <i>Nature</i> , 2011, 477, 583-586.	13.7	67
35	New approaches to <i>Prunus</i> transcriptome analysis. <i>Genetica</i> , 2011, 139, 755-769.	0.5	43
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44	The maternal and early embryonic transcriptome of the milkweed bug <i>Oncopeltus fasciatus</i> . <i>BMC Genomics</i> , 2011, 12, 61.	1.2	110
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55	Transcriptome analysis of rice mature root tissue and root tips in early development by massive parallel sequencing. <i>Journal of Experimental Botany</i> , 2012, 63, 2141-2157.	2.4	41
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1359	Comparative analysis of ovarian transcriptomes between prolific and non-prolific goat breeds via high-throughput sequencing. <i>Reproduction in Domestic Animals</i> , 2018, 53, 344-351.	0.6	9
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1362	Transcriptome analysis of gene expression patterns during embryonic development in golden cuttlefish (<i>Sepia esculenta</i>). <i>Genes and Genomics</i> , 2018, 40, 253-263.	0.5	12
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1819	Multi-omics Characterization of Interaction-mediated Control of Human Protein Abundance levels. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S114-S125.	2.5	16
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1821	Lisinopril Preserves Physical Resilience and Extends Life Span in a Genotype-Specific Manner in <i>Drosophila melanogaster</i> . <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019, 74, 1844-1852.	1.7	14
1822	Alterations in GRHL2-OVOL2-ZEB1 axis and aberrant activation of Wnt signaling lead to altered gene transcription in posterior polymorphous corneal dystrophy. <i>Experimental Eye Research</i> , 2019, 188, 107696.	1.2	16
1823	C/EBP β -LIP induces cancer-type metabolic reprogramming by regulating the let-7/LIN28B circuit in mice. <i>Communications Biology</i> , 2019, 2, 208.	2.0	13
1824	Expression of a Degradation-Resistant β -Catenin Mutant in Osteocytes Protects the Skeleton From Mechanodeprivation-Induced Bone Wasting. <i>Journal of Bone and Mineral Research</i> , 2019, 34, 1964-1975.	3.1	10
1825	CBS-miRSeq: A comprehensive tool for accurate and extensive analyses of microRNA-sequencing data. <i>Computers in Biology and Medicine</i> , 2019, 110, 234-243.	3.9	7
1826	In vitro expansion of endogenous human alveolar epithelial type II cells in fibroblast-free spheroid culture. <i>Biochemical and Biophysical Research Communications</i> , 2019, 515, 579-585.	1.0	28
1827	Detection of novel biomarkers for early detection of Non-Muscle-Invasive Bladder Cancer using Competing Endogenous RNA network analysis. <i>Scientific Reports</i> , 2019, 9, 8434.	1.6	34
1828	Co-expression network analysis identifies gonad- and embryo-associated protein modules in the sentinel species <i>Gammarus fossarum</i> . <i>Scientific Reports</i> , 2019, 9, 7862.	1.6	13

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1830	Transcriptome Analysis of the Breast Muscle of Xichuan Black-Bone Chickens Under Tyrosine Supplementation Revealed the Mechanism of Tyrosine-Induced Melanin Deposition. <i>Frontiers in Genetics</i> , 2019, 10, 457.	1.1	19
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1833	Dissecting the genetic control of root and leaf tissue-specific anthocyanin pigmentation in carrot (<i>Daucus carota</i> L.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2485-2507.	1.8	27
1834	Rapid molecular evolution of pain insensitivity in multiple African rodents. <i>Science</i> , 2019, 364, 852-859.	6.0	57
1835	Comparative transcriptomic analysis of dermal wound healing reveals de novo skeletal muscle regeneration in <i>Acomys cahirinus</i> . <i>PLoS ONE</i> , 2019, 14, e0216228.	1.1	27
1836	Systems analysis reveals complex biological processes during virus infection fate decisions. <i>Genome Research</i> , 2019, 29, 907-919.	2.4	21
1837	Effects of Predator-Prey Interactions on Predator Traits: Differentiation of Diets and Venoms of a Marine Snail. <i>Toxins</i> , 2019, 11, 299.	1.5	9
1838	NLRP6 Deficiency in CD4 T Cells Decreases T Cell Survival Associated with Increased Cell Death. <i>Journal of Immunology</i> , 2019, 203, 544-556.	0.4	11
1839	Cell-Based Therapy Restores Olfactory Function in an Inducible Model of Hyposmia. <i>Stem Cell Reports</i> , 2019, 12, 1354-1365.	2.3	33
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1841	The Peritoneal Surface Proteome in a Model of Chronic Peritoneal Dialysis Reveals Mechanisms of Membrane Damage and Preservation. <i>Frontiers in Physiology</i> , 2019, 10, 472.	1.3	9
1842	Simplicity DiffExpress: A Bespoke Cloud-Based Interface for RNA-seq Differential Expression Modeling and Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 356.	1.1	1
1843	Ovule Gene Expression Analysis in Sexual and Aposporous Apomictic <i>Hypericum perforatum</i> L. (<i>Hypericaceae</i>) Accessions. <i>Frontiers in Plant Science</i> , 2019, 10, 654.	1.7	14
1844	BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019, 10, 433.	1.0	25
1845	Annotation and Expression of IDN2-like and FDM-like Genes in Sexual and Aposporous <i>Hypericum perforatum</i> L. accessions. <i>Plants</i> , 2019, 8, 158.	1.6	1
1846	RNA-seq analyses of antibiotic resistance mechanisms in <i>Serratia marcescens</i> . <i>Molecular Medicine Reports</i> , 2019, 20, 745-754.	1.1	6

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1848	Alteration of Proteomes in First-Generation Cultures of <i>Bacillus pumilus</i> Spores Exposed to Outer Space. <i>MSystems</i> , 2019, 4, .	1.7	8
1849	Convergent genetic aberrations in murine and human T lineage acute lymphoblastic leukemias. <i>PLoS Genetics</i> , 2019, 15, e1008168.	1.5	5
1850	Methylation and PTEN activation in dental pulp mesenchymal stem cells promotes osteogenesis and reduces oncogenesis. <i>Nature Communications</i> , 2019, 10, 2226.	5.8	102
1851	The dynamics of mito-nuclear coevolution: A perspective from bivalve species with two different mechanisms of mitochondrial inheritance. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 534-547.	0.6	4
1852	Hand2 Selectively Reorganizes Chromatin Accessibility to Induce Pacemaker-like Transcriptional Reprogramming. <i>Cell Reports</i> , 2019, 27, 2354-2369.e7.	2.9	23
1853	Upregulation of peroxide scavenging enzymes and multidrug efflux proteins highlight an active sodium hypochlorite response in <i>Pseudomonas fluorescens</i> biofilms. <i>Biofouling</i> , 2019, 35, 329-339.	0.8	7
1854	Pharmacological systems analysis defines EIF4A3 functions in cell-cycle and RNA stress granule formation. <i>Communications Biology</i> , 2019, 2, 165.	2.0	29
1855	Towards the new normal: Transcriptomic convergence and genomic legacy of the two subgenomes of an allopolyploid weed (<i>Capsella bursa-pastoris</i>). <i>PLoS Genetics</i> , 2019, 15, e1008131.	1.5	27
1856	diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering. <i>Communications Biology</i> , 2019, 2, 183.	2.0	162
1857	Identification of potential biomarkers for diagnosis of pancreatic and biliary tract cancers by sequencing of serum microRNAs. <i>BMC Medical Genomics</i> , 2019, 12, 62.	0.7	19
1858	Intraductal Adaptation of the 4T1 Mouse Model of Breast Cancer Reveals Effects of the Epithelial Microenvironment on Tumor Progression and Metastasis. <i>Anticancer Research</i> , 2019, 39, 2277-2287.	0.5	19
1859	Comparative transcriptome profiling of the response to <i>Pyrenochaeta lycopersici</i> in resistant tomato cultivar Mogeor and its background genotype "susceptible Moneymaker". <i>Functional and Integrative Genomics</i> , 2019, 19, 811-826.	1.4	12
1860	Using RNA-seq to characterize responses to 4-hydroxyphenylpyruvate dioxygenase (HPPD) inhibitor herbicide resistance in waterhemp (<i>Amaranthus tuberculatus</i>). <i>BMC Plant Biology</i> , 2019, 19, 182.	1.6	21
1861	Knockdown of RAD18 inhibits glioblastoma development. <i>Journal of Cellular Physiology</i> , 2019, 234, 21100-21112.	2.0	8
1862	Banana (<i>Musa acuminata</i>) transcriptome profiling in response to rhizobacteria: <i>Bacillus amyloliquefaciens</i> Bs006 and <i>Pseudomonas fluorescens</i> Ps006. <i>BMC Genomics</i> , 2019, 20, 378.	1.2	31
1863	Species-specific transcriptomic responses in <i>Daphnia magna</i> exposed to a bio-plastic production intermediate. <i>Environmental Pollution</i> , 2019, 252, 399-408.	3.7	5
1864	Obesity Reduces mTORC1 Activity in Mucosal-Associated Invariant T Cells, Driving Defective Metabolic and Functional Responses. <i>Journal of Immunology</i> , 2019, 202, 3404-3411.	0.4	48

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1866	Genomic <i>scp</i> DNA <i>scp</i> methylation distinguishes subtypes of human focal cortical dysplasia. <i>Epilepsia</i> , 2019, 60, 1091-1103.	2.6	61
1867	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 139-173.	2.8	101
1868	RNA sequencing of mesenchymal stem cells reveals a blocking of differentiation and immunomodulatory activities under inflammatory conditions in rheumatoid arthritis patients. <i>Arthritis Research and Therapy</i> , 2019, 21, 112.	1.6	19
1869	Mandibular dysmorphology due to abnormal embryonic osteogenesis in FGFR2-related craniosynostosis mice. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	1.2	19
1870	Cytosporone B as a Biological Preservative: Purification, Fungicidal Activity and Mechanism of Action against <i>Geotrichum citri-aurantii</i> . <i>Biomolecules</i> , 2019, 9, 125.	1.8	11
1871	Infection of <i>Aedes albopictus</i> Mosquito C6/36 Cells with the <i>w</i> Melpop Strain of <i>Wolbachia</i> Modulates Dengue Virus-Induced Host Cellular Transcripts and Induces Critical Sequence Alterations in the Dengue Viral Genome. <i>Journal of Virology</i> , 2019, 93, .	1.5	11
1872	aFold “ using polynomial uncertainty modelling for differential gene expression estimation from RNA sequencing data. <i>BMC Genomics</i> , 2019, 20, 364.	1.2	9
1873	Spatial control of oxygen delivery to three-dimensional cultures alters cancer cell growth and gene expression. <i>Journal of Cellular Physiology</i> , 2019, 234, 20608-20622.	2.0	17
1874	The extracellular matrix protects <i>Bacillus subtilis</i> colonies from <i>Pseudomonas</i> invasion and modulates plant co-colonization. <i>Nature Communications</i> , 2019, 10, 1919.	5.8	102
1875	Metatranscriptomic analysis of an <i>in vitro</i> biofilm model reveals strain-specific interactions among multiple bacterial species. <i>Journal of Oral Microbiology</i> , 2019, 11, 1599670.	1.2	17
1876	Cross-platform Data Analysis Reveals a Generic Gene Expression Signature for Microsatellite Instability in Colorectal Cancer. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	10
1877	Antagonizing Increased <i>miR-135a</i> Levels at the Chronic Stage of Experimental TLE Reduces Spontaneous Recurrent Seizures. <i>Journal of Neuroscience</i> , 2019, 39, 5064-5079.	1.7	28
1878	DegNorm: normalization of generalized transcript degradation improves accuracy in RNA-seq analysis. <i>Genome Biology</i> , 2019, 20, 75.	3.8	22
1879	The Stat3-Fam3a axis promotes muscle stem cell myogenic lineage progression by inducing mitochondrial respiration. <i>Nature Communications</i> , 2019, 10, 1796.	5.8	38
1880	The Selective Expansion and Targeted Accumulation of Bone Marrow-Derived Macrophages Drive Cardiac Vasculitis. <i>Journal of Immunology</i> , 2019, 202, 3282-3296.	0.4	9
1881	The diurnal transcriptional landscape of the microalga <i>Tetrademus obliquus</i> . <i>Algal Research</i> , 2019, 40, 101477.	2.4	9
1882	Tissue-specific sex differences in human gene expression. <i>Human Molecular Genetics</i> , 2019, 28, 2976-2986.	1.4	41

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1884	Identification of Metabolically Distinct Adipocyte Progenitor Cells in Human Adipose Tissues. <i>Cell Reports</i> , 2019, 27, 1528-1540.e7.	2.9	108
1885	MLSeq: Machine learning interface for RNA-sequencing data. <i>Computer Methods and Programs in Biomedicine</i> , 2019, 175, 223-231.	2.6	36
1886	An Integrated Chemical Proteomics Approach for Quantitative Profiling of Intracellular ADP-Ribosylation. <i>Scientific Reports</i> , 2019, 9, 6655.	1.6	26
1887	Interplay between small RNA pathways shapes chromatin landscapes in <i>C. elegans</i> . <i>Nucleic Acids Research</i> , 2019, 47, 5603-5616.	6.5	20
1888	Charting DENR-dependent translation reinitiation uncovers predictive uORF features and links to circadian timekeeping via Clock. <i>Nucleic Acids Research</i> , 2019, 47, 5193-5209.	6.5	30
1889	Comparative analysis of the root and leaf transcriptomes in <i>Chelidonium majus</i> L.. <i>PLoS ONE</i> , 2019, 14, e0215165.	1.1	13
1890	Highly efficient hypothesis testing methods for regression-type tests with correlated observations and heterogeneous variance structure. <i>BMC Bioinformatics</i> , 2019, 20, 185.	1.2	3
1891	Whole transcriptome analysis of an estuarine amphipod exposed to highway road dust. <i>Science of the Total Environment</i> , 2019, 675, 141-150.	3.9	4
1892	RNA sequencing and swarm intelligence-enhanced classification algorithm development for blood-based disease diagnostics using spliced blood platelet RNA. <i>Nature Protocols</i> , 2019, 14, 1206-1234.	5.5	84
1893	Differential gene expression in response to eCry3.1Ab ingestion in an unselected and eCry3.1Ab-selected western corn rootworm (<i>Diabrotica virgifera virgifera</i> LeConte) population. <i>Scientific Reports</i> , 2019, 9, 4896.	1.6	12
1894	The origins and evolution of chromosomes, dosage compensation, and mechanisms underlying venom regulation in snakes. <i>Genome Research</i> , 2019, 29, 590-601.	2.4	114
1895	ORE identifies extreme expression effects enriched for rare variants. <i>Bioinformatics</i> , 2019, 35, 3906-3912.	1.8	8
1896	Two Chloroflexi classes independently evolved the ability to persist on atmospheric hydrogen and carbon monoxide. <i>ISME Journal</i> , 2019, 13, 1801-1813.	4.4	129
1897	Heterogeneity in the perirenal region of humans suggests presence of dormant brown adipose tissue that contains brown fat precursor cells. <i>Molecular Metabolism</i> , 2019, 24, 30-43.	3.0	85
1898	Transcriptomics of cardiac biopsies reveals differences in patients with or without diagnostic parameters for heart failure with preserved ejection fraction. <i>Scientific Reports</i> , 2019, 9, 3179.	1.6	35
1899	A Systematic Investigation of the Malignant Functions and Diagnostic Potential of the Cancer Secretome. <i>Cell Reports</i> , 2019, 26, 2622-2635.e5.	2.9	57
1900	Development of a multicellular pancreatic tumor microenvironment system using patient-derived tumor cells. <i>Lab on A Chip</i> , 2019, 19, 1193-1204.	3.1	25

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1902	Transcriptomic Analysis of the <i>Brucella melitensis</i> Rev.1 Vaccine Strain in an Acidic Environment: Insights Into Virulence Attenuation. <i>Frontiers in Microbiology</i> , 2019, 10, 250.	1.5	14
1903	Human Pluripotent Stem Cell-Derived Multipotent Vascular Progenitors of the Mesothelium Lineage Have Utility in Tissue Engineering and Repair. <i>Cell Reports</i> , 2019, 26, 2566-2579.e10.	2.9	28
1904	Engraftment and proliferation potential of embryonic lung tissue cells in irradiated mice with emphysema. <i>Scientific Reports</i> , 2019, 9, 3657.	1.6	7
1905	Atopic Dermatitis Is an IL-13â€™Dominant Disease with Greater Molecular Heterogeneity Compared to Psoriasis. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1480-1489.	0.3	283
1906	<i>Mycobacterium tuberculosis</i> 6C sRNA binds multiple mRNA targets via C-rich loops independent of RNA chaperones. <i>Nucleic Acids Research</i> , 2019, 47, 4292-4307.	6.5	50
1907	Lipid Uptake Is an Androgen-Enhanced Lipid Supply Pathway Associated with Prostate Cancer Disease Progression and Bone Metastasis. <i>Molecular Cancer Research</i> , 2019, 17, 1166-1179.	1.5	51
1908	Gene regulation of <i>Sclerotinia sclerotiorum</i> during infection of <i>Glycine max</i> : on the road to pathogenesis. <i>BMC Genomics</i> , 2019, 20, 157.	1.2	45
1909	Sex-specific lipid molecular signatures in obesity-associated metabolic dysfunctions revealed by lipidomic characterization in ob/ob mouse. <i>Biology of Sex Differences</i> , 2019, 10, 11.	1.8	30
1910	Metabolomic and transcriptomic changes underlying cold and anaerobic stresses after storage of table grapes. <i>Scientific Reports</i> , 2019, 9, 2917.	1.6	33
1911	Temporal dynamics of bacterial and fungal communities during the infection of <i>Brassica rapa</i> roots by the protist <i>Plasmodiophora brassicae</i> . <i>PLoS ONE</i> , 2019, 14, e0204195.	1.1	45
1912	Assessment of a Highly Multiplexed RNA Sequencing Platform and Comparison to Existing High-Throughput Gene Expression Profiling Techniques. <i>Frontiers in Genetics</i> , 2019, 10, 150.	1.1	4
1913	The effect of resistance exercise upon age-related systemic and local skeletal muscle inflammation. <i>Experimental Gerontology</i> , 2019, 121, 19-32.	1.2	16
1914	Liver macrophages regulate systemic metabolism through non-inflammatory factors. <i>Nature Metabolism</i> , 2019, 1, 445-459.	5.1	72
1915	Single-Cell RNA-Seq Technologies and Related Computational Data Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 317.	1.1	611
1916	Human Tumor-Associated Macrophage and Monocyte Transcriptional Landscapes Reveal Cancer-Specific Reprogramming, Biomarkers, and Therapeutic Targets. <i>Cancer Cell</i> , 2019, 35, 588-602.e10.	7.7	636
1917	An integrated whole genome analysis of <i>Mycobacterium tuberculosis</i> reveals insights into relationship between its genome, transcriptome and methylome. <i>Scientific Reports</i> , 2019, 9, 5204.	1.6	26
1918	Genome-wide association study in frontal fibrosing alopecia identifies four susceptibility loci including HLA-B*07:02. <i>Nature Communications</i> , 2019, 10, 1150.	5.8	82

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1920	A complete statistical model for calibration of RNA-seq counts using external spike-ins and maximum likelihood theory. <i>PLoS Computational Biology</i> , 2019, 15, e1006794.	1.5	9
1921	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. <i>Genome Biology</i> , 2019, 20, 54.	3.8	92
1922	A 5-gene prognostic nomogram predicting survival probability of glioblastoma patients. <i>Brain and Behavior</i> , 2019, 9, e01258.	1.0	8
1923	Differential metabolic activity and discovery of therapeutic targets using summarized metabolic pathway models. <i>Npj Systems Biology and Applications</i> , 2019, 5, 7.	1.4	30
1924	Single-cell transcriptome analysis of <i>Physcomitrella</i> leaf cells during reprogramming using microcapillary manipulation. <i>Nucleic Acids Research</i> , 2019, 47, 4539-4553.	6.5	39
1925	Integrative genomic analysis of peritoneal malignant mesothelioma: understanding a case with extraordinary chemotherapy response. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003566.	0.5	6
1926	Birch pollen allergen immunotherapy reprograms nasal epithelial transcriptome and recovers microbial diversity. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 2293-2296.e11.	1.5	11
1927	n-3 PUFA biosynthesis by the copepod <i>Apocyclops royi</i> determined by fatty acid profile and gene expression analysis. <i>Biology Open</i> , 2019, 8, .	0.6	35
1928	Optimisation of laboratory methods for whole transcriptomic RNA analyses in human left ventricular biopsies and blood samples of clinical relevance. <i>PLoS ONE</i> , 2019, 14, e0213685.	1.1	9
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1930	Gene Expression Pattern and Regulatory Network of $\hat{\pm}$ -Toxin Treatment in <i>Bombyx mori</i> . <i>International Journal of Genomics</i> , 2019, 2019, 1-11.	0.8	1
1931	Physiological profile of undifferentiated bovine blastocyst-derived trophoblasts. <i>Biology Open</i> , 2019, 8, .	0.6	16
1932	miR-147b-mediated TCA cycle dysfunction and pseudohypoxia initiate drug tolerance to EGFR inhibitors in lung adenocarcinoma. <i>Nature Metabolism</i> , 2019, 1, 460-474.	5.1	57
1933	Differences in gene regulation in a tephritid model of prezygotic reproductive isolation. <i>Insect Molecular Biology</i> , 2019, 28, 689-702.	1.0	6
1934	Sexual conflict drives male manipulation of female postmating responses in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8437-8444.	3.3	72
1935	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. <i>Science</i> , 2019, 364, .	6.0	576
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1938	Loss of p53 Causes Stochastic Aberrant X-Chromosome Inactivation and Female-Specific Neural Tube Defects. <i>Cell Reports</i> , 2019, 27, 442-454.e5.	2.9	37
1939	Characterization of the transcriptional profiles in common buckwheat (<i>Fagopyrum esculentum</i>) under PEG-mediated drought stress. <i>Electronic Journal of Biotechnology</i> , 2019, 39, 42-51.	1.2	12
1940	WRN helicase is a synthetic lethal target in microsatellite unstable cancers. <i>Nature</i> , 2019, 568, 551-556.	13.7	253
1941	Prolonged Bat Call Exposure Induces a Broad Transcriptional Response in the Male Fall Armyworm (<i>Spodoptera frugiperda</i> ; Lepidoptera: Noctuidae) Brain. <i>Frontiers in Behavioral Neuroscience</i> , 2019, 13, 36.	1.0	15
1942	MtGA2ox10 encoding C20-GA2-oxidase regulates rhizobial infection and nodule development in <i>Medicago truncatula</i> . <i>Scientific Reports</i> , 2019, 9, 5952.	1.6	22
1943	Metabolic comparison of aerial and submerged mycelia formed in the liquid surface culture of <i>Cordyceps militaris</i> . <i>MicrobiologyOpen</i> , 2019, 8, e00836.	1.2	16
1944	Novel Data Transformations for RNA-seq Differential Expression Analysis. <i>Scientific Reports</i> , 2019, 9, 4820.	1.6	28
1945	Intracolon Plasticity in Mammary Tumors Revealed through Large-Scale Single-Cell Resolution 3D Imaging. <i>Cancer Cell</i> , 2019, 35, 618-632.e6.	7.7	119
1946	A statistical normalization method and differential expression analysis for RNA-seq data between different species. <i>BMC Bioinformatics</i> , 2019, 20, 163.	1.2	24
1947	Topconfects: a package for confident effect sizes in differential expression analysis provides a more biologically useful ranked gene list. <i>Genome Biology</i> , 2019, 20, 67.	3.8	43
1948	Identification of special key genes for alcohol-related hepatocellular carcinoma through bioinformatic analysis. <i>PeerJ</i> , 2019, 7, e6375.	0.9	29
1949	Isolation and molecular characterization of hemocyte sub-populations in kuruma shrimp <i>Marsupenaeus japonicus</i> . <i>Fisheries Science</i> , 2019, 85, 521-532.	0.7	16
1950	Bioinformatics Databases and Tools on Dietary MicroRNA. , 2019, , 2219-2232.		0
1951	The role of the GATA transcription factor AreB in regulation of nitrogen and carbon metabolism in <i>Aspergillus nidulans</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	16
1952	Comparative Analysis of the Liver Transcriptome among Cattle Breeds Using RNA-seq. <i>Veterinary Sciences</i> , 2019, 6, 36.	0.6	8
1953	Triggering method in assisted reproduction alters the cumulus cell transcriptome. <i>Reproductive BioMedicine Online</i> , 2019, 39, 211-224.	1.1	7
1954	A RNA sequencing-based six-gene signature for survival prediction in patients with glioblastoma. <i>Scientific Reports</i> , 2019, 9, 2615.	1.6	40

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1956	Differential expression of circulating miRNAs as a novel tool to assess BAG3-associated familial dilated cardiomyopathy. <i>Bioscience Reports</i> , 2019, 39, .	1.1	14
1957	Comparison of RNA-Seq and Microarray Gene Expression Platforms for the Toxicogenomic Evaluation of Liver From Short-Term Rat Toxicity Studies. <i>Frontiers in Genetics</i> , 2018, 9, 636.	1.1	149
1958	Proximal recolonization by self-renewing microglia re-establishes microglial homeostasis in the adult mouse brain. <i>PLoS Biology</i> , 2019, 17, e3000134.	2.6	115
1959	Identification and characterization of genes with absolute mRNA abundances changes in tumor cells with varied transcriptome sizes. <i>BMC Genomics</i> , 2019, 20, 134.	1.2	4
1960	Globular structures in roots accumulate phosphorus to extremely high concentrations following phosphorus addition. <i>Plant, Cell and Environment</i> , 2019, 42, 1987-2002.	2.8	9
1961	Genetic and transcriptomic dissection of the fiber length trait from a cotton (<i>Gossypium hirsutum</i> L.) MAGIC population. <i>BMC Genomics</i> , 2019, 20, 112.	1.2	32
1962	Intratumoural Heterogeneity Underlies Distinct Therapy Responses and Treatment Resistance in Glioblastoma. <i>Cancers</i> , 2019, 11, 190.	1.7	39
1963	Aging-like Spontaneous Epigenetic Silencing Facilitates Wnt Activation, Stemness, and BrafV600E-Induced Tumorigenesis. <i>Cancer Cell</i> , 2019, 35, 315-328.e6.	7.7	107
1964	Linking gene expression and oenological traits: Comparison between <i>Torulaspora delbrueckii</i> and <i>Saccharomyces cerevisiae</i> strains. <i>International Journal of Food Microbiology</i> , 2019, 294, 42-49.	2.1	27
1965	Transcriptomic analysis reveals adaptive strategies to chronic low nitrogen in Tibetan wild barley. <i>BMC Plant Biology</i> , 2019, 19, 68.	1.6	22
1966	CircHMGC1 Promotes Hepatoblastoma Cell Proliferation by Regulating the IGF Signaling Pathway and Glutaminolysis. <i>Theranostics</i> , 2019, 9, 900-919.	4.6	60
1967	Quiescence Modulates Stem Cell Maintenance and Regenerative Capacity in the Aging Brain. <i>Cell</i> , 2019, 176, 1407-1419.e14.	18.5	265
1968	Human macrophages survive and adopt activated genotypes in living zebrafish. <i>Scientific Reports</i> , 2019, 9, 1759.	1.6	20
1969	CD8+ T cells from patients with narcolepsy and healthy controls recognize hypocretin neuron-specific antigens. <i>Nature Communications</i> , 2019, 10, 837.	5.8	80
1970	Gene expression and metabolite profiling analyses of developing pomegranate fruit peel reveal interactions between anthocyanin and punicalagin production. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	12
1971	Machine learning analysis of gene expression data reveals novel diagnostic and prognostic biomarkers and identifies therapeutic targets for soft tissue sarcomas. <i>PLoS Computational Biology</i> , 2019, 15, e1006826.	1.5	75
1972	microRNA expression profile in porcine oocytes with different developmental competence derived from large or small follicles. <i>Molecular Reproduction and Development</i> , 2019, 86, 426-439.	1.0	17

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1974	Normalization for Single-Cell RNA-Seq Data Analysis. <i>Methods in Molecular Biology</i> , 2019, 1935, 11-23.	0.4	1
1975	The anti-cancer drug 5-fluorouracil affects cell cycle regulators and potential regulatory long non-coding RNAs in yeast. <i>RNA Biology</i> , 2019, 16, 727-741.	1.5	10
1976	The Genome Sequence of the Eastern Woodchuck (<i>Marmota monax</i>) – A Preclinical Animal Model for Chronic Hepatitis B. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3943-3952.	0.8	13
1977	MCF-7 as a Model for Functional Analysis of Breast Cancer Risk Variants. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1735-1745.	1.1	7
1978	Mip6 binds directly to the Mex67 UBA domain to maintain low levels of Msn2/4 stress-dependent mRNAs. <i>EMBO Reports</i> , 2019, 20, e47964.	2.0	6
1979	Identification of Hub Genes and Key Modules in Stomach Adenocarcinoma Using nsNMF-Based Data Integration Technique. , 2019, , .		6
1980	DOT1L complex suppresses transcription from enhancer elements and ectopic RNAi in <i>Caenorhabditis elegans</i> . <i>Rna</i> , 2019, 25, 1259-1273.	1.6	7
1981	A Targeted Gene Panel That Covers Coding, Non-coding and Short Tandem Repeat Regions Improves the Diagnosis of Patients With Neurodegenerative Diseases. <i>Frontiers in Neuroscience</i> , 2019, 13, 1324.	1.4	4
1982	Chicken adaptive response to low energy diet: main role of the hypothalamic lipid metabolism revealed by a phenotypic and multi-tissue transcriptomic approach. <i>BMC Genomics</i> , 2019, 20, 1033.	1.2	7
1983	Molecular mechanisms underlying nuchal hump formation in dolphin cichlid, <i>Cyrtocara moorii</i> . <i>Scientific Reports</i> , 2019, 9, 20296.	1.6	18
1984	Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. <i>Clinical Cancer Research</i> , 2019, 25, 7351-7362.	3.2	61
1985	NDRindex: A method for the quality assessment of single-cell RNA-Seq preprocessing data. , 2019, , .		0
1986	Characterization of Holstein and Normande whole milk miRNomes highlights breed specificities. <i>Scientific Reports</i> , 2019, 9, 20345.	1.6	18
1987	An influential meal: host plant dependent transcriptional variation in the beet armyworm, <i>Spodoptera exigua</i> (Lepidoptera: Noctuidae). <i>BMC Genomics</i> , 2019, 20, 845.	1.2	5
1988	Two predictive precision medicine tools for hepatocellular carcinoma. <i>Cancer Cell International</i> , 2019, 19, 290.	1.8	13
1989	Identifying candidate diagnostic markers for early stage of non-small cell lung cancer. <i>PLoS ONE</i> , 2019, 14, e0225080.	1.1	1
1990	Missiles of Mass Disruption: Composition and Glandular Origin of Venom Used as a Projectile Defensive Weapon by the Assassin Bug <i>Platymeris rhadamanthus</i> . <i>Toxins</i> , 2019, 11, 673.	1.5	16

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1992	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. <i>BMC Biology</i> , 2019, 17, 108.	1.7	109
1993	Dichotomy of Dosage Compensation along the Neo Z Chromosome of the Monarch Butterfly. <i>Current Biology</i> , 2019, 29, 4071-4077.e3.	1.8	66
1994	Selection signatures in goats reveal copy number variants underlying breed-defining coat color phenotypes. <i>PLoS Genetics</i> , 2019, 15, e1008536.	1.5	50
1995	A genome-wide transcriptomic analysis of protein-coding genes in human blood cells. <i>Science</i> , 2019, 366, .	6.0	329
1996	Differentiation into an Effector Memory Phenotype Potentiates HIV-1 Latency Reversal in CD4 ⁺ T Cells. <i>Journal of Virology</i> , 2019, 93, .	1.5	72
1997	Suppression of FOXM1 activities and breast cancer growth in vitro and in vivo by a new class of compounds. <i>Npj Breast Cancer</i> , 2019, 5, 45.	2.3	54
1998	The dynamics of the inflammatory response during BBN-induced bladder carcinogenesis in mice. <i>Journal of Translational Medicine</i> , 2019, 17, 394.	1.8	21
1999	MS CD49d+CD154+ Lymphocytes Reprogram Oligodendrocytes into Immune Reactive Cells Affecting CNS Regeneration. <i>Cells</i> , 2019, 8, 1508.	1.8	7
2000	A Complete Genome Screening Program of Clinical Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates Identifies the Origin and Progression of a Neonatal Intensive Care Unit Outbreak. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	16
2001	Multiplatform biomarker identification using a data-driven approach enables single-sample classification. <i>BMC Bioinformatics</i> , 2019, 20, 601.	1.2	4
2002	A multi-omics digital research object for the genetics of sleep regulation. <i>Scientific Data</i> , 2019, 6, 258.	2.4	8
2003	Transcriptomics of Tasmanian Devil (<i>Sarcophilus harrisii</i>) Ear Tissue Reveals Homogeneous Gene Expression Patterns across a Heterogeneous Landscape. <i>Genes</i> , 2019, 10, 801.	1.0	6
2004	Transcription Factor Networks in Leaves of <i>Cichorium endivia</i> : New Insights into the Relationship between Photosynthesis and Leaf Development. <i>Plants</i> , 2019, 8, 531.	1.6	9
2005	Small RNA-sequence analysis of plasma-derived extracellular vesicle miRNAs in smokers and patients with chronic obstructive pulmonary disease as circulating biomarkers. <i>Journal of Extracellular Vesicles</i> , 2019, 8, 1684816.	5.5	96
2006	Excessive ER-phagy mediated by the autophagy receptor FAM134B results in ER stress, the unfolded protein response, and cell death in HeLa cells. <i>Journal of Biological Chemistry</i> , 2019, 294, 20009-20023.	1.6	46
2007	Coding and Non-Coding RNA Abnormalities in Bipolar Disorder. <i>Genes</i> , 2019, 10, 946.	1.0	23
2008	The human tissue-resident CCR5 ⁺ T cell compartment maintains protective and functional properties during inflammation. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	41

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2010	RADAR: differential analysis of MeRIP-seq data with a random effect model. <i>Genome Biology</i> , 2019, 20, 294.	3.8	46
2011	Splice-Junction-Based Mapping of Alternative Isoforms in the Human Proteome. <i>Cell Reports</i> , 2019, 29, 3751-3765.e5.	2.9	64
2012	Spliceosomal disruption of the non-canonical BAF complex in cancer. <i>Nature</i> , 2019, 574, 432-436.	13.7	163
2013	A perturbed gene network containing PI3K, AKT, RAS, ERK and WNT/β-catenin pathways in leukocytes is linked to ASD genetics and symptom severity. <i>Nature Neuroscience</i> , 2019, 22, 1624-1634.	7.1	71
2014	Spatial sorting enables comprehensive characterization of liver zonation. <i>Nature Metabolism</i> , 2019, 1, 899-911.	5.1	125
2015	Joint between-sample normalization and differential expression detection through a t ₀ -regularized regression. <i>BMC Bioinformatics</i> , 2019, 20, 593.	1.2	1
2016	A Latent Gaussian Copula Model for Mixed Data Analysis in Brain Imaging Genetics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1350-1360.	1.9	4
2017	miR-181c Activates Mitochondrial Calcium Uptake by Regulating MICU1 in the Heart. <i>Journal of the American Heart Association</i> , 2019, 8, e012919.	1.6	18
2018	mTORC1-Rps15 Axis Contributes to the Mechanisms Underlying Global Translation Reduction During Senescence of Mouse Embryonic Fibroblasts. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 337.	1.8	6
2019	RNA sequencing of transplant-stage idiopathic pulmonary fibrosis lung reveals unique pathway regulation. <i>ERJ Open Research</i> , 2019, 5, 00117-2019.	1.1	43
2020	Normalization Methods for the Analysis of Unbalanced Transcriptome Data: A Review. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 358.	2.0	72
2021	The role and robustness of the Gini coefficient as an unbiased tool for the selection of Gini genes for normalising expression profiling data. <i>Scientific Reports</i> , 2019, 9, 17960.	1.6	25
2022	Unraveling the Molecular Signature of Extracellular Vesicles From Endometrial-Derived Mesenchymal Stem Cells: Potential Modulatory Effects and Therapeutic Applications. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 431.	2.0	38
2023	Single-Cell RNA Sequencing of the Cardiovascular System: New Looks for Old Diseases. <i>Frontiers in Cardiovascular Medicine</i> , 2019, 6, 173.	1.1	47
2024	Transcriptome-wide analysis associates ID2 expression with combined pre- and post-capillary pulmonary hypertension. <i>Scientific Reports</i> , 2019, 9, 19572.	1.6	11
2025	Cytokine sensitivity screening highlights BMP4 pathway signaling as a therapeutic opportunity in ER + breast cancer. <i>FASEB Journal</i> , 2019, 33, 1644-1657.	0.2	13
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2028	The developmental transcriptome of <i>Trichopria drosophilae</i> (Hymenoptera: Diapriidae) and insights into cuticular protein genes. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 245-254.	0.4	5
2029	<i>Escherichia coli</i> O157:H7 transcriptome datasets for comparison of RNA-seq and microarray platforms. <i>Data in Brief</i> , 2019, 22, 126-131.	0.5	1
2030	Identifying cis Elements for Spatiotemporal Control of Mammalian DNA Replication. <i>Cell</i> , 2019, 176, 816-830.e18.	13.5	144
2031	Transcriptome analysis and metabolic profiling reveal the key role of ω -linolenic acid in dormancy regulation of European pear. <i>Journal of Experimental Botany</i> , 2019, 70, 1017-1031.	2.4	27
2032	Dasatinib and navitoclax act synergistically to target NUP98-NSD1+/FLT3-ITD+ acute myeloid leukemia. <i>Leukemia</i> , 2019, 33, 1360-1372.	3.3	40
2033	Identification of a circulating miRNA signature in extracellular vesicles collected from amyotrophic lateral sclerosis patients. <i>Brain Research</i> , 2019, 1708, 100-108.	1.1	82
2034	Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 447-458.	5.9	68
2035	Tumor-derived IFN triggers chronic pathway agonism and sensitivity to ADAR loss. <i>Nature Medicine</i> , 2019, 25, 95-102.	15.2	240
2036	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. <i>Cancer Cell</i> , 2019, 35, 95-110.e8.	7.7	65
2037	SUPT4H1 Depletion Leads to a Global Reduction in RNA. <i>Cell Reports</i> , 2019, 26, 45-53.e4.	2.9	15
2038	Transcription Factor PU.1 Promotes Conventional Dendritic Cell Identity and Function via Induction of Transcriptional Regulator DC-SCRIPT. <i>Immunity</i> , 2019, 50, 77-90.e5.	6.6	59
2039	Taxonomic and functional heterogeneity of the gill microbiome in a symbiotic coastal mangrove lucinid species. <i>ISME Journal</i> , 2019, 13, 902-920.	4.4	38
2040	Evaluation of variability in human kidney organoids. <i>Nature Methods</i> , 2019, 16, 79-87.	9.0	176
2041	AS03-Adjuvanted H5N1 Avian Influenza Vaccine Modulates Early Innate Immune Signatures in Human Peripheral Blood Mononuclear Cells. <i>Journal of Infectious Diseases</i> , 2019, 219, 1786-1798.	1.9	16
2042	Morpho-regulation in diverse chicken feather formation: Integrating branching modules and sex hormone-dependent morpho-regulatory modules. <i>Development Growth and Differentiation</i> , 2019, 61, 124-138.	0.6	13
2043	Widespread cis-regulation of RNA editing in a large mammal. <i>Rna</i> , 2019, 25, 319-335.	1.6	5
2044	The role of a class III gibberellin oxidase in tomato internode elongation. <i>Plant Journal</i> , 2019, 97, 603-615.	2.8	28

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2046	Clinicopathological, microenvironmental and genetic determinants of molecular subtypes in KEAP1/NRF2 mutant lung cancer. <i>International Journal of Cancer</i> , 2019, 144, 788-801.	2.3	16
2047	Molecular characterization of a precision-cut rat liver slice model for the evaluation of antifibrotic compounds. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 316, G15-G24.	1.6	8
2048	Ectonucleoside Triphosphate Diphosphohydrolase-3 Antibody Targets Adult Human Pancreatic Î² Cells for In Vitro and In Vivo Analysis. <i>Cell Metabolism</i> , 2019, 29, 745-754.e4.	7.2	59
2049	Assessment of agronomic parameters and gene expression profiling of flax (<i>Linum usitatissimum</i> L.) upon treatment with brassinosteroid and its biosynthetic inhibitor. <i>Industrial Crops and Products</i> , 2019, 128, 270-281.	2.5	4
2050	The transcriptome of the marine calanoid copepod <i>Temora longicornis</i> under heat stress and recovery. <i>Marine Environmental Research</i> , 2019, 143, 10-23.	1.1	29
2051	Indole Inhibits ToxR Regulon Expression in <i>Vibrio cholerae</i> . <i>Infection and Immunity</i> , 2019, 87, .	1.0	25
2052	Intermuscular adipose tissue directly modulates skeletal muscle insulin sensitivity in humans. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 316, E866-E879.	1.8	97
2053	RNA sequencing differential gene expression analysis of isolated perfused bovine udders experimentally inoculated with <i>Streptococcus agalactiae</i> . <i>Journal of Dairy Science</i> , 2019, 102, 1761-1767.	1.4	4
2054	A Peninsular Structure Coordinates Asynchronous Differentiation with Morphogenesis to Generate Pancreatic Islets. <i>Cell</i> , 2019, 176, 790-804.e13.	13.5	103
2055	(Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	34
2056	Cytoneuclear interactions remain stable during allopolyploid evolution despite repeated whole-genome duplications in <i>Brassica</i> . <i>Plant Journal</i> , 2019, 98, 434-447.	2.8	32
2057	IDH3Î± regulates one-carbon metabolism in glioblastoma. <i>Science Advances</i> , 2019, 5, eaat0456.	4.7	59
2058	Transcriptomic signature reveals mechanism of flower bud distortion in witches' broom disease of soybean (<i>Glycine max</i>). <i>BMC Plant Biology</i> , 2019, 19, 26.	1.6	15
2059	Characterization of the hepatic transcriptome following phenobarbital induction in mice with AIP. <i>Molecular Genetics and Metabolism</i> , 2019, 128, 382-390.	0.5	7
2060	A tumor-specific endogenous repetitive element is induced by herpesviruses. <i>Nature Communications</i> , 2019, 10, 90.	5.8	25
2061	Translation control of the immune checkpoint in cancer and its therapeutic targeting. <i>Nature Medicine</i> , 2019, 25, 301-311.	15.2	184
2062	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. <i>Nature Neuroscience</i> , 2019, 22, 307-316.	7.1	120

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2064	Loss of <i>Nmp4</i> optimizes osteogenic metabolism and secretion to enhance bone quality. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 316, E749-E772.	1.8	12
2065	Genetic control of longissimus dorsi muscle gene expression variation and joint analysis with phenotypic quantitative trait loci in pigs. <i>BMC Genomics</i> , 2019, 20, 3.	1.2	33
2066	Bacterial and viral pathogen-associated molecular patterns induce divergent early transcriptomic landscapes in a bovine macrophage cell line. <i>BMC Genomics</i> , 2019, 20, 15.	1.2	19
2067	Identification of a 6-gene signature predicting prognosis for colorectal cancer. <i>Cancer Cell International</i> , 2019, 19, 6.	1.8	69
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2069	Integrative Genomics Analysis Identifies ACVR1B as a Candidate Causal Gene of Emphysema Distribution. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 60, 388-398.	1.4	15
2070	Transcriptome analysis of strawberry (<i>Fragaria</i> — <i>ananassa</i>) fruits under osmotic stresses and identification of genes related to ascorbic acid pathway. <i>Physiologia Plantarum</i> , 2019, 166, 979-995.	2.6	13
2071	Limited short-term effects on human prostate cancer xenograft growth and epidermal growth factor receptor gene expression by the ghrelin receptor antagonist [D-Lys3]-GHRP-6. <i>Endocrine</i> , 2019, 64, 393-405.	1.1	5
2072	Transcriptomic responses to low temperature stress in the Nile tilapia, <i>Oreochromis niloticus</i> . <i>Fish and Shellfish Immunology</i> , 2019, 84, 1145-1156.	1.6	73
2073	Transcriptomic response of the <i>Crassostrea virginica</i> gonad after exposure to a water-accommodation fraction of hydrocarbons and the potential implications in reproduction. <i>Marine Genomics</i> , 2019, 43, 9-18.	0.4	7
2074	Identification of a universal 6â€œncRNA prognostic signature for three pathologic subtypes of renal cell carcinoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 7375-7385.	1.2	26
2075	Conduct and Quality Control of Differential Gene Expression Analysis Using High-Throughput Transcriptome Sequencing (RNASeq). <i>Methods in Molecular Biology</i> , 2019, 1834, 29-43.	0.4	8
2076	International Space Station conditions alter genomics, proteomics, and metabolomics in <i>Aspergillus nidulans</i> . <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1363-1377.	1.7	32
2077	Multifactorial Inheritance and Complex Diseases. , 2019, , 323-358.		3
2078	USP1 inhibition destabilizes KPNA2 and suppresses breast cancer metastasis. <i>Oncogene</i> , 2019, 38, 2405-2419.	2.6	73
2079	Control Interventions Can Impact Alveolarization and the Transcriptome in Developing Mouse Lungs. <i>Anatomical Record</i> , 2019, 302, 346-363.	0.8	6
2080	A quantitative framework for characterizing the evolutionary history of mammalian gene expression. <i>Genome Research</i> , 2019, 29, 53-63.	2.4	78

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2082	Molecular characterization of a precision-cut rat lung slice model for the evaluation of antifibrotic drugs. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2019, 316, L348-L357.	1.3	14
2083	<i>Acinetobacter baumannii</i> OxyR Regulates the Transcriptional Response to Hydrogen Peroxide. <i>Infection and Immunity</i> , 2019, 87, .	1.0	48
2084	Transcriptional effects of cadmium on iron homeostasis differ in calamine accessions of <i>Noccaea caerulescens</i> . <i>Plant Journal</i> , 2019, 97, 306-320.	2.8	27
2085	The Itaconate Pathway Is a Central Regulatory Node Linking Innate Immune Tolerance and Trained Immunity. <i>Cell Metabolism</i> , 2019, 29, 211-220.e5.	7.2	232
2086	A broken promise: microbiome differential abundance methods do not control the false discovery rate. <i>Briefings in Bioinformatics</i> , 2019, 20, 210-221.	3.2	132
2087	Clustering transformed compositional data using <i>K</i> -means, with applications in gene expression and bicycle sharing system data. <i>Journal of Applied Statistics</i> , 2019, 46, 47-65.	0.6	34
2088	A Unified Model for Joint Normalization and Differential Gene Expression Detection in RNA-Seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 442-454.	1.9	13
2089	Effect of normalization methods on the performance of supervised learning algorithms applied to HTSeq-FPKM-UQ data sets: 7SK RNA expression as a predictor of survival in patients with colon adenocarcinoma. <i>Briefings in Bioinformatics</i> , 2019, 20, 985-994.	3.2	55
2090	Comparative analysis of differential gene expression tools for RNA sequencing time course data. <i>Briefings in Bioinformatics</i> , 2019, 20, 288-298.	3.2	93
2091	Transcriptomic analysis of epigenetic modification genes in the termite <i>Reticulitermes speratus</i> . <i>Insect Science</i> , 2020, 27, 202-211.	1.5	12
2092	New evolving strategies revealed by transcriptomic analysis of a <i>fur</i> ^Δ mutant of the cyanotrophic bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT 5344. <i>Microbial Biotechnology</i> , 2020, 13, 148-161.	2.0	5
2093	Comparative study on seasonal hair follicle cycling by analysis of the transcriptomes from cashmere and milk goats. <i>Genomics</i> , 2020, 112, 332-345.	1.3	44
2094	DFseq: Distribution-Free Method to Detect Differential Gene Expression for RNA-Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 558-565.	1.9	0
2095	Sex-specific impact of prenatal androgens on social brain default mode subsystems. <i>Molecular Psychiatry</i> , 2020, 25, 2175-2188.	4.1	33
2096	Identification of Expression Profiles Defining Distinct Prognostic Subsets of Radioactive-Iodine Refractory Differentiated Thyroid Cancer from the DECISION Trial. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 312-317.	1.9	8
2097	Single-cell RNA-Seq: a next generation sequencing tool for a high-resolution view of the individual cell. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 3730-3735.	2.0	2
2098	Early transcriptional responses to soybean cyst nematode HG Type 0 show genetic differences among resistant and susceptible soybeans. <i>Theoretical and Applied Genetics</i> , 2020, 133, 87-102.	1.8	17

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2100	An EMS-induced mutation in a tetratricopeptide repeat-like superfamily protein gene (Chir_A12G008870) on chromosome A12 is responsible for the liy short fiber phenotype in cotton. <i>Theoretical and Applied Genetics</i> , 2020, 133, 271-282.	1.8	12
2101	Overexpression of chromatin remodeling and tyrosine kinase genes in iAMP21-positive acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2020, 61, 604-613.	0.6	7
2102	SINC: a scale-invariant deep-neural-network classifier for bulk and single-cell RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 1779-1784.	1.8	4
2103	Prepupae and pupae transcriptomic characterization of <i>Trichogramma chilonis</i> . <i>Genomics</i> , 2020, 112, 1651-1659.	1.3	7
2104	Targeting aurora kinase B alleviates spinal microgliosis and neuropathic pain in a rat model of peripheral nerve injury. <i>Journal of Neurochemistry</i> , 2020, 152, 72-91.	2.1	14
2105	tRic: a user-friendly data portal to explore the expression landscape of tRNAs in human cancers. <i>RNA Biology</i> , 2020, 17, 1674-1679.	1.5	18
2106	Characterization of Chinese hamster ovary cells with disparate chromosome numbers: Reduction of the amount of mRNA relative to total protein. <i>Journal of Bioscience and Bioengineering</i> , 2020, 129, 121-128.	1.1	5
2107	Genetic and genomic analysis of the seed-filling process in maize based on a logistic model. <i>Heredity</i> , 2020, 124, 122-134.	1.2	17
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2406	Transcriptome-Based Analysis of Tomato Genotypes Resistant to Bacterial Spot (<i>Xanthomonas</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.8	8
2407	Dynamic RNA acetylation revealed by quantitative cross-evolutionary mapping. <i>Nature</i> , 2020, 583, 638-643.	13.7	175
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2409	Common risk variants in <i>NPHS1</i> and <i>TNFSF15</i> are associated with childhood steroid-sensitive nephrotic syndrome. <i>Kidney International</i> , 2020, 98, 1308-1322.	2.6	39
2410	RNA-Seq Reproducibility Assessment of the Sequencing Quality Control Project. <i>Cancer Informatics</i> , 2020, 19, 117693512092249.	0.9	5
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2413	Gray whale transcriptome reveals longevity adaptations associated with DNA repair and ubiquitination. <i>Aging Cell</i> , 2020, 19, e13158.	3.0	27
2414	HARMONIES: A Hybrid Approach for Microbiome Networks Inference via Exploiting Sparsity. <i>Frontiers in Genetics</i> , 2020, 11, 445.	1.1	12
2415	Decoding Gene Networks Modules That Explain the Recovery of <i>Hymenoglossum cruentum</i> Cav. After Extreme Desiccation. <i>Frontiers in Plant Science</i> , 2020, 11, 574.	1.7	8
2416	RNA-seq Reveals Differentially Expressed Genes between Two indica Inbred Rice Genotypes Associated with Drought-Yield QTLs. <i>Agronomy</i> , 2020, 10, 621.	1.3	21
2417	ADORA1 Inhibition Promotes Tumor Immune Evasion by Regulating the ATF3-PD-L1 Axis. <i>Cancer Cell</i> , 2020, 37, 324-339.e8.	7.7	126
2418	Transcriptomic and metabolomic analyses of <i>Lycium ruthenicum</i> and <i>Lycium barbarum</i> fruits during ripening. <i>Scientific Reports</i> , 2020, 10, 4354.	1.6	17
2419	RASflow: an RNA-Seq analysis workflow with Snakemake. <i>BMC Bioinformatics</i> , 2020, 21, 110.	1.2	38
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2429	Characterization of <i>Arabidopsis thaliana</i> Promoter Bidirectionality and Antisense RNAs by Inactivation of Nuclear RNA Decay Pathways. <i>Plant Cell</i> , 2020, 32, 1845-1867.	3.1	50
2430	Time-Course RNAseq Reveals <i>Exserohilum turcicum</i> Effectors and Pathogenicity Determinants. <i>Frontiers in Microbiology</i> , 2020, 11, 360.	1.5	23
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2438	Normalization Methods on Single-Cell RNA-seq Data: An Empirical Survey. <i>Frontiers in Genetics</i> , 2020, 11, 41.	1.1	51
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