

AfterQC: automatic filtering, trimming, error removing

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Integrated transcriptomic analysis of <i>Trichosporon Asahii</i> uncovers the core genes and pathways of fluconazole resistance. <i>Scientific Reports</i> , 2017, 7, 17847.	1.6	7
2	SOAPnuke: a MapReduce acceleration-supported software for integrated quality control and preprocessing of high-throughput sequencing data. <i>GigaScience</i> , 2018, 7, 1-6.	3.3	1,265
3	Bioinformatics Analysis for Cell-Free Tumor DNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2018, 1754, 67-95.	0.4	15
4	Hair follicle dermal condensation forms via Fgf20 primed cell cycle exit, cell motility, and aggregation. <i>ELife</i> , 2018, 7, .	2.8	62
5	De novo assembly of middle-sized genome using MinION and Illumina sequencers. <i>BMC Genomics</i> , 2018, 19, 700.	1.2	18
6	Single Cell Gene Expression to Understand the Dynamic Architecture of the Heart. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 167.	1.1	16
7	fastp: an ultra-fast all-in-one FASTQ preprocessor. <i>Bioinformatics</i> , 2018, 34, i884-i890.	1.8	11,005
8	Detection of Urothelial Bladder Carcinoma via Microfluidic Immunoassay and Single-Cell DNA Copy-Number Alteration Analysis of Captured Urinary-Exfoliated Tumor Cells. <i>Cancer Research</i> , 2018, 78, 4073-4085.	0.4	34
9	Conducting metagenomic studies in microbiology and clinical research. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8629-8646.	1.7	26
10	Systematic evaluation of error rates and causes in short samples in next-generation sequencing. <i>Scientific Reports</i> , 2018, 8, 10950.	1.6	224
11	A prototypical non-malignant epithelial model to study genome dynamics and concurrently monitor micro-RNAs and proteins in situ during oncogene-induced senescence. <i>BMC Genomics</i> , 2018, 19, 37.	1.2	46
12	MutScan: fast detection and visualization of target mutations by scanning FASTQ data. <i>BMC Bioinformatics</i> , 2018, 19, 16.	1.2	15
13	Zearalenone exposure elevated the expression of tumorigenesis genes in mouse ovarian granulosa cells. <i>Toxicology and Applied Pharmacology</i> , 2018, 356, 191-203.	1.3	29
14	Regulatory variants: from detection to predicting impact. <i>Briefings in Bioinformatics</i> , 2019, 20, 1639-1654.	3.2	82
15	A practical guide for DNase-seq data analysis: from data management to common applications. <i>Briefings in Bioinformatics</i> , 2019, 20, 1865-1877.	3.2	7
16	Using QC-Blind for Quality Control and Contamination Screening of Bacteria DNA Sequencing Data Without Reference Genome. <i>Frontiers in Microbiology</i> , 2019, 10, 1560.	1.5	8
17	Analysis of Gut Microbiota and Their Metabolic Potential in Patients with Schizophrenia Treated with Olanzapine: Results from a Six-Week Observational Prospective Cohort Study. <i>Journal of Clinical Medicine</i> , 2019, 8, 1605.	1.0	37
18	Variant analysis pipeline for accurate detection of genomic variants from transcriptome sequencing data. <i>PLoS ONE</i> , 2019, 14, e0216838.	1.1	24

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19	Pseudogene repair driven by selection pressure applied in experimental evolution. <i>Nature Microbiology</i> , 2019, 4, 386-389.	5.9	21
20	Improved phylogenomic sampling of free-living nematodes enhances resolution of higher-level nematode phylogeny. <i>BMC Evolutionary Biology</i> , 2019, 19, 121.	3.2	78
21	First Draft Genome Sequence of <i>Xanthomonas axonopodis</i> pv. <i>eucalyptorum</i> , Causal Agent of Bacterial Leaf Blight on Eucalypt. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
22	FastqPuri: high-performance preprocessing of RNA-seq data. <i>BMC Bioinformatics</i> , 2019, 20, 226.	1.2	26
23	Integrative Differential Expression Analysis for Multiple EXperiments (IDEAMEX): A Web Server Tool for Integrated RNA-Seq Data Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 279.	1.1	60
24	Tracing the Evolution of the Plastome and Mitogenome in the Chloropicophyceae Uncovered Convergent tRNA Gene Losses and a Variant Plastid Genetic Code. <i>Genome Biology and Evolution</i> , 2019, 11, 1275-1292.	1.1	20
25	Complete genome of DENV2 isolated from mosquitoes in Mexico. <i>Infection, Genetics and Evolution</i> , 2019, 71, 98-107.	1.0	1
26	The genetic basis for adaptation of model-designed syntrophic co-cultures. <i>PLoS Computational Biology</i> , 2019, 15, e1006213.	1.5	17
27	Draft Genome Sequence of <i>Erwinia psidii</i> , Causal Agent of Bacterial Blight of Guava (<i>Psidium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 2019, 8, .	0.3	5
28	Using long and linked reads to improve an Atlantic herring (<i>Clupea harengus</i>) genome assembly. <i>Scientific Reports</i> , 2019, 9, 17716.	1.6	11
29	Meglumine acridone acetate, the ionic salt of CMA and N-methylglucamine, induces apoptosis in human PBMCs via the mitochondrial pathway. <i>Scientific Reports</i> , 2019, 9, 18240.	1.6	6
30	Calorie restriction reprograms diurnal rhythms in protein translation to regulate metabolism. <i>FASEB Journal</i> , 2019, 33, 4473-4489.	0.2	14
31	Detection and Surveillance of Bladder Cancer Using Urine Tumor DNA. <i>Cancer Discovery</i> , 2019, 9, 500-509.	7.7	143
32	ALEdb 1.0: a database of mutations from adaptive laboratory evolution experimentation. <i>Nucleic Acids Research</i> , 2019, 47, D1164-D1171.	6.5	93
33	Modulation of vitamin D signaling by the pioneer factor CEBPA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 96-106.	0.9	33
34	In vivo transcriptome changes of human white blood cells in response to vitamin D. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2019, 188, 71-76.	1.2	53
35	PPIP: Automated Software for Identification of Bioactive Endogenous Peptides. <i>Journal of Proteome Research</i> , 2019, 18, 721-727.	1.8	2
36	An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 728-738.	1.9	14

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37	Comparative genomic and transcriptomic analyses reveal different pathogenicity-related genes among three eucalyptus fungal pathogens. <i>Fungal Genetics and Biology</i> , 2020, 137, 103332.	0.9	9
38	Parachute geckos free fall into synonymy: Gekko phylogeny, and a new subgeneric classification, inferred from thousands of ultraconserved elements. <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106731.	1.2	31
39	A comparative synthesis of transcriptomic analyses reveals major differences between WSSV-susceptible <i>Litopenaeus vannamei</i> and WSSV-refractory <i>Macrobrachium rosenbergii</i> . <i>Developmental and Comparative Immunology</i> , 2020, 104, 103564.	1.0	23
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41	Functional role of Tet-mediated RNA hydroxymethylcytosine in mouse ES cells and during differentiation. <i>Nature Communications</i> , 2020, 11, 4956.	5.8	44
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43	Synthetic cross-phyla gene replacement and evolutionary assimilation of major enzymes. <i>Nature Ecology and Evolution</i> , 2020, 4, 1402-1409.	3.4	13
44	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. <i>BMC Genomics</i> , 2020, 21, 514.	1.2	23
45	Wnt Genes in Wing Pattern Development of Coliadinae Butterflies. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	19
46	Molecular Epidemiology of <i>Acinetobacter calcoaceticus</i> - <i>Acinetobacter baumannii</i> Complex Isolated From Children at the Hospital Infantil de México Federico Gómez. <i>Frontiers in Microbiology</i> , 2020, 11, 576673.	1.5	16
47	Keep Calm and Survive: Adaptation Strategies to Energy Crisis in Fruit Trees under Root Hypoxia. <i>Plants</i> , 2020, 9, 1108.	1.6	17
48	Kinetic profiling of metabolic specialists demonstrates stability and consistency of in vivo enzyme turnover numbers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23182-23190.	3.3	65
49	SeQual: Big Data Tool to Perform Quality Control and Data Preprocessing of Large NGS Datasets. <i>IEEE Access</i> , 2020, 8, 146075-146084.	2.6	5
50	First Draft Genome Sequence of Thermophilic <i>Laceyella tengchongensis</i> BKK01, Isolated from Municipal Solid Waste in Thailand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
51	Natural epialleles of <i>Arabidopsis</i> SUPERMAN display superwoman phenotypes. <i>Communications Biology</i> , 2020, 3, 772.	2.0	11
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55	Two new bacilladnaviruses associated with the diatom <i>Haslea ostrearia</i> . <i>European Journal of Phycology</i> , 2020, 55, 444-453.	0.9	1
56	The Draft Genome Dataset of the Asian Cricket <i>Teleogryllus occipitalis</i> for Molecular Research Toward Entomophagy. <i>Frontiers in Genetics</i> , 2020, 11, 470.	1.1	15
57	Larger, unfiltered datasets are more effective at resolving phylogenetic conflict: Introns, exons, and UCEs resolve ambiguities in Golden-backed frogs (<i>Anura: Ranidae</i> ; genus <i>Hylarana</i>). <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106899.	1.2	30
58	Similarities and spatial variations of bacterial and fungal communities in field rice planthopper (<i>Hemiptera: Delphacidae</i>) populations. <i>Insect Science</i> , 2020, 27, 947-963.	1.5	15
59	Integrating genomic features for non-invasive early lung cancer detection. <i>Nature</i> , 2020, 580, 245-251.	13.7	379
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61	Data of de novo genome assembly of the <i>Chlamydia psittaci</i> strain isolated from the livestock in Volga Region, Russian Federation. <i>Data in Brief</i> , 2020, 29, 105190.	0.5	4
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63	Whole-transcriptome analysis of the toxic effects of zearalenone exposure on ceRNA networks in porcine granulosa cells. <i>Environmental Pollution</i> , 2020, 261, 114007.	3.7	26
64	Integrative analysis of in vivo recording with single-cell RNA-seq data reveals molecular properties of light-sensitive neurons in mouse V1. <i>Protein and Cell</i> , 2020, 11, 417-432.	4.8	13
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66	Comprehensive fundamental somatic variant calling and quality management strategies for human cancer genomes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	10
67	System-level analyses of keystone genes required for mammalian tooth development. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2021, 336, 7-17.	0.6	27
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69	Exploring antibiotic resistance in environmental integron-cassettes through intl-attC amplicons deep sequencing. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 363-372.	0.8	8
70	Senescence Reprogramming by TIMP1 Deficiency Promotes Prostate Cancer Metastasis. <i>Cancer Cell</i> , 2021, 39, 68-82.e9.	7.7	66
71	Urinary Nucleic Acid in Tumor: Bioinformatics Approaches. <i>Methods in Molecular Biology</i> , 2021, 2292, 95-104.	0.4	1
72	SeqErr: measuring and suppressing sequencer errors in next-generation sequencing data. <i>Genome Biology</i> , 2021, 22, 37.	3.8	15

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74	Bioinformatics resources for SARS-CoV-2 discovery and surveillance. <i>Briefings in Bioinformatics</i> , 2021, 22, 631-641.	3.2	38
76	Reduction of alternative electron acceptors drives biofilm formation in <i>Shewanella</i> algae. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 9.	2.9	15
77	Infant gut microbiota modulation by human milk disaccharides in humanized microbiome mice. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	15
78	Dual functions of SPOP and ERG dictate androgen therapy responses in prostate cancer. <i>Nature Communications</i> , 2021, 12, 734.	5.8	26
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82	Sequence analysis of new variants of porcine epidemic diarrhea virus in Luzon, Philippines, in 2017. <i>Archives of Virology</i> , 2021, 166, 1859-1867.	0.9	5
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85	Genome Sequence of <i>Streptomyces cavourensis</i> BUU135, Isolated from Soil from a Tropical Fruit Farm in Thailand. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
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89	Environmental conditions dictate differential evolution of vancomycin resistance in <i>Staphylococcus aureus</i> . <i>Communications Biology</i> , 2021, 4, 793.	2.0	18
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94	Virome comparison of deferred blood donations obtained from different geographic regions in the Sao Paulo State, Brazil. <i>Transfusion and Apheresis Science</i> , 2021, 60, 103106.	0.5	1
95	Macrophyte meadows mediate the response of the sediment microbial community to ultraviolet radiation. <i>Hydrobiologia</i> , 2021, 848, 4569-4583.	1.0	2

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97	A Large-Scale and Serverless Computational Approach for Improving Quality of NGS Data Supporting Big Multi-Omics Data Analyses. <i>Frontiers in Genetics</i> , 2021, 12, 699280.	1.1	3
98	Transcriptomic encoding of sensorimotor transformation in the midbrain. <i>ELife</i> , 2021, 10, .	2.8	27
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100	The carP lncRNA Is a carS-Related Regulatory Element with Broad Effects on the <i>Fusarium fujikuroi</i> Transcriptome. <i>Non-coding RNA</i> , 2021, 7, 46.	1.3	0
101	Effect of black ginseng and silkworm supplementation on obesity, the transcriptome, and the gut microbiome of diet-induced overweight dogs. <i>Scientific Reports</i> , 2021, 11, 16334.	1.6	11
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104	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
105	Comparative Transcriptome Analysis of the Expression of Antioxidant and Immunity Genes in the Spleen of a Cyanidin 3-O-Glucoside-Treated Alzheimer's Mouse Model. <i>Antioxidants</i> , 2021, 10, 1435.	2.2	14
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109	Effects of fecal microbiota transplantation in subjects with irritable bowel syndrome are mirrored by changes in gut microbiome. <i>Gut Microbes</i> , 2020, 12, 1794263.	4.3	31
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126	Functional attractors in microbial community assembly. <i>Cell Systems</i> , 2022, 13, 29-42.e7.	2.9	59

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127	The proliferation role of LH on porcine primordial germ cell-like cells (pPGCLCs) through ceRNA network construction. <i>Clinical and Translational Medicine</i> , 2021, 11, e560.	1.7	5
128	Music of metagenomics—a review of its applications, analysis pipeline, and associated tools. <i>Functional and Integrative Genomics</i> , 2022, 22, 3-26.	1.4	3
138	Draft Genome Sequence of Multidrug-Resistant <i>Proteus mirabilis</i> CKTH01, Isolated from Raw Chicken Meat. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
140	Draft Genome Sequence of <i>Haloferax volcanii</i> SS0101, Isolated from Salt Farms in Samut Sakhon, Thailand. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
144	ProkSeq for complete analysis of RNA-Seq data from prokaryotes. <i>Bioinformatics</i> , 2021, 37, 126-128.	1.8	11
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152	Single cell analysis reveals inhibition of angiogenesis attenuates the progression of heterotopic ossification in <i>Mx¹/Î⁺</i> mice. <i>Bone Research</i> , 2022, 10, 4.	5.4	7
153	Nonsurgical periodontal debridement affects subgingival bacterial diversity in human immunodeficiency virus (HIV)-1 infected patients with periodontitis. <i>Journal of Periodontology</i> , 2022, , .	1.7	0
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155	Phylogenomic Analysis of the Phylum Nematoda: Conflicts and Congruences With Morphology, 18S rRNA, and Mitogenomes. <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	28
157	Revisiting hematopoiesis: applications of the bulk and single-cell transcriptomics dissecting transcriptional heterogeneity in hematopoietic stem cells. <i>Briefings in Functional Genomics</i> , 2022, 21, 159-176.	1.3	15
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161	Atlantic herring (<i>Clupea harengus</i>) population structure in the Northeast Atlantic Ocean. <i>Fisheries Research</i> , 2022, 249, 106231.	0.9	4
162	The functional starter and its genomic insight for histamine degradation in fish sauce. <i>Food Microbiology</i> , 2022, 104, 103988.	2.1	8
163	A Chromosome-Level Genome Assembly of the European Beech (<i>Fagus sylvatica</i>) Reveals Anomalies for Organelle DNA Integration, Repeat Content and Distribution of SNPs. <i>Frontiers in Genetics</i> , 2021, 12, 691058.	1.1	17
164	In Silico Methods for the Identification of Viral-Derived Small Interfering RNAs (vsiRNAs) and Their Application in Plant Genomics. <i>Methods in Molecular Biology</i> , 2022, 2408, 71-84.	0.4	1
165	Association Between Common Variants of APOE, ABCA7, A2M, BACE1, and Cerebrospinal Fluid Biomarkers in Alzheimer's Disease: Data from the PUMCH Dementia Cohort. <i>Journal of Alzheimer's Disease</i> , 2022, 85, 1511-1518.	1.2	3
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169	TGF β -EGFR pathway in breast carcinogenesis, association with WWOX expression and estrogen activation. <i>Journal of Applied Genetics</i> , 2022, 63, 339-359.	1.0	1
170	Encounter With a Selfish Virus Sabotages Its Vector to Orient Toward Requisite Host Plant: A Case Study With Chili Leaf Curl Virus-Whitefly. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	4
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173	LABRADOR "A Computational Workflow for Virus Detection in High-Throughput Sequencing Data. <i>Viruses</i> , 2021, 13, 2541.	1.5	1
174	Specific metabolic response of patient-derived organoids to curcumin of colorectal cancer. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2022, 1203, 123260.	1.2	5
175	Whole-genome sequencing and genetic characteristics of representative porcine reproductive and respiratory syndrome virus (PRRSV) isolates in Korea. <i>Virology Journal</i> , 2022, 19, 66.	1.4	13
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193	Differential expression analysis of genes and long non-coding RNAs associated with KRAS mutation in colorectal cancer cells. <i>Scientific Reports</i> , 2022, 12, 7965.	1.6	8
194	miR-29a-5p Inhibits Prenatal Hair Placode Formation Through Targeting EDAR by ceRNA Regulatory Network. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	0

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