

The Galaxy platform for accessible, reproducible and collaborative 2018 update

Nucleic Acids Research

46, W537-W544

DOI: [10.1093/nar/gky379](https://doi.org/10.1093/nar/gky379)

Citation Report

#	ARTICLE	IF	CITATIONS
1	MULTI-X, a State-of-the-Art Cloud-Based Ecosystem for Biomedical Research. , 2018, , .		2
2	MetaFlow: an interactive user-friendly workflow for automated analysis of whole genome shotgun sequencing metagenomic data. , 2018, , .		0
3	Draft Genome Sequence of <i>Candidatus Bathyarchaeota</i> Archaeon BE326-BA-RLH, an Uncultured Denitrifier and Putative Anaerobic Methanotroph from South Africa's Deep Continental Biosphere. Microbiology Resource Announcements, 2018, 7, .	0.3	11
4	Draft Genome Sequences of 57 <i>Salmonella enterica</i> Strains from Selected U.S. Swine Feed Mills. Microbiology Resource Announcements, 2018, 7, .	0.3	2
5	Return on Investment for Three Cyberinfrastructure Facilities: A Local Campus Supercomputer, the NSF-Funded Jetstream Cloud System, and XSEDE (the eXtreme Science and Engineering Discovery) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50		
6	Optimized Storing of Workflow Outputs through Mining Association Rules. , 2018, , .		3
7	Complete Genome Sequence of the Polymyxin E (Colistin)-Producing <i>Paenibacillus</i> sp. Strain B-LR. Microbiology Resource Announcements, 2018, 7, .	0.3	2
8	Comparative analysis of nucleus-encoded plastid-targeting proteins in <i>Rafflesia cantleyi</i> against photosynthetic and non-photosynthetic representatives reveals orthologous systems with potentially divergent functions. Scientific Reports, 2018, 8, 17258.	1.6	20
9	Integration of <i>omics</i> Data and Phenotypic Data Within a Unified Extensible Multimodal Framework. Frontiers in Neuroinformatics, 2018, 12, 91.	1.3	6
10	Pergola: Boosting Visualization and Analysis of Longitudinal Data by Unlocking Genomic Analysis Tools. IScience, 2018, 9, 244-257.	1.9	5
11	The CbrB Regulon: Promoter dissection reveals novel insights into the CbrAB expression network in <i>Pseudomonas putida</i> . PLoS ONE, 2018, 13, e0209191.	1.1	10
12	Transparent Deployment of Scientific Workflows across Clouds - Kubernetes Approach. , 2018, , .		14
13	Future Cloud Systems Design: Challenges and Research Directions. IEEE Access, 2018, 6, 74120-74150.	2.6	29
14	A transcriptomics analysis of the Tbx5 paralogues in zebrafish. PLoS ONE, 2018, 13, e0208766.	1.1	11
15	Dissecting clinical outcome of porcine circovirus type 2 with in vivo derived transcriptomic signatures of host tissue responses. BMC Genomics, 2018, 19, 831.	1.2	4
16	Whole Genome Next-Generation Sequencing Mutation Identification in <i>Pseudomonas aeruginosa</i> . Current Protocols in Molecular Biology, 2018, 124, e69.	2.9	1
17	Salicylic acid-induced transcriptional reprogramming by the HAC-NPR1-TGA histone acetyltransferase complex in <i>Arabidopsis</i> . Nucleic Acids Research, 2018, 46, 11712-11725.	6.5	59
18	DNA damage sensitivity of SWI/SNF-deficient cells depends on TFIIF subunit p62/GTF2H1. Nature Communications, 2018, 9, 4067.	5.8	25

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19	Profiling the airway in the macaque model of tuberculosis reveals variable microbial dysbiosis and alteration of community structure. <i>Microbiome</i> , 2018, 6, 180.	4.9	23
20	SNPSelect: A scalable and flexible targeted sequence-based genotyping solution. <i>PLoS ONE</i> , 2018, 13, e0205577.	1.1	2
21	Functional Genomics. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1102, 11-30.	0.8	3
22	DAZL Regulates Germ Cell Survival through a Network of PolyA-Proximal mRNA Interactions. <i>Cell Reports</i> , 2018, 25, 1225-1240.e6.	2.9	66
23	Draft Genome Sequences of Two Carbapenemase-Producing <i>Klebsiella pneumoniae</i> Strains Isolated from Blood Cultures. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3
24	Bulked-Segregant Analysis Coupled to Whole Genome Sequencing (BSA-Seq) for Rapid Gene Cloning in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3583-3592.	0.8	57
25	MATHT: A web server for comprehensive transcriptome data analysis. <i>Journal of Theoretical Biology</i> , 2018, 455, 140-146.	0.8	2
26	Generation of <i>Mycoplasma hominis</i> gene-targeted mutants by targeting-induced local lesions in genomes (TILLING). <i>BMC Genomics</i> , 2018, 19, 525.	1.2	5
27	Identification and tissue-expression profiling of novel chicken c-type lectin-like domain containing proteins as potential targets for carbohydrate-based vaccine strategies. <i>Molecular Immunology</i> , 2019, 114, 216-225.	1.0	13
28	Depletion of the MFAP1/SPP381 Splicing Factor Causes R-Loop-Independent Genome Instability. <i>Cell Reports</i> , 2019, 28, 1551-1563.e7.	2.9	13
29	A general framework for quantitatively assessing ecological stochasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16892-16898.	3.3	482
30	A Novel Group of <i>Rhizobium tumorigenes</i> -Like <i>Agrobacteria</i> Associated with Crown Gall Disease of <i>Rhododendron</i> and <i>Blueberry</i> . <i>Phytopathology</i> , 2019, 109, 1840-1848.	1.1	10
31	Study of VIPER and TATE in kinetoplastids and the evolution of tyrosine recombinase retrotransposons. <i>Mobile DNA</i> , 2019, 10, 34.	1.3	5
32	The association between gut microbiota composition and BMI in Chinese male college students, as analysed by next-generation sequencing. <i>British Journal of Nutrition</i> , 2019, 122, 986-995.	1.2	46
33	Bis-naphthopyrone pigments protect filamentous ascomycetes from a wide range of predators. <i>Nature Communications</i> , 2019, 10, 3579.	5.8	36
34	Genome Sequence of <i>Pseudomonas</i> Phage UMP151, Isolated from the Female Bladder Microbiota. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
35	The bio.tools registry of software tools and data resources for the life sciences. <i>Genome Biology</i> , 2019, 20, 164.	3.8	39
36	Unravelling the genes forming the wing pattern supergene in the polymorphic butterfly <i>Heliconius numata</i> . <i>EvoDevo</i> , 2019, 10, 16.	1.3	23

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37	Architecture of antimicrobial skin defense. <i>Cytokine and Growth Factor Reviews</i> , 2019, 49, 70-84.	3.2	41
38	baerhunter: an <i>R</i> package for the discovery and analysis of expressed non-coding regions in bacterial RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 966-969.	1.8	8
39	Differential Inhibition of Target Gene Expression by Human microRNAs. <i>Cells</i> , 2019, 8, 791.	1.8	14
40	Reproducible Scientific Workflows for High Performance and Cloud Computing. , 2019, , .		5
41	HDAC7 regulates histone 3 lysine 27 acetylation and transcriptional activity at super-enhancer-associated genes in breast cancer stem cells. <i>Oncogene</i> , 2019, 38, 6599-6614.	2.6	82
42	First detection and characterisation of a VanA-type <i>Enterococcus faecalis</i> clinical isolate from Bulgaria. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 18, 260-262.	0.9	5
43	Pluripotency of <i>Wolbachia</i> against Arbovirus: the case of yellow fever. <i>Gates Open Research</i> , 0, 3, 161.	2.0	0
44	Complete Genome Sequence of <i>Agrobacterium tumefaciens</i> Myophage Milano. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
45	Complete Genome Sequence of <i>Serratia marcescens</i> Myophage Moabite. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
46	Complete Genome Sequence of the Novel <i>Klebsiella pneumoniae</i> Phage Marfa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
47	Complete Genome Sequence of <i>Staphylococcus aureus</i> Siphophage Sebago. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
48	Draft Genome Sequence of the Yeast <i>Kodamaea ohmeri</i> , a Symbiont of the Small Hive Beetle. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
49	Social support for collaboration and group awareness in life science research teams. <i>Source Code for Biology and Medicine</i> , 2019, 14, 4.	1.7	0
50	Bringing Molecular Dynamics Simulation Data into View. <i>Trends in Biochemical Sciences</i> , 2019, 44, 902-913.	3.7	111
51	Improve your Galaxy text life: The Query Tabular Tool. <i>F1000Research</i> , 2018, 7, 1604.	0.8	21
52	Complex Bacterial Consortia Reprogram the Colitogenic Activity of <i>Enterococcus faecalis</i> in a Gnotobiotic Mouse Model of Chronic, Immune-Mediated Colitis. <i>Frontiers in Immunology</i> , 2019, 10, 1420.	2.2	40
53	The <i>Drosophila</i> nuclear receptors EcR and ERR jointly regulate the expression of genes involved in carbohydrate metabolism. <i>Insect Biochemistry and Molecular Biology</i> , 2019, 112, 103184.	1.2	29
54	Are bacteria responsible for aroma deterioration upon storage of the black truffle <i>Tuber aestivum</i> : A microbiome and volatilome study. <i>Food Microbiology</i> , 2019, 84, 103251.	2.1	32

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83	Collection of Mitochondrial tRNA Sequences and Anticodon Identification for <i>Acheta domestica</i> . <i>Materials Science Forum</i> , 0, 967, 65-70.	0.3	0
84	The quorum sensing transcription factor AphA directly regulates natural competence in <i>Vibrio cholerae</i> . <i>PLoS Genetics</i> , 2019, 15, e1008362.	1.5	25
85	Highly efficient library preparation for Ion Torrent sequencing using Y-adapters. <i>BioTechniques</i> , 2019, 67, 229-237.	0.8	8
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100	Draft Genome Sequence of <i>Massilia</i> sp. Strain MC02, Isolated from a Sandy Loam Maize Soil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
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2051	Biom mineralization in Cave Bacteriaâ€”Popcorn and Soda Straw Crystal Formations, Morphologies, and Potential Metabolic Pathways. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
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