

Metagenomics: Tools and Insights for Analyzing Next-Gen from Biodiversity Studies

Bioinformatics and Biology Insights

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Web Resources for Metagenomics Studies. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 296-303.	3.0	29
2	Probing the diversity of healthy oral microbiome with bioinformatics approaches. <i>BMB Reports</i> , 2016, 49, 662-670.	1.1	39
3	Advances in Molecular Serotyping and Subtyping of <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 644.	1.5	103
4	The Oral Microbiome in Health and Its Implication in Oral and Systemic Diseases. <i>Advances in Applied Microbiology</i> , 2016, 97, 171-210.	1.3	171
5	Analysis of rumen microbial community in cattle through the integration of metagenomic and network-based approaches. , 2016, , .		3
6	16S Metagenomic Microbial Composition Analysis of Kefir Grain using MEGAN and BaseSpace. <i>Food Biotechnology</i> , 2016, 30, 219-230.	0.6	25
7	FARAO: the flexible all-round annotation organizer. <i>Bioinformatics</i> , 2016, 32, 3664-3666.	1.8	6
8	Microbiome alterations in HIV infection a review. <i>Cellular Microbiology</i> , 2016, 18, 645-651.	1.1	72
9	Metagenomics and Bioinformatics in Microbial Ecology: Current Status and Beyond. <i>Microbes and Environments</i> , 2016, 31, 204-212.	0.7	76
10	Metagenomics: Probing pollutant fate in natural and engineered ecosystems. <i>Biotechnology Advances</i> , 2016, 34, 1413-1426.	6.0	42
11	ampliMethProfiler: a pipeline for the analysis of CpG methylation profiles of targeted deep bisulfite sequenced amplicons. <i>BMC Bioinformatics</i> , 2016, 17, 484.	1.2	25
12	Metagenomic insights into effects of spent engine oil perturbation on the microbial community composition and function in a tropical agricultural soil. <i>Environmental Science and Pollution Research</i> , 2017, 24, 7139-7159.	2.7	44
13	MEGARes: an antimicrobial resistance database for high throughput sequencing. <i>Nucleic Acids Research</i> , 2017, 45, D574-D580.	6.5	328
14	One-year calorie restriction impacts gut microbial composition but not its metabolic performance in obese adolescents. <i>Environmental Microbiology</i> , 2017, 19, 1536-1551.	1.8	54
15	Diversity changes of microbial communities into hospital surface environments. <i>Journal of Infection and Chemotherapy</i> , 2017, 23, 439-445.	0.8	12
16	The state of rhizospheric science in the era of multi-omics: A practical guide to omics technologies. <i>Rhizosphere</i> , 2017, 3, 212-221.	1.4	66
17	Arbitrarily Primed PCR for Comparison of Meta Genomes and Extracting Useful Loci from Them. <i>Methods in Molecular Biology</i> , 2017, 1620, 267-280.	0.4	1
18	Integrated metagenomic analysis of the rumen microbiome of cattle reveals key biological mechanisms associated with methane traits. <i>Methods</i> , 2017, 124, 108-119.	1.9	21

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24	Metagenomic Analysis of Silage. Journal of Visualized Experiments, 2017, , .	0.2	7
25	Consensus Clustering for Binning Metagenome Sequences. Lecture Notes in Computer Science, 2017, , 273-284.	1.0	0
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