

Taxonomic structure and functional association of foxta

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Citation Report

#	ARTICLE	IF	CITATIONS
1	BusyBee Web: metagenomic data analysis by bootstrapped supervised binning and annotation. <i>Nucleic Acids Research</i> , 2017, 45, W171-W179.	6.5	84
2	Nanopore sequencing data analysis: state of the art, applications and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, 1256-1272.	3.2	91
3	Functional trade-off between strength and thermal capacity of dermal armor: Insights from girdled lizards. <i>Journal of the Mechanical Behavior of Biomedical Materials</i> , 2017, 74, 189-194.	1.5	46
4	From Pine Cones to Read Clouds: Rescaffolding the Megagenome of Sugar Pine (<i>Pinus lambertiana</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1563-1568.	0.8	19
5	The serine/threonine phosphatases of apicomplexan parasites. <i>Molecular Microbiology</i> , 2017, 106, 1-21.	1.2	33
6	Molluscan Genomics: Implications for Biology and Aquaculture. <i>Current Molecular Biology Reports</i> , 2017, 3, 297-305.	0.8	30
7	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	1,228
8	Nanopore sequencing enables near-complete de novo assembly of <i>Saccharomyces cerevisiae</i> reference strain CEN.PK113-7D. <i>FEMS Yeast Research</i> , 2017, 17, .	1.1	84
9	Remodeling the blood-brain barrier microenvironment by natural products for brain tumor therapy. <i>Acta Pharmaceutica Sinica B</i> , 2017, 7, 541-553.	5.7	55
10	Profiling bacterial communities by MinION sequencing of ribosomal operons. <i>Microbiome</i> , 2017, 5, 116.	4.9	105
11	Microsomal glutathione transferase 2 modulates LTC ₄ synthesis and ROS production in <i>Apostichopus japonicus</i> . <i>Molecular Immunology</i> , 2017, 91, 114-122.	1.0	8
12	Innovation in microbiome-based strategies for promoting metabolic health. <i>Current Opinion in Clinical Nutrition and Metabolic Care</i> , 2017, 20, 484-491.	1.3	32
13	A novel TNFAIP8 gene mediates l-arginine metabolism in <i>Apostichopus japonicus</i> . <i>Fish and Shellfish Immunology</i> , 2017, 69, 26-34.	1.6	7
14	High-Quality <i>de Novo</i> Genome Assembly of the <i>Dekkera bruxellensis</i> Yeast Using Nanopore MinION Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3243-3250.	0.8	44
15	Assessment of gene copy number variation of Scots pine thaumatin-like protein gene using real-time PCR based methods. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	4
16	Nanopore sequencing of complex genomic rearrangements in yeast reveals mechanisms of repeat-mediated double-strand break repair. <i>Genome Research</i> , 2017, 27, 2072-2082.	2.4	36
17	Mapping and phasing of structural variation in patient genomes using nanopore sequencing. <i>Nature Communications</i> , 2017, 8, 1326.	5.8	315
18	Comparative analysis of alignment tools for nanopore reads. , 2017, , .		1

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20	Influences on the Test-Retest Reliability of Functional Connectivity MRI and its Relationship with Behavioral Utility. <i>Cerebral Cortex</i> , 2017, 27, 5415-5429.	1.6	300
21	Reference-free Identification of Phage DNA Using Signal Processing on Nanopore Data. , 2017, , .		1
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27	The sea cucumber genome provides insights into morphological evolution and visceral regeneration. <i>PLoS Biology</i> , 2017, 15, e2003790.	2.6	202
28	Investigating Basal Autophagic Activity in Brain Regions Associated with Neurodegeneration using In Vivo and Ex Vivo Models. , 2017, 07, .		3
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30	Perspective: functional genomics towards new biotechnology in medicinal plants. <i>Plant Biotechnology Reports</i> , 2018, 12, 69-75.	0.9	17
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38	Draft genome of the milu (<i>Elaphurus davidianus</i>). <i>GigaScience</i> , 2018, 7, .	3.3	22
39	Avian transcriptomics: opportunities and challenges. <i>Journal of Ornithology</i> , 2018, 159, 599-629.	0.5	31
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49	Next-generation sequencing showing potential leachate influence on bacterial communities around a landfill in China. <i>Canadian Journal of Microbiology</i> , 2018, 64, 537-549.	0.8	14
50	Caveat Usor: Assessing Differences between Major Chemistry Databases. <i>ChemMedChem</i> , 2018, 13, 470-481.	1.6	12
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53	Population Genomics of Marine Zooplankton. <i>Population Genomics</i> , 2018, , 61-102.	0.2	24
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80	Genetic landscape of hepatitis B virus-associated diffuse large B-cell lymphoma. <i>Blood</i> , 2018, 131, 2670-2681.	0.6	77
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