

Non-coding RNA Analysis Using the Rfam Database

Current Protocols in Bioinformatics

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The State of Long Non-Coding RNA Biology. <i>Non-coding RNA</i> , 2018, 4, 17.	1.3	67
2	An improved genome assembly of the fluke <i>Schistosoma japonicum</i> . <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007612.	1.3	50
3	Discovering and Constructing ceRNA-miRNA-Target Gene Regulatory Networks during Anther Development in Maize. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3480.	1.8	43
4	A proteotranscriptomic study of silk-producing glands from the orb-weaving spiders. <i>Molecular Omics</i> , 2019, 15, 256-270.	1.4	8
5	Integrated Analysis of Small RNA, Transcriptome and Degradome Sequencing Provides New Insights into Floral Development and Abscission in Yellow Lupine (<i>Lupinus luteus</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 5122.	1.8	21
6	The genome of <i>Populus alba</i> x <i>Populus tremula</i> var. <i>glandulosa</i> clone 84K. <i>DNA Research</i> , 2019, 26, 423-431.	1.5	56
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8	MicroRNA regulation during <i>Nibeia albiflora</i> immuno-resistant against <i>Cryptocaryon irritans</i> challenge in fish skin. <i>Aquaculture</i> , 2019, 507, 211-221.	1.7	10
9	FGMP: assessing fungal genome completeness. <i>BMC Bioinformatics</i> , 2019, 20, 184.	1.2	25
10	Comparative Transcriptomic Profiling of <i>Yersinia enterocolitica</i> O:3 and O:8 Reveals Major Expression Differences of Fitness- and Virulence-Relevant Genes Indicating Ecological Separation. <i>MSystems</i> , 2019, 4, .	1.7	8
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14	Comprehensive Characterization of miRNA and PHAS Loci in the Diploid Strawberry (<i>Fragaria vesca</i>) Genome. <i>Horticultural Plant Journal</i> , 2019, 5, 255-267.	2.3	19
15	Effective Rotation-Invariant Point CNN with Spherical Harmonics Kernels. , 2019, , .		53
16	TRANSNAP: a web database providing comprehensive information on Japanese pear transcriptome. <i>Scientific Reports</i> , 2019, 9, 18922.	1.6	10
17	Regulatory context drives conservation of glycine riboswitch aptamers. <i>PLoS Computational Biology</i> , 2019, 15, e1007564.	1.5	6
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20	milRNApredictor: Genome-free prediction of fungi milRNAs by incorporating k-mer scheme and distance-dependent pair potential. <i>Genomics</i> , 2020, 112, 2233-2240.	1.3	6
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