Benjamin R Evans

List of Publications by Year in descending order

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759233 1058476 1,087 14 12 14 citations h-index g-index papers 16 16 16 2065 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Rooting the Animal Tree of Life. Molecular Biology and Evolution, 2021, 38, 4322-4333.	8.9	93
2	Giant tortoise genomes provide insights into longevity and age-related disease. Nature Ecology and Evolution, 2019, 3, 87-95.	7.8	79
3	Genetic Markers of Benzimidazole Resistance among Human Hookworms (Necator americanus) in Kintampo North Municipality, Ghana. American Journal of Tropical Medicine and Hygiene, 2019, 100, 351-356.	1.4	35
4	Improved reference genome of Aedes aegypti informs arbovirus vector control. Nature, 2018, 563, 501-507.	27.8	426
5	How Much Does Inbreeding Reduce Heterozygosity? Empirical Results from <i>Aedes aegypti</i> American Journal of Tropical Medicine and Hygiene, 2017, 96, 157-158.	1.4	13
6	Tracking the return of Aedes aegypti to Brazil, the major vector of the dengue, chikungunya and Zika viruses. PLoS Neglected Tropical Diseases, 2017, 11, e0005653.	3.0	77
7	Multiple introductions of the dengue vector, Aedes aegypti, into California. PLoS Neglected Tropical Diseases, 2017, 11, e0005718.	3.0	65
8	Patterns of Genome-Wide Variation in Glossina fuscipes fuscipes Tsetse Flies from Uganda. G3: Genes, Genomes, Genetics, 2016, 6, 1573-1584.	1.8	12
9	De Novo Genome Assembly Shows Genome Wide Similarity between Trypanosoma brucei brucei and Trypanosoma brucei rhodesiense. PLoS ONE, 2016, 11, e0147660.	2.5	21
10	Vectors as Epidemiological Sentinels: Patterns of Within-Tick Borrelia burgdorferi Diversity. PLoS Pathogens, 2016, 12, e1005759.	4.7	28
11	A Multipurpose, High-Throughput Single-Nucleotide Polymorphism Chip for the Dengue and Yellow Fever Mosquito, <i>Aedes aegypti</i> C3: Genes, Genomes, Genetics, 2015, 5, 711-718.	1.8	56
12	Are 100 enough? Inferring acanthomorph teleost phylogeny using Anchored Hybrid Enrichment. BMC Evolutionary Biology, 2015, 15, 113.	3.2	40
13	Ancient homology underlies adaptive mimetic diversity across butterflies. Nature Communications, 2014, 5, 4817.	12.8	87
14	Comparative Genomics Reveals Multiple Genetic Backgrounds of Human Pathogenicity in the Trypanosoma brucei Complex. Genome Biology and Evolution, 2014, 6, 2811-2819.	2.5	39