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List of Publications by Year in descending order

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623734 677142 23 892 14 22 citations g-index h-index papers 28 28 28 1337 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Next-generation gene drive for population modification of the malaria vector mosquito, <i>Anopheles gambiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22805-22814.	7.1	157
2	Development of a confinable gene drive system in the human disease vector Aedes aegypti. ELife, 2020, 9,	6.0	156
3	Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. Nature Communications, 2014, 5, 3966.	12.8	124
4	An Annotated Draft Genome for Radix auricularia (Gastropoda, Mollusca). Genome Biology and Evolution, 2017, 9, 585-592.	2.5	57
5	The genomic footprint of climate adaptation in <i>Chironomus riparius</i> . Molecular Ecology, 2018, 27, 1439-1456.	3.9	54
6	Genome-wide divergence among invasive populations of Aedes aegypti in California. BMC Genomics, 2019, 20, 204.	2.8	44
7	Hypoxia tolerance, longevity and cancer-resistance in the mole rat Spalax – a liver transcriptomics approach. Scientific Reports, 2017, 7, 14348.	3.3	38
8	Phylogeny of Syndermata (syn. Rotifera): Mitochondrial gene order verifies epizoic Seisonidea as sister to endoparasitic Acanthocephala within monophyletic Hemirotifera. Molecular Phylogenetics and Evolution, 2016, 96, 79-92.	2.7	35
9	Abundance of conserved CRISPR-Cas9 target sites within the highly polymorphic genomes of Anopheles and Aedes mosquitoes. Nature Communications, 2020, $11,1425.$	12.8	28
10	Genomic basis of ecological niche divergence among cryptic sister species of non-biting midges. BMC Genomics, 2013, 14, 384.	2.8	25
11	The fate of genes that cross species boundaries after a major hybridization event in a natural mosquito population. Molecular Ecology, 2018, 27, 4978-4990.	3.9	23
12	A High-Quality Genome Assembly from Short and Long Reads for the Non-biting Midge <i>Chironomus riparius </i> (Diptera). G3: Genes, Genomes, Genetics, 2020, 10, 1151-1157.	1.8	22
13	Evaluating the Hypoxia Response of Ruffe and Flounder Gills by a Combined Proteome and Transcriptome Approach. PLoS ONE, 2015, 10, e0135911.	2.5	21
14	Molecular evolution of antioxidant and hypoxia response in long-lived, cancer-resistant blind mole rats: The Nrf2–Keap1 pathway. Gene, 2016, 577, 293-298.	2.2	20
15	De novo Transcriptome Assembly and Comparison of C3, C3-C4, and C4 Species of Tribe Salsoleae (Chenopodiaceae). Frontiers in Plant Science, 2017, 8, 1939.	3.6	19
16	<i>Chironomus riparius</i> (Diptera) genome sequencing reveals the impact of minisatellite transposable elements on population divergence. Molecular Ecology, 2017, 26, 3256-3275.	3.9	15
17	Transcontinental dispersal of Anopheles gambiae occurred from West African origin via serial founder events. Communications Biology, 2019, 2, 473.	4.4	13
18	Hybrid Genome Assembly of a Neotropical Mutualistic Ant. Genome Biology and Evolution, 2019, 11, 2306-2311.	2.5	11

#	Article	IF	CITATIONS
19	AFS: identification and quantification of species composition by metagenomic sequencing. Bioinformatics, 2017, 33, 1396-1398.	4.1	10
20	Complete mitogenome sequence of Aedes (Stegomyia) aegypti derived from field isolates from California and South Africa. Mitochondrial DNA Part B: Resources, 2018, 3, 994-995.	0.4	7
21	Genomics and transcriptomics of epizoic Seisonidea (Rotifera, syn. Syndermata) reveal strain formation and gradual gene loss with growing ties to the host. BMC Genomics, 2021, 22, 604.	2.8	6
22	Host-dependent impairment of parasite development and reproduction in the acanthocephalan model. Cell and Bioscience, 2022, 12, .	4.8	3
23	The Population Genomics of Anopheles gambiae Species Complex: Progress and Prospects. Population Genomics, 2021, , 1.	0.5	0