

Alistair Miles

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

1,615
citations

430874

18
h-index

610901

24
g-index

34
all docs

34
docs citations

34
times ranked

2314
citing authors

#	ARTICLE	IF	CITATIONS
1	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	97
2	Novel genotyping approaches to easily detect genomic admixture between the major Afrotropical malaria vector species, <i>Anopheles coluzzii</i> and <i>An. gambiae</i> . Molecular Ecology Resources, 2021, 21, 1504-1516.	4.8	7
3	Genetic variation at the Cyp6m2 putative insecticide resistance locus in <i>Anopheles gambiae</i> and <i>Anopheles coluzzii</i> . Malaria Journal, 2021, 20, 234.	2.3	5
4	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	51
5	Resistance to pirimiphos-methyl in West African <i>Anopheles</i> is spreading via duplication and introgression of the Ace1 locus. PLoS Genetics, 2021, 17, e1009253.	3.5	33
6	Evolution of the Insecticide Target Rdl in African <i>Anopheles</i> Is Driven by Interspecific and Interkaryotypic Introgression. Molecular Biology and Evolution, 2020, 37, 2900-2917.	8.9	31
7	Whole-genome sequencing reveals high complexity of copy number variation at insecticide resistance loci in malaria mosquitoes. Genome Research, 2019, 29, 1250-1261.	5.5	79
8	The origins and relatedness structure of mixed infections vary with local prevalence of <i>P. falciparum</i> malaria. ELife, 2019, 8, .	6.0	52
9	The genomics of insecticide resistance: insights from recent studies in African malaria vectors. Current Opinion in Insect Science, 2018, 27, 111-115.	4.4	16
10	Panoptes: web-based exploration of large scale genome variation data. Bioinformatics, 2017, 33, 3243-3249.	4.1	6
11	Massive introgression drives species radiation at the range limit of <i>Anopheles gambiae</i> . Scientific Reports, 2017, 7, 46451.	3.3	28
12	High-throughput genotyping of <i>Anopheles</i> mosquitoes using intact legs by <i>scRNA-seq</i> . Molecular Ecology Resources, 2016, 16, 480-486.	4.8	5
13	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . Genome Research, 2016, 26, 1288-1299.	5.5	180
14	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . Nature Genetics, 2016, 48, 959-964.	21.4	169
15	Binding of <i>Plasmodium falciparum</i> Merozoite Surface Proteins DBLMSP and DBLMSP2 to Human Immunoglobulin M Is Conserved among Broadly Diverged Sequence Variants. Journal of Biological Chemistry, 2016, 291, 14285-14299.	3.4	27
16	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. DNA Research, 2014, 21, 661-671.	3.4	27
17	A Genome Wide Association Study of <i>Plasmodium falciparum</i> Susceptibility to 22 Antimalarial Drugs in Kenya. PLoS ONE, 2014, 9, e96486.	2.5	27
18	Key choices in the design of Simple Knowledge Organization System (SKOS). Web Semantics, 2013, 20, 35-49.	2.9	73

#	ARTICLE	IF	CITATIONS
19	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	21.4	424
20	OpenFlyData: An exemplar data web integrating gene expression data on the fruit fly <i>Drosophila melanogaster</i> . <i>Journal of Biomedical Informatics</i> , 2010, 43, 752-761.	4.3	22
21	Adventures in Semantic Publishing: Exemplar Semantic Enhancements of a Research Article. <i>PLoS Computational Biology</i> , 2009, 5, e1000361.	3.2	124
22	Linked data and provenance in biological data webs. <i>Briefings in Bioinformatics</i> , 2009, 10, 139-152.	6.5	32
23	OpenFlyData: The Way to Go for Biological Data Integration. <i>Lecture Notes in Computer Science</i> , 2009, , 47-54.	1.3	6
24	An expressed sequence tag analysis of a full-length, spliced-leader cDNA library from <i>Leishmania major</i> promastigotes. <i>Molecular and Biochemical Parasitology</i> , 1996, 76, 345-348.	1.1	46