Gareth L Maslen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1109555/publications.pdf

Version: 2024-02-01

27 papers

5,719 citations

331670
21
h-index

27 g-index

29 all docs 29 docs citations

29 times ranked 10638 citing authors

#	Article	IF	CITATIONS
1	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. Nucleic Acids Research, 2022, 50, D898-D911.	14.5	277
2	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic Acids Research, 2022, 50, D996-D1003.	14.5	141
3	The genome of the stable fly, Stomoxys calcitrans, reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. BMC Biology, 2021, 19, 41.	3.8	19
4	Ensembl Genomes 2020—enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	14.5	416
5	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	3.8	177
6	Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. Genome Biology, 2019, 20, 187.	8.8	71
7	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. Nucleic Acids Research, 2018, 46, D802-D808.	14.5	489
8	Advancing vector biology research: a community survey for future directions, research applications and infrastructure requirements. Pathogens and Global Health, 2016, 110, 164-172.	2.3	3
9	Ensembl Genomes 2016: more genomes, more complexity. Nucleic Acids Research, 2016, 44, D574-D580.	14.5	530
10	Association mapping by pooled sequencing identifies TOLL 11 as a protective factor against Plasmodium falciparum in Anopheles gambiae. BMC Genomics, 2015, 16, 779.	2.8	19
11	VectorBase: an updated bioinformatics resource for invertebrate vectors and other organisms related with human diseases. Nucleic Acids Research, 2015, 43, D707-D713.	14.5	556
12	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. Science, 2015, 347, 1258522.	12.6	492
13	Genome analysis of a major urban malaria vector mosquito, Anopheles stephensi. Genome Biology, 2014, 15, 459.	8.8	119
14	Ensembl Genomes 2013: scaling up access to genome-wide data. Nucleic Acids Research, 2014, 42, D546-D552.	14.5	205
15	Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. Nature Genetics, 2013, 45, 648-655.	21.4	424
16	Genome-wide screen identifies new candidate genes associated with artemisinin susceptibility in Plasmodium falciparum in Kenya. Scientific Reports, 2013, 3, 3318.	3.3	75
17	Effective Preparation of Plasmodium vivax Field Isolates for High-Throughput Whole Genome Sequencing. PLoS ONE, 2013, 8, e53160.	2.5	26
18	Characterization of Within-Host Plasmodium falciparum Diversity Using Next-Generation Sequence Data. PLoS ONE, 2012, 7, e32891.	2.5	102

#	Article	IF	Citations
19	Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. Nature, 2012, 487, 375-379.	27.8	450
20	Optimizing illumina next-generation sequencing library preparation for extremely at-biased genomes. BMC Genomics, $2012,13,1.$	2.8	772
21	An In-Solution Hybridisation Method for the Isolation of Pathogen DNA from Human DNA-rich Clinical Samples for Analysis by NGS. The Open Genomics Journal, 2012, 5, 18-29.	0.5	12
22	An optimized microarray platform for assaying genomic variation in Plasmodium falciparum field populations. Genome Biology, 2011, 12, R35.	9.6	26
23	An Effective Method to Purify Plasmodium falciparum DNA Directly from Clinical Blood Samples for Whole Genome High-Throughput Sequencing. PLoS ONE, 2011, 6, e22213.	2.5	68
24	Drug-Resistant Genotypes and Multi-Clonality in Plasmodium falciparum Analysed by Direct Genome Sequencing from Peripheral Blood of Malaria Patients. PLoS ONE, 2011, 6, e23204.	2.5	41
25	SnoopCGH: software for visualizing comparative genomic hybridization data. Bioinformatics, 2009, 25, 2732-2733.	4.1	9
26	Application of phage display to high throughput antibody generation and characterization. Genome Biology, 2007, 8, R254.	9.6	195
27	Atlas of protein expression: image capture, analysis, and design of terabyte image database. , 2006, , .		0