

# 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

526287

27  
g-index

29  
all docs

29  
docs citations

29  
times ranked

10638  
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimizing illumina next-generation sequencing library preparation for extremely at-biased genomes. BMC Genomics, 2012, 13, 1.	2.8	772
2	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
3	Ensembl Genomes 2016: more genomes, more complexity. Nucleic Acids Research, 2016, 44, D574-D580.	14.5	530
4	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. Science, 2015, 347, 1258522.	12.6	492
5	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. Nucleic Acids Research, 2018, 46, D802-D808.	14.5	489
6	Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. Nature, 2012, 487, 375-379.	27.8	450
7	Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. Nature Genetics, 2013, 45, 648-655.	21.4	424
8	Ensembl Genomes 2020"enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	14.5	416
9	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. Nucleic Acids Research, 2022, 50, D898-D911.	14.5	277
10	Ensembl Genomes 2013: scaling up access to genome-wide data. Nucleic Acids Research, 2014, 42, D546-D552.	14.5	205
11	Application of phage display to high throughput antibody generation and characterization. Genome Biology, 2007, 8, R254.	9.6	195
12	Evolutionary superscaffolding and chromosome anchoring to improve Anopheles genome assemblies. BMC Biology, 2020, 18, 1.	3.8	177
13	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic Acids Research, 2022, 50, D996-D1003.	14.5	141
14	Genome analysis of a major urban malaria vector mosquito, Anopheles stephensi. Genome Biology, 2014, 15, 459.	8.8	119
15	Characterization of Within-Host Plasmodium falciparum Diversity Using Next-Generation Sequence Data. PLoS ONE, 2012, 7, e32891.	2.5	102
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	Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. Genome Biology, 2019, 20, 187.	8.8	71
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	An optimized microarray platform for assaying genomic variation in Plasmodium falciparum field populations. Genome Biology, 2011, 12, R35.	9.6	26
21	Effective Preparation of Plasmodium vivax Field Isolates for High-Throughput Whole Genome Sequencing. PLoS ONE, 2013, 8, e53160.	2.5	26
22	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
23	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
24	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
25	SnoopCGH: software for visualizing comparative genomic hybridization data. Bioinformatics, 2009, 25, 2732-2733.	4.1	9
26	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
27	Atlas of protein expression: image capture, analysis, and design of terabyte image database. , 2006, , .		0