

Gavin Band

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3214533/publications.pdf>

Version: 2024-02-01

27
papers

12,501
citations

361413

20
h-index

526287

27
g-index

36
all docs

36
docs citations

36
times ranked

21907
citing authors

#	ARTICLE	IF	CITATIONS
1	The UK Biobank resource with deep phenotyping and genomic data. <i>Nature</i> , 2018, 562, 203-209.	27.8	5,221
2	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011, 476, 214-219.	27.8	2,400
3	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013, 45, 1353-1360.	21.4	1,213
4	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. <i>Nature Genetics</i> , 2010, 42, 985-990.	21.4	918
5	A Genetic Atlas of Human Admixture History. <i>Science</i> , 2014, 343, 747-751.	12.6	691
6	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. <i>Human Molecular Genetics</i> , 2011, 20, 345-353.	2.9	202
7	A novel locus of resistance to severe malaria in a region of ancient balancing selection. <i>Nature</i> , 2015, 526, 253-257.	27.8	182
8	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. <i>Nature Genetics</i> , 2012, 44, 1131-1136.	21.4	162
9	Resistance to malaria through structural variation of red blood cell invasion receptors. <i>Science</i> , 2017, 356, .	12.6	135
10	Admixture into and within sub-Saharan Africa. <i>ELife</i> , 2016, 5, .	6.0	120
11	Imputation-Based Meta-Analysis of Severe Malaria in Three African Populations. <i>PLoS Genetics</i> , 2013, 9, e1003509.	3.5	95
12	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. <i>Lancet Haematology</i> , 2018, 5, e333-e345.	4.6	90
13	Common variants in the HLA-DRB1 and HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. <i>Nature Genetics</i> , 2013, 45, 208-213.	21.4	86
14	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. <i>Nature Communications</i> , 2014, 5, 4204.	12.8	72
15	Characterisation of the opposing effects of G6PD deficiency on cerebral malaria and severe malarial anaemia. <i>ELife</i> , 2017, 6, .	6.0	64
16	A Genome-wide Association Analysis of a Broad Psychosis Phenotype Identifies Three Loci for Further Investigation. <i>Biological Psychiatry</i> , 2014, 75, 386-397.	1.3	44
17	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. <i>American Journal of Human Genetics</i> , 2016, 98, 1092-1100.	6.2	39
18	Malaria protection due to sickle haemoglobin depends on parasite genotype. <i>Nature</i> , 2022, 602, 106-111.	27.8	36

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19	Genome-wide association study of intraocular pressure identifies the GLCCI1/ICA1 region as a glaucoma susceptibility locus. <i>Human Molecular Genetics</i> , 2013, 22, 4653-4660.	2.9	29
20	Bayesian meta-analysis across genome-wide association studies of diverse phenotypes. <i>Genetic Epidemiology</i> , 2019, 43, 532-547.	1.3	27
21	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. <i>Malaria Journal</i> , 2015, 14, 333.	2.3	26
22	Two complement receptor one alleles have opposing associations with cerebral malaria and interact with β -thalassaemia. <i>ELife</i> , 2018, 7, .	6.0	25
23	Evidence of the interplay of genetics and culture in Ethiopia. <i>Nature Communications</i> , 2021, 12, 3581.	12.8	25
24	Using de novo assembly to identify structural variation of eight complex immune system gene regions. <i>PLoS Computational Biology</i> , 2021, 17, e1009254.	3.2	22
25	Environmental Correlation Analysis for Genes Associated with Protection against Malaria. <i>Molecular Biology and Evolution</i> , 2016, 33, 1188-1204.	8.9	21
26	The ferroportin Q248H mutation protects from anemia, but not malaria or bacteremia. <i>Science Advances</i> , 2019, 5, eaaw0109.	10.3	20
27	Haplotype heterogeneity and low linkage disequilibrium reduce reliable prediction of genotypes for the β -thalassaemia using genome-wide microarray data. <i>Wellcome Open Research</i> , 2020, 5, 287.	1.8	3