

Daniel Mead

List of Publications by Year in descending order

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22
papers

3,169
citations

566801

15
h-index

839053

18
g-index

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all docs

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docs citations

27
times ranked

8701
citing authors

#	ARTICLE	IF	CITATIONS
1	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016, 167, 1415-1429.e19.	13.5	1,052
2	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	13.5	573
3	Genetic architecture of artemisinin-resistant <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2015, 47, 226-234.	9.4	515
4	K13-Propeller Polymorphisms in <i>Plasmodium falciparum</i> Parasites From Sub-Saharan Africa. <i>Journal of Infectious Diseases</i> , 2015, 211, 1352-5.	1.9	203
5	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2016, 26, 1288-1299.	2.4	180
6	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 959-964.	9.4	169
7	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.	2.2	90
8	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. <i>Genome Biology</i> , 2017, 18, 50.	3.8	71
9	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. <i>Nature Genetics</i> , 2016, 48, 1303-1312.	9.4	66
10	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	5.8	50
11	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. <i>Nature Communications</i> , 2021, 12, 2298.	5.8	32
12	Massive introgression drives species radiation at the range limit of <i>Anopheles gambiae</i> . <i>Scientific Reports</i> , 2017, 7, 46451.	1.6	28
13	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. <i>DNA Research</i> , 2014, 21, 661-671.	1.5	27
14	Association mapping by pooled sequencing identifies TOLL 11 as a protective factor against <i>Plasmodium falciparum</i> in <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2015, 16, 779.	1.2	19
15	The genome sequence of the brown trout, <i>Salmo trutta</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2021, 6, 108.	0.9	15
16	An interactive genome browser of association results from the UK10K cohorts project. <i>Bioinformatics</i> , 2015, 31, 4029-4031.	1.8	12
17	The genome sequence of the ringlet, <i>Aphantopus hyperantus</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 0, 6, 165.	0.9	4
18	The genome sequence of the European turtle dove, <i>Streptopelia turtur</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 0, 6, 191.	0.9	4

#	ARTICLE	IF	CITATIONS
19	The genome sequence of the European golden eagle, <i>Aquila chrysaetos chrysaetos</i> Linnaeus 1758. Wellcome Open Research, 2021, 6, 112.	0.9	3
20	The genome sequence of the common pipistrelle, <i>Pipistrellus pipistrellus</i> Schreber 1774. Wellcome Open Research, 0, 6, 117.	0.9	2
21	The genome sequence of the European robin, <i>Erithacus rubecula</i> Linnaeus 1758. Wellcome Open Research, 0, 6, 172.	0.9	2
22	The genome sequence of the European water vole, <i>Arvicola amphibius</i> Linnaeus 1758. Wellcome Open Research, 0, 6, 162.	0.9	1