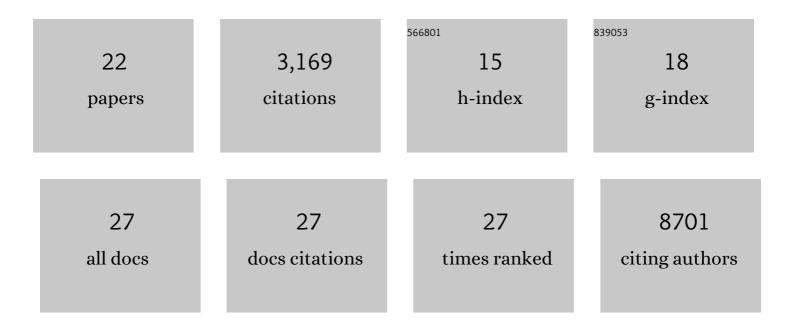
Daniel Mead

List of Publications by Year in descending order

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DANIEL MEAD

#	Article	IF	CITATIONS
1	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. Nature Communications, 2021, 12, 2298.	5.8	32
2	The genome sequence of the brown trout, Salmo trutta Linnaeus 1758. Wellcome Open Research, 2021, 6, 108.	0.9	15
3	The genome sequence of the European golden eagle, Aquila chrysaetos chrysaetos Linnaeus 1758. Wellcome Open Research, 2021, 6, 112.	0.9	3
4	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. Lancet Haematology,the, 2018, 5, e333-e345.	2.2	90
5	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	3.8	71
6	Massive introgression drives species radiation at the range limit of Anopheles gambiae. Scientific Reports, 2017, 7, 46451.	1.6	28
7	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	5.8	50
8	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
9	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . Genome Research, 2016, 26, 1288-1299.	2.4	180
10	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	13.5	1,052
11	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
12	Genomic analysis of local variation and recent evolution in Plasmodium vivax. Nature Genetics, 2016, 48, 959-964.	9.4	169
13	K13-Propeller Polymorphisms in Plasmodium falciparum Parasites From Sub-Saharan Africa. Journal of Infectious Diseases, 2015, 211, 1352-5.	1.9	203
14	Association mapping by pooled sequencing identifies TOLL 11 as a protective factor against Plasmodium falciparum in Anopheles gambiae. BMC Genomics, 2015, 16, 779.	1.2	19
15	Genetic architecture of artemisinin-resistant Plasmodium falciparum. Nature Genetics, 2015, 47, 226-234.	9.4	515
16	An interactive genome browser of association results from the UK10K cohorts project. Bioinformatics, 2015, 31, 4029-4031.	1.8	12
17	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. DNA Research, 2014, 21, 661-671.	1.5	27
18	The genome sequence of the common pipistrelle, Pipistrellus pipistrellus Schreber 1774. Wellcome Open Research, 0, 6, 117.	0.9	2

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#	Article	IF	CITATIONS
19	The genome sequence of the European water vole, Arvicola amphibius Linnaeus 1758. Wellcome Open Research, 0, 6, 162.	0.9	1
20	The genome sequence of the ringlet, Aphantopus hyperantus Linnaeus 1758. Wellcome Open Research, 0, 6, 165.	0.9	4
21	The genome sequence of the European robin, Erithacus rubecula Linnaeus 1758. Wellcome Open Research, 0, 6, 172.	0.9	2
22	The genome sequence of the European turtle dove, Streptopelia turtur Linnaeus 1758. Wellcome Open Research, 0, 6, 191.	0.9	4