

# David Wragg

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4314718/publications.pdf>

Version: 2024-02-01

19  
papers

807  
citations

623574

14  
h-index

752573

20  
g-index

23  
all docs

23  
docs citations

23  
times ranked

1087  
citing authors

#	ARTICLE	IF	CITATIONS
1	A locus conferring tolerance to Theileria infection in African cattle. PLoS Genetics, 2022, 18, e1010099.	1.5	6
2	Complex population structure and haplotype patterns in the Western European honey bee from sequencing a large panel of haploid drones. Molecular Ecology Resources, 2022, 22, 3068-3086.	2.2	9
3	Whole-Genome Sequence Data Suggest Environmental Adaptation of Ethiopian Sheep Populations. Genome Biology and Evolution, 2021, 13, .	1.1	20
4	Inherited Tolerance in Cattle to the Apicomplexan Protozoan Theileria parva is Associated with Decreased Proliferation of Parasite-Infected Lymphocytes. Frontiers in Cellular and Infection Microbiology, 2021, 11, 751671.	1.8	5
5	Digging into the Genomic Past of Swiss Honey Bees by Whole-Genome Sequencing Museum Specimens. Genome Biology and Evolution, 2020, 12, 2535-2551.	1.1	26
6	The wild species genome ancestry of domestic chickens. BMC Biology, 2020, 18, 13.	1.7	61
7	Genome Diversity and Signatures of Selection for Production and Performance Traits in Dromedary Camels. Frontiers in Genetics, 2019, 10, 893.	1.1	26
8	Genome-wide scans identify known and novel regions associated with prolificacy and reproduction traits in a sub-Saharan African indigenous sheep (Ovis aries). Mammalian Genome, 2019, 30, 339-352.	1.0	25
9	Developing reduced <sc>SNP</sc> assays from whole-genome sequence data to estimate introgression in an organism with complex genetic patterns, the Iberian honeybee (<i>Apis mellifera</i>). Tj ETQq1 1 0.784314 rgBT /Over		
10	Characterisation of the British honey bee metagenome. Nature Communications, 2018, 9, 4995.	5.8	51
11	Genomic signatures of adaptive introgression and environmental adaptation in the Sheko cattle of southwest Ethiopia. PLoS ONE, 2018, 13, e0202479.	1.1	30
12	Autosomal and Mitochondrial Adaptation Following Admixture: A Case Study on the Honeybees of Reunion Island. Genome Biology and Evolution, 2018, 10, 220-238.	1.1	13
13	Signatures of Selection for Environmental Adaptation and Zebu – Taurine Hybrid Fitness in East African Shorthorn Zebu. Frontiers in Genetics, 2017, 8, 68.	1.1	133
14	Using Whole-Genome Sequence Information to Foster Conservation Efforts for the European Dark Honey Bee, Apis mellifera mellifera. Frontiers in Ecology and Evolution, 2016, 4, .	1.1	34
15	Whole-genome resequencing of honeybee drones to detect genomic selection in a population managed for royal jelly. Scientific Reports, 2016, 6, 27168.	1.6	35
16	Signatures of positive selection in East African Shorthorn Zebu: A genome-wide single nucleotide polymorphism analysis. Scientific Reports, 2015, 5, 11729.	1.6	114
17	Genome-wide analysis reveals the extent of EAV-HP integration in domestic chicken. BMC Genomics, 2015, 16, 784.	1.2	20
18	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	0.6	97

#	ARTICLE	IF	CITATIONS
19	Endogenous Retrovirus EAV-HP Linked to Blue Egg Phenotype in Mapuche Fowl. PLoS ONE, 2013, 8, e71393.	1.1	56