

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	Signatures of Selection for Environmental Adaptation and Zebu – Taurine Hybrid Fitness in East African Shorthorn Zebu. <i>Frontiers in Genetics</i> , 2017, 8, 68.	1.1	133
2	Signatures of positive selection in East African Shorthorn Zebu: A genome-wide single nucleotide polymorphism analysis. <i>Scientific Reports</i> , 2015, 5, 11729.	1.6	114
3	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	0.6	97
4	The wild species genome ancestry of domestic chickens. <i>BMC Biology</i> , 2020, 18, 13.	1.7	61
5	Endogenous Retrovirus EAV-HP Linked to Blue Egg Phenotype in Mapuche Fowl. <i>PLoS ONE</i> , 2013, 8, e71393.	1.1	56
6	Characterisation of the British honey bee metagenome. <i>Nature Communications</i> , 2018, 9, 4995.	5.8	51
7	Whole-genome resequencing of honeybee drones to detect genomic selection in a population managed for royal jelly. <i>Scientific Reports</i> , 2016, 6, 27168.	1.6	35
8	Using Whole-Genome Sequence Information to Foster Conservation Efforts for the European Dark Honey Bee, <i>Apis mellifera mellifera</i> . <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	34
9	Genomic signatures of adaptive introgression and environmental adaptation in the Sheko cattle of southwest Ethiopia. <i>PLoS ONE</i> , 2018, 13, e0202479.	1.1	30
10	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>). <i>Tj ETQq0 0 0 ngBT /Overlock 10 Tf</i>	1.1	26
11	Genome Diversity and Signatures of Selection for Production and Performance Traits in Dromedary Camels. <i>Frontiers in Genetics</i> , 2019, 10, 893.	1.1	26
12	Digging into the Genomic Past of Swiss Honey Bees by Whole-Genome Sequencing Museum Specimens. <i>Genome Biology and Evolution</i> , 2020, 12, 2535-2551.	1.1	26
13	Genome-wide scans identify known and novel regions associated with prolificacy and reproduction traits in a sub-Saharan African indigenous sheep (<i>Ovis aries</i>). <i>Mammalian Genome</i> , 2019, 30, 339-352.	1.0	25
14	Genome-wide analysis reveals the extent of EAV-HP integration in domestic chicken. <i>BMC Genomics</i> , 2015, 16, 784.	1.2	20
15	Whole-Genome Sequence Data Suggest Environmental Adaptation of Ethiopian Sheep Populations. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	20
16	Autosomal and Mitochondrial Adaptation Following Admixture: A Case Study on the Honeybees of Reunion Island. <i>Genome Biology and Evolution</i> , 2018, 10, 220-238.	1.1	13
17	Complex population structure and haplotype patterns in the Western European honey bee from sequencing a large panel of haploid drones. <i>Molecular Ecology Resources</i> , 2022, 22, 3068-3086.	2.2	9
18	A locus conferring tolerance to <i>Theileria</i> infection in African cattle. <i>PLoS Genetics</i> , 2022, 18, e1010099.	1.5	6

#	ARTICLE	IF	CITATIONS
19	Inherited Tolerance in Cattle to the Apicomplexan Protozoan <i>Theileria parva</i> is Associated with Decreased Proliferation of Parasite-Infected Lymphocytes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 751671.	1.8	5