

Julia Metzger

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

40
papers

622
citations

14
h-index

24
g-index

43
ext. papers

899
ext. citations

4
avg, IF

4.08
L-index

#	Paper	IF	Citations
40	A comparison of strategies for generating artificial replicates in RNA-seq experiments.. <i>Scientific Reports</i> , 2022 , 12, 7170	4.9	0
39	Impact of model assumptions on demographic inferences: the case study of two sympatric mouse lemurs in northwestern Madagascar. <i>Bmc Ecology and Evolution</i> , 2021 , 21, 197	2.1	1
38	Hanoverian F/W-line contributes to segregation of Warmblood fragile foal syndrome type 1 variant PLOD1:c.2032G>A in Warmblood horses. <i>Equine Veterinary Journal</i> , 2021 , 53, 51-59	2.4	6
37	Past environmental changes affected lemur population dynamics prior to human impact in Madagascar. <i>Communications Biology</i> , 2021 , 4, 1084	6.7	2
36	De novo ZIC2 frameshift variant associated with frontonasal dysplasia in a Limousin calf. <i>BMC Genomics</i> , 2021 , 22, 1	4.5	48
35	Tracing selection signatures in the pig genome gives evidence for selective pressures on a unique curly hair phenotype in Mangalitza. <i>Scientific Reports</i> , 2020 , 10, 22142	4.9	4
34	Loss of Cx43 in Murine Sertoli Cells Leads to Altered Prepubertal Sertoli Cell Maturation and Impairment of the Mitosis-Meiosis Switch. <i>Cells</i> , 2020 , 9,	7.9	5
33	Genetics of Equine Orthopedic Disease. <i>Veterinary Clinics of North America Equine Practice</i> , 2020 , 36, 289-301	1.9	2
32	A structural UGDH variant associated with standard Munchkin cats. <i>BMC Genetics</i> , 2020 , 21, 67	2.6	1
31	Demographic assessment of the Dalmatian dog - effective population size, linkage disequilibrium and inbreeding coefficients. <i>Canine Medicine and Genetics</i> , 2020 , 7, 3	2.1	1
30	Genome-wide association analysis for lethal brachycephalic-like facial dysmorphism in Labrador Retrievers. <i>Animal Genetics</i> , 2020 , 51, 122-126	2.5	
29	Clinical, cytogenetic and molecular genetic characterization of a tandem fusion translocation in a male Holstein cattle with congenital hypospadias and a ventricular septal defect. <i>PLoS ONE</i> , 2020 , 15, e0227117	3.7	6
28	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019 , 9, 6095	4.9	12
27	Study of congenital Morgagnian cataracts in Holstein calves. <i>PLoS ONE</i> , 2019 , 14, e0226823	3.7	1
26	Genetic risk factors for osteochondrosis in various horse breeds. <i>Equine Veterinary Journal</i> , 2018 , 50, 556-563	2.4	16
25	An epistatic effect of KRT25 on SP6 is involved in curly coat in horses. <i>Scientific Reports</i> , 2018 , 8, 6374	4.9	9
24	Curly coat caused by a keratin 27 variant was transmitted from Fleckvieh into German Angus. <i>Animal Genetics</i> , 2018 , 49, 349-350	2.5	3

23	Genome data uncover four synergistic key regulators for extremely small body size in horses. <i>BMC Genomics</i> , 2018 , 19, 492	4.5	13
22	Autozygosity islands and ROH patterns in Nellore lineages: evidence of selection for functionally important traits. <i>BMC Genomics</i> , 2018 , 19, 680	4.5	19
21	A recessive lethal chondrodysplasia in a miniature zebu family results from an insertion affecting the chondroitin sulfat domain of aggrecan. <i>BMC Genetics</i> , 2018 , 19, 91	2.6	3
20	Whole-genome sequencing reveals a potential causal mutation for dwarfism in the Miniature Shetland pony. <i>Mammalian Genome</i> , 2017 , 28, 143-151	3.2	15
19	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. <i>BMC Genomics</i> , 2017 , 18, 565	4.5	66
18	Germline mutation within COL2A1 associated with lethal chondrodysplasia in a polled Holstein family. <i>BMC Genomics</i> , 2017 , 18, 762	4.5	8
17	Whole genome sequencing identifies missense mutation in MTBP in Shar-Pei affected with Autoinflammatory Disease (SPAID). <i>BMC Genomics</i> , 2017 , 18, 348	4.5	3
16	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. <i>Current Biology</i> , 2017 , 27, 2029-2035	4.5	45
15	Variant detection and runs of homozygosity in next generation sequencing data elucidate the genetic background of Lundehund syndrome. <i>BMC Genomics</i> , 2016 , 17, 535	4.5	8
14	Genome-wide association study for hereditary ataxia in the Parson Russell Terrier and DNA-testing for ataxia-associated mutations in the Parson and Jack Russell Terrier. <i>BMC Veterinary Research</i> , 2016 , 12, 225	2.7	4
13	Genome-wide association study for semen quality traits in German Warmblood stallions. <i>Animal Reproduction Science</i> , 2016 , 171, 81-6	2.1	16
12	Screening of whole genome sequences identified high-impact variants for stallion fertility. <i>BMC Genomics</i> , 2016 , 17, 288	4.5	15
11	Congenital Ichthyosis in 14 Great Dane Puppies With a New Presentation. <i>Veterinary Pathology</i> , 2016 , 53, 614-20	2.8	5
10	Implication of FKBP6 for male fertility in horses. <i>Reproduction in Domestic Animals</i> , 2015 , 50, 195-199	1.6	8
9	Runs of homozygosity reveal signatures of positive selection for reproduction traits in breed and non-breed horses. <i>BMC Genomics</i> , 2015 , 16, 764	4.5	77
8	Segregation of the hereditary thrombopathia-associated polymorphism in polled German Fleckvieh cattle. <i>Animal Genetics</i> , 2015 , 46, 584-5	2.5	1
7	A Novel SLC27A4 Splice Acceptor Site Mutation in Great Danes with Ichthyosis. <i>PLoS ONE</i> , 2015 , 10, e0141514	3.7	17
6	Next generation sequencing gives an insight into the characteristics of highly selected breeds versus non-breed horses in the course of domestication. <i>BMC Genomics</i> , 2014 , 15, 562	4.5	18

5	A study of Shar-Pei dogs refutes association of the TmeatmouthTduplication near HAS2 with Familial Shar-Pei Fever. <i>Animal Genetics</i> , 2014 , 45, 763-4	2.5	5
4	Analysis of copy number variants by three detection algorithms and their association with body size in horses. <i>BMC Genomics</i> , 2013 , 14, 487	4.5	40
3	A genome-wide association study identifies risk loci to equine recurrent uveitis in German warmblood horses. <i>PLoS ONE</i> , 2013 , 8, e71619	3.7	39
2	Expression levels of LCORL are associated with body size in horses. <i>PLoS ONE</i> , 2013 , 8, e56497	3.7	70
1	Genome-wide linkage and association analysis identifies major gene loci for guttural pouch tympany in Arabian and German warmblood horses. <i>PLoS ONE</i> , 2012 , 7, e41640	3.7	12