Julia Metzger

List of Publications by Year
in descending order

42 papers	1,206 citations	516561 16 h-index	395590 33 g-index
43 all docs	43 docs citations	43 times ranked	1686 citing authors

#	Article	IF	Citations
1	De novo ZIC2 frameshift variant associated with frontonasal dysplasia in a Limousin calf. BMC Genomics, 2021, 22, 1.	1.2	259
2	Runs of homozygosity reveal signatures of positive selection for reproduction traits in breed and non-breed horses. BMC Genomics, 2015, 16, 764.	1.2	125
3	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. BMC Genomics, 2017, 18, 565.	1.2	116
4	Expression Levels of LCORL Are Associated with Body Size in Horses. PLoS ONE, 2013, 8, e56497.	1.1	91
5	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. Current Biology, 2017, 27, 2029-2035.e5.	1.8	75
6	Analysis of copy number variants by three detection algorithms and their association with body size in horses. BMC Genomics, 2013, 14, 487.	1.2	49
7	A Genome-Wide Association Study Identifies Risk Loci to Equine Recurrent Uveitis in German Warmblood Horses. PLoS ONE, 2013, 8, e71619.	1.1	45
8	The horse Y chromosome as an informative marker for tracing sire lines. Scientific Reports, 2019, 9, 6095.	1.6	39
9	Autozygosity islands and ROH patterns in Nellore lineages: evidence of selection for functionally important traits. BMC Genomics, 2018, 19, 680.	1.2	34
10	Genetic risk factors for osteochondrosis in various horse breeds. Equine Veterinary Journal, 2018, 50, 556-563.	0.9	27
11	Genome-wide association study for semen quality traits in German Warmblood stallions. Animal Reproduction Science, 2016, 171, 81-86.	0.5	25
12	Next generation sequencing gives an insight into the characteristics of highly selected breeds versus non-breed horses in the course of domestication. BMC Genomics, 2014, 15, 562.	1.2	24
13	A Novel SLC27A4 Splice Acceptor Site Mutation in Great Danes with Ichthyosis. PLoS ONE, 2015, 10, e0141514.	1.1	23
14	Screening of whole genome sequences identified high-impact variants for stallion fertility. BMC Genomics, 2016, 17, 288.	1.2	21
15	An epistatic effect of KRT25 on SP6 is involved in curly coat in horses. Scientific Reports, 2018, 8, 6374.	1.6	18
16	Genome data uncover four synergistic key regulators for extremely small body size in horses. BMC Genomics, 2018, 19, 492.	1.2	18
17	Whole-genome sequencing reveals a potential causal mutation for dwarfism in the Miniature Shetland pony. Mammalian Genome, 2017, 28, 143-151.	1.0	17
18	Past environmental changes affected lemur population dynamics prior to human impact in Madagascar. Communications Biology, 2021, 4, 1084.	2.0	15

#	Article	IF	Citations
19	Genome-Wide Linkage and Association Analysis Identifies Major Gene Loci for Guttural Pouch Tympany in Arabian and German Warmblood Horses. PLoS ONE, 2012, 7, e41640.	1.1	15
20	Virological and Parasitological Characterization of Mini-LEWE Minipigs Using Improved Screening Methods and an Overview of Data on Various Minipig Breeds. Microorganisms, 2021, 9, 2617.	1.6	13
21	Variant detection and runs of homozygosity in next generation sequencing data elucidate the genetic background of Lundehund syndrome. BMC Genomics, 2016, 17, 535.	1.2	12
22	Implication of <scp>FKBP</scp>6 for Male Fertility in Horses. Reproduction in Domestic Animals, 2015, 50, 195-199.	0.6	11
23	Clinical, cytogenetic and molecular genetic characterization of a tandem fusion translocation in a male Holstein cattle with congenital hypospadias and a ventricular septal defect. PLoS ONE, 2020, 15, e0227117.	1.1	11
24	Loss of Cx43 in Murine Sertoli Cells Leads to Altered Prepubertal Sertoli Cell Maturation and Impairment of the Mitosis-Meiosis Switch. Cells, 2020, 9, 676.	1.8	11
25	Genetics of Equine Orthopedic Disease. Veterinary Clinics of North America Equine Practice, 2020, 36, 289-301.	0.3	11
26	Congenital Ichthyosis in 14 Great Dane Puppies With a New Presentation. Veterinary Pathology, 2016, 53, 614-620.	0.8	10
27	Hanoverian F/Wâ€‰ine contributes to segregation of Warmblood fragile foal syndrome type 1 variant PLOD1:c .2032G>A in Warmblood horses. Equine Veterinary Journal, 2021, 53, 51-59.	0.9	10
28	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. BMC Veterinary Research, 2016, 12, 225.	0.7	9
29	Whole genome sequencing identifies missense mutation in MTBP in Shar-Pei affected with Autoinflammatory Disease (SPAID). BMC Genomics, 2017, 18, 348.	1.2	9
30	Germline mutation within COL2A1 associated with lethal chondrodysplasia in a polled Holstein family. BMC Genomics, 2017, 18, 762.	1.2	9
31	Tracing selection signatures in the pig genome gives evidence for selective pressures on a unique curly hair phenotype in Mangalitza. Scientific Reports, 2020, 10, 22142.	1.6	8
32	A study of Sharâ€Pei dogs refutes association of the â€˜meatmouthâ€™ duplication near <scp>HAS</scp>2 with Familial Sharâ€Pei Fever. Animal Genetics, 2014, 45, 763-764.	0.6	7
33	Impact of model assumptions on demographic inferences: the case study of two sympatric mouse lemurs in northwestern Madagascar. Bmc Ecology and Evolution, 2021, 21, 197.	0.7	7
34	A structural UGDH variant associated with standard Munchkin cats. BMC Genetics, 2020, 21, 67.	2.7	6
35	A recessive lethal chondrodysplasia in a miniature zebu family results from an insertion affecting the chondroitin sulfat domain of aggrecan. BMC Genetics, 2018, 19, 91.	2.7	5
36	Curly coat caused by a keratin 27 variant was transmitted from Fleckvieh into German Angus. Animal Genetics, 2018, 49, 349-350.	0.6	5

#	Article	IF	Citations
37	Demographic assessment of the Dalmatian dog â€“ effective population size, linkage disequilibrium and inbreeding coefficients. Canine Medicine and Genetics, 2020, 7, 3.	1.4	5
38	Study of congenital Morgagnian cataracts in Holstein calves. PLoS ONE, 2019, 14, e0226823.	1.1	4
39	A comparison of strategies for generating artificial replicates in RNA-seq experiments. Scientific Reports, 2022, 12, 7170.	1.6	3
40	Segregation of the hereditary thrombopathiaâ€associated polymorphism in polled German Fleckvieh cattle. Animal Genetics, 2015, 46, 584-585.	0.6	1
41	Genomeâ€wide association analysis for lethal brachycephalicâ€like facial dysmorphia in Labrador Retrievers. Animal Genetics, 2020, 51, 122-126.	0.6	0
42	An FGA Frameshift Variant Associated with Afibrinogenemia in Dachshunds. Genes, 2021, 12, 1065.	1.0	0