Rebecca Bellone

List of Publications by Year
in descending order

77 papers	2,739 citations	236925 25 h-index	197818 49 g-index
85 all docs	85 docs citations	85 times ranked	2919 citing authors

#	Article	IF	Citations
1	A review of investigated risk factors for developing equine recurrent uveitis. Veterinary Ophthalmology, 2023, 26, 86-100.	1.0	2
2	Melanocortinâ€1 receptor influence in equine opioid sensitivity. Equine Veterinary Education, 2023, 35, 152-162.	0.6	2
3	A multimodal approach to management of ocular surface squamous cell carcinoma in horses. Equine Veterinary Education, 2022, 34, 455-458.	0.6	0
4	DNA methylation aging and transcriptomic studies in horses. Nature Communications, 2022, 13, 40.	12.8	34
5	First reported case of fragile foal syndrome type 1 in the Thoroughbred caused by PLOD1 c.2032G>A. Equine Veterinary Journal, 2022, 54, 1086-1093.	1.7	8
6	Prediction of histone post-translational modification patterns based on nascent transcription data. Nature Genetics, 2022, 54, 295-305.	21.4	53
7	Analysis of Genetic Diversity in the American Standardbred Horse Utilizing Short Tandem Repeats and Single Nucleotide Polymorphisms. Journal of Heredity, 2022, 113, 238-247.	2.4	6
8	Prevalence of clinical signs and factors impacting expression of myosin heavy chain myopathy in Quarter Horseâ€related breeds with the <scp>MYH1^{E321G}</scp> mutation. Journal of Veterinary Internal Medicine, 2022, 36, 1152-1159.	1.6	6
9	A genetic investigation of equine recurrent uveitis in the Icelandic horse breed. Animal Genetics, 2022, 53, 436-440.	1.7	2
10	A de novo missense mutation in <scp>KIT</scp> is responsible for dominant white spotting phenotype in a Standardbred horse. Animal Genetics, 2022, 53, 534-537.	1.7	5
11	Another lesson from unmapped reads: in-depth analysis of RNA-Seq reads from various horse tissues. Journal of Applied Genetics, 2022, 63, 571-581.	1.9	2
12	Wholeâ€genome sequencing identifies missense mutation in GRM6 as the likely cause of congenital stationary night blindness in a Tennessee Walking Horse. Equine Veterinary Journal, 2021, 53, 316-323.	1.7	11
13	A novel DDB2 mutation causes defective recognition of UV-induced DNA damages and prevalent equine squamous cell carcinoma. DNA Repair, 2021, 97, 103022.	2.8	7
14	â€œAdopt-a-Tissueâ€•Initiative Advances Efforts to Identify Tissue-Specific Histone Marks in the Mare. Frontiers in Genetics, 2021, 12, 649959.	2.3	8
15	Generation of a Biobank From Two Adult Thoroughbred Stallions for the Functional Annotation of Animal Genomes Initiative. Frontiers in Genetics, 2021, 12, 650305.	2.3	10
16	Mining the 99 Lives Cat Genome Sequencing Consortium database implicates genes and variants for the Ticked locus in domestic cats (FelisÂcatus). Animal Genetics, 2021, 52, 321-332.	1.7	9
17	Brainstem auditory evoked responses and bone conduction assessment in alpacas. Research in Veterinary Science, 2021, 136, 297-302.	1.9	3
18	Successful ATAC-Seq From Snap-Frozen Equine Tissues. Frontiers in Genetics, 2021, 12, 641788.	2.3	8

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19	Standardization of a SNP panel for parentage verification and identification in the domestic cat (Felis Â silvestris Â catus). Animal Genetics, 2021, 52, 675-682.	1.7	5
20	Response to comments on â€˜Wholeâ€genome sequencing identifies missense mutation in GRM6 as the likely cause of congenital stationary night blindness in a Tennessee Walking Horseâ€™. Equine Veterinary Journal, 2021, 53, 1297-1297.	1.7	0
21	Decoding the Equine Genome: Lessons from ENCODE. Genes, 2021, 12, 1707.	2.4	5
22	Identification of W13 in the American Miniature Horse and Shetland Pony Populations. Genes, 2021, 12, 1985.	2.4	3
23	A missense mutation in damageâ€specific DNA binding protein 2 is a genetic risk factor for ocular squamous cell carcinoma in Belgian horses. Equine Veterinary Journal, 2020, 52, 34-40.	1.7	11
24	Horses with equine recurrent uveitis have an activated CD4+ Tâ€cell phenotype that can be modulated by mesenchymal stem cells in vitro. Veterinary Ophthalmology, 2020, 23, 160-170.	1.0	27
25	Warmblood fragile foal syndrome type 1 mutation (PLOD1 c.2032G>A) is not associated with catastrophic breakdown and has a low allele frequency in the Thoroughbred breed. Equine Veterinary Journal, 2020, 52, 411-414.	1.7	14
26	Genetic investigation of equine recurrent uveitis in Appaloosa horses. Animal Genetics, 2020, 51, 111-116.	1.7	19
27	Functionally Annotating Regulatory Elements in the Equine Genome Using Histone Mark ChIP-Seq. Genes, 2020, 11, 3.	2.4	34
28	Evidence supports white spotting in donkeys as a homozygous lethal condition. Animal Genetics, 2020, 51, 840-842.	1.7	0
29	Whole genome sequencing identified a 16 kilobase deletion on ECA13 associated with distichiasis in Friesian horses. BMC Genomics, 2020, 21, 848.	2.8	6
30	Comparison of Poly-A+ Selection and rRNA Depletion in Detection of lncRNA in Two Equine Tissues Using RNA-seq. Non-coding RNA, 2020, 6, 32.	2.6	6
31	DDB2 Genetic Risk Factor for Ocular Squamous Cell Carcinoma Identified in Three Additional Horse Breeds. Genes, 2020, 11, 1460.	2.4	4
32	Distribution of the Warmblood Fragile Foal Syndrome Type 1 Mutation (PLOD1 c.2032G>A) in Different Horse Breeds from Europe and the United States. Genes, 2020, 11, 1518.	2.4	12
33	Novel Complex Unbalanced Dicentric X-Autosome Rearrangement in a Thoroughbred Mare with a Mild Effect on the Phenotype. Cytogenetic and Genome Research, 2020, 160, 597-609.	1.1	3
34	Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. American Journal of Human Genetics, 2020, 106, 893-904.	6.2	29
35	Genetics of Equine Ocular Disease. Veterinary Clinics of North America Equine Practice, 2020, 36, 303-322.	0.7	4
36	Genetic Testing in the Horse. Veterinary Clinics of North America Equine Practice, 2020, 36, 211-234.	0.7	6

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37	Risk factors for equine recurrent uveitis in a population of Appaloosa horses in western Canada. Veterinary Ophthalmology, 2020, 23, 515-525.	1.0	19
38	A De Novo MITF Deletion Explains a Novel Splashed White Phenotype in an American Paint Horse. Journal of Heredity, 2020, 111, 287-293.	2.4	15
39	Ten years of the horse reference genome: insights into equine biology, domestication and population dynamics in the postâ€genome era. Animal Genetics, 2019, 50, 569-597.	1.7	43
40	Additional Evidence for DDB2 T338M as a Genetic Risk Factor for Ocular Squamous Cell Carcinoma in Horses. International Journal of Genomics, 2019, 2019, 1-10.	1.6	7
41	Frameshift Variant in MFSD12 Explains the Mushroom Coat Color Dilution in Shetland Ponies. Genes, 2019, 10, 826.	2.4	14
42	Effects of high fat diet-induced obesity on mammary tumorigenesis in the PyMT/MMTV murine model. Cancer Biology and Therapy, 2019, 20, 487-496.	3.4	24
43	Limbal squamous cell carcinoma in a Rocky Mountain Horse: Case report and investigation of genetic contribution. Veterinary Ophthalmology, 2019, 22, 201-205.	1.0	10
44	Improved reference genome for the domestic horse increases assembly contiguity and composition. Communications Biology, 2018, 1, 197.	4.4	148
45	Ruling out <scp>BGN</scp> variants as simple Xâ€linked causative mutations for bilateral corneal stromal loss in Friesian horses. Animal Genetics, 2018, 49, 656-657.	1.7	6
46	Generation of an equine biobank to be used for Functional Annotation of Animal Genomes project. Animal Genetics, 2018, 49, 564-570.	1.7	33
47	Genetic risk for squamous cell carcinoma of the nictitating membrane parallels that of the limbus in Haflinger horses. Animal Genetics, 2018, 49, 457-460.	1.7	17
48	A missense mutation in damageâ€specific DNA binding protein 2 is a genetic risk factor for limbal squamous cell carcinoma in horses. International Journal of Cancer, 2017, 141, 342-353.	5.1	39
49	Genetic Testing as a Tool to Identify Horses with or at Risk for Ocular Disorders. Veterinary Clinics of North America Equine Practice, 2017, 33, 627-645.	0.7	4
50	Tissue resolved, gene structure refined equine transcriptome. BMC Genomics, 2017, 18, 103.	2.8	22
51	Two Variants in SLC24A5 Are Associated with â€œTiger-Eyeâ€•Iris Pigmentation in Puerto Rican Paso Fino Horses. G3: Genes, Genomes, Genetics, 2017, 7, 2799-2806.	1.8	17
52	Identification of long non-coding RNA in the horse transcriptome. BMC Genomics, 2017, 18, 511.	2.8	30
53	Variant in the <scp>RFWD</scp>3 gene associated with <scp>PATN</scp>1, a modifier of leopard complex spotting. Animal Genetics, 2016, 47, 91-101.	1.7	31
54	<scp>GO</scp>â€<scp>FAANG</scp> meeting: a Gathering On Functional Annotation of <scp>An</scp>imal Genomes. Animal Genetics, 2016, 47, 528-533.	1.7	65

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55	Redundant contribution of a Transient Receptor Potential cation channel Member 1 exon 11 single nucleotide polymorphism to equine congenital stationary night blindness. BMC Veterinary Research, 2016, 12, 121.	1.9	4
56	Morphological Variation in Gaited Horse Breeds. Journal of Equine Veterinary Science, 2016, 43, 55-65.	0.9	11
57	Limbal squamous cell carcinoma in <scp>H</scp>aflinger horses. Veterinary Ophthalmology, 2015, 18, 404-408.	1.0	31
58	Twenty-five thousand years of fluctuating selection on leopard complex spotting and congenital night blindness in horses. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130386.	4.0	43
59	Worldwide frequency distribution of the â€˜<scp>G</scp>ait keeperâ€™ mutation in the <scp>DMRT</scp>3 gene. Animal Genetics, 2014, 45, 274-282.	1.7	74
60	Genetic risk factors for insidious equine recurrent uveitis in <scp>A</scp>ppaloosa horses. Animal Genetics, 2014, 45, 392-399.	1.7	60
61	Novel variants in the <scp>KIT</scp> and <scp>PAX</scp>3 genes in horses with whiteâ€spotted coat colour phenotypes. Animal Genetics, 2013, 44, 763-765.	1.7	68
62	Accumulating Mutations in Series of Haplotypes at the KIT and MITF Loci Are Major Determinants of White Markings in Franches-Montagnes Horses. PLoS ONE, 2013, 8, e75071.	2.5	34
63	Evidence for a Retroviral Insertion in TRPM1 as the Cause of Congenital Stationary Night Blindness and Leopard Complex Spotting in the Horse. PLoS ONE, 2013, 8, e78280.	2.5	115
64	Reply to Bar-Oz and Lev-Yadun: Horse colors in time and space. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1213-E1213.	7.1	1
65	Congenital stationary night blindness is associated with the leopard complex in the miniature horse. Veterinary Ophthalmology, 2012, 15, 18-22.	1.0	34
66	Four Loci Explain 83% of Size Variation in the Horse. PLoS ONE, 2012, 7, e39929.	2.5	170
67	Genotypes of predomestic horses match phenotypes painted in Paleolithic works of cave art. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18626-18630.	7.1	85
68	Pleiotropic effects of pigmentation genes in horses. Animal Genetics, 2010, 41, 100-110.	1.7	61
69	Association analysis of candidate SNPs in TRPM1 with leopard complex spotting (LPâ€Š) and congenital stationary night blindness (CSNB) in horses. Animal Genetics, 2010, 41, 207-207.	1.7	12
70	Fine-mapping and mutation analysis of TRPM1: a candidate gene for leopard complex (LP) spotting and congenital stationary night blindness in horses. Briefings in Functional Genomics, 2010, 9, 193-207.	2.7	49
71	Causation for inherited equine night blindness. FASEB Journal, 2010, 24, 675.1.	0.5	0
72	Genome Sequence, Comparative Analysis, and Population Genetics of the Domestic Horse. Science, 2009, 326, 865-867.	12.6	680

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73	Missense Mutation in Exon 2 of SLC36A1 Responsible for Champagne Dilution in Horses. PLoS Genetics, 2008, 4, e1000195.	3.5	52
74	Differential Gene Expression of TRPM1, the Potential Cause of Congenital Stationary Night Blindness and Coat Spotting Patterns (LP) in the Appaloosa Horse (Equus caballus). Genetics, 2008, 179, 1861-1870.	2.9	146
75	Congenital ocular anomalies in purebred and crossbred Rocky and Kentucky Mountain horses in Canada. Canadian Veterinary Journal, 2008, 49, 675-81.	0.0	40
76	Analysis of a SNP in exon 7 of equine OCA2 and its exclusion as a cause for appaloosa spotting. Animal Genetics, 2006, 37, 525-525.	1.7	5
77	Comparative mapping of oculocutaneous albinism type II (OCA2), transient receptor potential cation channel, subfamily M member 1 (TRPM1) and two equine microsatellites, ASB08 and 1CA43, among four equid species by fluorescence in situ hybridization. Cytogenetic and Genome Research, 2006, 114, 93A-93A.	1.1	13