Tosso Leeb

List of Publications by Year
in descending order

401	10,011	47006 47	62596 80
papers	citations	h-index	g-index

432	432	432	8834
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	ABHD5 frameshift deletion in Golden Retrievers with ichthyosis. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	7
2	Genetics of inherited skin disorders in dogs. Veterinary Journal, 2022, 279, 105782.	1.7	4
3	Runs of homozygosity in Swiss goats reveal genetic changes associated with domestication and modern selection. Genetics Selection Evolution, 2022, 54, 6.	3.0	14
4	The Effects of FGF4 Retrogenes on Canine Morphology. Genes, 2022, 13, 325.	2.4	7
5	FYCO1 Frameshift Deletion in Wirehaired Pointing Griffon Dogs with Juvenile Cataract. Genes, 2022, 13, 334.	2.4	4
6	Independent DSG4 frameshift variants in cats with hair shaft dystrophy. Molecular Genetics and Genomics, 2022, 297, 147-154.	2.1	0
7	Independent COL5A1 Variants in Cats with Ehlers-Danlos Syndrome. Genes, 2022, 13, 797.	2.4	4
8	A COL5A2 In-Frame Deletion in a Chihuahua with Ehlers-Danlos Syndrome. Genes, 2022, 13, 934.	2.4	5
9	Canine reference genome accuracy impacts variant calling: Lessons learned from investigating embryonic lethal variants. Animal Genetics, 2022, 53, 706-708.	1.7	1
10	SLC25A12 Missense Variant in Nova Scotia Duck Tolling Retrievers Affected by Cerebellar Degenerationâ€"Myositis Complex (CDMC). Genes, 2022, 13, 1223.	2.4	2
11	Transcriptional Differences between Canine Cutaneous Epitheliotropic Lymphoma and Immune-Mediated Dermatoses. Genes, 2021, 12, 160.	2.4	2
12	COL6A1 related muscular dystrophy in Landseer dogs: A canine model for Ullrich congenital muscular dystrophy. Muscle and Nerve, 2021, 63, 608-616.	2.2	4
13	SUV39H2 epigenetic silencing controls fate conversion of epidermal stem and progenitor cells. Journal of Cell Biology, 2021, 220, .	5.2	6
14	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
15	X-Linked Hypohidrotic Ectodermal Dysplasia in Crossbred Beef Cattle Due to a Large Deletion in EDA. Animals, 2021, 11, 657.	2.3	6
16	A hypomyelinating leukodystrophy in German Shepherd dogs. Journal of Veterinary Internal Medicine, 2021, 35, 1455-1465.	1.6	4
17	Variants at the ASIP locus contribute to coat color darkening in Nellore cattle. Genetics Selection Evolution, 2021, 53, 40.	3.0	25
18	Dog10K_Boxer_Tasha_1.0: A Long-Read Assembly of the Dog Reference Genome. Genes, 2021, 12, 847.	2.4	19

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19	L2HGDH Missense Variant in a Cat with L-2-Hydroxyglutaric Aciduria. Genes, 2021, 12, 682.	2.4	1
20	Introgression of ASIP and TYRP1 Alleles Explains Coat Color Variation in Valais Goats. Journal of Heredity, 2021, 112, 452-457.	2.4	7
21	Improving the resolution of canine genomeâ€wide association studies using genotype imputation: A study of two breeds. Animal Genetics, 2021, 52, 703-713.	1.7	5
22	Effects of Cocoa Genotypes on Coat Color, Platelets and Coagulation Parameters in French Bulldogs. Genes, 2021, 12, 1092.	2.4	1
23	Deletion of the SELENOP gene leads to CNS atrophy with cerebellar ataxia in dogs. PLoS Genetics, 2021, 17, e1009716.	3.5	12
24	A Missense Variant in SLC39A4 in a Litter of Turkish Van Cats with Acrodermatitis Enteropathica. Genes, 2021, 12, 1309.	2.4	1
25	Dog colour patterns explained by modular promoters of ancient canid origin. Nature Ecology and Evolution, 2021, 5, 1415-1423.	7.8	24
26	Variants Affecting the C-Terminal Tail of UNC93B1 Are Not a Common Risk Factor for Systemic Lupus Erythematosus. Genes, 2021, 12, 1268.	2.4	0
27	PRKG2 Splice Site Variant in Dogo Argentino Dogs with Disproportionate Dwarfism. Genes, 2021, 12, 1489.	2.4	6
28	MYO5A Frameshift Variant in a Miniature Dachshund with Coat Color Dilution and Neurological Defects Resembling Human Griscelli Syndrome Type 1. Genes, 2021, 12, 1479.	2.4	8
29	MIA3 Splice Defect in Cane Corso Dogs with Dental-Skeletal-Retinal Anomaly (DSRA). Genes, 2021, 12, 1497.	2.4	5
30	Domestic animal genetics. PLoS Genetics, 2021, 17, e1009831.	3.5	0
31	Polyadenine insertion disrupting the G6PC1 gene in German Pinschers with glycogen storage disease type Ia (GSD1A). Animal Genetics, 2021, 52, 900-902.	1.7	0
32	LTBP3 Frameshift Variant in British Shorthair Cats with Complex Skeletal Dysplasia. Genes, 2021, 12, 1923.	2.4	1
33	LAMA2 Nonsense Variant in an Italian Greyhound with Congenital Muscular Dystrophy. Genes, 2021, 12, 1823.	2.4	2
34	Diagnostic and prognostic potential of eight whole blood microRNAs for equine sarcoid disease. PLoS ONE, 2021, 16, e0261076.	2.5	3
35	A deletion spanning the promoter and first exon of the hair cycleâ€specific ASIP transcript isoform in black and tan rabbits. Animal Genetics, 2020, 51, 137-140.	1.7	14
36	Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. Animal Genetics, 2020, 51, 78-86.	1.7	3

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37	A major facilitator superfamily domain 8 frameshift variant in a cat with suspected neuronal ceroid lipofuscinosis. Journal of Veterinary Internal Medicine, 2020, 34, 289-293.	1.6	3
38	Altered Basal Autophagy Affects Extracellular Vesicle Release in Cells of Lagotto Romagnolo Dogs With a Variant ATG4D. Veterinary Pathology, 2020, 57, 926-935.	1.7	2
39	An Integrative miRNA-mRNA Expression Analysis Reveals Striking Transcriptomic Similarities between Severe Equine Asthma and Specific Asthma Endotypes in Humans. Genes, 2020, 11, 1143.	2.4	11
40	A nonsense variant in the KRT14 gene in a domestic shorthair cat with epidermolysis bullosa simplex. Animal Genetics, 2020, 51, 829-832.	1.7	2
41	Mitochondrial PCK2 Missense Variant in Shetland Sheepdogs with Paroxysmal Exercise-Induced Dyskinesia (PED). Genes, 2020, 11, 774.	2.4	14
42	Transcriptome Profiling and Differential Gene Expression in Canine Microdissected Anagen and Telogen Hair Follicles and Interfollicular Epidermis. Genes, 2020, 11, 884.	2.4	8
43	Multiple FGF4 Retrocopies Recently Derived within Canids. Genes, 2020, 11, 839.	2.4	12
44	LAMB3 Missense Variant in Australian Shepherd Dogs with Junctional Epidermolysis Bullosa. Genes, 2020, 11, 1055.	2.4	8
45	CCDC66 frameshift variant associated with a new form of early-onset progressive retinal atrophy in Portuguese Water Dogs. Scientific Reports, 2020, 10, 21162.	3.3	7
46	A COL7A1 Variant in a Litter of Neonatal Basset Hounds with Dystrophic Epidermolysis Bullosa. Genes, 2020, 11, 1458.	2.4	6
47	NSDHL Frameshift Deletion in a Mixed Breed Dog with Progressive Epidermal Nevi. Genes, 2020, 11, 1297.	2.4	4
48	ATP2A2 SINE Insertion in an Irish Terrier with Darier Disease and Associated Infundibular Cyst Formation. Genes, 2020, 11, 481.	2.4	5
49	Genetic Variants Affecting Skeletal Morphology in Domestic Dogs. Trends in Genetics, 2020, 36, 598-609.	6.7	15
50	Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. American Journal of Human Genetics, 2020, 106, 893-904.	6.2	29
51	Novel Brown Coat Color (Cocoa) in French Bulldogs Results from a Nonsense Variant in HPS3. Genes, 2020, 11, 636.	2.4	6
52	YARS2 Missense Variant in Belgian Shepherd Dogs with Cardiomyopathy and Juvenile Mortality. Genes, 2020, 11, 313.	2.4	4
53	Abnormal keratinocyte differentiation in the nasal planum of Labrador Retrievers with hereditary nasal parakeratosis (HNPK). PLoS ONE, 2020, 15, e0225901.	2.5	7
54	A Genome-Wide Association Analysis in Noriker Horses Identifies a SNP Associated With Roan Coat Color. Journal of Equine Veterinary Science, 2020, 88, 102950.	0.9	8

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55	Whole Genome Sequencing Indicates Heterogeneity of Hyperostotic Disorders in Dogs. Genes, 2020, 11, 163.	2.4	4
56	The LCORL Locus Is under Selection in Large-Sized Pakistani Goat Breeds. Genes, 2020, 11, 168.	2.4	25
57	A Missense Variant Affecting the C-Terminal Tail of UNC93B1 in Dogs with Exfoliative Cutaneous Lupus Erythematosus (ECLE). Genes, 2020, 11, 159.	2.4	13
58	Investigating the epithelial barrier and immune signatures in the pathogenesis of equine insect bite hypersensitivity. PLoS ONE, 2020, 15, e0232189.	2.5	10
59	A DSG1 Frameshift Variant in a Rottweiler Dog with Footpad Hyperkeratosis. Genes, 2020, 11, 469.	2.4	5
60	Compound heterozygosity for <scp>TNXB</scp> genetic variants in a mixedâ€breed dog with Ehlersâ€Danlos syndrome. Animal Genetics, 2019, 50, 546-549.	1.7	11
61	A complex structural variant at the <scp>KIT</scp> locus in cattle with the Pinzgauer spotting pattern. Animal Genetics, 2019, 50, 423-429.	1.7	12
62	AKNA Frameshift Variant in Three Dogs with Recurrent Inflammatory Pulmonary Disease. Genes, 2019, 10, 567.	2.4	5
63	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. PLoS Genetics, 2019, 15, e1008411.	3.5	9
64	A novel KIT deletion variant in a German Riding Pony with whiteâ€spotting coat colour phenotype. Animal Genetics, 2019, 50, 761-763.	1.7	11
65	An <scp>ABCA</scp>12 missense variant in a Shorthorn calf with ichthyosis fetalis. Animal Genetics, 2019, 50, 749-752.	1.7	7
66	Frameshift Variant in MFSD12 Explains the Mushroom Coat Color Dilution in Shetland Ponies. Genes, 2019, 10, 826.	2.4	14
67	A missense variant in the NSDHL gene in a Chihuahua with a congenital cornification disorder resembling inflammatory linear verrucous epidermal nevi. Animal Genetics, 2019, 50, 768-771.	1.7	8
68	A RAPGEF6 variant constitutes a major risk factor for laryngeal paralysis in dogs. PLoS Genetics, 2019, 15, e1008416.	3.5	5
69	A comprehensive biomedical variant catalogue based on whole genome sequences of 582 dogs and eight wolves. Animal Genetics, 2019, 50, 695-704.	1.7	138
70	NME5 frameshift variant in Alaskan Malamutes with primary ciliary dyskinesia. PLoS Genetics, 2019, 15, e1008378.	3.5	21
71	Identification of Two Independent COL5A1 Variants in Dogs with Ehlersâ€“Danlos Syndrome. Genes, 2019, 10, 731.	2.4	13
72	Genome-wide association study and whole-genome sequencing identify a deletion in LRIT3 associated with canine congenital stationary night blindness. Scientific Reports, 2019, 9, 14166.	3.3	15

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73	Differences in miRNA differential expression in whole blood between horses with sarcoid regression and progression. Journal of Veterinary Internal Medicine, 2019, 33, 241-250.	1.6	10
74	Whole Genome Sequencing of Giant Schnauzer Dogs with Progressive Retinal Atrophy Establishes NECAP1 as a Novel Candidate Gene for Retinal Degeneration. Genes, 2019, 10, 385.	2.4	6
75	Identification of a Missense Variant in MFSD12 Involved in Dilution of Phaeomelanin Leading to White or Cream Coat Color in Dogs. Genes, 2019, 10, 386.	2.4	20
76	A SIX6 Nonsense Variant in Golden Retrievers with Congenital Eye Malformations. Genes, 2019, 10, 454.	2.4	6
77	Phenotypic Effects of FGF4 Retrogenes on Intervertebral Disc Disease in Dogs. Genes, 2019, 10, 435.	2.4	33
78	In silico and in vitro analysis of genetic variants of the equine CYP3A94, CYP3A95 and CYP3A97 isoenzymes. Toxicology in Vitro, 2019, 60, 116-124.	2.4	5
79	Xâ€linked cutaneous mosaicism in a dog. Veterinary Dermatology, 2019, 30, 361-362.	1.2	0
80	An ADAMTS3 missense variant is associated with Norwich Terrier upper airway syndrome. PLoS Genetics, 2019, 15, e1008102.	3.5	14
81	Genome-Wide Association Studies Based on Equine Joint Angle Measurements Reveal New QTL Affecting the Conformation of Horses. Genes, 2019, 10, 370.	2.4	15
82	The horse Y chromosome as an informative marker for tracing sire lines. Scientific Reports, 2019, 9, 6095.	3.3	39
83	Naegeliâ€“Franceschettiâ€“Jadassohn syndrome and dermatopathia pigmentosa reticularis: intrafamilial overlap of phenotypes in patients with the same <scp>KRT</scp> 14 frameshift variant. British Journal of Dermatology, 2019, 181, 864-866.	1.5	3
84	Christmas disease in a Hovawart family resembling human hemophilia B Leyden is caused by a single nucleotide deletion in a highly conserved transcription factor binding site of the F9 gene promoter. Haematologica, 2019, 104, 2307-2313.	3.5	6
85	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. National Science Review, 2019, 6, 810-824.	9.5	65
86	ATP13A2 missense variant in Australian Cattle Dogs with late onset neuronal ceroid lipofuscinosis. Molecular Genetics and Metabolism, 2019, 127, 95-106.	1.1	17
87	Bald thigh syndrome in sighthoundsâ€”Revisiting the cause of a well-known disease. PLoS ONE, 2019, 14, e0212645.	2.5	5
88	Selection signatures in goats reveal copy number variants underlying breed-defining coat color phenotypes. PLoS Genetics, 2019, 15, e1008536.	3.5	50
89	A TAC3 Missense Variant in a Domestic Shorthair Cat with Testicular Hypoplasia and Persistent Primary Dentition. Genes, 2019, 10, 806.	2.4	4
90	Comprehensive characterization of horse genome variation by wholeâ€genome sequencing of 88 horses. Animal Genetics, 2019, 50, 74-77.	1.7	33

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91	MicroRNA fingerprints in serum and whole blood of sarcoidâ€affected horses as potential nonâ€invasive diagnostic biomarkers. Veterinary and Comparative Oncology, 2019, 17, 107-117.	1.8	11
92	A second <scp>KRT</scp>71 allele in curly coated dogs. Animal Genetics, 2019, 50, 97-100.	1.7	9
93	Wholeâ€genome sequencing reveals a large deletion in the <scp>MITF</scp> gene in horses with white spotted coat colour and increased risk of deafness. Animal Genetics, 2019, 50, 172-174.	1.7	24
94	Complex Structural PPT1 Variant Associated with Non-syndromic Canine Retinal Degeneration. G3: Genes, Genomes, Genetics, 2019, 9, 425-437.	1.8	13
95	Concern Regarding the Publication by Posbergh etÂal. â€œA Nonsynonymous Change in Adhesion G Proteinâ€“Coupled Receptor L3 Associated With Risk for Equine Degenerative Myeloencephalopathy in the Caspian Horse,â€J Equine Vet Sci 2018;70:96â€“100. Journal of Equine Veterinary Science, 2019, 72, 124.	0.9	1
96	<scp>NHLRC</scp>1 dodecamer repeat expansion demonstrated by whole genome sequencing in a Chihuahua with Lafora disease. Animal Genetics, 2019, 50, 118-119.	1.7	11
97	Genetic variant in the NSDHL gene in a cat with multiple congenital lesions resembling inflammatory linear verrucous epidermal nevi. Veterinary Dermatology, 2019, 30, 64-e18.	1.2	6
98	A nonâ€coding regulatory variant in the 5â€²â€region of the MITF gene is associated with whiteâ€spotted coat in Brown Swiss cattle. Animal Genetics, 2019, 50, 27-32.	1.7	17
99	Title is missing!. , 2019, 15, e1008536.		0
100	Title is missing!. , 2019, 15, e1008536.		0
101	Title is missing!. , 2019, 15, e1008536.		0
102	Title is missing!. , 2019, 15, e1008536.		0
103	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
104	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
105	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
106	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
107	A Nonsense Variant in the ACADVL Gene in German Hunting Terriers with Exercise Induced Metabolic Myopathy. G3: Genes, Genomes, Genetics, 2018, 8, 1545-1554.	1.8	9
108	Exclusion of adrenoceptor alpha 2 variants in a horse insensitive to medetomidine. Animal Genetics, 2018, 49, 141-141.	1.7	1

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109	Asian horses deepen the MSY phylogeny. Animal Genetics, 2018, 49, 90-93.	1.7	32
110	A splice site variant in the <scp>SUV</scp>39H2 gene in Greyhounds with nasal parakeratosis. Animal Genetics, 2018, 49, 137-140.	1.7	7
111	A novel <scp>MLPH</scp> variant in dogs with coat colour dilution. Animal Genetics, 2018, 49, 94-97.	1.7	31
112	Systemic Scedosporium prolificans infection in an 11â€monthâ€old Border collie with cobalamin deficiency secondary to selective cobalamin malabsorption (canine Imerslundâ€GrÃsbeck syndrome). Journal of Small Animal Practice, 2018, 59, 253-256.	1.2	10
113	A frameshift variant in the <scp>EDA</scp> gene in Dachshunds with Xâ€linked hypohidrotic ectodermal dysplasia. Animal Genetics, 2018, 49, 651-654.	1.7	13
114	Genomeâ€wide association study and heritability estimate for ectopic ureters in Entlebucher mountain dogs. Animal Genetics, 2018, 49, 645-650.	1.7	5
115	A frameshift variant in the <scp>COL</scp>5A1 gene in a cat with Ehlersâ€Danlos syndrome. Animal Genetics, 2018, 49, 641-644.	1.7	13
116	eQTL discovery and their association with severe equine asthma in European Warmblood horses. BMC Genomics, 2018, 19, 581.	2.8	13
117	Generation of an equine biobank to be used for Functional Annotation of Animal Genomes project. Animal Genetics, 2018, 49, 564-570.	1.7	33
118	Two <scp>MC</scp>1R lossâ€ofâ€function alleles in creamâ€coloured Australian Cattle Dogs and white Huskies. Animal Genetics, 2018, 49, 284-290.	1.7	24
119	MKLN1 splicing defect in dogs with lethal acrodermatitis. PLoS Genetics, 2018, 14, e1007264.	3.5	26
120	FEELnc: a tool for long non-coding RNA annotation and its application to the dog transcriptome. Nucleic Acids Research, 2017, 45, gkw1306.	14.5	281
121	Generalized myoclonic epilepsy with photosensitivity in juvenile dogs caused by a defective DIRAS family GTPase 1. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2669-2674.	7.1	39
122	A Nonsense Variant in the ST14 Gene in Akhal-Teke Horses with Naked Foal Syndrome. G3: Genes, Genomes, Genetics, 2017, 7, 1315-1321.	1.8	12
123	Whole genome sequencing reveals a novel deletion variant in the <scp>KIT</scp> gene in horses with white spotted coat colour phenotypes. Animal Genetics, 2017, 48, 483-485.	1.7	36
124	Ancient genomic changes associated with domestication of the horse. Science, 2017, 356, 442-445.	12.6	185
125	A SINE Insertion inATP1B2in Belgian Shepherd Dogs Affected by Spongy Degeneration with Cerebellar Ataxia (SDCA2). G3: Genes, Genomes, Genetics, 2017, 7, 2729-2737.	1.8	18
126	Frameâ€shift variant in the <scp>CHRNE</scp> gene in a juvenile dog with suspected myasthenia gravisâ€like disease. Animal Genetics, 2017, 48, 625-625.	1.7	5

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127	Basal Autophagy Is Altered in Lagotto Romagnolo Dogs with an ATG4D Mutation. Veterinary Pathology, 2017, 54, 953-963.	1.7	16
128	Canine Brachycephaly Is Associated with a Retrotransposon-Mediated Missplicing of SMOC2. Current Biology, 2017, 27, 1573-1584.e6.	3.9	80
129	Precision Medicine in Cats: Novel Niemannâ€Pick Type C1 Diagnosed by Wholeâ€Genome Sequencing. Journal of Veterinary Internal Medicine, 2017, 31, 539-544.	1.6	30
130	A Missense Variant inKCNJ10in Belgian Shepherd Dogs Affected by Spongy Degeneration with Cerebellar Ataxia (SDCA1). G3: Genes, Genomes, Genetics, 2017, 7, 663-669.	1.8	22
131	A genomeâ€wide association study for equine recurrent airway obstruction in European Warmblood horses reveals a suggestive new quantitative trait locus on chromosome 13. Animal Genetics, 2017, 48, 691-693.	1.7	14
132	A Large Deletion in the NSDHL Gene in Labrador Retrievers with a Congenital Cornification Disorder. G3: Genes, Genomes, Genetics, 2017, 7, 3115-3121.	1.8	15
133	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. Current Biology, 2017, 27, 2029-2035.e5.	3.9	75
134	A novelMITFvariant in a white American Standardbred foal. Animal Genetics, 2017, 48, 123-124.	1.7	8
135	Genetic testing in veterinary dermatology. Veterinary Dermatology, 2017, 28, 4.	1.2	12
136	A GJA9 frameshift variant is associated with polyneuropathy in Leonberger dogs. BMC Genomics, 2017, 18, 662.	2.8	20
137	LPS-induced modules of co-expressed genes in equine peripheral blood mononuclear cells. BMC Genomics, 2017, 18, 34.	2.8	12
138	A curated catalog of canine and equine keratin genes. PLoS ONE, 2017, 12, e0180359.	2.5	19
139	OCA2 splice site variant in German Spitz dogs with oculocutaneous albinism. PLoS ONE, 2017, 12, e0185944.	2.5	12
140	A de novo variant in the ASPRV1 gene in a dog with ichthyosis. PLoS Genetics, 2017, 13, e1006651.	3.5	34
141	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. BMC Genomics, 2017, 18, 565.	2.8	116
142	A single base deletion in the <scp>SLC</scp>45A2 gene in a Bullmastiff with oculocutaneous albinism. Animal Genetics, 2017, 48, 619-621.	1.7	14
143	Identification of key contributors in complex population structures. PLoS ONE, 2017, 12, e0177638.	2.5	13
144	A structural variant in the 5â€™-flanking region of the TWIST2 gene affects melanocyte development in belted cattle. PLoS ONE, 2017, 12, e0180170.	2.5	12

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145	Novel insights into the pathways regulating the canine hair cycle and their deregulation in alopecia X. PLoS ONE, 2017, 12, e0186469.	2.5	22
146	An Intronic MBTPS2 Variant Results in a Splicing Defect in Horses with Brindle Coat Texture. G3: Genes, Genomes, Genetics, 2016, 6, 2963-2970.	1.8	8
147	Neuronale Zeroidlipofuszinose bei einem adulten American Staffordshire Terrier. Tierarztliche Praxis Ausgabe K: Kleintiere - Heimtiere, 2016, 44, 431-437.	0.5	3
148	Genomeâ€wide association studies based on sequenceâ€derived genotypes reveal new QTL associated with conformation and performance traits in the Franchesâ€“Montagnes horse breed. Animal Genetics, 2016, 47, 227-229.	1.7	7
149	Initial characterization of stiff skinâ€like syndrome in West Highland white terriers. Veterinary Dermatology, 2016, 27, 210.	1.2	2
150	<scp>MFSD</scp>8 singleâ€base pair deletion in a Chihuahua with neuronal ceroid lipofuscinosis. Animal Genetics, 2016, 47, 631-631.	1.7	6
151	Multiple regulatory variants located in cell type-specific enhancers within the PKP2 locus form major risk and protective haplotypes for canine atopic dermatitis in German shepherd dogs. BMC Genetics, 2016, 17, 97.	2.7	8
152	A Splice Defect in the EDA Gene in Dogs with an X-Linked Hypohidrotic Ectodermal Dysplasia (XLHED) Phenotype. G3: Genes, Genomes, Genetics, 2016, 6, 2949-2954.	1.8	18
153	A RAB3GAP1 SINE Insertion in Alaskan Huskies with Polyneuropathy, Ocular Abnormalities, and Neuronal Vacuolation (POANV) Resembling Human Warburg Micro Syndrome 1 (WARBM1). G3: Genes, Genomes, Genetics, 2016, 6, 255-262.	1.8	26
154	Genetic variability of the equine casein genes. Journal of Dairy Science, 2016, 99, 5486-5497.	3.4	8
155	Genomic amplification of the caprine EDNRA locus might lead to a dose dependent loss of pigmentation. Scientific Reports, 2016, 6, 28438.	3.3	41
156	Selection signatures in Shetland ponies. Animal Genetics, 2016, 47, 370-372.	1.7	38
157	DNA-based analysis of protein variants reveals different genetic variability of the paralogous equine ÃŸ-lactoglobulin genes LGB1 and LGB2. Livestock Science, 2016, 187, 181-185.	1.6	4
158	Whole-Genome Sequencing of a Canine Family Trio Reveals a FAM83G Variant Associated with Hereditary Footpad Hyperkeratosis. G3: Genes, Genomes, Genetics, 2016, 6, 521-527.	1.8	19
159	Syringomyelia in a Newborn Male Simmental Calf. Journal of Veterinary Internal Medicine, 2015, 29, 1633-1637.	1.6	6
160	A breeding experiment confirms the dominant mode of inheritance of the brown coat colour associated with the ⁴⁹⁶Asp <scp>TYRP</scp>1 allele in goats. Animal Genetics, 2015, 46, 587-588.	1.7	5
161	Optimized methods for extracting circulating small RNAs from long-term stored equine samples. Acta Veterinaria Scandinavica, 2015, 58, 44.	1.6	11
162	A Nonsense Variant in COL6A1 in Landseer Dogs with Muscular Dystrophy. G3: Genes, Genomes, Genetics, 2015, 5, 2611-2617.	1.8	16

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163	Whole genome sequencing confirms <scp>KIT</scp> insertions in a white cat. Animal Genetics, 2015, 46, 98-98.	1.7	9
164	A novelKITvariant in an Icelandic horse with white-spotted coat colour. Animal Genetics, 2015, 46, 466-466.	1.7	37
165	Congenital aural atresia associated with agenesis of internal carotid artery in a girl with a FOXI3 deletion. American Journal of Medical Genetics, Part A, 2015, 167, 537-544.	1.2	27
166	A Deletion in the VLDLR Gene in Eurasier Dogs with Cerebellar Hypoplasia Resembling a Dandy-Walker-Like Malformation (DWLM). PLoS ONE, 2015, 10, e0108917.	2.5	29
167	The Transcriptome of Equine Peripheral Blood Mononuclear Cells. PLoS ONE, 2015, 10, e0122011.	2.5	17
168	Impaired Cell Cycle Regulation in a Natural Equine Model of Asthma. PLoS ONE, 2015, 10, e0136103.	2.5	24
169	Polycystic Kidneys and GM₂ Gangliosidosis-Like Disease in Neonatal Springboks (Antidorcas marsupialis). Veterinary Pathology, 2015, 52, 543-552.	1.7	6
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