Vidhya Jagannathan

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6297904/publications.pdf

Version: 2024-02-01

184 papers	4,067 citations	172457 29 h-index	175258 52 g-index
191 all docs	191 docs citations	191 times ranked	5042 citing authors

#	Article	IF	Citations
1	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics, 2018, 50, 362-367.	21.4	286
2	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
3	Ancient genomic changes associated with domestication of the horse. Science, 2017, 356, 442-445.	12.6	185
4	Evolutionary Genomics and Conservation of the Endangered Przewalskiâ€™s Horse. Current Biology, 2015, 25, 2577-2583.	3.9	161
5	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6889-97.	7.1	139
6	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
7	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. BMC Genomics, 2017, 18, 565.	2.8	116
8	Investigations on Transgenerational Epigenetic Response Down the Male Line in F2 Pigs. PLoS ONE, 2012, 7, e30583.	2.5	94
9	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. Current Biology, 2017, 27, 2029-2035.e5.	3.9	75
10	A Non-Synonymous HMGA2 Variant Decreases Height in Shetland Ponies and Other Small Horses. PLoS ONE, 2015, 10, e0140749.	2.5	73
11	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. National Science Review, 2019, 6, 810-824.	9.5	65
12	Comparison against 186 canid whole-genome sequences reveals survival strategies of an ancient clonally transmissible canine tumor. Genome Research, 2015, 25, 1646-1655.	5.5	63
13	Rapid Discovery of De Novo Deleterious Mutations in Cattle Enhances the Value of Livestock as Model Species. Scientific Reports, 2017, 7, 11466.	3.3	61
14	Independent Polled Mutations Leading to Complex Gene Expression Differences in Cattle. PLoS ONE, 2014, 9, e93435.	2.5	60
15	A transposable element insertion in <scp>APOB</scp> causes cholesterol deficiency in Holstein cattle. Animal Genetics, 2016, 47, 253-257.	1.7	59
16	Selection signatures in goats reveal copy number variants underlying breed-defining coat color phenotypes. PLoS Genetics, 2019, 15, e1008536.	3.5	50
17	A Missense Change in the ATG4D Gene Links Aberrant Autophagy to a Neurodegenerative Vacuolar Storage Disease. PLoS Genetics, 2015, 11, e1005169.	3.5	48
18	A Mutation in the FAM83G Gene in Dogs with Hereditary Footpad Hyperkeratosis (HFH). PLoS Genetics, 2014, 10, e1004370.	3.5	43

#	ARTICLE	IF	CITATIONS
19	Differential Expression of Serum MicroRNAs Supports CD4+ T Cell Differentiation into Th2/Th17 Cells in Severe Equine Asthma. Genes, 2017, 8, 383.	2.4	39
20	The horse Y chromosome as an informative marker for tracing sire lines. Scientific Reports, 2019, 9, 6095.	3.3	39
21	A COL11A2 Mutation in Labrador Retrievers with Mild Disproportionate Dwarfism. PLoS ONE, 2013, 8, e60149.	2.5	37
22	A novelKITvariant in an Icelandic horse with white-spotted coat colour. Animal Genetics, 2015, 46, 466-466.	1.7	37
23	A naturally occurring prfA truncation in a Listeria monocytogenes field strain contributes to reduced replication and cell-to-cell spread. Veterinary Microbiology, 2015, 179, 91-101.	1.9	37
24	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
25	A Mutation in the SUV39H2 Gene in Labrador Retrievers with Hereditary Nasal Parakeratosis (HNPK) Provides Insights into the Epigenetics of Keratinocyte Differentiation. PLoS Genetics, 2013, 9, e1003848.	3.5	35
26	A de novo variant in the ASPRV1 gene in a dog with ichthyosis. PLoS Genetics, 2017, 13, e1006651.	3.5	34
27	A Frameshift Mutation in the Cubilin Gene (CUBN) in Border Collies with Imerslund-GrÃsbeck Syndrome (Selective Cobalamin Malabsorption). PLoS ONE, 2013, 8, e61144.	2.5	34
28	Comprehensive characterization of horse genome variation by wholeâ€genome sequencing of 88 horses. Animal Genetics, 2019, 50, 74-77.	1.7	33
29	Deletion in the EVC2 Gene Causes Chondrodysplastic Dwarfism in Tyrolean Grey Cattle. PLoS ONE, 2014, 9, e94861.	2.5	32
30	Molecular Characterization of Three Canine Models of Human Rare Bone Diseases: Caffey, van den Ende-Gupta, and Raine Syndromes. PLoS Genetics, 2016, 12, e1006037.	3.5	32
31	Asian horses deepen the MSY phylogeny. Animal Genetics, 2018, 49, 90-93.	1.7	32
32	A novel <scp>MLPH</scp> variant in dogs with coat colour dilution. Animal Genetics, 2018, 49, 94-97.	1.7	31
33	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
34	Signal search analysis server. Nucleic Acids Research, 2003, 31, 3618-3620.	14.5	28
35	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
36	HTPSELEX--a database of high-throughput SELEX libraries for transcription factor binding sites. Nucleic Acids Research, 2006, 34, D90-D94.	14.5	26

#	ARTICLE	IF	CITATIONS
37	Meta-analysis of estrogen response in MCF-7 distinguishes early target genes involved in signaling and cell proliferation from later target genes involved in cell cycle and DNA repair. BMC Systems Biology, 2011, 5, 138.	3.0	26
38	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
39	MKLN1 splicing defect in dogs with lethal acrodermatitis. PLoS Genetics, 2018, 14, e1007264.	3.5	26
40	TECPR2 Associated Neuroaxonal Dystrophy in Spanish Water Dogs. PLoS ONE, 2015, 10, e0141824.	2.5	25
41	The LCORL Locus Is under Selection in Large-Sized Pakistani Goat Breeds. Genes, 2020, 11, 168.	2.4	25
42	Looking the Cow in the Eye: Deletion in the NID1 Gene Is Associated with Recessive Inherited Cataract in Romagnola Cattle. PLoS ONE, 2014, 9, e110628.	2.5	24
43	Imputation of sequence level genotypes in the Franches-Montagnes horse breed. Genetics Selection Evolution, 2014, 46, 63.	3.0	24
44	Impaired Cell Cycle Regulation in a Natural Equine Model of Asthma. PLoS ONE, 2015, 10, e0136103.	2.5	24
45	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
46	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
47	Dog colour patterns explained by modular promoters of ancient canid origin. Nature Ecology and Evolution, 2021, 5, 1415-1423.	7.8	24
48	A frameshift mutation in the cubilin gene (<scp>CUBN</scp>) in <scp>B</scp>eagles with <scp>I</scp>merslundâ€“<scp>G</scp>rÃsbeck syndrome (selective cobalamin malabsorption). Animal Genetics, 2014, 45, 148-150.	1.7	22
49	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
50	Novel insights into the pathways regulating the canine hair cycle and their deregulation in alopecia X. PLoS ONE, 2017, 12, e0186469.	2.5	22
51	Two Loci on Chromosome 5 Are Associated with Serum IgE Levels in Labrador Retrievers. PLoS ONE, 2012, 7, e39176.	2.5	21
52	NME5 frameshift variant in Alaskan Malamutes with primary ciliary dyskinesia. PLoS Genetics, 2019, 15, e1008378.	3.5	21
53	In Search of Epigenetic Marks in Testes and Sperm Cells of Differentially Fed Boars. PLoS ONE, 2013, 8, e78691.	2.5	21
54	A GJA9 frameshift variant is associated with polyneuropathy in Leonberger dogs. BMC Genomics, 2017, 18, 662.	2.8	20

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	Neuronal ceroid lipofuscinosis (NCL) is caused by the entire deletion of CLN8 in the AlpenlÃndische Dachsbracke dog. Molecular Genetics and Metabolism, 2017, 120, 269-277.	1.1	19
58	A curated catalog of canine and equine keratin genes. PLoS ONE, 2017, 12, e0180359.	2.5	19
59	Dog10K_Boxer_Tasha_1.0: A Long-Read Assembly of the Dog Reference Genome. Genes, 2021, 12, 847.	2.4	19
60	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
61	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
62	The Transcriptome of Equine Peripheral Blood Mononuclear Cells. PLoS ONE, 2015, 10, e0122011.	2.5	17
63	ATP13A2 missense variant in Australian Cattle Dogs with late onset neuronal ceroid lipofuscinosis. Molecular Genetics and Metabolism, 2019, 127, 95-106.	1.1	17
64	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
65	A Nonsense Variant in COL6A1 in Landseer Dogs with Muscular Dystrophy. G3: Genes, Genomes, Genetics, 2015, 5, 2611-2617.	1.8	16
66	A Nonsense Mutation in the IKBKG Gene in Mares with Incontinentia Pigmenti. PLoS ONE, 2013, 8, e81625.	2.5	16
67	Congenital Hepatic Fibrosis in the Franches-Montagnes Horse Is Associated with the Polycystic Kidney and Hepatic Disease 1 (PKHD1) Gene. PLoS ONE, 2014, 9, e110125.	2.5	15
68	Lethal chondrodysplasia in a family of Holstein cattle is associated with a de novo splice site variant of COL2A1. BMC Veterinary Research, 2016, 12, 100.	1.9	15
69	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
70	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
71	Differentially expressed microRNAs, including a large microRNA cluster on chromosome 24, are associated with equine sarcoid and squamous cell carcinoma. Veterinary and Comparative Oncology, 2019, 17, 155-164.	1.8	15
72	The challenge of modeling nuclear receptor regulatory networks in mammalian cells. Molecular and Cellular Endocrinology, 2011, 334, 91-97.	3.2	14

#	ARTICLE	IF	CITATIONS
73	Hairless Streaks in Cattle Implicate TSR2 in Early Hair Follicle Formation. PLoS Genetics, 2015, 11, e1005427.	3.5	14
74	DNA-based diagnosis of rare diseases in veterinary medicine: a 4.4Âkb deletion of ITGB4 is associated with epidermolysis bullosa in Charolais cattle. BMC Veterinary Research, 2015, 11, 48.	1.9	14
75	A CHRNB1 frameshift mutation is associated with familial arthrogryposis multiplex congenita in Red dairy cattle. BMC Genomics, 2016, 17, 479.	2.8	14
76	Canine NAPEPLD-associated models of human myelin disorders. Scientific Reports, 2018, 8, 5818.	3.3	14
77	Frameshift Variant in MFSD12 Explains the Mushroom Coat Color Dilution in Shetland Ponies. Genes, 2019, 10, 826.	2.4	14
78	An ADAMTS3 missense variant is associated with Norwich Terrier upper airway syndrome. PLoS Genetics, 2019, 15, e1008102.	3.5	14
79	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
80	Mitochondrial PCK2 Missense Variant in Shetland Sheepdogs with Paroxysmal Exercise-Induced Dyskinesia (PED). Genes, 2020, 11, 774.	2.4	14
81	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
82	Epidermolysis bullosa in Danish Hereford calves is caused by a deletion in LAMC2 gene. BMC Veterinary Research, 2015, 11, 23.	1.9	13
83	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
84	Identification of Two Independent COL5A1 Variants in Dogs with Ehlersâ€“Danlos Syndrome. Genes, 2019, 10, 731.	2.4	13
85	Chromosomal imbalance in pigs showing a syndromic form of cleft palate. BMC Genomics, 2019, 20, 349.	2.8	13
86	Complex Structural PPT1 Variant Associated with Non-syndromic Canine Retinal Degeneration. G3: Genes, Genomes, Genetics, 2019, 9, 425-437.	1.8	13
87	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
88	Torque ripple reduction in Permanent Magnet Synchronous Motor driven by field oriented control using Iterative Learning Control with space vector pulse width modulation. , 2013, , .		12
89	A frameshift mutation in MOCOS is associated with familial renal syndrome (xanthinuria) in Tyrolean Grey cattle. BMC Veterinary Research, 2016, 12, 276.	1.9	12
90	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

#	ARTICLE	IF	CITATIONS
91	LPS-induced modules of co-expressed genes in equine peripheral blood mononuclear cells. BMC Genomics, 2017, 18, 34.	2.8	12
92	OCA2 splice site variant in German Spitz dogs with oculocutaneous albinism. PLoS ONE, 2017, 12, e0185944.	2.5	12
93	Deletion of the SELENOP gene leads to CNS atrophy with cerebellar ataxia in dogs. PLoS Genetics, 2021, 17, e1009716.	3.5	12
94	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
95	A de novo missense mutation of FGFR2 causes facial dysplasia syndrome in Holstein cattle. BMC Genetics, 2017, 18, 74.	2.7	11
96	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
97	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
98	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
99	<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
100	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
101	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
102	Genetic Abnormalities in a Calf with Congenital Increased Muscular Tonus. Journal of Veterinary Internal Medicine, 2015, 29, 1418-1421.	1.6	9
103	Whole genome sequencing confirms <scp>KIT</scp> insertions in a white cat. Animal Genetics, 2015, 46, 98-98.	1.7	9
104	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
105	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. PLoS Genetics, 2019, 15, e1008411.	3.5	9
106	A second <scp>KRT</scp>71 allele in curly coated dogs. Animal Genetics, 2019, 50, 97-100.	1.7	9
107	A CNTNAP1 Missense Variant Is Associated with Canine Laryngeal Paralysis and Polyneuropathy. Genes, 2020, 11, 1426.	2.4	9
108	Genomic diversity and population structure of the Leonberger dog breed. Genetics Selection Evolution, 2020, 52, 61.	3.0	9

#	ARTICLE	IF	CITATIONS
109	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
110	Genetic variability of the equine casein genes. Journal of Dairy Science, 2016, 99, 5486-5497.	3.4	8
111	A novelMITFvariant in a white American Standardbred foal. Animal Genetics, 2017, 48, 123-124.	1.7	8
112	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
113	A de novo inâ€frame duplication in the <scp>COL</scp>1A2 gene in a Lagotto Romagnolo dog with osteogenesis imperfecta. Animal Genetics, 2019, 50, 786-787.	1.7	8
114	A Missense Variant in SCN8A in Alpine Dachsbracke Dogs Affected by Spinocerebellar Ataxia. Genes, 2019, 10, 362.	2.4	8
115	Transcriptome Profiling and Differential Gene Expression in Canine Microdissected Anagen and Telogen Hair Follicles and Interfollicular Epidermis. Genes, 2020, 11, 884.	2.4	8
116	X-Linked Duchenne-Type Muscular Dystrophy in Jack Russell Terrier Associated with a Partial Deletion of the Canine DMD Gene. Genes, 2020, 11, 1175.	2.4	8
117	LAMB3 Missense Variant in Australian Shepherd Dogs with Junctional Epidermolysis Bullosa. Genes, 2020, 11, 1055.	2.4	8
118	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
119	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
120	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
121	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
122	Abnormal keratinocyte differentiation in the nasal planum of Labrador Retrievers with hereditary nasal parakeratosis (HNPK). PLoS ONE, 2020, 15, e0225901.	2.5	7
123	Diagnostic potential of three serum <scp>microRNAs</scp> as biomarkers for equine sarcoid disease in horses and donkeys. Journal of Veterinary Internal Medicine, 2021, 35, 610-619.	1.6	7
124	ABHD5 frameshift deletion in Golden Retrievers with ichthyosis. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	7
125	<scp>MFSD</scp>8 singleâ€base pair deletion in a Chihuahua with neuronal ceroid lipofuscinosis. Animal Genetics, 2016, 47, 631-631.	1.7	6
126	A SIX6 Nonsense Variant in Golden Retrievers with Congenital Eye Malformations. Genes, 2019, 10, 454.	2.4	6

#	ARTICLE	IF	CITATIONS
127	A <scp>COL</scp>2A1 de novo variant in a Holstein bulldog calf. Animal Genetics, 2019, 50, 113-114.	1.7	6
128	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
129	A COL7A1 Variant in a Litter of Neonatal Basset Hounds with Dystrophic Epidermolysis Bullosa. Genes, 2020, 11, 1458.	2.4	6
130	Novel Brown Coat Color (Cocoa) in French Bulldogs Results from a Nonsense Variant in HPS3. Genes, 2020, 11, 636.	2.4	6
131	SUV39H2 epigenetic silencing controls fate conversion of epidermal stem and progenitor cells. Journal of Cell Biology, 2021, 220, .	5.2	6
132	PRKG2 Splice Site Variant in Dogo Argentino Dogs with Disproportionate Dwarfism. Genes, 2021, 12, 1489.	2.4	6
133	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
134	Genomeâ€wide association study and heritability estimate for ectopic ureters in Entlebucher mountain dogs. Animal Genetics, 2018, 49, 645-650.	1.7	5
135	AKNA Frameshift Variant in Three Dogs with Recurrent Inflammatory Pulmonary Disease. Genes, 2019, 10, 567.	2.4	5
136	A RAPGEF6 variant constitutes a major risk factor for laryngeal paralysis in dogs. PLoS Genetics, 2019, 15, e1008416.	3.5	5
137	A large deletion in the GP9 gene in Cocker Spaniel dogs with Bernard-Soulier syndrome. PLoS ONE, 2019, 14, e0220625.	2.5	5
138	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
139	Bald thigh syndrome in sighthoundsâ€"Revisiting the cause of a well-known disease. PLoS ONE, 2019, 14, e0212645.	2.5	5
140	ATP2A2 SINE Insertion in an Irish Terrier with Darier Disease and Associated Infundibular Cyst Formation. Genes, 2020, 11, 481.	2.4	5
141	A DSG1 Frameshift Variant in a Rottweiler Dog with Footpad Hyperkeratosis. Genes, 2020, 11, 469.	2.4	5
142	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
143	MIA3 Splice Defect in Cane Corso Dogs with Dental-Skeletal-Retinal Anomaly (DSRA). Genes, 2021, 12, 1497.	2.4	5
144	A COL5A2 In-Frame Deletion in a Chihuahua with Ehlers-Danlos Syndrome. Genes, 2022, 13, 934.	2.4	5

#	ARTICLE	IF	CITATIONS
145	<scp>IL</scp>26 gene inactivation in Equidae. Animal Genetics, 2013, 44, 770-772.	1.7	4
146	A single codon insertion in the PICALM gene is not associated with subvalvular aortic stenosis in Newfoundland dogs. Human Genetics, 2015, 134, 127-129.	3.8	4
147	DNA-based analysis of protein variants reveals different genetic variability of the paralogous equine ÄŸ-lactoglobulin genes LGB1 and LGB2. Livestock Science, 2016, 187, 181-185.	1.6	4
148	A TAC3 Missense Variant in a Domestic Shorthair Cat with Testicular Hypoplasia and Persistent Primary Dentition. Genes, 2019, 10, 806.	2.4	4
149	SLC19A3 Loss-of-Function Variant in Yorkshire Terriers with Leigh-Like Subacute Necrotizing Encephalopathy. Genes, 2020, 11, 1215.	2.4	4
150	NSDHL Frameshift Deletion in a Mixed Breed Dog with Progressive Epidermal Nevi. Genes, 2020, 11, 1297.	2.4	4
151	YARS2 Missense Variant in Belgian Shepherd Dogs with Cardiomyopathy and Juvenile Mortality. Genes, 2020, 11, 313.	2.4	4
152	Whole Genome Sequencing Indicates Heterogeneity of Hyperostotic Disorders in Dogs. Genes, 2020, 11, 163.	2.4	4
153	FYCO1 Frameshift Deletion in Wirehaired Pointing Griffon Dogs with Juvenile Cataract. Genes, 2022, 13, 334.	2.4	4
154	Independent COL5A1 Variants in Cats with Ehlers-Danlos Syndrome. Genes, 2022, 13, 797.	2.4	4
155	Reduction of transient and steady state speed pulsation in permanent magnet synchronous motor using Space Vector Pulse Width Modulation control. , 2013, , .		3
156	A de novo germline mutation of <scp>DLX</scp>3 in a Brown Swiss calf with trichoâ€dentoâ€osseusâ€like syndrome. Veterinary Dermatology, 2017, 28, 616.	1.2	3
157	Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. Animal Genetics, 2020, 51, 78-86.	1.7	3
158	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
159	A Missense Variant in ALDH5A1 Associated with Canine Succinic Semialdehyde Dehydrogenase Deficiency (SSADHD) in the Saluki Dog. Genes, 2020, 11, 1033.	2.4	3
160	Transcriptome of microglia reveals a speciesâ€specific expression profile in bovines with conserved and new signature genes. Glia, 2021, 69, 1932-1949.	4.9	3
161	Diagnostic and prognostic potential of eight whole blood microRNAs for equine sarcoid disease. PLoS ONE, 2021, 16, e0261076.	2.5	3
162	Initial characterization of stiff skinâ€like syndrome in West Highland white terriers. Veterinary Dermatology, 2016, 27, 210.	1.2	2

#	ARTICLE	IF	CITATIONS
163	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
164	Transcriptional Differences between Canine Cutaneous Epitheliotropic Lymphoma and Immune-Mediated Dermatoses. Genes, 2021, 12, 160.	2.4	2
165	A pathogenic HEXA missense variant in wild boars with Tay-Sachs disease. Molecular Genetics and Metabolism, 2021, 133, 297-306.	1.1	2
166	LAMA2 Nonsense Variant in an Italian Greyhound with Congenital Muscular Dystrophy. Genes, 2021, 12, 1823.	2.4	2
167	Genomic and Transcriptomic Characterization of Atypical Recurrent Flank Alopecia in the Cesky Fousek. Genes, 2022, 13, 650.	2.4	2
168	SLC25A12 Missense Variant in Nova Scotia Duck Tolling Retrievers Affected by Cerebellar Degenerationâ€"Myositis Complex (CDMC). Genes, 2022, 13, 1223.	2.4	2
169	Exclusion of adrenoceptor alpha 2 variants in a horse insensitive to medetomidine. Animal Genetics, 2018, 49, 141-141.	1.7	1
170	L2HGDH Missense Variant in a Cat with L-2-Hydroxyglutaric Aciduria. Genes, 2021, 12, 682.	2.4	1
171	A Missense Variant in SLC39A4 in a Litter of Turkish Van Cats with Acrodermatitis Enteropathica. Genes, 2021, 12, 1309.	2.4	1
172	LTBP3 Frameshift Variant in British Shorthair Cats with Complex Skeletal Dysplasia. Genes, 2021, 12, 1923.	2.4	1
173	Canine reference genome accuracy impacts variant calling: Lessons learned from investigating embryonic lethal variants. Animal Genetics, 2022, 53, 706-708.	1.7	1
174	Application of high performance computing in lattice physics code VISWAM. , 2014, , .		0
175	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
176	Independent DSG4 frameshift variants in cats with hair shaft dystrophy. Molecular Genetics and Genomics, 2022, 297, 147-154.	2.1	0
177	Title is missing!. , 2019, 15, e1008536.		0
178	Title is missing!. , 2019, 15, e1008536.		0
179	Title is missing!. , 2019, 15, e1008536.		0
180	Title is missing!. , 2019, 15, e1008536.		0

#	Article	IF	Citations
181	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
182	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
183	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
184	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0