Vidhya Jagannathan

List of Publications by Year
in descending order

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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	ABHD5 frameshift deletion in Golden Retrievers with ichthyosis. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	7
2	FYCO1 Frameshift Deletion in Wirehaired Pointing Griffon Dogs with Juvenile Cataract. Genes, 2022, 13, 334.	2.4	4
3	Genomic and Transcriptomic Characterization of Atypical Recurrent Flank Alopecia in the Cesky Fousek. Genes, 2022, 13, 650.	2.4	2
4	Independent DSG4 frameshift variants in cats with hair shaft dystrophy. Molecular Genetics and Genomics, 2022, 297, 147-154.	2.1	0
5	Independent COL5A1 Variants in Cats with Ehlers-Danlos Syndrome. Genes, 2022, 13, 797.	2.4	4
6	A COL5A2 In-Frame Deletion in a Chihuahua with Ehlers-Danlos Syndrome. Genes, 2022, 13, 934.	2.4	5
7	Canine reference genome accuracy impacts variant calling: Lessons learned from investigating embryonic lethal variants. Animal Genetics, 2022, 53, 706-708.	1.7	1
8	SLC25A12 Missense Variant in Nova Scotia Duck Tolling Retrievers Affected by Cerebellar Degenerationâ€"Myositis Complex (CDMC). Genes, 2022, 13, 1223.	2.4	2
9	Transcriptional Differences between Canine Cutaneous Epitheliotropic Lymphoma and Immune-Mediated Dermatoses. Genes, 2021, 12, 160.	2.4	2
10	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
11	SUV39H2 epigenetic silencing controls fate conversion of epidermal stem and progenitor cells. Journal of Cell Biology, 2021, 220, .	5.2	6
12	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
13	Dog10K_Boxer_Tasha_1.0: A Long-Read Assembly of the Dog Reference Genome. Genes, 2021, 12, 847.	2.4	19
14	L2HGDH Missense Variant in a Cat with L-2-Hydroxyglutaric Aciduria. Genes, 2021, 12, 682.	2.4	1
15	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
16	A pathogenic HEXA missense variant in wild boars with Tay-Sachs disease. Molecular Genetics and Metabolism, 2021, 133, 297-306.	1.1	2
17	Deletion of the SELENOP gene leads to CNS atrophy with cerebellar ataxia in dogs. PLoS Genetics, 2021, 17, e1009716.	3.5	12
18	A Missense Variant in SLC39A4 in a Litter of Turkish Van Cats with Acrodermatitis Enteropathica. Genes, 2021, 12, 1309.	2.4	1

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19	Dog colour patterns explained by modular promoters of ancient canid origin. Nature Ecology and Evolution, 2021, 5, 1415-1423.	7.8	24
20	PRKG2 Splice Site Variant in Dogo Argentino Dogs with Disproportionate Dwarfism. Genes, 2021, 12, 1489.	2.4	6
21	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
22	MIA3 Splice Defect in Cane Corso Dogs with Dental-Skeletal-Retinal Anomaly (DSRA). Genes, 2021, 12, 1497.	2.4	5
23	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
24	LTBP3 Frameshift Variant in British Shorthair Cats with Complex Skeletal Dysplasia. Genes, 2021, 12, 1923.	2.4	1
25	LAMA2 Nonsense Variant in an Italian Greyhound with Congenital Muscular Dystrophy. Genes, 2021, 12, 1823.	2.4	2
26	Diagnostic and prognostic potential of eight whole blood microRNAs for equine sarcoid disease. PLoS ONE, 2021, 16, e0261076.	2.5	3
27	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
28	Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. Animal Genetics, 2020, 51, 78-86.	1.7	3
29	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
30	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
31	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
32	Mitochondrial PCK2 Missense Variant in Shetland Sheepdogs with Paroxysmal Exercise-Induced Dyskinesia (PED). Genes, 2020, 11, 774.	2.4	14
33	A CNTNAP1 Missense Variant Is Associated with Canine Laryngeal Paralysis and Polyneuropathy. Genes, 2020, 11, 1426.	2.4	9
34	Transcriptome Profiling and Differential Gene Expression in Canine Microdissected Anagen and Telogen Hair Follicles and Interfollicular Epidermis. Genes, 2020, 11, 884.	2.4	8
35	Genomic diversity and population structure of the Leonberger dog breed. Genetics Selection Evolution, 2020, 52, 61.	3.0	9
36	SLC19A3 Loss-of-Function Variant in Yorkshire Terriers with Leigh-Like Subacute Necrotizing Encephalopathy. Genes, 2020, 11, 1215.	2.4	4

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37	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
38	LAMB3 Missense Variant in Australian Shepherd Dogs with Junctional Epidermolysis Bullosa. Genes, 2020, 11, 1055.	2.4	8
39	A Missense Variant in ALDH5A1 Associated with Canine Succinic Semialdehyde Dehydrogenase Deficiency (SSADHD) in the Saluki Dog. Genes, 2020, 11, 1033.	2.4	3
40	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
41	A COL7A1 Variant in a Litter of Neonatal Basset Hounds with Dystrophic Epidermolysis Bullosa. Genes, 2020, 11, 1458.	2.4	6
42	NSDHL Frameshift Deletion in a Mixed Breed Dog with Progressive Epidermal Nevi. Genes, 2020, 11, 1297.	2.4	4
43	ATP2A2 SINE Insertion in an Irish Terrier with Darier Disease and Associated Infundibular Cyst Formation. Genes, 2020, 11, 481.	2.4	5
44	Novel Brown Coat Color (Cocoa) in French Bulldogs Results from a Nonsense Variant in HPS3. Genes, 2020, 11, 636.	2.4	6
45	YARS2 Missense Variant in Belgian Shepherd Dogs with Cardiomyopathy and Juvenile Mortality. Genes, 2020, 11, 313.	2.4	4
46	Abnormal keratinocyte differentiation in the nasal planum of Labrador Retrievers with hereditary nasal parakeratosis (HNPK). PLoS ONE, 2020, 15, e0225901.	2.5	7
47	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
48	Whole Genome Sequencing Indicates Heterogeneity of Hyperostotic Disorders in Dogs. Genes, 2020, 11, 163.	2.4	4
49	The LCORL Locus Is under Selection in Large-Sized Pakistani Goat Breeds. Genes, 2020, 11, 168.	2.4	25
50	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
51	A DSG1 Frameshift Variant in a Rottweiler Dog with Footpad Hyperkeratosis. Genes, 2020, 11, 469.	2.4	5
52	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
53	AKNA Frameshift Variant in Three Dogs with Recurrent Inflammatory Pulmonary Disease. Genes, 2019, 10, 567.	2.4	5
54	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. PLoS Genetics, 2019, 15, e1008411.	3.5	9

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55	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
56	Frameshift Variant in MFSD12 Explains the Mushroom Coat Color Dilution in Shetland Ponies. Genes, 2019, 10, 826.	2.4	14
57	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
58	A RAPGEF6 variant constitutes a major risk factor for laryngeal paralysis in dogs. PLoS Genetics, 2019, 15, e1008416.	3.5	5
59	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
60	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
61	NME5 frameshift variant in Alaskan Malamutes with primary ciliary dyskinesia. PLoS Genetics, 2019, 15, e1008378.	3.5	21
62	A large deletion in the GP9 gene in Cocker Spaniel dogs with Bernard-Soulier syndrome. PLoS ONE, 2019, 14, e0220625.	2.5	5
63	Identification of Two Independent COL5A1 Variants in Dogs with Ehlersâ€“Danlos Syndrome. Genes, 2019, 10, 731.	2.4	13
64	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
65	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
66	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
67	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
68	A SIX6 Nonsense Variant in Golden Retrievers with Congenital Eye Malformations. Genes, 2019, 10, 454.	2.4	6
69	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
70	Chromosomal imbalance in pigs showing a syndromic form of cleft palate. BMC Genomics, 2019, 20, 349.	2.8	13
71	An ADAMTS3 missense variant is associated with Norwich Terrier upper airway syndrome. PLoS Genetics, 2019, 15, e1008102.	3.5	14
72	A Missense Variant in SCN8A in Alpine Dachsbracke Dogs Affected by Spinocerebellar Ataxia. Genes, 2019, 10, 362.	2.4	8

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73	The horse Y chromosome as an informative marker for tracing sire lines. Scientific Reports, 2019, 9, 6095.	3.3	39
74	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. National Science Review, 2019, 6, 810-824.	9.5	65
75	ATP13A2 missense variant in Australian Cattle Dogs with late onset neuronal ceroid lipofuscinosis. Molecular Genetics and Metabolism, 2019, 127, 95-106.	1.1	17
76	Bald thigh syndrome in sighthoundsâ€"Revisiting the cause of a well-known disease. PLoS ONE, 2019, 14, e0212645.	2.5	5
77	Selection signatures in goats reveal copy number variants underlying breed-defining coat color phenotypes. PLoS Genetics, 2019, 15, e1008536.	3.5	50
78	A TAC3 Missense Variant in a Domestic Shorthair Cat with Testicular Hypoplasia and Persistent Primary Dentition. Genes, 2019, 10, 806.	2.4	4
79	Comprehensive characterization of horse genome variation by wholeâ€genome sequencing of 88 horses. Animal Genetics, 2019, 50, 74-77.	1.7	33
80	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
81	A second <scp>KRT</scp>71 allele in curly coated dogs. Animal Genetics, 2019, 50, 97-100.	1.7	9
82	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
83	Complex Structural PPT1 Variant Associated with Non-syndromic Canine Retinal Degeneration. G3: Genes, Genomes, Genetics, 2019, 9, 425-437.	1.8	13
84	A <scp>COL</scp>2A1 de novo variant in a Holstein bulldog calf. Animal Genetics, 2019, 50, 113-114.	1.7	6
85	<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
86	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
87	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
88	Title is missing!. , 2019, 15, e1008536.		0
89	Title is missing!. , 2019, 15, e1008536.		0
90	Title is missing!. , 2019, 15, e1008536.		0

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91	Title is missing!. , 2019, 15, e1008536.		0
92	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
93	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
94	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
95	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. , 2019, 15, e1008411.		0
96	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
97	Canine NAPEPLD-associated models of human myelin disorders. Scientific Reports, 2018, 8, 5818.	3.3	14
98	Exclusion of adrenoceptor alpha 2 variants in a horse insensitive to medetomidine. Animal Genetics, 2018, 49, 141-141.	1.7	1
99	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
100	Asian horses deepen the MSY phylogeny. Animal Genetics, 2018, 49, 90-93.	1.7	32
101	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
102	A novel <scp>MLPH</scp> variant in dogs with coat colour dilution. Animal Genetics, 2018, 49, 94-97.	1.7	31
103	Genomeâ€wide association study and heritability estimate for ectopic ureters in Entlebucher mountain dogs. Animal Genetics, 2018, 49, 645-650.	1.7	5
104	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
105	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
106	MKLN1 splicing defect in dogs with lethal acrodermatitis. PLoS Genetics, 2018, 14, e1007264.	3.5	26
107	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
108	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

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109	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
110	Ancient genomic changes associated with domestication of the horse. Science, 2017, 356, 442-445.	12.6	185
111	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
112	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
113	Neuronal ceroid lipofuscinosis (NCL) is caused by the entire deletion of CLN8 in the AlpenlÄndische Dachsbracke dog. Molecular Genetics and Metabolism, 2017, 120, 269-277.	1.1	19
114	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
115	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
116	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
117	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
118	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. Current Biology, 2017, 27, 2029-2035.e5.	3.9	75
119	A novelMITFvariant in a white American Standardbred foal. Animal Genetics, 2017, 48, 123-124.	1.7	8
120	A GJA9 frameshift variant is associated with polyneuropathy in Leonberger dogs. BMC Genomics, 2017, 18, 662.	2.8	20
121	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
122	LPS-induced modules of co-expressed genes in equine peripheral blood mononuclear cells. BMC Genomics, 2017, 18, 34.	2.8	12
123	A curated catalog of canine and equine keratin genes. PLoS ONE, 2017, 12, e0180359.	2.5	19
124	OCA2 splice site variant in German Spitz dogs with oculocutaneous albinism. PLoS ONE, 2017, 12, e0185944.	2.5	12
125	A de novo variant in the ASPRV1 gene in a dog with ichthyosis. PLoS Genetics, 2017, 13, e1006651.	3.5	34
126	A de novo missense mutation of FGFR2 causes facial dysplasia syndrome in Holstein cattle. BMC Genetics, 2017, 18, 74.	2.7	11

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127	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. BMC Genomics, 2017, 18, 565.	2.8	116
128	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
129	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
130	Novel insights into the pathways regulating the canine hair cycle and their deregulation in alopecia X. PLoS ONE, 2017, 12, e0186469.	2.5	22
131	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
132	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
133	Initial characterization of stiff skinâ€like syndrome in West Highland white terriers. Veterinary Dermatology, 2016, 27, 210.	1.2	2
134	<scp>MFSD</scp>8 singleâ€base pair deletion in a Chihuahua with neuronal ceroid lipofuscinosis. Animal Genetics, 2016, 47, 631-631.	1.7	6
135	A CHRNB1 frameshift mutation is associated with familial arthrogryposis multiplex congenita in Red dairy cattle. BMC Genomics, 2016, 17, 479.	2.8	14
136	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
137	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
138	Genetic variability of the equine casein genes. Journal of Dairy Science, 2016, 99, 5486-5497.	3.4	8
139	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
140	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
141	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
142	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
143	A transposable element insertion in <scp>APOB</scp> causes cholesterol deficiency in Holstein cattle. Animal Genetics, 2016, 47, 253-257.	1.7	59
144	Genetic Abnormalities in a Calf with Congenital Increased Muscular Tonus. Journal of Veterinary Internal Medicine, 2015, 29, 1418-1421.	1.6	9

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145	A Nonsense Variant in COL6A1 in Landseer Dogs with Muscular Dystrophy. G3: Genes, Genomes, Genetics, 2015, 5, 2611-2617.	1.8	16
146	Whole genome sequencing confirms <scp>KIT</scp> insertions in a white cat. Animal Genetics, 2015, 46, 98-98.	1.7	9
147	A novelKITvariant in an Icelandic horse with white-spotted coat colour. Animal Genetics, 2015, 46, 466-466.	1.7	37
148	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
149	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
150	The Transcriptome of Equine Peripheral Blood Mononuclear Cells. PLoS ONE, 2015, 10, e0122011.	2.5	17
151	Hairless Streaks in Cattle Implicate TSR2 in Early Hair Follicle Formation. PLoS Genetics, 2015, 11, e1005427.	3.5	14
152	Impaired Cell Cycle Regulation in a Natural Equine Model of Asthma. PLoS ONE, 2015, 10, e0136103.	2.5	24
153	TECPR2 Associated Neuroaxonal Dystrophy in Spanish Water Dogs. PLoS ONE, 2015, 10, e0141824.	2.5	25
154	A Missense Change in the ATG4D Gene Links Aberrant Autophagy to a Neurodegenerative Vacuolar Storage Disease. PLoS Genetics, 2015, 11, e1005169.	3.5	48
155	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
156	Epidermolysis bullosa in Danish Hereford calves is caused by a deletion in LAMC2 gene. BMC Veterinary Research, 2015, 11, 23.	1.9	13
157	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
158	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
159	Evolutionary Genomics and Conservation of the Endangered Przewalskiâ€™s Horse. Current Biology, 2015, 25, 2577-2583.	3.9	161
160	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
161	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
162	A Non-Synonymous HMGA2 Variant Decreases Height in Shetland Ponies and Other Small Horses. PLoS ONE, 2015, 10, e0140749.	2.5	73

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163	Independent Polled Mutations Leading to Complex Gene Expression Differences in Cattle. PLoS ONE, 2014, 9, e93435.	2.5	60
164	Deletion in the EVC2 Gene Causes Chondrodysplastic Dwarfism in Tyrolean Grey Cattle. PLoS ONE, 2014, 9, e94861.	2.5	32
165	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
166	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
167	A Mutation in the FAM83G Gene in Dogs with Hereditary Footpad Hyperkeratosis (HFH). PLoS Genetics, 2014, 10, e1004370.	3.5	43
168	Application of high performance computing in lattice physics code VISWAM. , 2014, , .		0
169	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
170	Imputation of sequence level genotypes in the Franches-Montagnes horse breed. Genetics Selection Evolution, 2014, 46, 63.	3.0	24
171	<scp>IL</scp>26 gene inactivation in Equidae. Animal Genetics, 2013, 44, 770-772.	1.7	4
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