Vidhya Jagannathan

List of Publications by Year in Descending Order

171 papers	2,474 citations	23 h-index	42 g-index
191 ext. papers	3,469 ext. citations	4.3 avg, IF	4.79 L-index

#	Paper	IF	Citations
171	Independent COL5A1 Variants in Cats with Ehlers-Danlos Syndrome. *Genes*, **2022**, 13, 797	4.2	
170	A COL5A2 In-Frame Deletion in a Chihuahua with Ehlers-Danlos Syndrome. *Genes*, **2022**, 13, 934	4.2	0
169	ABHD5 frameshift deletion in Golden Retrievers with ichthyosis. *G3: Genes, Genomes, Genetics*, **2021**,	3.2	2
168	Polyadenine insertion disrupting the G6PC1 gene in German Pinschers with glycogen storage disease type Ia (GSD1A). *Animal Genetics*, **2021**, 52, 900-902	2.5	
167	Transcriptome of microglia reveals a species-specific expression profile in bovines with conserved and new signature genes. *Glia*, **2021**, 69, 1932-1949	9	0
166	Missense Variant in a Cat with L-2-Hydroxyglutaric Aciduria. *Genes*, **2021**, 12,	4.2	1
165	Improving the resolution of canine genome-wide association studies using genotype imputation: A study of two breeds. *Animal Genetics*, **2021**, 52, 703-713	2.5	0
164	Diagnostic potential of three serum microRNAs as biomarkers for equine sarcoid disease in horses and donkeys. *Journal of Veterinary Internal Medicine*, **2021**, 35, 610-619	3.1	3
163	SUV39H2 epigenetic silencing controls fate conversion of epidermal stem and progenitor cells. *Journal of Cell Biology*, **2021**, 220,	7.3	3
162	A pathogenic HEXA missense variant in wild boars with Tay-Sachs disease. *Molecular Genetics and Metabolism*, **2021**, 133, 297-306	3.7	1
161	Deletion of the SELENOP gene leads to CNS atrophy with cerebellar ataxia in dogs. *PLoS Genetics*, **2021**, 17, e1009716	6	3
160	Dog colour patterns explained by modular promoters of ancient canid origin. *Nature Ecology and Evolution*, **2021**, 5, 1415-1423	12.3	3
159	Frameshift Variant in a Miniature Dachshund with Coat Color Dilution and Neurological Defects Resembling Human Griscelli Syndrome Type 1. *Genes*, **2021**, 12,	4.2	2
158	Independent DSG4 frameshift variants in cats with hair shaft dystrophy. *Molecular Genetics and Genomics*, **2021**, 297, 147	3.1	
157	Diagnostic and prognostic potential of eight whole blood microRNAs for equine sarcoid disease.. *PLoS ONE*, **2021**, 16, e0261076	3.7	0
156	A Variant in a Litter of Neonatal Basset Hounds with Dystrophic Epidermolysis Bullosa. *Genes*, **2020**, 11,	4.2	2
155	Frameshift Deletion in a Mixed Breed Dog with Progressive Epidermal Nevi. *Genes*, **2020**, 11,	4.2	3

154	SINE Insertion in an Irish Terrier with Darier Disease and Associated Infundibular Cyst Formation. *Genes*, **2020**, 11,	4.2	3
153	Novel Brown Coat Color (Cocoa) in French Bulldogs Results from a Nonsense Variant in. *Genes*, **2020**, 11,	4.2	2
152	Missense Variant in Belgian Shepherd Dogs with Cardiomyopathy and Juvenile Mortality. *Genes*, **2020**, 11,	4.2	3
151	Abnormal keratinocyte differentiation in the nasal planum of Labrador Retrievers with hereditary nasal parakeratosis (HNPK). *PLoS ONE*, **2020**, 15, e0225901	3.7	5
150	A Genome-Wide Association Analysis in Noriker Horses Identifies a SNP Associated With Roan Coat Color. *Journal of Equine Veterinary Science*, **2020**, 88, 102950	1.2	4
149	Whole Genome Sequencing Indicates Heterogeneity of Hyperostotic Disorders in Dogs. *Genes*, **2020**, 11,	4.2	1
148	The Locus is under Selection in Large-Sized Pakistani Goat Breeds. *Genes*, **2020**, 11,	4.2	8
147	A Missense Variant Affecting the C-Terminal Tail of UNC93B1 in Dogs with Exfoliative Cutaneous Lupus Erythematosus (ECLE). *Genes*, **2020**, 11,	4.2	6
146	A Frameshift Variant in a Rottweiler Dog with Footpad Hyperkeratosis. *Genes*, **2020**, 11,	4.2	4
145	A deletion spanning the promoter and first exon of the hair cycle-specific ASIP transcript isoform in black and tan rabbits. *Animal Genetics*, **2020**, 51, 137-140	2.5	8
144	Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. *Animal Genetics*, **2020**, 51, 78-86	2.5	0
143	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	3.1	3
142	An Integrative miRNA-mRNA Expression Analysis Reveals Striking Transcriptomic Similarities between Severe Equine Asthma and Specific Asthma Endotypes in Humans. *Genes*, **2020**, 11,	4.2	3
141	A nonsense variant in the KRT14 gene in a domestic shorthair cat with epidermolysis bullosa simplex. *Animal Genetics*, **2020**, 51, 829-832	2.5	1
140	Mitochondrial PCK2 Missense Variant in Shetland Sheepdogs with Paroxysmal Exercise-Induced Dyskinesia (PED). *Genes*, **2020**, 11,	4.2	7
139	A Missense Variant Is Associated with Canine Laryngeal Paralysis and Polyneuropathy. *Genes*, **2020**, 11,	4.2	3
138	Transcriptome Profiling and Differential Gene Expression in Canine Microdissected Anagen and Telogen Hair Follicles and Interfollicular Epidermis. *Genes*, **2020**, 11,	4.2	1
137	Genomic diversity and population structure of the Leonberger dog breed. *Genetics Selection Evolution*, **2020**, 52, 61	4.9	4

136	Loss-of-Function Variant in Yorkshire Terriers with Leigh-Like Subacute Necrotizing Encephalopathy. *Genes*, **2020**, 11,	4.2	2
135	X-Linked Duchenne-Type Muscular Dystrophy in Jack Russell Terrier Associated with a Partial Deletion of the Canine Gene. *Genes*, **2020**, 11,	4.2	2
134	Missense Variant in Australian Shepherd Dogs with Junctional Epidermolysis Bullosa. *Genes*, **2020**, 11,	4.2	4
133	CCDC66 frameshift variant associated with a new form of early-onset progressive retinal atrophy in Portuguese Water Dogs. *Scientific Reports*, **2020**, 10, 21162	4.9	0
132	A comprehensive biomedical variant catalogue based on whole genome sequences of 582 dogs and eight wolves. *Animal Genetics*, **2019**, 50, 695-704	2.5	64
131	NME5 frameshift variant in Alaskan Malamutes with primary ciliary dyskinesia. *PLoS Genetics*, **2019**, 15, e1008378	6	12
130	A large deletion in the GP9 gene in Cocker Spaniel dogs with Bernard-Soulier syndrome. *PLoS ONE*, **2019**, 14, e0220625	3.7	1
129	Identification of Two Independent Variants in Dogs with Ehlers-Danlos Syndrome. *Genes*, **2019**, 10,	4.2	6
128	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	4.9	9
127	Differences in miRNA differential expression in whole blood between horses with sarcoid regression and progression. *Journal of Veterinary Internal Medicine*, **2019**, 33, 241-250	3.1	8
126	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	2.5	9
125	Identification of a Missense Variant in Involved in Dilution of Phaeomelanin Leading to White or Cream Coat Color in Dogs. *Genes*, **2019**, 10,	4.2	10
124	A Nonsense Variant in Golden Retrievers with Congenital Eye Malformations. *Genes*, **2019**, 10,	4.2	3
123	In silico and in vitro analysis of genetic variants of the equine CYP3A94, CYP3A95 and CYP3A97 isoenzymes. *Toxicology in Vitro*, **2019**, 60, 116-124	3.6	3
122	Chromosomal imbalance in pigs showing a syndromic form of cleft palate. *BMC Genomics*, **2019**, 20, 349	4.5	10
121	An ADAMTS3 missense variant is associated with Norwich Terrier upper airway syndrome. *PLoS Genetics*, **2019**, 15, e1008102	6	11
120	A Missense Variant in in Alpine Dachsbracke Dogs Affected by Spinocerebellar Ataxia. *Genes*, **2019**, 10,	4.2	3
119	The horse Y chromosome as an informative marker for tracing sire lines. *Scientific Reports*, **2019**, 9, 6095	4.9	12

118	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. *National Science Review*, **2019**, 6, 810-824	10.8	27
117	ATP13A2 missense variant in Australian Cattle Dogs with late onset neuronal ceroid lipofuscinosis. *Molecular Genetics and Metabolism*, **2019**, 127, 95-106	3.7	9
116	Bald thigh syndrome in sighthounds-Revisiting the cause of a well-known disease. *PLoS ONE*, **2019**, 14, e0212645	3.7	1
115	Compound heterozygosity for TNXB genetic variants in a mixed-breed dog with Ehlers-Danlos syndrome. *Animal Genetics*, **2019**, 50, 546-549	2.5	5
114	Frameshift Variant in Three Dogs with Recurrent Inflammatory Pulmonary Disease. *Genes*, **2019**, 10,	4.2	4
113	TSEN54 missense variant in Standard Schnauzers with leukodystrophy. *PLoS Genetics*, **2019**, 15, e1008416		5
112	A novel KIT deletion variant in a German Riding Pony with white-spotting coat colour phenotype. *Animal Genetics*, **2019**, 50, 761-763	2.5	5
111	Frameshift Variant in MFSD12 Explains the Mushroom Coat Color Dilution in Shetland Ponies. *Genes*, **2019**, 10,	4.2	4
110	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	2.5	7
109	A RAPGEF6 variant constitutes a major risk factor for laryngeal paralysis in dogs. *PLoS Genetics*, **2019**, 15, e1008416	6	3
108	A de novo in-frame duplication in the COL1A2 gene in a Lagotto Romagnolo dog with osteogenesis imperfecta. *Animal Genetics*, **2019**, 50, 786-787	2.5	3
107	Selection signatures in goats reveal copy number variants underlying breed-defining coat color phenotypes. *PLoS Genetics*, **2019**, 15, e1008536	6	24
106	A Missense Variant in a Domestic Shorthair Cat with Testicular Hypoplasia and Persistent Primary Dentition. *Genes*, **2019**, 10,	4.2	3
105	Comprehensive characterization of horse genome variation by whole-genome sequencing of 88 horses. *Animal Genetics*, **2019**, 50, 74-77	2.5	21
104	MicroRNA fingerprints in serum and whole blood of sarcoid-affected horses as potential non-invasive diagnostic biomarkers. *Veterinary and Comparative Oncology*, **2019**, 17, 107-117	2.5	6
103	A second KRT71 allele in curly coated dogs. *Animal Genetics*, **2019**, 50, 97-100	2.5	4
102	Whole-genome sequencing reveals a large deletion in the MITF gene in horses with white spotted coat colour and increased risk of deafness. *Animal Genetics*, **2019**, 50, 172-174	2.5	9
101	Complex Structural Variant Associated with Non-syndromic Canine Retinal Degeneration. *G3: Genes, Genomes, Genetics*, **2019**, 9, 425-437	3.2	10

100	A COL2A1 de novo variant in a Holstein bulldog calf. *Animal Genetics*, **2019**, 50, 113-114	2.5	5
99	NHLRC1 dodecamer repeat expansion demonstrated by whole genome sequencing in a Chihuahua with Lafora disease. *Animal Genetics*, **2019**, 50, 118-119	2.5	5
98	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	1.8	4
97	A non-coding regulatory variant in the 5′region of the MITF gene is associated with white-spotted coat in Brown Swiss cattle. *Animal Genetics*, **2019**, 50, 27-32	2.5	9
96	Selection signatures in goats reveal copy number variants underlying breed-defining coat color phenotypes **2019**, 15, e1008536		
95	Selection signatures in goats reveal copy number variants underlying breed-defining coat color phenotypes **2019**, 15, e1008536		
94	Selection signatures in goats reveal copy number variants underlying breed-defining coat color phenotypes **2019**, 15, e1008536		
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92	TSEN54 missense variant in Standard Schnauzers with leukodystrophy **2019**, 15, e1008411		
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90	TSEN54 missense variant in Standard Schnauzers with leukodystrophy **2019**, 15, e1008411		
89	TSEN54 missense variant in Standard Schnauzers with leukodystrophy **2019**, 15, e1008411		
88	A Nonsense Variant in the Gene in German Hunting Terriers with Exercise Induced Metabolic Myopathy. *G3: Genes, Genomes, Genetics*, **2018**, 8, 1545-1554	3.2	4
87	Canine NAPEPLD-associated models of human myelin disorders. *Scientific Reports*, **2018**, 8, 5818	4.9	8
86	Exclusion of adrenoceptor alpha 2 variants in a horse insensitive to medetomidine. *Animal Genetics*, **2018**, 49, 141	2.5	0
85	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	36.3	139
84	Asian horses deepen the MSY phylogeny. *Animal Genetics*, **2018**, 49, 90-93	2.5	13
83	A splice site variant in the SUV39H2 gene in Greyhounds with nasal parakeratosis. *Animal Genetics*, **2018**, 49, 137-140	2.5	7

82	A novel MLPH variant in dogs with coat colour dilution. *Animal Genetics*, **2018**, 49, 94-97	2.5	11
81	MKLN1 splicing defect in dogs with lethal acrodermatitis. *PLoS Genetics*, **2018**, 14, e1007264	6	18
80	Genome-wide association study and heritability estimate for ectopic ureters in Entlebucher mountain dogs. *Animal Genetics*, **2018**, 49, 645-650	2.5	3
79	A frameshift variant in the COL5A1 gene in a cat with Ehlers-Danlos syndrome. *Animal Genetics*, **2018**, 49, 641-644	2.5	9
78	Two MC1R loss-of-function alleles in cream-coloured Australian Cattle Dogs and white Huskies. *Animal Genetics*, **2018**, 49, 284-290	2.5	12
77	FEELnc: a tool for long non-coding RNA annotation and its application to the dog transcriptome. *Nucleic Acids Research*, **2017**, 45, e57	20.1	167
76	A Nonsense Variant in the Gene in Akhal-Teke Horses with Naked Foal Syndrome. *G3: Genes, Genomes, Genetics*, **2017**, 7, 1315-1321	3.2	8
75	Whole genome sequencing reveals a novel deletion variant in the KIT gene in horses with white spotted coat colour phenotypes. *Animal Genetics*, **2017**, 48, 483-485	2.5	16
74	Ancient genomic changes associated with domestication of the horse. *Science*, **2017**, 356, 442-445	33.3	149
73	A SINE Insertion in in Belgian Shepherd Dogs Affected by Spongy Degeneration with Cerebellar Ataxia (SDCA2). *G3: Genes, Genomes, Genetics*, **2017**, 7, 2729-2737	3.2	10
72	Frame-shift variant in the CHRNE gene in a juvenile dog with suspected myasthenia gravis-like disease. *Animal Genetics*, **2017**, 48, 625	2.5	4
71	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	3.7	14
70	A Missense Variant in in Belgian Shepherd Dogs Affected by Spongy Degeneration with Cerebellar Ataxia (SDCA1). *G3: Genes, Genomes, Genetics*, **2017**, 7, 663-669	3.2	13
69	LPS-induced modules of co-expressed genes in equine peripheral blood mononuclear cells. *BMC Genomics*, **2017**, 18, 34	4.5	8
68	A curated catalog of canine and equine keratin genes. *PLoS ONE*, **2017**, 12, e0180359	3.7	12
67	OCA2 splice site variant in German Spitz dogs with oculocutaneous albinism. *PLoS ONE*, **2017**, 12, e0185944	3.7	9
66	A de novo variant in the ASPRV1 gene in a dog with ichthyosis. *PLoS Genetics*, **2017**, 13, e1006651	6	29
65	A de novo missense mutation of FGFR2 causes facial dysplasia syndrome in Holstein cattle. *BMC Genetics*, **2017**, 18, 74	2.6	7

64	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. *BMC Genomics*, **2017**, 18, 565	4.5	66
63	Rapid Discovery of De Novo Deleterious Mutations in Cattle Enhances the Value of Livestock as Model Species. *Scientific Reports*, **2017**, 7, 11466	4.9	36
62	A Large Deletion in the Gene in Labrador Retrievers with a Congenital Cornification Disorder. *G3: Genes, Genomes, Genetics*, **2017**, 7, 3115-3121	3.2	10
61	A de novo germline mutation of DLX3 in a Brown Swiss calf with tricho-dento-osseus-like syndrome. *Veterinary Dermatology*, **2017**, 28, 616-e150	1.8	2
60	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. *Current Biology*, **2017**, 27, 2029-2035.e5	6.9	43
59	A novel MITF variant in a white American Standardbred foal. *Animal Genetics*, **2017**, 48, 123-124	2.5	4
58	A GJA9 frameshift variant is associated with polyneuropathy in Leonberger dogs. *BMC Genomics*, **2017**, 18, 662	4.5	17
57	Differential Expression of Serum MicroRNAs Supports CD4+ T Cell Differentiation into Th2/Th17 Cells in Severe Equine Asthma. *Genes*, **2017**, 8,	4.2	23
56	A single base deletion in the SLC45A2 gene in a Bullmastiff with oculocutaneous albinism. *Animal Genetics*, **2017**, 48, 619-621	2.5	10
55	A structural variant in the 5′flanking region of the TWIST2 gene affects melanocyte development in belted cattle. *PLoS ONE*, **2017**, 12, e0180170	3.7	8
54	Novel insights into the pathways regulating the canine hair cycle and their deregulation in alopecia X. *PLoS ONE*, **2017**, 12, e0186469	3.7	13
53	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	2.7	13
52	A frameshift mutation in MOCOS is associated with familial renal syndrome (xanthinuria) in Tyrolean Grey cattle. *BMC Veterinary Research*, **2016**, 12, 276	2.7	9
51	DNA-based analysis of protein variants reveals different genetic variability of the paralogous equine β-lactoglobulin genes LGB1 and LGB2. *Livestock Science*, **2016**, 187, 181-185	1.7	3
50	Whole-Genome Sequencing of a Canine Family Trio Reveals a FAM83G Variant Associated with Hereditary Footpad Hyperkeratosis. *G3: Genes, Genomes, Genetics*, **2016**, 6, 521-7	3.2	15
49	A transposable element insertion in APOB causes cholesterol deficiency in Holstein cattle. *Animal Genetics*, **2016**, 47, 253-7	2.5	39
48	An Intronic MBTPS2 Variant Results in a Splicing Defect in Horses with Brindle Coat Texture. *G3: Genes, Genomes, Genetics*, **2016**, 6, 2963-70	3.2	6
47	Molecular Characterization of Three Canine Models of Human Rare Bone Diseases: Caffey, van den Ende-Gupta, and Raine Syndromes. *PLoS Genetics*, **2016**, 12, e1006037	6	27

46	Initial characterization of stiff skin-like syndrome in West Highland white terriers. *Veterinary Dermatology*, **2016**, 27, 210-e53	1.8	2
45	MFSD8 single-base pair deletion in a Chihuahua with neuronal ceroid lipofuscinosis. *Animal Genetics*, **2016**, 47, 631	2.5	4
44	A CHRNB1 frameshift mutation is associated with familial arthrogryposis multiplex congenita in Red dairy cattle. *BMC Genomics*, **2016**, 17, 479	4.5	7
43	A Splice Defect in the EDA Gene in Dogs with an X-Linked Hypohidrotic Ectodermal Dysplasia (XLHED) Phenotype. *G3: Genes, Genomes, Genetics*, **2016**, 6, 2949-54	3.2	13
42	Genetic variability of the equine casein genes. *Journal of Dairy Science*, **2016**, 99, 5486-5497	4	6
41	A missense change in the ATG4D gene links aberrant autophagy to a neurodegenerative vacuolar storage disease. *PLoS Genetics*, **2015**, 11, e1005169	6	37
40	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	3.3	16
39	Epidermolysis bullosa in Danish Hereford calves is caused by a deletion in LAMC2 gene. *BMC Veterinary Research*, **2015**, 11, 23	2.7	8
38	DNA-based diagnosis of rare diseases in veterinary medicine: a 4.4 kb deletion of ITGB4 is associated with epidermolysis bullosa in Charolais cattle. *BMC Veterinary Research*, **2015**, 11, 48	2.7	10
37	Comparison against 186 canid whole-genome sequences reveals survival strategies of an ancient clonally transmissible canine tumor. *Genome Research*, **2015**, 25, 1646-55	9.7	48
36	Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. *Current Biology*, **2015**, 25, 2577-83	6.3	115
35	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	11.5	89
34	A single codon insertion in the PICALM gene is not associated with subvalvular aortic stenosis in Newfoundland dogs. *Human Genetics*, **2015**, 134, 127-9	6.3	3
33	Genetic Abnormalities in a Calf with Congenital Increased Muscular Tonus. *Journal of Veterinary Internal Medicine*, **2015**, 29, 1418-21	3.1	9
32	A Nonsense Variant in COL6A1 in Landseer Dogs with Muscular Dystrophy. *G3: Genes, Genomes, Genetics*, **2015**, 5, 2611-7	3.2	11
31	Whole genome sequencing confirms KIT insertions in a white cat. *Animal Genetics*, **2015**, 46, 98	2.5	6
30	A novel KIT variant in an Icelandic horse with white-spotted coat colour. *Animal Genetics*, **2015**, 46, 466	2.5	20
29	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**, 167A, 537-44	2.5	19

28	A deletion in the VLDLR gene in Eurasier dogs with cerebellar hypoplasia resembling a Dandy-Walker-like malformation (DWLM). *PLoS ONE*, **2015**, 10, e0108917	3.7	18
27	The transcriptome of equine peripheral blood mononuclear cells. *PLoS ONE*, **2015**, 10, e0122011	3.7	14
26	Hairless Streaks in Cattle Implicate TSR2 in Early Hair Follicle Formation. *PLoS Genetics*, **2015**, 11, e1005427	6	11
25	Impaired Cell Cycle Regulation in a Natural Equine Model of Asthma. *PLoS ONE*, **2015**, 10, e0136103	3.7	16
24	TECPR2 Associated Neuroaxonal Dystrophy in Spanish Water Dogs. *PLoS ONE*, **2015**, 10, e0141824	3.7	16
23	A Non-Synonymous HMGA2 Variant Decreases Height in Shetland Ponies and Other Small Horses. *PLoS ONE*, **2015**, 10, e0140749	3.7	36
22	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*, **2015**, 6, 255-62	3.2	16
21	Independent polled mutations leading to complex gene expression differences in cattle. *PLoS ONE*, **2014**, 9, e93435	3.7	48
20	Deletion in the EVC2 gene causes chondrodysplastic dwarfism in Tyrolean Grey cattle. *PLoS ONE*, **2014**, 9, e94861	3.7	22
19	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	3.7	13
18	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	3.7	19
17	A mutation in the FAM83G gene in dogs with hereditary footpad hyperkeratosis (HFH). *PLoS Genetics*, **2014**, 10, e1004370	6	37
16	A frameshift mutation in the cubilin gene (CUBN) in Beagles with Imerslund-Gräsbeck syndrome (selective cobalamin malabsorption). *Animal Genetics*, **2014**, 45, 148-50	2.5	18
15	Imputation of sequence level genotypes in the Franches-Montagnes horse breed. *Genetics Selection Evolution*, **2014**, 46, 63	4.9	22
14	IL26 gene inactivation in Equidae. *Animal Genetics*, **2013**, 44, 770-2	2.5	4
13	Torque ripple reduction in Permanent Magnet Synchronous Motor driven by field oriented control using Iterative Learning Control with space vector pulse width modulation **2013**,		7
12	Reduction of transient and steady state speed pulsation in permanent magnet synchronous motor using Space Vector Pulse Width Modulation control **2013**,		3
11	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	6	29

List of Publications

10	A COL11A2 mutation in Labrador retrievers with mild disproportionate dwarfism. *PLoS ONE*, **2013**, 8, e60149	3.7	28
9	A frameshift mutation in the cubilin gene (CUBN) in Border Collies with Imerslund-Gr□beck syndrome (selective cobalamin malabsorption). *PLoS ONE*, **2013**, 8, e61144	3.7	28
8	In search of epigenetic marks in testes and sperm cells of differentially fed boars. *PLoS ONE*, **2013**, 8, e78691	3.7	6
7	A nonsense mutation in the IKBKG gene in mares with incontinentia pigmenti. *PLoS ONE*, **2013**, 8, e81625	3.7	16
6	Investigations on transgenerational epigenetic response down the male line in F2 pigs. *PLoS ONE*, **2012**, 7, e30583	3.7	81
5	Two loci on chromosome 5 are associated with serum IgE levels in Labrador retrievers. *PLoS ONE*, **2012**, 7, e39176	3.7	17
4	The challenge of modeling nuclear receptor regulatory networks in mammalian cells. *Molecular and Cellular Endocrinology*, **2011**, 334, 91-7	4.4	11
3	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	3.5	21
2	HTPSELEX--a database of high-throughput SELEX libraries for transcription factor binding sites. *Nucleic Acids Research*, **2006**, 34, D90-4	20.1	20
1	Signal search analysis server. *Nucleic Acids Research*, **2003**, 31, 3618-20	20.1	23