Bertram Brenig

List of Publications by Year
in descending order

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255	3,781	172457	214800
papers	citations	29 h-index	47 g-index

270	270	270	4317
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Safety Evaluation of Lactobacillus delbrueckii subsp. lactis CIDCA 133: a Health-Promoting Bacteria. Probiotics and Antimicrobial Proteins, 2022, 14, 816-829.	3.9	12
2	Hybrid Assembly Improves Genome Quality and Completeness of Trametes villosa CCMB561 and Reveals a Huge Potential for Lignocellulose Breakdown. Journal of Fungi (Basel, Switzerland), 2022, 8, 142.	3.5	8
3	RNA-seq of nine canine prostate cancer cell lines reveals diverse therapeutic target signatures. Cancer Cell International, 2022, 22, 54.	4.1	2
4	Very low allele frequency of small calf syndrome causing GALNT2â€splice acceptor variant in the worldwide Holstein cattle population. Animal Genetics, 2022, 53, 472-473.	1.7	0
5	The Space-Exposed Kombucha Microbial Community Member Komagataeibacter oboediens Showed Only Minor Changes in Its Genome After Reactivation on Earth. Frontiers in Microbiology, 2022, 13, 782175.	3.5	5
6	Bacteriocin Producing Streptococcus agalactiae Strains Isolated from Bovine Mastitis in Brazil. Microorganisms, 2022, 10, 588.	3.6	7
7	Protein speciation is likely to increase the chance of proteins to be determined in 2â€ÐE/MS. Electrophoresis, 2022, , .	2.4	1
8	Comparative Genomics and In Silico Evaluation of Genes Related to the Probiotic Potential of Bifidobacterium breve 1101A. , 2022, 1, 161-182.		5
9	Î±/Î²-Hydrolase D16B Truncation Results in Premature Sperm Capacitation in Cattle. International Journal of Molecular Sciences, 2022, 23, 7777.	4.1	3
10	Co-culturing fructophilic lactic acid bacteria and yeast enhanced sugar metabolism and aroma formation during cocoa beans fermentation. International Journal of Food Microbiology, 2021, 339, 109015.	4.7	35
11	Characterization of a new multidrug-resistant Brazilian K. pneumoniae isolate and 172 Klebsiella spp. sequenced strains: Genomic island, multilocus sequence typing and capsule locus dataset. Data in Brief, 2021, 34, 106746.	1.0	0
12	Shotgun metagenomic analysis of kombucha mutualistic community exposed to Marsâ€like environment outside the International Space Station. Environmental Microbiology, 2021, 23, 3727-3742.	3.8	17
13	Comparative genomics with a multidrug-resistant Klebsiella pneumoniae isolate reveals the panorama of unexplored diversity in Northeast Brazil. Gene, 2021, 772, 145386.	2.2	2
14	A Missense Mutation in the KLF7 Gene Is a Potential Candidate Variant for Congenital Deafness in Australian Stumpy Tail Cattle Dogs. Genes, 2021, 12, 467.	2.4	5
15	Characterization of the first vaginal Lactobacillus crispatus genomes isolated in Brazil. PeerJ, 2021, 9, e11079.	2.0	5
16	Probiogenomics of Lactobacillus delbrueckii subsp. lactis CIDCA 133: In Silico, In Vitro, and In Vivo Approaches. Microorganisms, 2021, 9, 829.	3.6	12
17	Comparative mitogenomics of Agaricomycetes: Diversity, abundance, impact and coding potential of putative open-reading frames. Mitochondrion, 2021, 58, 1-13.	3.4	10
18	Bacterial Cellulose Retains Robustness but Its Synthesis Declines After Exposure to a Mars-like Environment Simulated Outside the International Space Station. Astrobiology, 2021, 21, 706-717.	3.0	16

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19	In Silico Prediction of Transcription Factor Collaborations Underlying Phenotypic Sexual Dimorphism in Zebrafish (Danio rerio). Genes, 2021, 12, 873.	2.4	0
20	Molecular Characterization and Survive Abilities of Salmonella Heidelberg Strains of Poultry Origin in Brazil. Frontiers in Microbiology, 2021, 12, 674147.	3.5	14
21	Genome-Wide Association Studies Reveal Neurological Genes for Dog Herding, Predation, Temperament, and Trainability Traits. Frontiers in Veterinary Science, 2021, 8, 693290.	2.2	13
22	Comparative genomics and in silico gene evaluation involved in the probiotic potential of Bifidobacterium longum 51A. Gene, 2021, 795, 145781.	2.2	7
23	Sperm Lipid Markers of Male Fertility in Mammals. International Journal of Molecular Sciences, 2021, 22, 8767.	4.1	38
24	Metagenome-Assembled Genome Sequences Obtained from a Reactivated Kombucha Microbial Community Exposed to a Mars-Like Environment outside the International Space Station. Microbiology Resource Announcements, 2021, 10, e0054921.	0.6	4
25	An RNA-Seq-Based Framework for Characterizing Canine Prostate Cancer and Prioritizing Clinically Relevant Biomarker Candidate Genes. International Journal of Molecular Sciences, 2021, 22, 11481.	4.1	13
26	BTK and PI3K Inhibitors Reveal Synergistic Inhibitory Anti-Tumoral Effects in Canine Diffuse Large B-Cell Lymphoma Cells. International Journal of Molecular Sciences, 2021, 22, 12673.	4.1	4
27	Processed pseudogene confounding the identification of a putative lethal recessive deletion in the bovine 60S ribosomal protein L11 gene (<scp>uL</scp>5). Animal Genetics, 2020, 51, 146-147.	1.7	0
28	Using ITS2 metabarcoding and microscopy to analyse shifts in pollen diets of honey bees and bumble bees along a massâ€flowering crop gradient. Molecular Ecology, 2020, 29, 5003-5018.	3.9	24
29	Intra-Protein Coevolution Is Increasingly Functional with Greater Proximity to Fertilization. Cytogenetic and Genome Research, 2020, 160, 295-308.	1.1	1
30	Skin exhibits of Dark Ronald XX are homozygous wild type at the Warmblood fragile foal syndrome causative missense variant position in lysyl hydroxylase gene PLOD1. Animal Genetics, 2020, 51, 838-840.	1.7	5
31	Frameshift Variant in Novel Adenosine-A1-Receptor Homolog Associated With Bovine Spastic Syndrome/Late-Onset Bovine Spastic Paresis in Holstein Sires. Frontiers in Genetics, 2020, 11, 591794.	2.3	3
32	Whole-genome sequencing reveals misidentification of a multidrug-resistant urine clinical isolate as Corynebacterium urealyticum. Journal of Global Antimicrobial Resistance, 2020, 23, 16-19.	2.2	5
33	Establishment and characterization of stable red, far-red (fR) and near infra-red (NIR) transfected canine prostate cancer cell lines. Cancer Cell International, 2020, 20, 139.	4.1	2
34	Exploring the Relationship Among Divergence Time and Coding and Non-coding Elements in the Shaping of Fungal Mitochondrial Genomes. Frontiers in Microbiology, 2020, 11, 765.	3.5	11
35	Exploring the contribution of fructophilic lactic acid bacteria to cocoa beans fermentation: Isolation, selection and evaluation. Food Research International, 2020, 136, 109478.	6.2	24
36	Endangered Pinzgauer cattle subtype Jochberger Hummel are genetically distinct. Animal Genetics, 2020, 51, 590-594.	1.7	1

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37	Osteogenesis imperfecta in a male holstein calf associated with a possible oligogenic origin. Veterinary Quarterly, 2020, 40, 58-67.	6.7	6
38	Analysis of Copy-Number Variations and Feline Mammary Carcinoma Survival. Scientific Reports, 2020, 10, 1003.	3.3	8
39	Complete genome analysis of Glutamicibacter creatinolyticus from mare abscess and comparative genomics provide insight of diversity and adaptation for Glutamicibacter. Gene, 2020, 741, 144566.	2.2	14
40	Analyzing the Dietary Diary of Bumble Bee. Frontiers in Plant Science, 2020, 11, 287.	3.6	16
41	Genetic diversity and population structure of six ethiopian cattle breeds from different geographical regions using high density single nucleotide polymorphisms. Livestock Science, 2020, 234, 103979.	1.6	5
42	PDA Indolylmaleimides Induce Anti-Tumor Effects in Prostate Carcinoma Cell Lines Through Mitotic Death. Frontiers in Veterinary Science, 2020, 7, 558135.	2.2	4
43	Genomic Characterization of Multidrug-Resistant Escherichia coli BH100 Sub-strains. Frontiers in Microbiology, 2020, 11, 549254.	3.5	5
44	Association of Î±/Î²-Hydrolase D16B with Bovine Conception Rate and Sperm Plasma Membrane Lipid Composition. International Journal of Molecular Sciences, 2020, 21, 627.	4.1	12
45	Biochemical parameters, dynamic tensiometry and circulating nucleic acids for cattle blood analysis: a review. PeerJ, 2020, 8, e8997.	2.0	21
46	Suitability of ultrasound-guided fine-needle aspiration biopsy for transcriptome sequencing of the canine prostate. Scientific Reports, 2019, 9, 13216.	3.3	13
47	Genetic mechanism underlying sexual plasticity and its association with colour patterning in zebrafish (Danio rerio). BMC Genomics, 2019, 20, 341.	2.8	15
48	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
49	Efficient phenotypic sex classification of zebrafish using machine learning methods. Ecology and Evolution, 2019, 9, 13332-13343.	1.9	10
50	Calm Before the Storm: A Glimpse into the Secondary Metabolism of Aspergillus welwitschiae, the Etiologic Agent of the Sisal Bole Rot. Toxins, 2019, 11, 631.	3.4	6
51	Re-sequencing and optical mapping reveals misassemblies and real inversions on Corynebacterium pseudotuberculosis genomes. Scientific Reports, 2019, 9, 16387.	3.3	6
52	Interdigital Hyperplasia in Holstein Cattle Is Associated With a Missense Mutation in the Signal Peptide Region of the Tyrosine-Protein Kinase Transmembrane Receptor Gene. Frontiers in Genetics, 2019, 10, 1157.	2.3	4
53	Phenotypic plasticity induced using high ambient temperature during embryogenesis in domesticated zebrafish, Danio rerio. Reproduction in Domestic Animals, 2019, 54, 435-444.	1.4	19
54	Genetic diversity analysis of Thai indigenous pig population using microsatellite markers. Asian-Australasian Journal of Animal Sciences, 2019, 32, 1491-1500.	2.4	18

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55	Comparative High-Resolution Transcriptome Sequencing of Lymphoma Cell Lines and de novo Lymphomas Reveals Cell-Line-Specific Pathway Dysregulation. Scientific Reports, 2018, 8, 6279.	3.3	11
56	TiHo-0906: a new feline mammary cancer cell line with molecular, morphological, and immunocytological characteristics of epithelial to mesenchymal transition. Scientific Reports, 2018, 8, 13231.	3.3	7
57	Draft genome sequence of Trametes villosa (Sw.) Kreisel CCMB561, a tropical white-rot Basidiomycota from the semiarid region of Brazil. Data in Brief, 2018, 18, 1581-1587.	1.0	6
58	Sex discrimination in rainbow trout (Oncorhynchus mykiss) using various sources of DNA and different genetic markers. Aquaculture, 2018, 497, 373-379.	3.5	3
59	A genome-wide association study reveals a locus for bilateral iridal hypopigmentation in Holstein Friesian cattle. BMC Genetics, 2017, 18, 30.	2.7	3
60	Morgagnian cataract resulting from a naturally occurring nonsense mutation elucidates a role of CPAMD8 in mammalian lens development. PLoS ONE, 2017, 12, e0180665.	2.5	16
61	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
62	P5005 Hitchhiking effects influence allele frequencies and exclusion probabilities of microsatellites used for parentage control in Holstein Friesian cattle. Journal of Animal Science, 2016, 94, 117-118.	0.5	0
63	P6024 Holstein Friesian lethal haplotype 5 is caused by a 138kbp deletion on chromosome 9. Journal of Animal Science, 2016, 94, 160-160.	0.5	0
64	P6029 Congenital cataract formation in Holstein Friesian cattle. Journal of Animal Science, 2016, 94, 163-163.	0.5	0
65	Multiplex Gene Expression Profiling of 16 Target Genes in Neoplastic and Non-Neoplastic Canine Mammary Tissues Using Branched-DNA Assay. International Journal of Molecular Sciences, 2016, 17, 1589.	4.1	4
66	Longitudinal Claudin Gene Expression Analyses in Canine Mammary Tissues and Thereof Derived Primary Cultures and Cell Lines. International Journal of Molecular Sciences, 2016, 17, 1655.	4.1	6
67	Genomic amplification of the caprine EDNRA locus might lead to a dose dependent loss of pigmentation. Scientific Reports, 2016, 6, 28438.	3.3	41
68	Recent development of allele frequencies and exclusion probabilities of microsatellites used for parentage control in the German Holstein Friesian cattle population. BMC Genetics, 2016, 17, 18.	2.7	11
69	The Holstein Friesian Lethal Haplotype 5 (HH5) Results from a Complete Deletion of TBF1M and Cholesterol Deficiency (CDH) from an ERV-(LTR) Insertion into the Coding Region of APOB. PLoS ONE, 2016, 11, e0154602.	2.5	50
70	Characterization of the novel indolylmaleimides' PDA-66 and PDA-377 effect on canine lymphoma cells. Oncotarget, 2016, 7, 35379-35389.	1.8	8
71	A 20 bp Duplication in Exon 2 of the Aristaless-Like Homeobox 4 Gene (ALX4) Is the Candidate Causative Mutation for Tibial Hemimelia Syndrome in Galloway Cattle. PLoS ONE, 2015, 10, e0129208.	2.5	12
72	Porcine SOX9 Gene Expression Is Influenced by an 18bp Indel in the 5â€™-Untranslated Region. PLoS ONE, 2015, 10, e0139583.	2.5	16

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73	Analytical and statistical consideration on the use of the ISAG-ICAR-SNP bovine panel for parentage control, using the Illumina BeadChip technology: example on the German Holstein population. Genetics Selection Evolution, 2015, 47, 3.	3.0	9
74	Species identification and quantification in meat and meat products using droplet digital PCR (ddPCR). Food Chemistry, 2015, 173, 1054-1058.	8.2	163
75	Prevalence of the Prefoldin Subunit 5 Gene Deletion in Canine Mammary Tumors. PLoS ONE, 2015, 10, e0131280.	2.5	15
76	A study based on records taken at time of hoof trimming reveals a strong association between the IQ motif-containing GTPase-activating protein 1 (IQGAP1) gene and sole hemorrhage in Holstein cattle. Journal of Dairy Science, 2014, 97, 507-519.	3.4	17
77	Monozygotic incomplete caudal duplication in a German Holstein calf. Veterinary Record Case Reports, 2014, 2, e000048.	0.2	2
78	Early pregnancy diagnosis in dairy cows using circulating nucleic acids. Theriogenology, 2013, 79, 173-179.	2.1	15
79	Osteogenesis imperfecta in dachshunds. Veterinary Record, 2013, 172, 319-319.	0.3	2
80	Molecular genetics of coat colour variations in White Galloway and White Park cattle. Animal Genetics, 2013, 44, 450-453.	1.7	45
81	Analysis of Circulating DNA Distribution in Pregnant and Nonpregnant Dairy Cows1. Biology of Reproduction, 2013, 88, 29.	2.7	6
82	The G32E Functional Variant Reduces Activity of PPARD by Nuclear Export and Post-Translational Modification in Pigs. PLoS ONE, 2013, 8, e75925.	2.5	8
83	Genome Aberrations in Canine Mammary Carcinomas and Their Detection in Cell-Free Plasma DNA. PLoS ONE, 2013, 8, e75485.	2.5	46
84	PrPSc Spreading Patterns and Prion Types. , 2013, , .		0
85	Structural variations in mammary carcinomas and their detection in cell-free plasma DNA in a clinical dog model.. Journal of Clinical Oncology, 2013, 31, 1537-1537.	1.6	0
86	Novel polysome messages and changes in translational activity appear after induction of adipogenesis in 3T3-L1 cells. BMC Molecular Biology, 2012, 13, 9.	3.0	15
87	Extrinsic and intrinsic regulation of DOR/TP53INP2 expression in mice: effects of dietary fat content, tissue type and sex in adipose and muscle tissues. Nutrition and Metabolism, 2012, 9, 86.	3.0	6
88	Phenotype Selection Reveals Coevolution of Muscle Glycogen and Protein and PTEN as a Gate Keeper for the Accretion of Muscle Mass in Adult Female Mice. PLoS ONE, 2012, 7, e39711.	2.5	9
89	Detergents modify proteinase K resistance of PrPSc in different transmissible spongiform encephalopathies (TSEs). Veterinary Microbiology, 2012, 157, 23-31.	1.9	16
90	Polymorphisms in the bovine HSP90AB1 gene are associated with heat tolerance in Thai indigenous cattle. Tropical Animal Health and Production, 2012, 44, 921-928.	1.4	69

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91	Polymorphism and gene organization of water buffalo MHCâ€DQB genes show homology to the BoLA DQB region. Animal Genetics, 2011, 42, 378-385.	1.7	17
92	Further resolution of porcine phylogeny in Southeast Asia by Thai mtDNA haplotypes. Animal Genetics, 2011, 42, 445-450.	1.7	7
93	PrPSc spreading patterns in the brain of sheep linked to different prion types. Veterinary Research, 2011, 42, 32.	3.0	16
94	Molecular analysis of carbohydrate Nâ€acetylgalactosamine 4â€O sulfotransferase 8 (CHST8) as a candidate gene for bovine spongiform encephalopathy susceptibility. Animal Genetics, 2010, 41, 85-88.	1.7	2
95	Cloning, mapping and molecular characterization of porcine progesterone receptor membrane component 2 (PGRMC2) gene. Genetics and Molecular Biology, 2010, 33, 471-474.	1.3	12
96	Prion Interaction with the 37-kDa/67-kDa Laminin Receptor on Enterocytes as a Cellular Model for Intestinal Uptake of Prions. Journal of Molecular Biology, 2010, 402, 293-300.	4.2	21
97	Shotgun metagenomics of biological stains using ultra-deep DNA sequencing. Forensic Science International: Genetics, 2010, 4, 228-231.	3.1	20
98	A genome-wide scan reveals candidate susceptibility loci for pig hernias in an intercross between White Duroc and Erhualian1. Journal of Animal Science, 2009, 87, 2469-2474.	0.5	31
99	A whole genome scan for quantitative trait loci for leg weakness and its related traits in a large F2 intercross population between White Duroc and Erhualian1. Journal of Animal Science, 2009, 87, 1569-1575.	0.5	13
100	MLPH Genotype--Melanin Phenotype Correlation in Dilute Dogs. Journal of Heredity, 2009, 100, S75-S79.	2.4	19
101	Disease-specific motifs can be identified in circulating nucleic acids from live elk and cattle infected with transmissible spongiform encephalopathies. Nucleic Acids Research, 2009, 37, 550-556.	14.5	75
102	Detection of classical and atypical/Nor98 scrapie by the paraffinâ€embedded tissue blot method. Veterinary Record, 2009, 164, 677-681.	0.3	13
103	Infectious nucleic acids in prion disease: halfway there. Trends in Biochemical Sciences, 2009, 34, 4-5.	7.5	4
104	Tissue Calcium Content in Piglets with Inguinal or Scrotal Hernias or Cryptorchidism. Journal of Comparative Pathology, 2009, 140, 182-186.	0.4	3
105	The equine MSH-R TaqI RFLP is not informative for hair colour in Arabian horses. Animal Genetics, 2009, 27, 64-64.	1.7	7
106	A Genome Wide Detection of Quantitative Trait Loci on Pig Maternal Infanticide Behavior in a Large Scale White DurocÂÃ—ÂErhualian Resource Population. Behavior Genetics, 2009, 39, 213-219.	2.1	19
107	Genome-wide QTL mapping for three traits related to teat number in a White Duroc Ã— Erhualian pig resource population. BMC Genetics, 2009, 10, 6.	2.7	37
108	A linkage map of the porcine genome from a largeâ€scale White Durocâ€ƒÃ—â€ƒErhualian resource population and evaluation of factors affecting recombination rates. Animal Genetics, 2009, 40, 47-52.	1.7	60

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109	Exclusion of a T>C sequence variant in exon 7 of the canine G_{Î±s} gene (GNAS1) as a causal gene for liver cancer. Animal Genetics, 2009, 40, 792-792.	1.7	0
110	Molecular and functional characterization of a cDNA encoding 4-hydroxy-3-methylbut-2-enyl diphosphate reductase from Dunaliella salina. Journal of Plant Physiology, 2009, 166, 968-977.	3.5	20
111	A whole genome scanning for quantitative trait loci on traits related to sperm quality and ejaculation in pigs. Animal Reproduction Science, 2009, 114, 210-218.	1.5	20
112	Similarities between Forms of Sheep Scrapie and Creutzfeldt-Jakob Disease Are Encoded by Distinct Prion Types. American Journal of Pathology, 2009, 175, 2566-2573.	3.8	36
113	Serum Nucleic Acids in an Experimental Bovine Transmissible Spongiform Encephalopathy Model. Zoonoses and Public Health, 2009, 56, 384-390.	2.2	5
114	Isolation and characterization of a stress-inducible Dunaliella salina Lcy-Î² gene encoding a functional lycopene Î²-cyclase. Applied Microbiology and Biotechnology, 2008, 79, 819-28.	3.6	65
115	A genome-wide scan for quantitative trait loci affecting limb bone lengths and areal bone mineral density of the distal femur in a White Duroc Ã— Erhualian F2 population. BMC Genetics, 2008, 9, 63.	2.7	19
116	Chromosomal assignment of eight porcine genes involved in apoptosis. Animal Genetics, 2008, 39, 330-331.	1.7	2
117	Radiation hybrid mapping of seven porcine calcium channel genes (CATSPER1â€“4 and) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.7	1
118	Characterization and linkage mapping of 15 porcine STS markers to fineâ€map chromosomal regions associated with hernia inguinalis/scrotalis. Animal Genetics, 2008, 39, 671-672.	1.7	3
119	Maternal infanticide in sows: Incidence and behavioural comparisons between savaging and non-savaging sows at parturition. Applied Animal Behaviour Science, 2008, 109, 238-248.	1.9	43
120	Invasion of Tumorigenic HT1080 Cells Is Impeded by Blocking or Downregulating the 37-kDa/67-kDa Laminin Receptor. Journal of Molecular Biology, 2008, 378, 530-539.	4.2	59
121	Implication of Complex Vertebral Malformation and Bovine Leukocyte Adhesion Deficiency DNA-Based Testing on Disease Frequency in the Holstein Population. Journal of Dairy Science, 2008, 91, 4854-4859.	3.4	23
122	Accumulation of Pathological Prion Protein PrPSc in the Skin of Animals with Experimental and Natural Scrapie. PLoS Pathogens, 2007, 3, e66.	4.7	46
123	Sequence analysis of the equine <i>SLC26A2</i> gene locus on chromosome 14q15â†'q21. Cytogenetic and Genome Research, 2007, 118, 55-62.	1.1	8
124	Characterization of the porcine multicopy ribosomal protein SA/37-kDa laminin receptor gene family. Gene, 2007, 395, 135-143.	2.2	5
125	Analysis and mapping of CACNB4, CHRNA1, KCNJ3, SCN2A and SPG4, physiological candidate genes for porcine congenital progressive ataxia and spastic paresis. Journal of Animal Breeding and Genetics, 2007, 124, 269-276.	2.0	4
126	Characterization of thePGK2Associated MicrosatelliteS0719on SSC7 Suitable for Parentage and QTL Diagnosis. Animal Biotechnology, 2006, 17, 43-49.	1.5	0

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127	Molecular characterization and exclusion of porcine GUSB as a candidate gene for congenital hernia inguinalis/scrotalis. BMC Veterinary Research, 2006, 2, 14.	1.9	6
128	Application of bovine microsatellite markers for genetic diversity analysis of European bison (Bison) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.0	7
129	Chromosomal assignment of porcine oncogenic and apoptopic genes CACNA2D2, TUSC4, ATP2A1, COL1A1, TAC1, BAK1 and CASP9. Animal Genetics, 2006, 37, 523-525.	1.7	1
130	The mutation causing the black-and-tan pigmentation phenotype of Mangalitza pigs maps to the porcine ASIP locus but does not affect its coding sequence. Mammalian Genome, 2006, 17, 58-66.	2.2	54
131	FISH-mapping of <i>LEP</i> and <i>SLC26A2</i> genes in sheep, goat and cattle R-banded chromosomes: comparison between bovine, ovine and caprine chromosome 4 (BTA4/OAR4/CHI4) and human chromosome 7 (HSA7). Cytogenetic and Genome Research, 2006, 115, 7-9.	1.1	12
132	Genotyping of Ovine Prion Protein Gene (PRNP) Variants by PCR with Melting Curve Analysis,. Clinical Chemistry, 2006, 52, 1426-1429.	3.2	12
133	Molecular phylogeny of selected predaceous leeches with reference to the evolution of body size and terrestrialism. Theory in Biosciences, 2005, 124, 55-64.	1.4	16
134	Frequency of the canine leucocyte adhesion deficiency (CLAD) mutation among Irish red setters in Germany. Journal of Animal Breeding and Genetics, 2005, 122, 140-142.	2.0	9
135	Identification and characterization of novel peroxisome proliferator-activated receptor-gamma (PPAR-gamma) transcriptional variants in pig and human. Journal of Animal Breeding and Genetics, 2005, 122, 45-53.	2.0	20
136	Phylogenetics of the European Dahomey miniature cattle based on mitochondrial D-loop region DNA sequence. Animal Genetics, 2005, 36, 179-181.	1.7	8
137	Assignment of the porcine SKI and GABRD genes to chromosome 6q22â€“q23. Animal Genetics, 2005, 36, 272-273.	1.7	0
138	Identification of a mutation in the ovine uroporphyrinogen decarboxylase (UROD) gene associated with a type of porphyria. Animal Genetics, 2005, 36, 297-302.	1.7	15
139	Targeted oligonucleotide-mediated microsatellite identification (TOMMI) from large-insert library clones. BMC Genetics, 2005, 6, 54.	2.7	13
140	PRIONS. , 2005, , 287-298.		0
141	Bov-tA Short Interspersed Nucleotide Element Sequences in Circulating Nucleic Acids from Sera of Cattle with Bovine Spongiform Encephalopathy (BSE) and Sera of Cattle Exposed to BSE. Vaccine Journal, 2005, 12, 814-820.	3.1	14
142	Assignment of the equine colony stimulating factor 1 receptor gene (CSF1R) to equine chromosome 14q15â†'q16 (ECA14q15â†'q16) by in situ hybridization and radiation hybrid panel mapping. Cytogenetic and Genome Research, 2005, 109, 534G-534G.	1.1	2
143	Racing, ornamental and city pigeons carry shiga toxin producing Escherichia coli (STEC) with different Shiga toxin subtypes, urging further analysis of their epidemiological role in the spread of STEC. Berliner Und Munchener Tierarztliche Wochenschrift, 2005, 118, 456-63.	0.7	12
144	Characterization and chromosome localization of a processed pseudogene related to the bovine laminin receptor gene family. Cytogenetic and Genome Research, 2004, 107, 123-127.	1.1	2

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145	Molecular characterization of porcine hyaluronidase genes 1, 2, and 3 clustered on SSC13q21. Cytogenetic and Genome Research, 2004, 106, 98-106.	1.1	8
146	Assignment of the ovine uroporphyrinogen decarboxylase (UROD) gene to chromosome 1p34â†'p36 by fluorescence in situ hybridization. Cytogenetic and Genome Research, 2004, 106, 142B-142B.	1.1	1
147	Assignment of the equine solute carrier 26A2 gene (SLC26A2) to equine chromosome 14q15â†'q21 (ECA14q15â†'q21) by in situ hybridization and radiation hybrid panel mapping. Cytogenetic and Genome Research, 2004, 107, 139A-139A.	1.1	4
148	Assignment of thephosphoglycerate kinase 1(PGK1) gene to porcine chromosome Xq12-q13 byfluorescence in situhybridization and hybrid panel analyses. Animal Genetics, 2004, 35, 143-145.	1.7	3
149	Characterization of five single nucleotide polymorphisms in the porcine stearoyl-CoA desaturase (SCD) gene. Animal Genetics, 2004, 35, 255-257.	1.7	20
150	Molecular cloning and analysis of the swamp and river buffalo leptin gene. Animal Genetics, 2004, 35, 462-463.	1.7	20
151	Characterization of Two SNPs (Single Nucleotide Polymorphisms) in the Porcine INSL3 Gene and Their Exclusion as a Common Genetic Basis of Hernia Inguinalis in Pigs. Biochemical Genetics, 2004, 42, 11-19.	1.7	9
152	Analysis of sequence variability of the bovine prion protein gene (PRNP) in German cattle breeds. Neurogenetics, 2004, 5, 19-25.	1.4	132
153	Molecular characterization of the porcine testis-specificphosphoglycerate kinase 2 (PGK2) gene and its association with male fertility. Mammalian Genome, 2004, 15, 996-1006.	2.2	19
154	Analysis of mitochondrial D-loop region casts new light on domestic water buffalo (Bubalus bubalis) phylogeny. Molecular Phylogenetics and Evolution, 2004, 30, 308-324.	2.7	78
155	Diagnostic polymorphisms in the mitochondrial cytochrome b gene allow discrimination between cattle, sheep, goat, roe buck and deer by PCR-RFLP. BMC Genetics, 2004, 5, 30.	2.7	55
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157	Forensic DNA-typing of dog hair: DNA-extraction and PCR amplification. Forensic Science International, 2004, 141, 149-151.	2.2	61
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