

Rudiger Brauning

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

2,021
citations

471509

17
h-index

289244

40
g-index

44
all docs

44
docs citations

44
times ranked

3251
citing authors

#	ARTICLE	IF	CITATIONS
1	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	12.6	436
2	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	8.8	331
3	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18644-18649.	7.1	196
4	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. <i>Nature Communications</i> , 2018, 9, 859.	12.8	126
5	Construction of relatedness matrices using genotyping-by-sequencing data. <i>BMC Genomics</i> , 2015, 16, 1047.	2.8	122
6	Linkage disequilibrium over short physical distances measured in sheep using a high-density SNP chip. <i>Animal Genetics</i> , 2014, 45, 754-757.	1.7	113
7	Brain urea increase is an early Huntington's disease pathogenic event observed in a prodromal transgenic sheep model and HD cases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E11293-E11302.	7.1	78
8	A physical map of the bovine genome. <i>Genome Biology</i> , 2007, 8, R165.	9.6	73
9	The constituents of <i>Microctonus</i> sp. parasitoid venoms. <i>Insect Molecular Biology</i> , 2008, 17, 313-324.	2.0	69
10	SNPchip v.3: integrating and standardizing single nucleotide polymorphism data for livestock species. <i>BMC Genomics</i> , 2015, 16, 283.	2.8	69
11	Whole Genome Sequencing for Determining the Source of <i>Mycobacterium bovis</i> Infections in Livestock Herds and Wildlife in New Zealand. <i>Frontiers in Veterinary Science</i> , 2018, 5, 272.	2.2	44
12	Estimation of linkage disequilibrium and effective population size in New Zealand sheep using three different methods to create genetic maps. <i>BMC Genetics</i> , 2017, 18, 68.	2.7	43
13	Genome-Wide DNA Methylation Patterns and Transcription Analysis in Sheep Muscle. <i>PLoS ONE</i> , 2014, 9, e101853.	2.5	37
14	Copy number variants in the sheep genome detected using multiple approaches. <i>BMC Genomics</i> , 2016, 17, 441.	2.8	27
15	Linkage Disequilibrium Estimation in Low Coverage High-Throughput Sequencing Data. <i>Genetics</i> , 2018, 209, 389-400.	2.9	26
16	The Accuracy, Feasibility and Challenges of Sequencing Short Tandem Repeats Using Next-Generation Sequencing Platforms. <i>PLoS ONE</i> , 2014, 9, e113862.	2.5	24
17	Complete Genome Sequence of the Telford Type S Strain of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	22
18	Mutations in the leptin receptor gene associated with delayed onset of puberty are also associated with decreased ovulation and lambing rates in prolific Davigdale sheep. <i>Reproduction, Fertility and Development</i> , 2016, 28, 1318.	0.4	17

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19	Single-Nucleotide Polymorphisms in the LEPR Gene Are Associated with Divergent Phenotypes for Age at Onset of Puberty in Daisdale Ewes1. <i>Biology of Reproduction</i> , 2014, 90, 33.	2.7	16
20	Genomic signatures of inbreeding in a critically endangered parrot, the kākāpō. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	16
21	An ovine hepatorenal fibrocystic model of a Meckel-like syndrome associated with dysmorphic primary cilia and TMEM67 mutations. <i>Scientific Reports</i> , 2017, 7, 1601.	3.3	15
22	The effects of transcription and recombination on mutational dynamics of short tandem repeats. <i>Nucleic Acids Research</i> , 2018, 46, 1321-1330.	14.5	14
23	Exclusion and Genomic Relatedness Methods for Assignment of Parentage Using Genotyping-by-Sequencing Data. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3239-3247.	1.8	11
24	Application of Low Coverage Genotyping by Sequencing in Selectively Bred Arctic Charr (<i>Salvelinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.8	10
25	Development of a predicted physical map of microsatellite locus positions for pinnipeds, with wider applicability to the Carnivora. <i>Molecular Ecology Resources</i> , 2011, 11, 503-513.	4.8	9
26	GBS Data Identify Pigmentation-Specific Genes of Potential Role in Skin-Photosensitization in Two Tunisian Sheep Breeds. <i>Animals</i> , 2020, 10, 5.	2.3	9
27	PATH: a task for the inference of phylogenies. <i>Bioinformatics</i> , 2002, 18, 646-647.	4.1	7
28	A high density linkage map and quantitative trait loci for tree growth for New Zealand mānuka (<i>Leptospermum scoparium</i>). <i>New Zealand Journal of Crop and Horticultural Science</i> , 2019, 47, 261-272.	1.3	7
29	Beyond the genome: a perspective on the use of DNA methylation profiles as a tool for the livestock industry. <i>Animal Frontiers</i> , 2021, 11, 90-94.	1.7	7
30	Population Connectivity and Traces of Mitochondrial Introgression in New Zealand Black-Billed Gulls (<i>Larus bulleri</i>). <i>Genes</i> , 2018, 9, 544.	2.4	6
31	A Multi-Omic Huntington's Disease Transgenic Sheep-Model Database for Investigating Disease Pathogenesis. <i>Journal of Huntington's Disease</i> , 2021, 10, 423-434.	1.9	6
32	Identifying chromosomal selection sweep regions in facial eczema selection line animals using an ovine 50K SNP array. <i>Animal Genetics</i> , 2014, 45, 240-247.	1.7	5
33	Using genotyping-by-sequencing to predict gender in animals. <i>Animal Genetics</i> , 2019, 50, 307-310.	1.7	5
34	A multiway analysis for identifying high integrity bovine BACs. <i>BMC Genomics</i> , 2009, 10, 46.	2.8	4
35	SOLiD SAGE sequencing shows differential gene expression in jejunal lymph node samples of resistant and susceptible red deer (<i>Cervus elaphus</i>) challenged with <i>Mycobacterium avium</i> subsp. paratuberculosis. <i>Veterinary Immunology and Immunopathology</i> , 2016, 169, 102-110.	1.2	4
36	SNP discovery and population structure analysis in Lassi and Marecha camel breeds using a genotyping by sequencing method. <i>Animal Genetics</i> , 2020, 51, 620-623.	1.7	4

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37	The Use of "Genotyping-by-Sequencing" to Recover Shared Genealogy in Genetically Diverse Eucalyptus Populations. <i>Forests</i> , 2021, 12, 904.	2.1	4
38	Genome-wide DNA methylation analysis: no evidence for stable hemimethylation in the sheep muscle genome. <i>Animal Genetics</i> , 2015, 46, 185-189.	1.7	3
39	Ovine keratome: identification, localisation and genomic organisation of keratin and keratin-associated proteins. <i>Animal Genetics</i> , 2018, 49, 361-370.	1.7	3
40	An entropy-reducing data representation approach for bioinformatic data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	1
41	Genomic Tools for the Identification of Loci Associated with Facial Eczema in New Zealand Sheep. <i>Genes</i> , 2021, 12, 1560.	2.4	0