

Ruedi Fries

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4625121/publications.pdf>

Version: 2024-02-01

103
papers

8,434
citations

66234

42
h-index

46693

89
g-index

111
all docs

111
docs citations

111
times ranked

6601
citing authors

#	ARTICLE	IF	CITATIONS
1	Macrophages in dermal disease progression of phospholipase D4-deficient Fleckvieh calves. <i>Veterinary Pathology</i> , 2022, 59, 319-327.	0.8	2
2	Investigating the impact of reference assembly choice on genomic analyses in a cattle breed. <i>BMC Genomics</i> , 2021, 22, 363.	1.2	15
3	Activation of cryptic splicing in bovine WDR19 is associated with reduced semen quality and male fertility. <i>PLoS Genetics</i> , 2020, 16, e1008804.	1.5	26
4	Title is missing!. , 2020, 16, e1008804.		0
5	Title is missing!. , 2020, 16, e1008804.		0
6	Title is missing!. , 2020, 16, e1008804.		0
7	Title is missing!. , 2020, 16, e1008804.		0
8	Title is missing!. , 2020, 16, e1008804.		0
9	Title is missing!. , 2020, 16, e1008804.		0
10	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019, 9, 6095.	1.6	39
11	Genetics of adaptation in modern chicken. <i>PLoS Genetics</i> , 2019, 15, e1007989.	1.5	81
12	A splice donor variant in CCDC189 is associated with asthenospermia in Nordic Red dairy cattle. <i>BMC Genomics</i> , 2019, 20, 286.	1.2	21
13	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. <i>Nature Genetics</i> , 2018, 50, 362-367.	9.4	286
14	Short communication: Genomic prediction using imputed whole-genome sequence variants in Brown Swiss Cattle. <i>Journal of Dairy Science</i> , 2018, 101, 1292-1296.	1.4	35
15	Maternal placenta modulates a deleterious fetal mutation. <i>Biology of Reproduction</i> , 2017, 97, 249-257.	1.2	6
16	Evaluation of the accuracy of imputed sequence variant genotypes and their utility for causal variant detection in cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 24.	1.2	94
17	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. <i>Current Biology</i> , 2017, 27, 2029-2035.e5.	1.8	75
18	Highly accurate sequence imputation enables precise QTL mapping in Brown Swiss cattle. <i>BMC Genomics</i> , 2017, 18, 999.	1.2	22

#	ARTICLE	IF	CITATIONS
19	Detection of two non-synonymous SNPs in SLC45A2 on BTA20 as candidate causal mutations for oculocutaneous albinism in Braunvieh cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 73.	1.2	17
20	Meta-analysis of sequence-based association studies across three cattle breeds reveals 25 QTL for fat and protein percentages in milk at nucleotide resolution. <i>BMC Genomics</i> , 2017, 18, 853.	1.2	61
21	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. <i>BMC Genomics</i> , 2017, 18, 565.	1.2	116
22	Genome-wide association studies of fertility and calving traits in Brown Swiss cattle using imputed whole-genome sequences. <i>BMC Genomics</i> , 2017, 18, 910.	1.2	36
23	A nonsense mutation in the COL7A1 gene causes epidermolysis bullosa in Vorderwald cattle. <i>BMC Genetics</i> , 2016, 17, 149.	2.7	29
24	A missense mutation in TUBD1 is associated with high juvenile mortality in Braunvieh and Fleckvieh cattle. <i>BMC Genomics</i> , 2016, 17, 400.	1.2	48
25	A frameshift mutation in GON4L is associated with proportionate dwarfism in Fleckvieh cattle. <i>Genetics Selection Evolution</i> , 2016, 48, 25.	1.2	18
26	A multi-trait meta-analysis with imputed sequence variants reveals twelve QTL for mammary gland morphology in Fleckvieh cattle. <i>Genetics Selection Evolution</i> , 2016, 48, 14.	1.2	66
27	Confirmation of a non-synonymous SNP in PNPLA8 as a candidate causal mutation for Weaver syndrome in Brown Swiss cattle. <i>Genetics Selection Evolution</i> , 2016, 48, 21.	1.2	31
28	A frameshift mutation in ARMC3 is associated with a tail stump sperm defect in Swedish Red (Bos) Tj ETQq0 0 0 rgBTJ/Overlock 10 Tf 50	2.7	38
29	Copy number variation in the region harboring SOX9 gene in dogs with testicular/ovotesticular disorder of sex development (78,XX; SRY-negative). <i>Scientific Reports</i> , 2015, 5, 14696.	1.6	22
30	Short communication: Validation of 4 candidate causative trait variants in 2 cattle breeds using targeted sequence imputation. <i>Journal of Dairy Science</i> , 2015, 98, 4162-4167.	1.4	22
31	Homozygous haplotype deficiency reveals deleterious mutations compromising reproductive and rearing success in cattle. <i>BMC Genomics</i> , 2015, 16, 312.	1.2	79
32	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. <i>BMC Genomics</i> , 2014, 15, 823.	1.2	242
33	In frame exon skipping in UBE3B is associated with developmental disorders and increased mortality in cattle. <i>BMC Genomics</i> , 2014, 15, 890.	1.2	47
34	Classic Selective Sweeps Revealed by Massive Sequencing in Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004148.	1.5	254
35	A Nonsense Mutation in TMEM95 Encoding a Nondescript Transmembrane Protein Causes Idiopathic Male Subfertility in Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004044.	1.5	88
36	Evaluation of variant identification methods for whole genome sequencing data in dairy cattle. <i>BMC Genomics</i> , 2014, 15, 948.	1.2	44

#	ARTICLE	IF	CITATIONS
37	A nonsense mutation in PLD4 is associated with a zinc deficiency-like syndrome in Fleckvieh cattle. BMC Genomics, 2014, 15, 623.	1.2	31
38	Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. Nature Genetics, 2014, 46, 858-865.	9.4	697
39	Imputation of high-density genotypes in the Fleckvieh cattle population. Genetics Selection Evolution, 2013, 45, 3.	1.2	85
40	Assessment of the genomic variation in a cattle population by re-sequencing of key animals at low to medium coverage. BMC Genomics, 2013, 14, 446.	1.2	64
41	Ectopic KIT Copy Number Variation Underlies Impaired Migration of Primordial Germ Cells Associated with Gonadal Hypoplasia in Cattle (<i>Bos taurus</i>). PLoS ONE, 2013, 8, e75659.	1.1	29
42	Combining evidence of selection with association analysis increases power to detect regions influencing complex traits in dairy cattle. BMC Genomics, 2012, 13, 48.	1.2	31
43	Identification of QTL for UV-Protective Eye Area Pigmentation in Cattle by Progeny Phenotyping and Genome-Wide Association Analysis. PLoS ONE, 2012, 7, e36346.	1.1	53
44	Identification and Dissection of Four Major QTL Affecting Milk Fat Content in the German Holstein-Friesian Population. PLoS ONE, 2012, 7, e40711.	1.1	85
45	Genome-wide association study uncovers four QTL predisposing to supernumerary teats in cattle. Animal Genetics, 2012, 43, 689-695.	0.6	19
46	Genome-Wide Association Study Identifies Two Major Loci Affecting Calving Ease and Growth-Related Traits in Cattle. Genetics, 2011, 187, 289-297.	1.2	96
47	A Novel Mutation in the Maternally Imprinted PEG3 Domain Results in a Loss of MIMT1 Expression and Causes Abortions and Stillbirths in Cattle (<i>Bos taurus</i>). PLoS ONE, 2010, 5, e15116.	1.1	55
48	Dissection of Genetic Factors Modulating Fetal Growth in Cattle Indicates a Substantial Role of the Non-SMC Condensin I Complex, Subunit G (<i>NCAPG</i>) Gene. Genetics, 2009, 183, 951-964.	1.2	138
49	Haplotypes of the porcine peroxisome proliferator-activated receptor delta gene are associated with backfat thickness. BMC Genetics, 2009, 10, 76.	2.7	15
50	Variation in neighbouring genes of the dopaminergic and serotonergic systems affects feather pecking behaviour of laying hens. Animal Genetics, 2009, 40, 192-199.	0.6	65
51	Whole genome sequencing of a single <i>Bos taurus</i> animal for single nucleotide polymorphism discovery. Genome Biology, 2009, 10, R82.	13.9	88
52	Alleles of the bovine DGAT1 variable number of tandem repeat associated with a milk fat QTL at chromosome 14 can stimulate gene expression. Physiological Genomics, 2006, 25, 116-120.	1.0	25
53	A major genetic component of BSE susceptibility. BMC Biology, 2006, 4, 33.	1.7	98
54	Association of the melanocortin 4 receptor with feed intake and daily gain in F2 Mangalitsa x Pietrain pigs. Animal Genetics, 2006, 37, 245-247.	0.6	37

#	ARTICLE	IF	CITATIONS
55	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. <i>Mammalian Genome</i> , 2006, 17, 58-66.	1.0	54
56	Characterization of the bovine ampk?1 gene. <i>Mammalian Genome</i> , 2005, 16, 194-200.	1.0	5
57	Genomewide Scan for Anal Atresia in Swine Identifies Linkage and Association With a Chromosome Region on <i>Sus scrofa</i> Chromosome 1. <i>Genetics</i> , 2005, 171, 1207-1217.	1.2	7
58	Detection and characterization of SNPs useful for identity control and parentage testing in major European dairy breeds. <i>Animal Genetics</i> , 2004, 35, 44-49.	0.6	94
59	DGAT1 polymorphism in <i>Bos indicus</i> and <i>Bos taurus</i> cattle breeds. <i>Journal of Dairy Research</i> , 2004, 71, 182-187.	0.7	102
60	Evidence for Multiple Alleles at the DGAT1 Locus Better Explains a Quantitative Trait Locus With Major Effect on Milk Fat Content in Cattle. <i>Genetics</i> , 2004, 167, 1873-1881.	1.2	111
61	Assessment of the gene content of the chromosomal regions flanking bovine DGAT1. <i>Genomics</i> , 2004, 83, 172-180.	1.3	18
62	DGAT1 , a new positional and functional candidate gene for intramuscular fat deposition in cattle. <i>Animal Genetics</i> , 2003, 34, 354-357.	0.6	171
63	Molecular cloning, mapping, and functional analysis of the bovine sulfate transporter SLC26a2 gene. <i>Gene</i> , 2003, 319, 161-166.	1.0	8
64	Genomic organization of the DGAT2/MOGAT gene family in cattle (<i>Bos taurus</i>) and other mammals. <i>Cytogenetic and Genome Research</i> , 2003, 102, 42-47.	0.6	26
65	Association of a lysine-232/alanine polymorphism in a bovine gene encoding acyl-CoA:diacylglycerol acyltransferase (DGAT1) with variation at a quantitative trait locus for milk fat content. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9300-9305.	3.3	307
66	Digital DNA signatures for animal tagging. <i>Nature Biotechnology</i> , 2001, 19, 508-508.	9.4	16
67	Chromosomal localization of the genes encoding SCNN1A, BTG1, IFNG and MAOA on chicken chromosome 1 by fluorescence in-situ hybridization. <i>Chromosome Research</i> , 2001, 9, 515-518.	1.0	3
68	Construction and characterization of a gridded cattle BAC library. <i>Animal Genetics</i> , 2000, 31, 347-351.	0.6	23
69	Characterization and chromosomal localization of the chicken avidin gene family. <i>Animal Genetics</i> , 2000, 31, 367-375.	0.6	28
70	Chromosomal mapping of adenosine receptor genes in chicken suggests clustering of two members of the gene family. <i>Chromosome Research</i> , 2000, 8, 173-176.	1.0	2
71	A DNA polymorphism influencing $\hat{\pm}$ (1,2)fucosyltransferase activity of the pig FUT1 enzyme determines susceptibility of small intestinal epithelium to <i>Escherichia coli</i> F18 adhesion. <i>Immunogenetics</i> , 2000, 52, 129-136.	1.2	122
72	Structural Analysis and Transcript Processing of the Bovine Proteolipid Protein (PLP) Gene. <i>DNA Sequence</i> , 2000, 10, 379-385.	0.7	1

#	ARTICLE	IF	CITATIONS
73	The dynamics of chromosome evolution in birds and mammals. <i>Nature</i> , 1999, 402, 411-413.	13.7	280
74	Construction and characterization of a porcine P1-derived artificial chromosome (PAC) library covering 3.2 genome equivalents and cytogenetical assignment of six type I and type II loci. <i>Mammalian Genome</i> , 1999, 10, 569-572.	1.0	68
75	Molecular cloning and chromosomal assignment of the porcine 54 and 56 kDa vacuolar H(+)-ATPase subunit gene (V-ATPase). <i>Mammalian Genome</i> , 1999, 10, 266-270.	1.0	10
76	High-resolution, human–bovine comparative mapping based on a closed YAC contig spanning the bovine mh locus. <i>Mammalian Genome</i> , 1999, 10, 289-293.	1.0	3
77	A 5Å– genome coverage bovine BAC library: production, characterization, and distribution. <i>Mammalian Genome</i> , 1999, 10, 706-709.	1.0	53
78	A bovine YAC library containing four- to five-fold genome equivalents. <i>Mammalian Genome</i> , 1999, 10, 837-838.	1.0	25
79	The cattle interleukin-13 gene: genomic organization, chromosomal location, and evolution of the promoter. <i>Immunogenetics</i> , 1999, 49, 872-878.	1.2	14
80	Evolutionarily conserved telomeric location of BBC1 and MC1R on a microchromosome questions the identity of MC1R and a pigmentation locus on chromosome 1 in chicken. <i>Chromosome Research</i> , 1998, 6, 651-654.	1.0	18
81	SHORT COMMUNICATIONS. Mapping of five members of the cyclin gene family on chicken chromosomes by FISH. <i>Chromosome Research</i> , 1998, 6, 231-238.	1.0	15
82	A deletion in the bovine myostatin gene causes the double“ muscled phenotype in cattle. <i>Nature Genetics</i> , 1997, 17, 71-74.	9.4	1,323
83	Cosmid-derived markers anchoring the bovine genetic map to the physical map. <i>Mammalian Genome</i> , 1997, 8, 29-36.	1.0	34
84	Polymorphic CA-microsatellites for the integration of the bovine genetic and physical map. <i>Mammalian Genome</i> , 1997, 8, 52-55.	1.0	23
85	Two $\hat{\pm}(1,2)$ fucosyltransferase genes on porcine Chromosome 6q11 are closely linked to the blood group inhibitor (S) and Escherichia coli F18 receptor (ECF18R) loci. <i>Mammalian Genome</i> , 1997, 8, 736-741.	1.0	130
86	The bovine glutamine synthase gene (GLUL) maps to 10q33 and a pseudogene (GLULP) to 16q21. <i>Mammalian Genome</i> , 1997, 8, 794-795.	1.0	0
87	Chromosomal localization and molecular characterization of 53 cosmid-derived bovine microsatellites. <i>Mammalian Genome</i> , 1995, 6, 629-635.	1.0	71
88	Combined Q banding and fluorescence in situ hybridization for the identification of bovine chromosomes 1 to 7. <i>Cytogenetic and Genome Research</i> , 1995, 69, 1-6.	0.6	37
89	Isolation of the human genomic brain-2/N-Oct 3 gene (POUF3) and assignment to chromosome 6q16. <i>Genomics</i> , 1995, 26, 272-280.	1.3	32
90	Comparative Genome Map of Human and Cattle. <i>Genomics</i> , 1995, 27, 489-496.	1.3	315

#	ARTICLE	IF	CITATIONS
91	The bovine lactoferrin gene (LTF) maps to Chromosome 22 and syntenic group U12. <i>Mammalian Genome</i> , 1994, 5, 486-489.	1.0	22
92	A genetic linkage map of the bovine genome. <i>Nature Genetics</i> , 1994, 6, 227-235.	9.4	537
93	Establishment of a Partially Informative Porcine Somatic Cell Hybrid Panel and Assignment of the Loci for Transition Protein 2 (TNP2) and Protamine 1 (PRM1) to Chromosome 3 and Polyubiquitin (UBC) to Chromosome 14. <i>Genomics</i> , 1994, 21, 558-566.	1.3	23
94	The bovine genome map. <i>Mammalian Genome</i> , 1993, 4, 405-428.	1.0	167
95	Physically mapped, cosmid-derived microsatellite markers as anchor loci on bovine chromosomes. <i>Mammalian Genome</i> , 1993, 4, 720-727.	1.0	163
96	Isolation, sequencing, and expression analysis of a bovine apolipoprotein E (APOE) cDNA and chromosomal localization of the APOE locus. <i>Mammalian Genome</i> , 1993, 4, 53-57.	1.0	10
97	Mapping of bovine markers CYP21, PRL, and BOLA DRBP1 by genetic linkage analysis in reference pedigrees. <i>Genomics</i> , 1992, 14, 526-528.	1.3	39
98	RASA contains a polymorphic microsatellite and maps to bovine syntenic group U22 on Chromosome 7q2.4-qter. <i>Mammalian Genome</i> , 1992, 3, 559-563.	1.0	15
99	Mapping of bovine cyokeratin sequences to four different sites on three chromosomes. <i>Cytogenetic and Genome Research</i> , 1991, 57, 135-141.	0.6	34
100	The thyroglobulin gene is syntenic with the MYC and MOS protooncogenes and carbonic anhydrase II and maps to chromosome 14 in cattle. <i>Cytogenetic and Genome Research</i> , 1990, 53, 32-36.	0.6	22
101	The bovine genome contains polymorphic microsatellites. <i>Genomics</i> , 1990, 8, 403-406.	1.3	82
102	The loci for parathyroid hormone and γ -globin are closely linked and map to chromosome 15 in cattle. <i>Genomics</i> , 1988, 3, 302-307.	1.3	38
103	Assignment of the porcine major histocompatibility complex to chromosome 7 by in situ hybridization. <i>Cytogenetic and Genome Research</i> , 1985, 39, 206-209.	0.6	61