

Ruedi Fries

List of Publications by Year in descending order

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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	A deletion in the bovine myostatin gene causes the double-muscling phenotype in cattle. <i>Nature Genetics</i> , 1997, 17, 71-74.	9.4	1,323
2	Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. <i>Nature Genetics</i> , 2014, 46, 858-865.	9.4	697
3	A genetic linkage map of the bovine genome. <i>Nature Genetics</i> , 1994, 6, 227-235.	9.4	537
4	Comparative Genome Map of Human and Cattle. <i>Genomics</i> , 1995, 27, 489-496.	1.3	315
5	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
6	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
7	The dynamics of chromosome evolution in birds and mammals. <i>Nature</i> , 1999, 402, 411-413.	13.7	280
8	Classic Selective Sweeps Revealed by Massive Sequencing in Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004148.	1.5	254
9	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
10	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
11	The bovine genome map. <i>Mammalian Genome</i> , 1993, 4, 405-428.	1.0	167
12	Physically mapped, cosmid-derived microsatellite markers as anchor loci on bovine chromosomes. <i>Mammalian Genome</i> , 1993, 4, 720-727.	1.0	163
13	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. <i>Genetics</i> , 2009, 183, 951-964.	1.2	138
14	Two $\alpha(1,2)$ 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
15	A DNA polymorphism influencing $\alpha(1,2)$ fucosyltransferase activity of the pig FUT1 enzyme determines susceptibility of small intestinal epithelium to Escherichia coli F18 adhesion. <i>Immunogenetics</i> , 2000, 52, 129-136.	1.2	122
16	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. <i>BMC Genomics</i> , 2017, 18, 565.	1.2	116
17	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
18	DGAT1 polymorphism in Bos indicus and Bos taurus cattle breeds. <i>Journal of Dairy Research</i> , 2004, 71, 182-187.	0.7	102

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19	A major genetic component of BSE susceptibility. <i>BMC Biology</i> , 2006, 4, 33.	1.7	98
20	Genome-Wide Association Study Identifies Two Major Loci Affecting Calving Ease and Growth-Related Traits in Cattle. <i>Genetics</i> , 2011, 187, 289-297.	1.2	96
21	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
22	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
23	Whole genome sequencing of a single <i>Bos taurus</i> animal for single nucleotide polymorphism discovery. <i>Genome Biology</i> , 2009, 10, R82.	13.9	88
24	A Nonsense Mutation in <i>TMEM95</i> Encoding a Nondescript Transmembrane Protein Causes Idiopathic Male Subfertility in Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004044.	1.5	88
25	Identification and Dissection of Four Major QTL Affecting Milk Fat Content in the German Holstein-Friesian Population. <i>PLoS ONE</i> , 2012, 7, e40711.	1.1	85
26	Imputation of high-density genotypes in the Fleckvieh cattle population. <i>Genetics Selection Evolution</i> , 2013, 45, 3.	1.2	85
27	The bovine genome contains polymorphic microsatellites. <i>Genomics</i> , 1990, 8, 403-406.	1.3	82
28	Genetics of adaptation in modern chicken. <i>PLoS Genetics</i> , 2019, 15, e1007989.	1.5	81
29	Homozygous haplotype deficiency reveals deleterious mutations compromising reproductive and rearing success in cattle. <i>BMC Genomics</i> , 2015, 16, 312.	1.2	79
30	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. <i>Current Biology</i> , 2017, 27, 2029-2035.e5.	1.8	75
31	Chromosomal localization and molecular characterization of 53 cosmid-derived bovine microsatellites. <i>Mammalian Genome</i> , 1995, 6, 629-635.	1.0	71
32	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
33	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
34	Variation in neighbouring genes of the dopaminergic and serotonergic systems affects feather pecking behaviour of laying hens. <i>Animal Genetics</i> , 2009, 40, 192-199.	0.6	65
35	Assessment of the genomic variation in a cattle population by re-sequencing of key animals at low to medium coverage. <i>BMC Genomics</i> , 2013, 14, 446.	1.2	64
36	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

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37	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
38	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>). <i>PLoS ONE</i> , 2010, 5, e15116.	1.1	55
39	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
40	A 5Å— genome coverage bovine BAC library: production, characterization, and distribution. <i>Mammalian Genome</i> , 1999, 10, 706-709.	1.0	53
41	Identification of QTL for UV-Protective Eye Area Pigmentation in Cattle by Progeny Phenotyping and Genome-Wide Association Analysis. <i>PLoS ONE</i> , 2012, 7, e36346.	1.1	53
42	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
43	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
44	Evaluation of variant identification methods for whole genome sequencing data in dairy cattle. <i>BMC Genomics</i> , 2014, 15, 948.	1.2	44
45	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
46	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019, 9, 6095.	1.6	39
47	The loci for parathyroid hormone and β -globin are closely linked and map to chromosome 15 in cattle. <i>Genomics</i> , 1988, 3, 302-307.	1.3	38
48	A frameshift mutation in ARMC3 is associated with a tail stump sperm defect in Swedish Red (<i>Bos</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.7	38
49	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
50	Association of the melanocortin 4 receptor with feed intake and daily gain in F2 Mangalitsa x Pietrain pigs. <i>Animal Genetics</i> , 2006, 37, 245-247.	0.6	37
51	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
52	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
53	Mapping of bovine cytokeratin sequences to four different sites on three chromosomes. <i>Cytogenetic and Genome Research</i> , 1991, 57, 135-141.	0.6	34
54	Cosmid-derived markers anchoring the bovine genetic map to the physical map. <i>Mammalian Genome</i> , 1997, 8, 29-36.	1.0	34

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55	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
56	Combining evidence of selection with association analysis increases power to detect regions influencing complex traits in dairy cattle. <i>BMC Genomics</i> , 2012, 13, 48.	1.2	31
57	A nonsense mutation in PLD4 is associated with a zinc deficiency-like syndrome in Fleckvieh cattle. <i>BMC Genomics</i> , 2014, 15, 623.	1.2	31
58	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
59	Ectopic KIT Copy Number Variation Underlies Impaired Migration of Primordial Germ Cells Associated with Gonadal Hypoplasia in Cattle (<i>Bos taurus</i>). <i>PLoS ONE</i> , 2013, 8, e75659.	1.1	29
60	A nonsense mutation in the COL7A1 gene causes epidermolysis bullosa in Vorderwald cattle. <i>BMC Genetics</i> , 2016, 17, 149.	2.7	29
61	Characterization and chromosomal localization of the chicken avidin gene family. <i>Animal Genetics</i> , 2000, 31, 367-375.	0.6	28
62	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
63	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
64	A bovine YAC library containing four- to five-fold genome equivalents. <i>Mammalian Genome</i> , 1999, 10, 837-838.	1.0	25
65	Alleles of the bovine DGAT1 variable number of tandem repeat associated with a milk fat QTL at chromosome 14 can stimulate gene expression. <i>Physiological Genomics</i> , 2006, 25, 116-120.	1.0	25
66	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
67	Polymorphic CA-microsatellites for the integration of the bovine genetic and physical map. <i>Mammalian Genome</i> , 1997, 8, 52-55.	1.0	23
68	Construction and characterization of a gridded cattle BAC library. <i>Animal Genetics</i> , 2000, 31, 347-351.	0.6	23
69	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
70	The bovine lactoferrin gene (LTF) maps to Chromosome 22 and syntenic group U12. <i>Mammalian Genome</i> , 1994, 5, 486-489.	1.0	22
71	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
72	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

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73	Highly accurate sequence imputation enables precise QTL mapping in Brown Swiss cattle. <i>BMC Genomics</i> , 2017, 18, 999.	1.2	22
74	A splice donor variant in <i>CCDC189</i> is associated with asthenospermia in Nordic Red dairy cattle. <i>BMC Genomics</i> , 2019, 20, 286.	1.2	21
75	Genome-wide association study uncovers four QTL predisposing to supernumerary teats in cattle. <i>Animal Genetics</i> , 2012, 43, 689-695.	0.6	19
76	Evolutionarily conserved telomeric location of <i>BBC1</i> and <i>MC1R</i> on a microchromosome questions the identity of <i>MC1R</i> and a pigmentation locus on chromosome 1 in chicken. <i>Chromosome Research</i> , 1998, 6, 651-654.	1.0	18
77	Assessment of the gene content of the chromosomal regions flanking bovine <i>DGAT1</i> . <i>Genomics</i> , 2004, 83, 172-180.	1.3	18
78	A frameshift mutation in <i>GON4L</i> is associated with proportionate dwarfism in Fleckvieh cattle. <i>Genetics Selection Evolution</i> , 2016, 48, 25.	1.2	18
79	Detection of two non-synonymous SNPs in <i>SLC45A2</i> on <i>BTA20</i> as candidate causal mutations for oculocutaneous albinism in Braunvieh cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 73.	1.2	17
80	Digital DNA signatures for animal tagging. <i>Nature Biotechnology</i> , 2001, 19, 508-508.	9.4	16
81	<i>RASA</i> 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
82	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
83	Haplotypes of the porcine peroxisome proliferator-activated receptor delta gene are associated with backfat thickness. <i>BMC Genetics</i> , 2009, 10, 76.	2.7	15
84	Investigating the impact of reference assembly choice on genomic analyses in a cattle breed. <i>BMC Genomics</i> , 2021, 22, 363.	1.2	15
85	The cattle interleukin-13 gene: genomic organization, chromosomal location, and evolution of the promoter. <i>Immunogenetics</i> , 1999, 49, 872-878.	1.2	14
86	Isolation, sequencing, and expression analysis of a bovine apolipoprotein E (<i>APOE</i>) cDNA and chromosomal localization of the <i>APOE</i> locus. <i>Mammalian Genome</i> , 1993, 4, 53-57.	1.0	10
87	Molecular cloning and chromosomal assignment of the porcine 54 and 56 kDa vacuolar H(+)-ATPase subunit gene (<i>V-ATPase</i>). <i>Mammalian Genome</i> , 1999, 10, 266-270.	1.0	10
88	Molecular cloning, mapping, and functional analysis of the bovine sulfate transporter <i>SLC26a2</i> gene. <i>Gene</i> , 2003, 319, 161-166.	1.0	8
89	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
90	Maternal placenta modulates a deleterious fetal mutation. <i>Biology of Reproduction</i> , 2017, 97, 249-257.	1.2	6

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91	Characterization of the bovine ampk?1 gene. Mammalian Genome, 2005, 16, 194-200.	1.0	5
92	High-resolution, human–bovine comparative mapping based on a closed YAC contig spanning the bovine mh locus. Mammalian Genome, 1999, 10, 289-293.	1.0	3
93	Chromosomal localization of the genes encoding SCNN1A, BTG1, IFNG and MAOA on chicken chromosome 1 by fluorescence in-situ hybridization. Chromosome Research, 2001, 9, 515-518.	1.0	3
94	Chromosomal mapping of adenosine receptor genes in chicken suggests clustering of two members of the gene family. Chromosome Research, 2000, 8, 173-176.	1.0	2
95	Macrophages in dermal disease progression of phospholipase D4–deficient Fleckvieh calves. Veterinary Pathology, 2022, 59, 319-327.	0.8	2
96	Structural Analysis and Transcript Processing of the Bovine Proteolipid Protein (PLP) Gene. DNA Sequence, 2000, 10, 379-385.	0.7	1
97	The bovine glutamine synthase gene (GLUL) maps to 10q33 and a pseudogene (GLULP) to 16q21. Mammalian Genome, 1997, 8, 794-795.	1.0	0
98	Title is missing!. , 2020, 16, e1008804.		0
99	Title is missing!. , 2020, 16, e1008804.		0
100	Title is missing!. , 2020, 16, e1008804.		0
101	Title is missing!. , 2020, 16, e1008804.		0
102	Title is missing!. , 2020, 16, e1008804.		0
103	Title is missing!. , 2020, 16, e1008804.		0