

# Christa Kuehn

## List of Publications by Year in descending order

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107  
papers

4,343  
citations

126858

33  
h-index

118793

62  
g-index

111  
all docs

111  
docs citations

111  
times ranked

7819  
citing authors

#	ARTICLE	IF	CITATIONS
1	A medium-density genetic linkage map of the bovine genome. <i>Mammalian Genome</i> , 1997, 8, 21-28.	1.0	313
2	Suppression of high transverse momentum D mesons in central Pb-Pb collisions at $\sqrt{s_{\mathrm{NN}}}=2.76\mathrm{TeV}$ . <i>Journal of High Energy Physics</i> , 2012, 2012, 1.	1.6	228
3	Charmonium and $e+e^{-}$ pair photoproduction at mid-rapidity in ultra-peripheral Pb-Pb collisions at $\sqrt{s_{\mathrm{NN}}}=2.76\mathrm{TeV}$ . <i>European Physical Journal C</i> , 2013, 73, 2617.	1.4	203
4	Measurement of inelastic, single- and double-diffraction cross sections in proton-proton collisions at the LHC with ALICE. <i>European Physical Journal C</i> , 2013, 73, 2456.	1.4	202
5	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
6	Identification of novel transcripts and noncoding RNAs in bovine skin by deep next generation sequencing. <i>BMC Genomics</i> , 2013, 14, 789.	1.2	152
7	Heat stress directly impairs gut integrity and recruits distinct immune cell populations into the bovine intestine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10333-10338.	3.3	148
8	Dissection of Genetic Factors Modulating Fetal Growth in Cattle Indicates a Substantial Role of the Non-SMC Condensin I Complex, Subunit G (NCAPG) Gene. <i>Genetics</i> , 2009, 183, 951-964.	1.2	138
9	Energy dependence of the transverse momentum distributions of charged particles in pp collisions measured by ALICE. <i>European Physical Journal C</i> , 2013, 73, 2662.	1.4	101
10	A genome-wide association study indicates LCORL/NCAPG as a candidate locus for withers height in German Warmblood horses. <i>Animal Genetics</i> , 2013, 44, 467-471.	0.6	101
11	Measurement of quarkonium production at forward rapidity in $\sqrt{s}=7\mathrm{TeV}$ pp collisions at $\sqrt{s}=7\mathrm{TeV}$ . <i>European Physical Journal C</i> , 2014, 74, 2974.	1.4	89
12	Production of $K_S^0$ and $\phi$ in Pb-Pb collisions at $\sqrt{s_{\mathrm{NN}}}=5.02\mathrm{TeV}$ . <i>European Physical Journal C</i> , 2016, 76, 245.	1.4	89
13	Growth of Long Range Forward-Backward Multiplicity Correlations with Centrality in Au-Au Collisions at $\sqrt{s_{\mathrm{NN}}}=2.76\mathrm{TeV}$ . <i>Physical Review Letters</i> , 2009, 103, 172301.	2.9	79
14	A systems biology approach using metabolomic data reveals genes and pathways interacting to modulate divergent growth in cattle. <i>BMC Genomics</i> , 2013, 14, 798.	1.2	76
15	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. <i>Genome Biology</i> , 2020, 21, 285.	3.8	74
16	Mapping of QTL for Body Conformation and Behavior in Cattle. <i>Genetics</i> , 2003, 94, 496-506.		72
17	Metabolomic profiles indicate distinct physiological pathways affected by two loci with major divergent effect on <i>Bos taurus</i> growth and lipid deposition. <i>Physiological Genomics</i> , 2010, 42A, 79-88.	1.0	70
18	The SNP c.1326T>G in the non-SMC condensin I complex, subunit G (NCAPG) gene encoding a p.Ile442Met variant is associated with an increase in body frame size at puberty in cattle. <i>Animal Genetics</i> , 2011, 42, 650-655.	0.6	69

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19	An experimental approach for studying the genetic and physiological background of nutrient transformation in cattle with respect to nutrient secretion and accretion type. <i>Archives Animal Breeding</i> , 2002, 45, 317-330.	0.5	63
20	Systems Biology Analysis Merging Phenotype, Metabolomic and Genomic Data Identifies Non-SMC Condensin I Complex, Subunit G (NCAPG) and Cellular Maintenance Processes as Major Contributors to Genetic Variability in Bovine Feed Efficiency. <i>PLoS ONE</i> , 2015, 10, e0124574.	1.1	62
21	Comparative expression profiling of <i>E. coli</i> and <i>S. aureus</i> inoculated primary mammary gland cells sampled from cows with different genetic predispositions for somatic cell score. <i>Genetics Selection Evolution</i> , 2011, 43, 24.	1.2	59
22	Mining long noncoding RNA in livestock. <i>Animal Genetics</i> , 2017, 48, 3-18.	0.6	59
23	Induction of Allograft Tolerance by Monoclonal CD3 Antibodies: A Matter of Timing. <i>American Journal of Transplantation</i> , 2012, 12, 2909-2919.	2.6	57
24	Beef versus dairy cattle: a comparison of feed conversion, carcass composition, and meat quality. <i>Archives Animal Breeding</i> , 2007, 50, 59-70.	0.5	56
25	Association of an ACSL1 gene variant with polyunsaturated fatty acids in bovine skeletal muscle. <i>BMC Genetics</i> , 2011, 12, 96.	2.7	55
26	A QTL for the degree of spotting in cattle shows synteny with the KIT locus on chromosome 6. , 1999, 90, 629-634.		49
27	A mammary gland EST showing linkage disequilibrium to a milk production QTL on bovine Chromosome 14. <i>Mammalian Genome</i> , 2001, 12, 646-650.	1.0	43
28	Mapping of quantitative trait loci for lactation persistency traits in German Holstein dairy cattle. <i>Journal of Animal Breeding and Genetics</i> , 2006, 123, 89-96.	0.8	41
29	Dominance and parent-of-origin effects of coding and non-coding alleles at the acylCoA-diacylglycerol-acyltransferase (DGAT1) gene on milk production traits in German Holstein cows. <i>BMC Genetics</i> , 2007, 8, 62.	2.7	41
30	Selection signatures in four German warmblood horse breeds: Tracing breeding history in the modern sport horse. <i>PLoS ONE</i> , 2019, 14, e0215913.	1.1	41
31	Novel transcripts discovered by mining genomic DNA from defined regions of bovine chromosome 6. <i>BMC Genomics</i> , 2009, 10, 186.	1.2	37
32	Comparison of estimated breeding values, daughter yield deviations and de-regressed proofs within a whole genome scan for QTL. <i>Journal of Animal Breeding and Genetics</i> , 2001, 118, 357-370.	0.8	36
33	Monitoring the immune response to vaccination with an inactivated vaccine associated to bovine neonatal pancytopenia by deep sequencing transcriptome analysis in cattle. <i>Veterinary Research</i> , 2013, 44, 93.	1.1	36
34	Characterization of functional traits with focus on udder health in heifers with divergent paternally inherited haplotypes on BTA18. <i>BMC Veterinary Research</i> , 2019, 15, 241.	0.7	36
35	A male bovine linkage map for the ADR granddaughter design. <i>Journal of Animal Breeding and Genetics</i> , 2000, 117, 289-306.	0.8	34
36	Increased expression of thyroid hormone responsive protein (THRSP) is the result but not the cause of higher intramuscular fat content in cattle. <i>International Journal of Biological Sciences</i> , 2017, 13, 532-544.	2.6	34

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37	Biological Network Approach for the Identification of Regulatory Long Non-Coding RNAs Associated With Metabolic Efficiency in Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 1130.	1.1	34
38	Differences in milk production, glucose metabolism, and carcass composition of 2 Charolais $\times$ Holstein F2 families derived from reciprocal paternal and maternal grandsire crosses. <i>Journal of Dairy Science</i> , 2010, 93, 3007-3018.	1.4	33
39	In vivo model to study the impact of genetic variation on clinical outcome of mastitis in uniparous dairy cows. <i>BMC Veterinary Research</i> , 2020, 16, 33.	0.7	33
40	Detection of single-nucleotide polymorphisms coding for three ovine prion protein variants by primer extension assay and capillary electrophoresis. <i>Electrophoresis</i> , 2003, 24, 634-638.	1.3	31
41	Multiplicity and transverse momentum evolution of charge-dependent correlations in pp, p $\bar{p}$ , and p $\bar{p}$ collisions at the LHC. <i>European Physical Journal C</i> , 2016, 76, 86.	1.4	30
42	Genetic selection for bovine chromosome 18 haplotypes associated with divergent somatic cell score affects postpartum reproductive and metabolic performance. <i>Journal of Dairy Science</i> , 2019, 102, 9983-9994.	1.4	30
43	Glucose-Dependent Insulin Response and Milk Production in Heifers Within a Segregating Resource Family Population. <i>Journal of Dairy Science</i> , 2007, 90, 3247-3254.	1.4	29
44	Multiple QTL on chromosome six in dairy cattle affecting yield and content traits. <i>Journal of Animal Breeding and Genetics</i> , 2002, 119, 69-82.	0.8	28
45	A whole genome scan for differences in recombination rates among three <i>Bos taurus</i> breeds. <i>Mammalian Genome</i> , 2001, 12, 724-728.	1.0	25
46	A gene-based high-resolution comparative radiation hybrid map as a framework for genome sequence assembly of a bovine chromosome 6 region associated with QTL for growth, body composition, and milk performance traits. <i>BMC Genomics</i> , 2006, 7, 53.	1.2	25
47	Long noncoding RNAs are associated with metabolic and cellular processes in the jejunum mucosa of pre-weaning calves in response to different diets. <i>Oncotarget</i> , 2018, 9, 21052-21069.	0.8	25
48	Targeted Construction of a High-Resolution, Integrated, Comprehensive, and Comparative Map for a Region Specific to Bovine Chromosome 6 Based on Radiation Hybrid Mapping. <i>Genomics</i> , 2002, 79, 768-776.	1.3	21
49	99th Dahlem Conference on Infection, Inflammation and Chronic Inflammatory Disorders: Immune therapies of type 1 diabetes: new opportunities based on the hygiene hypothesis. <i>Clinical and Experimental Immunology</i> , 2010, 160, 106-112.	1.1	20
50	Gene expression profile of <i>Musculus longissimus dorsi</i> in bulls of a Charolais $\times$ Holstein F2 -cross with divergent intramuscular fat content. <i>Genomics Data</i> , 2016, 7, 131-133.	1.3	19
51	Detection of QTL for body weight and body fat content in mice using genetic markers. <i>Journal of Animal Breeding and Genetics</i> , 1996, 113, 373-379.	0.8	17
52	Different milk diets have substantial effects on the jejunal mucosal immune system of pre-weaning calves, as demonstrated by whole transcriptome sequencing. <i>Scientific Reports</i> , 2018, 8, 1693.	1.6	17
53	Plasma ghrelin is positively associated with body fat, liver fat and milk fat content but not with feed intake of dairy cows after parturition. <i>Journal of Endocrinology</i> , 2013, 216, 217-229.	1.2	16
54	In-Depth Analysis Reveals Production of Circular RNAs from Non-Coding Sequences. <i>Cells</i> , 2020, 9, 1806.	1.8	16

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55	Multiple splice variants within the bovine silver homologue (SILV) gene affecting coat color in cattle indicate a function additional to fibril formation in melanophores. BMC Genomics, 2007, 8, 335.	1.2	15
56	Analysis of pig transcriptomes suggests a global regulation mechanism enabling temporary bursts of circular RNAs. RNA Biology, 2019, 16, 1190-1204.	1.5	15
57	Beyond Back Splicing, a Still Poorly Explored World: Non-Canonical Circular RNAs. Genes, 2020, 11, 1111.	1.0	15
58	Hepatic Transcriptome Analysis Identifies Divergent Pathogen-Specific Targeting-Strategies to Modulate the Innate Immune System in Response to Intramammary Infection. Frontiers in Immunology, 2020, 11, 715.	2.2	15
59	The Mammalian Cervical Vertebrae Blueprint Depends on the <i>Tbr1</i> ( <i>brachyury</i> ) Gene. Genetics, 2015, 199, 873-883.	1.2	14
60	Detection of genetic variants affecting cattle behaviour and their impact on milk production: a genome-wide association study. Animal Genetics, 2016, 47, 12-18.	0.6	14
61	TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM: Factors influencing bovine intramuscular adipose tissue development and cellularity1. Journal of Animal Science, 2017, 95, 2244-2254.	0.2	13
62	Agouti Signaling Protein and Its Receptors as Potential Molecular Markers for Intramuscular and Body Fat Deposition in Cattle. Frontiers in Physiology, 2018, 9, 172.	1.3	13
63	Epistatic interactions between at least three loci determine the "erect-tail" phenotype in cattle. Genetics Selection Evolution, 2016, 48, 26.	1.2	12
64	Consensus and comprehensive linkage maps of the bovine sex chromosomes. Animal Genetics, 2001, 32, 115-117.	0.6	11
65	Identification of a two-marker-haplotype on Bos taurus autosome 18 associated with somatic cell score in German Holstein cattle. BMC Genetics, 2009, 10, 50.	2.7	11
66	Genomic prediction of unordered categorical traits: an application to subpopulation assignment in German Warmblood horses. Genetics Selection Evolution, 2016, 48, 13.	1.2	11
67	Different mitochondrial DNA copy number in liver and mammary gland of lactating cows with divergent genetic background for milk production. Molecular Biology Reports, 2018, 45, 1209-1218.	1.0	11
68	Analysis of structure and gene expression of bovine CCDC3 gene indicates a function in fat metabolism. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2010, 156, 19-25.	0.7	10
69	Unmapped reads from cattle RNAseq data: A source for missing and misassembled sequences in the reference assemblies and for detection of pathogens in the host. Genomics, 2017, 109, 36-42.	1.3	10
70	Identification and Annotation of Potential Function of Regulatory Antisense Long Non-Coding RNAs Related to Feed Efficiency in Bos taurus Bulls. International Journal of Molecular Sciences, 2020, 21, 3292.	1.8	10
71	Comparative Analysis of the Circular Transcriptome in Muscle, Liver, and Testis in Three Livestock Species. Frontiers in Genetics, 2021, 12, 665153.	1.1	10
72	TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM: Factors influencing bovine intramuscular adipose tissue development and cellularity. Journal of Animal Science, 2017, 95, 2244.	0.2	10

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73	Refined positioning of a quantitative trait locus affecting somatic cell score on chromosome 18 in the German Holstein using linkage disequilibrium. <i>Journal of Dairy Science</i> , 2009, 92, 4046-4054.	1.4	9
74	Evaluation of a replacement method for mammary gland biopsies by comparing gene expression in udder tissue and mammary epithelial cells isolated from milk. <i>Research in Veterinary Science</i> , 2012, 93, 970-974.	0.9	9
75	Marker assisted selection of heifers improved milk somatic cell count compared to selection on conventional pedigree breeding values. <i>Archives Animal Breeding</i> , 2008, 51, 23-32.	0.5	9
76	Bovine neonatal pancytopenia (BNP): novel insights into the incidence, vaccination-associated epidemiological factors and a potential genetic predisposition for clinical and subclinical cases. <i>Research in Veterinary Science</i> , 2014, 96, 537-542.	0.9	8
77	312 Consequences of birth weight differences on carcass traits as well as muscle and adipose tissue cellularity in crossbred bulls. <i>Journal of Animal Science</i> , 2017, 95, 154-154.	0.2	8
78	Variants of the bovine retinoic acid receptor-related orphan receptor C gene are in linkage disequilibrium with QTL for milk production traits on chromosome 3 in a beef × dairy crossbred population. <i>Archives Animal Breeding</i> , 2012, 55, 346-355.	0.5	8
79	Indication of Premelanosome Protein (PMEL) Expression Outside of Pigmented Bovine Skin Suggests Functions Beyond Eumelanogenesis. <i>Genes</i> , 2020, 11, 788.	1.0	7
80	Differentially Expressed miRNA-Gene Targets Related to Intramuscular Fat in Musculus Longissimus Dorsi of Charolais × Holstein F2-Crossbred Bulls. <i>Genes</i> , 2020, 11, 700.	1.0	7
81	Single-cell RNA sequencing of freshly isolated bovine milk cells and cultured primary mammary epithelial cells. <i>Scientific Data</i> , 2021, 8, 177.	2.4	7
82	Assignment of the locus for arachnomelia syndrome to bovine chromosome 23 in Simmental cattle. <i>Animal Genetics</i> , 2009, 40, 894-899.	0.6	6
83	Energy expenditure, urea kinetics, and body weight gain within a segregating resource family population. <i>Journal of Dairy Science</i> , 2010, 93, 5118-5128.	1.4	6
84	Vertebral and spinal dysplasia: A novel dominantly inherited congenital defect in Holstein cattle. <i>Veterinary Journal</i> , 2015, 204, 287-292.	0.6	6
85	A novel RNAseq-assisted method for MHC class I genotyping in a non-model species applied to a lethal vaccination-induced alloimmune disease. <i>BMC Genomics</i> , 2016, 17, 365.	1.2	6
86	Annotation of novel transcripts putatively relevant for bovine fat metabolism. <i>Molecular Biology Reports</i> , 2011, 38, 2975-2986.	1.0	5
87	Retinol binding protein 4 abundance in plasma and tissues is related to body fat deposition in cattle. <i>Scientific Reports</i> , 2019, 9, 8056.	1.6	5
88	Identification of Regulatory Functions of LncRNAs Associated With <i>T. circumcincta</i> Infection in Adult Sheep. <i>Frontiers in Genetics</i> , 2021, 12, 685341.	1.1	5
89	Cows selected for divergent mastitis susceptibility display a differential liver transcriptome profile after experimental <i>Staphylococcus aureus</i> mammary gland inoculation. <i>Journal of Dairy Science</i> , 2020, 103, 6364-6373.	1.4	5
90	Metabogenomic analysis to functionally annotate the regulatory role of long non-coding RNAs in the liver of cows with different nutrient partitioning phenotype. <i>Genomics</i> , 2022, 114, 202-214.	1.3	5

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91	Mapping of the bovine blood group systems J, N <sup>2</sup> , R <sup>2</sup> , and Z show evidence for oligo-genetic inheritance. <i>Animal Genetics</i> , 2002, 33, 107-117.	0.6	4
92	Investigations in the character of QTL affecting negatively correlated milk traits. <i>Journal of Animal Breeding and Genetics</i> , 2004, 121, 40-51.	0.8	4
93	Development and evaluation of a milk protein transcript depletion method for differential transcriptome analysis in mammary gland tissue. <i>BMC Genomics</i> , 2019, 20, 400.	1.2	4
94	A 50-kb deletion disrupting the RSPO2 gene is associated with tetradysmelia in Holstein Friesian cattle. <i>Genetics Selection Evolution</i> , 2020, 52, 68.	1.2	4
95	1089 Mitochondrial biogenesis and DNA content in metabolically tissues of lactating cows with divergent milk production. <i>Journal of Animal Science</i> , 2016, 94, 522-523.	0.2	2
96	0786 Factors influencing bovine intramuscular adipose tissue development and cellularity. <i>Journal of Animal Science</i> , 2016, 94, 378-378.	0.2	2
97	Metabolomics in Animal Breeding. , 2012, , 107-123.		2
98	Different Blood Cell-Derived Transcriptome Signatures in Cows Exposed to Vaccination Pre- or Postpartum. <i>PLoS ONE</i> , 2015, 10, e0136927.	1.1	2
99	Genetic and genomic characterization followed by single-step genomic evaluation of withers height in German Warmblood horses. <i>Journal of Applied Genetics</i> , 2022, 63, 369.	1.0	2
100	Angiotensin-2 (ANGPT2) as a candidate gene for somatic cell score in German Holstein cattle. <i>Journal of Dairy Science</i> , 2013, 96, 5388-5397.	1.4	1
101	From the comparative study of a circRNA originating from an mammalian ATXN2L intron to understanding the genesis of intron lariat-derived circRNAs. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194815.	0.9	1
102	Short communication: Evaluation of bovine milk residues from routine milk testing programs as DNA source for genotyping. <i>Journal of Dairy Science</i> , 2012, 95, 5436-5441.	1.4	0
103	Ultrasonographic Investigation of the Mechanisms Involved in Menstrual Cramps. <i>Journal of Minimally Invasive Gynecology</i> , 2015, 22, S16.	0.3	0
104	P6016 Epistatic interactions of more than two loci are involved in the rat-tail phenotype in cattle. <i>Journal of Animal Science</i> , 2016, 94, 156-156.	0.2	0
105	P3025 RNA depletion for highly abundant transcripts in bovine mammary gland improves the sensitivity of RNaseq analysis. <i>Journal of Animal Science</i> , 2016, 94, 64-64.	0.2	0
106	1467 RNaseq-based whole transcriptome analysis in the jejunum of preweaned calves under different milk feeding regimes. <i>Journal of Animal Science</i> , 2016, 94, 712-712.	0.2	0
107	Assignment of the fibroblast growth factor 10 (FGF10) gene to bovine chromosome 20q16-->q17 by fluorescence in situ hybridization and somatic cell panel analysis. <i>Cytogenetic and Genome Research</i> , 2005, 109, 533.	0.6	0