Karl Schellander

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Exosomal and Non-Exosomal Transport of Extra-Cellular microRNAs in Follicular Fluid: Implications for Bovine Oocyte Developmental Competence. PLoS ONE, 2013, 8, e78505.	1.1	257
2	Large-scale transcriptional analysis of bovine embryo biopsies in relation to pregnancy success after transfer to recipients. Physiological Genomics, 2006, 28, 84-96.	1.0	211
3	Molecular Mechanisms and Pathways Involved in Bovine Embryonic Genome Activation and Their Regulation by Alternative In Vivo and In Vitro Culture Conditions1. Biology of Reproduction, 2012, 87, 100.	1.2	130
4	Identification and characterization of miRNAs expressed in the bovine ovary. BMC Genomics, 2009, 10, 443.	1.2	129
5	Identification and expression profiling of microRNAs during bovine oocyte maturation using heterologous approach. Molecular Reproduction and Development, 2009, 76, 665-677.	1.0	129
6	Cellular and exosome mediated molecular defense mechanism in bovine granulosa cells exposed to oxidative stress. PLoS ONE, 2017, 12, e0187569.	1.1	106
7	Liposome-Mediated DNA uptake by sperm cells. Molecular Reproduction and Development, 1991, 30, 194-200.	1.0	99
8	Molecular and subcellular characterisation of oocytes screened for their developmental competence based on glucose-6-phosphate dehydrogenase activity. Reproduction, 2008, 135, 197-212.	1.1	96
9	Bovine pretransfer endometrium and embryo transcriptome fingerprints as predictors of pregnancy success after embryo transfer. Physiological Genomics, 2010, 42, 201-218.	1.0	94
10	MicroRNA Expression Profile in Bovine Granulosa Cells of Preovulatory Dominant and Subordinate Follicles during the Late Follicular Phase of the Estrous Cycle. PLoS ONE, 2015, 10, e0125912.	1.1	93
11	Gene expression profile of cumulus cells derived from cumulus - oocyte complexes matured either in vivo or in vitro. Reproduction, Fertility and Development, 2009, 21, 451.	0.1	83
12	Clinical and subclinical endometritis induced alterations in bovine endometrial transcriptome and miRNome profile. BMC Genomics, 2016, 17, 218.	1.2	76
13	Genome-Wide DNA Methylation Patterns of Bovine Blastocysts Developed In Vivo from Embryos Completed Different Stages of Development In Vitro. PLoS ONE, 2015, 10, e0140467.	1.1	76
14	QTL for microstructural and biophysical muscle properties and body composition in pigs. BMC Genetics, 2006, 7, 15.	2.7	74
15	Oxidative and endoplasmic reticulum stress defense mechanisms of bovine granulosa cells exposed to heat stress. Theriogenology, 2018, 110, 130-141.	0.9	74
16	The Expression Pattern of microRNAs in Granulosa Cells of Subordinate and Dominant Follicles during the Early Luteal Phase of the Bovine Estrous Cycle. PLoS ONE, 2014, 9, e106795.	1.1	73
17	Identification of genes differentially expressed during prenatal development of skeletal muscle in two pig breeds differing in muscularity. BMC Developmental Biology, 2007, 7, 109.	2.1	71
18	Bovine embryo survival under oxidativeâ€stress conditions is associated with activity of the NRF2â€mediated oxidativeâ€stressâ€response pathway. Molecular Reproduction and Development, 2014, 81, 497-513.	1.0	70

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19	Age-related changes in relative expression stability of commonly used housekeeping genes in selected porcine tissues. BMC Research Notes, 2011, 4, 441.	0.6	65
20	MicroRNAs: tiny molecules with a significant role in mammalian follicular and oocyte development. Reproduction, 2018, 155, R121-R135.	1.1	64
21	Combined line-cross and half-sib QTL analysis in Duroc–Pietrain population. Mammalian Genome, 2008, 19, 429-438.	1.0	63
22	Sulforaphane causes a major epigenetic repression of myostatin in porcine satellite cells. Epigenetics, 2012, 7, 1379-1390.	1.3	57
23	Controlled ovarian hyperstimulation induced changes in the expression of circulatory miRNA in bovine follicular fluid and blood plasma. Journal of Ovarian Research, 2015, 8, 81.	1.3	55
24	Endogenous and Exogenous Modulation of Nrf2 Mediated Oxidative Stress Response in Bovine Granulosa Cells: Potential Implication for Ovarian Function. International Journal of Molecular Sciences, 2019, 20, 1635.	1.8	53
25	Effect of the microenvironment and embryo density on developmental characteristics and gene expression profile of bovine preimplantative embryos cultured in vitro. Reproduction, 2009, 137, 415-425.	1.1	51
26	Genome-wide DNA methylation patterns of bovine blastocysts derived from in vivo embryos subjected to in vitro culture before, during or after embryonic genome activation. BMC Genomics, 2018, 19, 424.	1.2	50
27	MicroRNA-130b is involved in bovine granulosa and cumulus cells function, oocyte maturation and blastocyst formation. Journal of Ovarian Research, 2017, 10, 37.	1.3	49
28	Alterations in transcript abundance of bovine oocytes recovered at growth and dominance phases of the first follicular wave. BMC Developmental Biology, 2007, 7, 90.	2.1	47
29	MicroRNA-183-96-182 Cluster Regulates Bovine Granulosa Cell Proliferation and Cell Cycle Transition by Coordinately Targeting FOXO11. Biology of Reproduction, 2016, 94, 127.	1.2	47
30	A Genome-Wide Association Study in Large White and Landrace Pig Populations for Number Piglets Born Alive. PLoS ONE, 2015, 10, e0117468.	1.1	45
31	Quantification of DNA binding, uptake, transmission and expression in bovine sperm mediated gene transfer by RT-PCR: Effect of transfection reagent and DNA architecture. Theriogenology, 2007, 67, 1097-1107.	0.9	44
32	Evaluation of suitable reference genes for gene expression studies in porcine alveolar macrophages in response to LPS and LTA. BMC Research Notes, 2012, 5, 107.	0.6	43
33	Differential Expression of miRNAs and Their Target mRNAs in Endometria Prior to Maternal Recognition of Pregnancy Associates with Endometrial Receptivity for In Vivo- and In Vitro-Produced Bovine Embryos1. Biology of Reproduction, 2014, 91, 135.	1.2	43
34	Extracellular vesicle-coupled miRNA profiles in follicular fluid of cows with divergent post-calving metabolic status. Scientific Reports, 2019, 9, 12851.	1.6	43
35	MicroRNA 17–92 cluster regulates proliferation and differentiation of bovine granulosa cells by targeting PTEN and BMPR2 genes. Cell and Tissue Research, 2016, 366, 219-230.	1.5	42
36	Association study and expression analysis of porcine ESR1 as a candidate gene for boar fertility and sperm quality. Animal Reproduction Science, 2011, 128, 11-21.	0.5	41

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37	Expression Profiling of Muscle Reveals Transcripts Differentially Expressed in Muscle That Affect Water-Holding Capacity of Pork. Journal of Agricultural and Food Chemistry, 2008, 56, 10311-10317.	2.4	40
38	Transcriptional response of the bovine endometrium and embryo to endometrial polymorphonuclear neutrophil infiltration as an indicator of subclinical inflammation of the uterine environment. Reproduction, Fertility and Development, 2012, 24, 778.	0.1	40
39	LPS-induced expression of CD14 in the TRIF pathway is epigenetically regulated by sulforaphane in porcine pulmonary alveolar macrophages. Innate Immunity, 2016, 22, 682-695.	1.1	40
40	Degradation and oxidation postmortem of myofibrillar proteins in porcine skeleton muscle revealed by high resolution mass spectrometric proteome analysis. International Journal of Mass Spectrometry, 2011, 305, 217-227.	0.7	39
41	Gene Expression and DNA-Methylation of Bovine Pretransfer Endometrium Depending on Its Receptivity after In Vitro-Produced Embryo Transfer. PLoS ONE, 2012, 7, e42402.	1.1	39
42	Evaluation of suitable reference genes for gene expression studies in porcine PBMCs in response to LPS and LTA. BMC Research Notes, 2013, 6, 56.	0.6	39
43	Expression dynamics of Toll-like receptors mRNA and cytokines in porcine peripheral blood mononuclear cells stimulated by bacterial lipopolysaccharide. Veterinary Immunology and Immunopathology, 2012, 147, 211-222.	0.5	36
44	Deciphering transcriptome profiles of peripheral blood mononuclear cells in response to PRRSV vaccination in pigs. BMC Genomics, 2016, 17, 641.	1.2	36
45	Aberrant placenta gene expression pattern in bovine pregnancies established after transfer of cloned or in vitro produced embryos. Physiological Genomics, 2013, 45, 28-46.	1.0	35
46	Sulforaphane Epigenetically Regulates Innate Immune Responses of Porcine Monocyte-Derived Dendritic Cells Induced with Lipopolysaccharide. PLoS ONE, 2015, 10, e0121574.	1.1	34
47	Identification of expression QTL (eQTL) of genes expressed in porcine M. longissimus dorsi and associated with meat quality traits. BMC Genomics, 2010, 11, 572.	1.2	32
48	Association study and expression analysis of CD9 as candidate gene for boar sperm quality and fertility traits. Animal Reproduction Science, 2011, 125, 170-179.	0.5	32
49	Transcriptome profile of bovine elongated conceptus obtained from SCNT and IVP pregnancies. Molecular Reproduction and Development, 2013, 80, 315-333.	1.0	32
50	RNA Deep Sequencing Reveals Novel Candidate Genes and Polymorphisms in Boar Testis and Liver Tissues with Divergent Androstenone Levels. PLoS ONE, 2013, 8, e63259.	1.1	32
51	Alveolar macrophage phagocytic activity is enhanced with LPS priming, and combined stimulation of LPS and lipoteichoic acid synergistically induce pro-inflammatory cytokines in pigs. Innate Immunity, 2013, 19, 631-643.	1.1	31
52	Potential role of microRNAs in mammalian female fertility. Reproduction, Fertility and Development, 2017, 29, 8.	0.1	31
53	Prediction of oocyte developmental competence in ovine using glucose-6-phosphate dehydrogenase (G6PDH) activity determined at retrieval time. Journal of Assisted Reproduction and Genetics, 2012, 29, 153-158.	1.2	30
54	MicroRNA-424/503 cluster members regulate bovine granulosa cell proliferation and cell cycle progression by targeting SMAD7 gene through activin signalling pathway. Journal of Ovarian Research, 2018, 11, 34.	1.3	30

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55	Stage-specific expressed sequence tags obtained during preimplantation bovine development by differential display RT-PCR and suppression subtractive hybridization. Prenatal Diagnosis, 2002, 22, 1135-1142.	1.1	29
56	Association and expression quantitative trait loci (eQTL) analysis of porcine AMBP, GC and PPP1R3B genes with meat quality traits. Molecular Biology Reports, 2012, 39, 4809-4821.	1.0	28
57	Regulation of Nrf2 and NF-κB during lead toxicity in bovine granulosa cells. Cell and Tissue Research, 2020, 380, 643-655.	1.5	28
58	Dielectrophoretic behavior of in vitro-derived bovine metaphase II oocytes and zygotes and its relation to in vitro embryonic developmental competence and mRNA expression pattern. Reproduction, 2007, 133, 931-946.	1.1	27
59	Integrative Analysis of Metabolomic, Proteomic and Genomic Data to Reveal Functional Pathways and Candidate Genes for Drip Loss in Pigs. International Journal of Molecular Sciences, 2016, 17, 1426.	1.8	27
60	Transcriptome Fingerprint of Bovine 2-Cell Stage Blastomeres Is Directly Correlated with the Individual Developmental Competence of the Corresponding Sister Blastomere1. Biology of Reproduction, 2012, 87, 154.	1.2	26
61	PBMC transcriptome profiles identifies potential candidate genes and functional networks controlling the innate and the adaptive immune response to PRRSV vaccine in Pietrain pig. PLoS ONE, 2017, 12, e0171828.	1.1	26
62	Identification of the Novel Candidate Genes and Variants in Boar Liver Tissues with Divergent Skatole Levels Using RNA Deep Sequencing. PLoS ONE, 2013, 8, e72298.	1.1	26
63	Expression of Toll-like receptors and downstream genes in lipopolysaccharide-induced porcine alveolar macrophages. Veterinary Immunology and Immunopathology, 2012, 146, 62-73.	0.5	25
64	Sulforaphane protects granulosa cells against oxidative stress via activation of NRF2-ARE pathway. Cell and Tissue Research, 2018, 374, 629-641.	1.5	25
65	Detection of quantitative trait loci for carcass traits in the pig by using AFLP. Mammalian Genome, 2002, 13, 206-210.	1.0	24
66	QTL for the heritable inverted teat defect in pigs. Mammalian Genome, 2008, 19, 127-138.	1.0	24
67	Extracellular vesicles shuttle protective messages against heat stress in bovine granulosa cells. Scientific Reports, 2020, 10, 15824.	1.6	24
68	Identification of functional candidate genes for body composition by expression analyses and evidencing impact by association analysis and mapping. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2005, 1730, 31-40.	2.4	23
69	Application of MALDI-TOF-Mass Spectrometry to Proteome Analysis Using Stain-Free Gel Electrophoresis. Topics in Current Chemistry, 2012, 331, 37-54.	4.0	23
70	Oviductal, endometrial and embryonic gene expression patterns as molecular clues for pregnancy establishment. Animal Reproduction Science, 2012, 134, 9-18.	0.5	23
71	A genetical genomics approach reveals new candidates and confirms known candidate genes for drip loss in a porcine resource population. Mammalian Genome, 2013, 24, 416-426.	1.0	22
72	Genome-wide association analyses for boar taint components and testicular traits revealed regions having pleiotropic effects. BMC Genetics, 2015, 16, 36.	2.7	20

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73	Expression of homeobox-containing genes in cDNA libraries derived from cattle oocytes and preimplantation stage embryo. Molecular Reproduction and Development, 2001, 60, 297-301.	1.0	18
74	Identification and quantification of differentially expressed transcripts in in vitro-produced bovine preimplantation stage embryos. Molecular Reproduction and Development, 2003, 66, 105-114.	1.0	18
75	Quantitative expression analysis of blastocyst-derived gene transcripts in preimplantation developmental stages of in vitro-produced bovine embryos using real-time polymerase chain reaction technology. Reproduction, Fertility and Development, 2004, 16, 753.	0.1	18
76	Molecular mechanism underlying the differential MYF6 expression in postnatal skeletal muscle of Duroc and Pietrain breeds. Gene, 2011, 486, 8-14.	1.0	18
77	Massive deregulation of miRNAs from nuclear reprogramming errors during trophoblast differentiation for placentogenesis in cloned pregnancy. BMC Genomics, 2014, 15, 43.	1.2	18
78	Exploring maternal serum microRNAs during early pregnancy in cattle. Theriogenology, 2018, 121, 196-203.	0.9	18
79	Molecular characterization and evidencing of the porcine CRH gene as a functional-positional candidate for growth and body composition. Biochemical and Biophysical Research Communications, 2006, 342, 394-405.	1.0	17
80	Depletion of BIRC6 leads to retarded bovine early embryonic development and blastocyst formation in vitro. Reproduction, Fertility and Development, 2010, 22, 564.	0.1	17
81	Mapping of quantitative trait loci for mycoplasma and tetanus antibodies and interferon-gamma in a porcine F2 DurocÂ×ÂPietrain resource population. Mammalian Genome, 2010, 21, 409-418.	1.0	16
82	Epistatic QTL pairs associated with meat quality and carcass composition traits in a porcine Duroc × Pietrain population. Genetics Selection Evolution, 2010, 42, 39.	1.2	16
83	Detection of quantitative trait loci affecting serum cholesterol, LDL, HDL, and triglyceride in pigs. BMC Genetics, 2011, 12, 62.	2.7	16
84	Zona pellucida birefringence correlates with developmental capacity of bovine oocytes classified by maturational environment, COC morphology and G6PDH activity. Reproduction, Fertility and Development, 2012, 24, 568.	0.1	13
85	Embryo transcriptome response to environmental factors: Implication for its survival under suboptimal conditions. Animal Reproduction Science, 2014, 149, 30-38.	0.5	13
86	Hyaluronic acid and epidermal growth factor improved the bovine embryo quality by regulating the DNA methylation and expression patterns of the focal adhesion pathway. PLoS ONE, 2019, 14, e0223753.	1.1	11
87	Comparison of the innate immune responses of porcine monocyte-derived dendritic cells and splenic dendritic cells stimulated with LPS. Innate Immunity, 2015, 21, 242-254.	1.1	10
88	Sexual dimorphic expression and release of transcription factors in bovine embryos exposed to oxidative stress. Molecular Reproduction and Development, 2019, 86, 2005-2019.	1.0	10
89	Quercetin supports bovine preimplantation embryo development under oxidative stress condition via activation of the Nrf2 signalling pathway. Reproduction in Domestic Animals, 2020, 55, 1275-1285.	0.6	10
90	Age-related changes in phagocytic activity and production of pro-inflammatory cytokines by lipopolysaccharide stimulated porcine alveolar macrophages. Cytokine, 2012, 60, 707-717.	1.4	9

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91	Developmental competence of equine oocytes: impacts of zona pellucida birefringence and maternally derived transcript expression. Reproduction, Fertility and Development, 2014, 26, 441.	0.1	9
92	Metabolism-associated genome-wide epigenetic changes in bovine oocytes during early lactation. Scientific Reports, 2020, 10, 2345.	1.6	9
93	NRF2-mediated signaling is a master regulator of transcription factors in bovine granulosa cells under oxidative stress condition. Cell and Tissue Research, 2021, 385, 769-783.	1.5	9
94	The global gene expression outline of the bovine blastocyst: reflector of environmental conditions and predictor of developmental capacity. BMC Genomics, 2021, 22, 408.	1.2	9
95	Pathway Based Analysis of Genes and Interactions Influencing Porcine Testis Samples from Boars with Divergent Androstenone Content in Back Fat. PLoS ONE, 2014, 9, e91077.	1.1	9
96	Preliminary study of FMO1, FMO5, CYP21, ESR1, PLIN2 and SULT2A1 as candidate gene for compounds related to boar taint. Meat Science, 2015, 108, 67-73.	2.7	6
97	Association and expression analysis of porcine HNF1A gene related to meat and carcass quality traits. Meat Science, 2013, 94, 474-479.	2.7	5
98	Identification of gene co-expression clusters in liver tissues from multiple porcine populations with high and low backfat androstenone phenotype. BMC Genetics, 2015, 16, 21.	2.7	5
99	Transcriptome profile and association study revealed STAT3 gene as a potential quality marker of bovine gametes. Zygote, 2020, 28, 116-130.	0.5	5
100	The regulatory role of miR-20a in bovine cumulus cells and its contribution to oocyte maturation. Zygote, 2021, 29, 435-444.	0.5	4
101	Identifying genes associated with quantitative traits in pigs: integrating quantitative and molecular approaches for meat quality. Italian Journal of Animal Science, 2009, 8, 19-25.	0.8	3
102	Oregano essential oil showed limited effects on pigs' carcass quality and haematology whereas a transcriptome analysis revealed significant modulations in the jejunum and the ileum. Journal of Animal Physiology and Animal Nutrition, 2022, 106, 1017-1035.	1.0	3
103	Sulforaphane Enhanced Proliferation of Porcine Satellite Cells via Epigenetic Augmentation of SMAD7. Animals, 2022, 12, 1365.	1.0	3
104	The extent of the abundance of exosomal and nonâ€exosomal extracellular miRNAs in the bovine follicular fluid. Reproduction in Domestic Animals, 2022, 57, 1208-1217.	0.6	1
105	Heterogeneous expression of Toll-like receptors genes in lymphoid tissues of different ages pigs. Gene Reports, 2019, 15, 100401.	0.4	0