Xiaolong Wang

List of Publications by Year
in descending order

50	1,983	236833	265120
papers	citations	25	42
		h-index	g-index

52	52	52	1811
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Generation of gene-modified goats targeting MSTN and FGF5 via zygote injection of CRISPR/Cas9 system. Scientific Reports, 2015, 5, 13878.	1.6	151
2	Whole-genome sequencing of eight goat populations for the detection of selection signatures underlying production and adaptive traits. Scientific Reports, 2016, 6, 38932.	1.6	132
3	Discovery of cashmere goat (Capra hircus) microRNAs in skin and hair follicles by Solexa sequencing. BMC Genomics, 2013, 14, 511.	1.2	108
4	Rumen Bacterial Diversity of 80 to 110-Day-Old Goats Using 16S rRNA Sequencing. PLoS ONE, 2015, 10, e0117811.	1.1	98
5	Comparative Transcriptome Analysis of Fetal Skin Reveals Key Genes Related to Hair Follicle Morphogenesis in Cashmere Goats. PLoS ONE, 2016, 11, e0151118.	1.1	97
6	The origin of domestication genes in goats. Science Advances, 2020, 6, eaaz5216.	4.7	86
7	Disruption of FGF5 in Cashmere Goats Using CRISPR/Cas9 Results in More Secondary Hair Follicles and Longer Fibers. PLoS ONE, 2016, 11, e0164640.	1.1	75
8	Enhancing prime editing by Csy4-mediated processing of pegRNA. Cell Research, 2021, 31, 1134-1136.	5.7	74
9	Transcriptome profile analysis of adipose tissues from fat and short-tailed sheep. Gene, 2014, 549, 252-257.	1.0	71
10	Multiplex gene editing via CRISPR/Cas9 exhibits desirable muscle hypertrophy without detectable off-target effects in sheep. Scientific Reports, 2016, 6, 32271.	1.6	68
11	Characterization and Comparison of Microbiota in the Gastrointestinal Tracts of the Goat (Capra) Tj ETQq1 1 0.784314 rgBT /Overloc	1.5	67
12	Sheep and Goat Genome Engineering: From Random Transgenesis to the CRISPR Era. Frontiers in Genetics, 2019, 10, 750.	1.1	60
13	<scp>CRISPR</scp>/Cas9â€mediated <i><scp>MSTN</scp></i> disruption and heritable mutagenesis in goats causes increased body mass. Animal Genetics, 2018, 49, 43-51.	0.6	55
14	Exploring the Spatial-Temporal Microbiota of Compound Stomachs in a Pre-weaned Goat Model. Frontiers in Microbiology, 2018, 9, 1846.	1.5	54
15	Integrative analysis reveals ncRNA-mediated molecular regulatory network driving secondary hair follicle regression in cashmere goats. BMC Genomics, 2018, 19, 222.	1.2	53
16	Enhancement of prime editing via xrRNA motif-joined pegRNA. Nature Communications, 2022, 13, 1856.	5.8	51
17	Comparative transcriptome analysis reveals potentially novel roles of Homeobox genes in adipose deposition in fat-tailed sheep. Scientific Reports, 2017, 7, 14491.	1.6	50
18	Integrating miRNA and mRNA Expression Profiling Uncovers miRNAs Underlying Fat Deposition in Sheep. BioMed Research International, 2017, 2017, 1-11.	0.9	38

#	Article	IF	Citations
19	Whole-genome bisulfite sequencing of goat skins identifies signatures associated with hair cycling. BMC Genomics, 2018, 19, 638.	1.2	37
20	Low incidence of SNVs and indels in trio genomes of Cas9-mediated multiplex edited sheep. BMC Genomics, 2018, 19, 397.	1.2	36
21	Efficient generation of goats with defined point mutation (I397V) in GDF9 through CRISPR/Cas9. Reproduction, Fertility and Development, 2018, 30, 307.	0.1	36
22	Dynamics and stabilization of the rumen microbiome in yearling Tibetan sheep. Scientific Reports, 2019, 9, 19620.	1.6	35
23	Trio-Based Deep Sequencing Reveals a Low Incidence of Off-Target Mutations in the Offspring of Genetically Edited Goats. Frontiers in Genetics, 2018, 9, 449.	1.1	33
24	Comparative proteomic analyses using iTRAQ-labeling provides insights into fiber diversity in sheep and goats. Journal of Proteomics, 2018, 172, 82-88.	1.2	29
25	Programmable Base Editing of the Sheep Genome Revealed No Genome-Wide Off-Target Mutations. Frontiers in Genetics, 2019, 10, 215.	1.1	28
26	RNA-seq reveals transcriptome changes in goats following myostatin gene knockout. PLoS ONE, 2017, 12, e0187966.	1.1	27
27	Base pair editing in goat: nonsense codon introgression into *FGF5* results in longer hair. FEBS Journal, 2019, 286, 4675-4692.	2.2	25
28	The genetic diversity of seven indigenous Chinese goat breeds. Small Ruminant Research, 2008, 74, 231-237.	0.6	24
29	Effect of dietary concentrate to forage ratios on ruminal bacterial and anaerobic fungal populations of cashmere goats. Anaerobe, 2019, 59, 118-125.	1.0	24
30	Ruminal metagenomic analyses of goat data reveals potential functional microbiota by supplementation with essential oil-cobalt complexes. BMC Microbiology, 2019, 19, 30.	1.3	23
31	Trends towards revealing the genetic architecture of sheep tail patterning: Promising genes and investigatory pathways. Animal Genetics, 2021, 52, 799-812.	0.6	23
32	IRE1α regulates skeletal muscle regeneration through myostatin mRNA decay. Journal of Clinical Investigation, 2021, 131, .	3.9	22
33	Dietary supplementation with Essential-oils-cobalt for improving growth performance, meat quality and skin cell capacity of goats. Scientific Reports, 2018, 8, 11634.	1.6	21
34	Highly efficient generation of sheep with a defined FecBB mutation via adenine base editing. Genetics Selection Evolution, 2020, 52, 35.	1.2	21
35	Tβ4-overexpression based on the piggyBac transposon system in cashmere goats alters hair fiber characteristics. Transgenic Research, 2017, 26, 77-85.	1.3	18
36	Cyclic expression of Lhx2 is involved in secondary hair follicle development in cashmere goat. Gene Expression Patterns, 2014, 16, 31-35.	0.3	17

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37	Synchronous profiling and analysis of mRNAs and ncRNAs in the dermal papilla cells from cashmere goats. BMC Genomics, 2019, 20, 512.	1.2	17
38	Discovery of SNPs in RXFP2 related to horn types in sheep. Small Ruminant Research, 2014, 116, 133-136.	0.6	16
39	Redesigning small ruminant genomes with CRISPR toolkit: Overview and perspectives. Theriogenology, 2020, 147, 25-33.	0.9	15
40	A non‑synonymous mutation in <i><scp>GDF</scp>9</i> is highly associated with litter size in cashmere goats. Animal Genetics, 2016, 47, 630-631.	0.6	14
41	mRNA transcription and protein expression of PPARÎ³, FAS, and HSL in different parts of the carcass between fat-tailed and thin-tailed sheep. Electronic Journal of Biotechnology, 2015, 18, 215-220.	1.2	7
42	More abundant and healthier meat: will the MSTN editing epitome empower the commercialization of gene editing in livestock?. Science China Life Sciences, 2022, 65, 448-450.	2.3	7
43	Characterization of growth phenotypes and gastrointestinal tract microbiota in sheep fed with caragana. Journal of Applied Microbiology, 2021, 131, 2763-2779.	1.4	6
44	Optimized Cas9:sgRNA delivery efficiently generates biallelic MSTN knockout sheep without affecting meat quality. BMC Genomics, 2022, 23, 348.	1.2	6
45	PPARÎ³, FAS, HSL mRNA and protein expression during Tan sheep fat-tail development. Electronic Journal of Biotechnology, 2015, 18, 122-127.	1.2	5
46	CRISPR/Cas9-mediated MSTN gene editing induced mitochondrial alterations in C2C12 myoblast cells. Electronic Journal of Biotechnology, 2019, 40, 30-39.	1.2	5
47	Cytosine and adenine deaminase base-editors induce broad and nonspecific changes in gene expression and splicing. Communications Biology, 2021, 4, 882.	2.0	5
48	Optimisation of the clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9 : single-guide RNA (sgRNA) delivery system in a goat model. Reproduction, Fertility and Development, 2019, 31, 1533.	0.1	4
49	Meeting report on the 2019 international symposium of molecular design breeding in animals (Yangling, China) with the consensus on genome-editing agricultural animals and their regulation. Transgenic Research, 2020, 29, 263-265.	1.3	2
50	Deletions in the KAP6-1 gene are associated with fiber traits in cashmere-producing goats. Animal Biotechnology, 2021, , 1-7.	0.7	0