

# Xiaolong Wang

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

50  
papers

1,019  
citations

20  
h-index

30  
g-index

52  
ext. papers

1,646  
ext. citations

4.8  
avg. IF

4.1  
L-index

#	Paper	IF	Citations
50	Enhancement of prime editing via xrRNA motif-joined pegRNA.. <i>Nature Communications</i> , <b>2022</b> , 13, 1856	17.4	2
49	Optimized Cas9:sgRNA delivery efficiently generates biallelic MSTN knockout sheep without affecting meat quality.. <i>BMC Genomics</i> , <b>2022</b> , 23, 348	4.5	1
48	Enhancing prime editing by Csy4-mediated processing of pegRNA. <i>Cell Research</i> , <b>2021</b> , 31, 1134-1136	24.7	17
47	Characterization of growth phenotypes and gastrointestinal tract microbiota in sheep fed with caragana. <i>Journal of Applied Microbiology</i> , <b>2021</b> , 131, 2763-2779	4.7	3
46	Deletions in the gene are associated with fiber traits in cashmere-producing goats. <i>Animal Biotechnology</i> , <b>2021</b> , 1-7	1.4	
45	Cytosine and adenine deaminase base-editors induce broad and nonspecific changes in gene expression and splicing. <i>Communications Biology</i> , <b>2021</b> , 4, 882	6.7	1
44	More abundant and healthier meat: will the MSTN editing epitome empower the commercialization of gene editing in livestock?. <i>Science China Life Sciences</i> , <b>2021</b> , 1	8.5	3
43	Trends towards revealing the genetic architecture of sheep tail patterning: Promising genes and investigatory pathways. <i>Animal Genetics</i> , <b>2021</b> , 52, 799-812	2.5	4
42	The origin of domestication genes in goats. <i>Science Advances</i> , <b>2020</b> , 6, eaaz5216	14.3	28
41	Highly efficient generation of sheep with a defined FecB mutation via adenine base editing. <i>Genetics Selection Evolution</i> , <b>2020</b> , 52, 35	4.9	7
40	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. <i>Transgenic Research</i> , <b>2020</b> , 29, 263-265	3.3	2
39	Redesigning small ruminant genomes with CRISPR toolkit: Overview and perspectives. <i>Theriogenology</i> , <b>2020</b> , 147, 25-33	2.8	6
38	Characterization and Comparison of Microbiota in the Gastrointestinal Tracts of the Goat () During Prewaning Development. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2125	5.7	22
37	Synchronous profiling and analysis of mRNAs and ncRNAs in the dermal papilla cells from cashmere goats. <i>BMC Genomics</i> , <b>2019</b> , 20, 512	4.5	6
36	Effect of dietary concentrate to forage ratios on ruminal bacterial and anaerobic fungal populations of cashmere goats. <i>Anaerobe</i> , <b>2019</b> , 59, 118-125	2.8	11
35	CRISPR/Cas9-mediated MSTN gene editing induced mitochondrial alterations in C2C12 myoblast cells. <i>Electronic Journal of Biotechnology</i> , <b>2019</b> , 40, 30-39	3.1	2
34	Programmable Base Editing of the Sheep Genome Revealed No Genome-Wide Off-Target Mutations. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 215	4.5	19

33	Ruminal metagenomic analyses of goat data reveals potential functional microbiota by supplementation with essential oil-cobalt complexes. <i>BMC Microbiology</i> , <b>2019</b> , 19, 30	4.5	9
32	Sheep and Goat Genome Engineering: From Random Transgenesis to the CRISPR Era. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 750	4.5	27
31	Base pair editing in goat: nonsense codon introgression into FGF5 results in longer hair. <i>FEBS Journal</i> , <b>2019</b> , 286, 4675-4692	5.7	12
30	Optimisation of the clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9 : single-guide RNA (sgRNA) delivery system in a goat model. <i>Reproduction, Fertility and Development</i> , <b>2019</b> , 31, 1533-1537	1.8	3
29	Dynamics and stabilization of the rumen microbiome in yearling Tibetan sheep. <i>Scientific Reports</i> , <b>2019</b> , 9, 19620	4.9	19
28	CRISPR/Cas9-mediated MSTN disruption and heritable mutagenesis in goats causes increased body mass. <i>Animal Genetics</i> , <b>2018</b> , 49, 43-51	2.5	41
27	Comparative proteomic analyses using iTRAQ-labeling provides insights into fiber diversity in sheep and goats. <i>Journal of Proteomics</i> , <b>2018</b> , 172, 82-88	3.9	19
26	Dietary supplementation with Essential-oils-cobalt for improving growth performance, meat quality and skin cell capacity of goats. <i>Scientific Reports</i> , <b>2018</b> , 8, 11634	4.9	12
25	Low incidence of SNVs and indels in trio genomes of Cas9-mediated multiplex edited sheep. <i>BMC Genomics</i> , <b>2018</b> , 19, 397	4.5	20
24	Integrative analysis reveals ncRNA-mediated molecular regulatory network driving secondary hair follicle regression in cashmere goats. <i>BMC Genomics</i> , <b>2018</b> , 19, 222	4.5	21
23	Exploring the Spatial-Temporal Microbiota of Compound Stomachs in a Pre-weaned Goat Model. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1846	5.7	23
22	Efficient generation of goats with defined point mutation (I397V) in GDF9 through CRISPR/Cas9. <i>Reproduction, Fertility and Development</i> , <b>2018</b> , 30, 307-312	1.8	20
21	Trio-Based Deep Sequencing Reveals a Low Incidence of Off-Target Mutations in the Offspring of Genetically Edited Goats. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 449	4.5	22
20	Whole-genome bisulfite sequencing of goat skins identifies signatures associated with hair cycling. <i>BMC Genomics</i> , <b>2018</b> , 19, 638	4.5	18
19	T $\beta$ -overexpression based on the piggyBac transposon system in cashmere goats alters hair fiber characteristics. <i>Transgenic Research</i> , <b>2017</b> , 26, 77-85	3.3	15
18	Integrating miRNA and mRNA Expression Profiling Uncovers miRNAs Underlying Fat Deposition in Sheep. <i>BioMed Research International</i> , <b>2017</b> , 2017, 1857580	3	21
17	Comparative transcriptome analysis reveals potentially novel roles of Homeobox genes in adipose deposition in fat-tailed sheep. <i>Scientific Reports</i> , <b>2017</b> , 7, 14491	4.9	21
16	RNA-seq reveals transcriptome changes in goats following myostatin gene knockout. <i>PLoS ONE</i> , <b>2017</b> , 12, e0187966	3.7	15

15	Multiplex gene editing via CRISPR/Cas9 exhibits desirable muscle hypertrophy without detectable off-target effects in sheep. <i>Scientific Reports</i> , <b>2016</b> , 6, 32271	4.9	46
14	Comparative Transcriptome Analysis of Fetal Skin Reveals Key Genes Related to Hair Follicle Morphogenesis in Cashmere Goats. <i>PLoS ONE</i> , <b>2016</b> , 11, e0151118	3.7	48
13	Disruption of FGF5 in Cashmere Goats Using CRISPR/Cas9 Results in More Secondary Hair Follicles and Longer Fibers. <i>PLoS ONE</i> , <b>2016</b> , 11, e0164640	3.7	43
12	A non-synonymous mutation in GDF9 is highly associated with litter size in cashmere goats. <i>Animal Genetics</i> , <b>2016</b> , 47, 630-1	2.5	11
11	Whole-genome sequencing of eight goat populations for the detection of selection signatures underlying production and adaptive traits. <i>Scientific Reports</i> , <b>2016</b> , 6, 38932	4.9	66
10	PPAR $\alpha$ FAS, HSL mRNA and protein expression during Tan sheep fat-tail development. <i>Electronic Journal of Biotechnology</i> , <b>2015</b> , 18, 122-127	3.1	3
9	mRNA transcription and protein expression of PPAR $\alpha$ FAS, and HSL in different parts of the carcass between fat-tailed and thin-tailed sheep. <i>Electronic Journal of Biotechnology</i> , <b>2015</b> , 18, 215-220	3.1	6
8	Generation of gene-modified goats targeting MSTN and FGF5 via zygote injection of CRISPR/Cas9 system. <i>Scientific Reports</i> , <b>2015</b> , 5, 13878	4.9	112
7	Rumen bacterial diversity of 80 to 110-day-old goats using 16S rRNA sequencing. <i>PLoS ONE</i> , <b>2015</b> , 10, e0117811	3.7	52
6	Transcriptome profile analysis of adipose tissues from fat and short-tailed sheep. <i>Gene</i> , <b>2014</b> , 549, 252-73.8		51
5	Discovery of SNPs in RXFP2 related to horn types in sheep. <i>Small Ruminant Research</i> , <b>2014</b> , 116, 133-136.7		11
4	Cyclic expression of Lhx2 is involved in secondary hair follicle development in cashmere goat. <i>Gene Expression Patterns</i> , <b>2014</b> , 16, 31-5	1.5	11
3	Discovery of cashmere goat ( <i>Capra hircus</i> ) microRNAs in skin and hair follicles by Solexa sequencing. <i>BMC Genomics</i> , <b>2013</b> , 14, 511	4.5	64
2	The genetic diversity of seven indigenous Chinese goat breeds. <i>Small Ruminant Research</i> , <b>2008</b> , 74, 231-237		22
1	Base pair editing of goat embryos: nonsense codon introgression into FGF5 to improve cashmere yield		1