

# Yulin Chen

## 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.

54 papers	1,309 citations	20 h-index	35 g-index
61 ext. papers	2,010 ext. citations	5.4 avg, IF	4.26 L-index

#	Paper	IF	Citations
54	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
53	Generation of Double-Muscled Sheep and Goats by CRISPR/Cas9-Mediated Knockout of the Myostatin Gene. <i>Methods in Molecular Biology</i> , <b>2022</b> , 295-323	1.4	1
52	Dynamics of rumen gene expression, microbiome colonization, and their interplay in goats. <i>BMC Genomics</i> , <b>2021</b> , 22, 288	4.5	4
51	Enhancing prime editing by Csy4-mediated processing of pegRNA. <i>Cell Research</i> , <b>2021</b> , 31, 1134-1136	24.7	17
50	Modes of genetic adaptations underlying functional innovations in the rumen. <i>Science China Life Sciences</i> , <b>2021</b> , 64, 1-21	8.5	7
49	Taxonomic and functional adaption of the gastrointestinal microbiome of goats kept at high altitude (4800m) under intensive or extensive rearing conditions. <i>FEMS Microbiology Ecology</i> , <b>2021</b> , 97,	4.3	2
48	Selective Sweeps Uncovering the Genetic Basis of Horn and Adaptability Traits on Fine-Wool Sheep in China. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 604235	4.5	1
47	Deletions in the gene are associated with fiber traits in cashmere-producing goats. <i>Animal Biotechnology</i> , <b>2021</b> , 1-7	1.4	
46	An atlas of CNV maps in cattle, goat and sheep. <i>Science China Life Sciences</i> , <b>2021</b> , 64, 1747-1764	8.5	8
45	The origin of domestication genes in goats. <i>Science Advances</i> , <b>2020</b> , 6, eaaz5216	14.3	28
44	Effect of dietary nutrition on tail fat deposition and evaluation of tail-related genes in fat-tailed sheep. <i>Electronic Journal of Biotechnology</i> , <b>2020</b> , 46, 30-37	3.1	0
43	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
42	Transactivation of miR-202-5p by Steroidogenic Factor 1 (SF1) Induces Apoptosis in Goat Granulosa Cells by Targeting TGFBR2. <i>Cells</i> , <b>2020</b> , 9,	7.9	11
41	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
40	Redesigning small ruminant genomes with CRISPR toolkit: Overview and perspectives. <i>Theriogenology</i> , <b>2020</b> , 147, 25-33	2.8	6
39	Efficient generation of mouse models with the prime editing system. <i>Cell Discovery</i> , <b>2020</b> , 6, 27	22.3	80
38	Ancient Genomes Reveal the Evolutionary History and Origin of Cashmere-Producing Goats in China. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 2099-2109	8.3	13

37	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
36	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
35	Label-Free LC-MS/MS Proteomics Analyses Reveal Proteomic Changes Accompanying KO in C2C12 Cells. <i>BioMed Research International</i> , <b>2019</b> , 2019, 7052456	3	5
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	Role of OXCT1 in ovine adipose and preadipocyte differentiation. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 512, 779-785	3.4	3
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	Exosomal Micro RNAs Derived from Dermal Papilla Cells Mediate Hair Follicle Stem Cell Proliferation and Differentiation. <i>International Journal of Biological Sciences</i> , <b>2019</b> , 15, 1368-1382	11.2	32
30	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
29	CRISPR/Cas9-mediated knockout plays an essential role in the growth of dermal papilla cells through enhanced relative genes. <i>PeerJ</i> , <b>2019</b> , 7, e7230	3.1	1
28	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
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	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
25	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
24	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
23	Generation of gene-edited sheep with a defined Booroola fecundity gene (FecB) mutation in bone morphogenetic protein receptor type 1B (BMPR1B) via clustered regularly interspaced short palindromic repeat (CRISPR)/CRISPR-associated (Cas) 9. <i>Reproduction, Fertility and Development</i> , <b>2018</b> , 30, 1616-1621	1.8	16
22	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
21	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
20	Effects of all-trans retinoic acid on goat dermal papilla cells cultured in vitro. <i>Electronic Journal of Biotechnology</i> , <b>2018</b> , 34, 43-50	3.1	1

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	Effect of miR-125b on dermal papilla cells of goat secondary hair follicle. <i>Electronic Journal of Biotechnology</i> , <b>2017</b> , 25, 64-69	3.1	6
17	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
16	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
15	Biallelic $\beta$ -carotene oxygenase 2 knockout results in yellow fat in sheep via CRISPR/Cas9. <i>Animal Genetics</i> , <b>2017</b> , 48, 242-244	2.5	19
14	RNA-seq reveals transcriptome changes in goats following myostatin gene knockout. <i>PLoS ONE</i> , <b>2017</b> , 12, e0187966	3.7	15
13	Multiplex Gene Editing via CRISPR/Cas9 System in Sheep. <i>Bio-protocol</i> , <b>2017</b> , 7, e2385	0.9	2
12	Fibroblast growth factor 5-short (FGF5s) inhibits the activity of FGF5 in primary and secondary hair follicle dermal papilla cells of cashmere goats. <i>Gene</i> , <b>2016</b> , 575, 393-398	3.8	33
11	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
10	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
9	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
8	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
7	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
6	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
5	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
4	Transcriptome profile analysis of adipose tissues from fat and short-tailed sheep. <i>Gene</i> , <b>2014</b> , 549, 252-73.8	3.8	51
3	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , <b>2014</b> , 344, 1168-1173	33.3	294
2	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

1	Exploring differentially expressed genes by RNA-Seq in cashmere goat ( <i>Capra hircus</i> ) skin during hair follicle development and cycling. <i>PLoS ONE</i> , <b>2013</b> , 8, e62704	3-7	44
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