

# Jian-Lin Han

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3126736/publications.pdf>

Version: 2024-02-01

41  
papers

1,942  
citations

394421

19  
h-index

276875

41  
g-index

43  
all docs

43  
docs citations

43  
times ranked

1755  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rich maternal and paternal genetic diversity and divergent lineage composition in wild yak ( <i>Bos</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	1.5	4
2	Rich maternal and paternal genetic diversity and divergent lineage composition in wild yak ( <i>Bos</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.5	9
3	A single-nucleotide mutation within the TBX3 enhancer increased body size in Chinese horses. <i>Current Biology</i> , 2022, 32, 480-487.e6.	3.9	21
4	The Transcriptional Cell Atlas of Testis Development in Sheep at Pre-Sexual Maturity. <i>Current Issues in Molecular Biology</i> , 2022, 44, 483-497.	2.4	5
5	The de novo assembly of a European wild boar genome revealed unique patterns of chromosomal structural variations and segmental duplications. <i>Animal Genetics</i> , 2022, 53, 281-292.	1.7	6
6	Whole-Genome Resequencing of Worldwide Wild and Domestic Sheep Elucidates Genetic Diversity, Introgression, and Agronomically Important Loci. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	50
7	Galbase: a comprehensive repository for integrating chicken multi-omics data. <i>BMC Genomics</i> , 2022, 23, 364.	2.8	3
8	Functional and phylogenetic analyses of camel rumen microbiota associated with different lignocellulosic substrates. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	6.4	15
9	Metagenomic analysis reveals a dynamic microbiome with diversified adaptive functions to utilize high lignocellulosic forages in the cattle rumen. <i>ISME Journal</i> , 2021, 15, 1108-1120.	9.8	87
10	Whole-Genome Resequencing Reveals Adaptation Prior to the Divergence of Buffalo Subspecies. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	4
11	Historical Introgression from Wild Relatives Enhanced Climatic Adaptation and Resistance to Pneumonia in Sheep. <i>Molecular Biology and Evolution</i> , 2021, 38, 838-855.	8.9	44
12	Diversity of microbes colonizing forages of varying lignocellulose properties in the sheep rumen. <i>PeerJ</i> , 2021, 9, e10463.	2.0	18
13	Genetic Diversities and Historical Dynamics of Native Ethiopian Horse Populations ( <i>Equus caballus</i> ) Inferred from Mitochondrial DNA Polymorphisms. <i>Genes</i> , 2021, 12, 155.	2.4	3
14	Genome-wide comparative analyses reveal selection signatures underlying adaptation and production in Tibetan and Poll Dorset sheep. <i>Scientific Reports</i> , 2021, 11, 2466.	3.3	15
15	Mitochondrial genomes from modern and ancient Turano-Mongolian cattle reveal an ancient diversity of taurine maternal lineages in East Asia. <i>Heredity</i> , 2021, 126, 1000-1008.	2.6	11
16	A compendium and comparative epigenomics analysis of cis-regulatory elements in the pig genome. <i>Nature Communications</i> , 2021, 12, 2217.	12.8	63
17	A Mother's Story, Mitogenome Relationships in the Genus <i>Rupicapra</i> . <i>Animals</i> , 2021, 11, 1065.	2.3	6
18	Large-scale genomic analysis reveals the genetic cost of chicken domestication. <i>BMC Biology</i> , 2021, 19, 118.	3.8	22

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19	Genome Divergence and Dynamics in the Thin-Tailed Desert Sheep From Sudan. <i>Frontiers in Genetics</i> , 2021, 12, 659507.	2.3	5
20	High Genetic Diversity but Absence of Population Structure in Local Chickens of Sri Lanka Inferred by Microsatellite Markers. <i>Frontiers in Genetics</i> , 2021, 12, 723706.	2.3	4
21	Paternal Origins and Migratory Episodes of Domestic Sheep. <i>Current Biology</i> , 2020, 30, 4085-4095.e6.	3.9	49
22	Comparative population genomic analysis uncovers novel genomic footprints and genes associated with small body size in Chinese pony. <i>BMC Genomics</i> , 2020, 21, 496.	2.8	14
23	Genome-Wide Population Genetic Analysis of Commercial, Indigenous, Game, and Wild Chickens Using 600K SNP Microarray Data. <i>Frontiers in Genetics</i> , 2020, 11, 543294.	2.3	31
24	Three functional mutation sites affect the immune response of pigs through altering the expression pattern and IgV domain of the CD4 protein. <i>BMC Molecular and Cell Biology</i> , 2020, 21, 91.	2.0	0
25	Whole-genome resequencing provides insights into the evolution and divergence of the native domestic yaks of the Qinghai-Tibet Plateau. <i>BMC Evolutionary Biology</i> , 2020, 20, 137.	3.2	16
26	Genomic Diversity, Population Structure, and Signature of Selection in Five Chinese Native Sheep Breeds Adapted to Extreme Environments. <i>Genes</i> , 2020, 11, 494.	2.4	20
27	The origin of domestication genes in goats. <i>Science Advances</i> , 2020, 6, eaaz5216.	10.3	86
28	Evolutionary relationship and population structure of domestic Bovidae animals based on MHC-linked and neutral autosomal microsatellite markers. <i>Molecular Immunology</i> , 2020, 124, 83-90.	2.2	2
29	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits. <i>Nature Communications</i> , 2020, 11, 2815.	12.8	142
30	A Global Analysis of Y-STR INRA189 Polymorphism in Chinese Domestic Yak Breeds/Populations. <i>Animals</i> , 2020, 10, 393.	2.3	3
31	863 genomes reveal the origin and domestication of chicken. <i>Cell Research</i> , 2020, 30, 693-701.	12.0	144
32	Identification of Novel lncRNAs Differentially Expressed in Placentas of Chinese Ningqiang Pony and Yili Horse Breeds. <i>Animals</i> , 2020, 10, 119.	2.3	6
33	Temporal changes in microbial communities attached to forages with different lignocellulosic compositions in cattle rumen. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	32
34	EPAS1 Gain-of-Function Mutation Contributes to High-Altitude Adaptation in Tibetan Horses. <i>Molecular Biology and Evolution</i> , 2019, 36, 2591-2603.	8.9	80
35	The Genome Landscape of Tibetan Sheep Reveals Adaptive Introgression from Argali and the History of Early Human Settlements on the Qinghai-Tibetan Plateau. <i>Molecular Biology and Evolution</i> , 2019, 36, 283-303.	8.9	84
36	Was chicken domesticated in northern China? New evidence from mitochondrial genomes. <i>Science Bulletin</i> , 2018, 63, 743-746.	9.0	17

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37	Whole-genome resequencing reveals world-wide ancestry and adaptive introgression events of domesticated cattle in East Asia. <i>Nature Communications</i> , 2018, 9, 2337.	12.8	253
38	Genomic Reconstruction of the History of Native Sheep Reveals the Peopling Patterns of Nomads and the Expansion of Early Pastoralism in East Asia. <i>Molecular Biology and Evolution</i> , 2017, 34, 2380-2395.	8.9	94
39	Species composition and environmental adaptation of indigenous Chinese cattle. <i>Scientific Reports</i> , 2017, 7, 16196.	3.3	83
40	Whole-Genome Sequencing of Native Sheep Provides Insights into Rapid Adaptations to Extreme Environments. <i>Molecular Biology and Evolution</i> , 2016, 33, 2576-2592.	8.9	271
41	Mitogenomic Meta-Analysis Identifies Two Phases of Migration in the History of Eastern Eurasian Sheep. <i>Molecular Biology and Evolution</i> , 2015, 32, 2515-2533.	8.9	122