CITATION REPORT List of articles citing

Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals

DOI: 10.1038/s41588-018-0056-5 Nature Genetics, 2018, 50, 362-367.

Source: https://exaly.com/paper-pdf/68992203/citation-report.pdf

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

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

#	Paper	IF	Citations
252	Success and failure in replication of genotype-phenotype associations: How does replication help in understanding the genetic basis of phenotypic variation in outbred populations?. 2018 , 18, 739-754		14
251	Applications of genomic copy number variations on livestock: A review. 2018 , 17, 1313-1323		1
250	Association of Copy Number Variation at Intron 3 of With Navel Length in. <i>Frontiers in Genetics</i> , 2018 , 9, 627	4.5	9
249	Signatures of Selection in Admixed Dairy Cattle in Tanzania. Frontiers in Genetics, 2018, 9, 607	4.5	22
248	A Meta-Analysis Including Pre-selected Sequence Variants Associated With Seven Traits in Three French Dairy Cattle Populations. <i>Frontiers in Genetics</i> , 2018 , 9, 522	4.5	13
247	Genomic prediction for numerically small breeds, using models with pre-selected and differentially weighted markers. 2018 , 50, 49		18
246	Utility of whole-genome sequence data for across-breed genomic prediction. 2018 , 50, 27		32
245	Putative bovine topological association domains and CTCF binding motifs can reduce the search space for causative regulatory variants of complex traits. <i>BMC Genomics</i> , 2018 , 19, 395	4.5	16
244	Genome variants associated with RNA splicing variations in bovine are extensively shared between tissues. <i>BMC Genomics</i> , 2018 , 19, 521	4.5	19
243	Across-Experiment Transcriptomics of Sheep Rumen Identifies Expression of Lipid/Oxo-Acid Metabolism and Muscle Cell Junction Genes Associated With Variation in Methane-Related Phenotypes. <i>Frontiers in Genetics</i> , 2018 , 9, 330	4.5	5
242	Low genome-wide homozygosity in 11 Spanish ovine breeds. <i>Animal Genetics</i> , 2019 , 50, 501-511	2.5	4
241	Comparative Genomic Analysis of Three Salmonid Species Identifies Functional Candidate Genes Involved in Resistance to the Intracellular Bacterium. <i>Frontiers in Genetics</i> , 2019 , 10, 665	4.5	11
240	Conservation, acquisition, and functional impact of sex-biased gene expression in mammals. <i>Science</i> , 2019 , 365,	33.3	67
239	Sequence-based GWAS, network and pathway analyses reveal genes co-associated with milk cheese-making properties and milk composition in Montbliarde cows. 2019 , 51, 34		26
238	The Impact of Genomic and Traditional Selection on the Contribution of Mutational Variance to Long-Term Selection Response and Genetic Variance. 2019 , 213, 361-378		4
237	Landscape of Loci and Candidate Genes for Muscle Fatty Acid Composition in Pigs Revealed by Multiple Population Association Analysis. <i>Frontiers in Genetics</i> , 2019 , 10, 1067	4.5	2
236	Functional annotation of the cattle genome through systematic discovery and characterization of chromatin states and butyrate-induced variations. <i>BMC Biology</i> , 2019 , 17, 68	7.3	22

Multi-trait meta-analyses reveal 25 quantitative trait loci for economically important traits in Brown Swiss cattle. <i>BMC Genomics</i> , 2019 , 20, 695	4.5	13
Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. 2019 , 116, 19398-19408		44
Reaffirmation of known major genes and the identification of novel candidate genes associated with carcass-related metrics based on whole genome sequence within a large multi-breed cattle population. <i>BMC Genomics</i> , 2019 , 20, 720	4.5	26
Ide novo 3.8-Mb inversion affecting the EDA and XIST genes in a heterozygous female calf with generalized hypohidrotic ectodermal dysplasia. <i>BMC Genomics</i> , 2019 , 20, 715	4.5	2
Genome Sequence Analysis Reveals Selection Signatures in Endangered Trypanotolerant West African Muturu Cattle. <i>Frontiers in Genetics</i> , 2019 , 10, 442	4.5	19
A Large-Scale Genome-Wide Association Study in U.S. Holstein Cattle. <i>Frontiers in Genetics</i> , 2019 , 10, 412	4.5	54
Genome-wide association study reveals candidate genes associated with body measurement traits in Chinese Wagyu beef cattle. <i>Animal Genetics</i> , 2019 , 50, 386-390	2.5	12
Meta-analysis of genome-wide association studies for loin muscle area and loin muscle depth in two Duroc pig populations. 2019 , 14, e0218263		13
Accurate sequence variant genotyping in cattle using variation-aware genome graphs. 2019 , 51, 21		19
Weighting sequence variants based on their annotation increases the power of genome-wide association studies in dairy cattle. 2019 , 51, 20		6
Variance of gametic diversity and its application in selection programs. 2019 , 102, 5279-5294		12
Genome Scan for Genomic Regions and Genes Associated with Growth Trait in Pacific White Shrimp Litopeneaus vannamei. 2019 , 21, 374-383		21
A splice donor variant in CCDC189 is associated with asthenospermia in Nordic Red dairy cattle. <i>BMC Genomics</i> , 2019 , 20, 286	4.5	11
Whole genome sequencing of canids reveals genomic regions under selection and variants influencing morphology. 2019 , 10, 1489		103
A guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. 2019 , 19, 997-1014		11
Prioritizing candidate genes for fertility in dairy cows using gene-based analysis, functional annotation and differential gene expression. <i>BMC Genomics</i> , 2019 , 20, 255	4.5	16
Meta-analysis of genome-wide association studies provides insights into genetic control of tomato flavor. 2019 , 10, 1534		48
Joint imputation of whole-genome sequence variants and large chromosomal deletions in cattle. 2019 , 102, 11193-11206		1
	Swiss cattle. <i>BMC Genomics</i> , 2019, 20, 695 Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. 2019, 116, 19398-19408 Reaffirmation of known major genes and the identification of novel candidate genes associated with carcass-related metrics based on whole genome sequence within a large multi-breed cattle population. <i>BMC Genomics</i> , 2019, 20, 720 Idle novo 3.8-Mb inversion affecting the EDA and XIST genes in a heterozygous female calf with generalized hypohidrotic ectodermal dysplasia. <i>BMC Genomics</i> , 2019, 20, 715 Genome Sequence Analysis Reveals Selection Signatures in Endangered Trypanotolerant West African Muturu Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 442 A Large-Scale Genome-Wide Association Study in U.S. Holstein Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 412 Genome-wide association study reveals candidate genes associated with body measurement traits in Chinese Wagyu beef cattle. <i>Animal Genetics</i> , 2019, 50, 386-390 Meta-analysis of genome-wide association studies for loin muscle area and loin muscle depth in two Duroc pig populations. 2019, 14, e0218263 Accurate sequence variant genotyping in cattle using variation-aware genome graphs. 2019, 51, 21 Weighting sequence variants based on their annotation increases the power of genome-wide association studies in dairy cattle. 2019, 51, 20 Variance of gametic diversity and its application in selection programs. 2019, 102, 5279-5294 Genome Scan for Genomic Regions and Genes Associated with Growth Trait in Pacific White Shrimp Litopeneaus vannamei. 2019, 21, 374-383 A splice donor variant in CCDC189 is associated with asthenospermia in Nordic Red dairy cattle. <i>BMC Genomics</i> , 2019, 20, 286 Whole genome sequencing of canids reveals genomic regions under selection and variants influencing morphology. 2019, 10, 1489 A guinea fowl genome assembly provides new evidence on evolution following domestication and almotation and differential gene expression. <i>BMC Genomics</i> , 2019,	Aurge-Scale Genome-Wide Association Study in U.S. Holstein Cattle. Frontiers in Genetics, 2019, 10, 412 Alarge-Scale Genome-Wide Association Study in U.S. Holstein Cattle. Frontiers in Genetics, 2019, 10, 402 Genome-wide association study reveals candidate genes associated with carcassered to the Cattle associated with carcassered to the Cattle oppulation. BMC Genomics, 2019, 20, 720 Genome Sequence Analysis Reveals Selection Signatures in Endangered Trypanotolerant West African Muturu Cattle. Frontiers in Genetics, 2019, 10, 442 A Large-Scale Genome-Wide Association Study in U.S. Holstein Cattle. Frontiers in Genetics, 2019, 10, 442 A Large-Scale Genome-Wide Association Study in U.S. Holstein Cattle. Frontiers in Genetics, 2019, 10, 412 Genome-wide association study reveals candidate genes associated with body measurement traits in Chinese Wagyu beef cattle. Animal Genetics, 2019, 50, 386-390 Meta-analysis of genome-wide association studies for loin muscle area and loin muscle depth in two Duroc pig bopulations. 2019, 14, e0218263 Accurate sequence variants based on their annotation increases the power of genome-wide association studies in dairy cattle. 2019, 51, 20 Variance of gametic diversity and its application in selection programs. 2019, 102, 5279-5294 Genome Scan for Genomic Regions and Genes Associated with Growth Trait in Pacific White Shrimp Litopeneaus vannamei. 2019, 21, 374-383 A splice donor variant in CCDC189 is associated with asthenospermia in Nordic Red dairy cattle. BMC Genomics, 2019, 20, 286 Whole genome sequencing of canids reveals genomic regions under selection and variants influencing morphology. 2019, 10, 1489 A guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. 2019, 19, 997-1014 Prioritizing candidate genes for fertility in dairy cows using gene-based analysis, functional annotation and differential gene expression. BMC Genomics, 2019, 20, 255 Meta-analysis of genome-wide association studies provides in

217	Combining multi-population datasets for joint genome-wide association and meta-analyses: The case of bovine milk fat composition traits. 2019 , 102, 11124-11141		5
216	A multi-breed reference panel and additional rare variants maximize imputation accuracy in cattle. 2019 , 51, 77		21
215	Biological Network Approach for the Identification of Regulatory Long Non-Coding RNAs Associated With Metabolic Efficiency in Cattle. <i>Frontiers in Genetics</i> , 2019 , 10, 1130	4.5	18
214	Growth Performance and Meat Quality Evaluations in Three-Way Cross Cattle Developed for the Tibetan Plateau and their Molecular Understanding by Integrative Omics Analysis. 2019 , 67, 541-550		10
213	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. 2019, 7, 65-8	38	70
212	1000 Bull Genomes Project to Map Simple and Complex Genetic Traits in Cattle: Applications and Outcomes. 2019 , 7, 89-102		104
211	Harnessing genomic information for livestock improvement. 2019 , 20, 135-156		128
210	Whole genome sequencing of a MAGIC population identified genomic loci and candidate genes for major fiber quality traits in upland cotton (Gossypium hirsutum L.). 2019 , 132, 989-999		26
209	Genetics of bull semen characteristics in a multi-breed cattle population. 2019 , 123, 202-208		17
208	A SNP in PLAG1 is associated with body height trait in Chinese cattle. <i>Animal Genetics</i> , 2020 , 51, 87-90	2.5	7
207	Assessing genomic diversity and signatures of selection in Original Braunvieh cattle using whole-genome sequencing data. <i>BMC Genomics</i> , 2020 , 21, 27	4.5	20
206	Relationship of Icelandic cattle with Northern and Western European cattle breeds, admixture and population structure. 2020 , 69, 25-38		3
205	Genome-wide association study identifies genomic loci associated with flight reaction in cattle. 2020 , 137, 477-485		2
204	Confirmed effects of candidate variants for milk production, udder health, and udder morphology in dairy cattle. 2020 , 52, 55		11
203	A genome-wide association analysis for body, udder, and leg conformation traits recorded in Murciano-Granadina goats. 2020 , 103, 11605-11617		1
202	A de novo frameshift mutation in ZEB2 causes polledness, abnormal skull shape, small body stature and subfertility in Fleckvieh cattle. 2020 , 10, 17032		1
201	A multi-breed GWAS for morphometric traits in four Beninese indigenous cattle breeds reveals loci associated with conformation, carcass and adaptive traits. <i>BMC Genomics</i> , 2020 , 21, 783	4.5	5
200	Performances of Adaptive MultiBLUP, Bayesian regressions, and weighted-GBLUP approaches for genomic predictions in Belgian Blue beef cattle. <i>BMC Genomics</i> , 2020 , 21, 545	4.5	2

(2020-2020)

199	Heritability Estimates of Antler and Body Traits in White-Tailed Deer (Odocoileus virginianus) From Genomic-Relatedness Matrices. 2020 , 111, 429-435	3
198	Bovine breed-specific augmented reference graphs facilitate accurate sequence read mapping and unbiased variant discovery. 2020 , 21, 184	19
197	Meta-analysis of GWAS in canola blackleg (Leptosphaeria maculans) disease traits demonstrates increased power from imputed whole-genome sequence. 2020 , 10, 14300	14
196	Signatures of selection reveal candidate genes involved in economic traits and cold acclimation in five Swedish cattle breeds. 2020 , 52, 52	11
195	Whole genome analysis of water buffalo and global cattle breeds highlights convergent signatures of domestication. 2020 , 11, 4739	19
194	Genetic control of temperament traits across species: association of autism spectrum disorder risk genes with cattle temperament. 2020 , 52, 51	9
193	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock. 2020 , 16, e1008780	3
192	Improving Genomic Prediction of Crossbred and Purebred Dairy Cattle. <i>Frontiers in Genetics</i> , 2020 , 11, 598580	3
191	Breed- and trait-specific associations define the genetic architecture of calving performance traits in cattle. 2020 , 98,	5
190	Uncovering Sub-Structure and Genomic Profiles in Across-Countries Subpopulations of Angus Cattle. 2020 , 10, 8770	1
189	Genetic Variants Affecting Skeletal Morphology in Domestic Dogs. 2020 , 36, 598-609	3
188	Activation of cryptic splicing in bovine WDR19 is associated with reduced semen quality and male fertility. 2020 , 16, e1008804	11
187	Selection signatures in tropical cattle are enriched for promoter and coding regions and reveal missense mutations in the damage response gene HELB. 2020 , 52, 27	10
186	Identification of Genomic Characteristics and Selective Signals in a Du'an Goat Flock. 2020 , 10,	2
185	BGVD: An Integrated Database for Bovine Sequencing Variations and Selective Signatures. 2020 , 18, 186-193	17
184	Multiple association analysis of loci and candidate genes that regulate body size at three growth stages in Simmental beef cattle. 2020 , 21, 32	10
183	Expression profiles of the MXD3 gene and association of sequence variants with growth traits in Xianan and Qinchuan cattle. 2020 , 6, 399-409	4
182	Meta-analysis for milk fat and protein percentage using imputed sequence variant genotypes in 94,321 cattle from eight cattle breeds. 2020 , 52, 37	9

181	Epigenomics and genotype-phenotype association analyses reveal conserved genetic architecture of complex traits in cattle and human. <i>BMC Biology</i> , 2020 , 18, 80	7.3	12
180	The Locus is under Selection in Large-Sized Pakistani Goat Breeds. 2020 , 11,		8
179	Effect direction meta-analysis of GWAS identifies extreme, prevalent and shared pleiotropy in a large mammal. 2020 , 3, 88		13
178	Whole-genome analyses identify loci and selective signals associated with body size in cattle. 2020 , 98,		13
177	Genomic Regions Associated With Skeletal Type Traits in Beef and Dairy Cattle Are Common to Regions Associated With Carcass Traits, Feed Intake and Calving Difficulty. <i>Frontiers in Genetics</i> , 2020 , 11, 20	4.5	11
176	Beyond large-effect loci: large-scale GWAS reveals a mixed large-effect and polygenic architecture for age at maturity of Atlantic salmon. 2020 , 52, 9		27
175	Genome-Wide Association Study Identifies Genomic Loci Associated With Neurotransmitter Concentration in Cattle. <i>Frontiers in Genetics</i> , 2020 , 11, 139	4.5	3
174	Genomic regions associated with muscularity in beef cattle differ in five contrasting cattle breeds. 2020 , 52, 2		12
173	Genetic architecture of quantitative traits in beef cattle revealed by genome wide association studies of imputed whole genome sequence variants: II: carcass merit traits. <i>BMC Genomics</i> , 2020 , 21, 38	4.5	15
172	Whole-genome resequencing reveals diversity, global and local ancestry proportions in Yunling cattle. 2020 , 137, 641-650		5
171	Whole genome analyses revealed genomic difference between European taurine and East Asian taurine. 2021 , 138, 56-68		1
170	All sheeps and sizes: a genetic investigation of mature body size across sheep breeds reveals a polygenic nature. <i>Animal Genetics</i> , 2021 , 52, 99-107	2.5	7
169	Heterogeneity of a dwarf phenotype in Dutch traditional chicken breeds revealed by genomic analyses. 2021 , 14, 1095-1108		2
168	Pathways involved in pony body size development. <i>BMC Genomics</i> , 2021 , 22, 58	4.5	O
167	A meta-analysis of genome-wide association studies for average daily gain and lean meat percentage in two Duroc pig populations. <i>BMC Genomics</i> , 2021 , 22, 12	4.5	7
166	Concordance rate in cattle and sheep between genotypes differing in Illumina GenCall quality score. <i>Animal Genetics</i> , 2021 , 52, 208-213	2.5	3
165	Genome-wide fine-mapping identifies pleiotropic and functional variants that predict many traits across global cattle populations. 2021 , 12, 860		14
164	Genetic Regulation of Biomarkers as Stress Proxies in Dairy Cows. 2021 , 12,		2

Admixture mapping reveals loci for carcass mass in red deer x sika hybrids in Kintyre, Scotland.

Sequence-based GWAS and post-GWAS analyses reveal a key role of SLC37A1, ANKH, and regulatory regions on bovine milk mineral content. 2021, 11, 7537 A QTL for conformation of back and croup influences lateral gait quality in Icelandic horses. BMC Genomics, 2021, 22, 267 4.5 Mutant alleles differentially shape cattle complex traits and fitness.	3
161 Genomics, 2021 , 22, 267 4-5	O
160 Mutant alleles differentially shape cattle complex traits and fitness.	
	Ο
How imputation can mitigate SNP ascertainment Bias. <i>BMC Genomics</i> , 2021 , 22, 340 4.5	3
Association between Natriuretic peptide receptor 2 (npr2) rs208158047 polymorphism and fattening performance of young bulls. 2021 ,	
157 Genetics of tibia bone properties of crossbred commercial laying hens in different housing systems.	О
156 Genetic variation in recombination rate in the pig. 2021 , 53, 54	1
Evolutionary and phylogenetic insights from a nuclear genome sequence of the extinct, giant, "subfossil" koala lemur. 2021 , 118,	2
Analysis of pedigree data and whole-genome sequences in 12 cattle breeds reveals extremely low within-breed Y-chromosome diversity. <i>Animal Genetics</i> , 2021 , 52, 725-729	Ο
Exploiting within-breed variability in the autochthonous Reggiana breed identified several candidate genes affecting pigmentation-related traits, stature and udder defects in cattle. <i>Animal Genetics</i> , 2021 , 52, 579-597	0
Detection of 15-bp Deletion Mutation within Gene and Its Effects on Growth Traits in Goats. 2021 , 11,	2
A Large-Scale Genome-Wide Association Study of Epistasis Effects of Production Traits and Daughter Pregnancy Rate in U.S. Holstein Cattle. 2021 , 12,	1
A conditional multi-trait sequence GWAS discovers pleiotropic candidate genes and variants for sheep wool, skin wrinkle and breech cover traits. 2021 , 53, 58	O
Admixture mapping reveals loci for carcass mass in red deer x sika hybrids in Kintyre, Scotland. 2021 , 11,	1
Mapping of quantitative trait loci underlying a magic trait in ongoing ecological speciation. <i>BMC</i> Genomics, 2021 , 22, 615 4.5	1
Integration of selection signatures and multi-trait GWAS reveals polygenic genetic architecture of carcass traits in beef cattle. 2021 , 113, 3325-3336	4
Detection and Visualization of Heterozygosity-Rich Regions and Runs of Homozygosity in Worldwide Sheep Populations. 2021 , 11,	O

145	Runs of homozygosity analysis reveals consensus homozygous regions affecting production traits in Chinese Simmental beef cattle. <i>BMC Genomics</i> , 2021 , 22, 678	4.5	2
144	The Quest for Genes Involved in Adaptation to Climate Change in Ruminant Livestock. 2021 , 11,		3
143	Introgression contributes to distribution of structural variations in cattle. 2021 , 113, 3092-3102		О
142	Molecular Genetics, Genetic Engineering and Dairy Foods. 2022 , 345-351		
141	Expression quantitative trait loci in sheep liver and muscle contribute to variations in meat traits. 2021 , 53, 8		1
140	Bovine breed-specific augmented reference graphs facilitate accurate sequence read mapping and unbiased variant discovery.		2
139	Evolutionary and phylogenetic insights from a nuclear genome sequence of the extinct, giant Bubfossillkoala lemur Megaladapis edwardsi.		1
138	A Multi-Breed Reference Panel and Additional Rare Variation Maximizes Imputation Accuracy in Cattle.		2
137	Multi-trait meta-analyses reveal 25 quantitative trait loci for economically important traits in Brown Swiss cattle.		1
136	The Bovine Genome Variation Database (BGVD): Integrated Web-database for Bovine Sequencing Variations and Selective Signatures.		4
135	Genomic architecture of artificially and sexually selected traits in a wild cervid.		2
134	Functional and population genetic features of copy number variations in two dairy cattle populations. <i>BMC Genomics</i> , 2020 , 21, 89	4.5	12
133	Selection signatures in two oldest Russian native cattle breeds revealed using high-density single nucleotide polymorphism analysis. 2020 , 15, e0242200		7
132	Application of multivariate single-step SNP best linear unbiased predictor model and revised SNP list for genomic evaluation of dairy cattle in Australia. 2020 , 103, 8305-8316		1
131	Using imputed whole-genome sequence variants to uncover candidate mutations and genes affecting milking speed and temperament in Holstein cattle. 2020 , 103, 10383-10398		8
130	RGD v2.0: a major update of the ruminant functional and evolutionary genomics database. 2021 ,		3
129	Ruminant-specific retrotransposons shape regulatory evolution of bovine immunity.		1
128	Direct introgression of untapped diversity into elite wheat lines. 2021 , 2, 819-827		2

127	Genome variants associated with RNA splicing variation in bovine are extensively shared between tissues.		
126	Animal models with group-specific additive genetic variances: extending genetic group models.		
125	A splice donor variant in CCDC189 is associated with asthenospermia in Nordic Red dairy cattle.		
124	Comparative genomic analysis of three salmonid species identifies functional candidate genes involved in resistance to the intracellular bacteriaPiscirickettsia salmonis.		
123	Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits.		
122	Assessing genomic diversity and signatures of selection in Original Braunvieh cattle using whole-genome sequencing data.		
121	Performing QTL and eQTL Analyses with the R-Package GenomicTools. 2020 , 2082, 15-38		
120	Using singleton densities to detect recent selection in Bos taurus.		
119	Genome-wide association study identifies quantitative trait loci affecting cattle temperament. 2022 , 43, 14-25		1
118	Activation of cryptic splicing in bovine WDR19 is associated with reduced semen quality and male fertility.		
117	Identification of Candidate Variants Associated With Bone Weight Using Whole Genome Sequence in Beef Cattle <i>Frontiers in Genetics</i> , 2021 , 12, 750746	4.5	1
116	Bench Research Informed by GWAS Results. 2021 , 10,		О
115	Using singleton densities to detect recent selection in 2021 , 5, 595-606		О
114	Mutant alleles differentially shape fitness and other complex traits in cattle. 2021 , 4, 1353		O
113	Genome-wide association study for meat tenderness in beef cattle identifies patterns of the genetic contribution in different post-mortem stages 2022 , 186, 108733		1
112	Genomic diversity and signatures of selection in meat and fancy rabbit breeds based on high-density marker data 2022 , 54, 3		Ο
111	Genomic landscape, polymorphism and possible LINE-associated delivery of G-quadruplex motifs in the bovine genes 2022 , 114, 110272		О
110	Selection and Drift: A Comparison between Historic and Recent Dutch Friesian Cattle and Recent Holstein Friesian Using WGS Data 2022 , 12,		1

109	Genome-wide association study with imputed whole-genome sequence variants including large deletions for female fertility in 3 Nordic dairy cattle breeds 2021 ,		1
108	Identification of important genomic footprints using eight different selection signature statistics in domestic cattle breeds <i>Gene</i> , 2022 , 816, 146165	3.8	4
107	Evaluation of truncating variants in the LCORL gene in relation to body size of goats from Switzerland <i>Animal Genetics</i> , 2022 ,	2.5	0
106	Genomic architecture of phenotypic extremes in a wild cervid <i>BMC Genomics</i> , 2022 , 23, 126	4.5	1
105	Functional annotation of regulatory elements in cattle genome reveals the roles of extracellular interaction and dynamic change of chromatin states in rumen development during weaning 2022 , 114, 110296		О
104	Signatures of selection in Nelore cattle revealed by whole-genome sequencing data 2022 , 114, 110304		1
103	Large-scale association study on daily weight gain in pigs reveals overlap of genetic factors for growth in humans <i>BMC Genomics</i> , 2022 , 23, 133	4.5	0
102	Discovering genomic regions associated with the phenotypic differentiation of European local pig breeds.		
101	Comparative analysis of inbreeding parameters and runs of homozygosity islands in 2 Italian autochthonous cattle breeds mainly raised in the Parmigiano-Reggiano cheese production region 2021 ,		1
100	Extensive Variation in Gene Expression is Revealed in 13 Fertility-Related Genes Using RNA-Seq, ISO-Seq, and CAGE-Seq From Brahman Cattle <i>Frontiers in Genetics</i> , 2022 , 13, 784663	4.5	
99	Genetic variation in PLAG1 is associated with early fertility in Australian Brahman cattle 2022,		0
98	Recovery of mitogenomes from whole genome sequences to infer maternal diversity in 1883 modern taurine and indicine cattle 2022 , 12, 5582		O
97	Genomic landscape, polymorphism and possible LINE-associated delivery of G-Quadruplex motifs in the bovine genes.		
96	Whole-genome resequencing of worldwide wild and domestic sheep elucidates genetic diversity, introgression and agronomically important loci. 2021 ,		4
95	Hmga2 deficiency is associated with allometric growth retardation, infertility, and behavioral abnormalities in mice. 2021 ,		1
94	The conservation of human functional variants and their effects across mammals.		
93	DataSheet_1.docx. 2019 ,		
92	Image_1.tif. 2019 ,		

(2018-2019)

Image_2.tif. 2019, 91 Table_1.xlsx. 2019, 90 89 Table_2.xlsx. 2019, 88 Table_3.xlsx. 2019, Table_4.xlsx. 2019, 87 86 Table_5.xlsx. 2019, 85 Data_Sheet_1.zip. 2019, Data_Sheet_1.xlsx. 2019, 84 83 Data_Sheet_2.pdf. 2019, 82 Image_1.PDF. **2018**, Image_2.pdf. 2018, 81 Image_3.pdf. **2018**, 80 79 Image_4.pdf. **2018**, 78 Image_5.pdf. **2018**, Image_6.pdf. 2018, 77 76 Image_7.pdf. **2018**, Table_1.XLSX. 2018, 75 Table_2.XLSX. 2018, 74



(2022-2019)

55	Image_3.tif. 2019 ,		
54	Table_1.xlsx. 2019 ,		
53	Table_1.DOCX. 2018 ,		
52	Data_Sheet_1.xlsx. 2020 ,		
51	Image_1.PDF. 2018 ,		
50	Table_1.PDF. 2018 ,		
49	Table_2.pdf. 2018 ,		
48	Table_3.pdf. 2018 ,		
47	lmage_1.TIF. 2018 ,		
46	Table_1.XLS. 2018 ,		
45	Ancestry-inclusive dog genomics challenges popular breed stereotypes <i>Science</i> , 2022 , 376, eabk0639	33.3	2
44	Genetic architectures and selection signatures of body height in Chinese indigenous donkeys revealed by next-generation sequencing <i>Animal Genetics</i> , 2022 ,	2.5	O
43	Genome of a giant isopod, Bathynomus jamesi, provides insights into body size evolution and adaptation to deep-sea environment <i>BMC Biology</i> , 2022 , 20, 113	7.3	0
42	Gene expression and RNA splicing explain large proportions of the heritability for complex traits in cattle.		O
41	The application of mixed linear models for the estimation of functional effects on bovine stature based on SNP summary statistics from a whole-genome association study.		
40	Improving Genomic Selection for Heat Tolerance in Dairy Cattle: Current Opportunities and Future Directions. <i>Frontiers in Genetics</i> , 13,	4.5	O
39	Along the Bos taurus genome, uncover candidate imprinting control regions. <i>BMC Genomics</i> , 2022 , 23,	4.5	
38	Meta-analysis across Nellore cattle populations identifies common metabolic mechanisms that regulate feed efficiency-related traits. <i>BMC Genomics</i> , 2022 , 23,	4.5	O

37	Whole genome resequencing reveals the genetic contribution of Kazakh and Swiss Brown cattle to a population of Xinjiang Brown cattle. <i>Gene</i> , 2022 , 146725	
36	Genome-wide association and genotype by environment interactions for growth traits in U.S. Red Angus cattle. <i>BMC Genomics</i> , 2022 , 23, 4.5	2
35	Genome-Wide Screening for SNPs Associated with Stature in Diverse Cattle Breeds. 2022, 14, 692	
34	Comparative transcriptome in large-scale human and cattle populations. 2022 , 23,	1
33	Ruminant-specific retrotransposons shape regulatory evolution of bovine immunity. 2022, 32, 1474-1486	1
32	Allele-biased expression of the bovine APOB gene associated with the cholesterol deficiency defect suggests cis-regulatory enhancer effects of the LTR retrotransposon insertion. 2022 , 12,	
31	Genome-Wide Screening for SNPs Associated with Stature in Diverse Cattle Breeds.	0
30	Meta-Analysis of SNPs Determining Litter Traits in Pigs. 2022 , 13, 1730	O
29	Nucleotide and structural polymorphisms of the eastern oyster genome paint a mosaic of divergence, selection, and human impacts.	0
28	The conservation of human functional variants and their effects across livestock species. 2022 , 5,	O
27	Genome-wide association analysis of milk production, somatic cell score, and body conformation traits in Holstein cows. 9,	0
26	Identification of Genomic Variants Causing Variation in Quantitative Traits: A Review. 2022 , 12, 1713	2
25	The prediction accuracies of linear type traits in Czech Holstein cattle when using ssGBLUP or wssGBLUP.	0
24	Genetic analysis of production traits and body size measurements and their relationships with metabolic diseases in German Holstein cattle. 2023 , 106, 421-438	O
23	Genome-Wide Association Study for Body Conformation Traits and Fitness in Czech Holsteins. 2022 , 12, 3522	0
22	Genetics of tibia bone properties of crossbred commercial laying hens in different housing systems.	O
21	Application of mixed linear models for the estimation of functional effects on bovine stature based on SNP summary statistics from a whole-genome association study. 2022 , 54,	0
20	Genomic diversity and relationship analyses of endangered German Black Pied cattle (DSN) to 68 other taurine breeds based on whole-genome sequencing. 13,	1

19	350. Imputation of low coverage sequence data by utilization of pre-phased reads and HBimpute. 2022 ,	Ο
18	399. LASSO and SVM: an alternative approach to identify associated genome regions for simple and complex traits in cattle. 2022 ,	O
17	639. The effect of allele ancestry on hip height and body weight of tropical beef cattle. 2022,	О
16	523. Sequence-based GWAS meta-analyses for beef production traits. 2022 ,	O
15	Genomic insight into the influence of selection, crossbreeding, and geography on population structure in poultry. 2023 , 55,	Ο
14	Recent advances in crustacean genomics and their potential application in aquaculture.	O
13	MicroRNA sequence variation can impact interactions with target mRNA in cattle. 2023, 868, 147373	0
12	FarmGTEx TWAS-server: an interactive web server for customized TWAS analysis in both human and farm animals.	2
11	389. Sequence-based multi-trait genome-wide association study for linear classification traits in Belgian Blue beef cattle. 2022 ,	Ο
10	512. The application of mixed linear models for the estimation of functional effects on bovine stature based on SNP summary. 2022 ,	O
9	387. Sequence-based association analyses on X chromosome in six dairy cattle breeds. 2022 ,	0
8	537. Large-scale Bmics fine-mapping identifies expression quantitative trait loci significantly affecting cattle phenotypes. 2022 ,	O
7	QTL Mapping: Strategy, Progress, and Prospects in Flax. 2023 , 69-99	O
6	Whole-genome sequencing of cryopreserved resources from French Large White pigs at two distinct sampling times reveals strong signatures of convergent and divergent selection between the dam and sire lines. 2023 , 55,	Ο
5	metaGE: Investigating Genotype Œnvironment interactions through meta-analysis.	0
4	Identification of Candidate Genes and Functional Pathways Associated with Body Size Traits in Chinese Holstein Cattle Based on GWAS Analysis. 2023 , 13, 992	Ο
3	Dynamic chromatin architectures provide insights into the genetics of cattle myogenesis. 2023, 14,	0
2	Integration of non-additive genome-wide association study with a multi-tissue transcriptome analysis of growth and carcass traits in Duroc pigs. 2023 , 100817	0

Large-Scale Phenotyping and Genotyping: State of the Art and Emerging Challenges. **2023**, 103-139

О