

Resource Summary Report

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NAGRP Bioinformatics Coordination Program

RRID:SCR_006564

Type: Tool

Proper Citation

NAGRP Bioinformatics Coordination Program (RRID:SCR_006564)

Resource Information

URL: <http://www.animalgenome.org/>

Proper Citation: NAGRP Bioinformatics Coordination Program (RRID:SCR_006564)

Description: We at NRSP-8 bioinformatics coordination program strive to serve the animal genomics research community to better use computer tools and methods, to best utilize available resources, and in working with researchers in the community, to effectively share, combine, manage, manipulate, and analyze information from genomics/genetics studies. This site is designed as an information center to serve the national animal genome research projects of cattle, chicken, pigs, sheep, horse, and aquaculture species. This is home to databases and web sites (being) built for structural, functional and application oriented studies of the animal genomics, to serve the purpose of research, education and related activities in the scientific, industrial and educational communities in the states and world wide. The challenges in bioinformatics support/research for animal genomics may involve * Effective data collection, organization and management * Rapid development of most needed bioinformatics tools and resources * Efficient use of these tools for innovative data analysis Projects: * Animal Trait Ontology (ATO) Project * Virtual Comparative Genomics * The Past, the Current, and the Potentials * Collaborative and Hosted Works

Abbreviations: NAGRP Bioinformatics Coordination Program

Synonyms: USDA NRSP-8 Program Bioinformatics Coordination Project, NAGRP NRSP-8 Bioinformatics Coordination Program, National Animal Genome Research Program NRSP-8 Bioinformatics Coordination Program, National Animal Genome Research Program Bioinformatics Coordination Project

Resource Type: data or information resource, portal, service resource, topical portal

Keywords: genome, bioinformatics, genomics, sequencing, aquaculture species, computing

Funding: USDA

Resource Name: NAGRP Bioinformatics Coordination Program

Resource ID: SCR_006564

Alternate IDs: nlx_149170

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260903T234843+0000

Ratings and Alerts

No rating or validation information has been found for NAGRP Bioinformatics Coordination Program.

No alerts have been found for NAGRP Bioinformatics Coordination Program.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 101 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Lukic B, et al. (2026) Gene expression profiling by RNA-sequencing reveals regulators of intramuscular fat in Black Slavonian pigs. Scientific reports, 16(1).

Silva EFP, et al. (2026) Genome-Wide Association Studies of Milk Composition Traits in Holstein Cattle Raised in Tropical and Subtropical Conditions. Animals : an open access journal from MDPI, 16(11).

Thambiraja M, et al. (2026) Genetic basis of immunity in Indian cattle as revealed by comparative analysis of Bos genome. Scientific reports, 16(1).

Xu L, et al. (2025) Genome-wide association study reveals new QTL and functional candidate genes for the small intestine length and cecum-colon length in Yorkshire pigs. Journal of animal science, 103.

Crooijmans RPMA, et al. (2025) IMAGE001: A new livestock multispecies SNP array to characterize genomic variation in European livestock gene bank collections. Animal genetics, 56(5), e70039.

Azam S, et al. (2025) Constructing a draft Indian cattle pangenome using short-read sequencing. Communications biology, 8(1), 605.

Huang M, et al. (2025) Genome-Wide Association Studies of Body Weight and Average Daily Gain in Chinese Dongliao Black Pigs. International journal of molecular sciences,

26(7).

Zhou J, et al. (2025) Integrated genome-wide association studies, meta-analysis, and Bayesian fine mapping reveal novel quantitative trait loci's and functional candidate genes for vulva traits in large white pigs. *Journal of animal science*, 103.

Yaman Y, et al. (2025) Exploring the polygenic landscape of wool traits in Turkish Merinos through multi-locus GWAS approaches: middle Anatolian Merino. *Scientific reports*, 15(1), 10611.

Koncagül S, et al. (2025) Genome-wide association studies for conformation traits in the Turkish Holstein cattle population. *Iranian journal of veterinary research*, 26(1), 59.

Knaga S, et al. (2025) Ovalbumin gene polymorphism: Implications for hatchability and egg quality changes during storage in Japanese quail. *Poultry science*, 104(2), 104788.

de Haas EN, et al. (2024) Genetic and neuro-epigenetic effects of divergent artificial selection for feather pecking behaviour in chickens. *BMC genomics*, 25(1), 1219.

Guo Z, et al. (2024) Effect of SNPs on Litter Size in Swine. *Current issues in molecular biology*, 46(7), 6328.

Jin J, et al. (2024) Calcium deposition in chicken eggshells: role of host genetics and gut microbiota. *Poultry science*, 103(10), 104073.

Sheng W, et al. (2024) Oxidative stress controls lncRNA-mediated sow granulosa cell functions in a FoxO1-dependent manner. *Journal of animal science and biotechnology*, 15(1), 171.

Bouzeraa L, et al. (2024) Decoding epigenetic markers: implications of traits and genes through DNA methylation in resilience and susceptibility to mastitis in dairy cows. *Epigenetics*, 19(1), 2391602.

Sun X, et al. (2024) Whole-Genome Resequencing Reveals Genetic Diversity and Wool Trait-Related Genes in Liangshan Semi-Fine-Wool Sheep. *Animals : an open access journal from MDPI*, 14(3).

Yang L, et al. (2024) Mapping and functional characterization of structural variation in 1060 pig genomes. *Genome biology*, 25(1), 116.

Long M, et al. (2024) Genome-Wide Association Study as an Efficacious Approach to Discover Candidate Genes Associated with Body Linear Type Traits in Dairy Cattle. *Animals : an open access journal from MDPI*, 14(15).

Badia-Bringué G, et al. (2023) Control of *Mycobacterium avium* subsp. *paratuberculosis* load within infected bovine monocyte-derived macrophages is associated with host genetics. *Frontiers in immunology*, 14, 1042638.