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, service resource, portal, 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: 20250422T055321+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 78 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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

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

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.

Chen Q, et al. (2023) Multi-Omics Reveals the Effect of Crossbreeding on Some Precursors of Flavor and Nutritional Quality of Pork. Foods (Basel, Switzerland), 12(17).

Kang Z, et al. (2023) Genome-wide single-nucleotide polymorphism data and mitochondrial hypervariable region 1 nucleotide sequence reveal the origin of the Akhal-Teke horse. Animal bioscience, 36(10), 1499.

Tuggle CK, et al. (2022) The Agricultural Genome to Phenome Initiative (AG2PI): creating a shared vision across crop and livestock research communities. Genome biology, 23(1), 3.

Stefos GC, et al. (2022) Genomic landscape, polymorphism and possible LINE-associated delivery of G-quadruplex motifs in the bovine genes. Genomics, 114(2), 110272.

Canive M, et al. (2021) Identification of loci associated with pathological outcomes in Holstein cattle infected with Mycobacterium avium subsp. paratuberculosis using whole-genome sequence data. Scientific reports, 11(1), 20177.

Bermann M, et al. (2021) Validation of single-step GBLUP genomic predictions from threshold models using the linear regression method: An application in chicken mortality. Journal of animal breeding and genetics = Zeitschrift fur Tierzuchtung und Zuchtungsbiologie, 138(1), 4.

Li D, et al. (2021) Genomic Analyses Revealed the Genetic Difference and Potential Selection Genes of Growth Traits in Two Duroc Lines. Frontiers in veterinary science, 8, 725367.

Duan X, et al. (2021) Genome-Wide Association Analysis of Growth Curve Parameters in Chinese Simmental Beef Cattle. Animals : an open access journal from MDPI, 11(1).

Billa PA, et al. (2021) Nutrigenomic analyses reveal miRNAs and mRNAs affected by feed restriction in the mammary gland of midlactation dairy cows. PloS one, 16(4), e0248680.

Canive M, et al. (2021) Identification of loci associated with susceptibility to Mycobacterium avium subsp. paratuberculosis infection in Holstein cattle using combinations of diagnostic tests and imputed whole-genome sequence data. PloS one, 16(8), e0256091.

Hieber JK, et al. (2021) Identification of Genomic Regions for Carcass Quality Traits within the American Simmental Association Carcass Merit Program. Animals : an open access journal from MDPI, 11(2).

Wu P, et al. (2021) A combined GWAS approach reveals key loci for socially-affected traits in Yorkshire pigs. Communications biology, 4(1), 891.

Fulton JE, et al. (2021) The impact of endogenous Avian Leukosis Viruses (ALVE) on production traits in elite layer lines. Poultry science, 100(6), 101121.

Fabbri MC, et al. (2021) Genetic diversity and population history of eight Italian beef cattle breeds using measures of autozygosity. PloS one, 16(10), e0248087.

Tu Y, et al. (2021) Identifying Signatures of Selection Related to Comb Development. The journal of poultry science, 58(1), 5.

Tiezzi F, et al. (2021) Gut microbiome mediates host genomic effects on phenotypes: a case study with fat deposition in pigs. Computational and structural biotechnology journal, 19, 530.