

Resource Summary Report

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ArkDB - Genomes For The Rest of Us

RRID:SCR_001838

Type: Tool

Proper Citation

ArkDB - Genomes For The Rest of Us (RRID:SCR_001838)

Resource Information

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

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Description: The ArkDB database system aims to provide a comprehensive public repository for genome mapping data from farmed and other animal Species. The system also aims to provide a route in to genomic and other sequence from the initial viewpoint of linkage mapping, RH mapping, physical mapping or - possibly more importantly - QTL mapping data. Sponsors: ArkDB is funded by Biotechnology and Biological Sciences Research Council (BBSRC), UK. Cat, Chicken, Cow, Deer, Duck, Horse, Pig, Quail, Salmon, Sea Bass, Sheep, Turkey, QLT map, Linkage map, RH map, Farm animal, Genome map, Sequence, Mapping

Synonyms: ArkDB

Resource Type: data or information resource, database

Defining Citation: [PMID:11125062](#)

Keywords: duck, farm animal, cat, chicken, cow, deer, genome map, horse, linkage map, mapping, model organism comparative genomic, pig, qtl map, quail, rh map, salmon, sea bass, sequence, sheep, turkey

Availability: Free, Freely available

Resource Name: ArkDB - Genomes For The Rest of Us

Resource ID: SCR_001838

Alternate IDs: nif-0000-02568, r3d100012788

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260729T044017+0000

Ratings and Alerts

No rating or validation information has been found for ArkDB - Genomes For The Rest of Us.

No alerts have been found for ArkDB - Genomes For The Rest of Us.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Satta V, et al. (2021) Genetic characterization and implications for conservation of the last autochthonous Mouflon population in Europe. Scientific reports, 11(1), 14729.

Fu Y, et al. (2020) A gene prioritization method based on a swine multi-omics knowledgebase and a deep learning model. Communications biology, 3(1), 502.

Liu X, et al. (2017) Mitochondrial-nuclear crosstalk, haplotype and copy number variation distinct in muscle fiber type, mitochondrial respiratory and metabolic enzyme activities. Scientific reports, 7(1), 14024.

Meng Q, et al. (2017) Identification of growth trait related genes in a Yorkshire purebred pig population by genome-wide association studies. Asian-Australasian journal of animal sciences, 30(4), 462.

Fulgione D, et al. (2016) Unexpected but welcome. Artificially selected traits may increase fitness in wild boar. Evolutionary applications, 9(6), 769.

Wright D, et al. (2015) The Genetic Architecture of Domestication in Animals. Bioinformatics and biology insights, 9(Suppl 4), 11.

Wang K, et al. (2015) Genome Wide Association Analysis Reveals New Production Trait Genes in a Male Duroc Population. PloS one, 10(9), e0139207.

Kaczensky P, et al. (2011) Connectivity of the Asiatic wild ass population in the Mongolian Gobi. Biological conservation, 144(2), 920.

Fan B, et al. (2011) Genome-wide association study identifies Loci for body composition and structural soundness traits in pigs. PloS one, 6(2), e14726.

Rothschild MF, et al. (2007) Advances in QTL mapping in pigs. International journal of biological sciences, 3(3), 192.

Goh G, et al. (2007) High-resolution gene maps of horse chromosomes 14 and 21: additional insights into evolution and rearrangements of HSA5 homologs in mammals.

Genomics, 89(1), 89.

Chen K, et al. (2007) Genetic resources, genome mapping and evolutionary genomics of the pig (*Sus scrofa*). *International journal of biological sciences*, 3(3), 153.

Bie Petersen C, et al. (2007) Various domains of the B-cell regulatory molecule CD72 has diverged at different rates in mammals: cloning, transcription and mapping of porcine CD72. *Developmental and comparative immunology*, 31(5), 530.

Siwek M, et al. (2006) Detection of QTL for innate: non-specific antibody levels binding LPS and LTA in two independent populations of laying hens. *Developmental and comparative immunology*, 30(7), 659.

Lagerstr m MC, et al. (2006) The G protein-coupled receptor subset of the chicken genome. *PLoS computational biology*, 2(6), e54.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.

Honkatukia M, et al. (2005) Fishy taint in chicken eggs is associated with a substitution within a conserved motif of the FMO3 gene. *Genomics*, 86(2), 225.

Brunner RM, et al. (2003) The telomeric region of BTA18 containing a potential QTL region for health in cattle exhibits high similarity to the HSA19q region in humans. *Genomics*, 81(3), 270.

Clark J, et al. (2003) A future for transgenic livestock. *Nature reviews. Genetics*, 4(10), 825.

Nebert DW, et al. (2003) Update on human genome completion and annotations: gene nomenclature. *Human genomics*, 1(1), 66.