Resource Summary Report

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Bovine Genome Database

RRID:SCR_000148
Type: Tool

Proper Citation

Bovine Genome Database (RRID:SCR_000148)

Resource Information

URL: http://bovinegenome.org/

Proper Citation: Bovine Genome Database (RRID:SCR_000148)

Description: Database and integrated tools to improve annotation of the bovine genome and to integrate the genome sequence with other genomics data.

Abbreviations: BGD

Synonyms: The Bovine Genome Database, BovineGenome.org

Resource Type: database, data or information resource

Defining Citation: PMID:21123190, PMID:21092105

Keywords: genome browser, genome

Funding: USDA National Institute of Food and Agriculture 2007-35616-17882;
USDA National Institute of Food and Agriculture 2010-65205-20407

Availability: Acknowledgement requested

Resource Name: Bovine Genome Database

Resource ID: SCR_000148

Alternate IDs: OMICS_04529

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250403T060005+0000

Ratings and Alerts

No rating or validation information has been found for Bovine Genome Database.

No alerts have been found for Bovine Genome Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Bahbahani H, et al. (2018) Genomic signatures of adaptive introgression and environmental adaptation in the Sheko cattle of southwest Ethiopia. PloS one, 13(8), e0202479.

Hampel A, et al. (2018) Estimation of Recombination Rate and Maternal Linkage Disequilibrium in Half-Sibs. Frontiers in genetics, 9, 186.

Loya TJ, et al. (2017) The hnRNP-like Nab3 termination factor can employ heterologous prion-like domains in place of its own essential low complexity domain. PloS one, 12(10), e0186187.

Neupane M, et al. (2017) Loci and pathways associated with uterine capacity for pregnancy and fertility in beef cattle. PloS one, 12(12), e0188997.

Knowlton MN, et al. (2017) Naming CRISPR alleles: endonuclease-mediated mutation nomenclature across species. Mammalian genome : official journal of the International Mammalian Genome Society, 28(7-8), 367.

Uemoto Y, et al. (2017) Effect of two non-synonymous ecto-5'-nucleotidase variants on the genetic architecture of inosine 5'-monophosphate (IMP) and its degradation products in Japanese Black beef. BMC genomics, 18(1), 874.

Olsen HG, et al. (2016) Fine mapping of a QTL on bovine chromosome 6 using imputed full sequence data suggests a key role for the group-specific component (GC) gene in clinical mastitis and milk production. Genetics, selection, evolution : GSE, 48(1), 79.

Elsik CG, et al. (2016) Bovine Genome Database: new tools for gleaning function from the Bos taurus genome. Nucleic acids research, 44(D1), D834.

Chen Z, et al. (2016) Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. Epigenetics, 11(7), 501.

Pinnapureddy AR, et al. (2015) Large animal models of rare genetic disorders: sheep as phenotypically relevant models of human genetic disease. Orphanet journal of rare diseases, 10, 107.

Rai AN, et al. (2015) Application of Functional Genomics for Bovine Respiratory Disease Diagnostics. Bioinformatics and biology insights, 9(Suppl 2), 13.

Galperin MY, et al. (2011) The 2011 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. Nucleic acids research, 39(Database issue), D1.

Childers CP, et al. (2011) Bovine Genome Database: integrated tools for genome annotation and discovery. Nucleic acids research, 39(Database issue), D830.

Reese JT, et al. (2010) Bovine Genome Database: supporting community annotation and analysis of the Bos taurus genome. BMC genomics, 11, 645.

Vu GT, et al. (2010) A simple, high throughput method to locate single copy sequences from Bacterial Artificial Chromosome (BAC) libraries using High Resolution Melt analysis. BMC genomics, 11, 301.