Resource Summary Report

Generated by dkNET on Apr 16, 2025

Trace Archive

RRID:SCR_013788
Type: Tool

Proper Citation

Trace Archive (RRID:SCR_013788)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/Traces/trace.cgi

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Description: An online repository which houses sequencing data from gel and capillary platforms (such as Applied Biosystems ABI 3730®). Most sequences are derived from Whole Genome Shotgun sequencing. Large data sets as well as only a few sequences can be obtained.

Synonyms: Trace Archive, NCBI Trace Archive

Resource Type: data repository, service resource, storage service resource

Keywords: repository, sequencing data, gel platform, capillary platform, whole genome shotgun sequencing

Funding:

Resource Name: Trace Archive

Resource ID: SCR_013788

Alternate URLs: https://www.ncbi.nlm.nih.gov/Traces

Record Creation Time: 20220129T080318+0000

Record Last Update: 20250416T063650+0000

Ratings and Alerts

No rating or validation information has been found for Trace Archive.

No alerts have been found for Trace Archive.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 144 mentions in open access literature.

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

Harhay GP, et al. (2021) A Conserved Histophilus somni 23S Intervening Sequence Yields Functional, Fragmented 23S rRNA. Microbiology spectrum, 9(3), e0143121.

Premzl M, et al. (2020) Author Correction: Comparative genomic analysis of eutherian connexin genes. Scientific reports, 10(1), 10779.

Premzl M, et al. (2020) Comparative genomic analysis of eutherian interferon genes. Genomics, 112(6), 4749.

Cheng RL, et al. (2020) Nudivirus Remnants in the Genomes of Arthropods. Genome biology and evolution, 12(5), 578.

Premzl M, et al. (2019) Comparative genomic analysis of eutherian connexin genes. Scientific reports, 9(1), 16938.

Tsui B, et al. (2019) Extracting allelic read counts from 250,000 human sequencing runs in Sequence Read Archive. Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing, 24, 196.

Hecker N, et al. (2019) Convergent gene losses illuminate metabolic and physiological changes in herbivores and carnivores. Proceedings of the National Academy of Sciences of the United States of America, 116(8), 3036.

Lopes-Marques M, et al. (2019) The Singularity of Cetacea Behavior Parallels the Complete Inactivation of Melatonin Gene Modules. Genes, 10(2).

Jebb D, et al. (2018) Recurrent loss of HMGCS2 shows that ketogenesis is not essential for the evolution of large mammalian brains. eLife, 7.

Li Y, et al. (2018) Plant Phenotypic Traits Eventually Shape Its Microbiota: A Common Garden Test. Frontiers in microbiology, 9, 2479.

Grandi N, et al. (2018) HERV-W group evolutionary history in non-human primates:

characterization of ERV-W orthologs in Catarrhini and related ERV groups in Platyrrhini. BMC evolutionary biology, 18(1), 6.

Premzl M, et al. (2018) Comparative genomic analysis of eutherian adiponectin genes. Heliyon, 4(6), e00647.

Filiault DL, et al. (2018) The Aquilegia genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. eLife, 7.

Kalbfleisch TS, et al. (2018) Improved reference genome for the domestic horse increases assembly contiguity and composition. Communications biology, 1, 197.

VanBelzen DJ, et al. (2017) Mechanism of Deletion Removing All Dystrophin Exons in a Canine Model for DMD Implicates Concerted Evolution of X Chromosome Pseudogenes. Molecular therapy. Methods & clinical development, 4, 62.

Yoshida Y, et al. (2017) Comparative genomics of the tardigrades Hypsibius dujardini and Ramazzottius varieornatus. PLoS biology, 15(7), e2002266.

Metz S, et al. (2016) FullSSR: Microsatellite Finder and Primer Designer. Advances in bioinformatics, 2016, 6040124.

Šev?íková T, et al. (2016) A Comparative Analysis of Mitochondrial Genomes in Eustigmatophyte Algae. Genome biology and evolution, 8(3), 705.

Wolfgruber TK, et al. (2016) High Quality Maize Centromere 10 Sequence Reveals Evidence of Frequent Recombination Events. Frontiers in plant science, 7, 308.

Bao W, et al. (2016) Expressed miRNAs target feather related mRNAs involved in cell signaling, cell adhesion and structure during chicken epidermal development. Gene, 591(2), 393.