Resource Summary Report

Generated by RRID on Apr 13, 2025

Human BAC Ends Database

RRID:SCR_007727
Type: Tool

Proper Citation

Human BAC Ends Database (RRID:SCR_007727)

Resource Information

URL: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_intro.html

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Description: The Human BAC Ends Database is a database of sequences from the ends of bacterial artificial chromosome (BAC) clones. A whole genome sequencing approach has been described in a map-as-you-go strategy. The complete sequence of a seed BAC is searched against a BAC end database and the minimally overlapping clones in each direction are selected for sequencing. As coverage increases, BAC end sequences provide samples for whole genome survey. It currently contains 743,000 end sequences from 470,000 clones (20 X clone coverage and 12% sequence coverage), generated by TIGR, UofWashington and CalTech, providing a sequence marker every 5 kb across the genome. The coverage by paired-ends on chromosome 22 is over 5X. The project is funded by DOE.

Synonyms: Human BAC Ends

Resource Type: database, data or information resource

Keywords: bac, bacterial artificial chromosome, FASEB list

Funding:

Resource Name: Human BAC Ends Database

Resource ID: SCR_007727

Alternate IDs: nif-0000-02992

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250412T055209+0000

Ratings and Alerts

No rating or validation information has been found for Human BAC Ends Database.

No alerts have been found for Human BAC Ends Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 55 mentions in open access literature.

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

Raczynska KD, et al. (2014) The SERRATE protein is involved in alternative splicing in Arabidopsis thaliana. Nucleic acids research, 42(2), 1224.

Dlugosch KM, et al. (2013) Allele identification for transcriptome-based population genomics in the invasive plant Centaurea solstitialis. G3 (Bethesda, Md.), 3(2), 359.

Ahn JE, et al. (2013) Insight into hypoxia tolerance in cowpea bruchid: metabolic repression and heat shock protein regulation via hypoxia-inducible factor 1. PloS one, 8(4), e57267.

Xie M, et al. (2013) Transcriptome profiling of fruit development and maturation in Chinese white pear (Pyrus bretschneideri Rehd). BMC genomics, 14(1), 823.

Damon C, et al. (2012) Metatranscriptomics reveals the diversity of genes expressed by eukaryotes in forest soils. PloS one, 7(1), e28967.

Hu P, et al. (2012) Microarray meta-analysis identifies acute lung injury biomarkers in donor lungs that predict development of primary graft failure in recipients. PloS one, 7(10), e45506.

McNulty SN, et al. (2012) Transcriptomic and proteomic analyses of a Wolbachia-free filarial parasite provide evidence of trans-kingdom horizontal gene transfer. PloS one, 7(9), e45777.

Kim DW, et al. (2012) SpiroESTdb: a transcriptome database and online tool for sparganum expressed sequences tags. BMC research notes, 5, 130.

Ghatak P, et al. (2011) Unveiling the role of Dps in the organization of mycobacterial nucleoid. PloS one, 6(1), e16019.

Hu L, et al. (2011) Genome-wide identification and phylogenetic analysis of the ERF gene

family in cucumbers. Genetics and molecular biology, 34(4), 624.

Jaeckisch N, et al. (2011) Comparative genomic and transcriptomic characterization of the toxigenic marine dinoflagellate Alexandrium ostenfeldii. PloS one, 6(12), e28012.

Montaño AM, et al. (2011) Evolutionary origin of peptidoglycan recognition proteins in vertebrate innate immune system. BMC evolutionary biology, 11, 79.

Sierra R, et al. (2010) Discovery of Phytophthora infestans genes expressed in planta through mining of cDNA libraries. PloS one, 5(3), e9847.

Preechaphol R, et al. (2010) Isolation and characterization of genes functionally involved in ovarian development of the giant tiger shrimp Penaeus monodon by suppression subtractive hybridization (SSH). Genetics and molecular biology, 33(4), 676.

Tam PP, et al. (2010) The Puf family of RNA-binding proteins in plants: phylogeny, structural modeling, activity and subcellular localization. BMC plant biology, 10, 44.

Takata N, et al. (2010) Phylogenetic footprint of the plant clock system in angiosperms: evolutionary processes of pseudo-response regulators. BMC evolutionary biology, 10, 126.

Wu X, et al. (2010) Genes encoding hub and bottleneck enzymes of the Arabidopsis metabolic network preferentially retain homeologs through whole genome duplication. BMC evolutionary biology, 10, 145.

Desgagné-Penix I, et al. (2010) Integration of deep transcriptome and proteome analyses reveals the components of alkaloid metabolism in opium poppy cell cultures. BMC plant biology, 10, 252.

Cibrián-Jaramillo A, et al. (2010) Using phylogenomic patterns and gene ontology to identify proteins of importance in plant evolution. Genome biology and evolution, 2, 225.

Kim DW, et al. (2009) GarlicESTdb: an online database and mining tool for garlic EST sequences. BMC plant biology, 9, 61.