Resource Summary Report

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AceView

RRID:SCR_002277
Type: Tool

Proper Citation

AceView (RRID:SCR_002277)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/ieb/research/acembly/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented May 10, 2017. A pilot effort that has developed a centralized, web-based biospecimen locator that presents biospecimens collected and stored at participating Arizona hospitals and biospecimen banks, which are available for acquisition and use by researchers. Researchers may use this site to browse, search and request biospecimens to use in qualified studies. The development of the ABL was guided by the Arizona Biospecimen Consortium (ABC), a consortium of hospitals and medical centers in the Phoenix area, and is now being piloted by this Consortium under the direction of ABRC. You may browse by type (cells, fluid, molecular, tissue) or disease. Common data elements decided by the ABC Standards Committee, based on data elements on the National Cancer Institute''s (NCI''s) Common Biorepository Model (CBM), are displayed. These describe the minimum set of data elements that the NCI determined were most important for a researcher to see about a biospecimen. The ABL currently does not display information on whether or not clinical data is available to accompany the biospecimens. However, a requester has the ability to solicit clinical data in the request. Once a request is approved, the biospecimen provider will contact the requester to discuss the request (and the requester''s questions) before finalizing the invoice and shipment. The ABL is available to the public to browse. In order to request biospecimens from the ABL, the researcher will be required to submit the requested required information. Upon submission of the information, shipment of the requested biospecimen(s) will be dependent on the scientific and institutional review approval. Account required. Registration is open to everyone., documented August 29, 2016. AceView offers an integrated view of the human, nematode and Arabidopsis genes reconstructed by co-alignment of all publicly available mRNAs and ESTs on the genome sequence. Our goals are to offer a reliable up-to-date resource on the genes and their functions and to stimulate further validating experiments at the bench. AceView provides a curated, comprehensive and non-redundant

sequence representation of all public mRNA sequences (mRNAs from GenBank or RefSeq, and single pass cDNA sequences from dbEST and Trace). These experimental cDNA sequences are first co-aligned on the genome then clustered into a minimal number of alternative transcript variants and grouped into genes. Using exhaustively and with high quality standards the available cDNA sequences evidences the beauty and complexity of mammals' transcriptome, and the relative simplicity of the nematode and plant transcriptomes. Genes are classified according to their inferred coding potential; many presumably non-coding genes are discovered. Genes are named by Entrez Gene names when available, else by AceView gene names, stable from release to release. Alternative features (promoters, introns and exons, polyadenylation signals) and coding potential, including motifs, domains, and homologies are annotated in depth; tissues where expression has been observed are listed in order of representation; diseases, phenotypes, pathways, functions, localization or interactions are annotated by mining selected sources, in particular PubMed, GAD and Entrez Gene, and also by performing manual annotation, especially in the worm. In this way, both the anatomy and physiology of the experimentally cDNA supported human, mouse and nematode genes are thoroughly annotated. Our goals are to offer an up-to-date resource on the genes, in the hope to stimulate further experiments at the bench, or to help medical research. AceView can be queried by meaningful words or groups of words as well as by most standard identifiers, such as gene names, Entrez Gene ID, UniGene ID, GenBank accessions.

Abbreviations: AceView/WormGenes

Synonyms: AceView genes, AceView/WormGenes, The AceView Genes

Resource Type: data or information resource, database

Keywords: est, exon, expression, function, gene, alignment, arabidopsis, cdna, co-alignment, coding, disease, genome, genomic, human, intron, localization, mammal, mouse, mrna, nematode, pathway, phenotype, plant, polyadenylation, promoter, rat, sequence, signal, tissue, transcript, transcriptome, worm, blast, gold standard

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: AceView

Resource ID: SCR_002277

Alternate IDs: nif-0000-21007

Old URLs: http://www.ncbi.nih.gov/IEB/Research/Acembly/

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250422T055021+0000

Ratings and Alerts

No rating or validation information has been found for AceView.

No alerts have been found for AceView.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 186 mentions in open access literature.

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

Zhao W, et al. (2025) GoFCards: an integrated database and analytic platform for gain of function variants in humans. Nucleic acids research, 53(D1), D976.

Werr L, et al. (2025) TERT Expression and Clinical Outcome in Pulmonary Carcinoids. Journal of clinical oncology : official journal of the American Society of Clinical Oncology, 43(2), 214.

Olszewska M, et al. (2024) Effects of Tcte1 knockout on energy chain transportation and spermatogenesis: implications for male infertility. Human reproduction open, 2024(2), hoae020.

Shaw TI, et al. (2024) Comprehensive genomic analysis reveals molecular heterogeneity in pediatric ALK-positive anaplastic large cell lymphoma. Research square.

Jurida L, et al. (2024) A common gene signature of the right ventricle in failing rat and human hearts. Nature cardiovascular research, 3(7), 819.

Patterson MR, et al. (2024) E7-mediated repression of miR-203 promotes LASP1-dependent proliferation in HPV-positive cervical cancer. Oncogene, 43(28), 2184.

Newman JRB, et al. (2023) Shifts in isoform usage underlie transcriptional differences in regulatory T cells in type 1 diabetes. Communications biology, 6(1), 988.

Guaita-Cespedes M, et al. (2023) Deciphering the sex bias in housekeeping gene expression in adipose tissue: a comprehensive meta-analysis of transcriptomic studies. Biology of sex differences, 14(1), 20.

Morrison KR, et al. (2023) Elevated basal AMP-activated protein kinase activity sensitizes colorectal cancer cells to growth inhibition by metformin. Open biology, 13(4), 230021.

Marini P, et al. (2023) M3 Receptor Pathway Stimulates Rapid Transcription of the CB1

Receptor Activation through Calcium Signalling and the CNR1 Gene Promoter. International journal of molecular sciences, 24(2).

Hebbar N, et al. (2022) CAR T cells redirected to cell surface GRP78 display robust anti-acute myeloid leukemia activity and do not target hematopoietic progenitor cells. Nature communications, 13(1), 587.

Saul N, et al. (2022) Identification of healthspan-promoting genes in Caenorhabditis elegans based on a human GWAS study. Biogerontology, 23(4), 431.

Ghasemi S, et al. (2022) A novel likely pathogenic variant in the FBXO32 gene associated with dilated cardiomyopathy according to whole?exome sequencing. BMC medical genomics, 15(1), 234.

Meng H, et al. (2022) Defining the mammalian coactivation of hepatic 12-h clock and lipid metabolism. Cell reports, 38(10), 110491.

Aggarwal P, et al. (2022) Genetic susceptibility to patient-reported xerostomia among long-term oropharyngeal cancer survivors. Scientific reports, 12(1), 6662.

Shaw TI, et al. (2021) Integrative network analysis reveals USP7 haploinsufficiency inhibits E-protein activity in pediatric T-lineage acute lymphoblastic leukemia (T-ALL). Scientific reports, 11(1), 5154.

Fornerod M, et al. (2021) Integrative Genomic Analysis of Pediatric Myeloid-Related Acute Leukemias Identifies Novel Subtypes and Prognostic Indicators. Blood cancer discovery, 2(6), 586.

Schwartz JR, et al. (2021) The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. Nature communications, 12(1), 985.

Kwak YD, et al. (2021) Chromatin architecture at susceptible gene loci in cerebellar Purkinje cells characterizes DNA damage-induced neurodegeneration. Science advances, 7(51), eabg6363.

Mehravar M, et al. (2021) Exon and intron sharing in opposite direction-an undocumented phenomenon in human genome-between Pou5f1 and Tcf19 genes. BMC genomics, 22(1), 718.