Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 18, 2025

Gene Index Project

RRID:SCR_002148
Type: Tool

Proper Citation

Gene Index Project (RRID:SCR_002148)

Resource Information

URL: http://compbio.dfci.harvard.edu/tgi/

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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 on August 19,2019.The goal of The Gene Index Project is to use the available Expressed Sequence Transcript (EST) and gene sequences, along with the reference genomes wherever available, to provide an inventory of likely genes and their variants and to annotate these with information regarding the functional roles played by these genes and their products. The promise of genome projects has been a complete catalog of genes in a wide range of organisms. While genome projects have been successful in providing reference genome sequences, the problem of finding genes and their variants in genomic sequence remains an ongoing challenge. TGI has created an inventory that contains genes and their variants together with description. In addition, this resource is attempting to use these catalogs to find links between genes and pathways in different species and to provide lists of features within completed genomes that can aid in the understanding of how gene expression is regulated. DATABASES *Eukaryotic Gene Orthologues (formerly known as TOGA - TIGR Orthologous Gene Alignment): Eukaryotic Gene Orthologues (EGO) at DFGI are generated by pair-wise comparison between the Tentative Consensus (TC) sequences that comprise the Dana Farber Gene Indices from individual organisms. The reciprocal pairs of the best match were clustered into individual groups and multiple sequence alignments were displayed for each group. *GeneChip Oncology Database (GCOD):Cancer gene expression database is a collection of publicly available microarray expression data on Affymetrix GeneChip Arrays related to human cancers. Currently only datasets with available raw data (Affymetrix .CEL files) are processed. All processed datasets were subjected to extensive manual curation, uniform processing and consistent quality control. You can browse the experiments in our collection, perform statistical analysis, and download processed data; or to search gene expression profiles using Entrez gene symbol, Unigene ID, or Affymetrix probeset ID. *Gene Indices: As of July 1, 2008, there are 111 publicly available gene indices. They are separated into 4 categories for better organization and easier access. Animal: 41, Plant: 45, Protist: 15, Fungal: 10 *Genomic Maps: Human, mouse, rat, chicken, drosophila melanogaster, zebrafish, mosquito, caenorhabditis elegans, Arabidopsis thaliana, rice, yeast, fission yeast Dana-Farber Cancer Institute (DFCI) Gene Indices Software Tools: *TGI Clustering tools (TGICL): a software system for fast clustering of large EST datasets. *GICL: this package contains the scripts and all the necessary pre-compiled binaries for 32bit Linux systems. *clview: an assembly file viewer. *SeqClean:a script for automated trimming and validation of ESTs or other DNA sequences by screening for various contaminants, low quality and low-complexity sequences. *cdbfasta/cdbyank: fast indexing/retrieval of fasta records from flat file databases. *DAS/XML Genomic Viewer The Genomic viewer borrows modules from http://www.biodas.org (lstein (at) cshl.org) & http://webreference.com.

Abbreviations: TGI, DFCI TGI

Synonyms: DFCI Gene Index Project, Gene Index Project, DFCI

Resource Type: database, software resource, portal, topical portal, data or information resource

Defining Citation: PMID:7566098

Keywords: functional, gene, genome, index, organism, pathway, product, role, sequence, species, transcript, variant, bio.tools

Funding: DOE DBI-0552416

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Gene Index Project

Resource ID: SCR_002148

Alternate IDs: biotools:tigr_gene_indices, nif-0000-20942

Alternate URLs: https://bio.tools/tigr_gene_indices

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250418T054956+0000

Ratings and Alerts

No rating or validation information has been found for Gene Index Project.

No alerts have been found for Gene Index Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 129 mentions in open access literature.

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

Kumar R, et al. (2024) Advances in genomic tools for plant breeding: harnessing DNA molecular markers, genomic selection, and genome editing. Biological research, 57(1), 80.

Torres CA, et al. (2020) Photooxidative stress activates a complex multigenic response integrating the phenylpropanoid pathway and ethylene, leading to lignin accumulation in apple (Malus domestica Borkh.) fruit. Horticulture research, 7, 22.

Canedo-Téxon A, et al. (2019) Novel findings to the biosynthetic pathway of magnoflorine and taspine through transcriptomic and metabolomic analysis of Croton draco (Euphorbiaceae). BMC plant biology, 19(1), 560.

Lian JL, et al. (2019) How exposure to ALS-inhibiting gametocide tribenuron-methyl induces male sterility in rapeseed. BMC plant biology, 19(1), 124.

Bradai M, et al. (2018) Genome wide identification of wheat and Brachypodium type one protein phosphatases and functional characterization of durum wheat TdPP1a. PloS one, 13(1), e0191272.

Szurman-Zubrzycka ME, et al. (2018) HorTILLUS-A Rich and Renewable Source of Induced Mutations for Forward/Reverse Genetics and Pre-breeding Programs in Barley (Hordeum vulgare L.). Frontiers in plant science, 9, 216.

Piriyapongsa J, et al. (2018) Uncovering full-length transcript isoforms of sugarcane cultivar Khon Kaen 3 using single-molecule long-read sequencing. PeerJ, 6, e5818.

Yu Y, et al. (2018) XPAT: a toolkit to conduct cross-platform association studies with heterogeneous sequencing datasets. Nucleic acids research, 46(6), e32.

Raimundo J, et al. (2018) Successive Domain Rearrangements Underlie the Evolution of a Regulatory Module Controlled by a Small Interfering Peptide. Molecular biology and evolution, 35(12), 2873.

She M, et al. (2017) Comprehensive molecular analysis of arginase-encoding genes in common wheat and its progenitor species. Scientific reports, 7(1), 6641.

Wang D, et al. (2017) Comparative transcription analysis of different Antirrhinum phyllotaxy nodes identifies major signal networks involved in vegetative-reproductive transition. PloS one, 12(6), e0178424.

Chong Z, et al. (2017) novoBreak: local assembly for breakpoint detection in cancer genomes. Nature methods, 14(1), 65.

Woldesemayat AA, et al. (2017) An integrated and comparative approach towards identification, characterization and functional annotation of candidate genes for drought tolerance in sorghum (Sorghum bicolor (L.) Moench). BMC genetics, 18(1), 119.

Yeo FKS, et al. (2017) High-resolution mapping of genes involved in plant stage-specific partial resistance of barley to leaf rust. Molecular breeding : new strategies in plant improvement, 37(4), 45.

Peng Z, et al. (2017) Transcriptome profiles reveal gene regulation of peanut (Arachis hypogaea L.) nodulation. Scientific reports, 7, 40066.

Sepiol CJ, et al. (2017) Genome-Wide Identification of Chalcone Reductase Gene Family in Soybean: Insight into Root-Specific GmCHRs and Phytophthora sojae Resistance. Frontiers in plant science, 8, 2073.

Fagernes CE, et al. (2017) Extreme anoxia tolerance in crucian carp and goldfish through neofunctionalization of duplicated genes creating a new ethanol-producing pyruvate decarboxylase pathway. Scientific reports, 7(1), 7884.

Voldoire E, et al. (2017) Expansion by whole genome duplication and evolution of the sox gene family in teleost fish. PloS one, 12(7), e0180936.

Barraza A, et al. (2016) The Class II Trehalose 6-phosphate Synthase Gene PvTPS9 Modulates Trehalose Metabolism in Phaseolus vulgaris Nodules. Frontiers in plant science, 7, 1589.

Wang Z, et al. (2016) Comprehensive analysis of trihelix genes and their expression under biotic and abiotic stresses in Populus trichocarpa. Scientific reports, 6, 36274.