Resource Summary Report

Generated by RRID on May 17, 2025

GeneNest

RRID:SCR_007677
Type: Tool

Proper Citation

GeneNest (RRID:SCR_007677)

Resource Information

URL: http://genenest.molgen.mpg.de/

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Description: GeneNest is a comprehensive visualization of gene indices of several organisms. The aim of GeneNest is to represent each gene by a single cluster of ESTs and/or mRNAs. Further subdivision of a cluster into contigs may be caused by alternative splicing, genomic sequences, or artifacts like chimeric sequences. Consensus sequence derived from GeneNest contigs are a basis for mapping genes onto the genome, and for analysis of splice isoforms. Organisms included are human, mouse, arabidopsis, zebrafish, drosophila, and sheep. human, mouse, arabidopsis, zebrafish, drosophila, sheep, EST, mRNA, alternative splicing, genomic sequences

Synonyms: GeneNest

Resource Type: database, data or information resource

Keywords: est, alternative splicing, arabidopsis, drosophila, genomic sequences, human, mouse, mrna, sheep, zebrafish

Funding:

Resource Name: GeneNest

Resource ID: SCR_007677

Alternate IDs: nif-0000-02883

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250517T055834+0000

Ratings and Alerts

No rating or validation information has been found for GeneNest.

No alerts have been found for GeneNest.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Rampp M, et al. (2006) The MIGenAS integrated bioinformatics toolkit for web-based sequence analysis. Nucleic acids research, 34(Web Server issue), W15.

Hagens O, et al. (2006) Characterization of FBX25, encoding a novel brain-expressed F-box protein. Biochimica et biophysica acta, 1760(1), 110.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Khabar KS, et al. (2005) AU-rich transient response transcripts in the human genome: expressed sequence tag clustering and gene discovery approach. Genomics, 85(2), 165.

Beissbarth T, et al. (2003) Analysis of CREM-dependent gene expression during mouse spermatogenesis. Molecular and cellular endocrinology, 212(1-2), 29.