

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

Sequence Tag Alignment and Consensus Knowledgebase Database

RRID:SCR_002156

Type: Tool

Proper Citation

Sequence Tag Alignment and Consensus Knowledgebase Database
(RRID:SCR_002156)

Resource Information

URL: <http://ww2.sanbi.ac.za/Dbases.html>

Proper Citation: Sequence Tag Alignment and Consensus Knowledgebase Database
(RRID:SCR_002156)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 23, 2016. The STACKdb is knowledgebase generated by processing EST and mRNA sequences obtained from GenBank through a pipeline consisting of masking, clustering, alignment and variation analysis steps. The STACK project aims to generate a comprehensive representation of the sequence of each of the expressed genes in the human genome by extensive processing of gene fragments to make accurate alignments, highlight diversity and provide a carefully joined set of consensus sequences for each gene. The STACK project is comprised of the STACKdb human gene index, a database of virtual human transcripts, as well as stackPACK, the tools used to create the database. STACKdb is organized into 15 tissue-based categories and one disease category. STACK is a tool for detection and visualization of expressed transcript variation in the context of developmental and pathological states. The data system organizes and reconstructs human transcripts from available public data in the context of expression state. The expression state of a transcript can include developmental state, pathological association, site of expression and isoform of expressed transcript. STACK consensus transcripts are reconstructed from clusters that capture and reflect the growing evidence of transcript diversity. The comprehensive capture of transcript variants is achieved by the use of a novel clustering approach that is tolerant of sub-sequence diversity and does not rely on pairwise alignment. This is in contrast with other gene indexing projects. STACK is generated at least four times a year and represents the exhaustive processing of all publicly available human EST data extracted from GenBank. This processed information can be explored through 15 tissue-specific categories, a disease-related category and a whole-body index

Synonyms: STACKdb

Resource Type: data or information resource, software resource, software application, database, data visualization software, data processing software

Defining Citation: [PMID:11125101](#)

Keywords: exonic, expressed, expressed sequence tag (est), expression, fragment, gene, alignment, alternative gene, cdna, clone, cluster, developmental, disease, diversity, genome, homo sapiens, human, isoform, knowledgebase, meta-cluster, mrna, pathological, sequence, tissue, transcript, variant, visualization

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Sequence Tag Alignment and Consensus Knowledgebase Database

Resource ID: SCR_002156

Alternate IDs: nif-0000-20946

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260808T190228+0000

Ratings and Alerts

No rating or validation information has been found for Sequence Tag Alignment and Consensus Knowledgebase Database.

No alerts have been found for Sequence Tag Alignment and Consensus Knowledgebase Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.