

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

BETSY

RRID:SCR_026239

Type: Tool

Proper Citation

BETSY (RRID:SCR_026239)

Resource Information

URL: <https://github.com/jefftc/changlab>

Proper Citation: BETSY (RRID:SCR_026239)

Description: Software system for performing bioinformatics analyses. System includes knowledge base where the capabilities of bioinformatics software is explicitly and formally encoded. Backwards-chaining rule-based expert system comprised of data model that can capture richness of biological data, and inference engine that reasons on knowledge base to produce workflows. Knowledge base is populated with rules to analyze microarray and next generation sequencing data.

Synonyms: Bioinformatics Expert SYstem

Resource Type: software resource, source code

Defining Citation: [PMID:28052928](#)

Keywords: produce workflows, performing bioinformatics analyses, microarray data analysis, next generation sequencing data analysis,

Funding: Cancer Prevention and Research Institute of Texas ;
NIH

Availability: Free, Available for download, Freely available,

Resource Name: BETSY

Resource ID: SCR_026239

License URLs: <https://github.com/jefftc/changlab?tab=License-1-ov-file#readme>

Record Creation Time: 20250108T053322+0000

Record Last Update: 20260804T043854+0000

Ratings and Alerts

No rating or validation information has been found for BETSY.

No alerts have been found for BETSY.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.