

# Resource Summary Report

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## BETSY

RRID:SCR\_026239

Type: Tool

### Proper Citation

BETSY (RRID:SCR\_026239)

### Resource Information

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

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**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:** 20260815T183230+0000

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## Ratings and Alerts

No rating or validation information has been found for BETSY.

No alerts have been found for BETSY.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.