

# Resource Summary Report

Generated by T1D on Aug 1, 2026

## Tunable Biclustering Algorithm

RRID:SCR\_017121

Type: Tool

### Proper Citation

Tunable Biclustering Algorithm (RRID:SCR\_017121)

### Resource Information

**URL:** <https://github.com/KhiabanianLab/TuBA>

**Proper Citation:** Tunable Biclustering Algorithm (RRID:SCR\_017121)

**Description:** Software tool as graph based unsupervised biclustering algorithm to identify alterations in tumors based on hypothesis that gene pairs relevant to clinical process share statistically significant number of samples with extreme expression.

**Abbreviations:** TuBA

**Resource Type:** data processing software, data analysis software, software application, software resource

**Keywords:** graph, unsupervised, algorithm, identify, alteration, tumor, gene, pair, significant, expression

**Availability:** Free, Available for download, Freely available

**Resource Name:** Tunable Biclustering Algorithm

**Resource ID:** SCR\_017121

**Record Creation Time:** 20220129T080333+0000

**Record Last Update:** 20260801T042805+0000

### Ratings and Alerts

No rating or validation information has been found for Tunable Biclustering Algorithm.

No alerts have been found for Tunable Biclustering Algorithm.

### Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Panda A, et al. (2020) Tissue- and development-stage-specific mRNA and heterogeneous CNV signatures of human ribosomal proteins in normal and cancer samples. Nucleic acids research, 48(13), 7079.

Singh A, et al. (2019) TuBA: Tunable biclustering algorithm reveals clinically relevant tumor transcriptional profiles in breast cancer. GigaScience, 8(6).