# **Resource Summary Report**

Generated by NIF on May 15, 2025

## **BAIT**

RRID:SCR\_000511

Type: Tool

### **Proper Citation**

BAIT (RRID:SCR\_000511)

#### **Resource Information**

URL: http://sourceforge.net/projects/bait/

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**Description:** Software to create strand inheritance plots in data derived from the Strand-Seq sequencing protocol. The software is designed to be flexible with a range of species, and basic template folders can called to read in species-specific data.

Abbreviations: BAIT

Synonyms: BAIT - Software to help analyse Strand-Seq data

**Resource Type:** software application, data visualization software, data analysis software,

data processing software, software resource

**Defining Citation: PMID:24028793** 

**Keywords:** create strand inheritance plots, strand-seq, bio.tools

**Funding:** 

Availability: Free, Available for download, Freely available

Resource Name: BAIT

Resource ID: SCR\_000511

Alternate IDs: biotools:bait, OMICS 01531

Alternate URLs: https://bio.tools/bait

License: BSD License

**Record Creation Time:** 20220129T080202+0000

Record Last Update: 20250514T061146+0000

### **Ratings and Alerts**

No rating or validation information has been found for BAIT.

No alerts have been found for BAIT.

### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 1 mentions in open access literature.

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

Hills M, et al. (2013) BAIT: Organizing genomes and mapping rearrangements in single cells. Genome medicine, 5(9), 82.