

# Resource Summary Report

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## End Sequence Analysis ToolKit (ESAT)

RRID:SCR\_015812

Type: Tool

### Proper Citation

End Sequence Analysis ToolKit (ESAT) (RRID:SCR\_015812)

### Resource Information

**URL:** <https://github.com/garber-lab/ESAT>

**Proper Citation:** End Sequence Analysis ToolKit (ESAT) (RRID:SCR\_015812)

**Description:** Software for the analysis of short reads obtained from end-sequence RNA-seq. ESAT is designed for expression analysis of Digital expression (DGE) libraries that target transcript "ends."

**Abbreviations:** ESAT

**Synonyms:** End Sequence Analysis ToolKit

**Resource Type:** source code, data processing software, software resource, data analysis software, software toolkit, sequence analysis software, software application

**Defining Citation:** [PMID:27470110](#)

**Keywords:** short read, rna-seq, expression analysis, dge, digital expression library, transcript end, sequence analysis, alignment, sam file, bam file

**Availability:** Free, Available for download

**Resource Name:** End Sequence Analysis ToolKit (ESAT)

**Resource ID:** SCR\_015812

**Record Creation Time:** 20220129T080327+0000

**Record Last Update:** 20260818T043524+0000

### Ratings and Alerts

- Used for bioinformatics analysis by the Human Islet Research Network community. Contact(s): [Rita Bortell](#), [David Harlan](#), [Dale Greiner](#) - Human Islets Research Network <https://hirnetwork.org/>

No alerts have been found for End Sequence Analysis ToolKit (ESAT).

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Nanaware PP, et al. (2025) The antigen presentation landscape of cytokine-stressed human pancreatic islets. Cell reports, 44(8), 115927.

Wang Y, et al. (2023) Transcriptional and chromatin profiling of human blood innate lymphoid cell subsets sheds light on HIV-1 pathogenesis. The EMBO journal, 42(16), e114153.

Pamudurti NR, et al. (2022) circMbl functions in cis and in trans to regulate gene expression and physiology in a tissue-specific fashion. Cell reports, 39(4), 110740.

Singh PK, et al. (2021) The Tomato ddm1b Mutant Shows Decreased Sensitivity to Heat Stress Accompanied by Transcriptional Alterations. Genes, 12(9).

Qaisar N, et al. (2021) Type I IFN-Driven Immune Cell Dysregulation in Rat Autoimmune Diabetes. ImmunoHorizons, 5(10), 855.

Gao KM, et al. (2021) Human nasal wash RNA-Seq reveals distinct cell-specific innate immune responses in influenza versus SARS-CoV-2. JCI insight, 6(22).

Rinaldi VD, et al. (2020) An atlas of cell types in the mouse epididymis and vas deferens. eLife, 9.

Afik S, et al. (2017) Defining the 5' and 3' landscape of the Drosophila transcriptome with Exo-seq and RNaseH-seq. Nucleic acids research, 45(11), e95.

Derr A, et al. (2016) End Sequence Analysis Toolkit (ESAT) expands the extractable information from single-cell RNA-seq data. Genome research, 26(10), 1397.