

# Resource Summary Report

Generated by [NIF](#) on Aug 7, 2026

## MachiBase

RRID:SCR\_003078

Type: Tool

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### Proper Citation

MachiBase (RRID:SCR\_003078)

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### Resource Information

**URL:** <http://machibase.gi.k.u-tokyo.ac.jp/>

**Proper Citation:** MachiBase (RRID:SCR\_003078)

**Description:** Database for Drosophila melanogaster transcription profiling that allows users to search the Drosophila genome, see sequence overviews, and look at various transcripts. The data were generated in conjunction with the recently developed high-throughput genome sequencer Illumina / Solexa using a newly developed 5'-end mRNA collection method. Approximately 25 million 25-27 nucleotide (nt) 5'-end mRNA tags from the embryos, larvae, young males, young females, old males, old females, and S2 (culture cell line) of D. melanogaster were collected. By arranging this vast amount of expression tag with other annotated data, they have built a one-stop service for Drosophila melanogaster transcription profiling.

**Abbreviations:** MachiBase

**Resource Type:** database, data or information resource

**Defining Citation:** [PMID:18842623](#)

**Keywords:** transcription profiling, genome, sequence, transcript, mrna, promoter, gene expression, development, embryo, larvae, young, male, female, old, s2, culture, cell line, expressed sequence tag, solexa

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

**Resource Name:** MachiBase

**Resource ID:** SCR\_003078

**Alternate IDs:** OMICS\_01878, nif-0000-03092

**Record Creation Time:** 20220129T080217+0000

**Record Last Update:** 20260807T042547+0000

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## Ratings and Alerts

No rating or validation information has been found for MachiBase.

No alerts have been found for MachiBase.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Dreos R, et al. (2021) Computational identification and experimental characterization of preferred downstream positions in human core promoters. PLoS computational biology, 17(8), e1009256.