

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

MachiBase

RRID:SCR_003078

Type: Tool

Proper Citation

MachiBase (RRID:SCR_003078)

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: data or information resource, database

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: 20260804T043210+0000

Ratings and Alerts

No rating or validation information has been found for MachiBase.

No alerts have been found for MachiBase.

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 [ASWG](#) .

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