

# Beetle Atlas

The Tribolium gene expression atlas

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# Beetle Atlas

## User's Manual

<https://www.beetleatlas.org>

December 2023

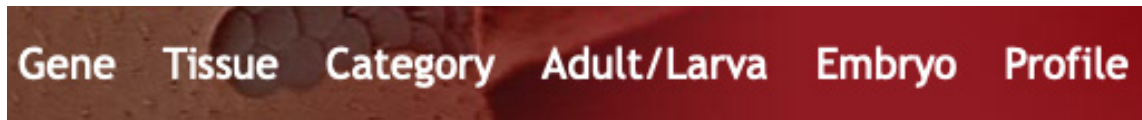
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# 1. Introduction

BEETLE ATLAS is a definitive, tissue-specific transcriptomic resource based on RNA-Seq data for the *Tribolium* community and beyond. From a simple web search BeetleAtlas allows users to explore the spatial expression pattern of genes of interest in embryos, larvae and adults of the red flour beetle, *Tribolium castaneum*. Thus, in its simplest form, BeetleAtlas will provide an answer to the key question in functional genomics “Where is my gene of interest expressed?”. For each tissue you can obtain the transcript abundance (FPKM) and enrichment (compared to whole beetle), and for all conditions there is information on gene splice variants (i.e. isoforms).

Different types of search are available from the menu:

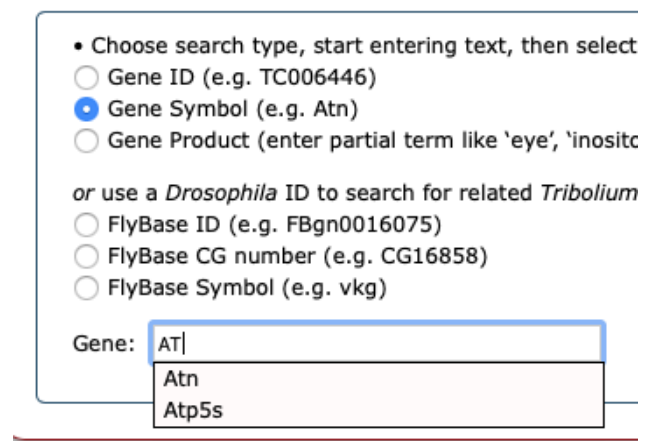


- GENE: For a particular gene, find details of its expression in different tissues or in embryos.
- TISSUE: For a given tissue, find the genes of a particular category with the greatest expression.
- CATEGORY: For a given tissue, find highly expressed genes corresponding to certain assigned keywords.
- ADULT/LARVA: For a given tissue, find the genes that show different expression between larva and adult.
- EMBRYO: Find genes expressed at different stages of embryo development.
- PROFILE: Find genes with a pattern of expression similar to a gene of interest.

Each type of search will be described in turn, but before starting we would emphasize:

## 2. Autocomplete is there to help you

For every field in which a gene name or identifier is entered there is an autocomplete facility based on the entries in the database underlying BeetleAtlas. The autosuggest for a Symbol starts after two characters and that for a gene ID after six. The reason for using this is to save yourself the frustration of making a query, only to discover that the gene is not in the database. If the gene is not in the autocomplete menu you can be sure that it is not in the database: check for typos or that you have the appropriate search type selected.



### 3. Different Types of Search

#### (i) Gene Search

For a particular *Tribolium* gene, find the pattern of expression in different tissues.

- Choose search type, start entering text, then select from the autosuggest menu •
  - Gene ID (e.g. TC006446)
  - Gene Symbol (e.g. Atn)
  - Gene Product (enter partial term like 'eye', 'inositol')
- or use a *Drosophila* ID to search for related *Tribolium* genes
  - FlyBase ID (e.g. FBgn0016075)
  - FlyBase CG number (e.g. CG16858)
  - FlyBase Symbol (e.g. vkg)

Gene:

Searching for tissue-specific expression data for a single gene is quite straightforward: select the type of input (to inform the autocomplete), enter the search term, click on the correct autocomplete text (p. 3) and hit the search button. One can search using *Drosophila* identifiers as well as those for *Tribolium*. The results, which are similar for most other searches, are discussed in the section 4.

#### (ii) Tissue Search

Find which genes have the greatest expression in a particular tissue.

First select a 'stage' and next the tissue of interest. Then choose 'enrichment' or 'abundance' for greatest expression:

Display:

**ANATOMICAL KEY** [show](#)

Tissue search allows one to search for the genes with the greatest expression in a particular tissue. First one chooses the tissue — there is a pop-up anatomical guide to assist you, if required. Then one selects whether one wishes to see the genes with the greatest absolute expression (abundance) or those which are most highly expressed relative to other tissues (enhancement). Finally one selects how many results one wishest to see (20–100).

#### (iii) Category Search

Find genes of a particular category most expressed in individual tissues.

1. Select a 'stage' and next the tissue of interest. Then choose 'enrichment' or 'abundance' for greatest expression:

2. Select a category (keyword), how many genes you wish displayed, and press 'Search'.

Category:

**ANATOMICAL KEY** [show](#)

Category search offers a pull-down list from which one can select any of 24 functional categories for gene products, and allows one to see which are expressed in a particular tissue.

#### (iv) Adult/Larvae Search

Find which genes show the greatest difference in expression between larva and adult for a given tissue.

1. Select whether expression should be greater in the adult or larval stage:

Adult > Larval  
 Larval > Adult

2. Choose the tissue, how many genes you wish displayed, and press 'Search'.

Tissue:  Display:

**ANATOMICAL KEY** [show](#)

This type of search simply allows one to find genes in a particular tissue that are much more highly expressed either in adult or in larvae.

#### (v) Embryo Search

Find genes expressed in the embryo.

Select a peak of embryo expression.

0–1 h  
 1–24 h  
 24–36 h  
 36–72 h

Do you wish to see genes expressed only in embryo?  
 Yes  No

Display:

The embryo search allows one to identify genes, the expression of which is predominantly at a particular embryonic stage, which one chooses from the choices offered. There is the option to restrict the choice of genes to those that are only expressed in the embryo.

#### (vi) Profile Search

For a particular *Tribolium* gene, find others with a similar profile of expression across tissues.

Choose search type before entering ID or symbol

Gene ID (e.g. TC000470)  
 Gene Symbol (e.g. Sobp)

Include embryo data in profile?  
 Embryo/Larva/Adult  Larva/Adult only

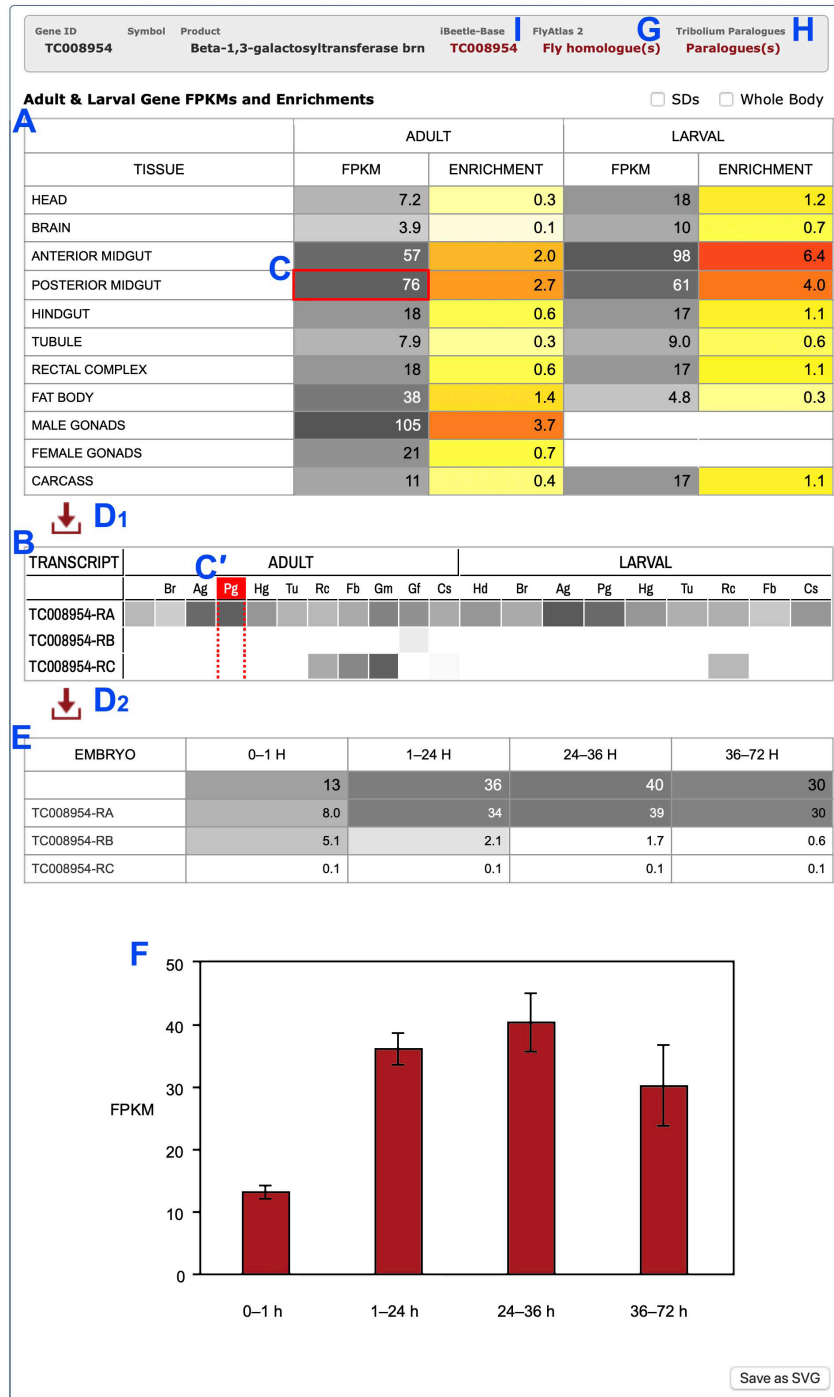
Correlation statistic and stringency (Defaults advised initially)  
 Pearson  Spearman  $r >$

Gene:  Display:

The purpose of the profile search is to help identify the function of genes for which this is unknown. The search employs the pattern of expression of a query gene across different tissues and retrieves genes with a similar pattern of expression. The results one obtains may differ depending on the statistical model used for the comparison, and one can select either Pearson or Spearman statistics. Likewise, there is an option to exclude comparison with expression in the embryo. It is suggested

that one experiments with these options to obtain a suitable number of results to a particular query. If one obtains a large number of genes with a similar expression profile, there is the option to increase the stringency of the comparison by selecting a higher  $r$  value.

## 4. Presentation of Results

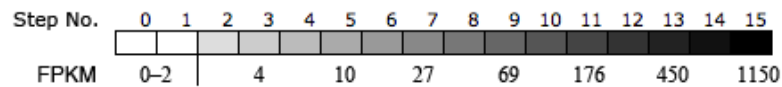


### Adult and Larval Expression

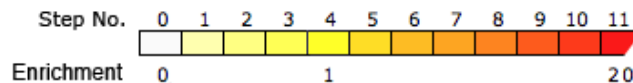
The overall data for gene transcripts in different tissues are tabulated first (A), and below this those for individual transcripts in a more compact form (B). It is possible to locate the transcript expression corresponding to that of the gene in particular tissue by clicking on the gene cell (C),

causing the corresponding transcript cells (C') to be highlighted. The data can be downloaded in spreadsheet format (D<sub>1</sub> and D<sub>2</sub>).

For abundance values the white-to-black spectrum illustrated below is used. For FPKMs this has a 15-step log<sub>1.6</sub> scale, but all values below 2 FPKM (considered background) are coloured white, and no discrimination is employed for values above 1150 FPKM (pure black).



For enrichment values a divergent white/yellow/red spectrum is used: This employs an asymmetric log scale running from white to yellow (0-1) to represent genes with 'decreased enrichment', and then from yellow through orange and a wider range of reds to encompass values of 'increased enrichment'.



### Embryonic Expression

Embryonic expression is presented in the form of both a single table for both gene and individual transcripts (E) and a bar chart of the overall gene expression (F). The latter can be downloaded in scaleable vector graphics (SVG) format.

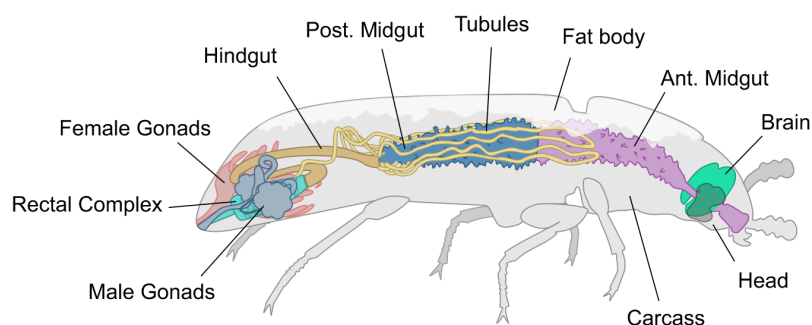
### Links out

For each retrieved gene there are links out to *Drosophila* homologues (G) and *Tribolium* paralogues (H) — where these exist — and to the corresponding entry in iBeetleBase (I).

## Appendix I: Technical

### Insects & Tissues

*Tribolium castaneum* (San Bernardino strain) stocks were maintained on organic whole-wheat flour supplemented with 5% (w/w) yeast powder at 30 °C at a constant 50% relative humidity and 12:12 light–dark cycles. The tissues are in the ‘Anatomical key’, available on each results page and reproduced below.



### RNA-Seq

RNA was isolated in triplicate using the Qiagen miRNeasy kit. The quality of RNA samples was analysed using an Agilent Bioanalyzer.

### Computational Analysis

Total RNA was analysed using the Tuxedo pipeline (Trapnell *et al.* (2012) Nature Protocols 7, 562–578).

### Tribolium Database & Third-Party Data

The RNA-Seq data were loaded into a MySQL database (TriboliumDB), which underlies this web application. It uses version Tcas5.2 of the Tribolium reference genome sequence: ([https://www.ncbi.nlm.nih.gov/assembly/GCF\\_000002335.3/](https://www.ncbi.nlm.nih.gov/assembly/GCF_000002335.3/)) and version ogs3 of the gff gene annotations: (<http://ibeetle-base.uni-goettingen.de/download OGS3.gff.gz>).



## Appendix II: Citing, Linking and Contact

### Authorship & Acknowledgements

The dataset underlying this web application was generated by Kenneth V. Halberg and Muhammad Naseem, University of Copenhagen, Denmark. The web application and the underlying database is by David P. Leader, University of Glasgow, UK.

### Citation in Publications

Any published work relying on the data here should cite the URL of the website ([www.beetleatlas.org](http://www.beetleatlas.org)). A manuscript for formal bibliographic citation is currently (2023) in preparation.

### Linking to BeetleAtlas

You are welcome to link to BeetleAtlas from your own website.

If you wish to link directly to the results of a search for a specific gene you need to provide the two parameters, GENE\_ID and ID\_TYPE, in a query of the type:

```
https://motif.mvls.gla.ac.uk/BeetleAtlas/index.html?  
    search=gene&gene=GENE_ID&idtype=ID_TYPE
```

where:

GENE\_ID is the identifier appropriate to the ID type.

ID\_TYPE can be any of 'geneID', 'geneSymbol' or 'geneName'. e.g.

```
https://motif.mvls.gla.ac.uk/BeetleAtlas/index.html?  
    search=gene&gene=TC006446&idtype=geneID
```

```
https://motif.mvls.gla.ac.uk/BeetleAtlas/index.html?  
    search=gene&gene=Atn&idtype=geneSymbol
```

```
https://motif.mvls.gla.ac.uk/BeetleAtlas/index.html?  
    search=gene&gene=allatotropin&idtype=geneName
```

### Contact

Bug reports, feedback and feature requests are welcomed. There is a feedback form on the website, or you may email us directly:

[david.leader@glasgow.ac.uk](mailto:david.leader@glasgow.ac.uk)

[kahalberg@bio.ku.dk](mailto:kahalberg@bio.ku.dk)