

## General information

### *Ciona robusta* **Ensembl based annotation.**

Genome assembly version considered: [GCF\\_000224145.1](#).

Annotation versions considered:

- RefSeq: [v. 104](#)
- Ensembl: [v. 95](#)
- Aniseed: [KH.2012](#)

RefSeq and Aniseed transcripts were re-mapped on the Ensembl genome assembly using [gmap](#) tool (max intron length=50000).

## TABLE GUIDE

- Annotated\_by: data resource (RefSeq, Ensembl or Aniseed);
- Transcript\_ID: identifier of the transcript (the name is a link to its position on the Jbrowse build on the Ensembl assembly);
- Region: chromosome or scaffold identifier;
- Start: start position of the gene on the region;
- End: end position of the gene on the region;
- Strand: +: forward, -: reverse;
- Functional\_Annotation: predicted function annotation (when available);
- Note: chromosome or scaffold identifier for the resource.

### “Search” box:

Typing a gene name or a chromosome name or a keyword in the annotation column, only rows with the corresponding result will be shown. Exact or partial matches are allowed.

### Filtering:

Annotated\_by, Region and Strand columns have a filter box, below the column name. Clicking on the box, a dropdown menu with the list of all the elements of the column will appear. After selecting one element, only rows with the corresponding result will be shown.

### Sorting:

All the columns can be sorted in ascending/descending order by clicking on the arrows next to the column name. By default, the displayed genes are sorted by Region, Start and End.