

General information

Strongylocentrotus purpuratus **Ensembl based annotation.**

Genome assembly version considered: v. 3.1.

Annotation versions considered:

- RefSeq: v. 101
- Ensembl: v. 37
- Echinobase: Build 8

RefSeq transcripts were re-mapped on the Ensembl genome assembly using **gmap** tool (max intron length=9000). Echinobase transcripts were predicted on the version 3.1 of the genome.

TABLE GUIDE

- Annotated_by: data resource (RefSeq, Ensembl or Echinobase);
- Transcript_ID: identifier of the transcript (the name is a link to its position on the Jbrowse built 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);

“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.