USER GUIDE

Table information:

- GeneID: the name of the gene is a link to its position on the JBrowse;
- Scaffolds: scaffold names;
- Start: start position of the gene on the scaffold;
- End: end position of the gene on the scaffold;
- Strand: +: forward, -: reverse;
- Annotation: gene information (when available). Possible values:
    - o Uniprot (ID: description);
    - o Uniref90 (UniRef90_ID: description);
    - o EC number (number: description);
    - o Pw level (1, 2, 3);
    - o Taxonomy;
    - o Transcript length.

"Search" box:

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

Filtering:

Name, Scaffolds 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 Scaffolds, Start and End.