

# USER MANUAL

## Table of Contents

<b>Basic definitions.....</b>	<b>1</b>
<b>Entering new data .....</b>	<b>2</b>
<b>Deleting data .....</b>	<b>2</b>
<b>Current Batches, Need Identification, Frozen and Archived Batches .....</b>	<b>2</b>
<b>Deceased/ Allocated Fish.....</b>	<b>2</b>
<b>Printing tank labels and QR code.....</b>	<b>3</b>
<b>Support Tickets .....</b>	<b>3</b>
<b>Permits and lines evaluation.....</b>	<b>3</b>

## Basic definitions

**Genomic Feature** – a term to describe mutations, transgenes (reporters, knock-ins), other tools for genetic engineering that one can combine in a new **Zebrafish Line**.

**Zebrafish Line** – a collection of **Genomic Features** that are maintained in a genetic pool, irrespective of their zygosity state.

**Zebrafish Batch** – the concrete representation of the abstract class „**Zebrafish line**“. One egg laying from a given zebrafish line on a given date. A batch could be kept in one or several tanks. At any given time, there can be multiple batches of one line in the facility.

For example, if you cross five pairs of one established line today and keep the eggs, you will register those as one batch. If you do that again tomorrow, that will be another batch and so on.

Every new **Batch** belongs to a **Zebrafish Line**, which is a combination of **Genomic Features**. To start registering fish:

1. Create records for the **Genomic Features** you want to combine in a new line.
2. Create a new **Zebrafish Line** record.
3. Add your first **Batch**.

If the **Zebrafish Line** is already existing, skip steps 1 and 2. If the **Genomic Feature** records exist, skip step 1.

## Entering new data

Entering data is done through the respective forms that you will find under the respective menu items. Most of the forms are self explanatory. Here some important points:

1. In the 'New Line' form you only need to choose the genomic features you want combined. Click once to select and one more time to de-select. Your choice will appear bellow. You can give the line a custom name if you wish so, but the name will be generated upon submission as a combination of the genomic features. The reason is that in the past we had cases of two lines with the same features. This is not possible now.
2. In both 'New Feature' and 'New Line' forms, there is the possibility to change the status to archive, if the respective entity is not any more available. This will remove it from the select lists in the 'New Line' and 'New Batch' form. In this way, these items do not get in the way when new records are generated.
3. In the 'New Batch' form you can specify whether some or all of the animals have been identified. You can also select the tank and specify the genotype and the count of fish per tank. The totals are calculated automatically.
4. Moving fish and editing tanks is done through the 'New Batch' form. It cannot be done through the 'Tanks' menu.

## Deleting data

Only the super user can delete records, if mistakes have been done on entry. Generally, records cannot be deleted. You can assign, however, a batch to a different line, if you made a mistake when choosing.

## Current Batches, Need Identification, Frozen and Archived Batches

**Current Batches** are all living batches present in the facility at this very moment.

**Archived Batches** are batches for which the animal count is 0.

For those batches, from which sperm freezing has been done, the batch record must be edited and tagged as **Frozen?->yes**. This will automatically add the record to menu **Frozen**.

By default, all newly generated batch records are marked as **Identified?->no** and can be found also in the menu **Need Identification**. After they have been identified, either phenotypically or by genotyping, the record must be tagged as **Identified?->yes**. This will remove the record from the menu **Need Identification**.

## Deceased/ Allocated Fish

If fish have been sacrificed, found dead, were send to another lab or have jumped out (allocated), these need to be recorded. This is a two step process.

1. Choose the 'New Dead/ Allocated' form and select the respective tank. The relevant information will be automatically filled in. Fill in the rest and submit.
2. Go to the respective batch and open it for editing. REDUCE the count of fish in that tank with the number of removed fish. Submit.

## Printing tank labels and QR code

Go to menu 'Tanks' and open the details page of the tank of interest. Press Print Tank Label at the top of the page. Print the label on your favorite label printer.

We use 24 mm wide x 67 mm long labels on P-touch from Brother.

Once you have printed the label, you can scan the QR code with the camera of your mobile device - usually a tablet. The first time you scan the code you will have to log in to the database. Then, you need to scan the same label once again and you will be redirected to the label page. The genotype on the label is a hyperlink to the tank record. The Batch ID on the label is a hyperlink to the Batch record.

## Support Tickets

Support is provided in the form of tickets on a first come, first served basis. At the moment only CRISPR mutagenesis is available. However, one could offer in future transgenesis, freezing etc.

## Permits and lines evaluation

In Germany generating new lines is regulated and you need a permit (Genehmigung) which is issued based on an application for animal experimentation (Tierversuchsantrag). When you enter a new line record you can indicate whether this line is regulated. If yes, you can select the respective permit from the menu. The new line needs to be evaluated in three stages. After each stage, you can edit the line record and indicate that it has been evaluated. At this point you can upload the filled evaluation form to the zebrafish line record. The forms and the instructions you can find under Downloads.

31.10.2016, Freiburg im Breisgau