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SOP#: MA016	REVISION LEVEL:. 1	DATE: 15 March 2007
AUTHOR: N Olivier	REVIEWER: L Solomon	

Purpose:

All data generated at the ACGT Microarray Facility must to be entered in the University of Pretoria BASE database. This is for public access as well as back-up purposes. The database can be accessed from any location in the world.

Scope:

This SOP outlines the steps required for entering microarray data into the BASE database of the University of Pretoria. The data is entered in MIAME format, the format required for export to public microarray databases.

Procedure:

Access to the BASE database:

Users need an account on the BASE server to enable data entry. Access the ACGT Microarray Facility website (<http://www.microarray.up.ac.za>) and follow the link called “Apply for service access”. Complete the required fields and fill the “Base@UP” checkbox. A message will be sent to the site administrator to create a new account on the BASE server, and this information will be returned to you once the new account has been created.

Entering the database:

Access the BASE server (<http://www.bi.up.ac.za:8080/base2>) and login using the details provided by the site administrator. To change the password, open the file menu and select the “**change password**” option. Change the password and save the changes. This will be in effect from the next time the user needs to log onto the database. Contact information

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can also be added or changed by opening the file menu and selecting the “**contact information**” or “**other information**” options and to save the information when complete.

“Loading files to the database”

It is necessary to upload files to the database, e.g. protocols etc. To upload files, Open the “**View**” menu, and select the “**Files**” option. If a new directory must be created, select the “**New directory**” option, enter the name and a description for the directory, and select the “**Save**” option. The window will close automatically. To upload a file, select the “**Upload file**” option and an Upload new file window will open. To select the file, select the Browse option, and browse to the selected file. Highlight the file and select the upload option. Select the Type of file by using the drop-down menu, so select the Protocol option if the file is a protocol. Enter a description of the file and select the “**Upload**” option. The window will close automatically.

“Adding protocols”

Open the “**Administrate**” menu, and select the Protocols option. The protocols owned by the user will open. Select the –view/presets drop down list, select the “**Owned by others**” option and all the shared protocols will be displayed. If the relevant protocol is not available, select the “**New**” option and a Create protocol window will open. Enter a name for the protocol and select the type of protocol from the drop-down list. To select the file, open the “**Select**” option. The file directory will open. Select the file from the appropriate folder and select the “**Ok**” option. Enter a description of the protocol and select the “**Save**” option. The window will close automatically.

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“Adding a new biosource”

Open the “**View**” menu and select the “**Biosources**” option. If you need to add a new Biosource, select the “**New**” option. A Create biosource window will open. Provide a name for the biosource, preferably the two part scientific name of the specific organism, and if required, add the specific ecotype/strain info in the name as well. In the external ID field, provide the common name of the organism. In the description field add all relevant information on the organism. Also provide the details of the strain used. When all information has been entered, select the “**Save**” button and the Create biosource window will close. In the main Biosource window, the new biosource will be listed, along with all the relevant information entered.

“Adding a sample”

In the main Biosource window the organisms will be listed in the table. In the Samples column of the table there will be a green circle with a plus inside. Select this item and a Create sample window will open. The naming conventions for sample names are as follows, and **MUST** be followed:

Abcd_e_fghi_xxx

Abcd – This is a 4 letter acronym for the scientific name of the organism, with the first letter of the genus, and the first three letters of the species, e.g. Arabidopsis thaliana = Atha

e – This is a very brief description of the tissue of the organism used, e.g leaf or root or thymus. Keep this as short as possible, and use an acceptable acronym if available.

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fghi – This is an acronym for the user, with the first letter of the person’s name, and the first three letters of the surname, e.g. John Smith = jsmi

xxx – All samples for a user must be numbered consecutively, even if the samples are from different organisms or for different projects, e.g. 001

Add the name of the sample as per the naming conventions above. The external ID is a descriptive name for the sample. Add the amount of sample taken (in μg). If possible, add a protocol for the specific sampling of the organism (see Adding Protocols).

Follow the “**Annotations & parameters**” tab, and input all the relevant information. Select the category, and input the relevant information in the box on the right of the category list. Select the “**add**” button and proceed to the following category. When all the annotation information has been entered, please select the “**Save**” option and the window will close.

“Adding extracts”

An extract is a nucleic acid isolation performed on a specific sample. Open the “**View**” menu and select the “**Samples**” option. In the Extract column of the sample the extract was prepared from there is a green circle with a plus sign inside. Select the green circle and a Create extract window will open. The extract name will be derived from the sample name, with only a suffix added to the name to indicate the number of extracts performed, e.g. e1 or e2. This does not have to be changed by the user. Enter a short descriptive External Id, as well as the amount of extract prepared. To specify the protocol, select the

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“**Select**” option, highlight the appropriate protocol and select the “**Ok**” option. Add a description of the extract, and select the “**Annotations & parameters**” tab. Select the appropriate category on the left and input the values in the box on the right followed by the “**Add**” option. Once all the relevant annotation information has been entered, select the “**Save**” option. The window will close automatically.

“Adding labelled extracts”

A labelled extract is the dye-coupled target prepared from a specific extract. Open the “**View**” menu and select the “**Extracts**” option. In the Labelled Extracts column of the extract the labelling was prepared from there is a green circle with a plus sign inside. Select the green circle and a Create labelled extract window will open. The labelled extract name will be derived from the extract name, and does not have to be changed by the user. Enter a short descriptive External Id, and select the dye molecule used to label the extract. Add the amount of labelled extract prepared (in µg) and select the appropriate protocol used to perform the labelling. Add a description of the labelled extract and select the “**Save**” option.

“Adding hybridizations”

A hybridization is one or more labelled extracts added to a microarray slide to generate data. Open the “**View**” menu and select the “**Hybridizations**” option. Select the “**New**” option and a Create hybridization window will open. The naming conventions for hybridization names are as follows, and **MUST** be followed:

abcdxxx_efghyyy_zzz

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abcd – four letter acronym for the user (as above).

xxx – the number of the sample used to generate the labelled extract, e,g, 001

efgh – four letter acronym for the user (as above).

yyy – the number of the sample used to generate the labelled extract, e,g, 009

zzz – the number of the hybridization, starting at 001 and numbered consecutively for every hybridization performed by the user, irrespective of whether the hybridizations are for the same project or on the same organism.

Select the appropriate protocol from the protocol list. Select the relevant hardware component for the hybridization from the list. Leave the array slides unchecked. Open the “**Labeled extracts**” tab, and select the “**Add labelled extracts**” option. Highlight the extracts used in the hybridisations, and select the “**Ok**” option. In put the amount of labelled extract used (in µg). Select the “**Save**” option and the window will automatically close.

“Adding a scan”

A scan is a data scan performed following a hybridization. Open the “**View**” menu and select the “**Hybridizations**” option. In the Scans column of the Hybridization the scan was prepared from there is a green circle with a plus sign inside. Select the green circle and a Create scan extract window will open. The scan name will be derived from the hybridization name, and does not have to be changed by the user. Select the scanner used for the scan, as well as the protocol used. Enter a description of the scan, select the “**Save**” option and the window will close automatically.

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“Adding a raw bioassay”

A raw bioassay is the data generated following data acquisition. Open the “**View**” menu and select the “**Scans**” option. In the Raw bioassay column of the Scan the Raw bioassay was prepared from there is a green circle with a plus sign inside. Select the green circle and a Create scan extract window will open. The Raw bioassay name will be derived from the scan name, and does not have to be changed by the user. Select the Raw data type from the drop-down list, used for the scan, as well as the protocol used. Enter a description of the scan, select the “**Save**” option and the window will close automatically.