

# Phenotype Database

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User manual for entering study (meta)data in  
the Generic Study Capture Framework & Assay Modules

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→ For any questions that could not be answered through this guide, please email  
[servicedesk@ctmm-trait.nl](mailto:servicedesk@ctmm-trait.nl)

# 1. Introduction

## 1.1 Generic Study Capture Framework (GSCF)

GSCF is a web application that is designed to store the design of molecular (biological) studies in a database. It serves as a linking hub for data and the various assay modules. Before data can be entered into modules, the study design needs to be present in GSCF. The following image (tab headers) illustrates what type of information can be stored in GSCF.

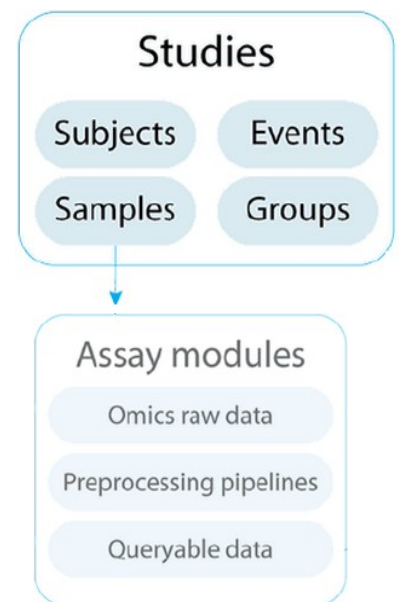
Show Study

Study Information	Subjects	Events timeline	Events table	Assays	Samples	Persons	Publications
title	PPS3						
description	Excessive intake of dietary fat is known to be a contributing factor in the development of obesity. In this study, we determined the dose-dependent effects of dietary fat on the development of this metabolic condition with a focus on changes in gene expression in the small intestine. C57BL/6J mice were fed diets with either 10, 20, 30 or 45 energy% (E%) derived from fat for four weeks (n=10 mice/diet). We found a significant higher weight gain in mice fed the 30E% and 45E% fat diet compared to mice on the control diet. These data indicate that the main shift towards an obese phenotype lies between a 20E% and 30E% dietary fat intake. Analysis of differential gene expression in the small intestine showed a fat-dose dependent gradient in differentially expressed genes, with the highest numbers in mice fed the 45E% fat diet. The main shift in fat-induced differential gene expression was found between the 30E% and 45E% fat diet. Furthermore, approximately 70% of the differentially expressed genes were regulated in a fat-dose dependent manner. Many of these genes were involved in lipid metabolism-related processes and were already differentially expressed on a 30E% fat diet. Taken together, we conclude that up to 20E% of dietary fat, the small intestine has an effective 'buffer capacity' for fat handling. From 30E% of dietary fat, a switch towards an obese phenotype is triggered. We further speculate that especially fat-dose dependently regulated lipid metabolism-related genes are involved in development of obesity.						
code	NuGO_PPS3						
startDate	2008-04-01 00:00:00.0						

## 1.2 Assay modules

Users can enter samples for their particular study in GSCF and indicate where the assay data, containing the measurements, is stored. In these assay modules users can easily import for example bulks of numerical data from Excel files. The following modules are currently available for GSCF:

- Clinical Chemistry (ClinicalChem)
- Metabolomics
- Microbiome
- Physiology
- Proteomics
- Quantitative polymerase chain reaction (qPCR)
- Questionnaire
- Simple Assay Module (SAM)
- Transcriptomics



For example, the Simple Assay Module (SAM) is used to store clinical data, such as rules based medicine assays, but also physical measurements such as body weight of mice. The accompanying image illustrates how GSCF and assay modules are related.

## 2. Getting started in GSCF: study wizard and data importer

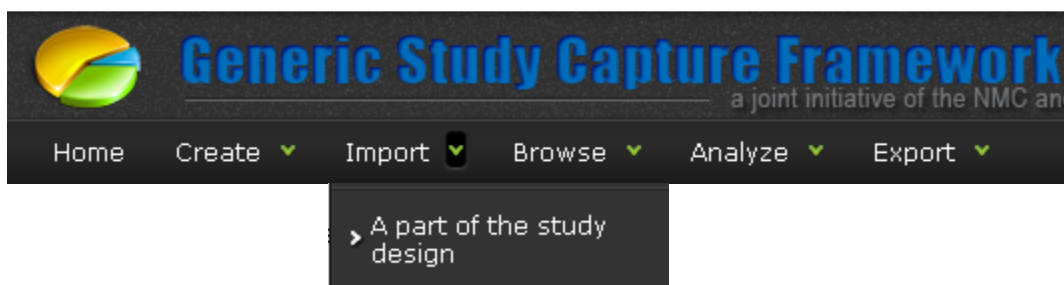
Using the menu on top of the application, you can either create, view or import study data. Generally, there are two ways to get your data into the database.

1. Start the **study wizard**, which will guide you step-by-step. This will allow you to describe the study design, all events and sampling events that take place and the time point the events take place; but also into what event groups your subjects are organized. Based on subjects, event groups and events, GSCF will create samples (samplenames). Samples are the link between GSCF and the assay modules, where you can store specific data (such as clinical chemistry or metabolomic values). (Go to chapter 2.1 for a more detailed description.)

*Advantage: full description of your study design; easy to compare with other GSCF-created studies that are fully described.*

*Disadvantage: because a lot of information can be stored to describe your study, it takes some time before you can start using the modules. Especially when your study contains a lot of samples (>1000), the wizard can become a bit slow.*

2. If you have a list of all subjects/samples in your study, you can also use the *short way* to get data into the system using the **importer** function. First a study needs to be created and (meta)data fields entered.



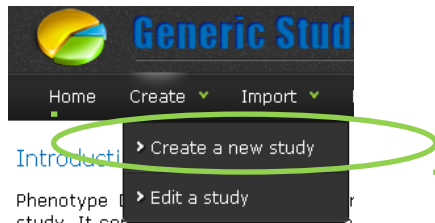
Then use 'Import > A part of study design' to import your Excel sheet containing a subject list with additional information, or a list with samples/samplenames and additional data. These samplenames can then be used in the various assay modules to add data measurements. (Go to section 2.3 for a more detailed description.)

*Advantage: you can quickly enter data into the module, since only minimal necessary information is imported.*

*Disadvantage: comparing two studies is more difficult if users only fill in minimal study (meta)data.*

## 2.1 Create a new study (wizard)

For creating a new study, you need a login. See the Access control document on how to become a user. Click on 'Create > Create a new study' using the menu on top. This will start the study wizard as shown below.



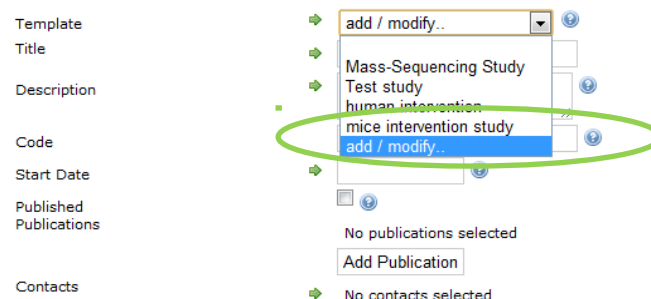
### Step 1: Start



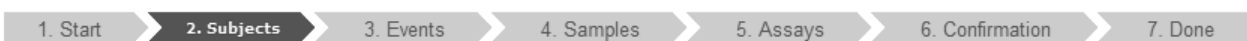
Define basic properties of your study. Fields indicated by an arrow are required.

The first step when creating a new study is adding an appropriate template holding information fields that need to be entered for this study (templates, see section 3 pg 14). Standard fields are already available when creating a new study template, yet it is possible to add more fields in order to describe your study sufficiently. Once a template has been generated it is ready for use. Also, using the same steps, a new template can be created for another study (or e.g. for a particular different set of subjects within that study), and an already existing template can be modified.

Other information such as known publications or contact persons for the study (owner, writer and reader) can be entered during this step.



### Step 2: Subjects



#### **Manual upload of study subjects**

When using the importer wizard it is possible to manually add a number of subjects: report the number of subjects in your study and choose the template containing the required

information fields describing these subjects. Then add these subjects to your study and enter the required information in the table.

Number Of Subjects To Add

Of Species

With Template

Human template

Name	Species	Individ. Id	Gender	Age (Years) (years)
1	Homo sapiens		Male	0
2	Homo sapiens		Female	0
3	Homo sapiens		Female	0
4	Homo sapiens		Male	0

### Import study subjects

If you have an excel file with a list of subjects and related information, a separate importer can be used. Especially when you have detailed subject information this importer can be used very efficiently. After creating a study, select 'quick save' and continue on to the tab 'Import > A part of study design' (more information on the importing of subjects is described in section 2.3 page 10).

### Step 3: (Sampling) Events

1. Start > 2. Subjects > **3. Events** > 4. Samples > 5. Assays > 6. Confirmation > 7. Done

Two types of events can be defined in the events step. In case anything happened to subject(s) in your study, but no sample was extracted for additional testing, a treatment/challenge event can be assigned (e.g. subjects were administered a particular drug). A *sampling* event can be defined when the event resulted in the extraction of samples, on which measurements could be/were performed (e.g. a blood sample was taken on which glucose levels were determined).

First choose between treatment or sampling event:

Choose The Type Of Event

☐ treatment, challenge, etc.

☒ sampling event

Then choose the appropriate (sampling) event template:

After you have added an event or sampling event, it will appear in a list below and you can modify this event if necessary. Here, you also need to create any event *groups* that occur in your study. Make sure that each event is linked to a group. Next, subjects can be assigned to the generated group(s) (see next step).

- Important: each (sampling) event should be added separately.
- Important: a combination of sampling events, subjects and groups will automatically create samples (samplenames) (note: it is also possible to upload samples using the importer wizard, in this case the uploaded samplenames will appear).

Group	Start Time	Duration	Sample Template	Control
Group 1	0s	0s	Blood	Y
Group 2	1w	0s	Blood	Y
	2w	0s	Blood	Y

### **Subjects into event groups**

Click 'next': this in-between-step allows you to select subjects and indicate to which event group they belong.

	Subjects	Group 1	Group 2
Human	Subject 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject 2	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject 3	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject 4	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject 5	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject 6	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject 7	<input type="checkbox"/>	<input checked="" type="checkbox"/>
	Subject 8	<input type="checkbox"/>	<input checked="" type="checkbox"/>
	Subject 9	<input type="checkbox"/>	<input checked="" type="checkbox"/>

- Note: shown are the event groups created in Step 3. In the step between Step 3 and 4 you can mark which subjects belong to which group.

### Step 4: Samples

1. Start	2. Subjects	3. Events	4. Samples	5. Assays	6. Confirmation	7. Done
----------	-------------	-----------	------------	-----------	-----------------	---------

This step provides a table showing all the samples (samplenames) that were created. Note that (unless samples were uploaded using the wizard importer) a combination of sampling events, subjects and groups automatically created samples (samplenames). Shown will be each sampling event and the subjects on which this (sampling) event occurred. It is possible to make manual adjustments to the shown data and/or fill out empty fields when necessary.

### Step 5: Assays

1. Start	2. Subjects	3. Events	4. Samples	5. Assays	6. Confirmation	7. Done
----------	-------------	-----------	------------	-----------	-----------------	---------

In this step, assays need to be created; this 'assay' is the part in which the actual measurements or data files belonging to a set of samples are stored. For each different sampling event a new assay needs to be created. There are different modules available depending on the particular assay (as mentioned in section 1.2, page 3). Within these modules users first have to create (a) new platform(s) (see section 4.2 page 17). After assays have been generated it is possible to upload the measurements for the matching samples, using features to provide information on the measurements (see section 4.3 page 17 and section 4.4 page 19 for detailed explanation of feature and measurement upload, respectively).

The example below shows a study containing a sampling event with template 'Clinical Chemistry'. In this case, the experiment name that will be shown in the assay overview is 'blood\_clinchem' and this assay can be found in the module 'simple assay module'. The assay name should give a good indication for which measurements were performed, e.g., for gene expression experiments (module = qPCR) using a generated template called 'mRNA expression', the target gene name 'Gene A' could be entered.



Template

Name

Module

Clinical Chemistry Platform

Clinical Chemistry

blood\_clinchem

simple assay module

Metagenomics  
clean transcriptomics database  
metabolomics  
simple assay module

### Samples into assays

After you click 'next', an in-between step allows you to select for which samples measurements can be found in what assay(s). Select multiple rows by click and dragging. Use checkboxes to indicate to what assay these samples belong.

(It is possible to attach multiple assays to one sample.)

Sample Type	Sample Name	blood_clinchem	blood_transcr
Blood	Subject1_Blood_Group1_0sBlood	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject10_Blood_Group2_0sBlood	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject11_Blood_Group2_0sBlood	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject2_Blood_Group1_0sBlood	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject3_Blood_Group1_0sBlood	<input checked="" type="checkbox"/>	<input type="checkbox"/>

### Step 6: Confirmation

1. Start	2. Subjects	3. Events	4. Samples	5. Assays	6. Confirmation	7. Done
----------	-------------	-----------	------------	-----------	-----------------	---------

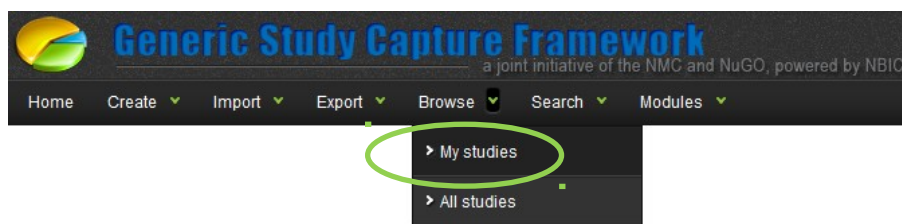
In this step a summary will be given of the study that was just defined. Here it is possible to check your data and in case corrections are required it is possible to go back to the corresponding steps in the wizard and make the required adjustments.

### Step 7. Done

You can view or edit the newly created study, or create a new study.













## 2.2 Edit a study

To view or edit an already existing study go to 'Browse > My studies'.



Now you see a list of studies that you have created, or studies where you have the role of reader. Click on the magnifying glass on the left to view a certain study, or click on the pencil in the middle to enter the wizard. This will allow you to edit this study (unless only reader access was assigned for this study).

Study List

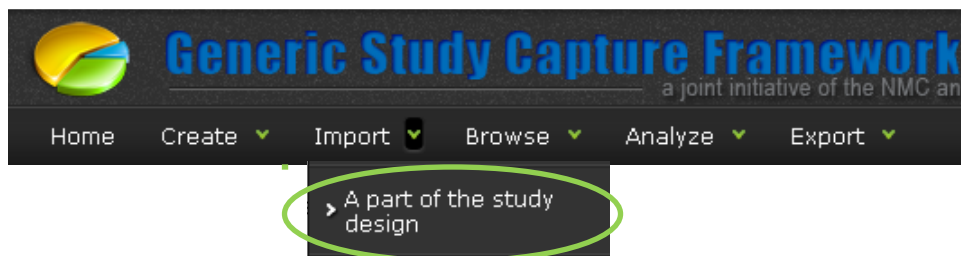
	Code	Title	Subjects	Events	Assays
  	codeX	Diclofenac2	19 Homo sapiens	-	simple assay module
  	6957	Effect of Nutritional Interventions on Inflammatory Status in Healthy Overweight Men (Foodmix)	35 Homo sapiens	Compound treatment, Oral Glucose Tolerance Test (OGTT), high fat post-prandial challenge	simple assay module, metabolomics
  	NuGO_PPSH	Human PPS: an intervention study	10 Homo sapiens	Fasting, Food intake	simple assay module, metabolomics
  	10 OAD	Identification of biomarkers and disease	262 Mus	Bodyweight, Compound treatment,	simple assay module

## 2.3 Import part of study design

Instead of walking through the wizard step by step and manually entering the data, GSCF also allows users to import a part of the study design (Sample, SamplingEvent, Feature, Event, Subject, Assay, Study and Platform). The following examples show the import of *subjects* and *samples*.

### Example: importing subjects

Click on 'Import > A part of the study design' using the menu on top.



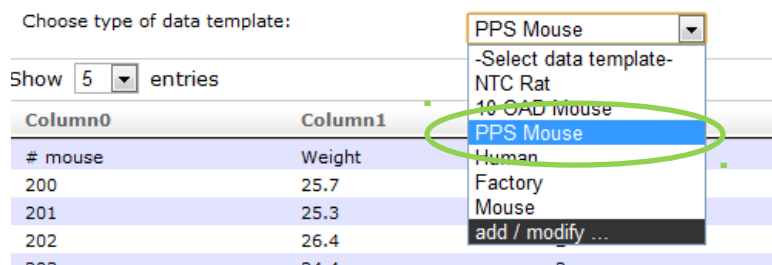
### Step 1: Import file

Select your excel file. The excel sheet should have this format: every study, subject, sample or event has its own row.

- It does not matter in *what column* which information is stored, as you can map the field in the template on the columns in your excel sheet.
- It does not matter *how many headers* are included in your excel sheet, as you can define in which row the first subject/ sample or event can be found.

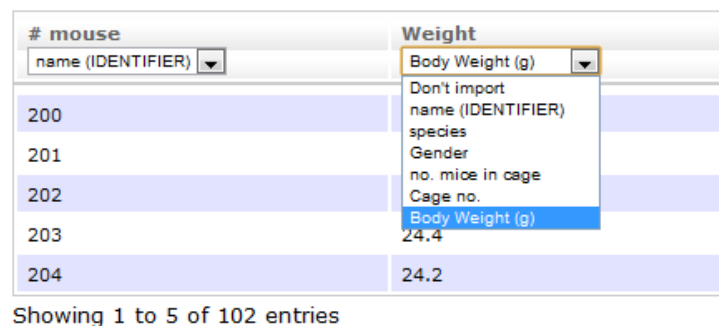
	A	B	C	D	E
1	# mouse	Weight	Cage number	Number of mice in cage	
2	200	25.7	1	2	
3	201	25.3	1	2	
4	202	26.4	2	2	
5	203	24.4	2	2	
6	204	24.2	3	3	

Make sure to select the correct data template; e.g. a mouse subject template for a mouse study (human subject template for a study with human subjects). The importer will show a preview of your uploaded excel file.



### Step 2: Assign properties

Map the information in your excel sheet on the columns, using the dropdowns. For importing subjects, name and species are minimum obligatory fields. If a certain field in the subject data template is missing, go to back to Step 1, where you can modify or add fields for a certain template.



### Step 3: Add information

Add information to the table when necessary. Multiple rows can be selected by click and dragging.

Name	Species	Body Weight (G)	Cage
200	Mus muscl	25.7	1
201	Aira	25.3	1
202	Homo sapiens	26.4	2
203	Mus musculus	24.4	2
204	Rattus norvegicus	24.2	3
	air		
	add more...		
	Mus muscl		

#### Step 4: Confirmation

Check whether the information is correctly mapped and click 'next'. Click on the study title to view your imported study data.

Show Study

Study Information	Subjects	Events timeline	Events table	Assays	Samples
name	species	Body Weight (g)	Cage no.		
200	Mus musculus	25.7	1		
201	Mus musculus	25.3	1		
202	Mus musculus	26.4	2		
203	Mus musculus	24.4	2		

#### Example: importing my own samples and samplenames

It is possible to upload samples and samplenames instead of having to go through the wizard step by step. Click on 'Import > A part of the study design' using the menu on top. This will start the short wizard as described above.

As before, choose the excel file with appropriate subject and sample data. A time point should also be present in this file. For example:

	A	B	C	D	E	F	G	H	I
1	Subject ID	SampleName	Label	Strain	genotype	Gender	name	old	starttime
2	L_022	L_22_OrganSampling_Ldlr_9whf_9wLiver	LDLR_9wHF	C57BL/6	LDLr-/-	Male	22	0w	0w
3	L_041	L_41_OrganSampling_Ldlr_9whf_9wLiver	LDLR_9wHF	C57BL/6	LDLr-/-	Male	41	0w	0w
4	L_050	L_50_OrganSampling_Ldlr_9whf_9wLiver	LDLR_9wHF	C57BL/6	LDLr-/-	Male	50	0w	0w
5	L_076	L_76_OrganSampling_Ldlr_9whf_9wLiver	LDLR_9wHF	C57BL/6	LDLr-/-	Male	76	0w	0w
6	L_077	L_77_OrganSampling_Ldlr_9whf_9wLiver	LDLR_9wHF	C57BL/6	LDLr-/-	Male	77	0w	0w

Samples can be uploaded directly, or matched to existing subjects (in which case the Subject identifier needs to be present in the file as well – shown here in column 'A') using the checkbox shown below. This latter is especially handy for uploading measurements from different kinds of sampling events for the same subject.

Choose type of data:

Sample

☒ Attach Samples to Existing Subjects

using this sampling template:

SamplingEvent

Describe your subjects, samples and events, by using existing templates:

## Assign properties to columns

Below you see a preview of your imported file, please correct the automatically detected types.

Show editable table before importing ☒

**Sample**

Current import mapping: none Clear Match Save Load Delete

Show  entries

SubjectID	SampleName	Label	Strain	Genotype	Gender
Subject name	name (IDENTIFIER)	Don't import	Don't import	Don't import	Don't import
L_022	L_022_OrganSampling_Ldlr_9whf_9wLiver	LDLR_9wHF	C57BL/6 mouse	LDLr-/-	Male
L_041	L_041_OrganSampling_Ldlr_9whf_9wLiver	LDLR_9wHF	C57BL/6 mouse	LDLr-/-	Male
L_050	L_050_OrganSampling_Ldlr_9whf_9wLiver	LDLR_9wHF	C57BL/6 mouse	LDLr-/-	Male
L_076	L_076_OrganSampling_Ldlr_9whf_9wLiver	LDLR_9wHF	C57BL/6 mouse	LDLr-/-	Male
L_077	L_077_OrganSampling_Ldlr_9whf_9wLiver	LDLR_9wHF	C57BL/6 mouse	LDLr-/-	Male

Showing 1 to 5 of 16 entries prev next

The important step during import is to map your columns with GSCF terms, to indicate how your excel sheet is structured. For uploading sample(names), choose 'name' and match back to the subject identifier (Subject name). A time point should also be present in this file (if a time point is not assigned this will result in the erroneous creation of 'empty' sampling events, so be sure to include a time point). Any data you want to skip can be indicated by selecting 'Don't import'; e.g. when sample names and subject information are present in the same file, but subject information is already uploaded, the columns containing subject information can be set to 'Don't import'.

Fill in missing values and continue the importer. After correct uploading of the samples, go back to the tab Events timeline of the study and edit the name of the newly generated event. Go through the subsequent steps and check the correct samples were assigned to the sampling-event. Finally, create a new assay to hold the measurements of the uploaded samples and mark which samples belong to the assay. The wizard will then give a study summary. After 'save', you can view your study:

## Show Study

Study Information	Subjects	Events timeline	Events table	Assays	Samples	Persons	Publications
Parent Subject	Parent Sampling Event	Parent Event Group	name				
L_103	Blood sampling at 0 seconds		L_103_OrganSampling_Ldlr_9whf_9wLiver				
L_120	Blood sampling at 0 seconds		L_120_OrganSampling_Ldlr_9whf_9wLiver				
L_201	Blood sampling at 0 seconds		L_201_OrganSampling_Ldlr_16whf_16wLiver				
L_202	Blood sampling at 0 seconds		L_202_OrganSampling_Ldlr_16whf_16wLiver				
L_203	Blood sampling at 0 seconds		L_203_OrganSampling_Ldlr_16whf_16wLiver				
L_204	Blood sampling at 0 seconds		L_204_OrganSampling_Ldlr_16whf_16wLiver				
L_205	Blood sampling at 0 seconds		L_205_OrganSampling_Ldlr_16whf_16wLiver				
L_206	Blood sampling at 0 seconds		L_206_OrganSampling_Ldlr_16whf_16wLiver				
L_207	Blood sampling at 0 seconds		L_207_OrganSampling_Ldlr_16whf_16wLiver				
L_208	Blood sampling at 0 seconds		L_208_OrganSampling_Ldlr_16whf_16wLiver				
L_209	Blood sampling at 0 seconds		L_209_OrganSampling_Ldlr_16whf_16wLiver				
L_210	Blood sampling at 0 seconds		L_210_OrganSampling_Ldlr_16whf_16wLiver				

After this it is possible to attach measurements to the samples (see section 4.4 page 19).

*\*Note: it is possible to upload sample(names) without attaching them to existing subjects. In this case users have to go back to the Events timeline and create a new sampling-event and continue the uploading process from there on. However, while measurements can be added to these samples, the samples themselves cannot be removed from the study, so users are disadvised of uploading of samples in this manner!*

### 3. Templates

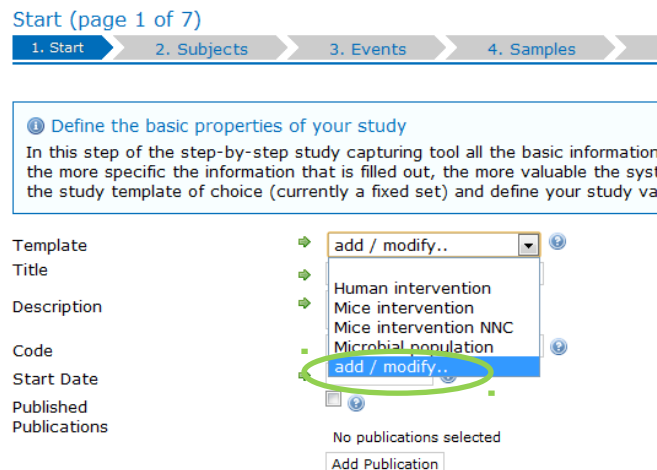
In order to allow flexibility to capture all information you require within a study and to make it possible to compare studies or study data, the system uses customizable templates and ontologies. Templates are available at all steps of the create study wizard and can be added or modified by someone with writer access to the particular study (templates can only be viewed by users with reader access) .

Templates are used in many parts of the study and are used to enter information on:

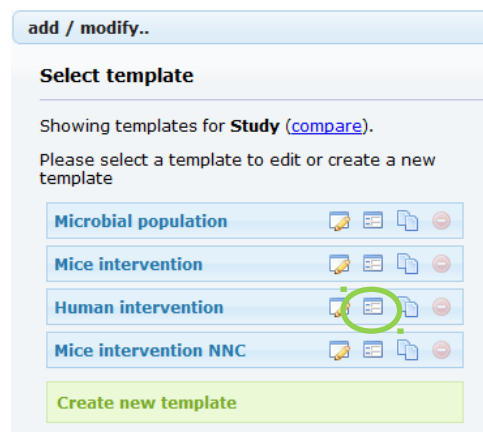
- **Study:** fields in this template should describe the study characteristics. Standard fields within the template are: "title, description, code, startdate and published". Other fields describing the study could also be added, e.g.: "study aim, study protocol and study institute(s)".
- **Subject:** fields in this template should describe subject characteristics. Standard fields within the template are: "name and species". It is possible to add more subject metadata, e.g.: "gender" or other variables.
- **Sample:** fields in this template should describe sample characteristics. Standard fields within the template are: "name and material".
- **Event:** fields in this template should describe event or sampling event characteristics. Standard fields within the template are: "startTime, duration and sampleTemplate".
- **Feature** (assay information field): fields in this template should describe the features for each assay, i.e. relevant information pertaining to the experiment. There are no standard fields within the template as these are particular for each different type of experiment. Features can be created individually, or imported from an excel file. The more detailed the fields the better traceable/queryable the study data.
- **Assay:** fields in this template should describe the assay characteristics. Standard fields within the template are: "name and module". The module used should depend on the type of assay.
- **Platform:** fields in this template should describe the platform characteristics. Standard fields within the template are "name, platformversion, platformtype and comments".

For example, to indicate the type of study design, choose an existing Study template, or 'add/modify templates'. This will show a pop-up where you can define the fields you want to appear next to default fields for study details.

Choose 'add/modify' to add or edit templates:



Now you can see a list of existing templates. By clicking the first icon you can change the name and description. For each template you can also describe additional fields.



Click on the second icon to modify template fields. In this screen you can create new fields for the particular template, indicate what is required for these fields and organize the fields:



add / modify..

### Human intervention (switch)

Currently, this template contains the following fields. Drag fields to reorder. Drag fields to the list of available fields to remove the field from the template.

title (Short text)

description (Long text)

code (Short text)

startDate (Date)

published (True/false)

‡ Institute (Short text)

‡ Consortium (Short text)

‡ Objectives (Long text)

‡ Study protocol (File)

‡ Central conclusion (Long text)

‡ objective related inclusion criteria

### Available fields

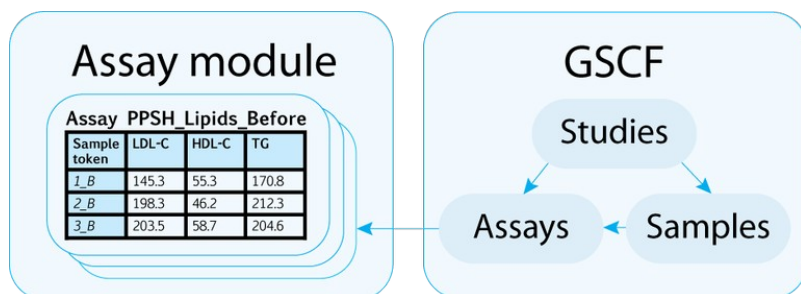
These fields are available for adding to the template. Drag a field to the template to add it.

Type (Dropdown selection of terms)

Create new field

## 4. Assay modules, experimental measurements

Measurements are stored in the experimental modules, mentioned in section 1.2 page 3. These modules are attached to the Generic Study Capture Framework (GSCF). Using these modules it is easy to import bulk numerical data from e.g. Excel files. In general, it is used to store clinical data, such as Rules Based Medicine assays, but also physical measurements such as body weight of mice.



### 4.1 Module section of Phenotype Database: relation to studies, samples and assays

The module section makes use of sample information created in GSCF. In section 2 it is described how users can create a study, define study information, import subjects and attach subject information. Then, by adding events and sampling events, together with subjects and subject groups, this will create samples (or samples can be imported).

The last step in GSCF is to define assays, in which measurements or data files are attached to samples.

Below is shown an example of different assay types from GSCF: the assay name and the module in which this particular assay can be found are shown on the left; also shown are a subset of the samples within this assay; clicking on the details link will take the users to the section where the measurements are stored.

#### Show Study

Study Information	Subjects	Events timeline	Events table	Assays	Samples	Persons
Assay Name	Module	Link	Samples			
tissue_transcr	clean transcriptomics database	<a href="#">details</a>	1029-49_OrganSampling_2b_1w3d, 1029-49_OrganSampling_49_OrganSampling_2b_1w3d_2, 1031-50_OrganSampling_1031-50_OrganSampling_2b_1w3d_2, 1033-37_OrganSampling_1033-37_OrganSampling_2a_3d_2, 1034-38_OrganSampling_1034-38_OrganSampling_2a_3d_2 and 222 more			
blood_clin	simple assay module	<a href="#">details</a>	1029-49_Blood_2b_0sTailBlood, 1029-49_Blood_2b_1w, 1050_Blood_2b_1w, 1033-37_Blood_2a_0s, 1034-38_Blood_2105_Blood_2e_0sTailBlood, 1045-105_Blood_2e_12w, 1045105_Blood_2e_6wTailBlood, 1045-105_Blood_2e_9wTailBlo106_Blood_2e_12w, 1054-54_Blood_2b_1w and 218 more			
bloodLC	metabolomics	<a href="#">details</a>	1029-49_Blood_2b_0sTailBlood, 1029-49_Blood_2b_1w, 1050_Blood_2b_0sTailBlood, 1031-50_Blood_2b_1w, 1031-5037_Blood_2a_0s, 1033-37_Blood_2a_3dBloodSacrifice, 10338_Blood_2a_3dBloodSacrifice, 1035-39_Blood_2a_0s, 103105_Blood_2e_0sTailBlood and 282 more			

## 4.2 Measurement platforms

### *Creating a measurement platform*

In each module section, platforms need to be created first that match the type of assays that were performed. Go to Measurement platforms, enter a new name, and click 'add'. For experiments in the qPCR module, a possible list of platforms could be as shown below (more platforms can be added).

Platform List for qPCR

Name	Comments	Platformtype	Platformversion	Template
MLPA gain P146-A1	SALSA MLPA kit MRC Holland	qPCR	v000	MLPA gain P146-A1
MLPA loss X-006	SALSA MLPA kit MRC Holland	qPCR	v000	MLPA loss X-006
qMSP, molecular beacon	Molecular beacon	qPCR	v000	qMSP, molecular beacon
qMSP, SYBR Green	SYBR Green	qPCR	v000	qMSP, SYBR Green
qRT-PCR SYBR Green	SYBR Green	qPCR	v000	qRT-PCR SYBR Green

## 4.3 Features

A feature is a substance or indicator that is measured when a sample is taken. For example, glucose, leptin, CD40, bodyweight, urea, but also e.g. gene expression or promoter methylation levels of a target gene.

### *How can I create a feature manually?*

Go to 'Browse > Features'. On top of the page, click 'Create new feature'. You now need to choose a Platform present in the list and enter the available fields.

Create a new feature for qPCR

Common fields:

Platform: qRT-PCR SYBR Green

Name (required):

Unit:

Template:

Feature templates (see section 3 page 14) can be created in this screen describing the measured feature in detail. For example, for a qPCR experiment think of information on the target and reference gene, primers used, detection method, annealing temperature, chemical suppliers and so on. It's possible to add experimental protocols as well to a feature

and analytical methods used. Furthermore, it's possible to create multiple feature versions describing the target and reference gene in different units (e.g. Ct value, ng/μl or Ct ratio).

### ***How can I import a list of features?***

Go to 'Import > Features'. This will start the feature importer.

1. **Locate and upload your Excel file** with feature names and units:

	A	B
1	Feature name	Unit
2	Alpha-1 Antitrypsin	mg/mL
3	Adiponectin	ug/mL
4	Alpha-2 Macroglobulin	mg/mL
5	Alpha-Fetoprotein	ng/mL

2. **Match your columns** with name and unit.
  3. **Check your input**, and make changes were needed.
  4. **Save** your features.
- Note: in addition to units, more columns holding feature characteristics can be uploaded from the Excel file as well during this step.

### ***Where can I see and edit my uploaded features?***

Go to 'Browse > Features'. By clicking on the magnifying glass the information held for that feature can be viewed. Clicking on the pencil icon enables users to edit a certain feature.

#### Feature list

Search: <input type="text"/>			
<input type="checkbox"/>	Name	Unit	Groups
<input type="checkbox"/>	3-hydroxybutyrate	mmol/l	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>
<input type="checkbox"/>	AST	U/l	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>
<input type="checkbox"/>	Adiponectin (0.20)	ug/mL	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>
<input type="checkbox"/>	Alpha-1 Antitrypsin		<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>
<input type="checkbox"/>	Alpha-1 Antitrypsin (0.011)	mg/mL	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>

## 4.4 Measurements

### ***What is a measurement?***

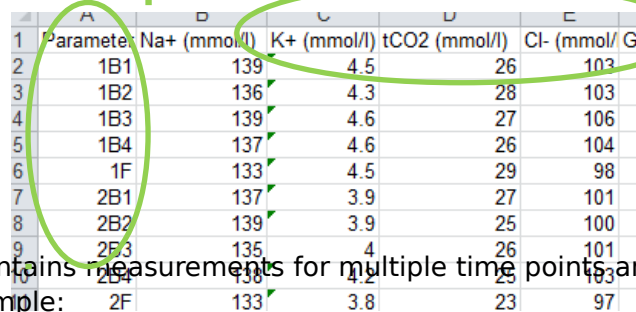
A measurement is a single value that belongs to a sample. For example, glucose level (= a feature present in the feature list) is measured for a sample.

### How can I import measurements?

Start the measurement importer by clicking, 'Import > Measurements'.

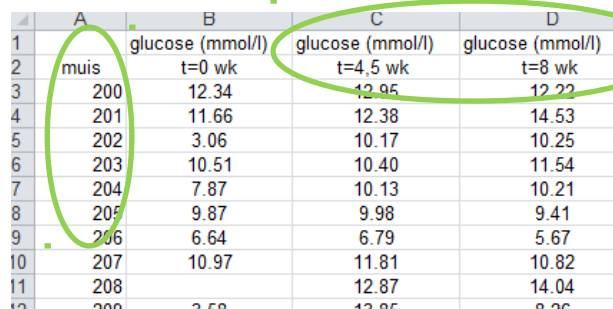
Important: to attach measurements to samples you need to have an assay with samples already available in GSCF (section 2).

1. **Choose the assay** for which you want to upload measurements.
  - Note: if your assay is not in the list, please check your assay and samples in GSCF, because only assays that contain samples for the particular module are listed here
2. **Locate and upload your Excel file** with measurements (see screenshot for an example)
3. **Choose your layout:**  
Sample layout has multiple features per *sample*. For example:



	A	B	C	D	E
1	Parameter	Na+ (mmol/l)	K+ (mmol/l)	tCO2 (mmol/l)	Cl- (mmol/l) G
2	1B1	139	4.5	26	103
3	1B2	136	4.3	28	103
4	1B3	139	4.6	27	106
5	1B4	137	4.6	26	104
6	1F	133	4.5	29	98
7	2B1	137	3.9	27	101
8	2B2	139	3.9	25	100
9	2B3	135	4	26	101
10	2B4	138	4.2	25	103
11	2F	133	3.8	23	97

Subject layout contains measurements for multiple time points and only one or a few features. For example:



	A	B	C	D
1		glucose (mmol/l)	glucose (mmol/l)	glucose (mmol/l)
2	muis	t=0 wk	t=4,5 wk	t=8 wk
3	200	12.34	12.95	12.22
4	201	11.66	12.38	14.53
5	202	3.06	10.17	10.25
6	203	10.51	10.40	11.54
7	204	7.87	10.13	10.21
8	205	9.87	9.98	9.41
9	206	6.64	6.79	5.67
10	207	10.97	11.81	10.82
11	208		12.87	14.04
12	209	2.58	12.85	8.26

4. **Match your columns** with features (and time points). Click on *Add new feature* if you want to add more features.  
**Match your rows** with subjects or sample names.

1. Choose Assay 2. Upload 3. Select Layout 4. Select Columns 5. Done

You have chosen the subject layout. On this page, we have tried to match your data with choice.

	fibrinogeen (mg/ml) Fibrinogen (0.0098)	fibrinogeen (mg/ml) Fibrinogen (0.0098)
10 Subject 10	t=5 wk 5w	t=10 wk 10w [Discard] 10w 5w 20w 15w
11 Subject 11	1.73	
12 Subject 12	2.76	
13 Subject 13	1.58	2.03
14	2.49	2.33
	2	2.49

5. **Done:** your data has been stored in the chosen assay and is ready for viewing.

### ***How can I view my uploaded measurements?***

Click '*Browse > Assays*' and click on the magnifying glass on the right, to view a certain assay with measurements.

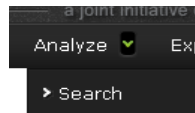
### ***Can I delete measurements?***

Yes, you can delete all measurements from an assay: Click *Browse > Assays* and click on the magnifying glass on the right. In this screen you can see all your measurements for this assay.

At the bottom, click on *Delete all measurements*.

## 5. Search

Data from GSCF and the assay modules can be queried by using the Search option. Use the menu on top of the page and click on 'Analyze > Search'.



On this page you can search for *any of the parameters/fields used in GSCF and the modules*. This can be Age, Subject Name, Cholesterol (or other feature and field names used in any of the modules).

*Search example: Let's assume you want to have a list of all blood samples, where subjects are of age 30 days or higher (among all your studies). First, you have to specify parameters. Note that while you type for a fieldname, you will get a list of possible fieldnames that exist in the database:*

### Search database

#### 1 Select criteria

N.B. Comparing numerical values is done without taking into account the units. E.g. a weight of 1 kg equals 1 grams.

Field	Operator	Value	
SamplingEvent.sampleTemplate	contains	blood	⊖
Age (RELTIME)	Equals		⊕

**1b** Age (RELTIME) Subject  
Age (years) Subject  
Cage Subject  
Cage no. Subject  
Cage no. (before exp.) Subject  
**2** No. mice in cage Subject  
Age child at sampling Sample  
Storage condition SamplingEvent  
# sequences Metagenomics  
**3** Forward primer Metagenomics  
Mid name Metagenomics

Search

*Choose your output format: results can be shown on either study-, sample or assay level.*

#### 2 Output type

Choose the type of output:

**3** Samples  
Studies  
Assays  
Search

Click Search and you will get a list of all the samples that match the specified criteria. Results of this search can be exported, for example as CSV file.

#### Query results: Sample search 1

2801 samples found with samplingevent.sampletemplate contains blood and subject.age (reltime) >= 30

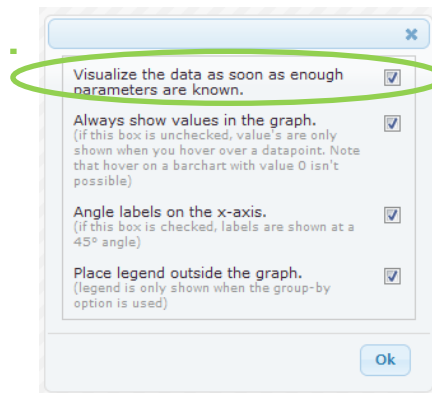
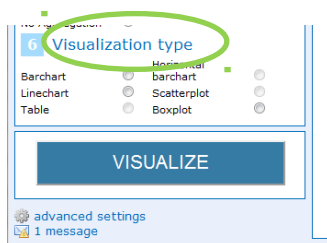
<input type="checkbox"/>	Name	Study	SamplingEvent sampleTemplate	Subject Age (RELTIME)
<input type="checkbox"/>	1029-49_Blood_2b_0sTailBlood	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w15mTailBlood	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w1hTailBlood	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w1s	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w2hTailBlood	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w30mTailBlood	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w3dBloodSacrifice	PPS1	Blood sacrifice	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w45m	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_All_-2w3d10hTailBlood	PPS1	Tail blood	12w

Showing 1 to 10 of 2,801 entries

First Previous 1 2 3 4 5 Next Last

- Search within results
- Refine by classification (Metagenomics)
- Search again
- Discard results
- Previous searches
- Export as CSV
- Export as fasta (Metagenomics)
- Export metadata (Metagenomics)

- Note: especially when you choose *sample* as the output format, this search can take several minutes, since the number of samples can be very high.





## 6. Export data

Both study data (GSCF) as well as measurements/assay data (modules) can be exported.

### 6.1 Export study (meta)data from GSCF

A whole study with GSCF data can be exported as a SimpleTox Excel file. To do this, navigate to 'Export > Export studies as SimpleTox Excel file'. Select which studies you want to export, and click 'Export'. The output will look like this:

	A	B	C	D	E	F	G	H	I	J	K	L
	SubjectID	DataFile	HybName	SampleNa	ArrayType	Label	StudyTitle	Array_ID	Species	name	species	Body Weig
1	Subject 6			Subject6_WholeBody	control	PPS3			Mus musc	Subject 6	Mus musculus	
2	Subject 8			Subject8_WholeBody	control	PPS3			Mus musc	Subject 8	Mus musculus	
3	Subject 5			Subject5_WholeBody	control	PPS3			Mus musc	Subject 5	Mus musculus	
4	Subject 7			Subject7_WholeBody	control	PPS3			Mus musc	Subject 7	Mus musculus	
5	Subject 10			Subject10_WholeBod	control	PPS3			Mus musc	Subject 10	Mus musculus	
6	Subject 3			Subject3_WholeBody	Minocyclin	PPS3			Mus musc	Subject 3	Mus musculus	
7	Subject 9			Subject9_WholeBody	Minocyclin	PPS3			Mus musc	Subject 9	Mus musculus	
8	Subject 1			Subject1_WholeBody	control	PPS3			Mus musc	Subject 1	Mus musculus	
9	Subject 4			Subject4_WholeBody	Minocyclin	PPS3			Mus musc	Subject 4	Mus musculus	
10	Subject 2			Subject2_WholeBody	control	PPS3			Mus musc	Subject 2	Mus musculus	
11	Subject 16			Subject16_WholeBod	HF-AL	PPS3			Mus musc	Subject 16	Mus musculus	
12	Subject 12			Subject12_WholeBod	cHF	PPS3			Mus musc	Subject 12	Mus musculus	
13	Subject 17			Subject17_WholeBod	cHF	PPS3			Mus musc	Subject 17	Mus musculus	
14	Subject 14			Subject14_WholeBod	HF-AL	PPS3			Mus musc	Subject 14	Mus musculus	
15	Subject 13			Subject13_WholeBod	HF-AL	PPS3			Mus musc	Subject 13	Mus musculus	
16	Subject 20			Subject20_WholeBod	Chow	PPS3			Mus musc	Subject 20	Mus musculus	

### 6.2 Export assay data

If you want to export a study, but also the data from the assays that belong to this study, use 'Export > Export Assay Data to File'. This will allow you to export measurements from a module, for example:

Select the study and assay(s) for export and submit.

Select the assay you want to export data from

With this exporter you can export (meta) data about samples from an assay to a file. First, select a study from the first list and then select an assay from that study from the second list.

Human PPS: an intervention study

antigen panel

Submit

haematological

clinical chemistry

antigen panel

LC

NMR

GC

clinical chemistry urine

In the next screen you can specify in more detail which fields you want to export. If you want to export assay data, make sure that measurements is checked:

### Select the columns that you want to be included in the resulting file

In this step you can make a selection from the available fields stored in the database a module (if available).

- ☒ Subject Data
  - ☒ name
  - ☒ species
  - ☒ Gender
  - ☒ Age (RELTIME)
  - ☒ Body Weight (g)
  - ☒ Cage
  - ☒ no. mice in cage
  - ☒ Cage no.
- ☒ Sampling Event Data
  - ☒ startTime
  - ☒ duration
  - ☒ sampleTemplate
  - ☒ Control
- ☒ Sample Data
  - ☒ name
- ☒ Event Group
  - ☒ name
- ☒ Measurements
  - Cholesterol

Finally, select the file type. All types can be opened in Excel.

### Select type of resulting file

- ☒ Tab delimited (.txt)
- ☐ Comma Separated: USA/UK (.csv)
- ☐ Semicolon Separated: European (.csv)

Submit

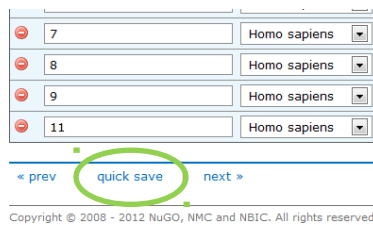
## 7. Tips and tricks

### General


- ✓ Use 'Import study data' to import large datasets (for example: many subjects) from an excel sheet into your study (see section 2).
- ✓ When you want to use the Search tool and choose *sample* as the output format, note that this search can take several minutes, as the number of samples could be very high.

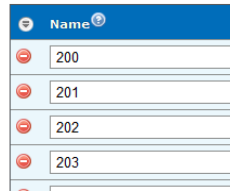
### Study wizard

- ✓ Use 'next' and 'previous' (at the bottom of the page) to navigate, or use 'quick save' at any time during the wizard, to complete it at another point in time.



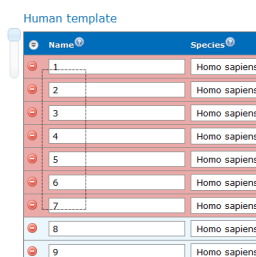
A screenshot of the Study wizard interface. It shows a table with four rows, each with a red minus icon, a text input field, and a dropdown menu. The text input fields contain the numbers 7, 8, 9, and 11. The dropdown menus are all set to 'Homo sapiens'. Below the table is a navigation bar with three buttons: '< prev', 'quick save', and 'next >'. The 'quick save' button is circled in green. At the bottom of the page, there is a small copyright notice: 'Copyright © 2008 - 2012 NuGO, NMC and NBIC. All rights reserved.'

- ✓ Hovering over question marks will show additional information on required fields: 
- ✓ Use the upper left icon to select all rows in a table:



A screenshot of a table with a blue header row labeled 'Name'. Below the header are four rows with red minus icons in the first column and text input fields containing the numbers 200, 201, 202, and 203.

- ✓ Select multiple rows by click and dragging over multiple rows:



A screenshot of a table titled 'Human template'. It has a blue header row with 'Name' and 'Species'. Below the header are nine rows. The first seven rows have red minus icons in the first column and text input fields containing the numbers 1 through 7. The last two rows have red minus icons in the first column and text input fields containing the numbers 8 and 9. The 'Species' column for all rows is set to 'Homo sapiens'.

## 8. FAQs

### *Where can I see a list of my studies?*

Click on 'Browse > My studies' to view your studies. It is possible that other users indicate you are reader of a study. These studies also appear in this list.

### *Where can I update study information?*

Click on 'Browse > My studies', and use the pencil on the left to edit a certain study. Just as creating a new study, this will start the study wizard. Using 'next' and 'previous' you can navigate through your study and update any information from this study.

### *How can I import events, or sampling events?*

Events or sampling events can be imported using a short wizard (the same way you can import subjects or samples, described in chapter 1.3). Use the following format if you want to import events. Describe starttime, endtime and a column for event description (second Diet treatment).

Subjectname	starttime	endtime		Diet treatment	Diet treatment
N_134_ADEM	0s	12w	ADEM/134	A	Green tea
N_010_ADMA	0s	12w	ADMA/10	B	Placebo
N_123_AHIF	0s	12w	AHIF/123	B	Placebo
N_158_ALAN	0s	12w	ALAN/158	B	Placebo

Use 'Import > Import part of study design', choose your file and indicate where your data begins. If your excel sheet contains subject names, you can link these events to the subjects you have in GSCF:

The result is one event, in which all subjects take part:

Show Study

Study information	Subjects	Events timeline	Events table	Assays	Samples	Persons	Persons
Name	Events	Subjects					
	diet (event)						
	start time						
Diet_0s	0s						187 Homo sapiens

### *How can I add more samples to my study?*

Click on 'Browse > My studies', and use the pencil on the left to edit a certain study. Samples are created as a combination of a sampling event, a subject and an event group; thus adding one of these three will allow more samples to be created.

For example, when adding an extra subject to the study: add the extra subject in Step 2, then navigate by clicking 'next' and this subject can be selected into a certain eventgroup. By clicking 'next' GSCF now creates new samples based on the new subject that was added to an eventgroup.

### *How can I add more samples to an assay?*

See previous question how to add more samples into your study. Then go to Step 5, and click 'next'. Now you reach the in-between step, where you can add samples to an assay.

### *How are sample names created in GSCF?*

Each sample name created in GSCF is composed of several fields. For example, the name 11\_UrineAfterFasting\_AllPersons\_1d has been created from:

Subject name: 11

Event group: All Persons

Sampling event: Urine After Fasting

Starttime Sampling event: 1 day

If there are more samples with the same content, then sample names get the addition \_1, \_2, \_3.

### *Can I change the sample names created by GSCF?*

Yes, you can change the names that are automatically created by GSCF. However, especially when you have a long list of samples, this has to be done all manually. Go to the Study 'Edit > Samples'.

Another option is to import samples, and thereby use your own samplenames. During the import you can attach samples to corresponding subjects that you have in GSCF. See section 2.3 page 11 for more details on sample import.

### *Where can I search among multiple studies?*

Click on 'Analyze > Search'. Select your GSCF fields and values you want to search for. Then select type of output (based on Studies, Samples or Assays).

For example, show me all samples from subjects that are at least 60 years of age:

## Search database

### 1 Select criteria

N.B. Comparing numerical values is done without taking into account

	Field	Operator	Value
	<input type="text" value="Age (years)"/>	<input type="text" value="&gt;="/> <input type="button" value="v"/>	<input type="text" value="60"/>
2	<div><div>Age (RELTIME) <i>Subject</i></div><div>Age (years) <i>Subject</i></div><div>Cage <i>Subject</i></div><div>Cage no. <i>Subject</i></div><div>Cage no. (before exp.) <i>Subject</i></div></div>		
3	<div><div>No. mice in cage <i>Subject</i></div><div>Age child at sampling <i>Sample</i></div><div>Storage condition <i>SamplingEvent</i></div></div>		

This will result in the following output:

Query results: Sample search 7

38 samples found with subject.age (years) >= 60

<input type="checkbox"/>	Name	Study	Subject Age (years)
<input type="checkbox"/>	18-144_Blood_Placebo_15w	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60
<input type="checkbox"/>	18-144_Blood_Placebo_-	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60
<input type="checkbox"/>	18-144_Blood_Placebo_0s	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60
<input type="checkbox"/>	18-144_Blood_Placebo_-_5	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60
<input type="checkbox"/>	18-144_Blood_Placebo_-_4	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60
<input type="checkbox"/>	18-144_Blood_Placebo_-_8	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60

*My samples do not appear in the module. What can I do?*

For samples to appear in a module attached to GSCF, make sure you have selected the right module for this assay. For example, make sure you selected module Simple Assay Module when you trying to view samples in this module. Second, make sure the right samples are actually in this assay. You can check this by clicking 'next' in Step 5. Here you can see a list of which samples are in what assay.

If the right samples do not exist yet for this assay and module, add the extra samples.