

MUMOL – Manual

Last update: 08.07.2022

1. Basics

1.1. Installation Guide

Download the software from the git-repository and store it at a location of your choice.

MUMOL can be downloaded at:

<https://github.com/mumol-munich/mumol>

Unzip the MUMOL project.

Download and install python 3.* (* = any version)

- ⇒ Hint: Some systems have problems with running MUMOL under python 3.10+. MUMOL should run stable on Python 3.9.

Current python versions can be found at:

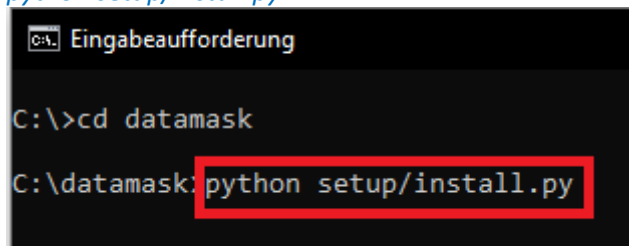
<https://www.python.org/downloads/>

Open a terminal or console window and navigate to the folder where you locally saved your MUMOL system. (e.g. <https://riptutorial.com/cmd/example/8646/navigating-in-cmd>)

Navigate to the project folder (we called it 'datamask' in this example – it is the folder which contains the readme file)

Type in the following command:

[python setup/install.py](#)



```
C:\>cd datamask
C:\datamask>python setup/install.py
```

Once installation is complete, activate the venv (virtual environment) and run the server. This can be achieved by using the following two commands:

windows

[.\\venv\\Scripts\\activate](#)

```
Eingabeaufforderung
C:\>cd datamask
C:\datamask>.\venv\Scripts\activate_
```

python app\manage.py runserver

```
Eingabeaufforderung
C:\>cd datamask
C:\datamask>.\venv\Scripts\activate
(venv) C:\datamask>python app\manage.py runserver_
```

After the first command, the console should display (venv) at the start of the line.

#linux

source ./venv/bin/activate

python app/manage.py runserver

Some installations in a clinical environment might encounter problems. These problems might be caused by Fire-Wall restrictions or by using Python 3.10+. These issues can usually be resolved by setting up a proxy on the local PC or switching to Python 3.9. Information how to configure a proxy on a local machine should be discussed with the local hospital IT as it might vary at each site.

1.2. User Registration

Administrative users who define the configurations can use the following login data.

User: **admin**

Password: **admin**

The first usage of MUMOL for a regular user requires a registration. This can be done in the registration form. Users need to be assigned to a project by the admin before they can start to work.

Registration

User

Required: 150 characters or fewer. Letters, digits and @/./+/-/_ only.

user.name@company.com

Please provide a valid email address.

User

Name

- Your password must contain at least 8 characters.
- Your password can't be a commonly used password.
- Your password can't be entirely numeric.

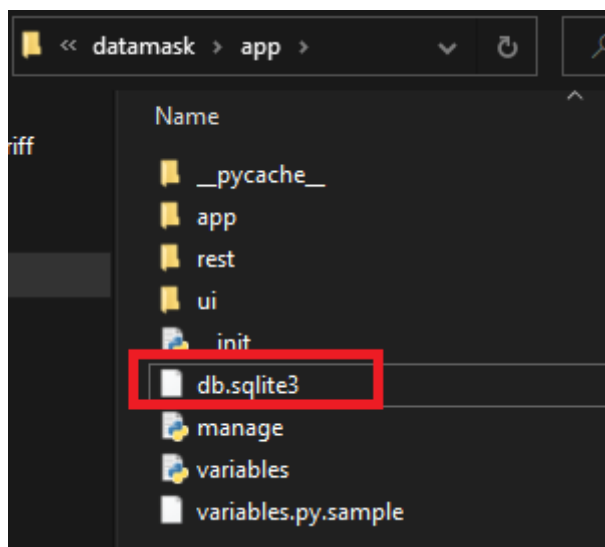
Enter the same password as before, for verification.

REGISTER

Already a member? [Login](#)

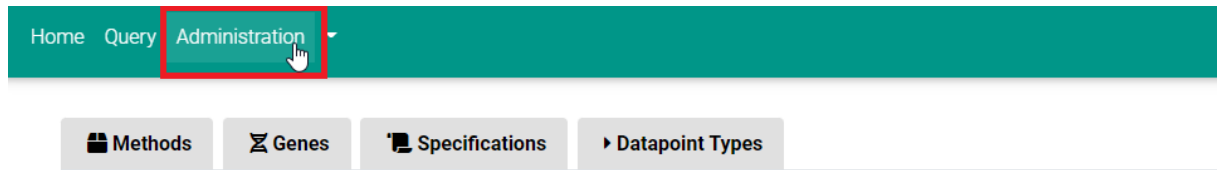
1.3. Direct Access to the database

While MUMOL offers a query page for quick data filtering and exports (see section 3.5), more experienced users can directly query the local sqlite database. (currently no user restriction)



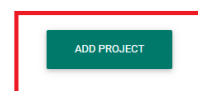
2. Administration

Enter the administration view on the top left corner

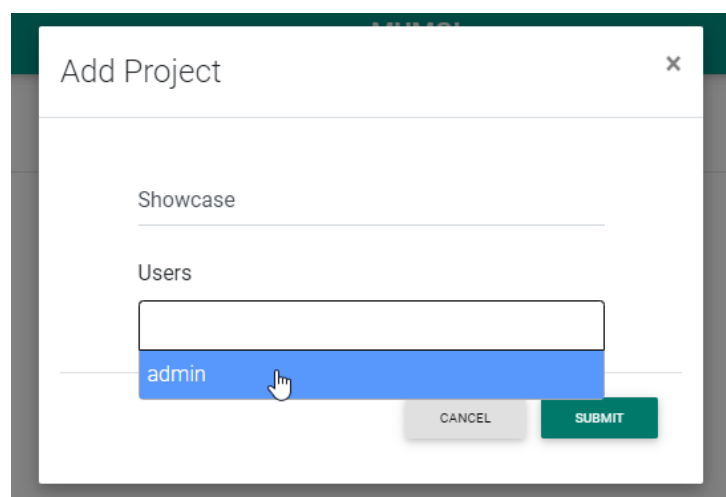


2.1. Setting up a project

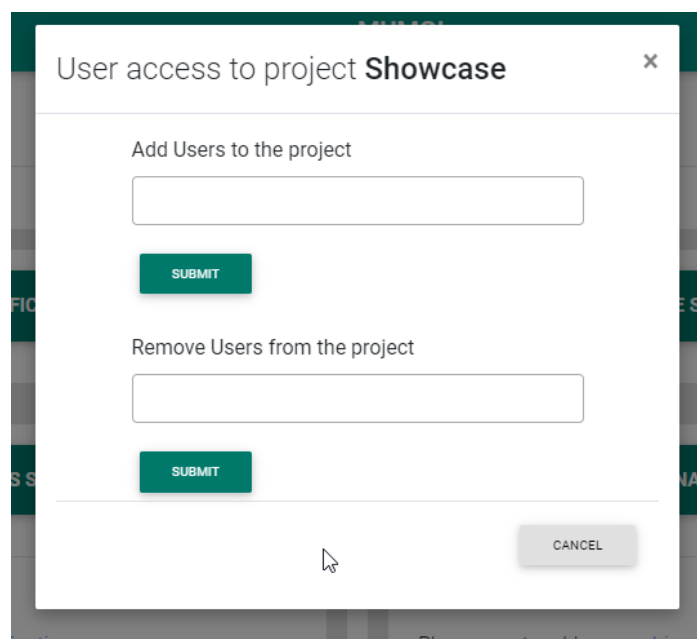
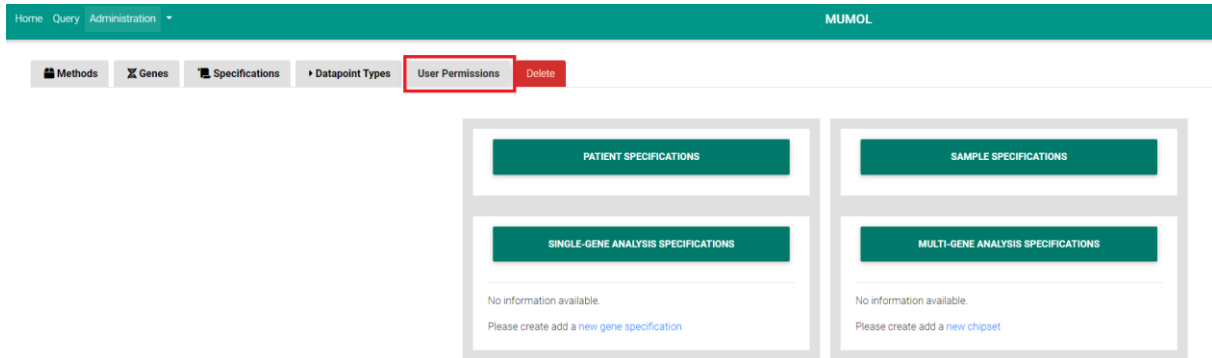
Click on „Add a project“.



Give the project a name and add the users, which should be, allow entering data later on.



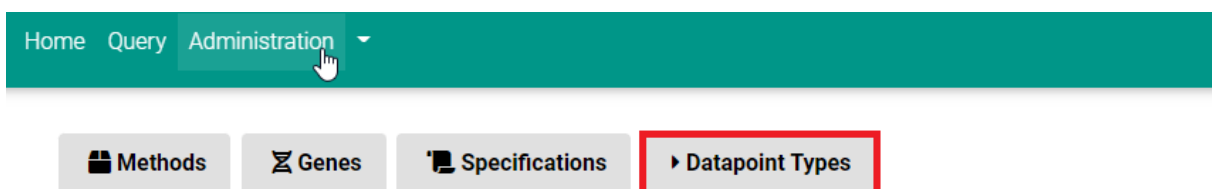
User Permissions can be set up later on as well under the **User Permissions** Tab



2.2. Datapoints

Data points are data fields which can be defined arbitrarily. They can later be added to a patient, a sample, a Gene Analysis or a Chipset Analysis configuration.

Click on Datapoint Types to define new Datapoints.



Note: Datapoints can also be defined on the fly while setting up the configuration of a patient, a sample, a Gene Analysis or a Chipset Analysis.

Within this view click on **ADD** to create a new datapoint.

A datapoint can be set up with a type (integer, numeric, varchar, Boolean, select, multiple), a name and a helptext. The helptext will later be displayed for the data manager to give instructions about the semantics of the data field. The type select will result in a selection drop down for the data manager. The type multiple will result in a dropdown as well, but allows multiple selections.

The screenshot shows the 'Add Datapoint Type' form. At the top, there's a title bar with a close button. Below it, the 'Type*' dropdown is set to 'varchar'. There are two input fields: 'Height' and 'Helptext'. Below these is a validation section with a table-like structure. The first row has 'Type*' as 'RegexValid:', 'Value*' as '^\\d+(\\.\\d+)?\$' (highlighted with a blue border), and 'Error Message*' as 'Only regular expressions sa'. A red 'X' icon is in the top right of this section. Below the table, there's a note: 'For validators which doesn't need value (eg: email validator), please enter None'. At the bottom of the validation section is a '+ ADD VALIDATORS' button. Below that is a red warning message: 'Default values are selected when added to specification result'. At the very bottom are 'CLOSE' and 'SUBMIT' buttons.

The screenshot shows the 'Add Datapoint Type' form with the 'Type*' dropdown menu open. The menu lists several options: 'varchar', 'integer' (highlighted in blue), 'numeric', 'varchar', 'boolean', 'select', and 'multiple'. Below the dropdown is a red warning message: 'Default values are selected when added to specification result'. At the bottom are 'CLOSE' and 'SUBMIT' buttons.

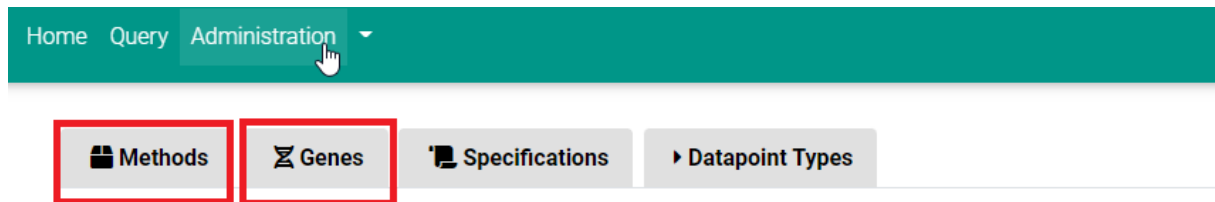
Additionally, a validator can be set up. The validator allows to restrict the input to specified patterns.

For the regex validator we use the syntax specified here:

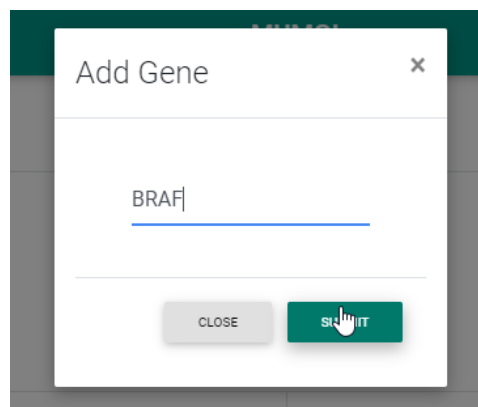
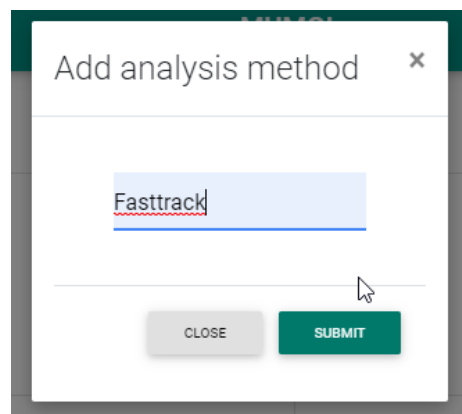
<https://docs.python.org/3/library/re.html>

2.3. Methods / Genes

While Genes and Methods can be defined on the fly while setting up a Gene Analysis or Chipset Analysis, they can also be set up and edited within the tab “**Methods**” and “**Genes**”.

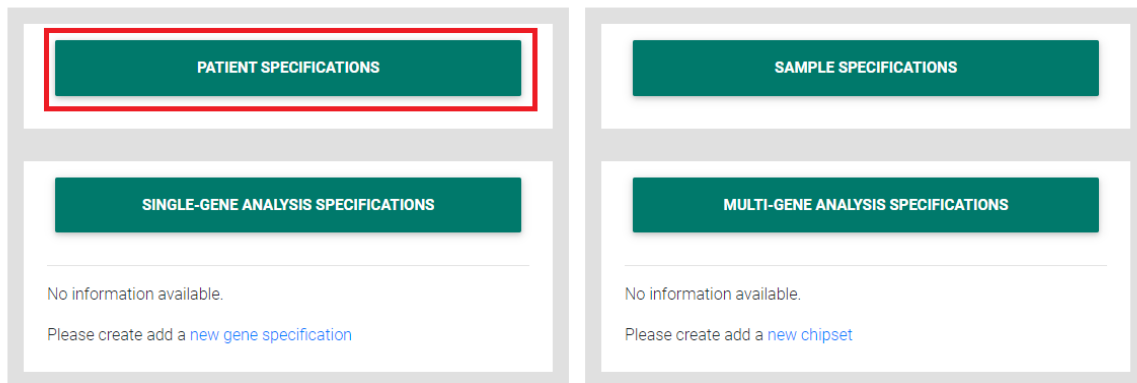


Methods and Genes are basically just a name value.



2.4. Configuring: patient

Switch to the project view and click on Patient specification.



Add datapoints created as explained in 2.2 to the patient specification. You can also add new datapoints on the fly.

Patient Specifications

Current

None

New

Datapoint Type	Mandatory	Default
Height	<input type="checkbox"/>	

helpText: None

SUBMIT

Datapoint Types ☐ Recommended

Exon

HGVS_c

HGVS_p

Height

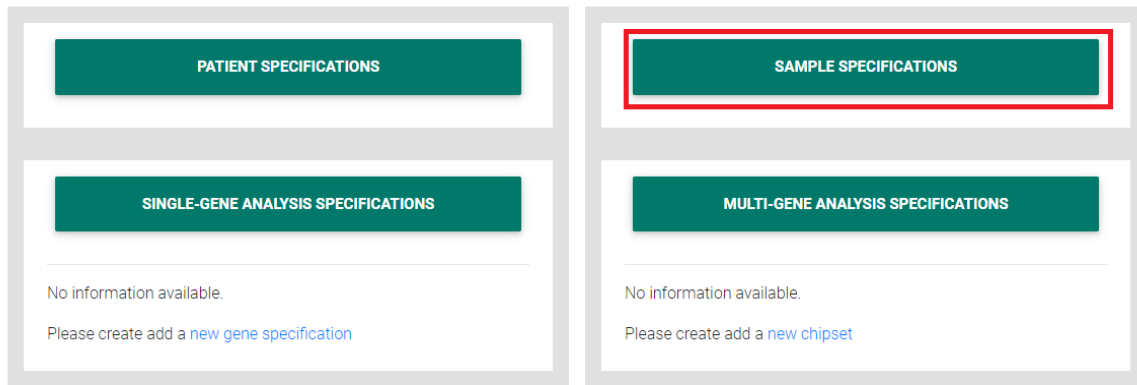
+ NEW DATAPOINT

The datapoints can be set up as mandatory. Another option is to add a default value.

Every patient already has the fixed datapoints: First Name, Last Name, Data of Birth. These values do not have to be set up since they are part of every configuration.

2.5. Configuring: sample

Switch to the project view and click on Sample specification.



Add datapoints created as explained in 2.2 to the sample specification. You can also add new datapoints on the fly.

Sample Specifications

Current

None

New

Datapoint Type	Mandatory	Default
ICD10 Code	<input checked="" type="checkbox"/>	C34
		helptext: None

SUBMIT

Datapoint Types ☐ Recommended

Exon

HGVS_c

HGVS_p

Height

ICD10 Code

+ NEW DATAPPOINT

The datapoints can be set up as mandatory. Another option is to add a default value.

Every sample already has the fixed datapoints: Date of entry, Visit of the Day. These values do not have to be set up since they are part of every configuration.

2.6. Configuring: Gene Analysis

Switch to the project view and click on Sample Single Gene Analysis Specification.

The image shows four buttons arranged in a 2x2 grid. The top row contains 'PATIENT SPECIFICATIONS' and 'SAMPLE SPECIFICATIONS'. The bottom row contains 'SINGLE-GENE ANALYSIS SPECIFICATIONS' (which is highlighted with a red border) and 'MULTI-GENE ANALYSIS SPECIFICATIONS'. Below each button is a text area with the message 'No information available.' and a link to 'Please create add a new gene specification' or 'Please create add a new chipset'.

Start with selecting a method as previously created under 2.3. Alternatively add the new method on the fly.

Select Genes which will be examined within the context of the project and the given method. The genes can also be created on the fly.

Add one or multiple results possible for the given method. E.g. “positive” or “negative”. Define the datapoints which apply for the combination of METHOD GENE and RESULT.

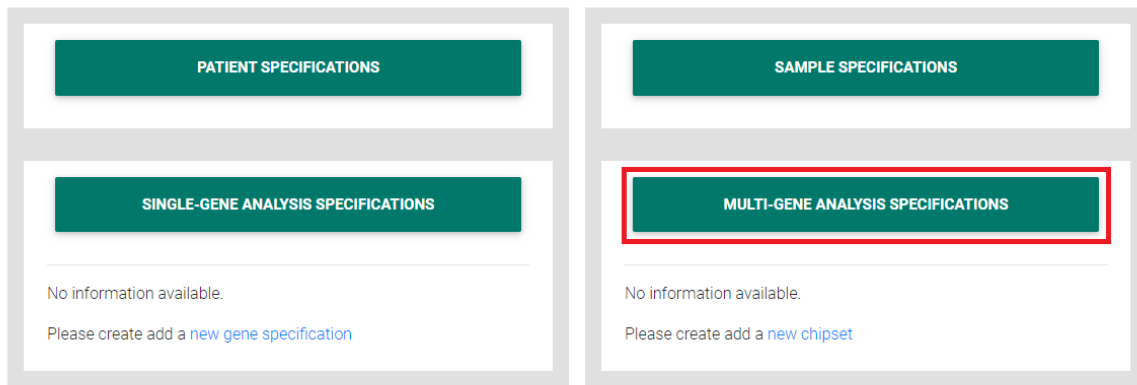
The datapoints can be set up as mandatory. Another option is to add a default value.

The image shows a 'New Gene Specification' form. It has three main sections: 'Select Analysis Method' with a dropdown menu showing 'Fasttrack', 'Select Gene' with a dropdown menu showing 'BRAP', 'EGFR', and 'KRAS', and 'Select Results'. The 'Select Results' section has a table with columns 'Datapoint Type', 'Mandatory', and 'Default'. The first row is 'Positive' with a red arrow pointing to the 'Exon' datapoint type. A red arrow also points from the 'Exon' datapoint type to the 'Datapoint Types' dropdown menu, which shows 'Exon', 'HIVL', 'HIVL', 'HIVL', 'HIVL', and 'HIVL'. Below the table are 'CLEAR', 'NEXT', and 'SUBMIT' buttons.

Each of these combinations is called a Single Gene Analysis Specifications. Most projects will require to set up multiple of these specifications for each method.

2.7. Configuring: Chipset Analysis

Switch to the project view and click on Multigene Analysis Specification.



Start with defining a chip. Add multiple Genes to the chip.

Add data points to the chip. The datapoints can be set up as mandatory. Another option is to add a default value.

New Chipset Specification

1 Chipset Information

Name*

NGS Panel

Manufacturer* selfmade

Version* 1

Genes* BRAF EGFR KRAS +

2 Datapoints

Datapoint Type	Mandatory	Default
Exon	<input checked="" type="checkbox"/>	help:st None
HGVSc	<input type="checkbox"/>	help:st None
HGVSp	<input type="checkbox"/>	help:st None

Datapoint Types

Exon HGVSc HGVSp Target VCD10 Code

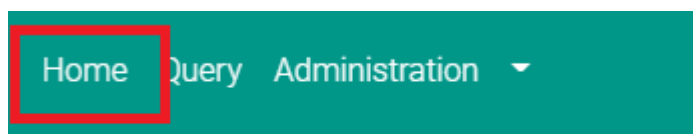
NEW DATAPPOINT

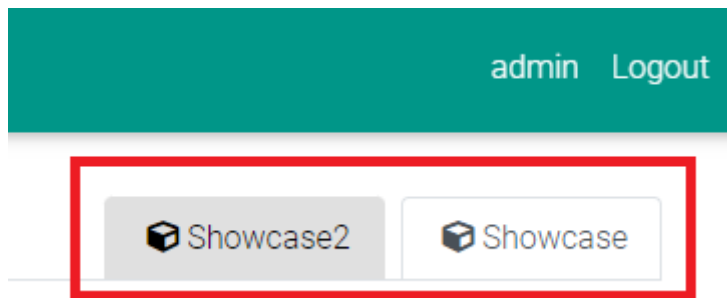
CLEAR NEXT SUBMIT

The result will be a matrix of genes and datapoints.

3. Data Entry

To document data, we have to switch to the “user view” after clicking on the “Home” button. We now can select between multiple projects.





3.1. Patient

After clicking on “Home” we are directed to the patient documentation form. This form allow documenting the identifying data as well as additionally added data points of a patient. A project specific patient ID will be randomly generated if not specified any further.

The image shows the 'Register Patient' form and a table. The form is highlighted with a red rectangle and contains the following fields: 'Firstname*' with value 'Max', 'Lastname*' with value 'Mustermann', 'Date of Birth*' with value '01.01.2000' and a calendar icon, 'Project Specific Patient ID' (empty), and 'Height' with value '180'. A green 'SUBMIT' button is at the bottom. To the right of the form, there are three buttons: 'DESELECT ALL', 'CSV', and 'DELETE'. Below these is a table with one column 'Patient ID' and one row with a checkbox. The table is empty, showing 'No data available in table'. Below the table, it says 'Showing 0 to 0 of 0 entries'.

3.2. Sample

We can click on a patient and get redirected to the sample view.

Register Patient

First Name*

Last Name*

DESELECT ALL
CSV
DELETE

Show 10 entries

<input type="checkbox"/>	Patient ID	First Name
<input type="checkbox"/>	3d6e3eb6-b5c4-4e7e-81a5-0c4969df9281	Max

There, we can add one or multiple samples for a patient in context of a project. As has been explained before, the sample form can be configured as explained under 2.5.

[Showcase](#) / [Patients](#) / [Mustermann, Max](#)

First Name*
Max

Last Name*
Mustermann

Date of Birth*
01.01.2000

Register Sample

Date of Entry*

Visit of the day*

ICD10 Code

SUBMIT

DESELECT ALL
DELETE

<input type="checkbox"/>	Date of Entry (Visit)
No data available in table	

Showing 0 to 0 of 0 entries

3.3. Gene Analysis

We can associate one or multiple single-gene analysis with a sample if we click on the sample date.

First Name*
Max

Last Name*
Mustermann

Date of Birth*
01.01.2000

Register Sample

Date of Entry*

Visit of the day*

DESELECT ALL
DELETE

<input type="checkbox"/>	Date of Entry (Visit)
<input type="checkbox"/>	11.01.2022 (1)

1 1 of 1

We can now choose between creating a single or multi gene analysis. In this case we select single gene analysis.

SINGLE-GENE ANALYSIS

+ New Gene Analysis

☐ Delete

No data available.
[Add gene analysis](#)

CHIPSET ANALYSIS

+ New Chipset Analysis

☐ Delete

No data available.
[Add chipset analysis](#)

In this view we can detail a method and its results. The form will display the data fields as previously defined as explained within section 2.6.

1 Analysis Method

2 Gene

3 Results

Select an Analysis Method

Select a Gene

Select Result

Fasttrack

BRAF

Positive

Exon

HGVS_c

HGVS_p

15

c.1799T>A

p.(V600E)

3.4. Chip Set

We can associate one or multiple single-gene analysis with a sample if we click on the sample date.

First Name*

Last Name*

Date of Birth*

Max

Mustermann

01.01.2000

Register Sample

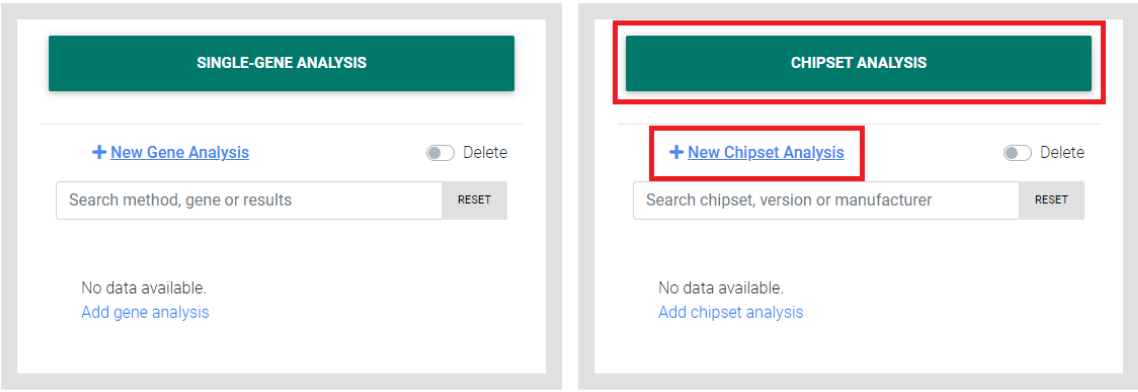
Date of Entry*

Visit of the day*

<input type="checkbox"/>	Date of Entry (Visit)
<input type="checkbox"/>	🔗 11.01.2022 (1)

1 1 of 1

We can now choose between creating a single or multi gene analysis. In this case we select chip set analysis.



The form will display a matrix with the data points on the x-axis and the genes at the y-axis as explained within section 2.7.

1 Chipset

Select Chipset
Select Chipset

Gene	Exon	HGVS_c	HGVS_p
BRAF			
EGFR			
KRAS	2	c.35G>T	p.G12C

BACKRESETSUBMIT

3.5. Query Page

All results can be displayed, filtered and exported at the query page.



Query Page - Gene Analysis

Project	Patient ID	First Name	Last Name	Date of Birth	Patient_Height
Project	Patient ID	First Name	Last Name	Date of Birth	Patient_Height
Showcase	3d6e3eb6-b5c4-4e7e-81a5-0c4969df9281	Max	Mustermann	01.01.2000	180

4. Contact

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