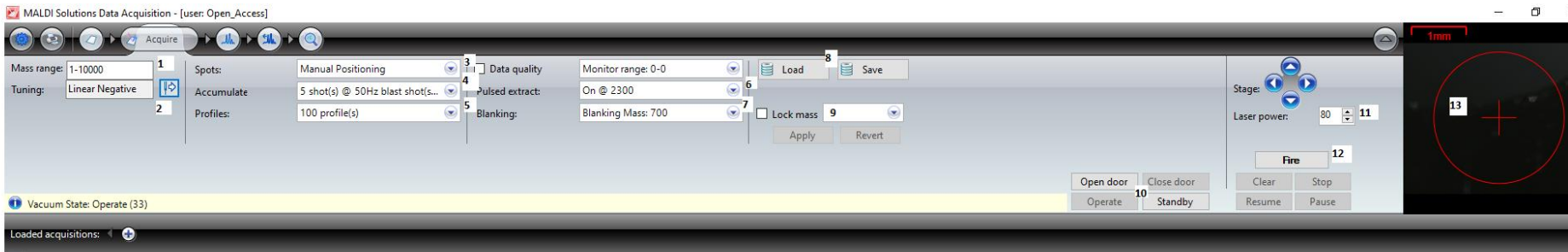


# Samples analyse on Shimadzu MALDI 8030

June 2023

1. CALIBRATE WITH STANDARD
2. APPLY CALIBRATION
3. ACQUIRE DATA FOR YOUR SAMPLE
4. PROCESS DATA
5. SAVE DATA AND DATA ANALYSE WITH [Mass++ \(V2.7.4\)](#)



1 – mass range from  $m/z$  500 to your mass

2 – select mode of ionisation Linear means positive and Linear negative is negative mode

3- select (a) raster for automatic firing of laser, or (b) dither, which is random movement of laser shots, (c) none of these then you select on your own where to shot the laser

4 – standard value is 5 shots, 200 Hz for raster and dither acquisition and 50 Hz for manual acquiring of data

5 – standard value 100 profiles increase for better s/n

6- Pulsed extraction choose close to a target mass or around middle of mass of interest

7- blanking mass means exclude your matrix peaks, keep distance of 200  $m/z$  to your target mass to keep full sensitivity

8- Load and save method you are using

9- Lock mass if you are using an internal standard (enter monoisotopic mass, and tolerance)

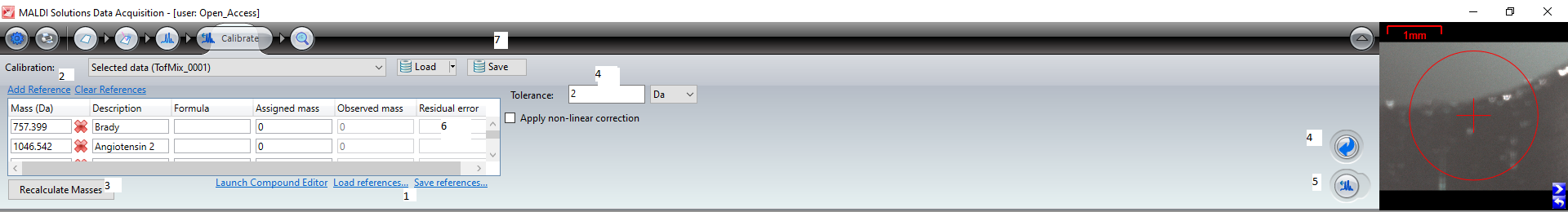
10- open when you want to insert the MALDI plate and when you finish your experiments and close door and put the instrument in stand-by mode

11- Laser power 20 for CHCA matrix; 70 for DHB or SA; increase if not enough signal yet; without matrix 10.

12 – Fire button; 13- camera and right click to move to certain position



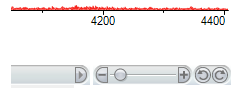
- 1- Baseline subtraction use low value
- 2- 10 for monoisotopic masses and above 100 for average masses
- 3- Smoothing method use off for monoisotopic masses and Gaussian for average masses
- 4- Peak width and smoothing filter use for average masses 10 kDa use 10, 100 kDa then 100 and 1 for monoisotopic masses
- 4- centroid for monoisotopic masses, and apex for average masses
- 5- threshold for peak picking depending on the peak height
- 6- monoisotopic peak picking change mass range if needed
- 7- load if you already have a processing method and save
- 8- Undo processing to original processing parameters
- 9- undo last change of processing parameters
- 10- apply processing parameters



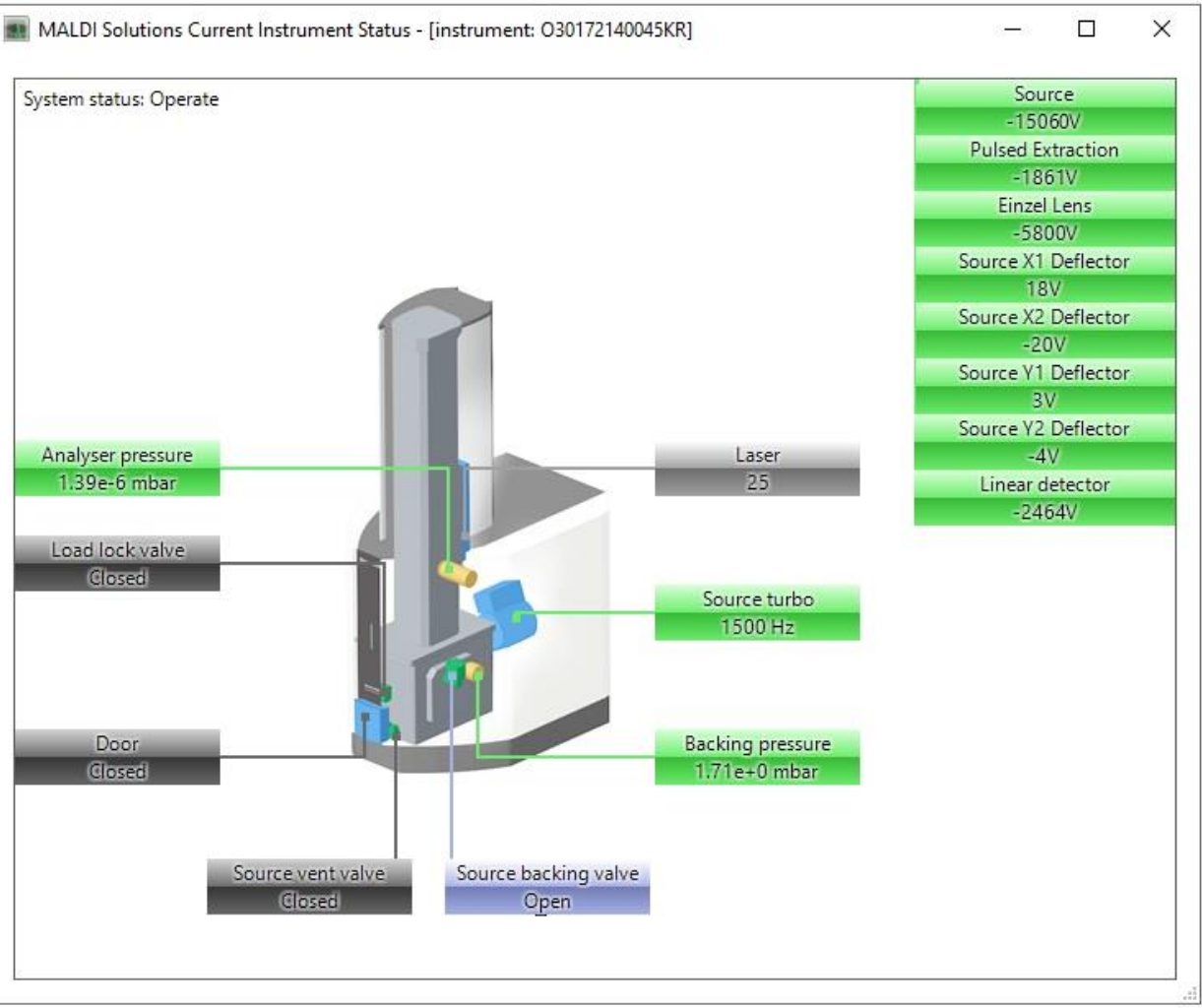
Created By Open\_Access, Data: TofMix\_0001:x1\_(Manual) 19 June 2023 14:37:29 Cal:Named Calibration "20230619\_CHCA\_Tofmix" by Open\_Access on 19 June 2023 14:50:25  
Shimadzu MALDI-8030: Tuning Linear, Power 20, P.Ext at 1500 (bin 95), Ion Gate Blanking: 500.00  
Processed data (Acquisition): 2023-06-19 14:37:29 (Unprocessed profile: #1 - 100)

1 Before you analyse your sample, you need to calibrate the TOF for each target and if you change matrix or acquisition or processing parameters. Acquire data first on your chosen calibrant mixture depending on mass range you need to use for your experiment

- 1- Load and save reference (mass list)
- 2 – if reference is not in database then add reference mass
- 3- Recalculate mass from elemental composition
- 4 – Set a tolerance value use tolerance above 0.3 Da only if you apply monoisotopic peak picking
- 5- Apply calibration
- 6- Check residual error should be below 0.1 Da for monoisotopic masses
- 7- Save calibration and then you can acquire data on your samples

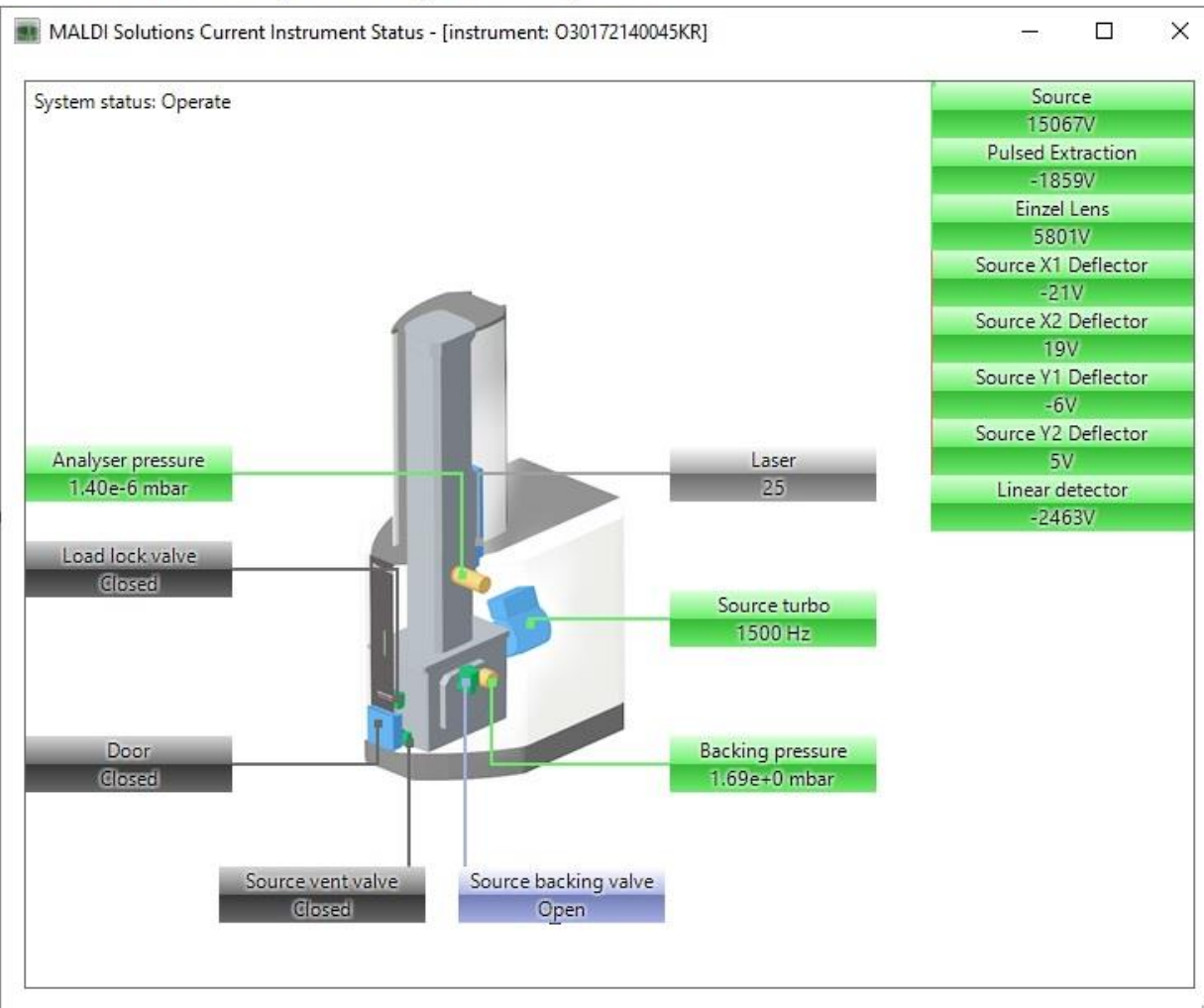


### Standard values operate mode (negative mode)



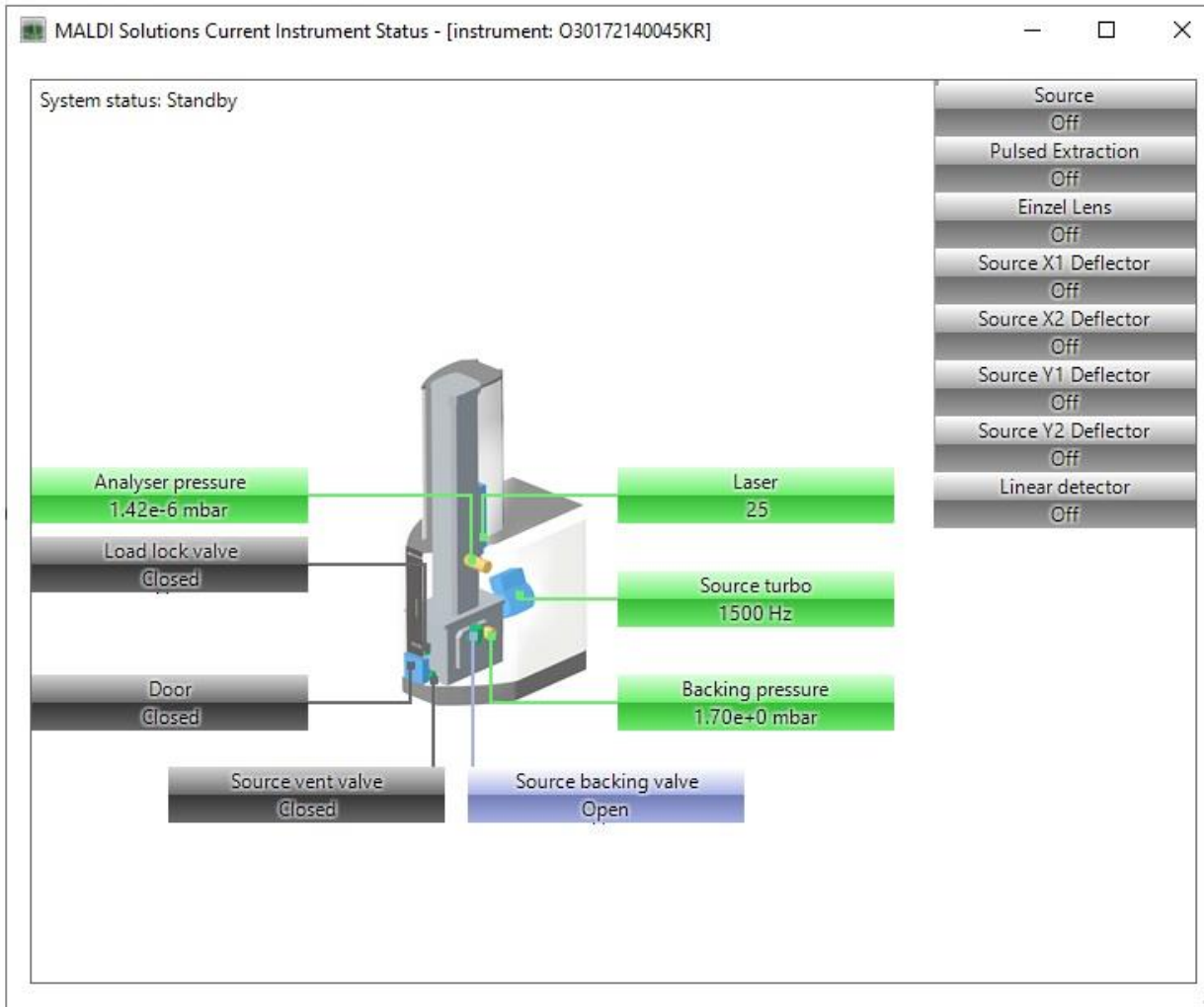
Instrument Reading values when in operation in Negative mode

Standard values in operate mode (positive mode)



Instrument Reading values when in operation in Positive mode

## Standard values for Standby-mode



Instrument Reading values when STAND-BY mode

When you finish your experiments

MALDI Solutions Data Acquisition - [user: Open\_Access]

Calibration: Selected data (New Acquisition 27) Load Save

Add Reference Clear References

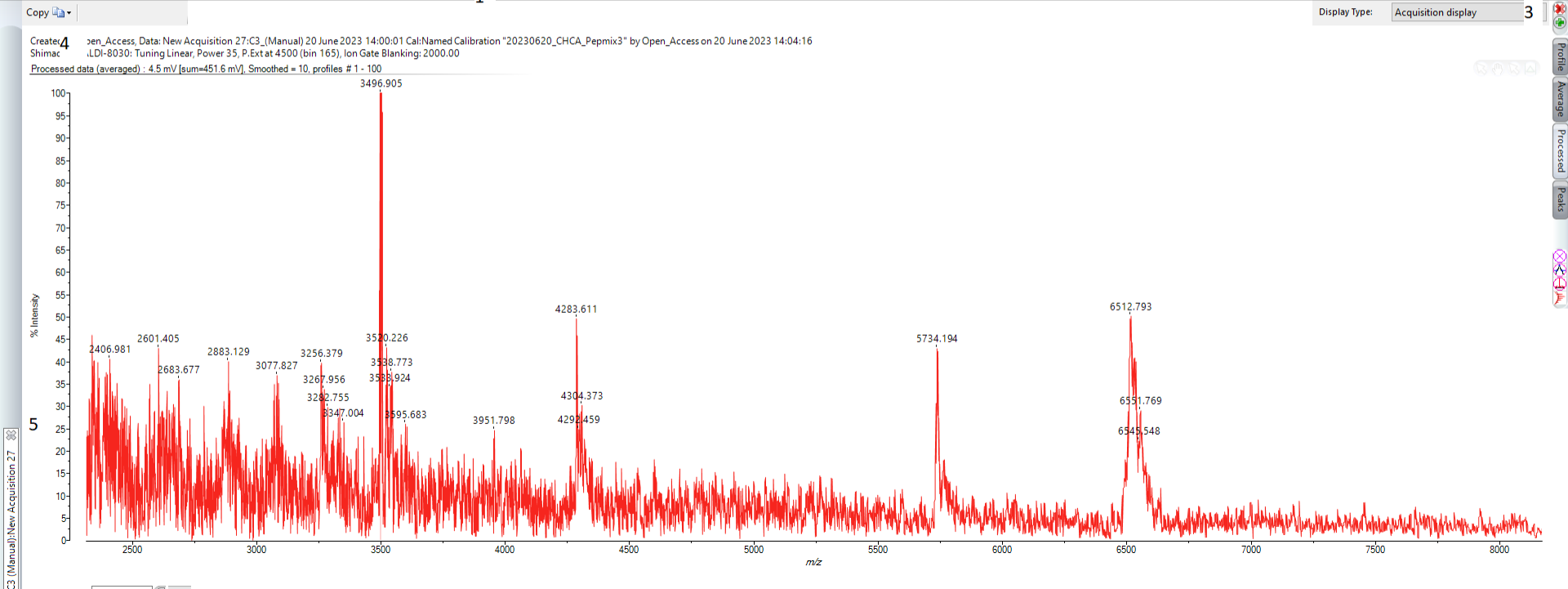
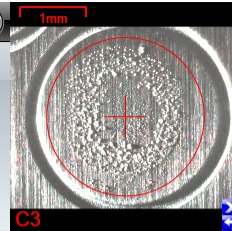
Mass (Da)	Description	Formula	Assigned mass	Observed mass	Residual error
3496.949	Insulin beta ox		0	0	
4283.433	Ubiquitin 2+		0	0	

Tolerance: 1 Da

Apply non-linear correction

Recalculate Masses Launch Compound Editor Load references... Save references...

Loaded acquisitions: New Acquisition 25 New Acquisition 26 New Acquisition 27



- 1- disk means save data and cross delete data
- 2- plus means load saved data
- 3- plus sign means add extra window
- 4- copy MALDI spectrum to your word or powerpoint
- 5- cross means remove data from display (not delete)
- 6- double click to display and right click to rename or batch export



Save Data As

Specify memorable attributes for this data

**Required**

Acquisition Name: New Acquisition 27

Research Group: Tabor

**Optional**

Project: 2023\_June

Batch ID:

**Automatically Provided**

Instrument: Shimadzu BenchTop

Instrument Mode: Linear

Instrument Serial Number: O30172140045KR

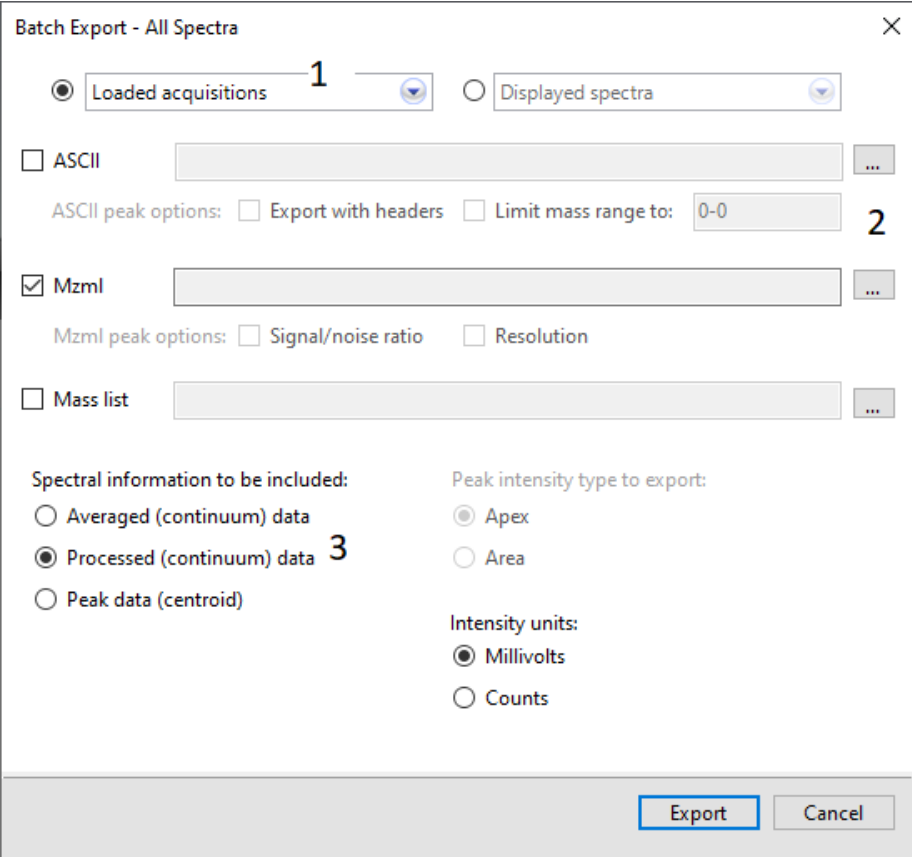
[Change who can see and modify this data](#)

Save Continue Without Saving...

Name of your sample

Type your research group if not there

Create a name by year/month when your samples analysed



- 1- loaded acquisitions select which file you want to export for data analysis
- 2- select ASCII or mzml and select where to export
- 3- select processed data and press export

Download Mass++  
for data analysis

<https://solutions.shimadzu.co.jp/form/msrl/license.html>

Select to download  
[Mass++ \(V2.7.4\) 64bit edition \(218MB, Updated on Mar. 20, 2015\)](#)

**Drag your data file (ASCII or mzml) into the MASS++ to visualise MALDI mass spectrum**