

Step-by-step tutorial: generating metadata and submitting to LIMS

Each data item submitted to the LIMS requires a metadata file. The LIMS system provides tools to generate these metadata files. If you are generating metadata for less than three (< 3) samples, it's recommended that you use the metadata form, as this will be the fastest method to produce your metadata files. If you are generating metadata for more than three (> 3) samples, it's recommended that you use the metadata batch processor to generate your metadata files. This tutorial provides step-by-step instructions for both methods.

Metadata Form (< 3 samples)

1. Go to the [LIMS metadata form](#).
 2. Enter information to the required fields (those with a blue asterisk)
 1. **LIMS Account:** The LIMS account is your account name: you can see this at the top right corner of the page. If you enter a non-existent account name, the system will tell you the account is invalid when you submit the form.
 2. **Experimental ID:** The experimental ID is the serial number analog for your sample. If you previously characterized your sample in the LIMS and are now submitting additional characterization information (e.g. you previously submitted an NMR spectrum and now you're submitting a mass spectrum), you **must** use the same experimental ID. If this is a new sample, then click the "Generate ID" button to generate a new unique identifier.
-

Metadata Batch (> 3 samples)

1. Go to the [LIMS metadata batch processor](#).

From:
<https://bpm-wiki.cnsi.ucsb.edu/> - NSF BioPACIFIC MIP Wiki

Permanent link:
<https://bpm-wiki.cnsi.ucsb.edu/doku.php?id=lims-guide-data-prep-tutorial&rev=1681149788>

Last update: **2023/04/10 18:03**

