# Adding mpIF/IF submission metadata into eLab Inventory Database

**Cases with GYN FFPE Blocks**

1. Create an excel spreadsheet with the following metadata key for each patient and site
   1. Patient ID
   2. Specimen Site
   3. Site Details
   4. Nomenclature (SPECTRUM-OV-*xxx site;* eg. SPECTRUM-OV-001 LA)
2. Save file as “*SPECTRUM\_Slides\_mpIF\_MMYY.xlsx*” in folder:

*GynLab/Weigelt Lab/Jamie/wet\_lab/SPECTRUM/Sample Submissions and Data/mpIF-IF*

1. Open PyCharm “sort\_columns.py” file
2. Run sort\_columns\_PPBC and compare\_sorted\_to\_submitted\_PPBC simultaneously
   1. Update file names:

Compare\_sorted\_to\_submitted\_PPBC(sorted\_filename, **submitted\_filename**, **saved\_filename**)

1. Import *Saved Filename* into excel and copy and paste data into eLab data entry spreadsheet
2. Save eLab data entry spreadsheet in folder:

*GynLab/Weigelt Lab/Jamie/wet\_lab/SPECTRUM/Sample Submissions and Data/mpIF-IF*

1. Click “Expand Columns and Copy Data to Clipboard” on eLab data entry spreadsheet
2. Open eLab Inventory in browser, click on “Inventory”, then “Sample List”
3. Click on the “Import” button
   1. Number of samples to add
   2. Location start position (PPBC Storage 🡪 FFPE Blocks 🡪 *select N/A box and next available spot*)
   3. Sample type to import: Tissue
   4. Click “Start Import”
4. Click the first empty field on the left and click “Paste from Clipboard”
5. Paste data into empty box
6. Double check that all fields are correct and accurate
7. Click “Import” on top right corner on eLab’s UI
8. Add each aliquot to their corresponding series
   1. Click on the sample series
   2. Click on “+ Series” button at the top of the page
   3. Locate the sample either using List View or Box View
   4. Add the sample to the series
   5. Double check in list that the correct sampled was added to the series

**Cases from Diagnostic Blocks**

1. Use the same saved excel spreadsheet as above, or create a new excel spreadsheet (see steps 1 and 2 above)
2. Open PyCharm “sort\_columns.py” file
3. Run sort\_columns\_PPBC and compare\_sorted\_to\_submitted\_diag simultaneously
   1. Update file names:

Compare\_sorted\_to\_submitted\_diag(sorted\_filename, **submitted\_filename**, **saved\_filename**)

1. Import *Saved Filename* into excel and copy and paste data into eLab data entry spreadsheet
2. Save eLab data entry spreadsheet in folder:

*GynLab/Weigelt Lab/Jamie/wet\_lab/SPECTRUM/Sample Submissions and Data/mpIF-IF*

1. Click “Expand Columns and Copy Data to Clipboard” on eLab data entry spreadsheet
2. Open eLab Inventory in browser, click on “Inventory”, then “Sample List”
3. Click on the “Import” button
   1. Number of samples to add
   2. Location start position (PPBC Storage 🡪 FFPE Blocks 🡪 *select N/A box and next available spot*)
   3. Sample type to import: Tissue
   4. Click “Start Import”
4. Click the first empty field on the left and click “Paste from Clipboard”
5. Paste data in empty box
6. Double check that all fields are correct and accurate
7. Click “Import” on right top corner of eLab’s UI
8. Add each aliquot to their corresponding series
   1. Click on the sample series
   2. Click on “+ Series” button at the top of the page
   3. Locate the sample either using List View or Box View
   4. Add the sample to the series
   5. Double check in list that the correct sampled was added to the series