

GeneXpert INSTRUMENT INTERFACE FOR BIKA LIMS DOCUMENTATION

INTRODUCTION

This document contains information about import of results from files directly generated by GeneXpert Instrument, to Bika Lims from functional and technical point of view. In the first part, it is explained what kind of preparations must be done in order to be able to upload results files to Bika, and how to upload files properly. And the second part explains how its implementation was done and added to Bika Lims step by step.

HOW IT WORKS

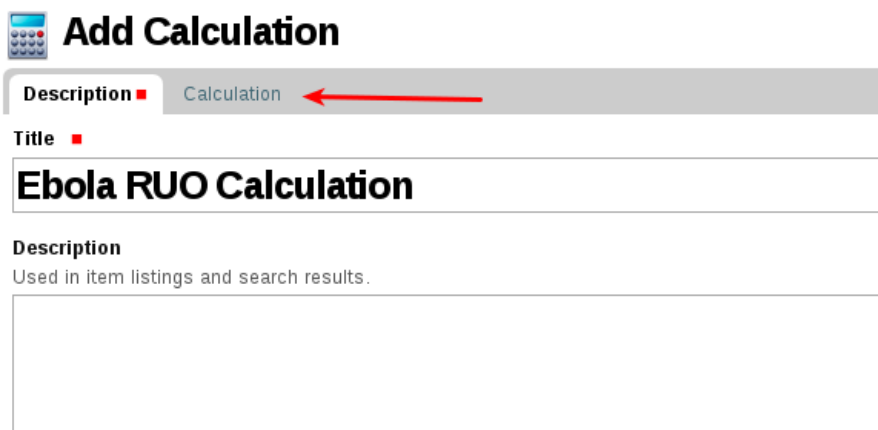
This part explains what users have to do to be able to upload result files from GeneXpert Instrument to the system. The very first step of this process is to create Analysis Services for each Assay that GeneXpert generates results for, if they do not exist in the system. For a better explanation, we will work with 'Ebola RUO' as an example.

Before adding Analysis Service (AS) for 'Ebola RUO' we must consider that GeneXpert doesn't extract direct results for 'Ebola RUO'. In order to get the final result, 'GP' and 'NP' results must be checked, and if they both are negative (NEG) or positive(POS) then the result is negative or positive accordingly. If they differ, or any of them is indeterminate, then the result is indeterminate. Thus, the AS of 'Ebola RUO' requires a *Calculation* to generate proper final results.

Adding Calculation

To create a calculation, follow these steps:

1. Go to *Calculations* page (<site_name>/bika_setup/bika_calculations) and click *Add*.
2. In the new page, enter Title (e.g. Ebola RUO Calc) and switch to *Calculation* tab.



Add Calculation

Description ■ Calculation ←

Title ■

Ebola RUO Calculation

Description

Used in item listings and search results.

Figure 1. Adding Calculation page.

3. As it is explained on that page, user can add *interim fields* there. In our case, we have only 2 Interim Fields which are 'NP' and 'GP' and can be added as shown in the next image:

Add Calculation

Description ■ Calculation

Calculation Interim Fields
 Define interim fields such as vessel mass, dilution factors, should your calculation require them. The field title specified here will be displayed. If 'Apply wide' is enabled the field will be shown in a selection box on the top of the worksheet, allowing to apply a specific value.

Keyword ■	Field Title ■	Default value	Unit	Hidden Field	Apply wide
GP	GP	1		<input type="checkbox"/>	<input checked="" type="checkbox"/>
NP	NP	1		<input type="checkbox"/>	<input checked="" type="checkbox"/>
				<input type="checkbox"/>	<input checked="" type="checkbox"/>

More

Figure 2. Adding GP and NP fields.

'Default Value' is a field to represent Interim Field's default value, when it is not found in result dictionary. We set it to '1' which stands for *INDETERMINATE* (see 'Creating AS' section) which prevents improper final result generations.

4. When interim fields are added, the next step is to enter *Calculation Formula*. Formulas must be valid Python codes. For our case we will add this line of code:

2 if (int([NP])==2 and int([GP])==2) else (3 if (int([NP])==3 and int([GP])==3) else 1)

This code line sets final result to '2' (*NOT DETECTED*, see 'Creating AS' section), if 'NP' and 'GP' are both '2'. Otherwise, final result is '3' (*DETECTED*, see 'Creating AS' section) if 'NP' and 'GP' are both '3'. And if none of previous cases happens, then result of this calculation will be set to '1'.

Add Calculation

Description ■ Calculation

Calculation Interim Fields
 Define interim fields such as vessel mass, dilution factors, should your calculation require them. The field title specified here will be displayed. If 'Apply wide' is enabled the field will be shown in a selection box on the top of the worksheet, allowing to apply a specific value.

Keyword ■	Field Title ■	Default value	Unit	Hidden Field	Apply wide
GP	GP	1		<input type="checkbox"/>	<input checked="" type="checkbox"/>
NP	NP	1		<input type="checkbox"/>	<input checked="" type="checkbox"/>
				<input type="checkbox"/>	<input checked="" type="checkbox"/>

More

Calculation Formula
 The formula you type here will be dynamically calculated when an analysis using this calculation is displayed.

To enter a Calculation, use standard maths operators, + - * / (), and all keywords available, both from other Analysis Services and brackets [].

E.g, the calculation for Total Hardness, the total of Calcium (ppm) and Magnesium (ppm) ions in water, is entered as [Ca] + [Mg].

2 if (int([NP])==2 and int([GP])==2) else (3 if (int([NP])==3 and int([GP])==3) else 1)

Change note
 Enter a comment that describes the changes you made.

Save Cancel

Figure 3. Overall view of Ebola RUO Calculation

Remember that a *Calculation* can be used for more than one AS. For now, this is the only calculation we need so we can save our *Calculation* and move on adding AS.

Creating Analysis Service

Creating AS is easy as just going to AS listing and clicking *Add* button. However, there are some important points that have to be considered.

1. **For each Assay** it is important to add AS. *Formatted Assay Name* must be keyword of AS, otherwise system won't be able to match analyses.

Formatting Assay Name: For GeneXpert Interface we decided to set *Keywords* same as Assay name but with extracting all special characters including *space* (“ ”) and *underscores* (“_”). Keywords are case sensitive and must be unique for Assay. Some examples of keyword formatting:

ASSAY	VALID KEYWORD	INVALID KEYWORDS
Ebola RUO	EbolaRUO	Ebola_RUO, EbolaRuo, Ebola RUO etc.
P0644 v1 50 I Tube Base	P0644v150TubeBase	P0644 v1 50 I Tube Base, P0644v150 I TubeBase, P0644_v1_50_Tube_Base, P0644TubeBase etc.

Let's set the keyword and proceed to setting previously created Calculation method to our AS.

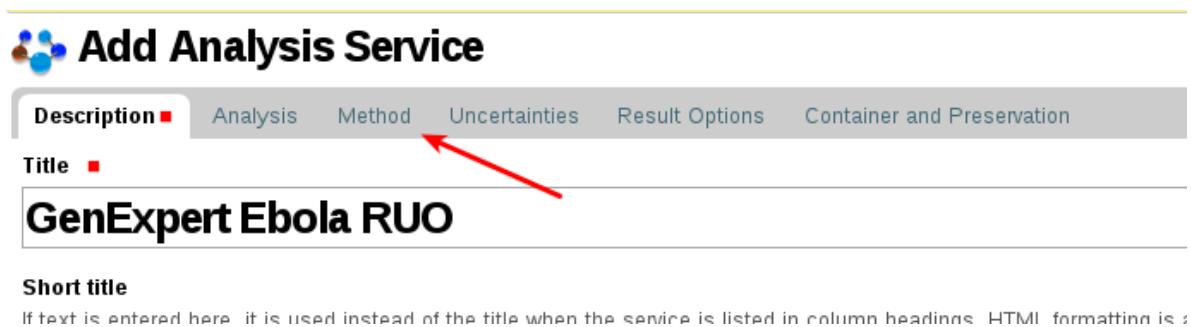
Analysis Keyword ■

The unique keyword used to identify the analysis service in import files of bulk AR requests and results imports from instruments. It is a calculations

Figure 4. Example of AS filled keyword field.

Now we have to go to 'Method' tab in order to add *Calculation* to this AS.

2. Click *Method* tab of AS creation page;



Add Analysis Service

Description Analysis **Method** Uncertainties Result Options Container and Preservation

Title

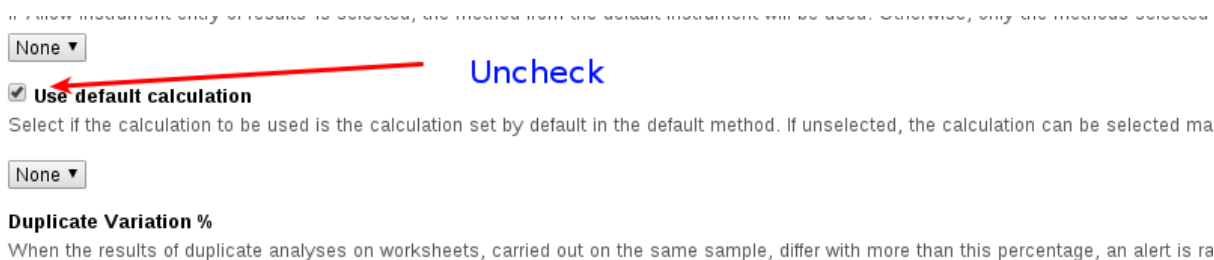
GenExpert Ebola RUO

Short title

If text is entered here, it is used instead of the title when the service is listed in column headings. HTML formatting is :

Figure 5. Tabs of AS add view.

3. Since we want to assign a *Calculation* for this AS, we have to disable using default calculation. Click '*Use default calculation*' to *Uncheck* it.



None ▼

☒ **Use default calculation**

Select if the calculation to be used is the calculation set by default in the default method. If unselected, the calculation can be selected manually.

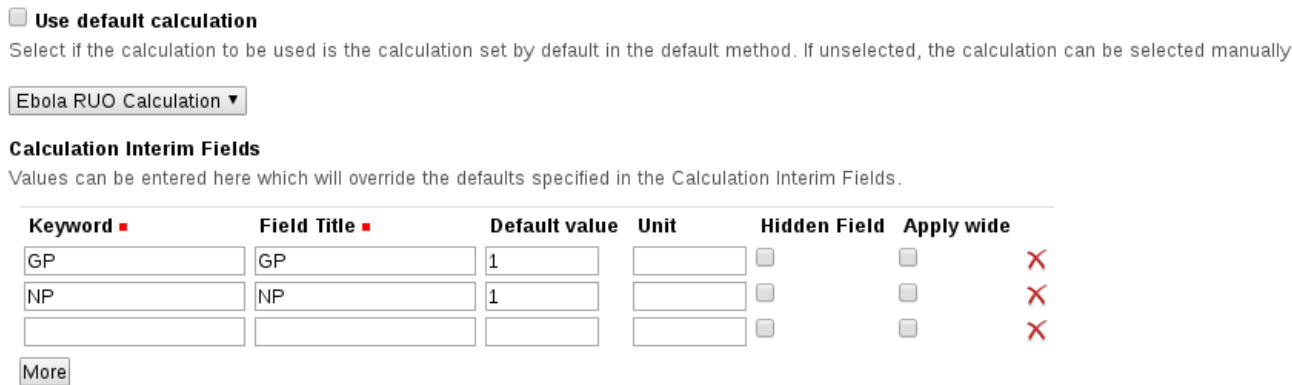
None ▼

Duplicate Variation %

When the results of duplicate analyses on worksheets, carried out on the same sample, differ with more than this percentage, an alert is raised.

Figure 6. Disabling Default Calculation for AS.

4. From the SelectBox Appeared choose the *Calculation* created before, and all interim fields must appear:



☐ **Use default calculation**

Select if the calculation to be used is the calculation set by default in the default method. If unselected, the calculation can be selected manually.

Ebola RUO Calculation ▼

Calculation Interim Fields

Values can be entered here which will override the defaults specified in the Calculation Interim Fields.

Keyword	Field Title	Default value	Unit	Hidden Field	Apply wide
GP	GP	1		<input type="checkbox"/>	<input type="checkbox"/>
NP	NP	1		<input type="checkbox"/>	<input type="checkbox"/>
				<input type="checkbox"/>	<input type="checkbox"/>

More

Figure 7. Fields inherited from *Calculation*.

Here user can override *Default Values*. This functionality mostly used when we use the same *Calculation* for more than one Analysis Services. In our case we don't have to override them.

Now it is time to define why '1', '2', and '3' were used as possible final results.

5. Go to *Results* tab, and there is a section (*Result Options*) which lets us define some values and texts that how they will be displayed. These values must be filled carefully and respectfully to GeneXpert Interface code. Result values of current version is the same as following figure:

Add Analysis Service

Description ■ Analysis Method Uncertainties **Result Options** Container and Preservation

Result Options

Please list all options for the analysis result if you want to restrict it to specific options only, e.g. 'Positive', 'Neg

Result Value ■	Display Value ■	
1	INDETERMINATE	✗
2	NOT DETECTED	✗
3	DETECTED	✗
		✗

More

Change note

Enter a comment that describes the changes you made.

Save Cancel

Figure 8. Defining Result Values for AS.

Remember that, this kind of calculation can be added to AS if it already exists as well, by editing them. It will work for next imports after that edit.

Setting Instrument's Interface

Until now, we have created a calculation and assigned it to the new AS, which has a keyword of an Assay from GeneXpert (*EbolaRUO*). The next step is to upload result files downloaded from GeneXpert Instrument, to the system. First, we must be sure there is an Interface assigned to our Instrument. We can check it from Instrument's Edit view:

Import Data Interface

Select an Import interface for this instrument.

- FOSS - Winescan FT120
- GenExpert**
- Horiba Jobin-Yvon - ICP
- Life Technologies - Qubit
- My Instrument

Figure 9. 'GeneXpert' Import Data Interface must be selected for GeneXpert Instrument.

New Interface special for GeneXpert must be in the Interface list. Choose 'GeneXpert' from the list if it is not selected and *Save*.

Uploading Results

When all previous steps done properly, import interface must appear on import page. Go to *Import* page, choose GeneXpert Instrument from Instrument list, GeneXpert Interface from Interface list, and upload result file.

Import

Select a data interface

Instrument Import Load Setup Data Auto Import Instrument Results

Instrument

GeneXpert® IV

If the system doesn't find any match (AnalysisRequest, Sample, Reference Analysis or Duplicate), it will use the record's identifier to find ma Calibration Test (Reference Analysis) and will link it to the instrument selected above.

If no instrument selected, no Calibration Test will be created for orphan IDs.

Import Interface

GenExpert

File Choose File ACCEL_mult...results.csv **Format** CSV

Advanced options

Analysis Requests state Received

Results override Override non-empty results (also with empty)

Submit

Figure 9. Import Interface of GeneXpert.

When import is done, logs, errors and warnings will be displayed if there is any.

Log trace

Parsing file ACCEL_mult_GeneXpert_results.csv

End of file reached successfully: 3 objects, 8 analyses, 3 results

Allowed Analysis Request states: sample_received

Allowed analysis states: sampled, sample_received, attachment_due, to_be_verified

SR-0005-R01 result for 'EbolaRUO:GP': '3'

SR-0005-R01 result for 'EbolaRUO:NP': '3'

SR-0005-R01: [u'Analysis EbolaRUO'] imported successfully

Import finished successfully: 1 ARs, 0 Instruments and 1 results updated

Errors

No analyses 'sampled, sample_received, attachment_due, to_be_verified' states found for 150129_LSP#103_38_Neg#6

No Reference Sample found for 150129_LSP#103_38_Neg#6

No analyses 'sampled, sample_received, attachment_due, to_be_verified' states found for LOD_75c_JeG_TF1_2

No Reference Sample found for LOD_75c_JeG_TF1_2

Warnings

Service keyword CIC not found

Service keyword QC-2 not found

Service keyword QC-1 not found

Service keyword GP not found

Service keyword SAC not found

Service keyword NP not found

Service keyword P0644v150lTubeBase not found

Figure 10. Examples of Log, Error and Warnings after Import.

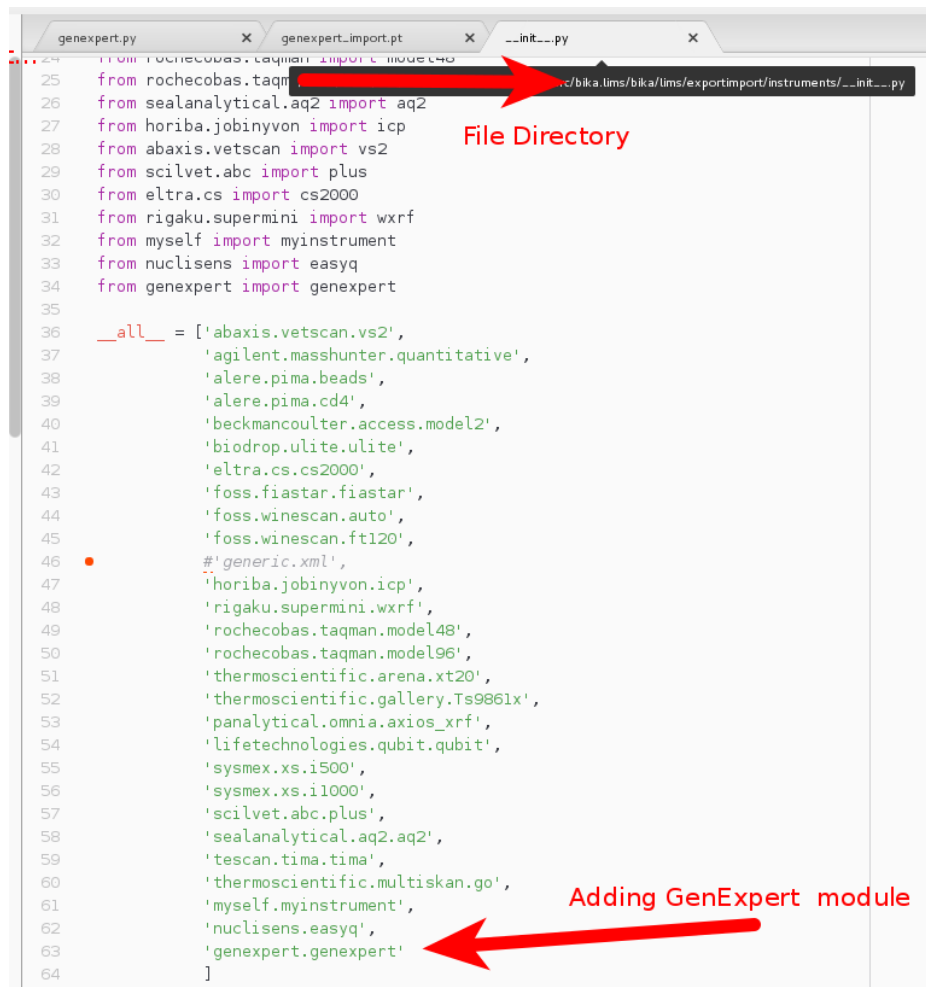
HOW IT IS DONE

Before reading this part, make sure that you have some acknowledgement about how to add a new Instrument Import Interface to Bika Lims. More information can be found on;

<https://github.com/bikalabs/bika.lims/wiki/creating-an-instrument-import-interface> .

To create the Import Interface of GeneXpert we followed steps shown below:

1. First of all, we added new 'GeneXpert' folder under 'bika/lims/exportimport/instruments/' directory, because all import interfaces are placed there, and when importing results, system imports modules exactly from that directory. To enable this folder to be as importable module, we added empty '__init__.py' file there, and also 'GeneXpert.py' file in order to add new classes, functions and etc.
2. Then, to make system see that interface, we had to add that empty interface to Bika's Interfaces list. It has been done by adding 'GeneXpert.GeneXpert' to the variable so-called '__all__' in '__init__' file of 'bika/lims/exportimport/instruments/' folder.



```
25 from rohecobas.taqm import model48
26 from sealanalytical.aq2 import aq2
27 from horiba.jobinyvon import icp
28 from abaxis.vetscan import vs2
29 from scilvet.abc import plus
30 from eltra.cs import cs2000
31 from rigaku.supermini import wxrf
32 from myself import myinstrument
33 from nuclisens import easyq
34 from genexpert import genexpert
35
36 __all__ = ['abaxis.vetscan.vs2',
37           'agilent.masshunter.quantitative',
38           'alere.pima.beads',
39           'alere.pima.cd4',
40           'beckmancoulter.access.model2',
41           'biobdrop.ulite.ulite',
42           'eltra.cs.cs2000',
43           'foss.fiastar.fiastar',
44           'foss.winescan.auto',
45           'foss.winescan.ft120',
46           '#generic.xml',
47           'horiba.jobinyvon.icp',
48           'rigaku.supermini.wxrf',
49           'rohecobas.taqm.model48',
50           'rohecobas.taqm.model96',
51           'thermoscientific.arena.xt20',
52           'thermoscientific.gallery.Ts9861x',
53           'panalytical.omnia.axios_xrf',
54           'lifetechnologies.qubit.qubit',
55           'sysmex.xs.i500',
56           'sysmex.xs.i1000',
57           'scilvet.abc.plus',
58           'sealanalytical.aq2.aq2',
59           'tescan.tima.tima',
60           'thermoscientific.multiskan.go',
61           'myself.myinstrument',
62           'nuclisens.easyq',
63           'genexpert.genexpert'
64 ]
```

Figure 11.New module is in Interfaces list.

Parser name also was added to the parsers list in the same file. It is important if we want to use Bika's auto-import of results functionality. We let the parser name be 'GeneXpertParser';

```

66 # Parsers are for auto-import. If empty, then auto-import won't run for that
67 # interface
68 PARSERS = [
69     ['abaxis.vetscan.vs2', 'AbaxisVetScanCSVVS2Parser'],
70     ['agilent.masshunter.quantitative', 'MasshunterQuantCSVParser'],
71     ['alere.pima.beads', 'AlerePimaSLKParser'],
72     ['alere.pima.cd4', 'AlerePimacd4SLKParser'],
73     ['beckmancoulter.access.model2', 'BeckmancoulterAccess2CSVParser'],
74     ['biobdrop.ulite.ulite', 'BioDropCSVParser'],
75     ['eltra.cs.cs2000', 'EltraCS2000CSVParser'],
76     ['foss.fiastar.fiastar', 'FOSSFIASStarCSVParser'],
77     ['foss.winescan.auto', 'WinescanAutoCSVParser'],
78     ['foss.winescan.ft120', 'WinescanFT120CSVParser'],
79     # ['generic.xml', ''],
80     ['horiba.jobinyvon.icp', 'HoribaJobinYvonCSVParser'],
81     ['rigaku.supermini.wxrf', 'RigakuSuperminiWXRFCsvParser'],
82     ['rochecobas.taqman.model48', 'RocheCobasTaqmanRSFParser'],
83     ['rochecobas.taqman.model96', 'RocheCobasTaqmanRSFParser'],
84     ['thermoscientific.arena.xt20', 'ThermoArena20XTRPRCSVParser'],
85     ['thermoscientific.gallery.ts9861x', 'ThermoGallery9861xTSVParser'],
86     ['panalytical.omnia.axios_xrf', 'AxiosXrfCSVParser'],
87     ['lifetechnologies.qubit.qubit', 'QubitCSVParser'],
88     ['sysmex.xs.i500', 'SysmexXS500iCSVParser'],
89     ['sysmex.xs.i1000', 'SysmexXS500iCSVParser'],
90     ['scilvet.abc.plus', 'AbaxisVetScanCSVVS2Parser'],
91     ['sealanalytical.aq2.aq2', 'SealAnalyticsAQ2CSVParser'],
92     ['tescan.tima.tima', 'TimaCSVParser'],
93     ['thermoscientific.multiskan.go', 'ThermoScientificMultiskanGOCsvParser'],
94     ['myself.myinstrument', 'MyInstrumentCSVParser'],
95     ['nuclisens.easyq', 'EasyQParser'],
96     ['genexpert.genexpert', 'GenExpertParser'],
97 ]
98

```

Parser of GenExpert Files

Figure 12. Adding GeneXpert parser to the Parsers List.

After editing '__init__' file of Instruments module, now system has an access to our Interface. We can move on and start adding a template and functions to parse and import results.

3. Templates are '*.pt' files which can be understood by anyone who knows how to code in HTML. They are used to define which parameters should be sent from users in order to set parameters of import process. For GeneXpert we also used Bika's default template, which allows users upload CSV file, and choose Analysis Requests states to be looked for, and disable/enable overriding results. We just created 'GeneXpert_import.pt' file under our new 'GeneXpert' folder, and filled it as the same as default template of Bika.


```

1  <p></p>
2  <label for="genexpert_file">File</label>&nbsp;
3  <input type="file" name="genexpert_file" id="genexpert_file"/>
4  &nbsp;&nbsp;
5  <label for="format">Format</label>&nbsp;
6  <select name="format" id="format">
7    <option value='csv'>CSV</option>
8  </select>
9  <p></p>
10 <h3>Advanced options</h3>
11 <table cellpadding="0" cellspacing="0">
12   <tr>
13     <td><label for="artoapply">Analysis Requests state</label>&nbsp;</td>
14     <td>
15       <select name="artoapply" id="artoapply">
16         <option value="received">Received</option>
17         <option value="received_tobeverified">Received and to be verified</option>
18       </select>
19     </td>
20   </tr>
21   <tr>
22     <td><label for="override">Results override</label></td>
23     <td>
24       <select name="override" id="override">
25         <option value="nooverride">Don't override results</option>
26         <option value="override">Override non-empty results</option>
27         <option value="overrideempty">Override non-empty results (also with empty)</option>
28       </select>
29     </td>
30   </tr>
31 </table>
32 <p></p>
33 <input name="firstsubmit" type="submit" value="Submit" id="firstsubmit" />
34 <p></p>
35

```

Figure 13. Template file overview.

4. Since we have the template, now we need an Import method to handle requests, and try to parse and import results. In Bika, all requests go to 'Import' method of Interface. In that method it is important to get parameters from request, build a parser and a result importer objects, and finally process values. 'Import' method for GeneXpert Interface is in 'GeneXpert.py' file. It simply reads requests and calls parser and importer functions. To know how everything done, please check comments inside code.

5. There are two more classes in GeneXpert.py file- GeneXpertParser and GeneXpertImporter, which are called by importer we added previously. Both of these classes are explained well in the comments and it is enough to know that, CSV parser reads files line-by-line, and depending on first word of line calls different methods. When the Parser reaches end of file, it adds all results to Raw Results, and Importer processes them.

Finally, all code changes and new files can be found on;

<https://github.com/naralabs/bika.lims/pull/88>