

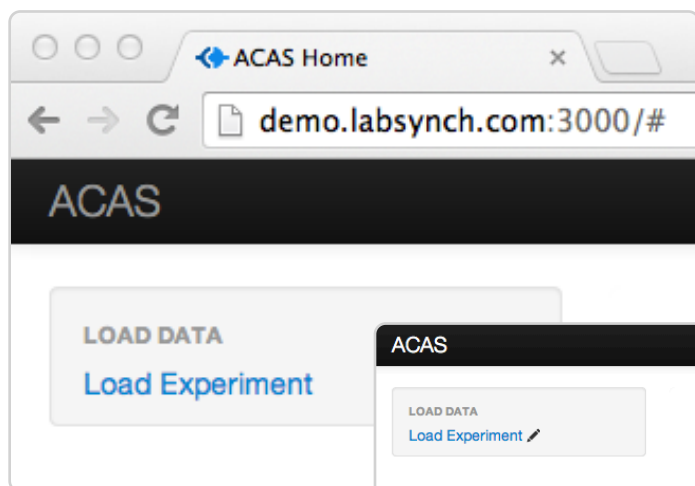
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# ACAS Tutorial

## *Simple Experiment Loader*

### Contents:

- Overall Workflow
- Loading a Generic Data File
- Loading a Concentration Data File
- Adding a Report File
- Adding Images
- Validation Errors
- Editing a Protocol
- Adding Files to Protocols

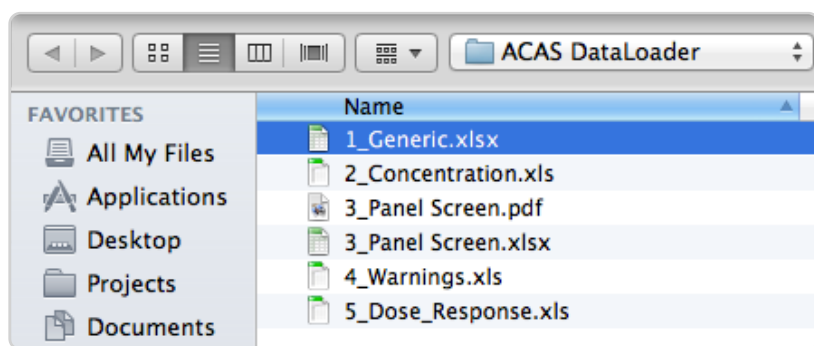
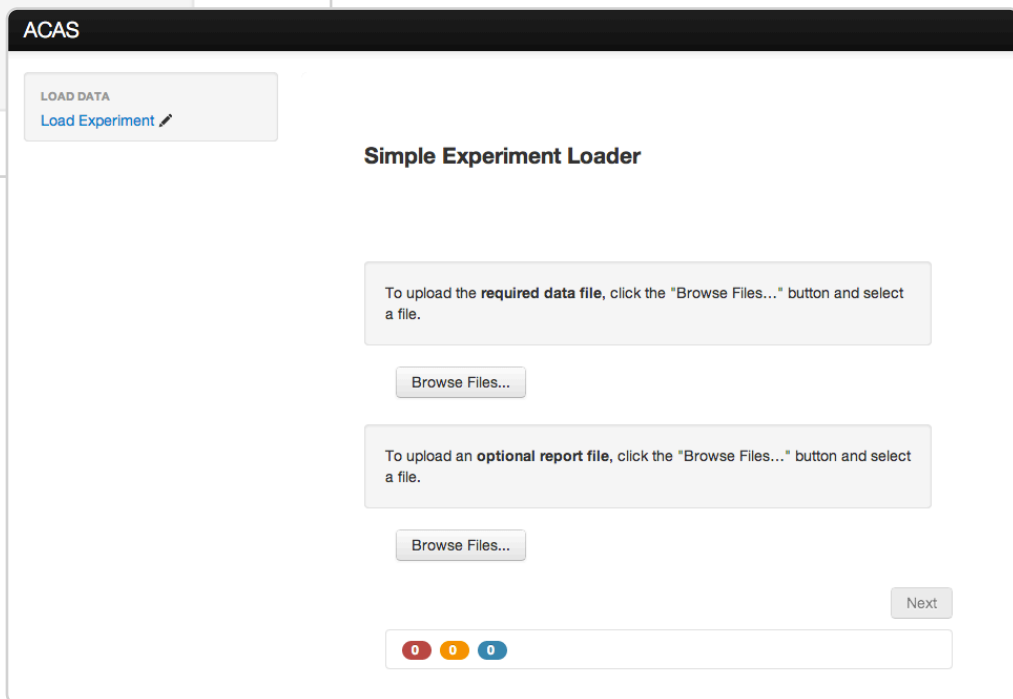


Open a browser window to ACAS. Clicking [Load Experiment](#) will take you to the Simple Experiment Loader.

The Simple Experiment Loader has three Browse for Files options.

The first allows you to upload a **data file**. This file is required to run the loader.

The second allows you to upload an **optional report file**.



Click [Browse Files...](#) and select the data file you would like to upload.

The data file browser accepts these file types: .xls, .xlsx, and .csv.

The report file browser accepts almost all file types except .exe.

	A	B	C	D	E
1	Experiment Meta Data				
2	Format	Generic			
3	Protocol Name	PAMPA Buffer A			
4	Experiment Name	Buffer A Test On5		Do not change green cells, they are required by the loader	
5	Scientist	jmcneil			
6	Notebook	JAM-000033			
7	Page	6			
8	Assay Date	2014-03-04			
9					
10	Calculated Results				
11	Datatype	Number	Number (hidden)	Text	
12	Corporate Batch ID	solubility (ug/mL)	log solubility (ug/mL)	Assay Comment	
13	CMPD-0000001-01	7.00	0.885446248	Great Value	
14	CMPD-0000002-01	4.00	0.497317153	Weak Value	
15	CMPD-0000003-01	fail	fail		
16	CMPD-0000004-01	3.97	0.598763775		
17	CMPD-0000005-01	>41	>1.61278385671974		
18	CMPD-0000006-01	>44	>1.64345267648619		
19	CMPD-0000007-01	>48	>1.68124123737559		
20					

This is what a generic sample data file looks like (in this case: solubility). The green cells are required by the loader to analyze the data in the file. However, all other fields may be changed. Keep in mind: some fields have format requirements.

Select the data file. It will appear in the Simple Experiment Loader, with options. If there is no report file, click the [Next](#) button.

**ACAS**

LOAD DATA  
[Load Experiment](#) ✎ \*

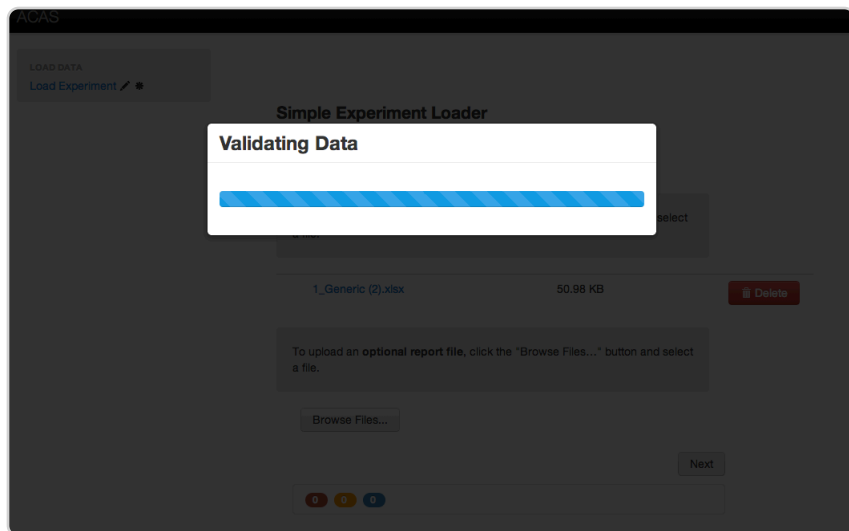
### Simple Experiment Loader

To upload the **required data file**, click the "Browse Files..." button and select a file.

1\_Generic (2).xlsx
50.98 KB
Delete

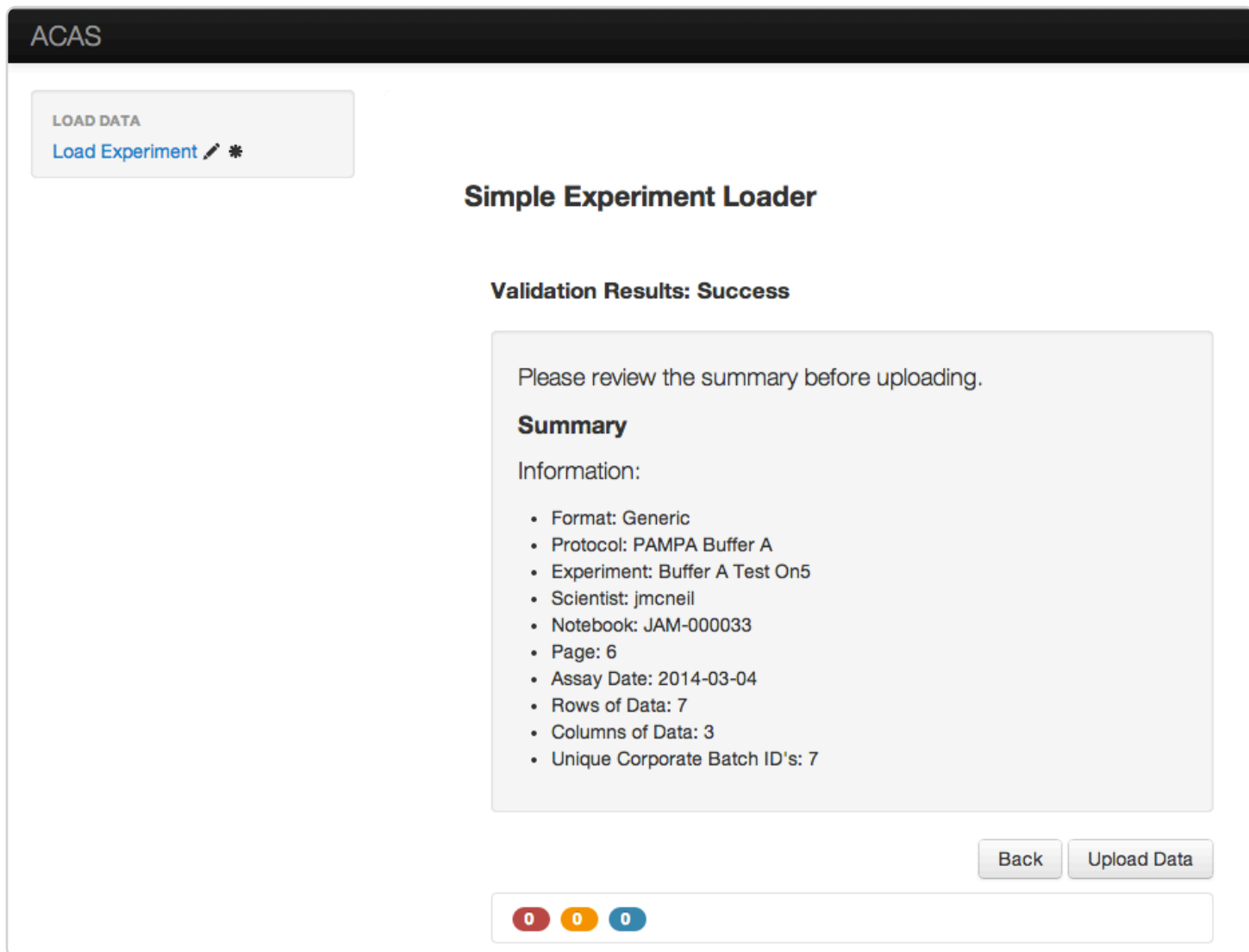
To upload an **optional report file**, click the "Browse Files..." button and select a file.

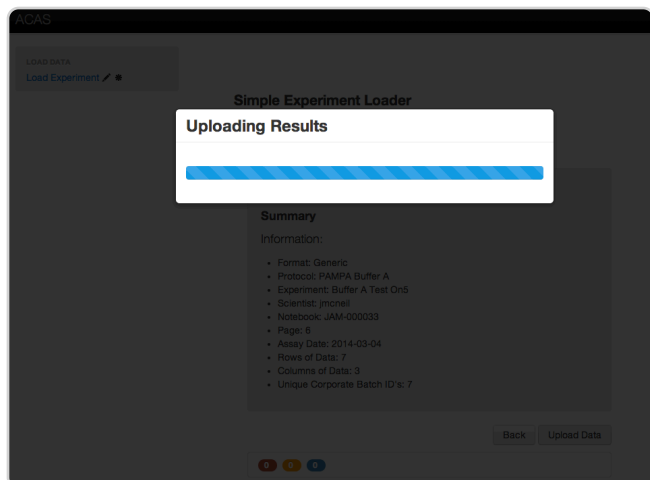
0
0
0



The file is then validated, and the results are displayed. Check the summary to make sure all the information is correct.

If correct, click the [Upload Data](#) button.





The results are uploaded, and a summary is displayed.

From there you can open the report in Seurat and email a link to the report. Clicking [Open Seurat Report](#) launches Seurat.

Alternatively, you can also load another experiment by clicking [Load Another](#).

# ACAS

[LOAD DATA](#)  
[Load Experiment](#)

## Simple Experiment Loader

**Upload Results: Success**

Upload completed.

### Summary

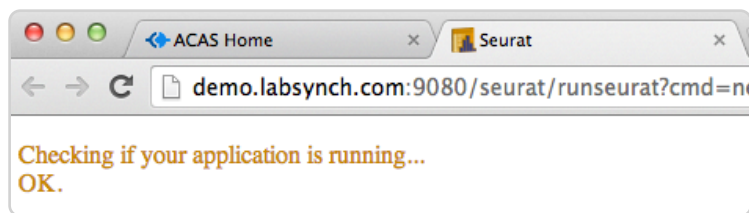
Information:

- Transaction Id: 21
- Format: Generic
- Protocol: PAMPA Buffer A
- Experiment: Buffer A Test On5
- Scientist: jmcneil
- Notebook: JAM-000033
- Page: 6
- Assay Date: 2014-03-04
- Rows of Data: 7
- Columns of Data: 3
- Unique Corporate Batch ID's: 7
- Experiment Code Name: EXPT-0000021

[Open Seurat Report\\*](#) [Email Link to Seurat Report](#)

\*Note: there may be a delay before data is visible in Seurat

[Load Another](#)

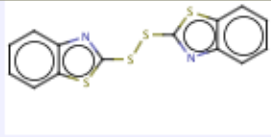
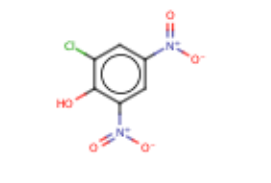
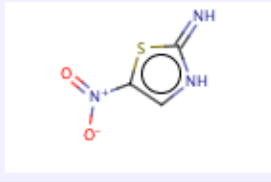
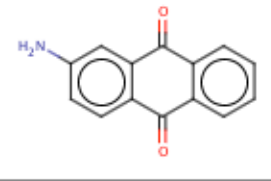


Seurat launches...

Assay Display (New Live Report)

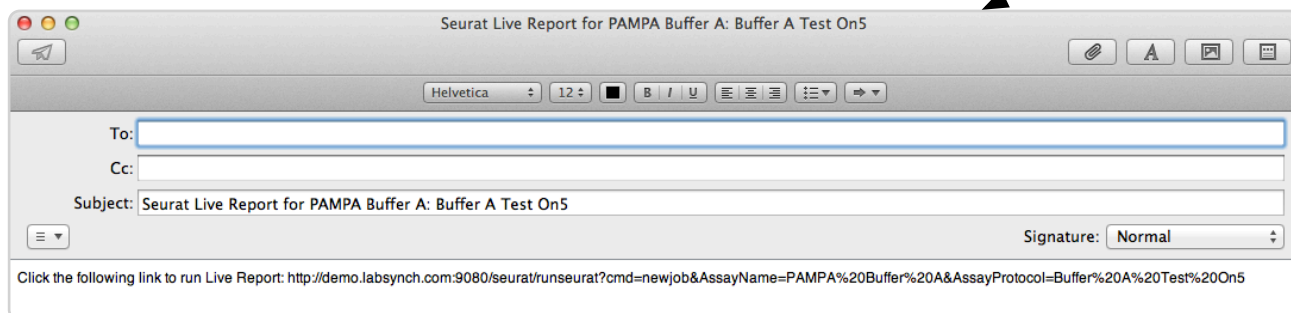
File Edit View Tools Help

Visualize Trellis Pie Chart SAR Table Add Data Hide Data Ff Operators

A: Corporate ID	B: Compound Structure	C: PAMPA Buffer A (Assay Comment)	D: PAMPA Buffer A (solubility) [ug/mL]
<a href="#">CMPD-0000002</a>		Weak Value	4.0
<a href="#">CMPD-0000003</a>			fail
<a href="#">CMPD-0000004</a>			3.97
<a href="#">CMPD-0000005</a>			> 41

Data loaded.

This is the format for emailing a Seurat report.



	A	B	C	D	E
1	<b>Experiment Meta Data</b>				
2	Format	Generic			
3	Protocol Name	PAMPA Buffer A			
4	Experiment Name	Buffer A Test On5		Do not change green cells, they are required by the loader	
5	Scientist	jmcneil			
6	Notebook	JAM-000033			
7	Page	6			
8	Assay Date	2014-03-04			
9					
10	<b>Calculated Results</b>				
11	Datatype	Number	Number (hidden)	Text	Number
12	Corporate Batch ID	solubility (ug/mL)	log solubility (ug/mL)	Assay Comment	Temp (K)
13	CMPD-0000001-01	7.00	0.885446248	Great Value	80
14	CMPD-0000002-01	4.00	0.497317153	Weak Value	30
15	CMPD-0000003-01	fail	fail		20
16	CMPD-0000004-01	3.97	0.598763775		
17	CMPD-0000005-01	>41	>1.61278385671974		
18	CMPD-0000006-01	>44	>1.64345267648619		
19	CMPD-0000007-01	>48	>1.68124		

### Validating Data

**Validation Results: Success but with warnings**

Please review the warnings and summary before uploading.

**Warnings: 1**

Warnings provide information on issues found in the upload file. You can proceed with warnings; however, it is recommended that, if possible, you make the changes suggested by the warnings and upload a new version of the file by using the 'Back' button at the bottom of this screen.

- Experiment 'Buffer A Test On5' already exists, so the loader will delete its current data and replace it with your new upload. If you do not intend to delete and reload data, enter a new experiment name.

**Summary**

Information:

- Format: Generic
- Protocol: PAMPA Buffer A
- Experiment: Buffer A Test On5
- Scientist: jmcneil
- Notebook: JAM-000033
- Page: 6
- Assay Date: 2014-03-04
- Rows of Data: 7
- Columns of Data: 4
- Unique Corporate Batch ID's: 7

Back Upload Data

It is possible to upload a different data set for the same experiment. Just alter the file and reupload.

The loader will give you a warning stating that the experiment already exists. It will replace the existing data with the new data.

In this example, the user added an additional data column (temperature) to the file. This will be displayed when the user opens the Seurat report.

## Uploading Results

Once uploaded, the results summary is shown, and again there are options to view the report in Seurat or email a link to the report.

## Simple Experiment Loader

### Upload Results: Success

Upload completed.

#### Summary

Information:

- Transaction Id: 22
- Format: Generic
- Protocol: PAMPA Buffer A
- Experiment: Buffer A Test On5
- Scientist: jmcneil
- Notebook: JAM-000033
- Page: 6
- Assay Date: 2014-03-04
- Rows of Data: 7
- Columns of Data: 4
- Unique Corporate Batch ID's: 7
- Experiment Code Name: EXPT-0000022

[Open Seurat Report\\*](#)

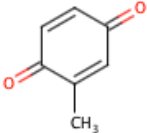
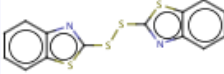
[Email Link to Seurat Report](#)

\*Note: there may be a delay before data is visible in Seurat

Assay Display (New Live Report)

File Edit View Tools Help

Visualize Trellis Pie Chart SAR Table Add Data Hide Data Operator

A: Corporate ID	B: Compound Structure	C: PAMPA Buffer A (Assay Comment)	D: PAMPA Buffer A (Temp) [K]	E: PAMPA Buffer A (solubility) [ug/mL]
<a href="#">CMPD-0000001</a>		Great Value	80	7.0
<a href="#">CMPD-0000002</a>		Weak Value	30	4.0

New temperature data.

[Load Another](#)



	A	B	C	D	E
1	<b>Experiment Meta Data</b>				
2	Format	Generic			
3	Protocol Name	CYP 3A4 Inhibition			
4	Experiment Name	Test Experiment On2		Do not change green cells, they are required by the loader	
5	Scientist	jmcneil			
6	Notebook	JM-576			
7	Page		12		
8	Assay Date	2014-02-28			
9					
10	<b>Calculated Results</b>				
11	Datatype	Number	Number	Number	
12	Corporate Batch ID	Inhibition (%) [10 uM]	Inhibition (%) [30 uM]	Inhibition (%) [100 uM]	
13	CMPD-0000051-01	10	45	80	
14	CMPD-0000052-01	40	70	retest	
15					

In the first example, a solubility data file was used. Other data types may also be uploaded, like inhibition at different concentrations.

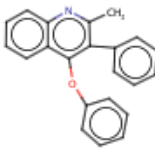
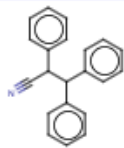
The steps to upload are the same.

The screenshots show the 'Simple Experiment Loader' interface. The first window shows the upload step. The second window shows 'Validation Results: Success'. The third window shows a 'Summary' of the upload results, including details like 'Format: Generic', 'Protocol: CYP 3A4 Inhibition', 'Experiment: Test Experiment On2', 'Scientist: jmcneil', and 'Notebook: JM-576'. The fourth window shows 'Upload Results: Success' with the message 'Upload completed.' and a 'Summary' of the data loaded.

Assay Display (New Live Report)

File Edit View Tools Help

Visualize Trellis Pie Chart SAR Table Add Data Hide Data Operators

A: Corporate ID	B: Compound Structure	C: CYP 3A4 Inhibition (Inhibition) at 10.0uM [%]	D: CYP 3A4 Inhibition (Inhibition) at 30.0uM [%]	E: CYP 3A4 Inhibition (Inhibition) at 100.0uM [%]
<a href="#">CMPD-0000051</a>		10	45	80
<a href="#">CMPD-0000052</a>		40	70	retest @100.0uM

The concentration data is shown, in this case, in multiple columns.

	A	B	C	D	E	F
1	<b>Experiment Meta Data</b>					
2	Format	Generic				
3	Protocol Name	Panel Screen				
4	Experiment Name	Expt On3				
5	Scientist	jmcneil				
6	Notebook	JAM-000033				
7	Page	6				
8	Assay Date	2013-07-08				
9						
10	<b>Calculated Results</b>					
11	Datatype	Text				
12	Corporate Batch ID	Assay Comment				
13	CMPD-0000001-01	See attached file				
14	CMPD-0000002-01	See attached file				
15	CMPD-0000003-01	See attached file				
16	CMPD-0000004-01	See attached file				
17	CMPD-0000005-01	See attached file				
18	CMPD-0000006-01	See attached file				
19	CMPD-0000007-01	See attached file				
20						

Do not change green cells, they are required by the loader

ACAS

LOAD DATA  
 Load Experiment / \*

### Simple Experiment Loader

To upload the required data file, click the "Browse Files..." button and select a file.

3\_Panel Screen.xlsx
49.78 KB
Delete

To upload an optional report file, click the "Browse Files..." button and select a file.

3\_Panel Screen.pdf
1.01 MB
Delete

Next

0
0
0

### Simple Experiment Loader

**Validation Results: Success**

Please review the summary before uploading.

**Summary**

Information:

- Format: Generic
- Protocol: Panel Screen
- Experiment: Expt On3
- Scientist: jmcneil
- Notebook: JAM-000033
- Page: 6
- Assay Date: 2013-07-08
- Rows of Data: 7
- Columns of Data: 1
- Unique Corporate Batch ID's: 7

### Simple Experiment Loader

**Upload Results: Success**

Upload completed.

**Summary**

Information:

- Transaction Id: 24
- Format: Generic
- Protocol: Panel Screen
- Experiment: Expt On3
- Scientist: jmcneil
- Notebook: JAM-000033
- Page: 6

In the next example, a report file is also uploaded with the data file.

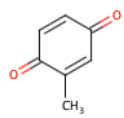
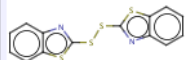
In Seurat, a link to the report file is shown in a new column.

Assay Display (New Live Report)

File Edit View Tools Help

Visualize
Trellis Pie Chart
SAR Table
Add Data
Hide Data

New Column Formula:

A: Corporate ID	B: Compound Structure	C: Panel Screen (Assay Comment)	D: Panel Screen (report file)
<a href="#">CMPD-0000001</a>		See attached file	<a href="#">Panel Screen - Expt On3 (experiments/EXPT-00000024/3_Panel Screen.pdf)</a>
<a href="#">CMPD-0000002</a>		See attached file	<a href="#">Panel Screen - Expt On3 (experiments/EXPT-00000024/3_Panel Screen.pdf)</a>



	A	B	C	D	E
1	<b>Experiment Meta Data</b>				
2	Format	Generic			
3	Protocol Name	PAMPA Buffer Other			
4	Experiment Name	Buffer other test On1			Do not change green cells, they are required by the loader
5	Scientist	jmcneil			
6	Notebook	JHN-123			
7	Page	6			
8	Assay Date	02-21-2014			
9	Extra Header row	not useful			
10					
11	<b>Calculated Results</b>				
12	Datatype	Number	Numbr	Text	Text
13	Corporate Batch ID	solubility (ug/mL)	log solubility other (ug/mL)	Assay Comment	Assay Comment
14	CMPD-0000001-101	7.68	0.885446248	Great Value	More
15	CMPD-0000002-01	3.14	0.497317153	Weak Value	Even More
16	CMPD-0000003-01	10.45	1.01912627		
17	CMPD-0000004-01	3.97	0.598763775		
18	CMPD-0000005-01	>41	>1.61278385671974		
19	CMPD-0000006-01	>44	>1.64345267648619		
20	CMPD-0000007-01	>48	>1.68124123737559		

If there is an error in the data file, the loader will fail to validate the file and report the errors. The errors can then be fixed and the file re-uploaded.

**Validation Results: Failed due to errors**

Please fix the following errors and use the 'Back' button at the bottom of this screen to upload a new version of the file.

**Errors: 2**

- These column headings are duplicated: Assay Comment. All column headings must be unique.
- Corporate Batch Id 'CMPD-0000001-101' has not been registered in the system. Contact your system administrator for help.

**Warnings: 5**

Warnings provide information on issues found in the upload file. You can proceed with warnings; however, it is recommended that, if possible, you make the changes suggested by the warnings and upload a new version of the file by using the 'Back' button at the bottom of this screen.

- A date is not in the proper format. Found: "02-21-2014" This was interpreted as "2014-02-21". Please enter dates in the following format: "2014-03-05", or click [here](#)
- The loader found an extra Experiment Meta Data row that will be ignored: 'Extra Header row'. Please remove this row.
- In column "log solubility other (ug/mL)", the loader found 'Numbr' as a datatype and interpreted it as 'Number'. Please enter 'Number', 'Text', or 'Date'.
- The following column headers have never been loaded in an experiment before: 'log solubility other'. If you have loaded a similar experiment before, please use the same headers that were used previously. If this is a new protocol, you can proceed without worry.
- Protocol 'PAMPA Buffer Other' does not exist, so it will be created. No user action is needed if you intend to create a new protocol.

**Summary**

In this example, the Assay Comment headers are duplicated. This is one of the errors listed.

The date format is also incorrect, the loader has detected and ignored an extra header row, etc. If it can, the loader will correct these issues.

The loader will try to allow you to continue uploading if there are only warnings, but true errors will cause a failure.

**Summary**

Information:

- Format: Generic
- Protocol: PAMPA Buffer Other
- Experiment: Buffer other test On1
- Scientist: jmcneil
- Notebook: JHN-123
- Page: 6
- Assay Date: 2014-02-21
- Rows of Data: 7
- Columns of Data: 3
- Unique Corporate Batch ID's: 7

2
5
0

	A	B	C
1	Experiment Meta Data		
2	Format	Dose Response	
3	Protocol Name	Fiona Test Protocol	
4	Experiment Name	Fiona Test Experiment 5-2	
5	Scientist	bob	
6	Notebook	12	
7	Page	7	
8	Assay Date	2015-05-08	
9			
10	Calculated Results		
11	Datatype	Text (hidden)	Text
12	Corporate Batch ID	Rendering Hint	curve id
13	CMPD-0000011-	4 parameter D-R	a sigmoid
14	CMPD-0000012-	4 parameter D-R	b sigmoid
15	CMPD-0000013-	4 parameter D-R	c sigmoid
16	CMPD-0000014-	4 parameter D-R	d sigmoid
17	CMPD-0000015-	4 parameter D-R	e sigmoid
18	CMPD-0000016-	4 parameter D-R	f sigmoid
19	CMPD-0000017-	4 parameter D-R	90803 sigmoid
20	CMPD-0000018-	4 parameter D-R	90816 sigmoid
21	CMPD-0000019-	4 parameter D-R	126226 sigmoid
22	CMPD-0000020-	4 parameter D-R	126877 sigmoid
23	CMPD-0000021-	4 parameter D-R	126915 sigmoid
24	CMPD-0000022-	4 parameter D-R	126933 sigmoid
25	CMPD-0000023-	4 parameter D-R	8778 biphasic
26	CMPD-0000024-	4 parameter D-R	8788 biphasic
27	CMPD-0000025-	4 parameter D-R	8806 biphasic
28	CMPD-0000026-	4 parameter D-R	8836 biphasic
29	CMPD-0000027-	4 parameter D-R	9629 biphasic
30			
31			
32			
33			
34	Raw Results		
35	temp id	x	y
36	curve id	Dose (uM)	Response (efficacy)
37	a		20 88.51
38	a		10 89.826 spilled
39	a		5 89.883

### Dose Response Fit Module

Upload Data

Model Fit

Model Fit Type

Select Model

Model Fit Type

- Select Model Fit Type
- EC50
- Ki

Model Fit Type

EC50

#### Global Fit Criteria

Smart Mode

Max:  None  Pin  Limit

Min:  None  Pin  Limit

Slope:  None  Pin  Limit

Inverse Agonist Mode

Inactive Threshold



20

Fit Data

### Curve Fit Summary

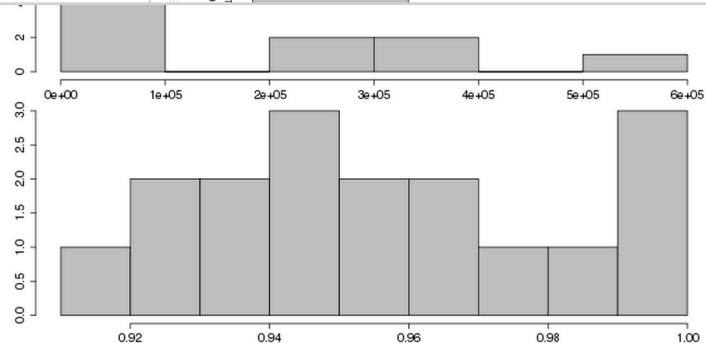
#### Model Equation

$$f(x) = c + \frac{\text{max} - \text{min}}{1 + \exp(\text{slope}(\log(\text{conc}) - \log(\text{ec50})))}$$

#### Fit Summary

- Attempted Fits: 17
- Successful Fits: 17
- Failed Fits: 0

#### Categories



\* Note - this summary is the result of the initial fit; curve curation may alter curves

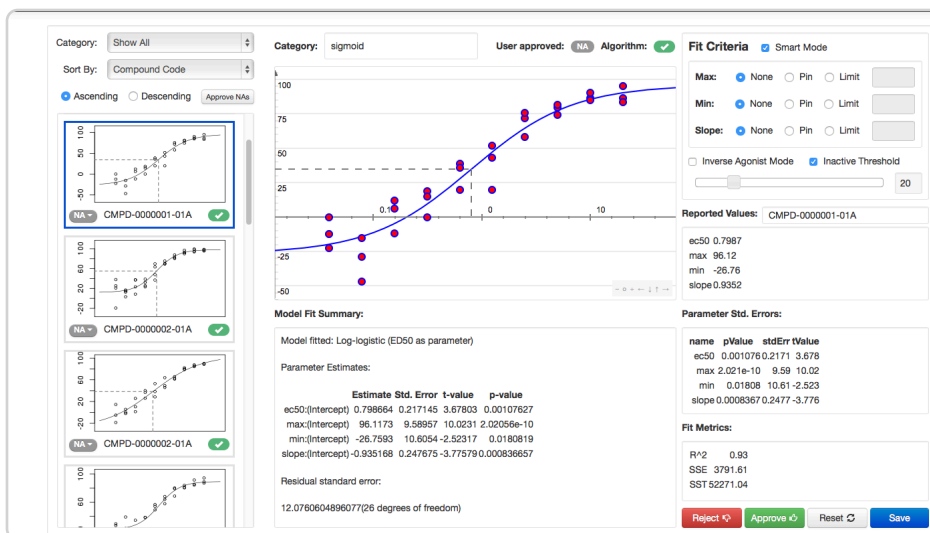
Fit Date: Tue Sep 29 2015 08:28:59 PM

Curate

Load and Fit Another

Load dose response data by going to the Dose Response module. Loading a file here is exactly like loading a file in SEL. Once the file has been uploaded successfully, it will ask you to choose between EC50 and KD. It will then show you a curve fit summary. From there, click the [Curate](#) button to open the curve curator.

In curve curator, you can reject and approve curves, knock out points, and change fit criteria. There is also a link to open the curves in Seurat.



Curve curator allows you to display certain categories of curves, sort by different parameters, and change the sort order in the curve summaries side bar. This allows you to narrow down the curves you are viewing.

Buttons:

Category:  Show All  sigmoid

Sort By: strong tested potency weak tested potency

Ascending  Descending Approve NAs

Category: Show All

Sort By:  Compound Code  EC50  SST  SSE  R^2  User Flag Status  Algorithm Flag Status

From here you can also quick approve and reject curves, and approve all NA curves.

Category: sigmoid User approved: NA Algorithm: Fit Criteria

Reason for flagging:  Compound Toxic  Pass Trend

Reported Values:

CMPD-0000011-01
ec50 0.6144 uM
max 104.4 efficacy
min 10.53 efficacy
slope 0.8687

Parameter Std. Error:

name	pValue	std
ec50	0.000014710	
max	2.013e-15	
min	0.1689	

Model fitted: Log-logistic (ED50 as parameter)

You can knock out points by clicking and dragging your mouse down over the specific points to be knocked out. Then pick the reason for flagging them. Knock points back in by clicking and dragging up over the same points.

You can reset a curve to its last save point by clicking the reset button. This will get rid of any changes made since the curve was first loaded or saved last.



You can also reject or approve a curve from the detailed view. Click **Save** once you are satisfied with your changes.

Category: strong tested potency User approved: Algorithm: Fit Criteria

Max:  None  Pin

Min:  None  Pin

Slope:  None  Pin

Inverse Agonist Mode  Inactive Threshold

Reported Values:

CMPD-0000012-01A
------------------

Reject Approve Reset Save

You can then open your curves in Seurat.

Show  entries Filter results:

Code	Kind	Name	Scientist	Date	Assay Stage	Status	Experiment Count
PROT-00000002	default	Fiona Test Protocol	unassigned	not recorded	unassigned	created	1

Showing 1 to 1 of 1 entries ◀ Previous Next ▶

To edit a protocol, go to Protocol Browser and use the search bar to find the protocol. You can search using a number of criteria, like protocol name and protocol code. You can also search for something in the description or details of a protocol.

Once you have found your protocol, click on it. It will open a preview below the search results. From there you can delete it, edit it, duplicate it, or create an experiment from it. Clicking [Edit](#) will open the edit view of the protocol in a new tab.

Status

\*Protocol Name

Code

Kind



Status

\*Protocol Name

Code

Kind

\*Scientist

\*Date

\*Notebook

Key Words

Assay Stage

Short Description

Assay Principle

You can add reference files to protocols. After filling out the form to make a new protocol (or while editing an existing protocol), scroll to the bottom of the form. There you can pick the file type and upload a file.

You can add and remove files there, as well. After you are done, click [Save](#).

**Comments**

**Attach Files**

File Type	File Name
<input type="text" value="Reference File"/>	<a href="#">TestPDF.pdf</a> <input type="button" value="x"/>