

General Information

Data Analysis

Model Fit

Status

Created

\*Protocol Name

Code

autofill when saved

Kind

Bio Activity

\*Scientist

Select Scientist

\*Date

yyyy-mm-dd

\*Notebook

Key Words

Add tags

Assay Stage

Select Assay Stage

Assay Activity

Select Assay Activity

Molecular Target

Select Target

Clone ID

Target Origin

Select Target Origin

Assay Type

Select Assay Type

To create a Plate Analysis Experiment, start by creating a new Plate Analysis Protocol. The Plate Analysis Protocol module has three tabs. Only the first two tabs are required to save a new protocol.

In the first tab, General Information, enter a Protocol Name, Scientist, Date, and Notebook. These are the only fields required. You may fill out the rest of the form if desired. You may also attach a reference file.

Assay Type

Select Assay Type

Assay Technology

Select Assay Technology

Cell Line

Select Cell Line

Curve Display Max/Min:

Max Y Curve Display

120

Min Y Curve Display

-20

Short Description

Short Description

Assay Principle

Assay Principle

Protocol Details

Protocol Details

Comments

Comments

Attach Files

File Type

Select Method

File Name

Browse Files...

Add file

Please fill in the required fields (in the first and second tab) to save or update this protocol.

Cancel

Save

Switch to the Data Analysis tab. Here you will enter your controls, assay parameters, and other details. Once you fill this out for protocol, those same details are autofilled in your experiment as soon as you choose a protocol for that experiment.

First enter some Standards. In the example below, a Positive Control, Negative Control, and Vehicle Control are all set. The Batch Name is validated against your database, and will be in an error state if there is a problem with the batch ID you are using.

[General Information](#) [Data Analysis](#) [Model Fit](#)

☒ Save data in HTS format

**Standards**

	Batch Name	Conc		Standard Type	
S1	<input type="text" value="CMPD-00000001"/>	<input type="text" value="1000"/> $\mu\text{M}$		<input type="text" value="Positive Control"/>	<input type="button" value="x"/>
S2	<input type="text" value="CMPD-00000002"/>	<input type="text" value="0"/> $\mu\text{M}$		<input type="text" value="Negative Control"/>	<input type="button" value="x"/>
S3	<input type="text" value="CMPD-00000003"/>	<input type="text" value=""/> $\mu\text{M}$		<input type="text" value="Vehicle Control"/>	<input type="button" value="x"/>

Pick either a Dilution Factor or a Compound Transfer Volume. You may also add an Assay Volume.

An Instrument Reader is required. In this example, Generic Plate is used.

**Assay Parameters**

☒ Dilution Factor

☐ Compound Transfer Volume

Assay Volume

\*Instrument Reader

**Assay Reads**

Read Number	Read Position	Read Name	<input type="checkbox"/> Match Read Name
R1	<input type="text" value="1"/>	<input type="text" value="Luminescence"/>	<input type="checkbox"/>

☒ Activity

Next enter some Assay Reads. Though not required, this example uses one read, Luminescence, as part of the analysis.

**Analysis Parameters**

\*Positive Control  
Signal Direction

Increasing Signal (highest = 100%)

\*Aggregate By

Assay Plate

\*Aggregation Method

Mean

\*Normalization

Plate Order Only

\*Positive Control

S1 CMPD-00000001 @ 1000 uM

\*Negative Control

S2 CMPD-00000002 @ 0 uM

\*Transformation

% efficacy

\*Positive Control

S1 CMPD-00000001 @ 1000 uM

\*Negative Control

S2 CMPD-00000002 @ 0 uM

SD

\*Negative Control

S2 CMPD-00000002 @ 0 uM

Add Transformation

All Analysis Parameters are required. All Positive and Negative Control options are filled in with the compound IDs entered earlier in the form. Choose which compound you would like to use for each Positive and Negative Control.

In this example, an extra Transformation Rule is also selected; both % Efficacy and SD will be run.

If you choose to fill in the curve fit rules in the Model Fit tab, those rules will be copied over to the new experiment.

Once you are done filling out the protocol forms, save the protocol. Next, create a new Plate Analysis Experiment.

General Information
Data Analysis
Model Fit

Status
Created

Code
autofill when saved

☒ Same as experiment code

\*Experiment Name

\*Scientist
Select Scientist

\*Date
yyyy-mm-dd

\*Protocol
Select Protocol

\*Notebook

Key Words
Add tags

Short Description
Short Description

Experiment Details
Experiment Details

The Experiment Name, Scientist, Date, Protocol, and Notebook are required for your new Plate Analysis Experiment. Select the protocol that you just created.

Once you have filled out the first tab, switch to the Data Analysis tab. Everything you filled in for the protocol will be filled in here. You may change any of these settings for this experiment.

Scroll down to Upload Data and Analyze. Here you can upload your plate. You may upload any number of plates. Put all plates in a compressed zip file before uploading. See the next canvas for plate file examples.

Experiment Details
Experiment Details

Comments
Comments

Attach Files
File Type
File Name
Select Method
Browse Files...

Add file

Cancel
Save

Upload Data and Analyze

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

Browse Files...

☐ Attach optional well flagging file

Next

0 0 0

# ACAS Tutorial

## Plate Analysis

A plate file follows this template. The Plate Information is required, as well as the layout of the plate.

Valid Compound IDs must be entered. The Plate Analysis module will return an error if any IDs are invalid.

The first tab in your plate file should have the Compound IDs. The second tab should have concentrations, and the third data.

	A	B	C	
1	Plate Information			
2	Assay Barcode	PB003		
3	Plate Order	1		
4	Plate Format	96		
5				
6	Plate			
7	Row/Col	1	2	
8	A	CMPD-0000001-01A	CMPD-0000010-01A	CMPD-
9	B	CMPD-0000001-01A	CMPD-0000011-01A	CMPD-
10	C	CMPD-0000001-01A	CMPD-0000012-01A	CMPD-
11	D	CMPD-0000001-01A	CMPD-0000013-01A	CMPD-
12	E	CMPD-0000002-01A	CMPD-0000014-01A	CMPD-
13	F	CMPD-0000002-01A	CMPD-0000015-01A	CMPD-
14	G	CMPD-0000002-01A	CMPD-0000016-01A	CMPD-
15	H	CMPD-0000002-01A	CMPD-0000017-01A	CMPD-
16				
17				

	A	B	C	D	E	F	G	H	
1	Plate Information								
2	Assay Conc Units	uM		Concentration of Tested lots in the assay plate. [uM]					
3	Plate Format	96							
4									
5	Plate								
6	Row/Col	1	2	3	4	5	6	7	
7	A	0	500	500	500	500	500	500	
8	B	0	500	500	500	500	500	500	
9	C	0	500	500	500	500	500	500	
10	D	0	500	500	500	500	500	500	
11	E	1000	500	500	500	500	500	500	
12	F	1000	500	500	500	500	500	500	
13	G	1000	500	500	500	500	500	500	
14	H	1000	500	500	500	500	500	500	
15									
16									

	A	B	C	D	E	F	G	
1	Plate Information							
2	Read Name	Activity						
3	Assay Barcode	PB003						
4	Plate Order	4						
5	Plate Format	96						
6								
7	Plate							
8	Row/Col	1	2	3	4	5	6	
9	A	1	72.74227906	65.63804044	58.57975162	60.70842604	86.88882396	70
10	B	0	75.78895057	83.02005059	97.1216446	91.4208727	103.3378534	97
11	C	0.002	80.88937835	89.18231832	92.04519063	99.34121972	106.7780949	11
12	D	0	68.89648059	78.69777268	68.49392039	101.0633383	111.7426711	10
13	E	99.45	45.41013942	41.95491426	41.15978294	96.31252856	100.0244733	10
14	F	101.4	24.00052942	20.07781499	19.80511291	74.95186509	90.93140744	85
15	G	100	11.31438903	9.069841198	8.828105295	68.58981563	78.65881524	78
16	H	100	2.169379952	6.195980891	5.925276635	42.15169927	60.95815322	36
17								

Once you have selected your plate zip file, click Next. ACAS will validate your file and give you preliminary results. If everything looks good, then click Upload Data.

**Dry Run Results: Success**

Please review the summary before uploading.

**Summary**

Information:

- Plates analyzed: 6 plates: PB0011 PB0012 PB0013 PB0021 PB0022 PB0023
- Unique compounds analyzed: 75
- Unique batches analyzed: 75
- Automatic hits: 0
- User hits: 0
- Flagged wells: 0
- Number of wells: 2304
- Hit rate: 0 %
- Z Prime: -0.05674
- Positive Control summary: Batch code: Count: 96 Mean: 863.30958 Median: 848.41972 Standard Deviation: 69.98522 CV: 0.08107
- Negative Control summary: Batch code: Count: 675 Mean: 372.01716 Median: 354.41682 Standard Deviation: 103.0716 CV: 0.27706
- Date analysis run: Thu Jan 12 00:30:29 +0000 2017
- Summary: [Summary](#)
- Spotfire: [Spotfire](#)
- Original Data File: [Original Data File](#)

[Back](#)[Upload Data](#)

0 0 0

**Upload Results: Success**

Upload completed.

**Summary**

Information:

- Plates analyzed: 6 plates: PB0011 PB0012 PB0013 PB0021 PB0022 PB0023
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- Unique batches analyzed: 75
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- Flagged wells: 0
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- Date analysis run: Thu Jan 12 00:30:53 +0000 2017
- Summary: [Summary](#)
- Spotfire: [Spotfire](#)
- Original Data File: [Original Data File](#)

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

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

[Re-Analyze](#)

0 0 0

The success summary will include details about the experiment, a link to open the experiment in your data viewer, and links to download files. You can download a summary file, the Spotfire file, and the original data file. You can also choose to Re-Analyze the experiment.

Plates analyzed: 6 plates:

PB0011  
PB0012  
PB0013  
PB0021  
PB0022  
PB0023

Unique compounds analyzed: 75

Unique batches analyzed: 75

Automatic hits: 0

User hits: 0

Flagged wells: 0

Number of wells: 2304

Hit rate: 0 %

Z Prime: -0.05674

Positive Control summary:

Batch code:

Count: 96

Mean: 863.30958

Median: 848.41972

Standard Deviation: 69.98522

CV: 0.08107

Negative Control summary:

Batch code:

Count: 675

Mean: 372.01716

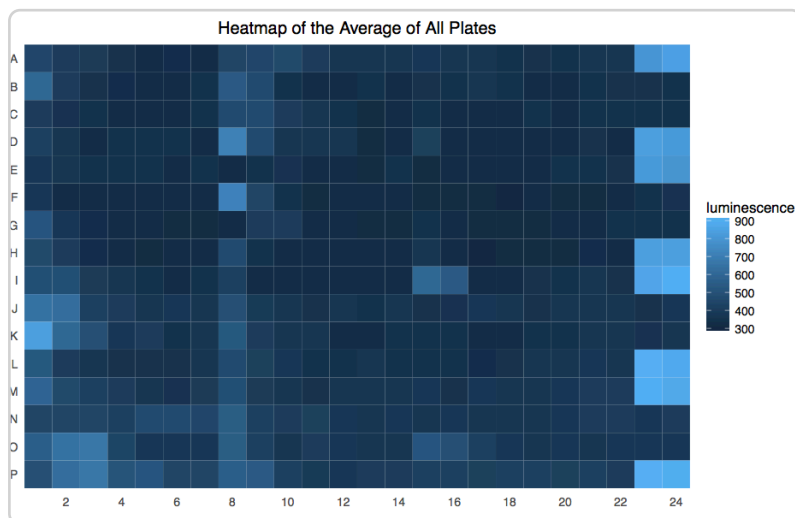
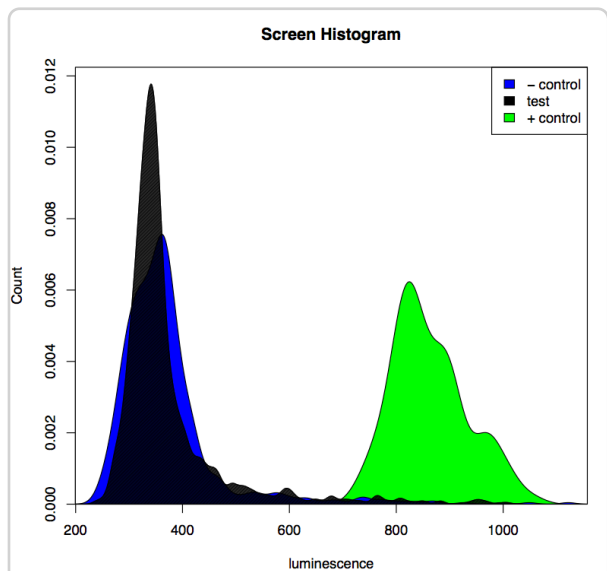
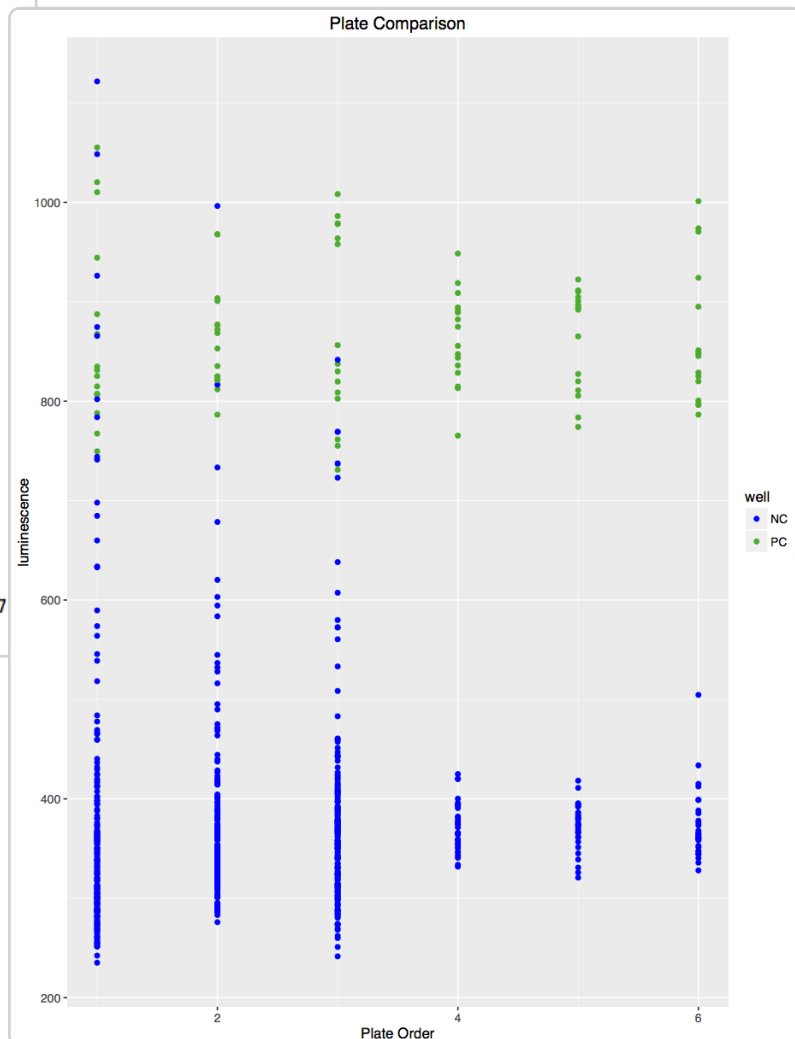
Median: 354.41682

Standard Deviation: 103.0716

CV: 0.27706

Date analysis run: Thu Jan 12 00:30:53 +0000 2017

Here is an example of a summary file for a Plate Analysis experiment that was run with six plates.



[General Information](#) [Data Analysis](#) **Model Fit**

**Fit Status: not started**

Model Fit Type

Fit Transformation

Transformation Unit

**Global Fit Criteria** ☒ Smart Mode

Max: ☒ None ☐ Pin ☐ Limit

Min: ☒ None ☐ Pin ☐ Limit

Slope: ☒ None ☐ Pin ☐ Limit

☐ Inverse Agonist Mode

Inactive Threshold  Theoretical Max

At this point if you would like to fit curve data for your experiment, you can do so by clicking on the Model Fit tab. Choose the Model Fit Type, Fit Transformation, and Transformation Unit. Then adjust the Global Fit Criteria if you so choose.

The Model Fit Type, Global Fit Criteria, and next steps work in the same way as the Dose Response module. You can fit your data, and then open in your data view or curate curves further.