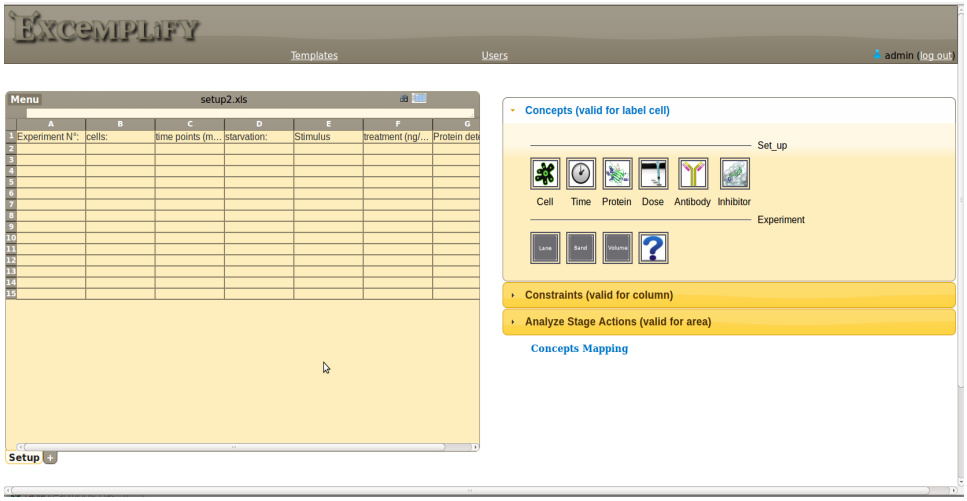
Brief Tutorial

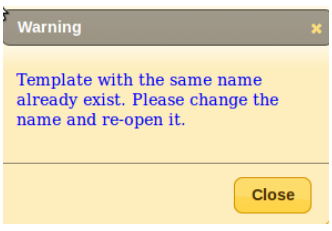
1. **User Group**
   There are three kinds of users in current version, which is **Admin User**, **Experimenter** and **Anonymous**.
   (a) Admin User:
      i. Create Set-up Template → http://sabio.h-its.org/excemplify
      ii. Mange User Accounts (create, edit, delete)→ http://sabio.h-its.org/excemplify/user
   (b) Experimenter
      i. Manage Experiments (create, update, delete, download and shareToPublic)→ http://sabio.h-its.org/excemplify/lab
   (c) Anonymous
      i. Review and download every public experiments → http://sabio.h-its.org/excemplify/public
   The first two kinds users need to be authorized to see corresponding pages.

2. **Create Set-up Template**
   (a) Click ***Menu*** and open a new empty set-up template (.xls) in the excel style workspace

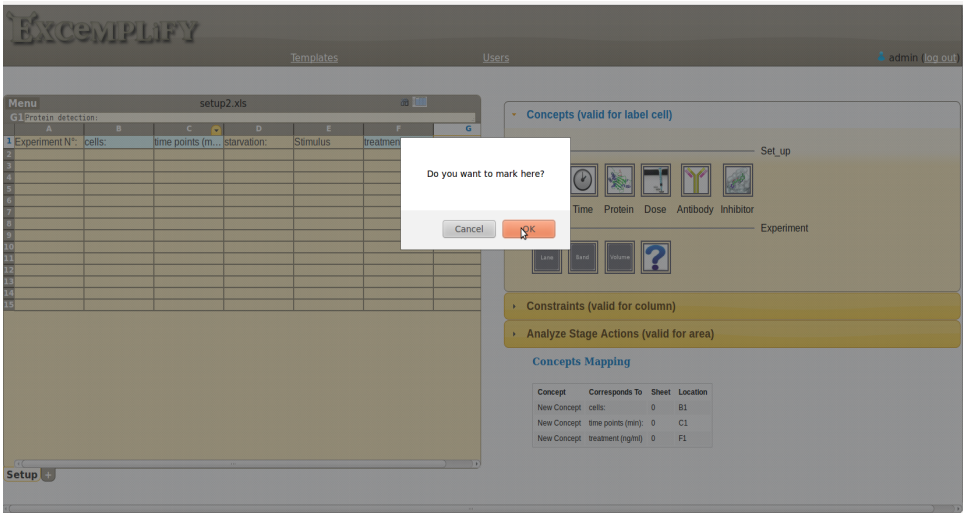


Step 1. Open an empty set-up template

Attention: please make sure the new set-up template has an unique template name, otherwise you will see warning icon like , click on it you will see the warning message .

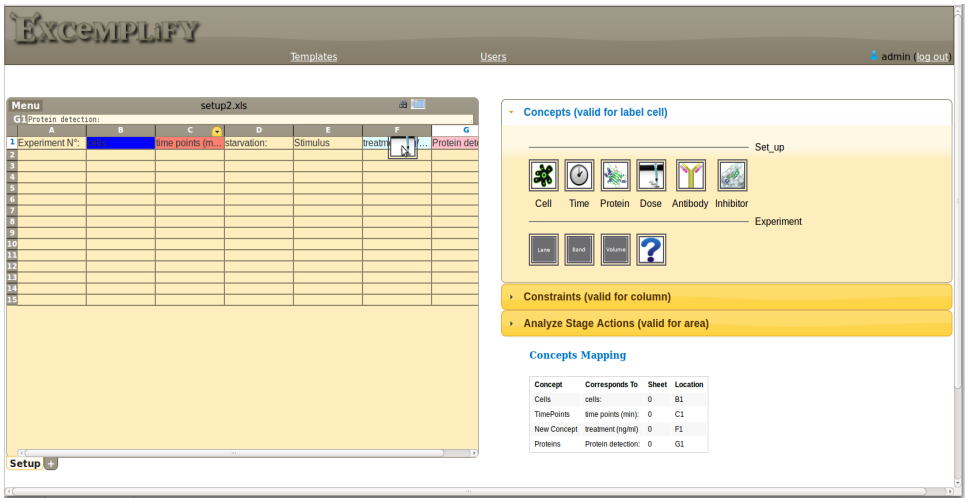


(b) Click on the important template cells and mark them.



Step2. Mark important template cells

(c) Use your mouse, **drag** concept icons in the right panel and **drop** on the corresponding marked cell to build the concepts mapping.



Step3. Build the concepts mapping

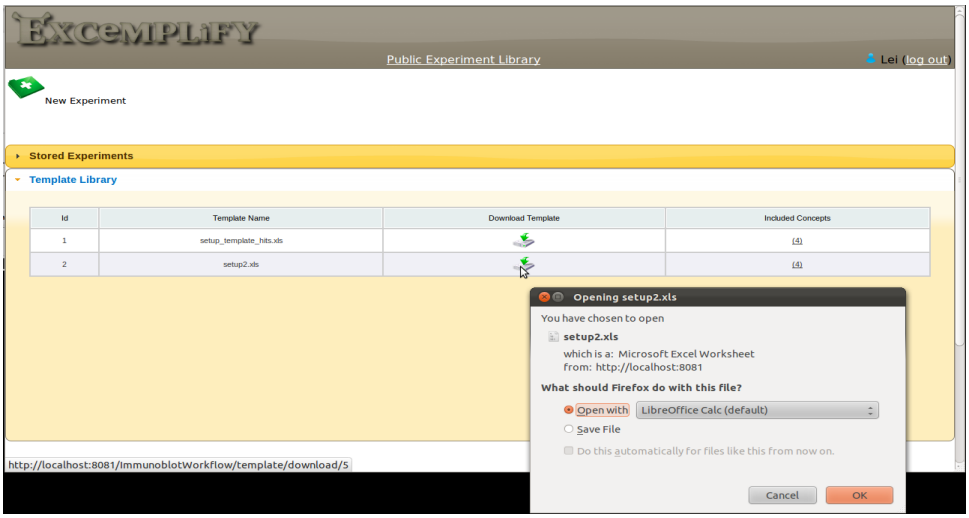
(d) Click ***Menu*** and save the template.

(e) You can check all templates by clicking the ***Templates*** link in the header bar

Attention: currently, we only consider **Cell**, **Time**, **Protein** and **Dose** concepts. Other concepts icons listed in the panel are not implemented yet.

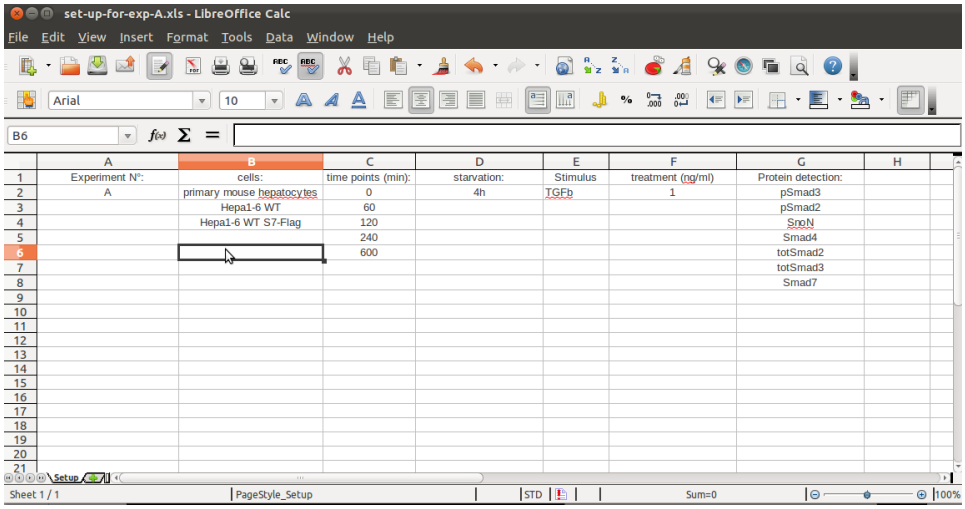
3. Manage Experiments

(a) Download one of the set-up templates from the ***Template Library*.**



1. Download the set-up template

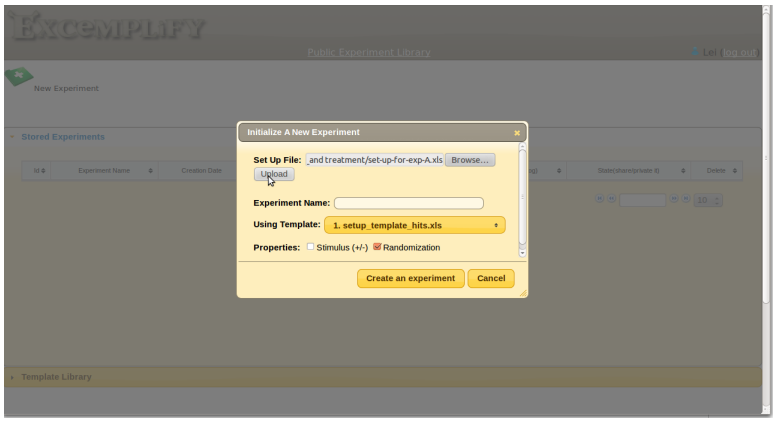
(b) Using your local excel tool to open the downloaded template, fill in your set-up information, and save it. (e.g. save it as “set-up-for-exp-A.xls”)



2. Use downloaded template and fill in the detail set up information

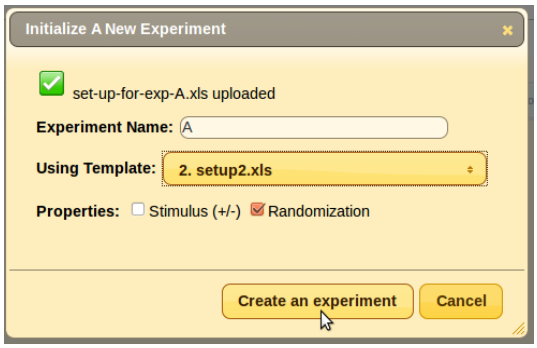
(c) Click the ***New Experiment*** button to initial your experiment

1) Choose your set-up file (e.g. set-up-for-exp-A.xls) and press the ***upload*** button, you will see the green icon ✅, if it is successfully uploaded.

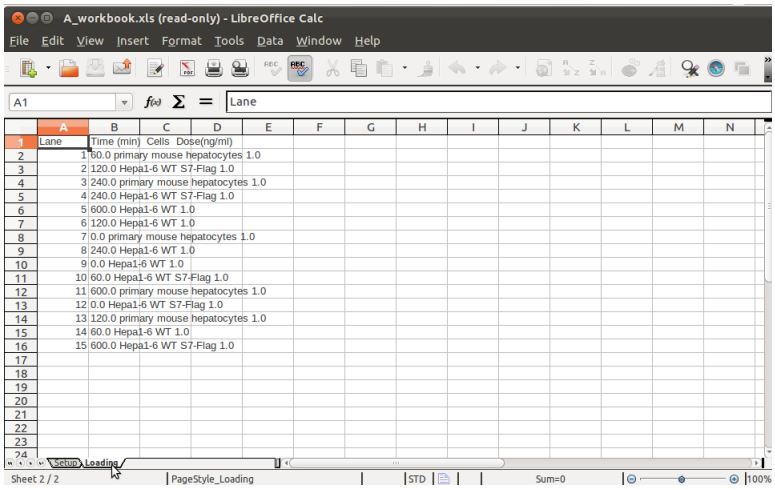


3.Upload the set-up file

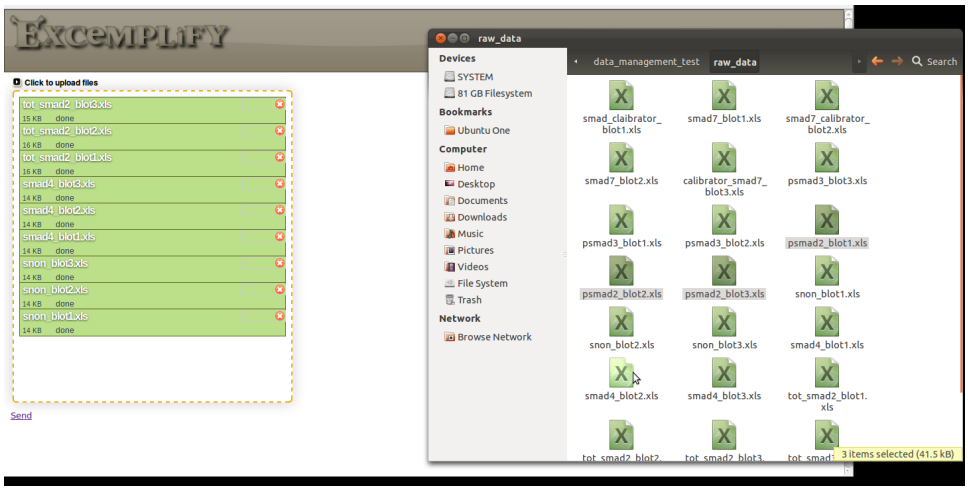
2) Fill in the experiment name, select the template you used from the drop down list, check other treatment properties (e.g. randomization, stimulus) and click ***Create an experiment*** button to finish experiment initialization. You will see the record for your new experiment show up in the ***Stored Experiments***.



3) Download the workbook for your new experiment, you will see the automatically generated loading sheet is appended after your original set-up sheet.

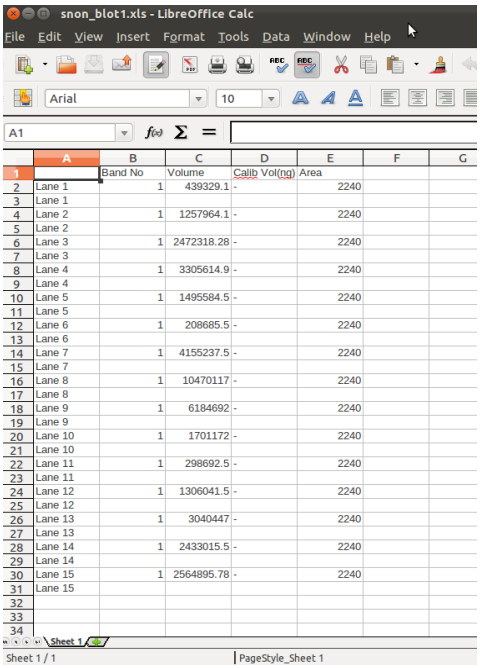


(d) Click icon to open the uploading page, **drag and drop** raw data **file/files** (.xls or .txt) into the dashed area. After successfully uploading, click the ***send*** button in the bottom.

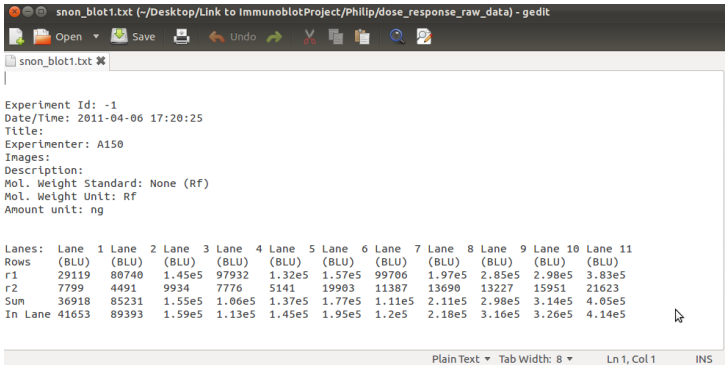


4.Upload raw data file/files

Attention: Please make sure the raw data file follows one of the two formates (machine bonded) which are listed below.



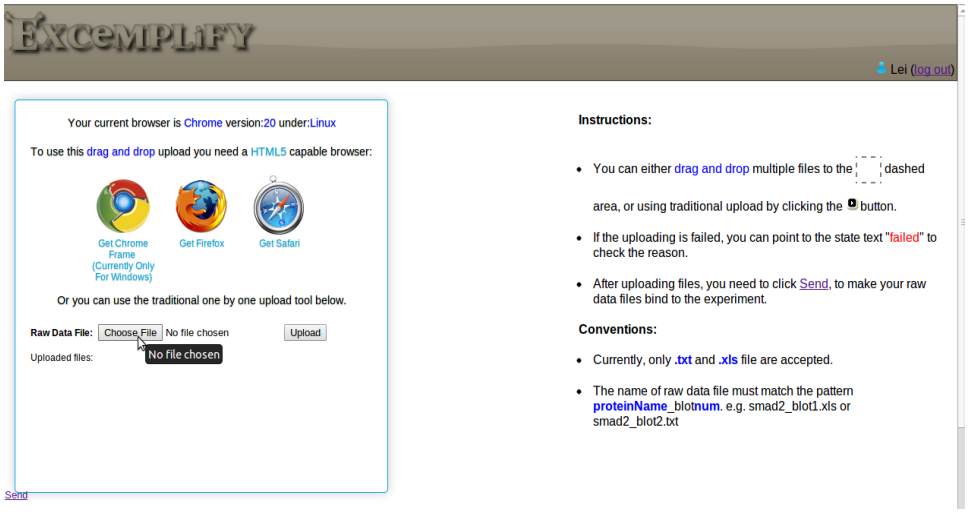
New machine output



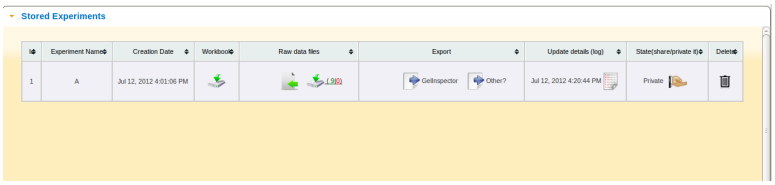
Old machine output

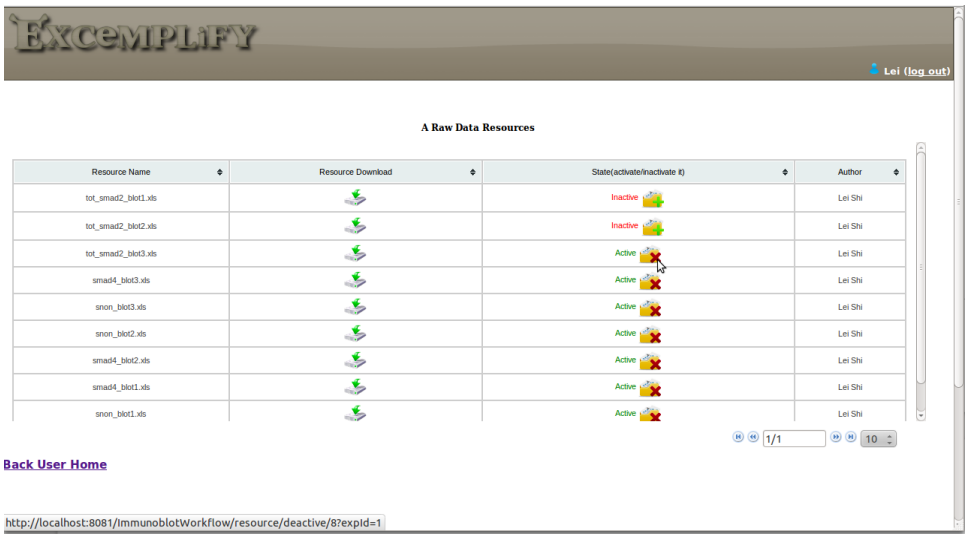
Attention: If your browser are Chrome or IE, there could be the case that your browser does not support our drag and drop uploading widget. You will see the warning page and another traditional

uploading tool instead. You can upload your raw data files one by one and afterwards click the ***send*** button.



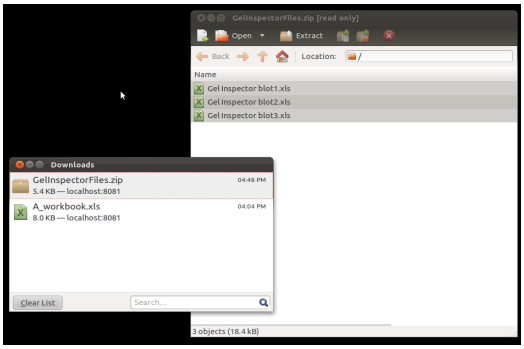
(e) By clicking the ***(active num/inactive num)*** link, you will enter the resource page where you can **activate** or **inactive** your raw data files, which will in sequence affect the workbook and the exported layout.

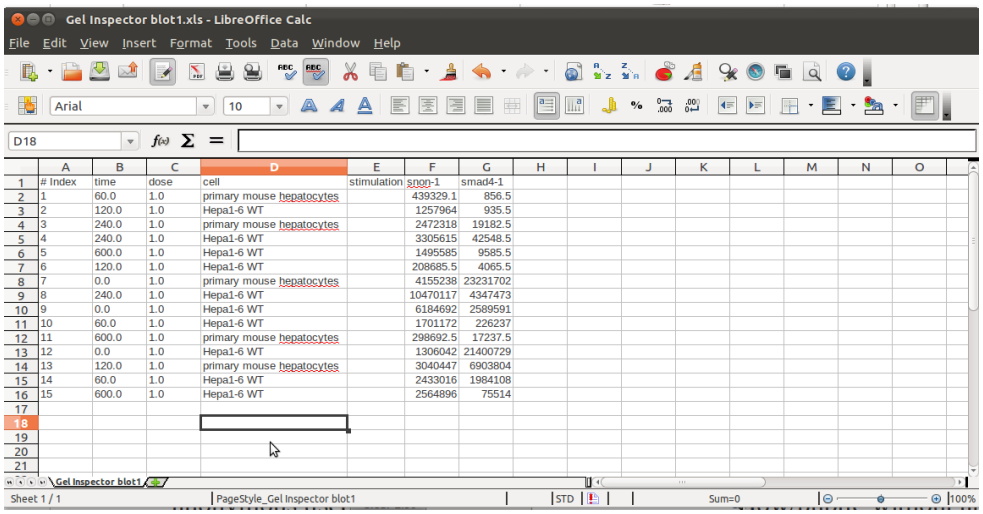




(f) Export your experiment data into different layouts. Currently, we only support Gelinspector layout.

i. A zip file which compressed separated sheets of Gelinspector layout for each blot.
ii. The workbook for such experiment will be updated after you click on the icon.





	A	B	C	D	E	F	G
1	# Index	time	dose	cell	stimulation	snon-1	smad4-1
2	1	60.0	1.0	primary mouse hepatocytes		439329.1	856.5
3	2	120.0	1.0	Hepa1-6 WT		1257964	935.5
4	3	240.0	1.0	primary mouse hepatocytes		2472318	19182.5
5	4	240.0	1.0	Hepa1-6 WT		3305615	42548.5
6	5	600.0	1.0	Hepa1-6 WT		1495585	9585.5
7	6	120.0	1.0	Hepa1-6 WT		208685.5	4065.5
8	7	0.0	1.0	primary mouse hepatocytes		4155238	23231702
9	8	240.0	1.0	Hepa1-6 WT		10470117	4347473
10	9	0.0	1.0	Hepa1-6 WT		6184692	2589591
11	10	60.0	1.0	Hepa1-6 WT		1701172	226237
12	11	600.0	1.0	primary mouse hepatocytes		298692.5	17237.5
13	12	0.0	1.0	Hepa1-6 WT		1306042	21400729
14	13	120.0	1.0	primary mouse hepatocytes		3040447	6903804
15	14	60.0	1.0	Hepa1-6 WT		2433016	1984108
16	15	600.0	1.0	Hepa1-6 WT		2564896	75514

5.Export

(g) You can make your experiment public by clicking on the hand shape share icon, so that anonymous user can see it under ./ImmunoblotWorkflow/public without any authentication.

4. More Attentions

(a) Since we haven't validated our current version application with sample experiment data which have stimulus treatment in each time points. So if you try the application with such kind of data, there could be some errors. Please send us the data package which breaks down the application.

(b) For each experiment, please make sure the uploaded raw data matches corresponding set up and generated loading. Currently, we have not implemented any validator to check the mismatch. The exported layouts will be strange if the raw data files do not match the loading.

(c) Please pay attention to your confidential data during test, because every experiment which is shared to public can be accessed by anonymous users without any user name and password.