# Creating reports & analysis of results – Single Antigen beads

1. Open Fusion 4.4
2. Enter ‘he user name and password
3. Click the LABScreen icon on the top left of the screen 

## Import data into Fusion

*This is a brief overview of what Cambridge Laboratory does, if more appropriate follow your own protocols.*

1. Click on yellow folder icon on the left hand pane. Default location is specific to laboratory.
2. The batch will then appear in the middle panel. Check that the batch has the correct catalogue ID number

* *If* ***!*** *appears next to the date select the correct date format using drop down button*

1. Check the negative control check box (column labelled NS).
2. Ensure the patient information fields (first & last names) have auto populated - indicating a patient record exists in the Fusion database.
3. Click import. The samples will appear in the right hand navigation panel. Repeat for all SAB batches.

## Analysis and report generation in Fusion

1. Hover over the navigation bar at the top right of the screen until it opens. Click the batch to be analysed, all analysed samples will then be displayed.
2. Double click the first sample to open
3. Click the >> icon to the left of the final assignment field to move all specificities across to the Ab Assignment/Final Assignment field then click save>>. All specificities will be highlighted in blue once they are transferred to the final assignment field.
4. Repeat assigning the specificities until the end of the batch then click ok. Repeat for both SAB-I and SAB-II.

## Export data from Fusion

1. Click ‘Specialty’ in the top centre of the reports screen and then select ‘Antibody Reaction’ from the drop down
2. Tick the batches required - SAB I and SAB II (all samples within will be selected)
3. Click the ‘Export Report’ button. A message should appear stating export was successful. Click OK

* *If there is an error when exporting the pathway may need to be reset for the export location. Go to Utilities* 🡪 *General Settings* 🡪 *Paths. Ensure the ‘Interface’ pathway is set to Z:\Tissue Typing\Luminex results\SAB export (this is specific for Cambridge, set to appropriate location for your laboratory)*

## Merge, rearrange and calculate cRF for exported data

1. Open the SAB I and SAB II export files, and the ‘SAB file merger v3’ available at GitHub
2. In the SAB I export file left click on the grey square in the top left of the worksheet to select all, and copy. Paste the data into the ‘SAB file merger v3’ tab labelled ‘SAB I’. Repeat for the SAB II export file. In the SAB I and II tabs delete the negative control row, otherwise an error message will appear when clicking the import button in Step 4.
3. Once both sets of data are in the ‘SAB file merger v3’ spreadsheet, go to the ‘IMPORT SHEET’ and check SAB I and SAB II appear in cells B3 and B4, respectively
4. Click Import button, followed by ‘OK’ when prompted. A new worksheet named ‘export ID… containing the merged information will be generated
5. Different colours correspond to which SAB tests were performed for that sample:
   1. Blue = SAB I
   2. Pink = SAB I & II
   3. Green = SAB II
6. Open the SAB export programme named ‘crf\_nov\_2012\_4\_RESTORED’ available at GitHub
7. Highlight the entire merged data in the SAB file merger programme by clicking on the top left grey square. Copy and paste into the worksheet named SAB I & II in the ‘crf\_nov\_2012\_4\_RESTORED’ programme.
8. Click on the ‘START SHEET’ worksheet and click the ‘Calculate’ button. This process may take a few minutes. A window will appear confirming data has been sorted, followed by another confirming that the cRF has been calculated. Click OK for both. It is essential that you do not use the PC for any other tasks while the program is running. Using the PC while the program is running can cause glitches and errors in the cRF calculation, which are difficult to detect (usually an inappropriate duplication of a calculated cRF).
9. The worksheet will now contain the new sorted data positioned to the right of the original data under columns labelled ‘Sorted\_Spec ’ alongside individual and total cRF %.
10. Highlight the entire worksheet by clicking on the square in the top left hand corner, copy the data and paste it into a new blank spreadsheet (File 🡪 New 🡪 Blank Document)
11. Perform a ‘Find & replace, replacing comma (‘,’) with comma space (‘, ’)
12. Format the cells carrying the numeric cRF values to zero decimal places
13. Hide the unsorted columns (C to G)
14. Save as ‘yySABxx ddmmyy SAB I & II cRF’ in a network drive and close the SAB file merger and the cRF calculator without saving any changes.