# Macro\_Intensity\_perCell.ijm

This macro treats a folder and measures the mean intensity of a given protein in a user-defined area (typically, a cell).

Steps of the macro

1/ The macro asks the user to:

* The channel representation: the protein of interest, and a potential channel to draw the cells (phalloidin for instance, but it can also be the same as the translocated protein channel).
* The name of the protein of interest, this to create an appropriately named analysis subfolder

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Description générée automatiquement

Remark: this means that all images treated together (*i.e.* in the same folder) should have the same order for the channel acquisitions.

2/ The macro asks for the folder to treat which contains all images that the user wants to treat. A “Intensity\_Analysis” subfolder is created in which all measurements and data will be saved.

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Description générée automatiquement

Click on OK. For each image finishing by the extension defined in the customizable parameters (in our case, “.tif”):

3/ Z-stack projections are made:

* + If it is a z-stack and the user has not chosen a projection on all the stack, the macro asks the user to choose the plans on which the projection will be made (maximum intensity projection). Click on OK.

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Description générée automatiquement

* + If it is a z-stack and the user has chosen a projection on all the stack, the projection on all slices will be done automatically (maximum intensity projection).
  + If it not a z-stack, the picture is kept as it is.

4/ The channel of cell contour is displayed.

1. If the code detects cell contours drawn from a previous analysis, it will load the old cell contours in the ROIManager. The user may simply click on OK or add or delete ROIs.
2. If no previous analysis was detected, the user must draw the contours and then add them to the ROIManager (by pressing the letter t on the keyboard). Several cells can be drawn and added to the ROIManager. Once done, click on OK.

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Description générée automatiquement

5/ The protein channel is extracted, the subtract background defined in customizable parameters is applied and the mean intensity for each drawn cell is measured and collected in arrays.

8/ Once all images are treated, a Results table is displayed and contains for each treated cell the cell area, the mean intensity of the translocated protein in the nuclei and in the cytoplasm and the ratio. This Results table in saved in the “Intensity\_Analysis” subdirectory where the cell ROIs are also saved.

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Description générée automatiquement