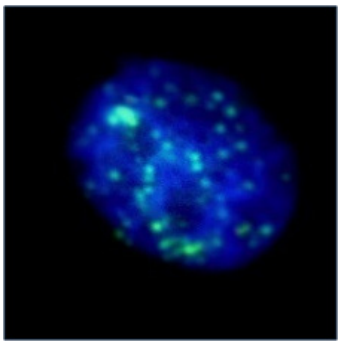
SYNENTEC

Nuclei Real Dot Count (1F)

GENERAL PURPOSE

The Nuclei Real Dot Count analysis algorithm is to be used in an end point assay, where cell nuclei are counted in a first fluorescence image (based e.g. on DAPI staining) and further stained sub structures (e.g. DNA string breaks with γH2AX-staining) in a second fluorescence image. The stained sub structures are counted and analysed on each cell nucleus area and their number and average intensities are stored as additional cell nuclei attributes.

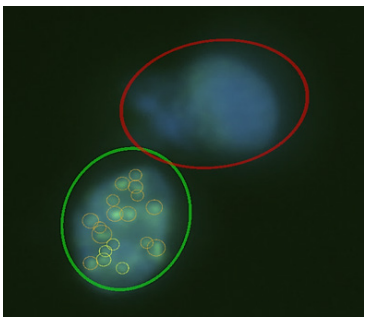


RESULT TABLE

Dot Count	Number of recognized sub structures
Nuclei Count	Number of recognized cell nuclei
Nuclei Dot positive	Number of cell nuclei, that own at least the desired number of sub structures („Dots“)
Nuclei Dot positive percent	Percentage ratio of Nuclei Dot positive counts with respect to the Nuclei Count
Cell Area Count Fluo 1	Number of recognized sub structures in the first addiationa fluorescence image
Avg Nucleus Fluorescence Intensity BC	Average fluorescence intensity of a cell nucleus over background level
Avg Fluo CH1 Intensity BC	Average fluorescence intensity of the cell sub structures in the first additional fluorescence image over background level
Avg Nucleus Size	Average Size of a cell nucleus
Sum of Nuclei Sizes	Total area of all recognized cell nuclei

EXAMPLE

Two labelled DAPI stained cell nuclei in a γH2AX assay: One with some identified double DNA string breaks (green labelled nucleus) and one without (red labelled nucleus).



SYNENTEC GmbH
Otto-Hahn-Str. 9A
25337 Elmshorn/Germany
Phone. +49 (0) 4121 46311-0
Email. appsupport@synentec.com

www.synentec.com