

Flow Cytometry Core Laboratory

Research Resources Branch /Central Laboratory Services Section
Gerontology Research Center/NI A/NI H

We're sorry, but your samples submitted to this laboratory for flow cytometric acquisition and/or analysis had the following problems:

Data acquisition

- Insufficient cell number
- Excessive number of clumps or cell aggregates
- Excessive debris or inadequate lysis of red blood cells
- Poor viability (live cell sort or physiological assays)
- Inconsistent cell number between samples (i.e. samples that run at 10 cells/sec or 3000 cells/sec on the FACScan)
- G_{0/1} peak shifts more than 10 channels (indicative of inconsistent cell numbers between samples)
- Absence of controls
 - Normal diploid control (for DNA ploidy analysis)
 - Unstained cells
 - Isotype controls (FITC-, PE-, or PerCP- IgG/IgM)
 - Cells stained with single color fluorochromes or antibodies for use as compensation controls
- Other _____

Data analysis

- Insufficient number of positive cells
- Absence of appropriate control
- Inappropriate gating requested by user
- Cell cycle analysis
 - Excessive debris
 - G_{0/1} CV greater than 10%
 - Poor cell cycle analysis model fit
 - Multiple G_{0/1} stemlines in "diploid" sample
- Other _____

We have reviewed our daily instrument quality control procedures and ascertained that the problem was not instrument related. Please feel free to contact us at x8840, x7098, or x8377 regarding the problems encountered with the sample. The staff of the Flow Cytometry Core Laboratory has nearly 45 years combined experience in flow cytometry and cell sorting. In most cases, we can suggest technical modifications or improvements to methods published in the literature to alleviate problems.