

# 04\_03\_PeakScanner\_capillar-electrophoresis

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MITTWOCH, 22.9.2021

## Goal-Setting

- Analysing data from capillary electrophoresis

## Terms / abbreviations

- CE = Capillar electrophoresis
- PS = PeakScanner (Analyzing program for CE data)
- SQ = Sample quality

## Risk areas

- None

## Required materials and / or information

- Data from CE, .zip file

## Templates, devices, software

- Access to the thermofisher cloud: [Cloud Dashboard \(thermofisher.com\)](https://thermofisher.com)

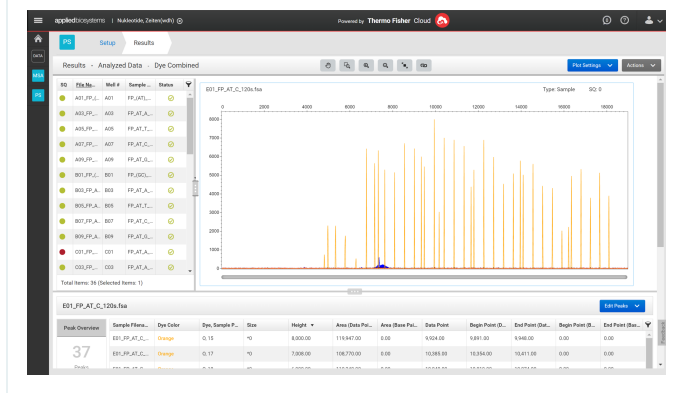
## Preliminary work

- Order primer with a fluorescent modification (e.g. 6FAM)
- Hand samples to IME
- Download the samples.zip file to the PC

## Operation

- Open the ThermoFisher Cloud in the browser
- Click in the dashboard to create a new project (top right)
- Import the .fsa files (data to analyze) to the project
- Click on the left to PS
  - PS-program opens up and all unanalysed samples can be seen
- Select the 600LIZ Size marker
- Click on analyse
  - Samples are getting analysed
- Click on results (top left)

## PS\_analysed samples



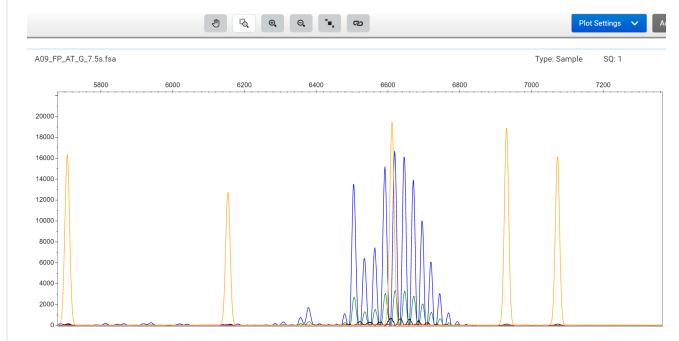
- Tip: click in the left table on "file name" to order the sample alphabetically
- The SQ should be green to get good data
  - If SQ is not green, the samples had a bad quality
- Click in the lower table on "Blue"
  - Now there are only the peaks from fragments with the 6FAM modification

## Raw CE Data



- Usually the peaks are ordered by height
- Plot analysis
  - The button to the right of the small hand can be used to select a part from the plot to analyse the length spectrum in the plot

## Plot analysis



## Troubleshooting

- For more information, contact an employee from the IME

- If bad SQ:
  - Order primer in HPLY purification
  - Purify the samples with a cleanup kit
  - Try different sample concentrations (done at the IME)

## Follow-up work

- Statistical analysis and evaluation