MOLECULAR SEROLOGY PROCEDURES MANUAL

Body Fluid Identification by Proteomic Mass Spectrometry -Analysis		
Status: Published		Document ID: 77459
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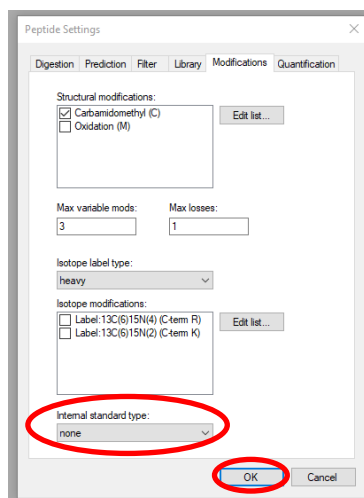# Body Fluid Identification by Proteomic Mass Spectrometry - Analysis

1 Purpose

1.1 Process data accumulated through the use of the liquid chromatographer and mass spectrometer in order to identify presence of specific body fluids on evidence samples using Skyline and R Script. Skyline is an open-source software for targeted proteomics data analysis.

2 Skyline Analysis Procedure

2.1 Double-click on Skyline (version 22.2.0.255) software on desktop.

2.2 On the Start Page click on Blank Document

2.3 Click Settings → Peptide Settings → Modifications and ensure "Internal standard type" to "None". If not, set to "None". Click OK.
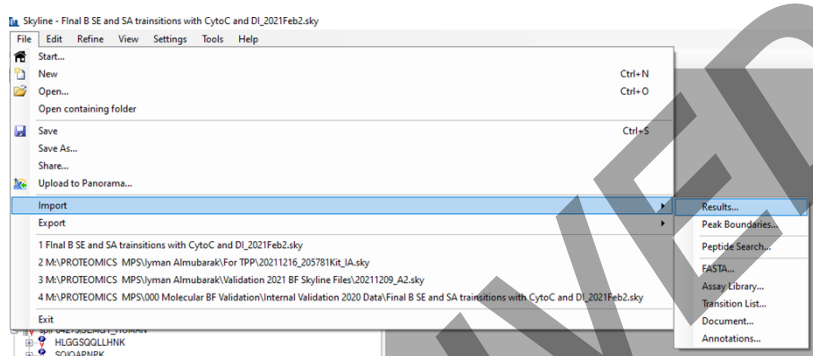
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2.4   Open the file labeled "Final B SE and SA transitions with Cyto C and DI_2021Feb" .sky file **FOUND IN M DRIVE: Molecular Serology_Data folder**

2.5   Click File → Save As → Rename File as DATE (YYYYMMDD)_Batch A
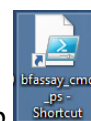
2.6   Select File → Import → Results

2.7   Click OK
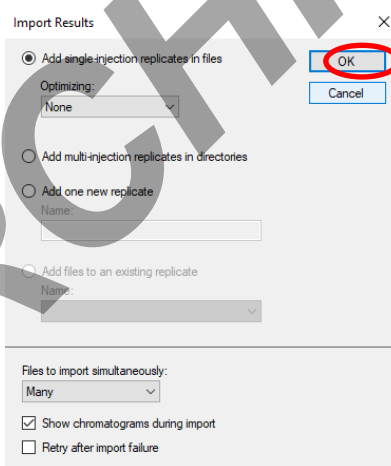
2.8   Select all samples within the batch found in Gertrude folder and click open.

2.9   Save file once all sample injections are imported and close software.

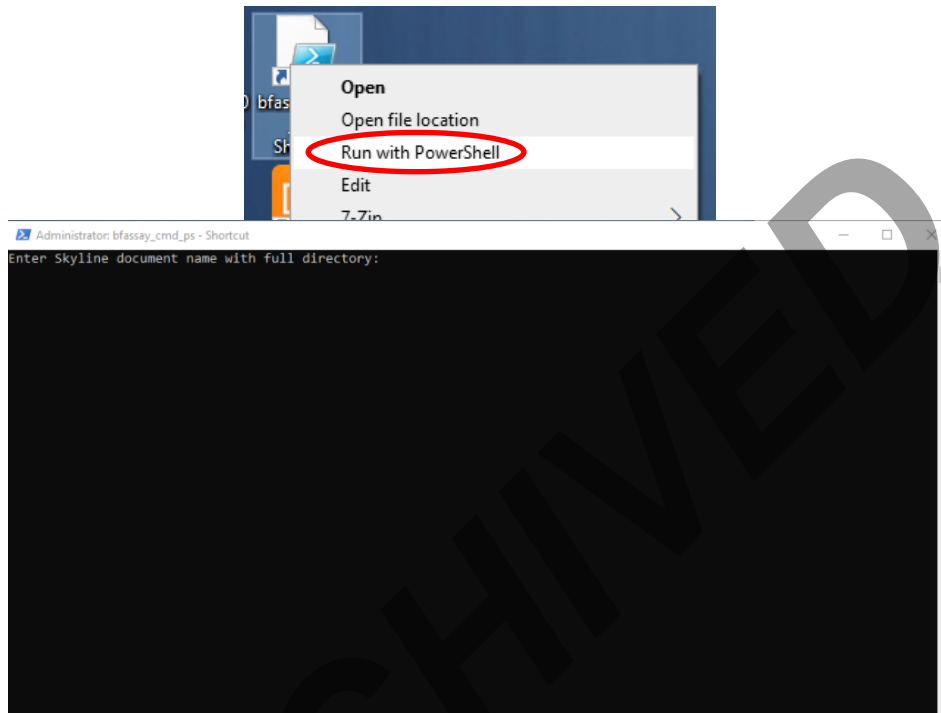# 3   MSDA (Molecular Serology Data Analysis)-Script Procedure

3.1   Find the bfassay_cmd_ps Shortcut icon on the processing computer desktop.
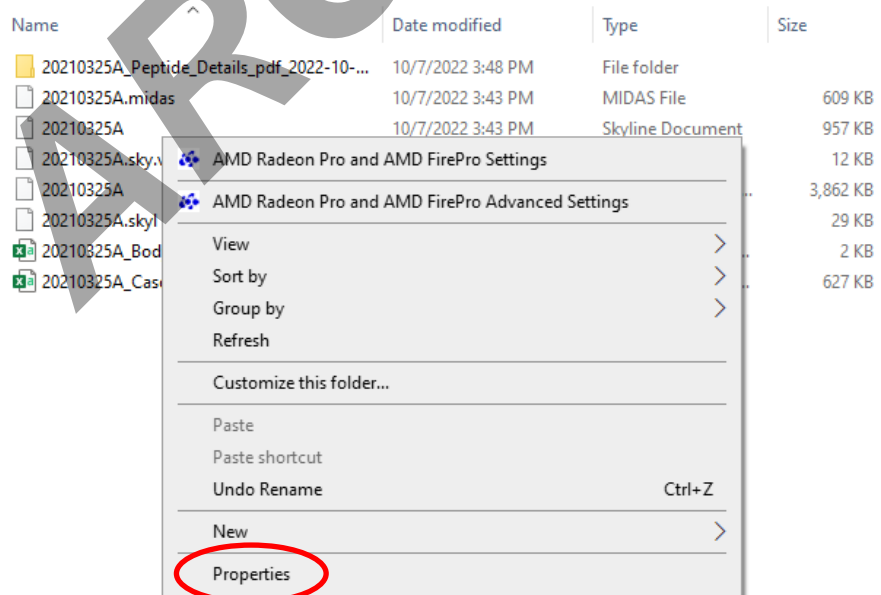
3.2   Right click on the bfassay_cmd_ps Shortcut icon and select Run with PowerShell.

3.3   Right click on the skyline file and select Properties.

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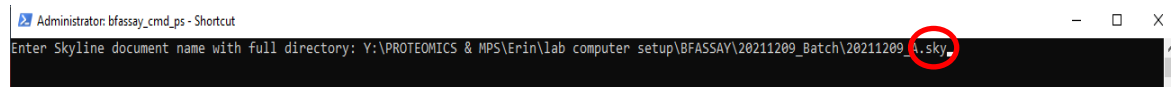3.4   Copy the location of the file and paste into bfassay_cmd_ps command window.
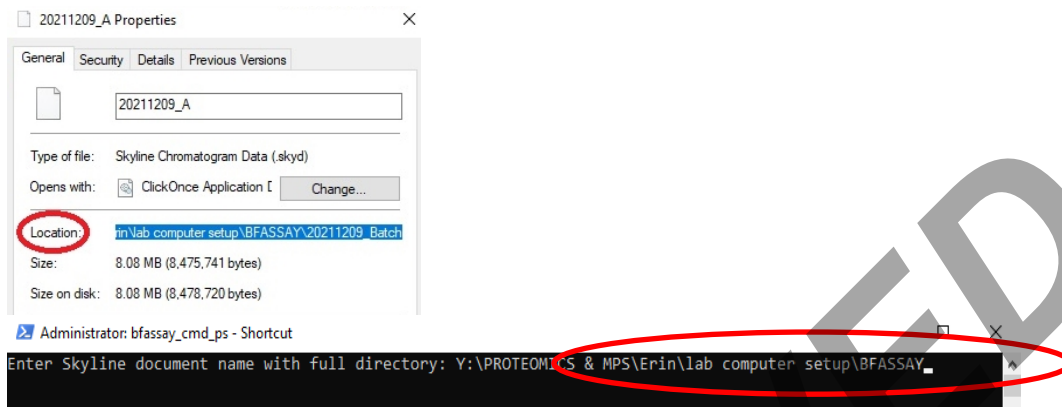
3.5   Write " \ " after pasting the location.

3.6   Copy the file name and paste in into bfassay_cmd_ps command window

3.7   Write "**.sky**" then press enter.

3.8   The script will run. The .csv export will be saved in the same folder as the Skyline documents, with the same name and the addition of 'CaseReport.csv' at the end.