Body Fluid Identification by Proteomic Mass Spectrometry - Liquid Chromatography & Mass Spectrometer Processing

Status: Published

DATE EFFECTIVE
08/16/2023

## Body Fluid Identification by Proteomic Mass Spectrometry -Liquid Chromatography & Mass Spectrometer Processing

## 1 Purpose

1.1 Samples are run through liquid chromatography to separate peptide markers. Marker peptides are identified by mass spectrometry.

## 2 Check Before Starting

- 2.1 Check the LC/MS instrument to see how many batches are in the queue. Do not proceed if there are two batches in the queue. Check the queue again the next business day.
- 2.2 Check the Pure Air tank. If pressure on the large gauge (right gauge) is  $\leq$  300 psi, <u>do not</u> proceed. Contact the Proteomics Team to change the Pure Air tank if it is less than 300 psi.



- 2.3 Check all volumes in reagent bottles. If reagent bottles do not have the volumes listed below, <u>do</u> <u>not proceed</u>. Contact the Proteomics Team to change the reagents bottles if their volumes are less than the volumes listed below.
  - 2.3.1 Methanol (50% methanol + 50% HPLC water) 200 mL
  - 2.3.2 Loading Solution (phase A 2% ACN + 98% HPLC water) 200 mL
  - 2.3.3 Bottle A (HPLC water) 160 mL

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#### 2.3.4 Bottle B (ACN) 120 mL

For samples that need to be rerun, follow the instructions above (2.1 to 2.3 above) and then 2.4 proceed to section 3.9.

#### 3 Liquid Chromatography – Mass Spectrometer Analysis Procedure

3.1 Retrieve the following reagents:

Cytochrome C (1pmol/ µl) at -80°C	
PCM Standard	
Phase A	
Acetone	
Acetonitrile	
Isopropanol	

3.2 If batch contains low concentration samples, make Low Conc resuspension mixture in a new 1.5 mL microcentrifuge tube. Work on ice or in a -20°C cold tube rack.

Low Conc. Resuspe	nsion Mi	xture	e – Enough for 9 Low Conc. Samples
Reagent			Volume
Phase A			93 µl
Cytochrome C (1 pm	ol/µl)		0.94 μl
Total volume:			93.94 μl

- 3.3 Resuspend samples as follows:
- 3.4 REGULAR samples: add 93µl Phase A and 0.94 µl Cytochrome C (1 pmol/µl) to reconstitute peptides. LIMS can do the math for total of samples
- 3.5 LOW Concentration Samples: add 10 µl of Low Conc resuspension mixture to reconstitute peptides.
- 3.6 Vortex.
- 3.7 Place in refrigerated centrifuge at 4°C and spin at 18,000 g for 30 minutes. Record instrument and temperature in LIMS.
- Pipette supernatant into LC Vial (avoid pellet if present) and store at 4°C. 3.8
- 3.9 Prepare the LC cleaning solution to be run alongside samples and controls:

#### LC Cleaning Solution

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Reagent	Volume
Acetone	2 µl
Acetonitrile	9 μl
Isopropanol	9 μl
<b>Total Volume:</b>	20 μl /sample

# 3.10 Place samples, controls, and prepared cleaning solution in Eksigent refrigerated auto sampler and fill out location of each vial in the input load plate on LIMS.

# 3.11 Fill in LIMS ouput data entry sheet and select the appropriate Acquistion Method for the sample type.

Sample Type	AcqMethod
PepCalMix, Phase A	Coll PepCalMix Col2 PepCalMix
Cleaning Sol	Col1 Cleaning Col2 Cleaning
ENeg, Ext Pos controls, Unknowns	Col1 Unknown Col2 Unknown
Reruns (High)	Col1 Unknown Hi Col2 Unknown Hi

- 3.12 Output Plate Name should be the date (YYYYMMDD), followed by a letter identifying batch order (e.g. A, B, C, etc.) an underscore, followed by analyst initials.
- 3.13 Ensure the output samples are in the desired injection order before loading plate (in its default vertical mode)
  - 3.13.1 Positive controls should be run after unknown samples when creating batch.
- 3.14 Export sample batch from the output plate in LIMS.
- 3.15 Open LIMS created batch excel sheet in the LIMS LCMS folder and confirm it is as desired and save document as .txt format.



- 3.16 Open analyst software.
- 3.17 Double click Hardware Configuration → Eksigent LC and MS → Activate Profile

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#### **MOLECULAR SEROLOGY PROCEDURES MANUAL**



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#### 3.19 Double click Build Acquisition Batch

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((Ų)) Tune and Calibrate	2	$\checkmark$	6/14/2019 4:12:40 P	CytoC Dig_10fmol/ul 10ul Loading_Col1	1
Compound Optimization	3	$\checkmark$	6/14/2019 4:45:41 P	CytoC Dig_10fmol/ul 10ul Loading_Col2	1
	4	$\checkmark$	6/14/2019 5:18:40 P	CytoC Dig_10fmol/ul 10ul Loading_Col1	1
AT Instrument Optimization	5	$\checkmark$	6/14/2019 5:51:41 P	Phase A_col2	1
	6	$\overline{\mathbf{V}}$	6/14/2019 6:24:40 P	Phase A C1	1
¥= Acquire (2)	7	V	6/14/2019 7:14:24 P	Phase A C2	1
	8	V	6/14/2019 8:04:06 P	SE 0.1ug/ul, 3 ul loading, Col1_Sample 1	1
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P® Explore (1)	13	Ŵ	6/15/2019 12:12:38	SE 0.1ug/ul, 3 ul loading, Col1 Sample 1	1
📑 Open Data File	14	V	6/15/2019 1:02:20 A	SE 0.1ug/ul, 3 ul loading, Col1_Sample 1	1

Right click to import acquisition batch. 3.20



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3.21 Select .txt batch list exported from LIMS. Click open.

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3.22 Select autosampler (ekspert nanoLC 400). Click OK.

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CTC-MPX Driver		Cancel
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Eksigent AS1	_	
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3.23 **Label and Position WITNESS**: Have a witness verify the selected autosampler, batch sample names, methods, and tube positions in autosampler match that in Vial Position column.

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#### 3.24 Click on Submit tab when sample list is ready.

3.25



#### Analyst - [Batch Editor: [Validation 2022\2022 - BuildingBatch1]] K Eile Edit View Acquire Tools Explore Window Script Help 🗂 🔂 Validation 2022\2022 🖹 🖨 🖶 🎒 🖪 👗 🎦 🛍 🔀 🕰 🗠 🛨 🛛 Acquire Mode 🛤 🗙 🛅 🗖 🗖 🖽 🛛 🗃 ĦĦħ&&& O ● <u>8</u> U & ¥ Ø & ← ⋈ ☆ **1** × P × Sample Locations Quantitation Submit E Configure Security Configuration Batch Owner name Hardware Configuration MS User Submit S Report Template Editor Ibmit Status (I)) Tune and Calibrate Number of samples in the Batch: 114. Number of DataFiles: 114. A Compound Optimization aU

3.26 Ensure "All samples" is selected and that the box for "apply new samples order" is unchecked. Click OK

Selected samples     All samples	
All samples	
Apply new samples order	

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#### 3.27 Click Queue button and double check all samples were submitted.

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3.28 Click Ready button.											
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#### 3.29 Click Start sample button. The Eksigent LC and 6500 MS will process all samples.

A Analyst - [Queue Manager [Local]]											
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