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| STANDARD OPERATING PROCEDURE |
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| **Title: Response curve for MRM assays run on 8040 triple quadrupole mass spectrometer (Shimadzu)** |
| **Version #: 1.2** | **Author: Hui Zhang Laboratory – Johns Hopkins University** |
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**Purpose**

The purpose of this document is to describe the characterization of a set of assays by response curve.

**Scope**

This procedure addresses the preparation and running of samples for generating a response curve in accordance with CPTAC Assay Characterization Guidance Experiment #1.

**Responsibilities**

It is the responsibility of person(s) performing this procedure to be familiar with laboratory safety procedures. The interpretation of results must be done by a person trained in the procedure and familiar with such interpretation.

**Equipment**

* Microcentrifuge
* Vacuum centrifuge

**Materials**

* Water: Optima LC/MS-grade (Fisher Scientific; cat. # W6-4)
* Acetonitrile: Optima LC/MS-grade (Fisher Scientific; cat. # A955-4)
* Formic Acid: LC-MS Ultra (Sigma-Aldrich; cat. # 14265)
* Methanol: Optima LC/MS-grade (Fisher Scientific; cat. # A456-4)
* Ammonium formate (Sigma-Aldrich; cat. # 70221)
* Ammonium hydroxide (Sigma-Aldrich; cat. # 320145)
* Polysulfoethyl A TopTips 100 – 200 µL (Glygen; cat. # TT2SSA.96)

**Reagents**

* 10 mM Ammonium formate in 25% ACN, pH 3.0
* 500 mM Ammonium formate in 25% ACN, pH 6.8
* 80:15:5 (vol:vol:vol) Methanol: Water: Ammonium hydroxide
* Crude unlabeled peptides (~60% purity)
* Stable isotope-labeled standards (SIS)
	+ Crude unlabeled peptides and SIS (both ~60% purity) from Thermo Fisher Scientific (PEPotec SRM peptide library): SIS peptides incorporate a fully atom-labeled 13C and 15N isotope at the C-terminal lysine (K) or arginine (R) position of each tryptic peptide, resulting in a mass shift of +8 or +10 Da, respectively. Peptides should be provided in 0.1% TFA/50% ACN and stored at -80 °C until use.
	+ Following de-salting via strong cation exchange (SCX) as detailed in Procedure #1 below, prepare stock solutions of the unlabeled and SIS peptides at a concentration of 2 nmol/µL in 0.2% FA and store at -20 °C. The peptide recovery following SCX clean-up is estimated to be 40%.
* Matrix
	+ Prepare a background matrix consisting of peptides from the trypsin digestion of human ovarian tissue according to the SOP entitled “SOP\_Tissue background matrix preparation v1\_2-HuiZhang lab.” This background matrix will be used for the preparation of the response curves and for the preparation of the mini-validation of repeatability experiments.

**Procedure**

1. SCX de-salting of crude peptides and SIS
	1. All centrifugation steps are performed at 2,000 rpm for 1.5 min, unless otherwise specified. De-salt 1 mg of each peptide via SCX.
		1. Condition Polysulfoethyl A TopTip 2x with 330 µL of Methanol
		2. Wash 2x with 330 µL of 10 mM Ammonium Formate in 25% ACN, pH 3.0
		3. Wash 2x with 330 µL of 500 mM Ammonium Formate in 25% ACN, pH 6.8
		4. Wash 2x with 330 µL of 10 mM Ammonium Formate in 25% ACN, pH 3.0
		5. Wash 2x with 330 µL of Water
		6. Wash 4x with 330 µL of 10 mM Ammonium Formate in 25% ACN, pH 3.0
		7. Slowly load acidified sample (pH < 3.0) 2x; centrifuge at 1,100 rpm for 5 min
		8. Wash 6x with 330 µL of 10 mM Ammonium Formate in 25% ACN, pH 3.0
		9. Allow TopTip to dry out. Elute sample 2x with 300 µL of 80:15:5 (vol:vol:vol) Methanol: Water: Ammonium hydroxide; centrifuge at 1,100 rpm for 5 min
		10. Dry eluted sample in a vacuum centrifuge
2. Preparation of samples
	1. Prepare stock SIS peptide mixture at a concentration of 5 pmol/µL per peptide in 0.2% FA.
	2. Prepare stock unlabeled peptide mixture at 50 pmol/µL per peptide in 0.2% FA.
	3. Dilute matrix to 0.1 µg/µL with 0.2% formic acid.
	4. Prepare samples with 7 points of varying concentrations by making 1:2 and 1:5 serial dilutions of the highest point on the curve (25 pmol/µL) using the diluted matrix to achieve the following final concentrations: 25, 5, 2.5, 0.5, 0.25, 0.05, 0.025 pmol/µL. Also prepare blank matrix containing SIS. Prepare an adequate volume of each sample for at least 6 runs (response curve concentration points) or 12 runs (blanks). The final preparation of each sample will contain background matrix, unlabeled peptides and SIS peptides (1.2 pmol/µL).
	5. Store samples at 4 °C (no longer than 48 hours) until LC-MRM MS analysis.
3. Execution of LC-MRM MS analysis
	1. Prepare 20 µL of each sample and spike with 2 µL of the SIS peptide mixture.
	2. Vortex samples, centrifuge briefly and transfer to autosampler vials. Add sufficient volume to each vial for all of the replicate injections.
	3. Perform LC-MRM MS analysis according to the SOPs entitled “SOP\_Liquid Chromatography CPTAC MRM 8040 Assays v1\_1-HuiZhang lab” and “SOP\_MRM mass spectrometry 8040 CPTAC Assays v1\_1-HuiZhang lab.”
4. Run order
	1. Run samples in order of increasing concentration as indicated below. Three replicates are acquired for each concentration. Three blanks are run prior to the first replicate run of the curve and two blanks are run following each curve.

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| Run order | Sample |
| 1 | Blank |
| 2 | Blank |
| 3 | Blank |
| 4 | 0.025 pmol/µL |
| 5 | 0.05 pmol/µL |
| 6 | 0.25 pmol/µL |
| 7 | 0.5 pmol/µL |
| 8 | 2.5 pmol/µL |
| 9 | 5 pmol/µL |
| 10 | 25 pmol/µL |
| 11 | Blank |
| 12 | Blank |
| 13 | Wash |
| 14 | Wash |

**Referenced Documents**

* SOP\_Liquid Chromatography CPTAC MRM 8040 Assays v1\_1-HuiZhang lab
* SOP\_MRM mass spectrometry 8040 CPTAC Assays v1\_1-HuiZhang lab
* SOP\_Tissue background matrix preparation v1\_2-HuiZhang lab

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