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# CIDC\_S16\_LC\_MS\_Celegans\_Extraction\_Protocol

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A sample preparation protocol for lyophilized *C. elegans* samples to be analyzed via LC-MSMS

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**protocols.io**

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*C. elegans*, *C. elegans* caenorhabditis *elegans*, LC-MSMS, LC-MS/MS, LC-MS, liquid chromatography, mass spectrometry, metabolomics, lipidomics

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## MATERIALS

☒ Glass beads, acid-washed, 425-600  $\mu\text{m}$  (30-40 U.S. sieve) **Sigma**

**Aldrich Catalog #G8772-100G**

☒ Acetonitrile **Sigma**

**Aldrich Catalog #34998**

☒ Methanol HPLC **Fisher**

**Scientific Catalog #9093-03**

☒ Eppendorf tubes 1.5 mL uncolored **Eppendorf**

**Centrifuge Catalog #022363204**

☒ 2-Propanol **Fisher**

**Scientific Catalog #A417-4**

☒ Water Optima™ LC/MS Grade **Fisher Scientific Contributed by**

**users Catalog #10728098**

☒ 2.0mm zirconium oxide beads (Next Advance SKU ZROB20) **Contributed by**

**users Catalog #ZROB20**

## Homogenization

- 1 Samples are removed from  $-80\text{ }^{\circ}\text{C}$
- 2 (3) 2.0mm zirconium oxide beads and ~ **75  $\mu\text{L}$**  volume of 0.5mm glass beads are added to each sample tube.
- 3 Samples are placed in Tissuelyser II using adapter trays chilled at  $-80\text{C}$  and homogenized at 1800rpm for **00:03:00**.
- 4 Samples are now homogenized.

## Extraction

- 5 **750  $\mu\text{L}$**  of 100% isopropanol is added to the 1.5mL Eppendorf tube containing the homogenized sample. The sample tube is lightly vortexed to create a suspension of homogenized sample and the resulting slurry is transferred to a new 2.0mL Eppendorf tube, leaving the beads behind in the original tube. This step is repeated so that a total of **1.5 mL** of solvent is transferred to the new 2.0mL Eppendorf tube.

- 6 Samples are vortexed for 🕒00:01:00 and then extracted over night at -20C
- 7 Samples are placed in the centrifuge and spun at max speed (22100G) for 🕒00:05:00
- 8 Supernatant of each sample is transferred to a new 2.0 mL Eppendorf labeled for RP chromatography and dried down using steps 14 through 18
- 9 The second round of the sequential extraction is 📏1.5 mL of 80/20 methanol/water per added directly to the pellet remaining after centrifugation.
- 10 Samples are shaken using the Fisher Scientific Isotemp High Speed Shaker at 1500rpm for 🕒00:30:00
- 11 2.0mL Eppendorfs are placed in the centrifuge and spun at max speed (22100G) for 🕒00:05:00
- 12 Supernatant of each sample is transferred to a new 2.0 mL Eppendorf labeled for HILIC chromatography and dried down using steps 14 through 18
- 13 Pellets are dried for 1 hour and stored at 🌡-80 °C

#### Sample drying/storage

- 14 Samples are placed in a Labconco CentriVap concentrator and monitored until they have completely dried (roughly 4-5 hours)
- 15 Once dry, samples are stored at 🌡-80 °C until they are to be run on the LC-MS instrument.
- 16 When preparing samples to run on LC-MS, reconstitute samples with 📏75 µL of 100% isopropanol for reverse phase and 80/20 methanol/water for HILIC.

- 17 Vortex for 1 minute, then centrifuge at max speed (22100G) for 🕒 00:05:00
- 18 Transfer to LC-MS vial
- 19 After LC-MS analysis, samples can be stored at -80C until ready for IMS analysis