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# Preparation of soluble and insoluble mitochondrial protein fractions for mass spectrometry analysis

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### **Abstract**

Preparation of soluble and insoluble mitochondrial protein fractions from HeLa cells for mass spectrometry analysis.



### Day 1

25m

10m

10m

- Centrifuge samples at 10000 rcf for 00:10:00 at 4 °C , and carefully aspirate the supernatant.
- Add  $\triangle$  60 µL of ice cold 0.5% TX-100 in PBS, vortex each sample for ~5 seconds, and leave samples to incubate on ice for  $\bigcirc$  00:15:00 . At the conclusion of the  $\bigcirc$  00:15:00 lysis incubation, vortex each sample for ~5 sec again.
- Centrifuge the samples at 12000 rcf for 00:10:00 at 1 4 °C.
- Using a pipette, carefully remove  $\Delta$  57  $\mu$ L of the supernatant (representing 95% of the lysis volume) and place this sample into a clean microfuge tube on ice, being sure not to disturb any pellets that have formed on the bottom of the tube. The volume removed represents the 'soluble' protein fraction. The tube containing the pellet represents the 'insoluble' protein fraction.
- Add  $\Delta$  57 µL of 0.5% TX-100 in PBS to each insoluble protein fraction by pipetting on the side of the tube. Gently flick each tube to rinse the sides of the tube.
- 7 Centrifuge the insoluble protein fractions at (3) 12000 rcf for (5) 00:10:00 at (4 °C).
- Using a pipette, carefully remove  $\Delta$  57  $\mu$ L of the supernatant from the insoluble protein fraction, and place into a clean microfuge tube (which will function as the waste collection tube for all samples).
- 9 Repeat steps 6 8, which will total 2 washes



- 10 Repeat step 6. You should now have two tubes for each sample (soluble and insoluble protein fractions), and one waste tube.
- 11 Thaw aliquots of recombinant Ag85A on ice, and add 4 180 ng of Ag85A to each insoluble protein fraction, and <u>A</u> 171 ng of Ag85A to each soluble fraction.
- 12 Equilibrate all samples to room temperature and then add 2x SDS solubilization buffer to a final concentration of 1x (2x: 10% w/v SDS, 200 mM HEPES pH 8.5). Vortex each samples for  $\sim 5$ seconds to mix.
- 13 Sonicate all samples in a waterbath sonicator set to 4 21 °C for 6 00:10:00 .

10m

45m

14 Add TCEP to a final concentration of [M] 10 millimolar (mM) and chloroacetamide to a final concentration of [M] 40 millimolar (mM) to each sample, vortex each sample for ~5 seconds to mix, and incubate samples at \$\ \ 37 \ O \ for \ 00:45:00 \ (standing).

#### Note

Make sure chloroacetamide is made up fresh from powder

- 15 Acidify each sample by adding phosphoric acid to a final concentration of 1.2%/sample (ensure pH < 4. More phosphoric acid can be added if the pH is not low enough at 1.2%/sample)
- 16 Add binding buffer ( [M] 100 millimolar (mM) triethylammonium bicarbonate, 90% v/v methanol pH 7.1 with phosphoric acid) to each sample at a ratio of 1:7, sample volume to binding buffer.
- 17 Vortex each sample for ~5 sec to mix
- 18 Load 🚨 400 µL of each sample into a S-Trap Mini column, and centrifuge at 😭 6500 rcf at Room temperature for 00:00:30 Discard the flow through.
- 19 Repeat step 18 until the full volume of each sample has been loaded on its column.

30s



- 20 Wash each column by adding 🛕 400 µL of binding buffer, centrifuging at 🚯 6500 rcf at 30s Room temperature for 00:00:30, and discarding the flow through.
- 21 Repeat step 20 three times, for a total of 4 washes.
- 22 Move the columns to a 1.5 mL LoBind microfuge tube (Eppendorf) and add △ 125 μL of digestion buffer directly to the column filter (digestion buffer: мі 50 millimolar (mM) triethylammonium bicarbonate supplemented with sequencing grade trypsin at a concentration of 1 ug trypsin to 50 ug of starting protein (which will differ between soluble and insoluble samples)).
- 23 Centrifuge samples at 1000x rcf for 00:00:30 at room temperature, and pipette the digestion buffer flow through directly back onto the column filter. Move the columns to clean 2.0 mL LoBind microfuge tubes.
- 24 Seal each sample to the LoBind microfuge tube with parafilm, and incubate samples overnight for at least (5) 16:00:00 at 37 deg C (static incubation)

## Day 2

- 25 Remove the parafilm and add 🚨 80 µL of digestion buffer without trypsin (50 mM triethylammonium bicarbonate) to each sample. Centrifuge samples at ( 🚯 3200 rcf for 00:01:00 at 🖁 Room temperature . Leave the flow through in the collection tube.
- 26 Add 🚨 80 µL of 0.2% v/v formic acid to each sample, and centrifuge at 🤮 3200 rcf for 00:01:00 at room temperature. Leave the flow through in the collection tube.
- 27 Add  $\perp$  80 µL of 50% v/v acetonitrile/0.2% v/v formic acid to each sample, and centrifuge at 1m **65**00 rcf for **6**00:01:00 .
- 28 Remove and discard the S-Trap columns from each sample.

30s

16h

3m

1m

1m



29 Lyophilise the total eluate from each sample, seal the samples with parafilm and store at

↓ -80 °C until needed for downstream processing.