Post-FASP Strong Anion Exchange Separation (SAX)

Adapted from Wisniewski et al, J Proteome Research, 2009

Materials

- 1. **Stock solution of Britton & Robinson Universal Buffer (BRUB)** (Britton, H.T.K and Robinson, R.A, *J. Chem. Soc.*, 1931, 1456-1462)
 - a. Prepare a 5x stock solution containing 0.1 M acetic acid, 0.1 M phosphoric acid and 0.1 M boric acid.
 - b. Adjust with NaOH to the required pH. For standard FASP processed sample, the following pH values are recommended: pH 3, 4, 5, 6, 8 and 11.
 - c. Before use, dilute 5-fold in DDW. Recommended amounts are $^{\sim}120\mu l$ diluted buffer per sample from buffers pH-3,4,5,6, 8, and $^{\sim}500\mu l$ diluted buffer per sample from buffer pH-11.
 - d. Add NaCl to the 1x pH-3 solution to a final concentration of 0.25M.
- 2. **Buffer B:** 80% (v/v) ACN, 0.5% (v/v) acetic acid.
- 3. **Buffer A:** 0.5% (v/v) acetic acid.
- 4. Anion-Exchange tip-column (in pipette tip) (SAX tip)
 - a. Stack 6 layers of Empore/Disk Anion Exchange (Varian, 1214-5012) in a 200μl pipette tip. Prepare 1 SAX tip for each sample.
 - b. Cut the top off the SAX tip (3-4mm) so it can conveniently be centrifuged.
- 5. StageTip
 - a. Stack 3 layers of Empore/C18 in a 200µl pipette tip (→ stageTip).

 Prepare 6 stageTips for each sample (1 for each pH), and label them properly.

Sample preparation

- 1. Elute peptides in FASP procedure or equivalent.
- 2. Verify the pH of each solution (after dilution) and correct with NaOH or BRUB.
- 3. Dissolve 20-50µg peptides with up to 200µl buffer 1x pH-11 and ensure pH is higher than 11 (correct with NaOH if necessary).

Anion Exchanger tip-column (SAX tip) activation

1. Assemble the tip-column in the eppendorf tube lid or adapter.

- 2. Wash with 100μ l Methanol. Centrifuge at $3000 \times g$ for 3 min. Ensure solution is not retained on top of the filter.
- 3. Wash with 100µl 1 M NaOH.
- 4. Wash **twice** with 100μl 1x pH-11 buffer.

StageTip conditioning

- 1. Assemble the tip-column in the eppendorf tube lid or adapter.
- 2. Wash StageTip with 100μ l Methanol. Centrifuge at $1000 \times g$ for 2 min. Ensure solution is not retained on top of the filter.
- 3. Wash StageTip with 100µl Buffer B
- 4. Wash StageTip twice with 100µl Buffer A

Sample loading and separation

- 1. Assemble the first (highest pH) StageTip-Sax tip apparatus as depicted in the drawing.
- 2. Load the diluted sample. If the sample volume exceeds the volume in the tip, you may perform the loading several times.
- 3. Centrifuge at 3000 x g for 3 min.
- 4. Add 100μ l 1x pH-11 buffer to the SAX tip and centrifuge at 1000 x g for 5 min.
- 5. Transfer the SAX tip to the next StageTip.
- 6. Continue with stages 4-5, eluting subsequently with 1x pH 8,6,5,4 and 3 buffer, each into its corresponding StageTip.
- 7. After each centrifugation step, make sure that no liquid remains above the filter.
- 8. Wash the StageTips with 100µl Buffer A.

