

# Phospho-seq

This protocol will take you through performing Phospho-seq with a 10x single-cell ATAC-seq kit. The pre-processing steps are contained here with the necessary modifications to the 10x protocol attached at the end. This protocol goes up to the sequencing of the libraries, please refer to the other protocols at [Phospho-seq.com](http://Phospho-seq.com) for preparing conjugated antibody pools and data processing and analysis.

## Materials

16% FA – 30 ul/sample – 500 ul

- 219  $\mu$ l 36.5% Formaldehyde (Sigma: F8775)
- 281  $\mu$ l 1X PBS (Cytiva: SH30256)

1M Glycine – 68.5 ul/sample – 10 ml

- 750.7 mg Glycine (BioBasic: GB0235)
- 10 ml H<sub>2</sub>O

1X PBS

Permeabilization buffer (100 ul/ sample - 1 ml)

- 1M Tris-HCl (Thermo: 15567027)- 10  $\mu$ l
- 5M NaCl (Thermo: AM9759) - 2  $\mu$ l
- 1M MgCl<sub>2</sub> (Sigma: M1787) - 3.33  $\mu$ l
- 10% NP40 (Thermo: 28324) - 10  $\mu$ l
- 10% BSA in H<sub>2</sub>O (Fisher: BP9706100) - 100  $\mu$ l
- H<sub>2</sub>O - 874  $\mu$ l

Wash Buffer (#1) (1 ml/ sample - 10 ml)

- 1M Tris-HCl - 100  $\mu$ l
- 5M NaCl - 20  $\mu$ l
- 1M MgCl<sub>2</sub> - 33.3  $\mu$ l
- 10% BSA in H<sub>2</sub>O - 1 ml
- H<sub>2</sub>O - 8850  $\mu$ l

Blocking Buffer (100 ul/ sample - 1 ml)

- PBS w/ 3% BSA - 909  $\mu$ l

**Note:** Make a 500 ml bottle of this (15 g BSA in 500 ml PBS), filter and store at 4C



2. take 1-2 million cells total for experiment
3. Centrifuge 300 rcf for 5 mins
4. Resuspend in 475  $\mu$ l PBS
5. Run through a 40  $\mu$ m Flowmi cell strainer (Bel-Art: H13680-0040) into a 1.5 ml tube

## Fixation and Permeabilization

1. Add 30  $\mu$ l 16% FA and pipette to mix
2. Leave at RT for 10 mins, swirl/invert occasionally
3. Quench fixation by adding 68.5  $\mu$ l of 1M Glycine
4. Fill tube with ice cold 1X PBS
5. Centrifuge for 5 mins at 400 rcf at 4C
6. Remove supernatant and add 1 ml cold 1X PBS
7. Centrifuge for 5 mins at 400 rcf at 4C
8. Discard supernatant and resuspend in 100  $\mu$ l permeabilization buffer
9. Incubate on ice for 5 mins
10. Add 1ml Wash buffer #1, centrifuge for 5 mins at 500 rcf at 4C
11. Resuspend in 100  $\mu$ l blocking buffer
12. Put on tube rotator at RT for 30 mins

## Hashing

**Note: This step is optional and the protocol is if you are using four separate hashing antibodies for one sample. For samples that are already separate, leave them separate and hash each one accordingly. Adjust accordingly for more or less hashes used and skip step if not hashing**

1. Add 500  $\mu$ l wash buffer #2, centrifuge for 5 mins at 500 rcf at 4C
2. Remove supernatant, add 300  $\mu$ l wash buffer #2, split into 4 x 100  $\mu$ l tubes, add further 400  $\mu$ l wash buffer to each and spin down 500 rcf at 4C
3. Remove supernatant and resuspend in 100  $\mu$ l staining buffer with 1  $\mu$ g hashing antibody per tube
4. Place on the tube rotator for 30 mins at RT
5. In the meantime prepare the SSB-bound antibodies

## Binding SSB to antibodies

1. Add an appropriate amount of pooled antibody to a 1.5 ml tube

**Note:** Usually I add approximately 0.5 µg of antibody mix per antibody – e.g. in a panel of 30 antibodies I would add 15 µg of antibody pool – but this can go as low as 0.1 ug/ab or as high as 1 ug/ab with expected changes in sensitivity.

2. Add H<sub>2</sub>O to fill up to 100 µl less 10µl and less the amount of SSB you put in (8ug/ug of antibody) e.g. for 20 µl of antibody pool with 10 ug, you will add roughly 16 µl of SSB, so you would add 100- 20 -10 -16 = 54 µl H<sub>2</sub>O

3. Add 10 µl 10X NEB buffer 4

4. Add SSB and pipette mix until well distributed

5. incubate at 37C for 30 mins

6. Add 50 µl of 3X PBS + 9% BSA to make a final concentration of 3% BSA in 1X PBS

## Staining and washes

1. After hashing, centrifuge at 600 rcf for 5 mins and resuspend in 500 µl wash buffer #2

2. Remove supernatant and repeat centrifugation

3. Remove supernatant and resuspend in wash buffer #2, count each sample and combine into one tube (1 million cells total)

**Note:** Counting is unnecessary when starting with small quantities of cells

4. Centrifuge at 600 rcf for 5 mins, remove supernatant

5. Resuspend in the 150 µl of Staining Buffer + ab

6. Put in the tube rotator at RT for 1 hr

7. Centrifuge at 600 rcf for 5 mins, remove super and add 500 µl wash buffer #2. Repeat this step

8. Remove supernatant and resuspend in 500 µl 1x nuclei buffer and run through a 40 µm flowmi filter

9. Centrifuge at 600 rcf for 5 mins to concentrate sample

10. Take off much of the supernatant to have about 30 µl left depending on size of pellet

11. Resuspend cells and count 2-5 µl of cells and adjust concentration accordingly

12. Load 30,000 cells into tagmentation reaction for 20,000 cell recovery overall

13. From here, follow the 10X scATAC protocol with indicated changes (scATAC kit version 1.1 protocol – adjust accordingly for version 2)

## Adjustments to 10X scATAC v1.1 protocol

1. At step 2.1 (barcoding reaction), spike in 0.5 µl of 1 uM each of bridge oligo A and bridge oligo B

**Note:** If not doing hashing or TSA blocking, bridge oligo A is unnecessary. Additionally this protocol assumes TotalSeqB oligos are being used for the protein antibodies

2. At step 2.5 (GEM incubation) add a 5 min at 40C at the beginning of the protocol (before the 72C for 5 min step)

3. At step 3.1o (Silane bead elution), add 43.5  $\mu$ l of Elution Solution I and recover 43  $\mu$ l of elution. Set aside 3  $\mu$ l of this elution to use as input into the ADT and HTO input PCRs to increase complexity. Continue with the remaining 40  $\mu$ l as written.
4. At step 3.2d (SPRI cleanup), rather than discarding the supernatant, save it as this is where the ADT and HTO fragments are. Continue with the bead bound fraction for the remainder of the protocol as this is where the ATAC fragments are
5. To clean up the supernatant after step 3.2d, add 32  $\mu$ l SPRI beads and let bind for 5 min. Collect the beads on the magnet and wash 2X with 80% EtOH. Remove all EtOH and resuspend in 42  $\mu$ l EB, allowing to bind for 5 min. Place the tubes back on the magnet and remove 42  $\mu$ l of the elute and combine with the 3  $\mu$ l set aside at step 3.1o for 45  $\mu$ l total.
6. If doing both HTOs and ADTs, split the 45  $\mu$ l fraction in two and input into two separate PCR reactions with the following parameters:

PCR reaction:

50  $\mu$ l 2X KAPA master mix (KAPA Biosystems: 07958935001)

2.5  $\mu$ l 10 uM P5 Primer (generic P5)

2.5  $\mu$ l 10 uM RPxx (TSA) or D7xx (TSB) primer

22.5  $\mu$ l input fragments

22.5  $\mu$ l H<sub>2</sub>O

RPxx Primer: CAAGCAGAAGACGGCATAACGAGATXXXXXXXXXXGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

D7xx Primer: CAAGCAGAAGACGGCATAACGAGATXXXXXXXXXXGTGACTGGAGTTCAGACGTGTGC

Generic P5 Primer: AATGATACGGCGACCACCGAGA

X's denote the i7 barcode in the primers

PCR Program:

1.95 C 3 min

2.95 C 20s                      Repeat steps 2-4 for 12-16 total cycles

3.60 C 30s

4.72 C 20s

5.72 C 5 min

6.4 C Hold

**Note:** Depending on the number of cells and antibody input into the reaction, I will remove 2  $\mu$ l of product after 12 cycles and look for product (188-205 bp) on a 2% e-gel. If no product is visible, I will run 2-4 more cycles.

7. After PCR, clean up the reactions with SPRI beads: Add 160  $\mu$ l SPRI beads to 100  $\mu$ l PCR reaction and let bind for 5 mins. Place on magnet and wash 2X with 80% EtOH. Remove all EtOH and resuspend in 20  $\mu$ l buffer EB. Let bind for 2 mins at RT and place back on magnet. Remove elute which is your ADT or HTO sequencing library.

## Sequencing

1. Run all libraries on a Bioanalyzer High Sensitivity DNA chip to determine molarity. For ATAC libraries, look for nucleosome banding pattern. For ADTs and HTOs look for strong, clean products at 188-205 bp.
2. Combine the libraries to aim for 20,000 reads per cell for the ATAC fraction, 5,000 reads per cell for the ADT fraction and 2,000 reads per cell for the HTO fraction
3. Run on whichever sequencer you have available as long as there is >26 bp Read 1, 8 bp i7 index, >34 bp Read 2 and 16 bp i5 index. A 75 cycle NextSeq high-output kit performs well for 20,000 cells for this with 34/8/16/34 sequencing recipe.