

Nuclei isolation from flash-frozen *Pleurobrachia* samples

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– PROTOCOL –

Materials

- | | |
|--|---|
| <input type="checkbox"/> BSA 1 % | <input type="checkbox"/> Nuclease-free water |
| <input type="checkbox"/> Buffer, lysis (stock) | <input type="checkbox"/> PBS for single cell |
| <input type="checkbox"/> Buffer, wash (stock) | <input type="checkbox"/> Petri dish |
| <input type="checkbox"/> Cell strainer 100 µm | <input type="checkbox"/> Pipettes |
| <input type="checkbox"/> Cell strainer Flowmi® 40 µm | <input type="checkbox"/> RNase inhibitor |
| <input type="checkbox"/> Dissecting needles | <input type="checkbox"/> RNaseZap™ |
| <input type="checkbox"/> Dounce homogenizers & pestels | <input type="checkbox"/> Samples |
| <input type="checkbox"/> DTT | <input type="checkbox"/> Scaple blades (new) |
| <input type="checkbox"/> Eppendorfs 0.5 mL | <input type="checkbox"/> Tips 1000 µL |
| <input type="checkbox"/> Eppendorfs 2 mL | <input type="checkbox"/> Tips 1000 µL low retention |
| <input type="checkbox"/> Eppendorfs 2 mL low bind | <input type="checkbox"/> Tips 200 µL |
| <input type="checkbox"/> Eppendorfs 5 mL | <input type="checkbox"/> Tips 200 µL low retention |
| <input type="checkbox"/> Falcon tubes 15 mL | <input type="checkbox"/> Tips 20 µL |
| <input type="checkbox"/> Gloves | <input type="checkbox"/> Tips 10 µL |
| <input type="checkbox"/> Ice boxes | <input type="checkbox"/> Tweezers |

Procedure

Make sure to set the temperature of the 4 °C centrifuge beforehand.

*Always **work on ice**, unless otherwise specified.*

*Always keep the working environment and materials as much **RNase-free** as possible.*

Place all the working solutions, tubes, and homogenizers on ice before starting.

Keep the frozen samples at -80 °C until use. Otherwise, place them in dry ice.

1. Add **2–5 mL of ice-cold working lysis buffer** into a Dounce homogenizer.
2. Transfer the samples from the tube to the homogenizers using tweezers.

If the starting material is too much, place it on a dry-ice-cooled petri dish, and split it in multiple samples using a sterile scalpel blade.

3. Homogenize samples on ice, with a maximum of 10 loose-pestel strokes, and a maximum of 10 tight-pestle strokes.
4. Rinse the pestles back into the homogenizers with **100–500 µL of lysis buffer**.

If the sample does not fully dissociate, incubate on ice with the lysis buffer for a couple of minutes.

5. Filter the homogenate through a 100 µm cell strainer into a 15 mL Falcon tube, using 1000 µL low retention tips.
6. Rinse the cell strainer with **1× PBS for single cell**.
7. Filter the homogenate through a 40 µm Flowmi® cell strainer into a clean 15 mL Falcon tube, using 1000 µL low retention tips.
8. Spin samples at 500–900 g for 5 min at 4 °C.
9. Discard the supernatant.
10. Resuspend the nuclei with **2 mL of working nuclei wash buffer**, gently pipetting with 1000 µL low retention tips.
11. Repeat steps 8–10 twice.
12. Resuspend samples in **500 µL of 1× PBS for single cell**.

– RECIPES –**Stock lysis buffer**

Compound	Quantity	Initial concentration	Final concentration (for 10 mL)
Tris-HCl (pH 7.5)	100.0 μ L	1 M	100 mM
NaCl	20.0 μ L	5 M	10 mM
MgCl ₂	30.0 μ L	1 M	3 mM

1. Add 5 mL of 20 \times PBS to a graduated cylinder.
2. Add 5 μ L of Triton X-100.
3. Fill up to 50 mL with ultrapure water.

6% goat serum in PBSTx

Compound	Quantity	Molar mass (g/mol)	Final concentration (for 5 mL)
Normal goat serum	300.0 μ L	–	6 %
Triton X-100	0.5 μ L	647.00	0.01 %
20 \times PBS	250.0 μ L	–	1 \times
Ultrapure water	–	–	–

1. Add 250 μ L of 20 \times PBS to a beaker.
2. Add 300 μ L of normal goat serum.
3. Add 0.5 μ L of Triton X-100.
4. Fill up to 5 mL with ultrapure water.

Proteinase K working solution

Compound	Quantity	Molar mass (g/mol)	Final concentration (for 10 mL)
20 mg/mL proteinase K stock solution	1.30 μ L	–	2.6 μ g/mL
PBST	–	–	–

1. Add 1.3 μ L of 20 mg/mL proteinase K stock solution to 8 mL of PBST.
2. Fill up to 10 mL with PBST.

1:500 DAPI staining solution

Compound	Quantity	Molar mass (g/mol)	Final concentration (for 500 μ L)
DAPI	1.0 μ L	–	1:500
1 \times PBS	499.0 μ L	–	–

– RESOURCES –

1. IHC in various ctenophore species.

- Burkhardt, P., Colgren, J., Medhus, A., Digel, L., Naumann, B., Soto-Angel, J. J., ... & Kittelmann, M. (2023). Syncytial nerve net in a ctenophore adds insights on the evolution of nervous systems. *Science*, 380(6642), 293-297. [10.1126/science.ade5645](https://doi.org/10.1126/science.ade5645)
- Jager, M., Chiori, R., Alié, A., Dayraud, C., Quéinnec, E., & Manuel, M. (2011). New insights on ctenophore neural anatomy: immunofluorescence study in *Pleurobrachia pileus* (Müller, 1776). *Journal of Experimental Zoology Part B: Molecular and Developmental Evolution*, 316(3), 171-187. [10.1002/jez.b.21386](https://doi.org/10.1002/jez.b.21386)
- Moroz, L. L., Kocot, K. M., Citarella, M. R., Dosung, S., Norekian, T. P., Povolotskaya, I. S., ... & Kohn, A. B. (2014). The ctenophore genome and the evolutionary origins of neural systems. *Nature*, 510(7503), 109-114. [10.1038/nature13400](https://doi.org/10.1038/nature13400)
- Sachkova, M. Y., Nordmann, E. L., Soto-Àngel, J. J., Meeda, Y., Górski, B., Naumann, B., ... & Burkhardt, P. (2021). Neuropeptide repertoire and 3D anatomy of the ctenophore nervous system. *Current Biology*, 31(23), 5274-5285. [10.1016/j.cub.2021.09.005](https://doi.org/10.1016/j.cub.2021.09.005)