



APR 02, 2024

BAF_Protocol_007a Chloroform/Methanol Precipitation

Nicholas Sherman¹

¹University of Virginia Biomolecular Analysis Facility Core



Nicholas Sherman

University of Virginia Biomolecular Analysis Facility Core

ABSTRACT

This protocol extends BAF_Protocol_007 as an alternative to acetone precipitation (normal method). The chloroform/methanol precipitation is a better method if the sample is high in lipid or other hydrophobic small molecules. This method also produces a protein pellet and not the normal liquid interface and as such is easier.

GUIDELINES

This precipitation would be substituted in for the acetone precipitation normally used in BAF_Protocol_007.

MATERIALS

Pre-cleaned microtubes 1.5 mL - SEAL-RITE[®] 1.5 ML MICROCENTRIFUGE TUBES color: natural, USA Scientific

Pipette tips - Fisher Brand, yellow, part number: 02-681-151

ABC - Fluka analytical Ammonium Bicarbonate, Sigma Aldrich, 09830-500G

VWR Analog Vortex mixer - CAT No: 58816-121

Centrifuge 5427 R, Eppendorf

Water - Fisher Chemical, W6-4, Optima LC/MS

Methanol - A456-212, Methanol, optima LC/MS

Chloroform - AC423550010, ACS Grade 99.8+%

OPEN ACCESS



DOI:

dx.doi.org/10.17504/protocols.io.n92ld83q9v5b/v1

Protocol Citation: Nicholas Sherman 2024.
BAF_Protocol_007a
Chloroform/Methanol
Precipitation. **protocols.io**
<https://dx.doi.org/10.17504/protocols.io.n92ld83q9v5b/v1>

License: This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: Working
We use this protocol and it's working

Created: Apr 02, 2024

Last Modified: Apr 02, 2024

PROTOCOL integer ID: 97659

Keywords: protein precipitation,
mass spectrometry, sample
cleanup, lipids

Chloroform/Methanol PPT		28m
1	100 uL of protein extract of sample added to Eppendorf tube.	1m
2	400 uL of Methanol was added, vortexed well.	2m
3	200 uL of Chloroform was added, vortexed well.	2m
4	300 uL of Water was added, vortexed well.	2m
5	Sample was centrifuged at 13,000 rpm for 2 minutes	4m
6	The upper layer was carefully removed (not disturbing the protein interface).	1m

- 7** 300 uL of Methanol was added, vortexed well. 2m
- 8** Samples were centrifuged at 13,000 rpm, for 2 minutes. 4m
- 9** Supernatants were discarded and the protein pellet was air dried. Resuspend in 100 mM Ammonium Bicarbonate in volume based on protein amount. 10m