



Jun 23, 2022

Amicon NMWCO Filter Concentration and Buffer Exchange

Lauren Adams¹¹Northwestern University

1 Works for me

 Share

This protocol is published without a DOI.

Kelleher Research Group

Tech. support email: kelleher-ofc@northwestern.edu

Kelleher KRG Research Group

Northwestern University, National Resource for Translational...

ABSTRACT

This Amicon NMWCO filter protocol helps concentration dilute elution fractions containing protein as well as assists with buffer exchange if necessary.

PROTOCOL CITATION

Lauren Adams 2022. Amicon NMWCO Filter Concentration and Buffer Exchange. **protocols.io**

<https://protocols.io/view/amicon-nmwco-filter-concentration-and-buffer-exchange-cbwvspe6>



LICENSE

————— This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

CREATED

Jun 23, 2022

LAST MODIFIED

Jun 23, 2022

PROTOCOL INTEGER ID

65205

MATERIALS TEXT

Amicon NMWCO Filter (MWCO dependent on the protein target)

Centrifuge

0.5% TFA or 0.2% FA in mass spec grade H₂O

LoBind microcentrifuge tubes

- 1 Wash the filter three times with Optima grade water and centrifuging at 14,000 x g. Equilibrate the column by washing once with the same buffer as the elution buffer containing the target protein for ~10-30 minutes or until the volume has decreased.
- 2 Load the elution fraction containing the target protein into the filter and centrifuge at 14,000 x g for ~10-30 minutes or until the volume has decreased. Repeat this until the total elution volume has decreased $\leq 25 \mu\text{L}$ for LC-MS or $\leq 80 \mu\text{L}$ for I2MS. If the buffer is already acidic (TFA or FA), no additional buffer exchange is required. However, if the elution buffer is not acidic (ex: 100 mM Tris Base), buffer exchange should be performed.
- 3 Gradually incorporate larger volumes of 0.2-0.5% TFA or FA to the sample volume after sequential centrifuge cycles until the majority of the final buffer is TFA or FA. Remove sample from filter by centrifuging upside down at 14,000 x g into a clean LoBind tube. Bring the final volume up to 25 μL for LC-MS or 80 μL for I2MS with 0.2-0.5% TFA or FA before analyzing by mass spectrometry.