

Bench Protocol to Perform TAILS

We have been performing TAILS for nearly 10 years and this is now a very streamlined and highly optimized approach.

The one request we have is to follow this protocol exactly. Exactly. After you achieve good results then you may consider specific modifications that may optimize results for your particular samples. In particular, do not even think of using aldehyde derivatized chromatography beads, ever. Beads lead to massive peptide losses and contamination by non-specific binding. We tried for years to get these to work adequately and gave up, preferring to develop the polymer.

Starting material: Ideally start with a total of 1 to 3 mg of proteome^{1,2}. To reduce costs for TMT or iTRAQ one can use a minimum of 250 µg (iTRAQ 4-plex) or 200 µg (TMT 6-plex) per channel. For dimethylation labeling experiments we recommend 1 mg per channel. For any given experiment use no less than 1 mg *total* protein (spread over all channels).

If you are not sure how to prepare your proteome samples, please refer to Appendix A at the end of this document for suggestions.

¹ *The reason is to avoid high peptide losses after the polymer pull out step of the internal tryptic peptides.*

² *It is highly recommended to begin with a precipitated protein sample. This initial precipitation step will remove small molecular weight primary amines (i.e. amino acids) that otherwise interfere with labeling. This is a very important consideration for tissue culture medium, which contains high levels of amino acids. Start with a gently dried protein pellet. Do not overdry as it is hard to dissolve and losses will always occur. Alternatively, for samples in solution, it is **crucial** that buffers do not contain primary amines. Measure and adjust protein concentrations and amounts before starting TAILS protocol.*

A: DIMETHYL LABELING

Advantages: Low cost, perfect for two sample comparisons, perfect to learn TAILS. We extensively tried, but now do not use or recommend three-plex dimethylation due to generally much lower peptide numbers identified.

Day 1: Reduction, Alkylation and Dimethylation

1. Add 6 M GuHCl³ to ≥3 M, final (starting protein concentration 1-2 mg/mL)
2. Add HEPES pH 7.5 to 100 mM, final
3. Check that pH = 7.5. *This is important. Use for example pH paper and a micropipette to minimize sample loss.*
4. Add fresh DTT (dithiothreitol) to 5 mM, final, and incubate for 60 min at 37 °C

5. Add IAA (iodoacetamide) to 15 mM, final, and incubate for 30 min at room temperature in the dark (make IAA fresh; e.g. as 0.5 M stock)
6. Add DTT to 15 mM, final (i.e. to be equal concentration to IAA) and incubate 20 min at room temperature to quench alkylation
7. IN FUMEHOOD: Prepare a 2 M working stock of CH₂O (light formaldehyde) and a 1 M working stock of NaBH₃CN (light sodium cyanoborohydride; light channel)
8. Add CH₂O (light dimethylation) to 40 mM, final
9. Immediately afterwards add NaBH₃CN to 20 mM, final
10. Adjust pH to 6-7 and incubate overnight at 37 °C ^{4, 5, 6}

³ Do not use urea, not even deionized urea.

⁴ *Alternatively incubate at 50 °C for 1 h, add fresh NaBH₃CN and incubate for an additional 1 hour (not recommended, but reduces protocol length considerably)*

⁵ *If using duplex dimethylation for quantitation add ¹³CD₂O (heavy formaldehyde) and NaBH₃CN (light sodium cyanoborohydride; heavy channel; +6) to the second sample. Note these conditions may differ from what you currently use for peptide labeling. Remember the key step in TAILS is labeling at the protein level and so conditions are different.*

⁶ *If using triplex dimethylation for quantitation, add CD₂O (medium formaldehyde) + NaBH₃CN (light sodium cyanoborohydride; medium channel; +4) and ¹³CD₂O (heavy formaldehyde) + NaBD₃CN (heavy sodium cyanoborohydride; super heavy channel; +8) appropriately, but not recommended*

Day 2: Precipitation and digestion

1. Add fresh formaldehyde (20 mM; either light, medium, or heavy) and sodium cyanoborohydride (10 mM; either light or heavy) and incubate 37 °C for 2 hours to ensure complete labeling
2. Quench reaction by adding 1 M Tris, pH 6.8 to 100 mM, final
3. Vortex sample and check that pH is 6-7
4. Incubate 37 °C for 1 hour
5. For quantitative experiments mix samples now⁷

⁷ *If using triplex dimethylation for quantitation, acidify sample to pH <2.5 in fume hood to eliminate residual NaBH₃CN and NaBD₃CN before mixing samples to avoid cross labeling between channels*

Chloroform/Methanol precipitation

Transfer sample to chemically resistant tubes (e.g. blue-capped Falcon brand) to avoid leeching of polymeric compounds and plasticizers into the sample. Note: maximum volume during chloroform/methanol precipitation will be 10x the starting volume.

6. Add 4 sample volumes freezer cold methanol, vortex
7. Add 2 samples volumes freezer cold chloroform, vortex
8. Add 3 sample volumes ice-cold water, vortex
9. Centrifuge >5,000 rcf and retain interphase containing the protein precipitate (2 min if using 1.5-2 mL Eppendorf tubes and 10 min if using 15 mL Falcon Tubes) **Note: It is advisable to leave some supernatant on top of the interphase to avoid disturbing the protein layer → this greatly improves yields.*
10. Add 750 µL freezer-cold methanol to the pellet and transfer to a 2 mL Eppendorf tube. Rinse Falcon tube with another 750 µL freezer cold methanol and combine. Centrifuge at >15,000 rcf and discard supernatant
11. Wash pellet 3-4x with 1.5 mL freezer cold methanol (initially vortex to ensure thorough washing and later gently lift pellet to minimize sample loss)
12. Invert tube and partially air-dry the pellet (very important: do not over dry or pellet will be difficult to re-solubilize)
13. Re-suspend in 100 mM NaOH. Start with 20 µL and add an additional 2-5 µL if necessary to re-suspend. If difficult to re-suspend, brief tip-probe sonication can help.
14. Immediately after re-solubilizing add water stepwise aiming for [protein] >1 mg/mL
15. Add 1 M HEPES pH 7.2 to 50 mM, final

⁸ The initial success rate of this step is highly sample dependent. Stepwise, add more water and HEPES if necessary to maintain solubility. Aim to keep protein sample as concentrated as possible without precipitation

16. Check pH 7.5-8 ⁹

⁹ Retain 20 µg sample for parallel digestion with LysargiNase (for C termini identification by a separate shotgun analysis) or half of the sample for GluC as a second TAILS analysis to increase coverage of N-termini, if desired. If using a second enzyme for a parallel TAILS analysis, it is advised to increase the initial amount of protein per channel.

17. Add trypsin at a protease:protein ratio of 1:100 and gently pipette up and down to mix sample. Use LysargiNase or GluC in a 1:50 ratio.
18. Incubate overnight at 37 °C or for 2-4 hours at 42 °C to shorten the protocol length
19. Validate complete digestion by analyzing a small aliquot by 10% SDS-PAGE and by checking that there are tryptic peptides by MALDI-TOF-MS (optional)
20. After trypsin digestion retain 10-20 µg sample for pre-TAILS analysis (equivalent to a shotgun analysis). This is useful to assign N termini to protein isoforms by the Isoform Assignment Score (IAS), see auf dem Keller, U., Prudova, A., Gioia, M., Butler, G.S., and Overall, C.M. 2010. A Statistics Based Platform for Quantitative N-Terminome Analysis and Identification of Protease Cleavage Products. Molecular Cellular Proteomics 9, 912-927 and to use 2+ peptides per protein for identification if this is a concern.

Day 3: Negative Selection Using HPG-ALDII Polymer

- . Polymer can be purchased at <http://www.flintbox.com/public/project/1948/>

1. Thaw frozen polymer solution at room temperature (not on ice)
2. Add HPG-ALDII polymer at a polymer:peptide ratio of 5:1 (w/w; check that the polymer has been pre-washed)
3. Immediately add NaBH₃CN to a 20 mM, final and mix gently
4. Check pH is 6-7
5. Incubate overnight at 37 °C ¹⁰

¹⁰ Day 3 and 4 can be combined following a shorter tryptic digest at 42 °C. On Day 3 check that the trypsin digestion has gone to completion (step 19).

Day 4: Sample Recovery

1. Add 1.0 M Tris pH 6.8 to 100 mM, final
2. Check that pH is 6-7
3. Incubate at 37 °C for 30 min
4. Pre-wash 10-kDa MWCO Amicon column (0.5 ml centrifugal filters):
 - a) Add 400 µL 100 mM NaOH, centrifuge 10,000 rcf for 10 min and discard flow-through
 - b) Add 400 µL dH₂O, centrifuge 10,000 rcf for 10 min and discard flow-through (repeat 2-3x)
5. Load the peptide-polymer mixture and spin 10,000 rcf for 15 min
6. Collect flow-through and transfer to a clean 1.5 mL tube
7. Repeat steps 5-6 until all peptide-polymer mixture is passed-through the filter
8. Wash filter by adding 200 µL 100 mM Tris pH 6.8
9. Combine all flow-through fractions
10. Refer to STAGE Tip protocol to desalt and store preTAILS and TAILS samples “on tip” prior to LC-MS

B: TANDEM MASS TAG (TMT) LABELING variant strategy

Day 1: Reduction, alkylation and labeling

1. Precipitate 200 µg protein per condition by chloroform-methanol precipitation as above (in 1.5 mL Eppendorf tube)
2. Re-dissolve pellet in 30 µL 6 M GuHCl
3. Add 50 µL nanopure water
4. Add 20 µL 1 M HEPES, pH 8.0 and mix
5. Add TCEP (not DTT or mercaptoethanol as thiols interfere with labeling) from TMT kit to 10 mM, final. If preparing TCEP stock solution in-house check pH after addition. Adjust to pH 8 if necessary.
6. Incubate for 30 min
7. Add iodoacetamide (IAA) to 25 mM, final
8. Incubate at 25 °C in the dark for 30 min

9. Dissolve TMT labels (0.8 mg each) in a volume of DMSO equal to the total reaction mix (~110-115 μ L), so the labeling is performed in 50% v/v DMSO. *This is critical and is different to the protocol suggested by manufactures for peptide labeling. TAILS employs labeling at the protein level.*
10. Add TMT labels to appropriate samples (e.g. 1:1), mix well
11. Incubate at 25 °C in the dark for 1 hour
12. Add 25 μ L 1 M ethanolamine (prepared fresh) and incubate for 30 min to quench unreacted TMT labels
13. Combine samples into a single tube. 6-plex samples fit into a 15 mL tube so aim for this. For 10-plex samples use a 50 mL Falcon tube, which the 2 mg of sample precipitates nicely as a visible pellet ¹⁵
14. Clean up unreacted reagents by acetone precipitation described below
15. Continue from dimethylation protocol Day 2, step 13 for pellet re-solubilization in NaOH and continue from there

¹⁵ For 10 plex you may try avoiding the 50 mL tube and transfer all sample into multiple 1.5 mL Eppendorf tubes after mixing for precipitation and then higher speed centrifugation is possible

¹⁶ *This protocol has been proven effective for 10-plex TMT labeling of 200 μ g sample per channel, for 6-plex TMT an increase in protein amount to 250 μ g per channel may be necessary to achieve as satisfying results (i.e. 1.5 mg total starting protein)*

Acetone/methanol precipitation

1. Add 8 sample volumes of freezer cold acetone and 1 sample volume of freezer cold methanol ¹⁷
2. Mix well by vortexing and let precipitation occur at -80 °C for 2 hours
3. Centrifuge at maximum speed for 15 min
4. Carefully discard supernatant
5. Wash pellet thoroughly with freezer cold methanol. Break up pellet by pipetting gently up and down
6. Centrifuge, repeat wash
7. Let pellet air dry. Do not over-dry pellet since this complicates re-solubilization

¹⁷ *Use chemically resistant tubes (e.g. blue-capped Falcon tubes) for this step to avoid leeching of polymeric compounds and plasticizers into the sample*

¹⁸ *Proper washing of the pellet with methanol is absolutely critical to avoid experimental induced N-terminal acetylation of tryptic peptides by residual acetone. This will compromise efficiency of the HPG polymer pull-out step resulting in carryover of acetylated and blocked tryptic peptides in the TAILS supernatant sample*

Appendix A: Proteome extraction from murine or human tissues

- We recommend using a ULTRA-TURRAX (IKA) high-speed homogenizer for proteome extractions from murine or human tissues. Alternatively a Cell Crusher instrument (<http://cellcrusher.com/>) can be used. Both work well in our hands.
- Choose your favourite extraction buffer. Depending on the type of experiment and tissue we usually use either (i) 100 mM HEPES, 150 mM NaCl, 10 mM EDTA, 1x HALT inhibitor cocktail, (ii) T-PER Tissue Protein Extraction Buffer (Pierce), or (iii) 6 M guanidine hydrochloride. These can be used also sequentially, exactly in this order, to prepare soluble proteins first and then the membrane or insoluble protein fractions from the residual.
- Use 10x excess of extraction buffer to tissue weight. For higher extraction yields, perform two cycles with 10-fold excess each (total ratio: 20:1 v/w).
- Centrifuge samples for at least 10 min at >10,000g to pellet cell debris and insoluble proteins. Pool supernatants in blue capped BD Falcon tubes. Discard pellet or use it for subsequent extraction with a different buffer.
- Perform chloroform-methanol Precipitation (as described elsewhere)
 - Keep in mind: Final volume will be 10x protein sample volume
 - Resolubilize protein pellet in 6 M GuHCl. Keep volume as small as possible.
- Determine protein concentration using Bradford Analysis
 - Dilute samples at least 1:10 and make sure to not pipette less than 5 μ L to avoid pipetting and dilution errors.
 - Use the appropriate amount of proteome for your TAILS analysis.