

S-Trap™ Universal Sample Prep Mini Kit



The ProtiFi™ **S-Trap™** technology combines robust Sodium Dodecyl Sulfate (SDS) solubilization of biological samples and enhanced contaminant removal for proteomic analysis by mass spectrometry. The **S-Trap™ Universal Sample Prep Mini Kit** provides all the solutions for the solubilization, reduction, alkylation, and digestion of 80 samples containing **100 µg - 300 µg of total protein**. The kit fully removes a broad range of contaminants incompatible with downstream proteomics analysis, such as detergents, salts, buffers, stabilizers, excipients, and others, while yielding high peptide recovery.

Additional Reagents/Solutions (Not Included)

Liquid Chromatography-Mass Spectrometry (LC-MS) grade is recommended, where applicable

- Protein sample (**100 µg - 300 µg of total protein**)
- Protease of choice (e.g. Trypsin; 1 µg per 10 µg sample)*
- LC-MS grade Water
- LC-MS grade Methanol (MeOH)
- LC-MS grade Acetonitrile (ACN)
- LC-MS grade Formic Acid (FA)
- Benzonase® (optional)*

* **Benzonase® and proteases are susceptible to freeze-thaw cycles.**

Equipment/Materials (Not Included)

- Single channel pipettes (P2 through P1000) and corresponding tips
- 1.7 mL sample tubes (optional)
- Benchtop centrifuge
- Vortex mixer
- Heat block (adjusted to 55 °C)
- pH paper (pH < 1, optional)
- Water bath or humidified incubator (adjusted to 47 °C)
- Lyophilizer or SpeedVac
- Positive pressure apparatus or vacuum manifold (optional)
- Sonicator (optional, recommended)

Contents: (80) S-Trap™ Mini Spin Columns

①	Solution 1	2x Lysis Solution	2 x 1.5 mL	10% (w/v) SDS, 100 mM TEAB in LC-MS grade Water, pH 7.55
②	Solution 2	Reductant	1 x 200 µL	120 mM TCEP in LC-MS grade Water
③	Solution 3	Alkylator	1 x 200 µL	500 mM MMTS in LC-MS grade IPA (mass shift is + 45.988, addition of SCH ₂)
④	Solution 4	Acidifier	1 x 550 µL	12.0% (v/v) Phosphoric Acid in LC-MS grade Water*
⑤	Solution 5	Binding/Wash Solution	4 x 3.0 mL (30.0 mL bottles)	100 mM TEAB (final) in 90% LC-MS grade MeOH, pH 7.5 Note: 27.0 mL LC-MS grade MeOH must be added to each bottle before use
⑥	Solution 6	Digestion Solution	1 x 28.5 mL	50 mM TEAB in LC-MS grade Water, pH 8.0
⑦	Solution 7	Elution Solution	1 x 9.75 mL	0.2% (v/v) LC-MS grade FA in LC-MS grade Water

All provided solutions, including Binding/Wash Solution with MeOH added, can be stored 1 month at 4 °C or up to 1 year at -20 °C. After thawing, mix thoroughly to ensure any precipitants are redissolved.

* **Acidifier must be stored tightly capped; it will degrade upon atmospheric exposure.**

IPA = isopropyl alcohol, MMTS = methyl methanethiosulfonate, RT = room temperature (20-25 °C), TCEP = (tris(2-carboxyethyl)phosphine), TEAB = triethylammonium bicarbonate, v/v = volume-to-volume ratio, w/v = weight-to-volume ratio, w/w = weight-to-weight ratio

Protocol:

Refer to Appendices for Sample-Specific Considerations, Alternative Proteases, and Troubleshooting Tips.

- ① 1. **Denature Protein.** To 23.0 µL of liquid sample, add 23.0 µL of **Solution 1 (2x Lysis Solution)**. For solid samples, dilute **Solution 1 (2x Lysis Solution)** to 1x by adding an equal volume of LC-MS grade water. Add 46.0 µL of 1x Solution 1 to a solid sample. Sonicate or vortex to fully solubilize and denature proteins.
2. If sample is viscous due to the presence of DNA, shear it thoroughly by probe sonication or enzymatically with a nuclease such as Benzonase™ (see Appendix D). Unsheared DNA will clog the protein trap.
3. Clarify sample as desired by centrifugation (e.g. 13,000 x g for 8 minutes). Transfer clarified lysate to tubes. Pellet can be analyzed separately (see Appendix D).
- ② 4. **Reduce.** Add 2.0 µL of **Solution 2 (Reductant)**. Vortex briefly and incubate at 55 °C for 15 minutes.
- ③ 5. **Alkylate.** Add 2.0 µL of **Solution 3 (Alkylator)**. Vortex briefly and incubate at RT for 10 minutes.
- ⑤ 6. While the sample is incubating, add 27.0 mL of LC-MS grade MeOH to a bottle of **Solution 5 (Binding/Wash Solution)**. Mix thoroughly.
- ④ 7. **Acidify.** Add 5.0 µL of **Solution 4 (Acidifier)** to the sample. Vortex briefly. pH paper can be used to ensure pH ≤ 1. Proceed to the next step immediately.
- ⑤ 8. Add 350 µL of **Solution 5 (Binding/Wash Solution) with MeOH added** to the sample. Mix thoroughly.
Note: The sample may appear translucent at this step due to colloidal protein formation. Do NOT centrifuge.
9. Transfer the entire sample, including any insoluble material, to the top of a **S-Trap™ Mini Spin Column** positioned in a 2.0 mL tube for waste flow-through.
Note: The column reservoir can hold ~600 µL of solution. For larger volumes, the column can be loaded multiple times with the solution from Step 8. When transferring into the column, do not disturb the matrix.
10. **Trap Protein.** Centrifuge the **S-Trap™ Mini Spin Column** and waste flow-through tube at 10,000 x g for 30 seconds. Visually confirm that all solution passed through the column. If not, centrifuge again until no liquid remains. If the solution still hasn't passed through, the column may be centrifuged as high as 15,000 x g until all solution passed through. Discard flow-through and return the column to the 2.0 mL tube.
Note: The S-Trap™ Mini Spin Columns end in a Luer taper. A vacuum manifold or positive pressure can be used to draw solution through the column.
- ⑤ 11. **Clean Protein.** Add 400 µL of **Solution 5 (Binding/Wash Solution) with MeOH added** to the **S-Trap™ Mini Spin Column** and centrifuge at 10,000 x g for 30 seconds. Visually confirm that all solution passed through the column. Repeat washes 3 times; discard flow-through as necessary. Return the column to the 2.0 mL tube.
Note: For best results, rotate the column 180° between centrifugations. Marking the outside edge of the column makes it easier to track rotations.
12. Centrifuge the **S-Trap™ Mini Spin Column** at 10,000 x g for 1 minute to fully remove all Binding/Wash Solution.
13. Transfer the protein-containing **S-Trap™ Mini Spin Column** to the clean 2.0 mL tube provided for digestion.
- ⑥ 14. Dilute trypsin in **Solution 6 (Digestion Solution)** to a final volume of 125 µL, ensuring that the amount of trypsin in this solution is at a 1:10 (w/w) ratio with the total amount of protein in the sample (e.g. 10 µg per 100 µg of sample).
15. Transfer the entire 125 µL of trypsin solution to the **S-Trap™ Mini Spin Column**. The matrix is hydrophilic and will absorb the solution; no centrifugation is necessary.
Note: If bubbles are present, flick the tube gently to remove them and/or spin the column very briefly using a benchtop centrifuge. If any solution flows through, pipette it back on top of the column.
16. **Incubate & Digest.** Loosely snap the cap on the **S-Trap™ Mini Spin Column** to limit evaporative loss so that trypsin solution is not pushed through the column due to thermal expansion; allow air to escape. Pipette any solution that passes through back on top of the column. Place the column and tube in a 47 °C water bath or humidified incubator for 2 hours. If using a water bath, make sure the column matrix sits below the water level to ensure even heating.
- ⑥ 17. **Elute 1.** Remove the **S-Trap™ Mini Spin Column** and tube from the incubator and add 80.0 µL of **Solution 6 (Digestion Solution)** to the top of the column. Centrifuge at 10,000 x g for 1 minute.
- ⑦ 18. **Elute 2.** Add 80.0 µL of **Solution 7 (Elution Solution)** to the top of the **S-Trap™ Mini Spin Column**. Centrifuge at 10,000 x g for 1 minute.
19. **Elute 3.** If hydrophobic peptides are of interest, add 80.0 µL of 50% (v/v) LC-MS grade ACN in 0.2% (v/v) LC-MS grade FA (solution not provided) to the top of the **S-Trap™ Mini Spin Column**. Centrifuge at 10,000 x g for 1 minute.
20. Lyophilize or SpeedVac eluted peptides collected from Steps 17-19 in the 2.0 mL tube. Resuspend as needed for subsequent analysis (e.g. Aqueous Buffer A such as 5% ACN, 0.1% FA).