PREOMICS

iST-NHS 96x HT

P.O.00151; P.O.00191

Pelleted cells & precipitated protein

Introduction

Sample preparation is one of the essential steps of bottom-up proteomics. The PreOmics® iST sample preparation kit is designed to assist researchers achieving best results with few sample preparation steps and little hands-on time. For sample-specific protocols and optimization visit www.preomics.com/resources or contact info@preomics.com.

Kit Contents

The kit includes all essential components for proteomic sample preparation: denaturing, reducing, and alkylating agents, enzymes, cartridges, and wash buffers for peptide clean-up.

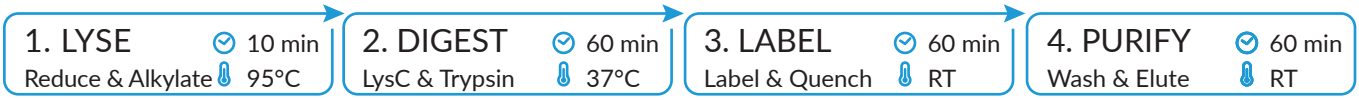
Component	Cap	Quantity	Buffer Properties				Description	Storage
			Organic	Acidic	Basic	Volatile		
DIGEST		24x					Trypsin/LysC mix to digest proteins.	-20°C
RESUSPEND		1x 20 mL				●	Reconstitutes lyophilized proteolytic enzymes.	RT
LYSE-NHS		1x 20 mL			●		Denatures, reduces, and alkylates proteins.	RT
STOP		1x 15 mL	●	●		●	Stops the enzymatic activity.	RT
WASH 1		1x 25 mL	●	●		●	Cleans peptides from hydrophobic contaminants.	RT
WASH 2		1x 25 mL		●		●	Cleans peptides from hydrophilic contaminants.	RT
ELUTE		1x 25 mL	●		●	●	Elutes the peptides from the cartridge.	RT
LC-LOAD		1x 25 mL		●		●	Loads peptides on reversed-phase LC-MS column.	RT
CARTRIDGE		96x					Cartridge for 1–100 µg protein starting material.	RT
WASTE PLATE		1x					Deep well plate for collecting waste after washes.	RT
MTP PLATE		1x					LoBind plate for collecting peptides after elution.	RT
ADAPTER PLATE		1x					Enables cartridges to be placed on top of 96w plates.	RT
ADAPTER		8x					Enables a cartridge to be placed into a tube.	RT

Pre-Requisites

Common lab equipment is required for the sample preparation.

Equipment	Quantity and Description
PIPETTE	Careful sample handling and pipetting reduces contaminations and improves quantification.
SAMPLE	Pelleted cells or precipitated protein. For other sample types contact PreOmics for adapted protocols.
96 WELL PLATES	96 deep well & 96 well skirted plates to balance WASTE & MTP PLATES in centrifuge.
HEATING BLOCK	Two MTP plate heaters are recommended to support protein denaturation and digestion.
CENTRIFUGE	Swing-bucket centrifuges are required for loading, washing, and elution.
SONICATOR	If the sample contains DNA, shear it by sonication (e.g., Diagenode Bioruptor®).
VACUUM EVAPORATOR	Vacuum manifolds evaporate volatile buffers from the eluate before LC-MS.
ULTRASONIC BATH	Optional: can be used to resuspend peptides.
LABELING REAGENT	Labeling reagent (e.g., 400 µg labeling reagent in 41 µL dry acetonitrile for 100 µg peptides).
LABELING BUFFER	Anhydrous acetonitrile & quenching buffer (5% hydroxylamine), as recommended by the manufacturer.

Procedure



Method

1. LYSE *Critical Note*

1.1. Add 50 µL **LYSE-NHS** to 1–100 µg of protein sample, place it in a HEATING BLOCK (95°C; 1,000 rpm; 10 min).*NOTE1*

1.2. Optional: Spin down droplets (RT; max. 300 rcf; 10 sec).

1.3. If the sample contains DNA, shear it in a SONICATOR (10 cycles; 30 sec ON/OFF). Let sample cool down to RT.

2. DIGEST

2.1. Add 210 µL **RESUSPEND** to **DIGEST** (1 tube for 4 reactions), shake (RT; 500 rpm; 10 min), pipette up/down.

2.2. Add 50 µL **DIGEST** to sample and place it in a pre-heated HEATING BLOCK (37°C; 500 rpm; 1–3 h). *NOTE2*

3. LABEL

3.1. Resuspend LABELING REAGENT in anhydrous acetonitrile (e.g., 4:1 ratio of label:peptides).

3.2. Add resuspended LABELING REAGENT to sample, pipette up/down, incubate shaking (RT; 500 rpm; 1 h).

3.3. Add 10 µL QUENCHING BUFFER (5% hydroxylamine) to sample, pipette up/down.

3.4. Add 100 µL **STOP** to sample (precipitation may occur), shake (RT; 500 rpm; 1 min), pipette up/down. *SP*

4. PURIFY

4.1. Use **ADAPTER PLATE** to place **CARTRIDGE** on top of **WASTE PLATE**. Label plate and wells.

4.2. Transfer sample to **CARTRIDGE**. Be careful not to damage the bottom layer of the **CARTRIDGE**.

4.3. Spin **CARTRIDGE** in a CENTRIFUGE (2,250 rcf; 1–3 min). If needed, adjust time to ensure complete flow-through.

4.4. Add 200 µL **WASH 1** to **CARTRIDGE**, repeat step 4.3.

4.5. Add 200 µL **WASH 2** to **CARTRIDGE**, repeat step 4.3. *SP*

4.6. Use **ADAPTER PLATE** to place **CARTRIDGE** on top of the **MTP PLATE**. Label plate and wells.

4.7. Add 100 µL **ELUTE** to **CARTRIDGE**, repeat step 4.3., keep flow-through in **MTP PLATE**.

4.8. Repeat step 4.7, keep flow-through in the same **MTP PLATE**.

4.9. Discard **CARTRIDGE** and place **MTP PLATE** in a vacuum evaporator (45°C; until completely dry). *SP*

4.10. Reconstitute peptides by adding **LC-LOAD** to **MTP PLATE**. For example, add 50 µL LC-LOAD to 100 µg protein starting material and perform a peptide quantitation assay. Adjust the volume according to specific requirements.

4.11. Sonicate **MTP PLATE** in an ULTRASONIC BATH (5 min) or shake (RT; 500 rpm; 5 min).

4.12. Spin **MTP PLATE** in a CENTRIFUGE (RT; 2,250 rcf; 15 min) and transfer the supernatant to a fresh autosample vial Be careful not to collect from the bottom. *NOTE3*

Critical Note	For automation processes, only use Protein LoBind plates as buffer reservoirs to avoid polymer contamination. Contact us at info@preomics.com for advice on buffer and plasticware usage on liquid handling platforms.
NOTE1	Volumes of buffers can be adjusted according to protein starting amounts. Lysis temperature should be between 60–95°C. Visit our FAQ website for more information and optimized procedures for chemical labeling: www.preomics.com/faq.
NOTE2	During the digestion, place the silicone mat lightly on top of the CARTRIDGE. Do not close the silicone mat tightly to prevent pressure buildup.
NOTE3	At this point, peptide concentration can be measured or directly injected for LC-MS analysis.
SP - Storage Point:	At this point, close the peptide containing tube or CARTRIDGE using the silicon mat. Peptides can be frozen at -20°C. Storage of peptides should not exceed two weeks at -20°C. For extended storage, finish the protocol and store at -80°C.

Data analysis

Consider the following as fixed modifications in your database search:

MODIFICATION	DESCRIPTION	COMPOSITION	SPECIFICITY	MASS
ALKYLATION	Specific cysteine modification	$C_6H_{11}NO$	[C]	+113.084Da