Frequently asked questions (FAQs) - Version 1.1
iST Sample Preparation Technology

PREOMICS

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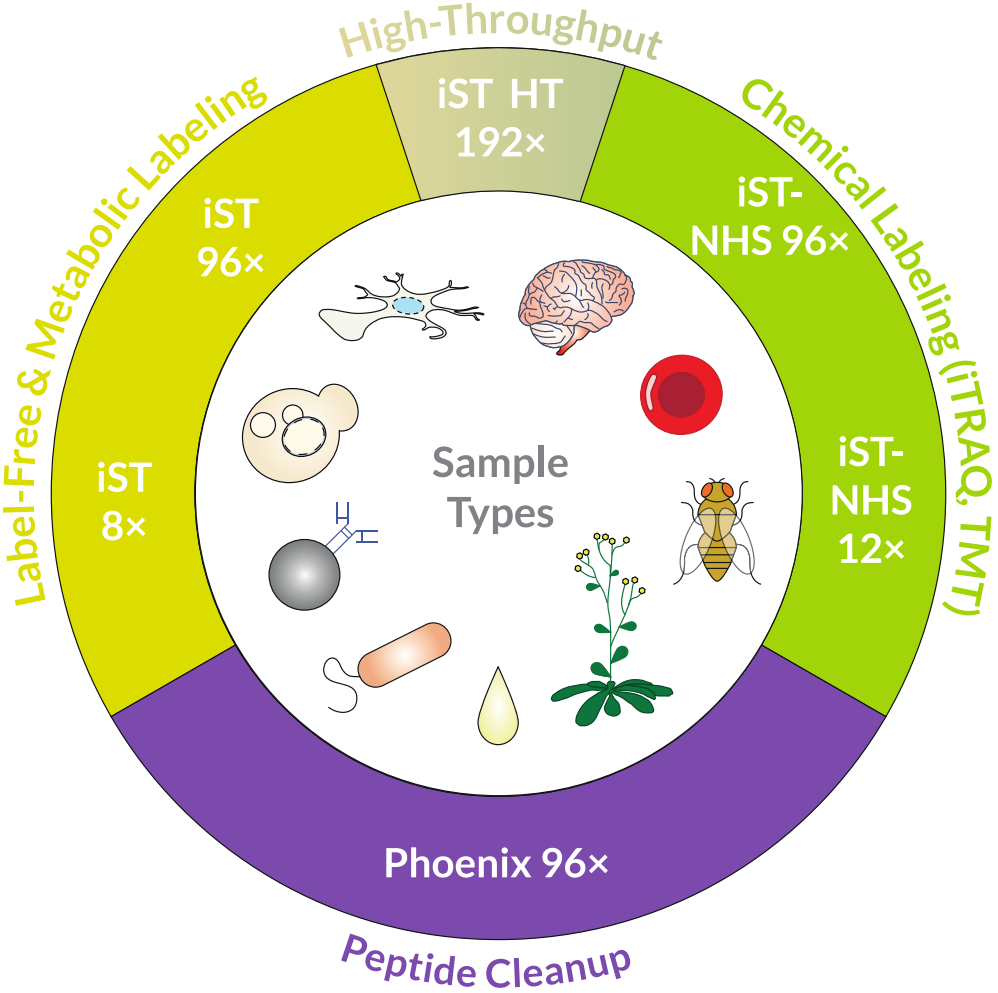
INTRODUCTION

Complex sample preparation workflows, extensive fractionation and proteolytic digestion are highly time consuming and restrict the overall technical reproducibility. PreOmics addresses these limitations and our iST technologies enable a robust and reproducible sample preparation with a significant time advantage compared to other commonly employed methods, which is essential for reliable and informative results.

The iST kits are compatible with label-free and metabolic labeling (e.g. SILAC). The iST-NHS kits are compatible with chemical labeling (e.g. iTRAQ™ or TMT™). Both, the iST and iST-NHS kits are complete sample preparation kits to process whole cells, tissues, body fluids, precipitated proteins and other sample types.
The PHOENIX kit is a specialized SPE (solid phase extraction) peptide cleanup kit and the input material is a solution containing peptides. The PHOENIX offers an easy-to-use solution to clean up peptide mixtures and efficiently remove detergents, polymers, salts, lipids and more for reliable LC-MS analyses.



FREQUENTLY ASKED QUESTIONS

1. SAMPLE PREPARATION

1.1 *Is my own lysis buffer compatible with the iST / iST-NHS kits?*

We strongly advise to use the LYSE or LYSE-NHS buffers provided with the iST or iST-NHS kits, respectively. If you want to use your own lysis buffer, the efficiency of cell lysis and thus protein identifications are likely adversely impacted. Please refer to the following table or contact us (info@preomics.com) to discuss the compatibility of your lysis buffer with the iST technology:

own lysis buffer	iST / iST-NHS compatible?	max. vol. own lysis buffer	remarks
PBS	yes	25 µL	dilute with 25 µL 2X concentrated LYSE / LYSE-NHS
RIPA (max. 0.1% SDS, 1% SDC, 1% Triton x-100)	yes	25 µL	dilute with 25 µL 2X concentrated LYSE / LYSE-NHS
urea (max. 2M; no thiourea)	yes	25 µL	dilute with 25 µL 2X concentrated LYSE / LYSE-NHS
thiourea	no	-	*perform protein precipitation*
high salt (e.g. >0.5M NaCl)	no	-	*perform protein precipitation*

1.2 *What is the maximum starting volume of my sample to be processed with the iST / iST-NHS kits?*

Your sample volume (liquid or solid, e.g. cell pellets) should not exceed 10 µL when combined with our LYSE / LYSE-NHS buffers. For sample volumes between 11-25 µL, use of our 2-fold concentrated lysis buffers (2X LYSE, 2X LYSE-NHS), which can be purchased upon request. The 2X lysis buffers are mixed 1:1 with samples ranging from 11-25 µL, e.g. 11 µL sample + 11 µL 2X LYSE, all downstream buffer volumes stay the same.

If your sample volume exceeds 25 µL, perform protein precipitation before processing with the standard iST or iST-NHS workflows.

1.3 *How do I perform protein precipitation?*

Several different protocols for protein precipitation exist. We recommend acetone precipitation:

1. Transfer protein lysate (not more than 300 µL) to a clean 2 mL microcentrifuge tube.
   > in case you have a larger sample volume, use either a 5 or 15 mL tube
2. Add ice-cold acetone (-20°C) to your sample
   > add at least 4-fold more acetone than sample, e.g. 300 µL sample + 1.2 mL acetone
3. Mix briefly
4. Incubate for one hour at -20°C
5. Spin in table-top centrifuge at 4°C for 15 min at 13,000 rpm
6. Carefully discard supernatant, make sure not to disturb the pellet
7. Air-dry the pellet for 5-10 min
8. Continue with PreOmics iST protocol: add 50 µL LYSE buffer, follow the iST protocol from here on
   > you can also freeze the pellet after air-drying at -20°C or -80°C until further use

1.4 *Can I add protease inhibitors to my sample?*
Although protease inhibitors are in general compatible with our iST protocols, we recommend not to add additional exogeneous proteins in order to not contaminate your sample.

1.5 *Can I use mechanical force disruption in combination with the iST / iST-NHS kits?*
For samples such as cells, yeast or tissue material, performing mechanical force disruption in LYSE or LYSE-NHS buffers will improve lysis efficiency. Many different mechanical force methods can be employed such as traditional bead milling, liquid nitrogen grinding, or commerical systems from various vendors (e.g. Bertin Instruments, Covaris, Hielscher, MP Biomedicals). We recommend the Bioruptor® Pico system (Diagenode), that allows direct placement of our CARTRIDGES.
Samples such as body fluids do not require additional mechnical force disruption.

1.6 *What are the minimum and maximum protein amounts for the iST / iST-NHS kits?*
Highly reproducible results are achieved with protein starting amounts ranging from 1 µg to 100 µg. For low input information please see 1.9.

1.7 *What is the maximum volume I can load on the PreOmics CARTRIDGES?*
The maximum volume is 250 µL.

1.8 *Which protein quantification methods are compatible with the iST / iST-NHS Kits?*
Most classical assays are compatible with our LYSE and LYSE-NHS buffers. We recommend the BCA assay or the tryptophan quantification method. Some assays require dilution with distilled water to achieve the best results:

BCA: none	microBCA: 1:100 with PBS	Bradford: 1:4
Coomassie: 1:20	Lowry: 1:4	Tryptophan: none

1.9 *Shall I adjust the buffer volumes depending on the protein starting amounts?*
For 20 µg protein starting material or less, add 10 µL LYSE and 10 µL DIGEST to your sample, keep all other buffers as indicated in the protocol. Accordingly, you may adjust the volumes for chemical labeling and quenching as recommended by the label manufacturer.

1.10 *Which lysis temperature shall I use?*
Perform the lysis/denaturation step at 95°C. Use lower temperatures only for temperature-sensitive samples such as immunoprecipitations. We have tested lower temperatures down to 60°C and do not see any differences in parameters assessed (e.g. IDs, alkylation rates).

1.11 *Can I use other enzymes for the protein digestion?*
The iST and iST-NHS kits come with a lyophilized enzyme mix consisting of LysC and trypsin. We plan to develop solutions for other enzymes in future products.

1.12 *How long shall I digest my samples?*
The digestion depends on your sample type and input material (see table below). Please note our recommendations to lower the enzyme amount for low input samples (<20 µg protein starting material, see 1.10).

Sample Type	Digestion Time
Precipitated proteins	1-3 hrs
Cell lines	1-3 hrs
Body fluids	1-3 hrs
Tissues (mammalian, plants)	3 hrs

Although not recommended, you can also digest your samples overnight (~18 hours). While this will reduce the missed cleavage rate even further, it will come at the cost of higher unspecific cleavages and much longer processing time of the overall workflow.

1.13 *Are the iST / iST-NHS workflows compatible with enrichment of phosphorylation sites?*
While our protocols are in general compatible with IP samples (modified protocols can be found to download on our website), the required input amounts for global phosphorylation enrichment experiments (~500 µg) usually exceed the peptide binding capacity of our CARTRIDGES. We plan to develop CARTRIDGES with higher binding capacities for applications with post-translational modifications.

1.14 *How can I automate my sample processing efforts?*
We are collaborating with many different providers of liquid handling systems to offer the best automation solutions for your needs. For platform-specific protocols and more information on either semi- or full-automation please contact us at info@preomics.com.

1.15 *Are the PreOmics kits compatible with absolute quantification?*
All of our kits (iST, iST-NHS, Phoenix) are compatible with absolute quantification strategies. For absolute quantification employing isotopically-labeled protein standards with our iST and iST-NHS kits, please add the respective absolute standard (e.g. DIGESTIF, PSAQ, SILAC-PrEST) together with your sample to the LYSE or LYSE-NHS buffer and proceed with the protocol accordingly.
For absolute quantification employing isotopically-labeled peptide standards with either the iST, iST-NHS or Phoenix kits, please introduce the respective standard (e.g. AQUA, QconCAT) before adding the STOP buffer to your samples.

1.16 *How do I assess the peptide recovery rate after the whole sample processing workflow?*
The best way to assess peptide recovery rates is by employing absolute quantification strategies (see 1.15). Our peptide recovery is >80% over a range of 1 - 100 µg protein starting material.

1.17 *Which kind of quality control does PreOmics provide for the kits?*
We perform strict QC measures for every buffer, kit and enzyme batch produced. Such measures include incoming goods control, polymer leaching tests for plasticware, LC/MS-based quality control for parameters including alkylation rate or missed cleavages on a standardized sample, and more. Upon request, PreOmics can provide certficate of analysis (CoA) to our clients.

1.18 *What are the differences between the 4x, 8x, 12x, 96x and 192x PreOmics` kits?*
Our kits are provided in pack sizes according to the number of samples that can be processed:

iST kits
◦ 4 reaction: test kits for first time users
◦ 8 reactions: small kits for initial experiments
◦ 96 reactions: medium kits with flexibility to process either up to 96 samples at once or multiple smaller batches, as all buffers and enzymes come aliquoted in 2 mL tubes
◦ 192 reactions: large kit suitable for liquid handling platforms, all buffers come in 20 mL vials for convenient transfer into liquid handling reservoirs

iST-NHS kits
◦ 4 reaction: test kits for first time users
◦ 12 reactions: small kits for initial experiments
◦ 96 reactions: medium kits with flexibility to process either up to 96 samples at once or multiple smaller batches, as all buffers and enzymes come aliquoted in 2 mL tubes
◦ 192 reactions: large kit suitable for liquid handling platforms, all buffers come in 20 mL vials for convenient transfer into liquid handling reservoirs

Phoenix kits
◦ 4 reaction: test kits for first time users
◦ 96 reactions: medium kits with flexibility to process either up to 96 samples at once or multiple smaller batches, as all buffers come aliquoted in 2 mL tubes

kit variant	buffer volumes provided	4 rxn	8 rxn	12 rxn	96 rxn	192 rxn
iST	in 2 mL tubes	yes	yes	-	yes	-
iST	in 20 mL vials	-	-	-	-	yes
iST-NHS	in 2 mL tubes	yes	-	yes	yes	yes
iST-NHS	in 20 mL vials	-	-	-	-	-
Phoenix	in 20 mL tubes	yes	-	-	yes	-

1.19 *Are the PreOmics kits copatible with peptide fractionation?*
Yes, all our kits are compatible with downstream peptide fractionation workflows. After peptides are dried completely in a vacuum concentrator, resuspend the peptides either in LC-LOAD or a resuspension buffer of your choice as input buffer for further peptide fractionation methods. PreOmics is also developing solutions for our own peptide fractionation workflows.

2. SAMPLE TYPE RECOMMENDATIONS

2.1 *How much raw material do I need for the iST / iST-NHS kits?*

Protein content varies considerably across distinct biological input material (e.g. different cell lines, strains, tissues, tissue regions, body fluids) and sample storage conditions (e.g. different storage temperatures, storage time, repeated freeze-thaw cycles, fresh frozen vs. FFPE, formaldehyde treatment). Hence, we advise to quantify protein concentration of your sample after the lysis (see 1.9). As a rule of thumb, a short overview of raw material amounts is given in the table below.
We do have a database with processing recommendations for >100 species and various sample types. Please contact us at info@preomics for further details on your specific sample of interest.

Material	Starting Amount	Protein Amount
Mammalian Cell Line (e.g. HeLa)	6E5 cells	100 µg
Yeast (*S.cerevisae*)	OD_{600} = 0.6	100 µg
Bacteria (*E.coli*)	OD_{600} = 0.5	100 µg
Immunoprecipitation	1 mL slurry	10 - 400 µg
Blood / Serum / Plasma (*H.sapiens*)	2 µL	100 µg
Mammalian Tissue	1 mm^3	100 µg
Plant Tissue (*A.thaliana*): shoot/root wet weight	50 mg / 100 mg	100 µg / 100 µg

2.2 *How do I process non-depleted plasma/serum samples?*

Non-depleted human plasma and serum have a high protein concentration, commonly around 50µg/µL. For processing of non-depleted plasma/serum, mix up to 2 µL plasma/serum with 50 µL LYSE/LYSE-NHS buffer and continue with the regular iST/iST-NHS protocol.

2.3 *How do I process depleted plasma/serum samples?*

Depending on the depletion process used, the resulting depleted plasma/serum sample may contain high concentration of salts and/or have a large volume, making the samples incompatible for direct processing with our iST/iST-NHS kits. We suggest performing protein precipitation (see 1.3) and using the resulting pellet as input material for our regular iST/iST-NHS protocol.

2.4 *How do I process CSF samples?*

CSF has a wide concentration range, we advise to perform a protein quantification assay to determine the concentration (see 1.8). For highly concentrated CSF samples, follow the recommendations for non-depleted plasma/serum (see 2.1) For diluted CSF samples (volume larger than 25 µL), perform protein precipitation (see 1.3) and continue with the regular iST/iST-NHS protocol.

2.5 *How do I process urine samples?*

Protein concentrations in urine samples vary substantially, we suggest either concentrating or precipitating the protein (see 1.3) before processing with the iST kits. As a rule of thumb, 10-100 mL human urine corresponds to ~100 µg protein, which needs to be concentrated down to 100 µL. Specifically for urine preparations, PreOmics provides an extra WASH0 buffer to effectively remove bilirubin contaminations: https://preomics.com/resources/protocols/PreOmics_iST_SamplePrepKit_Protocol_InD_Cartridge_8x_Urine_v3_1.pdf

2.6 *How do I process saliva samples?*

Protein concentrations in saliva samples vary substantially, a rough estimate is about 10 µg/µL. Either collect ~10 µL saliva by spitting into a microcentrifuge tube or perform mouth swab and place the swap in 50-100 µL LYSE / LYSE-NHS buffer to fully cover the swap. Keep all other buffer volumes as indicated in the regular protocols.

2.7 *How do I process adherent cell culture samples?*

If extracellular matrix or transmembrane proteins are not of interest, you can use cell culture-grade trypsin to detach the adherent cells, wash them once with PBS and then store the cell pellet fraction as input for our regular protocols. Alternatively, if extracellular matrix or transmembrane are of interest and affected by partial trypsin digestion, add 50-100 µL of our LYSE / LYSE-NHS buffer directly to the cells and scrape them off using a rubber policeman. Collect the scraped material and heat to 95°C for 10 min before continuing with the regular iST / iST-NHS protocol.

2.8 *How do I process mammalian tissue samples?*

Mammalian tissue samples are more difficult to lyse and require some kind of mechanical force disruption in the presence of our LYSE or LYSE-NHS buffers (see 1.5). Addition of glass beads in combination with ultrasonication enhances the efficiency of tissue homogenization and cell lysis (https://preomics.com/resources/application-notes/PreOmics_ApplicationNote_Tissue_final.pdf).

2.9 *How do I process FFPE samples?*

Processing of FFPE samples requires de-paraffinization of the FFPE punches/slides. In addition, de-paraffinized samples require a longer heat treatment for efficient de-crosslinking: increase the initial heating step from 10 to 60 min at 95°C. More details can be found here: https://preomics.com/resources/protocols/PreOmics_iST_SamplePrepKit_Protocol_InD_Cartridge_8x_FFPE_v3_2.pdf

2.10 *How do I process plant tissue samples?*

Plant tissues can be processed with our iST and iST-NHS kits but require cryogenic grinding or other means of mechanical force disruption initially. Specifically for plant preparations, PreOmics provides an extra WASH0 buffer to effectively remove secondary metabolite contaminations: https://preomics.com/resources/protocols/PreOmics_iST_SamplePrepKit_Protocol_InD_Cartridge_8x_Plants_v1_1.pdf

2.11 *How do I process immunoprecipitation samples?*

Enrichment of proteins via IP or coIP strategies is compatible with our iST and iST-NHS technologies. Depending on the type of bead material used, the sample transfer to our cartridges happens either directly after the IP (transfer of proteins; magnetic beads) or after the digestion (transfer of peptides; Agarose beads). For further information, please have a look at our two workflow recommendations:
https://preomics.com/resources/protocols/PreOmics_iST_SamplePrepKit_Protocol_InD_Cartridge_8x_IPs_Agarose_v3_1.pdf
https://preomics.com/resources/protocols/PreOmics_iST_SamplePrepKit_Protocol_InD_Cartridge_8x_IPs%20Magnetic_v3_1.pdf

2.12 *How do I process bacteria/yeast/algae/diatoms?*

Model organisms can be entirely processed with our iST or iST-NHS kits. We recommend mechanical force disruption in the presence of our lysis buffers to effectively disrupt tissues/lyse cells. For processing of algae and diatoms, our WASH0 buffer removes secondary metabolites (provided upon request).

3. CHEMICAL LABELING (iTRAQ™, TMT™)

3.1 *What is the difference between the iST and the iST-NHS kits?*

The lysis buffer in the iST-NHS kit, called LYSE-NHS, does not contain primary amines and therefore does not interfere with chemical labeling. The LYSE-NHS contains a distinct alkylation agent. Please consider the following as fixed modification in your database search:
Specific cysteine modification ($C_6H_{11}NO$), specificity [C], mass shift +113.084 Da

3.2 *How can I improve the labeling efficiency when performing chemical labeling in combination with the iST-NHS kits?*

Chemical labeling experiments require very high peptide labeling efficiencies (>98%) for proper quantification. When struggling with lower labeling efficiencies, please see the following points:

◦ Make sure that the sample input material (e.g. cell pellet) is not contaminated with residual buffers or cell culture media containing primary amines that interfere with chemical labeling.

◦ Use fresh labeling reagents to achieve the highest labeling efficiency. Resuspended labeling agent, which is not used throughout the experiment, should not be stored longer than two weeks at -20°C. Resuspended labeling reagent will hydrolyze over time leading to lower labeling efficiency.

◦ Use TMT at a label to peptide ratio of 4:1, i.e. 400 µg of TMT label per 100 µg of peptides. Higher ratios will slightly increase the labeling efficiency but commonly reduce peptide identification rates.

◦ Use an acetonitrile (ACN) concentration of at least 30% during the labeling reaction, i.e. 50 µL LYSE + 50 µL DIGEST + 42 µL of labeling reagent in dry ACN. Lower amounts of ACN will quickly hydrolyze the labeling agent. If you have resuspended the labeling reagent in a smaller ACN volume, add some dry ACN to the solution in order to achieve a final concentration of 30% ACN. Take the volume of the cell pellet and residual buffer/cell culture media into account for the final ACN concentration.

3.3 *Shall I perform the chemical labeling step on the cartridge or in the tube?*

Perform the labeling in an 1.5 mL microreaction tube and only to transfer the labeled peptides to our CARTRIDGES for the final peptide cleanup.

3.4 *When shall I mix channels after the chemical labeling?*

There are two options for channel mixing:
A. Perform workflow until addition of STOP buffer, then mix channels accordingly. The pooled sample can be split equally on different CARTRIDGES (binding capacity of 100 µg per CARTRIDGE).
B. Perform workflow until end of vacuum concentrator step. Resuspend individual channels in LC-LOAD and then pool channels accordingly.
We advise to measure the peptide concentration of each channel for optimal channel pooling results.

4. PEPTIDE CLEANUP

4.1 *Which sample types require additional wash steps?*

Most peptide samples can be cleaned up with the washing buffers presented in the iST / iST-NHS kits. However, for certain samples such as urine or plant tissues, our regular iST or iST-NHS protocols can be extended with one additional washing buffer called "WASH0" to remove metabolites. For cleaning up peptide samples with stronger sources of contamination, e.g. sugars, fat, polymers or high concentrations of detergents, we recommend to use our PHOENIX peptide cleanup kit instead that features yet another washing buffer called "WASHX".

4.2 *What are the differences between the PreOmics washing buffers?*

Washing Buffer	Organic	Acidic	Basic	Volatile	for which samples?
WASH0	yes	yes		yes	urine, plants
WASHX	yes	yes		yes	lipids, polymers, detergents
WASH1	yes	yes		yes	hydrophobic contaminations
WASH2		yes		yes	hydrophilic contaminations

4.3 *How do I elute my samples from the 96-well CARTRIDGE adapter plates?*

You can either stack the 96-well CARTRIDGE adapter plate on top of the provided collection plate, or you can stack it on top of standardized autosampler vials.

4.4 *How long do I need to concentrate my samples in the vacuum concentrator?*

Concentrate at 45°C until the sample is dry and no residual ELUTE buffer is left. This usually takes about 30 min. Depending on your sample, peptide ions might accumulate at the top layer and thus interfere with efficient evaporation. To overcome this, tap the sample briefly to mix the eluate and then continue to concentrate in the vacuum concentrator.

4.5 *Can I concentrate iST / iST-NHS eluates together with samples eluted from C18 columns in the same vacuum concentrator?*

Since our ELUTE buffer has a basic pH and C18 eluates have an acidic pH, do **not** place them in the same vacuum concentrator as this can damage the instrument.

4.6 *Which peptide quantification methods can I use after processing my samples?*

Peptide quantification should be done in our LC-LOAD buffer and not in the ELUTE buffer. We recommend quantitative colorimetric peptide assays.

4.7 *How can I resuspend dried peptides in the 96-well plate?*

After the vacuum concentrator step, you can add our LC-LOAD buffer to each well and shake in a horizontal plate shaker (500 rpm, 5 min).

4.8 *How shall I store resuspended peptide samples after processing them?*

Storage of peptides should not exceed two weeks at -20°C. For long-term storage, keep them at -80°C.

5. PHOENIX KITS

5.1 *Are the CARTRIDGES from the iST / iST-NHS and the PHOENIX kits the same?*
CARTRIDGES in the iST and iST-NHS kits are the same. CARTRIDGES in the PHOENIX kit are of different nature and have a slightly lower affinity for hydrophobic species.

5.2 *How do I load my peptide samples on the PHOENIX CARTRIDGES?*
It is essential to acidify the peptides, otherwise your sample will not bind to the CARTRIDGE. To do so, mix your peptides 1:1 with the provided STOP buffer and load everything on the CARTRIDGE. Spin at 3,800 rcf for 1-3 min to load the sample completely.

6. PreON PLATFORM

6.1 *What are the pre-installation requirements?*
We offer a full pre-installation requirement documentation upon request. Briefly, the PreON operates at: 100–240 V AC, 50/60 Hz, 650 VA. PreON dimensions are (WxDxH): 65 cm (25.6 in.) x 62 cm (24.4 in.) x 86 cm (34.0 in.) with a weight of 71.5 kg (157.6 lbs).

6.2 *Which sample types can be processed on the PreON?*
The PreON can process protein pellets, intact cells, body fluids and tissue lysates.

6.3 *How many samples can I process on the PreON per day?*
The sample throughput is 12 samples per run with the option to execute multiple runs per day. For iST workflows, up to three runs per day with a total of 36 samples are feasible. For iST-NHS workflows, up to two runs per day with a total of 24 samples are feasible.

6.4 *Can the PreON prepare both label-free and chemical labeling samples?*
Yes, the PreON can execute workflows for both label-free and chemical labeling samples with our ready-to-go iST and iST-NHS kits.

6.5 *Can I run my own methods on the PreON?*
The PreON works seamlessly with our ready-to-go iST and iST-NHS kits. Other methods or commercial products cannot be operated with the PreON.

6.6 *Which kind of maintenance does the PreON require?*
The PreON requires minimal maintenance such as cleaning the surfaces and emptying the solid and liquid waste containers. Once every six months we recommend to perform a tightness test for the pipetting unit (all required utensils provided).

6.7 *How is the PreON serviced?*
Our global and trusted partner PEAK-Service is the leading global provider for technical services for medical, analytical and industrial equipment. Contact us at info@preomics to inquire about further servicing options and pricing.

7. KIT SHIPPING & STORAGE

7.1 *Does PreOmics ship worldwide?*
Yes, we do ship our products worldwide. For the convenience of our US customers, we ship from our warehouse in New Jersey.

7.2 *How do you ship your products and how shall I store them?*
We ship at ambient temperature. Upon arrival, please store the lyophilized enzyme mix (red DIGEST tubes) at -20°C and the rest of the kit at room temperature.

7.3 *Can I freeze whole kits upon arrival?*
No, freezing is detrimental to our buffers. Only the lyophilized enzymes (red DIGEST tubes) in the iST and iST-NHS kits should be frozen upon arrival for long-term storage.

7.4 *How do I store resuspended DIGEST in case I have leftover solution?*
Resuspended DIGEST can be stored at 4°C for up to two weeks. For long-term storage, lyophilize the DIGEST again, lyophilized DIGEST can be stored at -20°C for up to nine months.

7.5 *How long can I store the iST / iST-NHS kits and PHOENIX kits?*
We guarantee a minimum remaining shelf live of three months after receiving our products. Please refer to the shelf life information printed on each kit box for further details.

7.6 *Can I still use kit after the shelf life has expired?*
The performance of our LYSE / LYSE-NHS will drop significantly after the expiration date. Thus, we do not recommend to use our kits after the shelf life has expired.

8. ACCESSORIES

8.1 *What is the Metal Heating Shaker Adapter?*
The Metal Heating Shaker Adapter guarantees optimal heat transfer for our CARTRIDGES compared to planar heating systems. It is compatible with any heating shaker in the SPSS format and many liquid handling platforms. It is also directly compatible with our 96-well CARTRIDGE adapter plates.

8.2 *When purchasing the iST / iST-NHS or PHOENIX 96 reaction kits, do I need to order the 96-well adapter plate too?*
All our kits in the 96 reaction format already contain the 96-well adapter plate required for convenient handling of larger sample numbers.

9. ORDERING

9.1 *How can I order your products?*

Customers from North America please order via PreOmics Inc. (USA), customers from the rest of the world please order via PreOmics GmbH (Germany).

We offer several options to order our products:

- Send an email to: order@preomics.com
- Call us +49-89-2314-163-0
- Fax us +49-89-2314-163-99
- Visit our webshop at www.preomics.com/products

9.2 *How does the PreOmics webshop work?*

1. Go to www.preomics.com/products
2. Select your products of choice and add them to your shopping cart
3. Select your delivery and billing address
4. Shipping costs and taxes will be added during the checkout procedure
5. Pay by credit card or PayPal

9.3 *Is it possible to order individual items from your kits?*

We provide complete solutions to ensure best results for your LC-MS/MS analyses. Adaptions to our lysis buffers might be necessary though for specific experimental questions. Upon request, we provide the following buffers: LYSE, 2X LYSE (2-fold concentrated), LYSE-NHS, 2X LYSE-NHS (2-fold concentrated).

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