

# BeatBox Tissue Kit 24x: Increased flexibility and input



The PreOmics BeatBox is a revolutionary technology for efficient and reliable throughput for tissue homogenization and cell lysis. The BeatBox is a fast and easy-to-use instrument that completes sample homogenization in as little as 10 minutes, without cross contamination and minimal heat induction. The BeatBox has a surprisingly small footprint and quiet operation compared to traditional tissue processing instrumentation.

Here we present the BeatBox Tissue Kit 24x, enabling efficient homogenization of various tissue types from 5 to 50 mg wet weight and up to 24 samples in parallel. BeatBox tissue homogenization can be seamlessly integrated into the PreOmics' iST sample preparation workflow.

## Technical details

Product Specifications	Description/Values
<b>Kit</b>	
24-tube format containing a Gyuto Bead	1 to 24 samples
<b>Input</b>	
Wet weight of mammalian tissue	5 – 50 mg
Lysis buffer volume	1000 µL (or sufficient liquid to cover tissue sample, e.g. 300 µL)

## Materials

Sample	CD1 mouse tissues (5 – 50 mg) Type: brain, liver, cardiac muscle (NeoBiotech, Nanterre, France)
BeatBox Tissue Kit 24x	PreOmics, P.O.00128
Tube adapter	Accessory part of BeatBox instrument PreOmics, P.O.00103
Tryptophan assay <sup>1</sup>	Tryptophan standard (Sigma-Aldrich, T0254), urea (Sigma-Aldrich, U5378)
Multimode microplate reader	Infinite® 200 (Tecan)

### Keywords

Homogenization, tissue, sample preparation, BeatBox, bead beating, proteomics, protein yields

### Key takeaways

Tissue amounts from 5 to 50 mg of wet weight independently of tissue type

Flexibility to homogenize 1 to 24 samples in parallel

Efficient protein extraction

Homogenate can directly be processed using the iST technology

No heat-generation

Methods

Two different tissue/cell homogenization techniques were compared; the BeatBox and conventional bead beating (Table 1). Various tissue types (brain, liver, and cardiac muscle) were prepared in quadruplicate to evaluate the homogenization efficiency. In addition, different wet weight tissue input amounts of mouse cardiac muscle tissue were prepared in triplicate. A tryptophan assay<sup>1</sup> was performed to measure the protein yield of the homogenates.

Depending on the starting amount of tissue (5-35 mg or 50 mg), homogenates with 30 µg or 100 µg of total protein were processed according to the iST mammalian tissue protocol<sup>2</sup>, respectively (starting at step 2; adding DIGEST). 300 ng of peptides were analyzed on an EASY-nLC™ 1200 system (ThermoFisher Scientific) coupled to a timsTOF Pro mass spectrometer (Bruker Daltonics) in DDA-PASEF mode with a 45 min gradient; data were analyzed by MaxQuant software, version 2.0.1.0 (*Mus musculus* canonical version UniProt database, February 2022).

The BeatBox workflow integrated with the iST empowers successful proteomics sample preparation for challenging

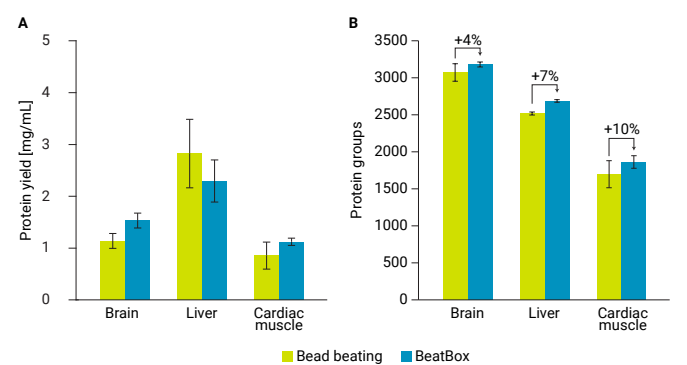
tissue samples. Firstly, the BeatBox tissue homogenization workflow results in increased protein extraction efficiency for specific tissue types (Figure 1A). Secondly, it increases the number of proteins identified compared to a bead beating workflow (Figure 1B). Although BeatBox liver tissue derived homogenate showed lower protein yields, the number of protein groups identified increased. This might be due to compact tissue (debris) spun down before protein quantification but accessible for iST buffers.

Thirdly, the BeatBox workflow enables the reliable processing of different tissue input amounts (wet weight) from 5 to 50 mg with comparable results to bead beating (Figure 2). Overall, Beatbox shows exceedingly reproducible protein extraction and identification across different starting amounts and tissue types (Figures 1 and 2).

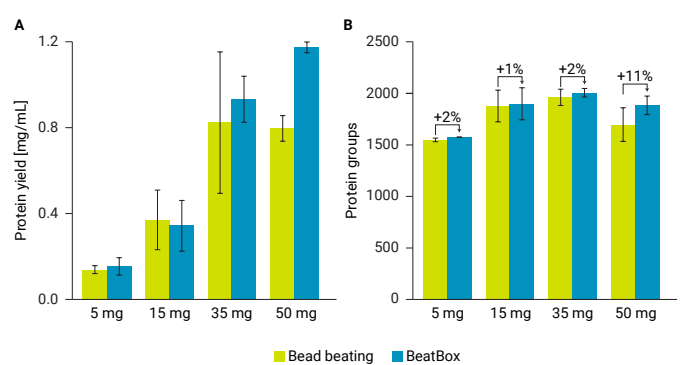
The main differences between the BeatBox homogenization and a conventional bead beating workflow are summarized in Table 2. In summary, the BeatBox enables an intuitive and easy-to-operate workflow.

Table 1 | Experimental parameters to homogenize tissue samples

	Homogenization techniques	
	BeatBox	Bead beating
Mouse brain and liver tissue (wet weight)	50 mg	
Mouse cardiac muscle (wet weight)	5, 15, 35, 50 mg	
LYSE buffer (Volume)	1000 µL	
Consumables	Ready to use kits	Tube with screwcaps with or without beads
Homogenization	10 min; Standard power setting	10x 1 min (4 m/sec, 4°C)
Proteomic sample preparation workflow	iST technology	



**Figure 1 | Comparing BeatBox and bead beating homogenization techniques using three mouse tissue types.** Mouse brain, liver and cardiac muscle of 50 mg of wet weight were processed in quadruplicate. A) Protein extraction yields from different tissue types and B) Protein groups identified per tissue type. The error bars represent the standard deviation.



**Figure 2 | Efficiency of homogenization from different starting amounts of cardiac muscle tissue using BeatBox and bead beating technique.** Tissue samples from 5 to 50 mg were processed in triplicate. A) Protein extraction yields from different tissue inputs and B) Protein identification from different tissue inputs. The error bars represent the standard deviation.

**Table 2 | Sample handling differences between BeatBox and bead beating workflows**

	Homogenization techniques	
	BeatBox	Bead beating
Homogenization tube	Tube with a gyuto bead	Tube with or without beads
Loss of sample during homogenization	Minimal as the tube is stationary	Cap might leak if not properly closed
Induction of heat	Minimal (allows operation at RT)	High (active cooling to 4°C required)
Homogenate recovery from the vessel	Easy in presence of single bead	Challenging with pipetting around many beads in the tube - potential for losses to large surfaces and incomplete sample retrieval

## Conclusions

BeatBox, in combination with the BeatBox Tissue Kit 24x, enables tissue processing for starting input amounts up to 50 mg, from 1 to 24 samples, in parallel. The BeatBox can be seamlessly combined with the iST kits, providing a complete and reliable proteomic sample preparation workflow from tissue to ready-to-measure peptides in less than 3 hours.

The BeatBox workflow (BeatBox instrument plus the BeatBox Tissue Kit 24x) is:

- Fast: 1-24 samples processed in parallel in less than 10 minutes
- Easy-to-use: Add your sample into preassembled kits and run it in just two clicks
- Flexible: Homogenize everything from cell pellets to tough muscle tissue
- Efficient: Enhance the proteome coverage using the BeatBox combined with the iST sample preparation for tissue input amounts ranging from 5 to 50 mg
- Revolutionary: Small footprint, silent, and maintaining a stable temperature

## Products

Product	Manufacturer	Product Code
BeatBox Instrument	PreOmics GmbH	P.O.00103
BeatBox Tissue Kit 24x	PreOmics GmbH	P.O.00128

## Ordering information:

<http://www.preomics.com/quote>  
order@preomics.com

## References

1. Wisniewski JK, Gaugaz F. Fast, and Sensitive Total Protein and Peptide Assays for Proteomic Analysis. Anal. Chem. (2015) 87: p4110–4116. DOI: 10.1021/ac504689z
2. PreOmics iST method 8rxn mammalian tissue protocol. <https://www.preomics.com/resources>