Multi Beads Shocker® Application Report

Multi-Beads Shocker® has proven its worth in proteome research!

Feature 1: Material preparation and analysis methods for successful proteomic research to discover biomarkers

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**Excerpt from the introduction of Multi-Beads Shocker® below*

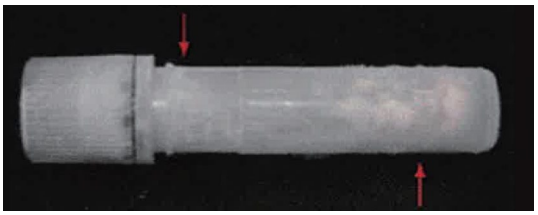
Overview

Sample preparation from frozen samples

There is a method in which a specimen frozen with liquid nitrogen is crushed to a powder form while still frozen, and then a solubilizing solution is added all at once to the cells that have been broken up. A mortar has traditionally been used to crush cells in this way. When the number of specimens is small or the specimens are relatively large, a mortar frozen with liquid nitrogen is sufficient, and the quality of the specimens is good. However, if you want to process 100 specimens in one or two days, a mortar is not sufficient. Also, very small specimens will disappear while being ground in a mortar. To crush multiple specimens in a short time, the "Multi-beads Shocker" sold by Yamato Scientific America is good (Figure 1). In this machine, a specimen and stainless steel beads that have also been frozen with liquid nitrogen are placed in a dedicated screw cap tube that has been frozen with liquid nitrogen, and the specimen is pulverized. Since the processing time is short, the temperature does not rise. With this method, the tissue is pulverized finely to a powder-like state. The pulverized samples can also be divided into small powders using a spatula cooled with liquid nitrogen for DNA and RNA extraction.

This method has been confirmed to be capable of stably extracting not only high-quality protein but also several tens RNA with a quality suitable for GeneChip analysis. Although this has not been confirmed, we believe from experience that it may also be suitable for DNA extraction for RLGS (Restriction Landmark Genomic Scanning).

Beads



Becomes powder

Reference: (Kondo Itaru) Sample preparation and analysis methods for successful proteome research: "Preparation of tissue samples for two-dimensional electrophoresis and mass spectrometry" Biotechnology Journal, Vol. 13-4, pp. 3-6, Yodosha, 2006.

Tadashi Kondo

Project leader of the Proteome Bioinformatics Project at the National Cancer Institute.
His research goal is to elucidate the mechanisms behind cancer pathology through comprehensive protein analysis and to improve the outcome of cancer treatment. Taking advantage of the favorable environment at the National Cancer Center Research Institute, he strives daily to achieve results that will rival those of top laboratories overseas.