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A Geno Technology, Inc. (USA) brand name

# FOCUS™ Extraction Buffers

## Chaotropic extraction buffers that preserve the native charge of proteins

## (Cat. #786-219, 786-220, 786-221, 786-222, 786-223, 786-233)

## INTRODUCTION

One of the most important considerations before running 2D gel electrophoresis is the choice of protein solubilization buffers. The suitable buffer must solubilize proteins effectively, without disturbing the native charge of the proteins. Urea, a common chaotrope, is widely used for solubilization and denaturation of proteins. One of the disadvantages of using urea is carbamylation. Urea in water exists in equilibrium with ammonium cyanate, the level of which increases with increasing temperature and pH. Cyanate reacts with α-amino and ε-amino groups of proteins and induces a change in the isoelectric point of proteins. This leads to artifactual results and therefore carbamylation must be avoided.

One way to minimize the risk of carbamylation is to prepare the urea based reagents fresh before each use. G-Biosciences has developed a series of dry urea based pre-mixed and ready-to-use solubilization buffers. Simply, add an appropriate volume of the supplied rehydration buffer to the dry buffer and then use to solubilize proteins, saving time and improving the quality of IEF/2D gel electrophoresis. FOCUS™ Extraction Buffers are also designed to be used as rehydration buffers for IPG strips.

FOCUS™ Extraction Buffers are experimentally optimized concentrations of critical agents, buffering and stabilizing agents, including urea, thiourea, Nonidet® P-40, CHAPS, and sulfobetaines (SB). The FOCUS™ Extraction Buffers are designed to produce optimal protein extraction and improved spot resolution for 2D gel analysis.

A range of FOCUS™ Extraction Buffers have been developed and depending on the nature of the samples, one or more of the buffers suitable for your applications can be ordered. FOCUS™ Extraction Buffer-I is suitable for most applications, however for stronger solubilization effects, we recommend FOCUS™ Extraction Buffer-II, -III, -IV, -V or -VI.

For analysis of a proteome, a single buffer may not be suitable and sequential solubilization using different FOCUS™ Extraction Buffers will help in identifying new proteins. ***"Improved Protein Extraction for 2D Electrophoresis by Sequential Solubilization with FOCUS™ Chaotropic Extraction Buffers"*** is available at GBiosciences.com.

## ITEM(S) SUPPLIED

| Cat # | FOCUS™ Extraction Buffer | Contents |
|---|---|---|
| 786-220 | FOCUS™ Extraction Buffer-I with DILUENT-I, For 50ml | Urea and NP-40 |
| 786-221 | FOCUS™ Extraction Buffer-II with DILUENT-II, For 50ml | Urea and CHAPS |
| 786-222 | FOCUS™ Extraction Buffer-III with DILUENT-III, For 50ml | Urea, Thiourea, ASB-16 & CHAPS |
| 786-223 | FOCUS™ Extraction Buffer-IV with DILUENT-III, For 50ml | Urea, Thiourea, SB 3-10 & CHAPS |
| 786-219 | FOCUS™ Extraction Buffer-V with DILUENT-II, For 50ml | Urea, Thiourea & CHAPS |
| 786-233 | FOCUS™ Extraction Buffer-VI with DILUENT-III, For 50ml | Urea, Thiourea, NDSB 201 & CHAPS |

## STORAGE CONDITION

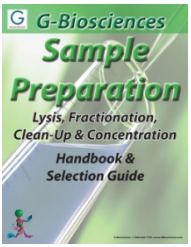
The buffers are shipped at ambient temperature. Upon arrival, store FOCUS™ Extraction Buffers at room temperature and DILUENT at 4°C.

## PROTOCOL

1. Allow the DILUENT to equilibrate to room temperature before using.
2. Shake the FOCUS™ Extraction Buffer bottle for 10-15 seconds to homogenize the dry powder mixture.
3. Weigh an appropriate quantity of FOCUS™ Extraction Buffer and dissolve in appropriate volume of DILUENT. For each gram of FOCUS™ Extraction Buffer dry powder mix, add 1.15ml of matching DILUENT, which will produce approximately 2ml buffer solution.
4. Vortex periodically and incubate the tube at room temperature, until completely dissolved and a clear solution is achieved.
   ***NOTE:*** *Some buffers (e.g. FOCUS™ Extraction Buffer -IV) may require warming to 30-35°C for 5-10 minutes.*
5. Add other needed agents, such as reducing agents, inhibitors (such as protease/phosphatase inhibitors), carrier ampholytes, bromophenol blue dye and proceed with your experiments.
6. Discard any unused buffer. For optimal results, make fresh each time.

## RELATED PRODUCTS

Download our Protein Cross-linkers Handbook.




http://info.gbiosciences.com/complete-protein-sample-preparation-handbook

*For other related products, visit our website at www.GBiosciences.com or contact us.*

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