



A Geno Technology, Inc. (USA) brand name

# **IBS-HP™ Buffer Kit**

For Inclusion Body Solubilization

(Cat. # 786-183HP)



#### INTRODUCTION

Bacterial expression of recombinant proteins is a commonly used technique. A major problem with bacterial expression is that non-bacterial and over-expressed proteins form aggregates of insoluble proteins, known as inclusion bodies. The reasons for inclusion body formation are poorly understood, however it is hypothesized that the exposed hydrophobic domains of partially or incorrectly folded proteins aggregate together to form the large insoluble aggregates. The large, aggregate nature of inclusion bodies allows for them to be separated by centrifugation.

Once separated from the soluble proteins, the large aggregates are themselves difficult to solubilize. The IBS-HP<sup>™</sup> Buffer kit contains a proprietary buffer that gently solubilizes both hydrophilic and hydrophobic proteins from the inclusion bodies.

The supplied IBS-HP<sup>™</sup> Buffer contains urea, thiourea and SDS. IBS-HP<sup>™</sup> Buffer is compatible for protein estimation with our NI<sup>™</sup> protein assay (Cat. # 786-005) and running SDS-PAGE analysis using PAGE-Perfect<sup>™</sup> kit (Cat. # 786-123). For other downstream processes the interfering agents can be removed by dialysis. We recommend Tube-O-DIALYZER<sup>™</sup>, micro-dialysis units for rapid dialysis.

## ITEM(S) SUPPLIED (Cat. # 786-183HP)

Description	Size
IBS-HP <sup>™</sup> Buffer	1 Bottle
DTT [1M in 1ml]*	1 Vial

<sup>\*</sup> See preparation before use

## STORAGE CONDITION

The kit is shipped at ambient temperature. Upon arrival, store DTT at 4°C and IBS-HP<sup>™</sup> Buffer at room temperature. After rehydration of the IBS-HP<sup>™</sup> Buffer, prepare 10-20ml aliquots and store at -20°C.

## ADDITIONAL ITEMS REQUIRED

Centrifuge and test tubes

#### PREPARATION BEFORE USE

- \*Add 1ml de-ionized water into DTT vial. Vortex until dissolved to achieve a 1M DTT solution. Store DTT solution at -20°C.
- Add 53ml of deionized water to the IBS-HP<sup>™</sup> Buffer. Swirl the bottle gently at intervals until the contents are completely dissolved (~60 minutes). Do NOT warm or heat to aid this process.
- 3. The rehydration process will result in 100ml IBS-HP<sup>™</sup> Buffer. Following rehydration, prepare 10-20ml aliquots and store at -20°C. When required, thaw at room temperature, do not heat the solution.

#### ISOLATION OF INCLUSION BODIES

Inclusion bodies are easily isolated following bacterial lysis by centrifugation. For inclusion bodies isolation, we recommend using Bacterial-PE  $LB^{\text{TM}}$  (Cat # 786-176). Briefly, incubate the bacterial cells in Bacterial-PE  $LB^{\text{TM}}$  and lysozyme until lysis is complete. At the end of incubation, centrifuge the lysate at 30,000xg for 30 minutes at 4°C. Collect the pellet and wash twice with 1 in 10 dilution of Bacterial-PE  $LB^{\text{TM}}$ . Collect the inclusion bodies for solubilization and folding.

## INCLUSION BODY SOLUBILIZATION PROTOCOL

- Determine the wet weight of inclusion bodies and resuspend each 100mg inclusion bodies in 1ml IBS-HP<sup>™</sup> Buffer.
- 2. If disulfide bonds are involved in folding, add  $20\mu$ I/ml 1M DTT to the suspended inclusion bodies to give a final concentration of 20mM DTT.
- 3. Suspend the inclusion bodies by vortexing or pipetting up and down until a homogeneous suspension is achieved.
- 4. Shake the suspension for 1 hour at 4°C for complete solubilization.
- 5. Remove insoluble material that may affect downstream processing by centrifugation at 30,000xg for 15 minutes.
- 6. Collect the supernatant for further analysis.

## REMOVAL OR OUENCHING OF SDS

If it is necessary to remove or quench the SDS present in the IBS-HP<sup>™</sup> buffer, dilute the protein solution 10-fold with a buffer containing 4% NP-40. Alternatively, dialyze the IBS-HP<sup>™</sup> buffer solubilized protein in an appropriate buffer containing 4% NP-40.

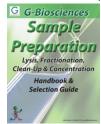
#### PROTEIN FOLDING

The presence of a denaturant results in unfolded proteins, so to obtain an active protein the proteins must be refolded. Every protein has unique folding properties and is therefore difficult to suggest a universal folding protocol.

We recommend determining the optimal folding protocol using our PROTEIN-Foldase Kit (Cat. # 786-185), which is designed to simplify protein folding optimization.

#### RELATED PRODUCTS

Download our Sample Preparation Handbook.



http://info.gbiosciences.com/complete-protein-sample-preparation-handbook/
For other related products, visit our website at www.GBiosciences.com or contact us.

Last saved: 8/28/2012 CMH



www.GBiosciences.com