



## Proteomics

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# Alkylation and In-gel Trypsin Digestion

## 1. Protocol usage

To identify proteins which have been separated by gel electrophoresis.

## 2. Principle

Gel separated proteins are proteolytically digested into peptides prior to identification by mass spectrometry. The process involves 'in-gel' reduction and alkylation, followed by digestion of the proteins and extraction of the peptide from the gel piece(s).

## 3. Protocol workflow

A protein band or spot is cut from a gel. The gel piece is washed to remove impurities, such as e.g. SDS. Any disulfide bound cysteines in proteins are reduced and reformation of disulphide bridges is prevented by alkylation. Proteins are digested to peptides by trypsin and the peptides are extracted from the gel:

- Preparing the gel piece
- Reduction
- Alkylation
- Digestion
- Extraction of peptides

## 4. Reagents and equipment

H<sub>2</sub>O, MilliQ

Acetonitrile (**ACN**) (purity >99,8%)

NH<sub>4</sub>HCO<sub>3</sub> (purity >99%)

1,4-dithiothreitol (**DTT**) (purity >99%)

Iodoacetamide (**IAA**) (purity >99%), Sigma I-6125

Sequencing Grade Modified Trypsin, Promega V5111

Formic Acid (**HCOOH**) (purity 98-100%)

Scalpel

Tweezers

Eppendorf tubes 1,5 ml or 0,5 ml (To avoid plasticizer contamination, tubes made of high quality polypropylene must be used.)

Tips

Gloves

Heating block

Vacuum centrifuge (SpeedVac)

## 5. Solutions

### **1 M ammonium bicarbonate - NH<sub>4</sub>HCO<sub>3</sub> stock solution**

Weight accurately 15,81 g of NH<sub>4</sub>HCO<sub>3</sub> in a 200 ml flask and fill to mark with water. Filter through 0,45 µm filter. The pH of the solution should be 8-9. This 1 M stock solution can be stored for one month at 4 °C. For 100 mM solution, mix 1,0 ml stock solution and 9,0 ml MilliQ water.



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### **20 mM DTT**

Accurately weigh DTT in an Eppendorf tube. Dissolve in 100 mM  $\text{NH}_4\text{HCO}_3$  in a ratio of 3,08 mg DTT : 1 ml  $\text{NH}_4\text{HCO}_3$ . This solution should be prepared fresh.

### **55 mM IAA**

Accurately weigh IAA in an Eppendorf tube. Dissolve in 100 mM  $\text{NH}_4\text{HCO}_3$  in a ratio of 10,2 mg IAA : 1 ml  $\text{NH}_4\text{HCO}_3$ . This solution should be prepared fresh and kept in the dark\* at RT.\* cover with foil or store in cupboard

### **0,02 $\mu\text{g}/\mu\text{l}$ trypsin solution**

Note: When working with trypsin, keep it always on ice. The trypsin stock solution is prepared by dissolving 20  $\mu\text{g}$  aliquot of trypsin in 20  $\mu\text{l}$  of Promega trypsin dilution buffer. The stock solution can be stored up to one month at  $-20^\circ\text{C}$ . Directly prior to use, dilute the trypsin stock solution (1 mg/ml) in a ratio 1:50 with a solution containing 40 mM  $\text{NH}_4\text{HCO}_3$  and 10 % ACN.

## **6. Instructions**

When you prepare solutions and handle your samples keep in mind that most common keratin contaminations arise from dust, hair or skin.

The volumes here are calculated for thin slices from a 1-DE gel band, so with a bigger piece of gel or small gel spot the volumes should be adjusted.

### **A. PREPARATION OF THE GEL PIECE**

Excise the stained protein band from the gel with a clean scalpel. If the gel is dried, rehydrate the gel piece in water and remove the cellophane. Cut the gel into approx. 1x1 mm pieces in an Eppendorf tube. Wash the gel pieces thoroughly by 3 x 10 min washes in  $\text{H}_2\text{O}$ .

#### ***Coomassie blue stained proteins***

Wash Coomassie stained gel pieces twice with 200  $\mu\text{l}$  of solution containing 0,04 M  $\text{NH}_4\text{HCO}_3$ / 50 % ACN for 15 min at  $37^\circ\text{C}$  or as long as required to remove all blue colour. Shrink the gel pieces by adding at least 200  $\mu\text{l}$  100% ACN. Wait until the gel pieces become white (about 5-10 min) and remove all ACN.

For **silver stained proteins**, no destaining is needed. Shrink the gel pieces by adding at least 200  $\mu\text{l}$  100% ACN. Wait until the gel pieces become white (about 5-10 min) and remove all ACN.

### **B. REDUCTION**

Rehydrate the gel pieces in 100  $\mu\text{l}$  20 mM DTT for 30 min at  $56^\circ\text{C}$ . Remove the excess liquid and shrink the gel pieces again with ACN as above.

### **C. ALKYLATION**

Rehydrate the gel pieces by adding 100  $\mu\text{l}$  55 mM IAA for 20 min in the dark RT. Remove the excess liquid and wash the gel pieces twice with 100  $\mu\text{l}$  100 mM  $\text{NH}_4\text{HCO}_3$ .

Dehydrate the gel pieces again with ACN as above, remove all ACN (and dry in a vacuum centrifuge for 5 min to evaporate all ACN).



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### D. DIGESTION

Add 10  $\mu$ l 0,02  $\mu$ g/ $\mu$ l trypsin solution and allow to absorb for 20 min on ice. Check if all solution was absorbed and add more if needed. Gel pieces should be completely saturated with trypsin solution. After 20 min, add about 20  $\mu$ l solution containing 40 mM  $\text{NH}_4\text{HCO}_3$ /10 % ACN to completely cover the gel pieces. Incubate up to 18 hours at 37 °C (overnight).

### E. EXTRACTION OF PEPTIDES

Add about 30-60  $\mu$ l ACN (equal volume with the digestion mixture), vortex and incubate 15 min at 37 °C. Collect the supernatant to another eppendorf tube and repeat the extraction with 150  $\mu$ l solution containing 50 % ACN / 5% HCOOH. Dry the solution in a vacuum centrifuge and store the dried peptides at -20 °C. Immediately prior to MS analysis, dissolve the peptides in 10  $\mu$ l 2% HCOOH by vortexing, incubate at 37 °C for 15 min and vortex again.

### 7. QC control

Sometimes we have problems with contaminating proteins such as keratins, or no proteins can be identified. To confirm that all reagents are working, or to define the origin of possible protein contaminations such as keratin, use a positive and a negative control for each batch of analyses.

A positive control is a gel piece containing 0,5 pmol BSA and negative control is a similar size gel piece without any protein. Customers using the facility should include a positive and negative gel piece.

A successful digestion results in the identification of numerous peptides from BSA in the positive control, whereas in the negative control only trypsin should be identified.

### 8. References

- Shevchenko et al. (1996) Anal. Chem. 68, 850-858.  
Shevchenko et al. (2006) Nature Protocols 1(6), 2856-2860.