

## **Methods**

### I. 1D SDS PAGE

4% Stacking gel

10% Separate gel

In situ alkylated with acrylamide.

Gel stained with silver staining

### II. in gel digestion (Trypsin)

Cut a band and cut small pieces around 1 mm square

Washed with water (500  $\mu$ l) at 37 degree -10min, 5 times

Destained with 100  $\mu$ l of **15mM Potassium ferricyanide, 50mM Sodium thiosulfate** at 37degree-10 min

Dehydrated with CH<sub>3</sub>CN (100 $\mu$ l) at 37 degree-10min

Evaporated with a concentrator

Digested with trypsin ( **100mM NH<sub>4</sub>HCO<sub>3</sub> pH8.5, 0.001%(w/v) Trypsin** )

The gels were covered with the trypsin solution at 37 degree -45min.  
37 degree - overnight

Extracted (1) with **50%CH<sub>3</sub>CN,0.1%TFA** at 37 degree -10 min

Extracted (2) with **15%isopropanol, 20%formic acid, 25%CH<sub>3</sub>CN** at 37 degree -15min

Extracted (3) with **80%CH<sub>3</sub>CN** at 37 degree -10min

**Sup (1), (2), (3) and (4)** were evaporated.

### III. LC-ESI-MS-MS

LC: DiNa(KYA TECH)

Column: Magic C18 0.1mm  $\phi$  x 50mm

Flow: 0.3  $\mu$ l / min

Solvent A: 0.1%HCOOH, Solvent B: 0.1%HCOOH/90%CH<sub>3</sub>CN

Gradient: 0%B(30min)  $\rightarrow$  1%/min  $\rightarrow$  80%B

MS: QSTAR (ABI)

Scan range: m/z 310-2000

Spray V: 1800V

Curtain gas: N<sub>2</sub>, 10

Collision gas: N<sub>2</sub>, 5

Collision energy: 20-50ev

### Determination of C terminal peptide

			A	B
	m/z	MW		
N-terminal	601.3	1200.6	GSH(M+16)AQNITAR	GSH(M+16)AQNITAR
Modification	599.86	1197.7	IGEPLVL(K+28)CK	IGEPLVL(K+28)CK
	503.81	1005.57	GAP(K+28)KPPQR	GAP(K+28)KPPQR
	572.82	1143.62	LEW(K+28)LNTGR	LEW(K+28)LNTGR
Insert	901.96	1801.92	-	VYQIA <sup>R</sup> PGKPEIVDSASE
1.C-terminal	866.45	1730.90	-	VYQIPGKPEIVDSASE
	946.43	945.43	-	PEIVDSASE
2.C-terminal	882.98	1763.97	-	VWEPVPLEEVQLVVE
3.C-terminal	650.83	1299.65	AVSISIIEPGEEG	AVSISIIEPGEEG

We digested the protein with trypsin, but we found that C terminal amino acids were not K or R peptides.

Therefore, we determined C terminal peptide of the protein.