

## Proteome Analysis Example using AXIMA

The comprehensive analysis of proteins referred to as “proteome analysis” is becoming a powerful trend in post-genome research. Introduced here is an example of proteome analysis of cyanobacterium *Anabeane sp.* stain PCC7120 using AXIMA-CFR.

### Peptide Mass Fingerprint (PMF)

The PMF method uses a mass spectrometer to identify proteins. First, proteins that have been separated using two-dimensional electrophoresis, etc. are digested by trypsin, and the obtained peptide fragment mass values are measured. Then, this data set is compared with the theoretical values calculated from DNA / protein databases for the protein identification. Figure 1 (a) shows the two-dimensional electrophoretic pattern, and (b) shows the PMF spectrum of one of the spots. Using the PMF method, this protein was identified as the gene product shown in Figure 2 (reverse side).

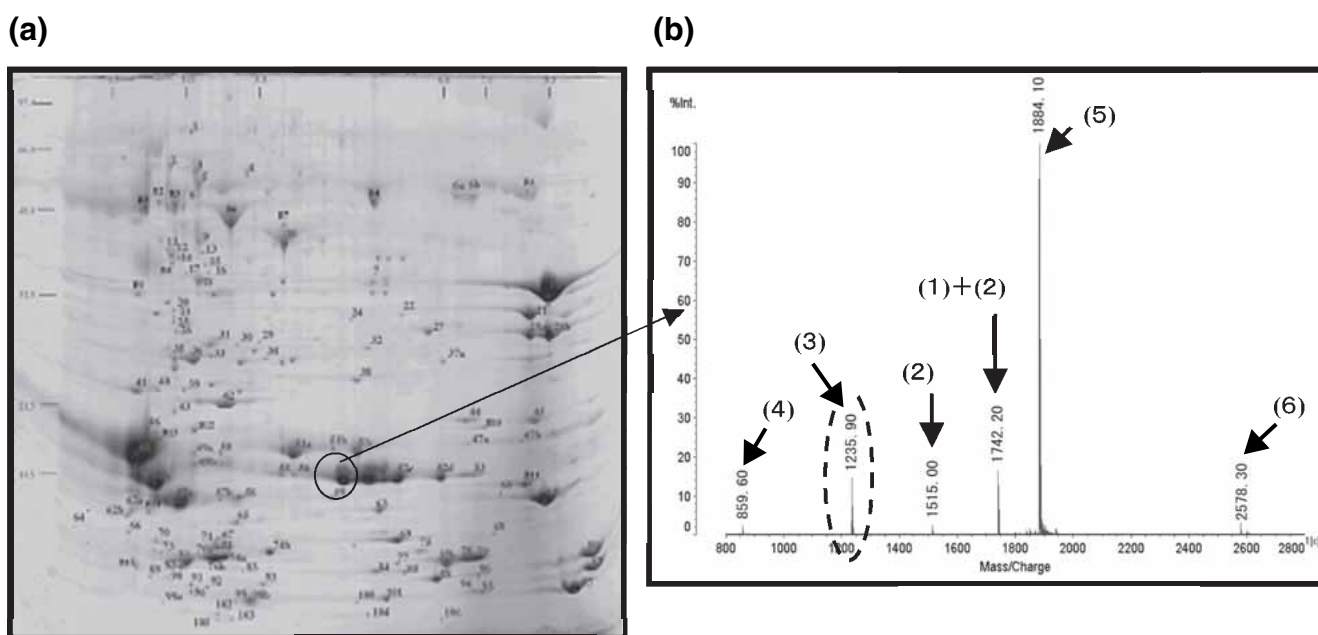


Fig. 1 Two-Dimensional Electrophoretic Pattern of *Anabeane sp.* stain PCC7120 whole protein (a) and PMF Spectrum (b)

## Gene

A29674:

*Anabaena* sp. PCC 7120  
C-PHYCOCYANIN ALPHA  
CHAIN

## Complete Protein Amino Acid Sequence

VK<sup>(1)</sup> TPITEAIAAADTQGR<sup>(2)</sup> FLGNTLQ SAR<sup>(3)</sup> GR  
YER AAASLEAAR<sup>(4)</sup> GLTSNAQR LIDGATQAVYQK  
PYTTQTPGPQFAADSR<sup>(5)</sup> GK SK CAR DVGHYLR  
IITYSLVAGGTGPLDEYLIAGLAEINSTFDLSPSWYVEALK  
HIK ANHGLSGQAANEANTYIDYAINALS<sup>(6)</sup>

Fig. 2 Identified Gene and Complete Amino Acid Sequence of the encoded protein.  
Numbers in parentheses correspond to numbers in Fig. 1.

## Analysis by PSD (Post Source Decay)

MS/MS analysis by PSD is an effective method for analyzing peptide structure. PSD with a Curved Field Reflectron allows rapid measurement because the entire range of fragment ions can be detected in a single measurement without having to change the reflectron electric field depending on the fragment ion mass. At the point where PSD analysis was performed on the peptide (3) mass peak in Fig. 1, the spectrum shown in Fig. 3 was obtained. The result confirmed the sequence of 9 of the 11 amino acids.

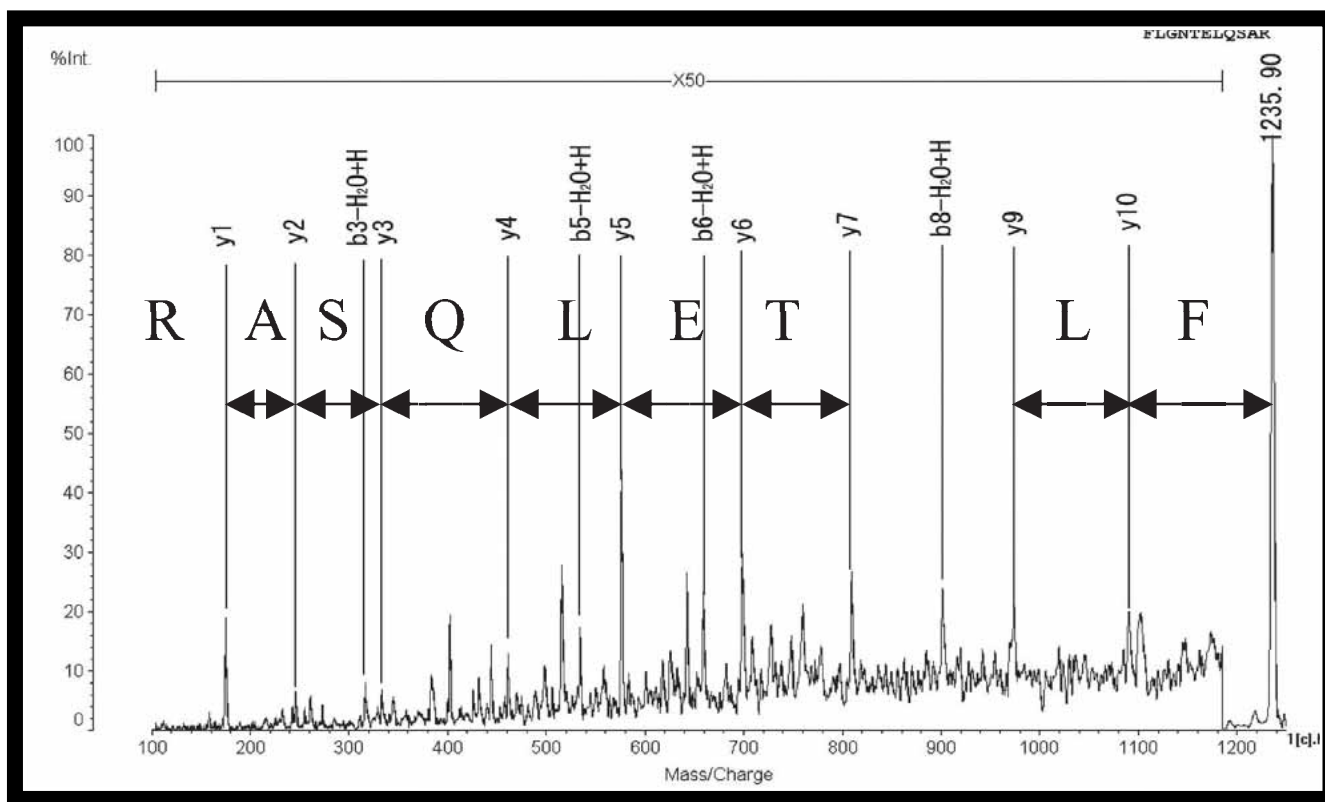


Fig. 3 PSD Spectrum of Peptides (3) - Corresponding amino acids are annotated by one letter code.  
The amino acid sequence deduced from the genome sequence is FLGNTLQ SAR.

The protein was thus identified using PMF, and further, the amino acid sequence of the digested peptide was ascertained by PSD analysis. AXIMA-CFR provides solutions for proteome analysis with high-accuracy and high-throughput performance.

Data provided by : Dr. Satsuka; Kazusa DNA Research Institute