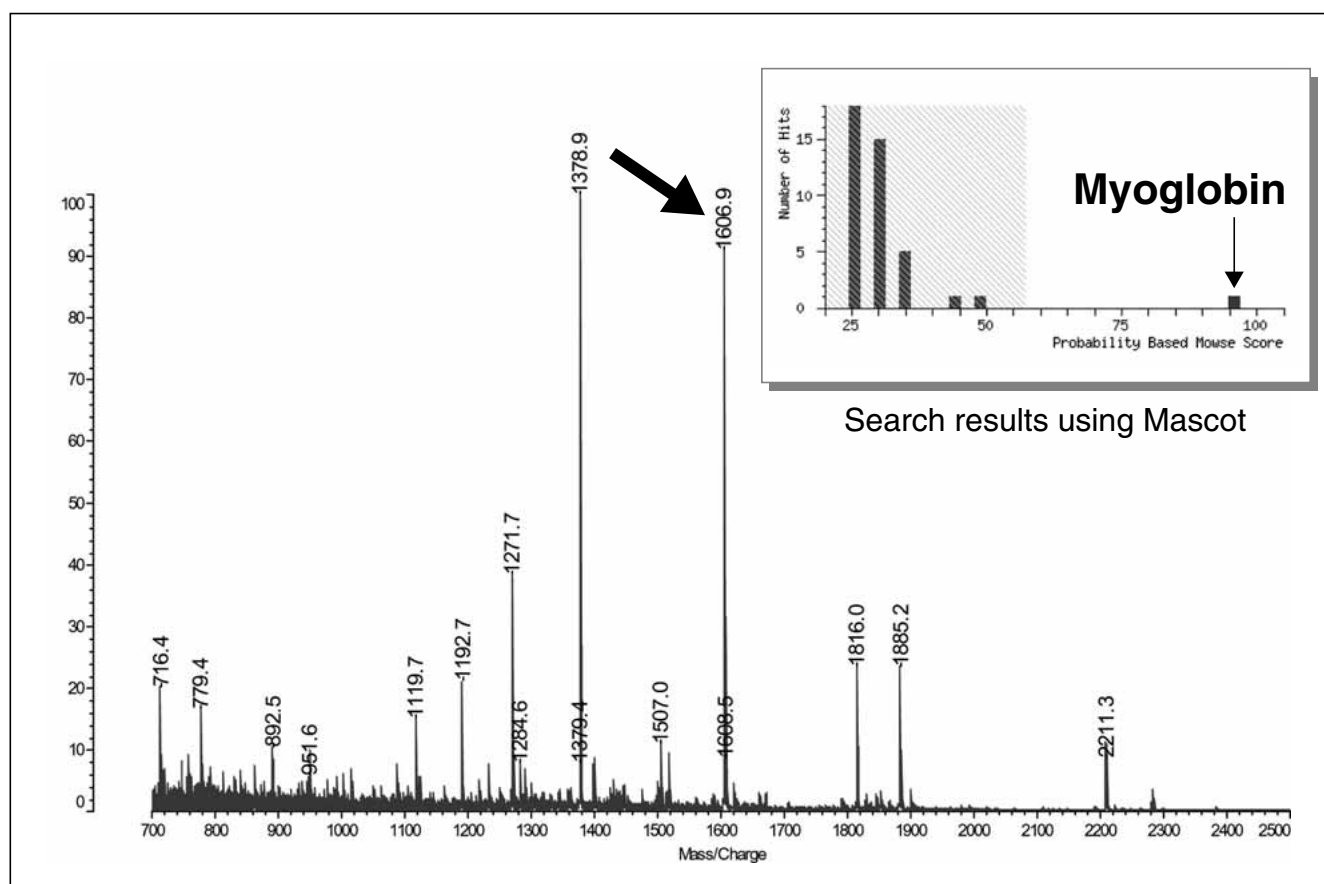


PMF (peptide mass fingerprint) and MS/MS ion search are widely used to enable high throughput protein identification. Introduced here is an example of high-score results.

Analysis of In-Gel Digest Sample (1) - Protein Identification by Peptide Mass Fingerprint -



Sample: Horse myoglobin

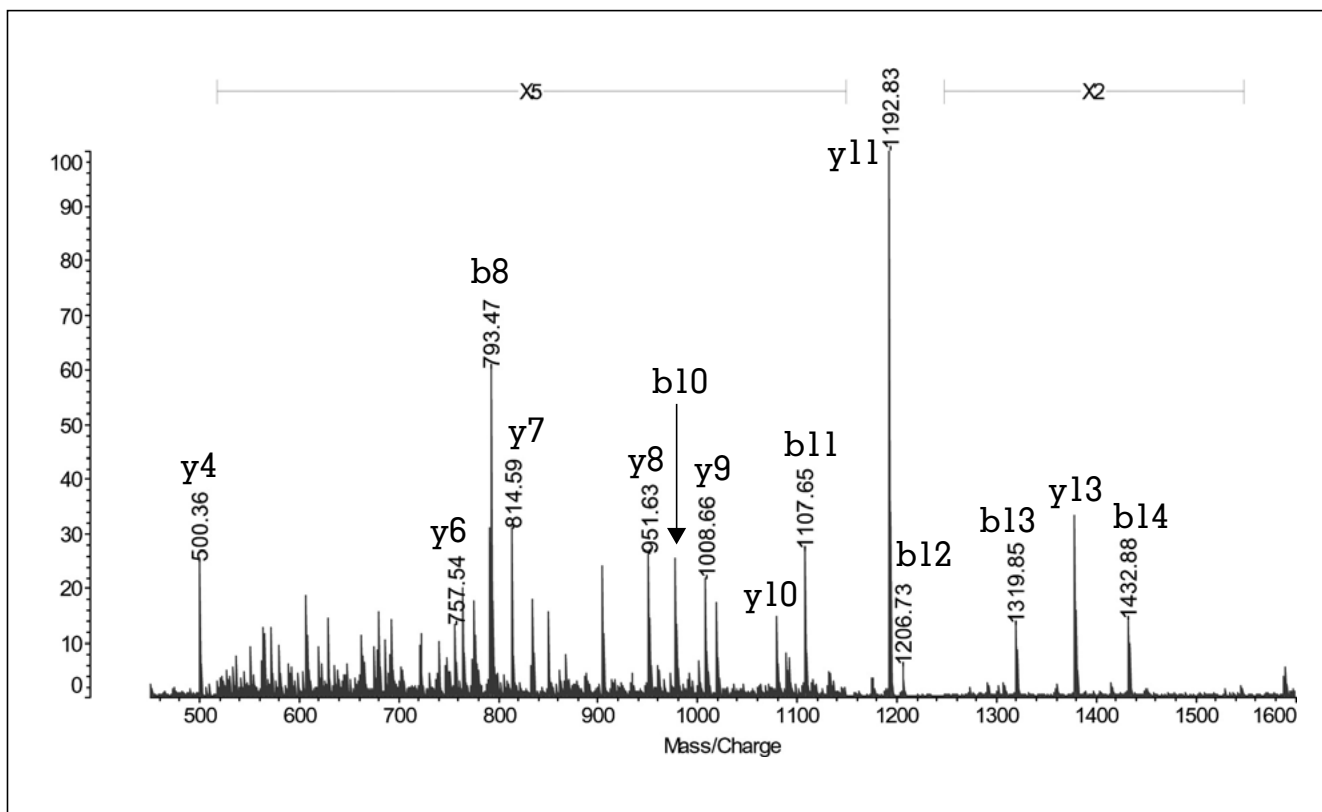
In-gel digestion procedure: 5 pmol of protein (myoglobin) was analyzed by SDS-PAGE, and after staining with CBB, the stained band was extracted and digested with trypsin.

Desalting: Zip Tip C18 (eluted with about 5 μ L)

MS analysis: About 0.5 μ L each of matrix (DHBA) solution and sample solution were mixed on a plate.

Analysis of In-Gel Digest Sample (2)

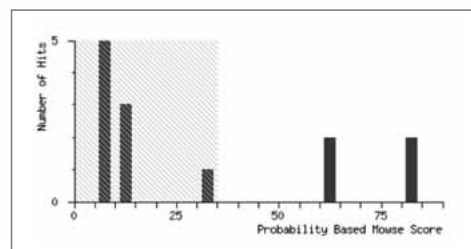
- Protein Identification by MS/MS Ion Search -



MS/MS spectrum of tryptic (m/z 1606.9)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
	1606.90	1605.89	1605.85	0.04	0	82	1	VEADIAGHGQEYLIR

Proteins matching the same set of peptides:	Total score:	Peptides matched:
<u>MYG_HORSE</u>	82	1
<u>1BJE</u>	82	1
<u>MYHO</u>	82	1
<u>1XCH</u>	82	1
<u>1YMA</u>	82	1
<u>1HRM</u>	82	1



Qualitative results using Mascot MS/MS Ion Search