

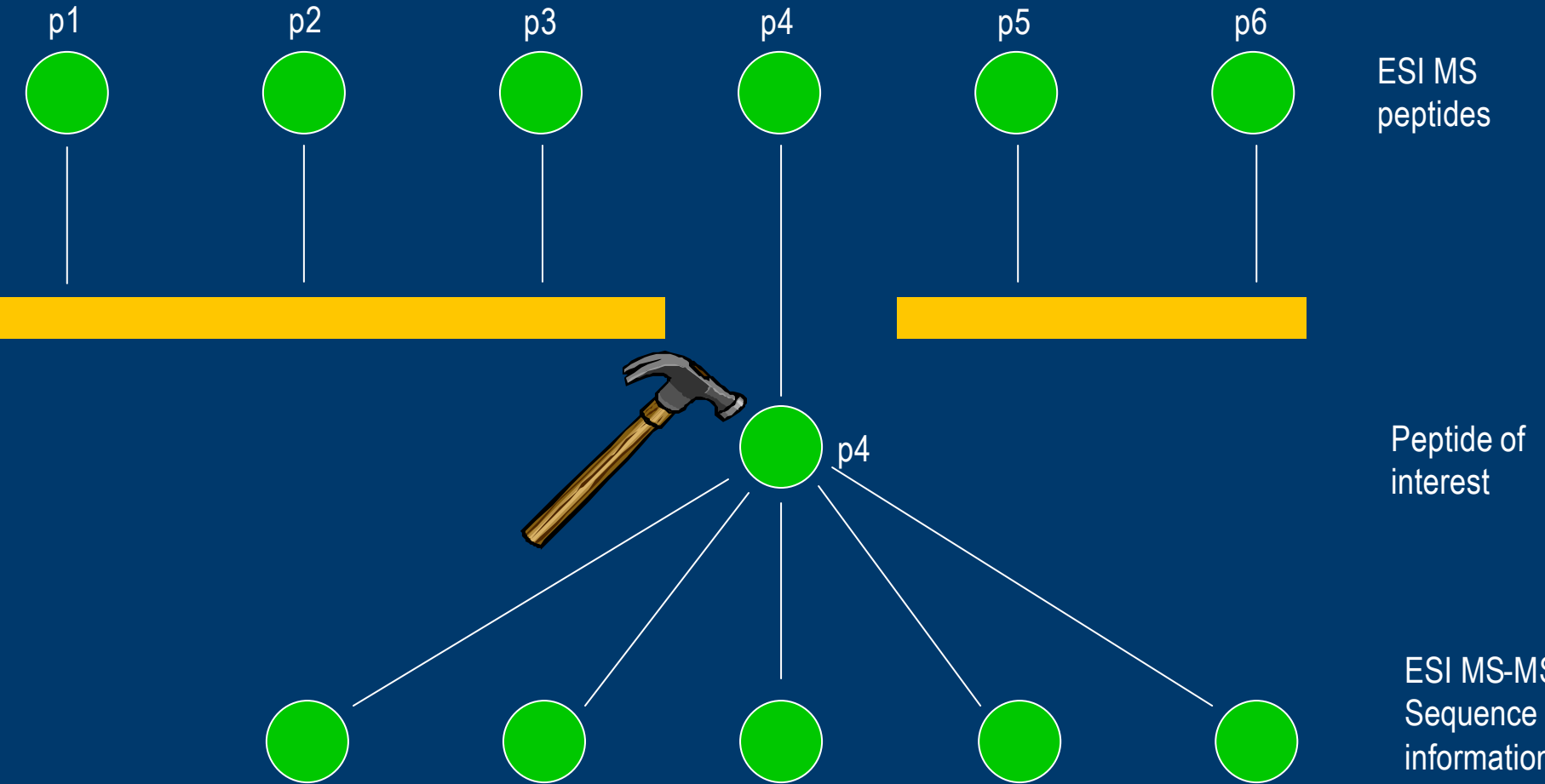
# Mass Spectrometry for proteomics

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- The peptide mixture is introduced into the tandem mass spectrometer
- The peptide of interest is selected and fragmented by applying energy
- The amino acid sequence can be read from the resulting tandem mass spectrum

# Sequence tagging

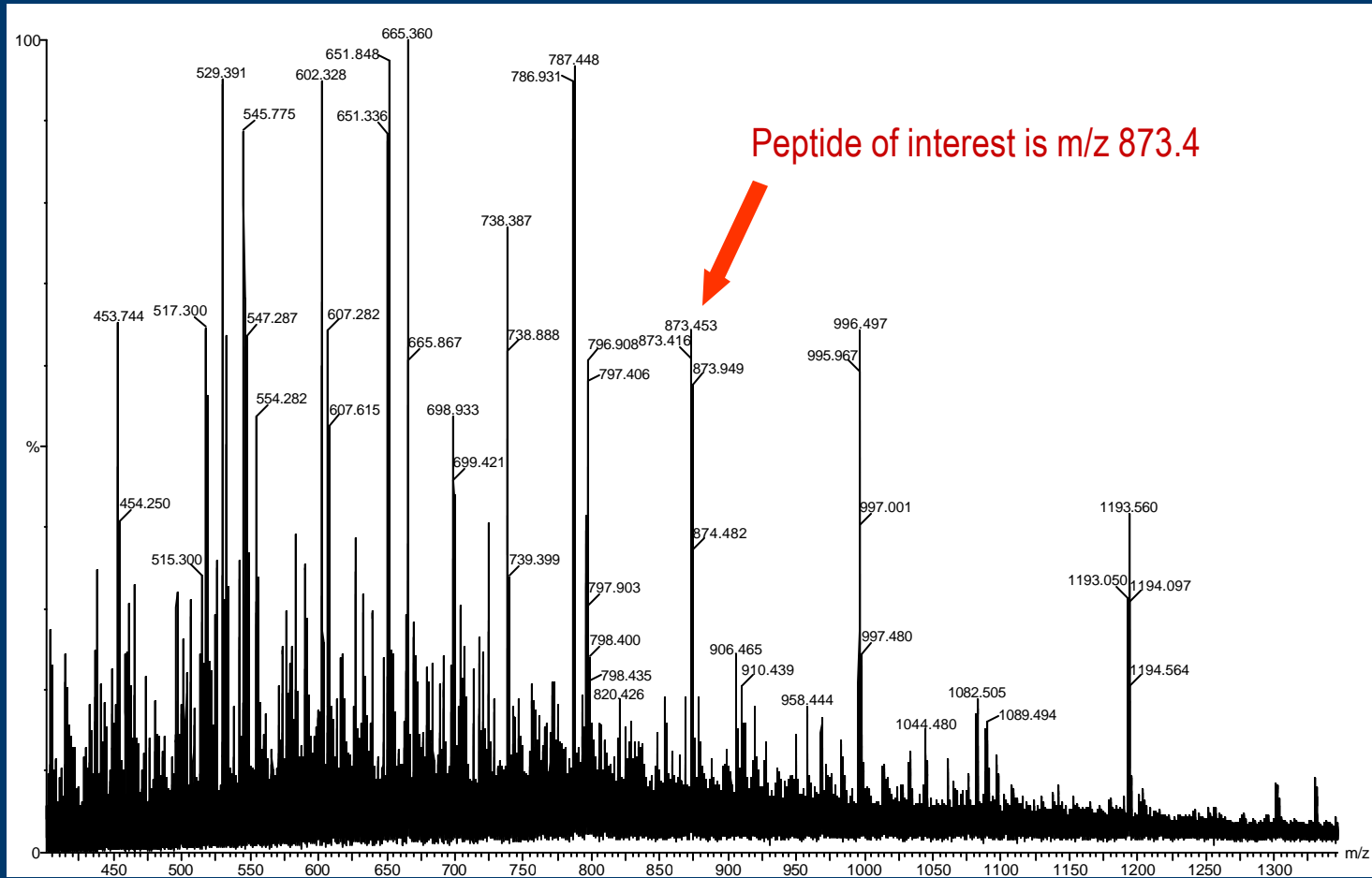
## Tandem mass spectrometry



# Sequence tagging

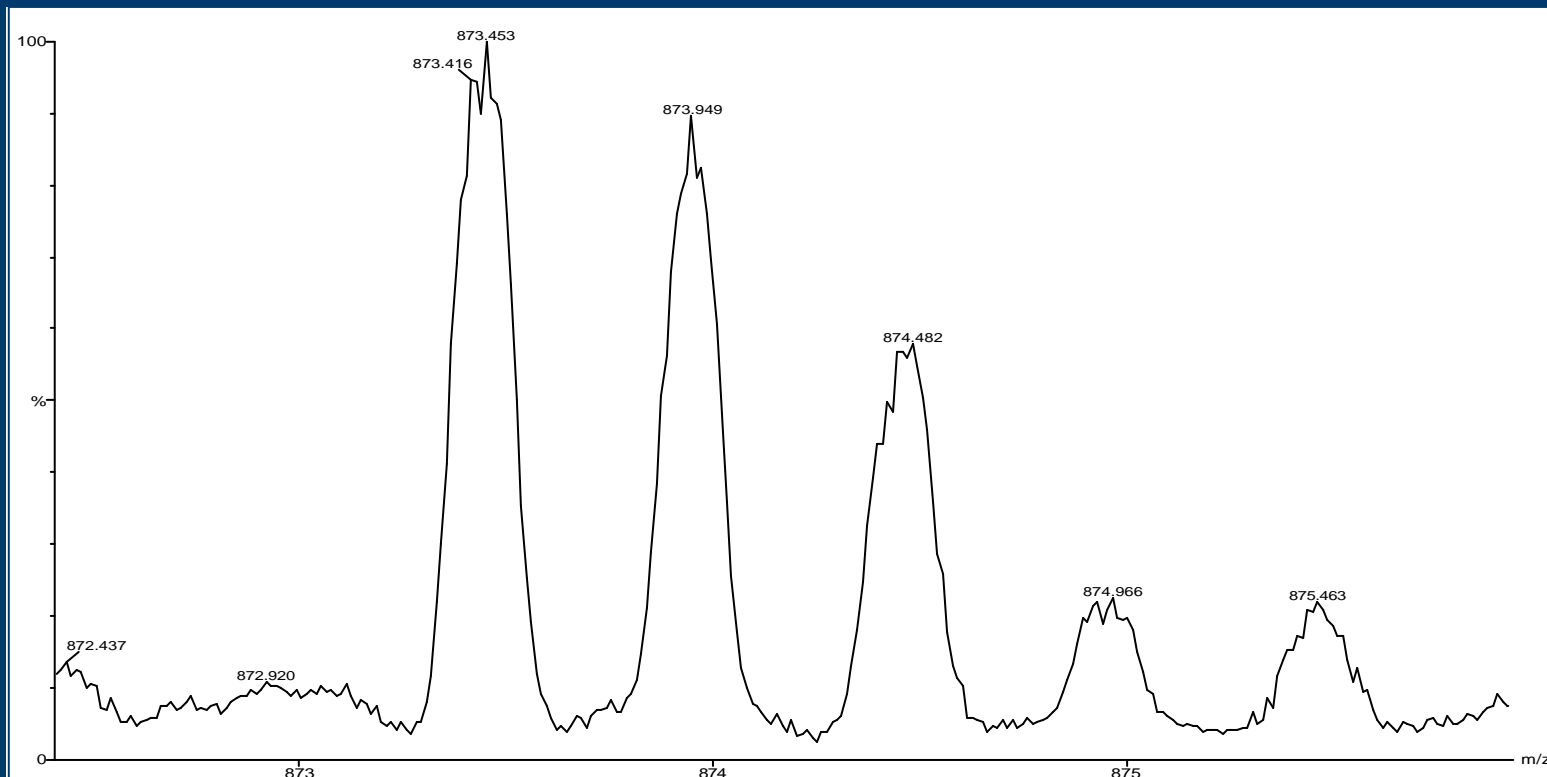
Identification of the spot of interest excised from the gel:

\* ESI MS results in a mass spectrum of the peptides present in the mixture.



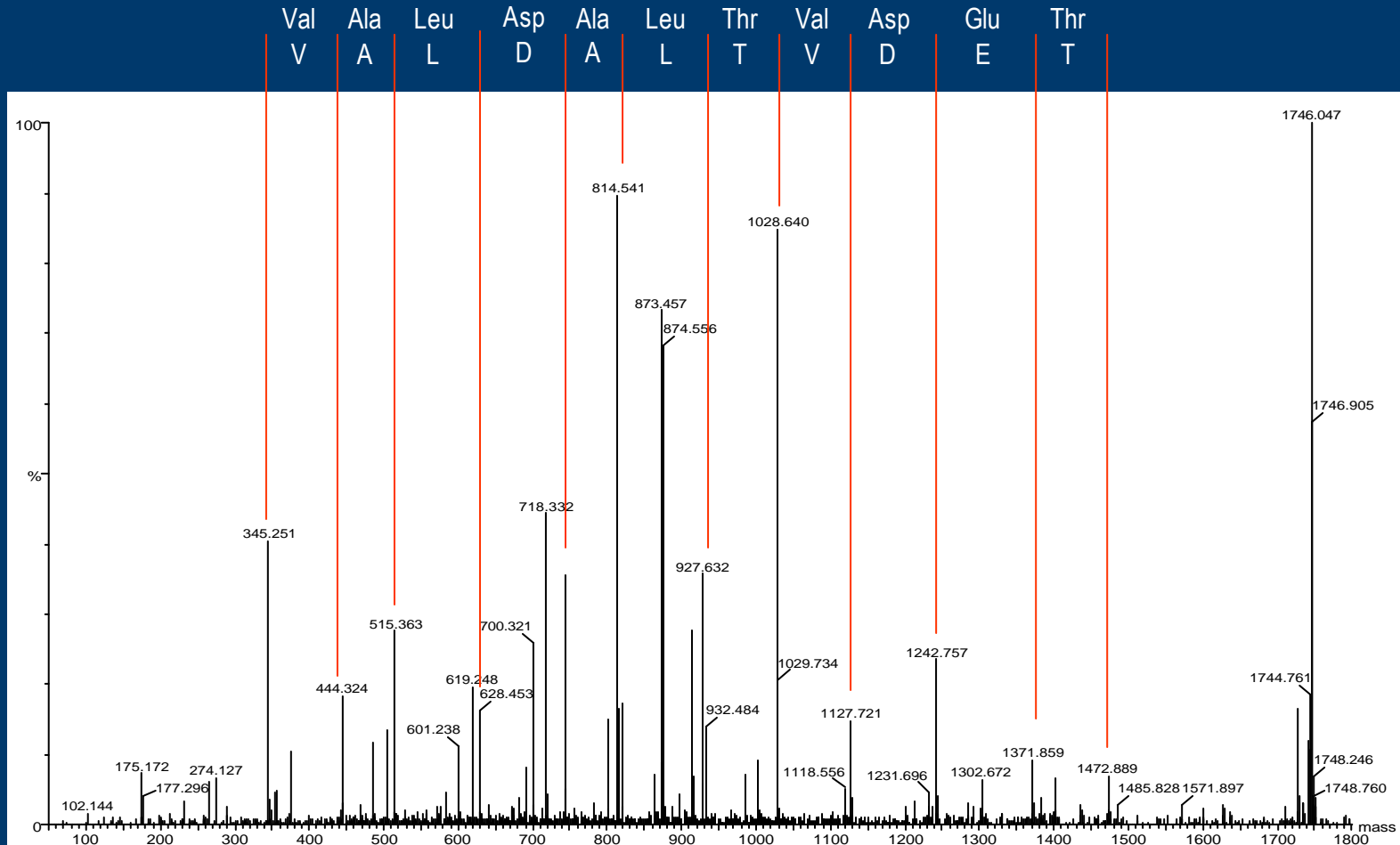
# Sequence tagging

- Zoomed-in mass spectrum
- Energy is applied to the mass of interest, resulting in a tandem mass spectrum (demonstrated on next slide)



# Sequence tagging

From the tandem mass spectrum the amino acid sequence can be determined



# Protein identification

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- Sequence information can be used for dBase searching
- Sequence of 10 amino acids or more is sufficient to identify the protein
- Sequence tags can also be used for cloning (8 amino acids sufficient)