Sample problem (in class) for amino acid sequence determination

(demonstration of how to align sequenced peptides from 2 different cleavage methods so the "overlaps" from one set of peptides with the other set of peptides tell you the order they were in, in the original longer peptide)

You have been asked to deduce the sequence of a heptapeptide (7 amino acid residues) from the following information.

A. Cleavage with a certain reagent or enzyme yielded 3 peptides, with sequences as follows:
Tyr-Lys
Glu-Ser
Ala-Phe-Arg
What was the cleavage reagent or enzyme used? _____

B. Cleavage with another reagent or enzyme also yielded 3 peptides, with sequences as follows:
Lys-Glu-Ser
Ala-Phe
Arg-Tyr
What was the cleavage reagent or enzyme used? _____

C. What is the sequence of the heptapeptide? (Use 3-letter abbreviations.)

_____ - _____ - _____ - _____ - _____ - _____ - _____

ANSWER

A. trypsin (all peptides except one end in Lys or Arg; the one that doesn't end in Lys or Arg must've been at the C-terminus of the original peptide, so it was "left" from the C-terminus of original peptide after the trypsin cleavages).

B. chymotrypsin (all peptides except one end in Tyr or Phe (or could have been Trp OR OTHER HYDROPHOBIC RESIDUES LIKE LEU OR ILE OR EVEN MET); the one peptide that doesn't end in an aromatic or hydrophobic residue must've been at the C-terminus of the original peptide, so it was "left" from the C-terminus of original peptide after the chymotrypsin cleavages).

trypsin

Tyr-Lys
Glu-Ser
Ala-Phe-Arg

chymotrypsin

Lys-Glu-Ser
Ala-Phe
Arg-Tyr

Ala - Phe - Arg - Tyr - Lys - Glu - Ser