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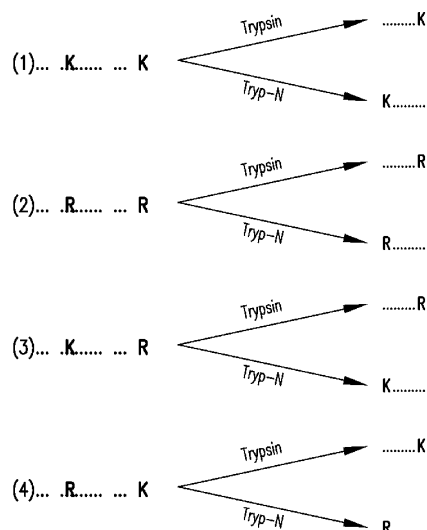
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- as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))
- as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))

- (54) **Title:** METHODS FOR DE NOVO PROTEIN SEQUENCING

**FIG.3**

(57) **Abstract:** A method for determining an amino acid sequence of a polypeptide, including: contacting first and second samples containing the polypeptide with a first protease (*e.g.*, Trypsin) and a second protease (*e.g.*, Tryp-N), respectively, to produce first and second sets of digested peptide fragments; fragmenting the sets of digested peptide fragments to produce sets of fragmented peptide ions; selecting pairs of peptide ions from the sets of peptide ions that differ in mass by a mass of an arginine or lysine amino acid residue; assigning an ion type (N-terminal or C-terminal peptide ion) to the selected pairs of peptide ions from the two sets; selecting a mass ladder of the same-type peptide ions in either set of peptide ions with incremental mass by the mass of amino acid residue(s), and assembling the identified amino acid residues from the mass ladder to determine the amino acid sequence of the polypeptide of interest.

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