atom bonded to the α carbon is substituted by the deuterium atom, by mass spectrometry. Thus, there is a problem that an accuracy is greatly reduced in the chiral analysis of amino acid residues that are originally included in bound amino acids with a very small amount.

SUMMARY

Thus, an embodiment of the disclosure is made in light of the above problems, and provides a chiral analysis method of bound amino acids and a chiral analysis system, by which an artifact generated during an analysis process of the bound amino acids, and a D-amino acid residue and/or an L-amino acid residue originally included in the bound amino acids can be very accurately distinguished.

According to one aspect, there is provided a chiral analysis method of a bound amino acid comprising:a step of hydrolyzing a bound amino acid using a deuterium chloride-deuterium oxide solution and/or deuterium oxide; a step of separating, by chiral separation, a D-form and an L-form of an amino acid generated by the hydrolyzation; a step of generating fragments from the separated amino acid; and a step of selecting and analyzing a predetermined fragment that contains an α carbon and does not contain a side chain from the generated fragments, by mass spectrometry.

According to another aspect, there is provided a chiral analysis system of a bound amino acid comprising: an chiral separation part that separates, by chiral separation, a D-form and an L-form of an amino acid generated by hydrolyzing the bound amino acid using a deuterium chloride-deuterium oxide solution and/or

deuterium oxide; a fragment generation part that generates fragments from the separated amino acid; and a mass spectrometry part that selects and analyzes a predetermined fragment that contains an α carbon and does not contain a side chain from the generated fragments, by mass spectrometry.

According to the present disclosure, a chiral analysis method of bound amino acids and a chiral analysis system are provided, by which an artifact generated during an analysis process of the bound amino acids, and a D-amino acid residue and/or an L-amino acid residue originally included in the bound amino acids can be very accurately distinguished.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a view illustrating an example of a structure of a chiral analysis system of bound amino acids of an embodiment; and

Fig. 2 is a view illustrating a result of a chiral analysis of aspartic acid and glutamic acid included in a hydrolysis product of a peptide.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

Next, embodiments of the present invention are described with reference to drawings.

A chiral analysis method of bound amino acids of the embodiment includes a step of hydrolyzing bound amino acids using a deuterium chloride-deuterium oxide solution and/or deuterium oxide (heavy water), a step of separating, by chiral separation, a D-form and an L-form of an amino acid generated by the hydrolyzation, a step of generating fragments from the separated amino acid, and a step of selecting and analyzing a predetermined