

That is, the present invention includes the following aspects.

(1)

1. A method wherein

a porous body in which a monoclonal antibody to be measured is immobilized in pores and nanoparticles on which a protease is immobilized are brought into contact with each other in a liquid to perform selective proteolysis of the monoclonal antibody,

a resulting peptide fragment is detected using liquid chromatography-mass spectrometry (LC-MS),

the porous body has an average pore diameter in a range of 10 nm – 200 nm,

the nanoparticles have an average particle size in a range of 50 nm – 500 nm,

the average particle size of the nanoparticles is larger than the average pore diameter of the porous body, and

a peptide fragment to be detected has an amino acid sequence that includes an amino acid derived from a CDR2 region of a heavy chain or a light chain of the monoclonal antibody,

wherein the monoclonal antibody is trastuzumab or trastuzumab-DM1, and

a detection target is a peptide having an amino acid sequence expressed in SEQ ID No: 1, 3, 6 and/or 7, and

wherein the detection target is detected by multiple reaction monitoring under conditions described in Table 2 or Table 3.

2. A method wherein

a porous body in which a monoclonal antibody to be measured is immobilized in pores and nanoparticles on which a protease is immobilized are brought into contact with each other in a liquid to perform selective proteolysis of the monoclonal antibody,

a resulting peptide fragment is detected using liquid chromatography-mass spectrometry (LC-MS),

the porous body has an average pore diameter in a range of 10 nm – 200 nm,

the nanoparticles have an average particle size in a range of 50 nm – 500 nm,

the average particle size of the nanoparticles is larger than the average pore diameter of the porous body, and

a peptide fragment to be detected has an amino acid sequence that includes an amino acid derived from a CDR2 region of a heavy chain or a light chain of the monoclonal antibody,

wherein the monoclonal antibody is bevacizumab, and

a detection target is a peptide having an amino acid sequence expressed in SEQ ID No: 9 – 11, and

wherein the detection target is detected by multiple reaction monitoring under conditions described in Table 4.

3. A method wherein

a porous body in which a monoclonal antibody to be measured is immobilized in pores and nanoparticles on which a protease is immobilized are brought into contact with each other in a liquid to perform selective proteolysis of the monoclonal antibody,

a resulting peptide fragment is detected using liquid chromatography-mass spectrometry (LC-MS),

the porous body has an average pore diameter in a range of 10 nm – 200 nm,

the nanoparticles have an average particle size in a range of 50 nm – 500 nm,

the average particle size of the nanoparticles is larger than the average pore diameter of the porous body, and

a peptide fragment to be detected has an amino acid sequence that includes an amino acid derived from a CDR2 region of a heavy chain or a light chain of the monoclonal antibody,

wherein the monoclonal antibody is rituximab, and

a detection target is a peptide having an amino acid sequence expressed in SEQ ID No: 13, 15 and/or 16, and

wherein the detection target is detected by multiple reaction monitoring under conditions described in Table 5.

Also disclosed are the following examples:

(1) A method is provided in which a porous body in which a monoclonal antibody to be measured is immobilized in pores and nanoparticles on which a protease is immobilized are brought into contact with each other in a liquid to perform selective proteolysis of the monoclonal antibody; a resulting peptide fragment is detected using liquid chromatography-mass

spectrometry (LC-MS); the porous body has an average pore diameter in a range of 10 nm – 200 nm; the nanoparticles have an average particle size in a range of 50 nm – 500 nm; the average particle size of the nanoparticles is larger than the average pore diameter of the porous body; and a peptide fragment to be detected has an amino acid sequence that includes an amino acid derived from a CDR2 region of a heavy chain or a light chain of the monoclonal antibody.

(2) In the method described in the above aspect (1), the monoclonal antibody is trastuzumab or trastuzumab-DM1, and a detection target is a peptide having an amino acid sequence expressed in SEQ ID No: 1, 3, 6 and/or 7.

(3) In the method described in the above aspect (2), the detection target is detected by multiple reaction monitoring under conditions described in Table 2 or 3.

(4) In the method described in the above aspect (1), the monoclonal antibody is bevacizumab, and a detection target is a peptide having an amino acid sequence expressed in SEQ ID No: 9 – 11.

(5) In the method described in the above aspect (4), the detection target is detected by multiple reaction monitoring under conditions described in Table 4.

(6) In the method described in the above aspect (1), the monoclonal antibody is rituximab, and a detection target is a peptide having an amino acid sequence expressed in SEQ ID No: 13, 15 and/or 16.

(7) In the method described in the above aspect (6), the detection target is detected by multiple reaction monitoring under conditions described in Table 5.

[0021]

The present specification incorporates a disclosure content of Japanese Patent Application No. 2015-046059 on which priority of the present application is based.

WHAT IS CLAIMED IS:

1. A method wherein

a porous body in which a monoclonal antibody to be measured is immobilized in pores and nanoparticles on which a protease is immobilized are brought into contact with each other in a liquid to perform selective proteolysis of the monoclonal antibody,

a resulting peptide fragment is detected using liquid chromatography-mass spectrometry (LC-MS),

the porous body has an average pore diameter in a range of 10 nm – 200 nm,

the nanoparticles have an average particle size in a range of 50 nm – 500 nm,

the average particle size of the nanoparticles is larger than the average pore diameter of the porous body, and

a peptide fragment to be detected has an amino acid sequence that includes an amino acid derived from a CDR2 region of a heavy chain or a light chain of the monoclonal antibody,

wherein the monoclonal antibody is trastuzumab or trastuzumab-DM1, and

a detection target is a peptide having an amino acid sequence expressed in SEQ ID No: 1, 3, 6 and/or 7, and

wherein the detection target is detected by multiple reaction monitoring under conditions described in Table 2 or Table 3.

2. A method wherein

a porous body in which a monoclonal antibody to be measured is immobilized in pores and nanoparticles on which a protease is immobilized are brought into contact with each other in a liquid to perform selective proteolysis of the monoclonal antibody,

a resulting peptide fragment is detected using liquid chromatography-mass spectrometry (LC-MS),

the porous body has an average pore diameter in a range of 10 nm – 200 nm,

the nanoparticles have an average particle size in a range of 50 nm – 500 nm,

the average particle size of the nanoparticles is larger than the average pore diameter of

the porous body, and

a peptide fragment to be detected has an amino acid sequence that includes an amino acid derived from a CDR2 region of a heavy chain or a light chain of the monoclonal antibody,

wherein the monoclonal antibody is bevacizumab, and

a detection target is a peptide having an amino acid sequence expressed in SEQ ID No: 9 – 11, and

wherein the detection target is detected by multiple reaction monitoring under conditions described in Table 4.

3. A method wherein

a porous body in which a monoclonal antibody to be measured is immobilized in pores and nanoparticles on which a protease is immobilized are brought into contact with each other in a liquid to perform selective proteolysis of the monoclonal antibody,

a resulting peptide fragment is detected using liquid chromatography-mass spectrometry (LC-MS),

the porous body has an average pore diameter in a range of 10 nm – 200 nm,

the nanoparticles have an average particle size in a range of 50 nm – 500 nm,

the average particle size of the nanoparticles is larger than the average pore diameter of the porous body, and

a peptide fragment to be detected has an amino acid sequence that includes an amino acid derived from a CDR2 region of a heavy chain or a light chain of the monoclonal antibody,

wherein the monoclonal antibody is rituximab, and

a detection target is a peptide having an amino acid sequence expressed in SEQ ID No: 13, 15 and/or 16, and

wherein the detection target is detected by multiple reaction monitoring under conditions described in Table 5.