[0062]

The present inventors have studied intensively to develop a means of specifically eliminating highly malignant disease-associated cells, and have focused on gpNMB (glycoprotein nonmetastatic melanoma protein B) as a common antigen for disease-associated cells involved in various diseases. As a result, the present inventors have succeeded in obtaining novel anti-gpNMB antibodies that bind to a new epitope on gpNMB, which is different from previously known antibodies, through diligent investigation using various experimental means and methods under various constraints. Based on these findings, the inventors have completed the following inventions.

[0063] In one aspect, the present disclosure refers to the use of a pharmaceutical composition in the manufacture of a medicament for removing disease-related cells such as senescent cells, cancer-related cells, and phagocytes, optionally wherein the cancer-related cells are selected from cancer cells, cancer stem cells, cancer progenitor cells, and cancer infiltration cells, and wherein the pharmaceutical composition comprises an anti-gpNMB antibody or its fragment or a derivative thereof that binds specifically to at least one site in a region from V78 to a PKD domain of human gpNMB (glycoprotein nonmetastatic melanoma protein B) having the amino acid sequence of SEQ ID NO 209. In another aspect, the present disclosure refers to the use of a pharmaceutical composition in the manufacture of a medicament for removing disease-related cells, wherein the pharmaceutical composition comprises an anti-gpNMB antibody or its fragment or a derivative thereof that binds to at least one site in a region from V78 to a PKD domain of human gpNMB (glycoprotein nonmetastatic melanoma protein B) having the amino acid sequence of SEQ ID NO 209 competitively with an anti-gpNMB antibody or its fragment or a derivative thereof as disclosed herein. In yet another aspect, the present disclosure refers to the use of a pharmaceutical composition in the manufacture of a medicament for removing disease-related cells, wherein the pharmaceutical composition comprises: a nucleic acid molecule having a polynucleotide sequence encoding an anti-gpNMB ntibody or its fragment or a derivative described herein; and/or a cloning vector or expression vector carrying at least one of the nucleic acid molecule; and/or a recombinant cell into which the vector has been introduced.

Specifically, aspects of the present invention include the following.

[Aspect 1] A pharmaceutical composition for removing disease-related cells, comprising an anti-gpNMB antibody or its fragment or a derivative thereof that binds specifically to at least one site in a region from V78 to a PKD domain of human gpNMB (glycoprotein nonmetastatic melanoma protein B) having the amino acid sequence of SEQ ID NO 209.

[Aspect 2] The pharmaceutical composition according to Aspect 1, wherein the anti-gpNMB antibody specifically binds to a region containing amino acid residue(s) D287 and/or H301 of human gpNMB having the amino acid sequence of SEQ ID NO 209.

[Aspect 3] The pharmaceutical composition according to Aspect 1 or 2, wherein the anti-gpNMB antibody specifically binds to a region containing amino acid residue(s) R214 and/or R215 of human gpNMB having the amino acid sequence of SEQ ID NO 209.
[Aspect 4] The pharmaceutical composition according to Aspect 2 or 3, wherein the anti-gpNMB antibody specifically binds to one or more regions selected from a region containing amino acid residue(s) K257 and/or D258, a region containing amino acid residue(s) H268 and/or D269, a region containing amino acid residue K282, a region containing amino acid residue K316, a region containing amino acid residue K186, and a region containing amino acid residue(s) H216 and/or R218 of human gpNMB having the amino acid sequence of SEQ ID NO 209.
[Aspect 5] The pharmaceutical composition according to Aspect 1, wherein the anti-gpNMB antibody binds specifically to at least one site in a region from V78 to S92 of human gpNMB having the amino acid sequence of SEQ ID NO 209.
[Aspect 6] The pharmaceutical composition according to any one of Aspects 1 to 5, wherein the anti-gpNMB antibody specifically binds to at least one site in a region from V78 to a PKD domain of mouse gpNMB having the amino acid sequence of SEQ ID NO 211.
[Aspect 7] The pharmaceutical composition according to any one of Aspects 1 to 6, wherein the anti-gpNMB antibody is a monoclonal antibody or its fragment or a derivative thereof.

CLAIMS

[Claim 1]

Use of a pharmaceutical composition in the manufacture of a medicament for removing disease-related cells such as senescent cells, cancer-related cells, and phagocytes, optionally wherein the cancer-related cells are selected from cancer cells, cancer stem cells, cancer progenitor cells, and cancer infiltration cells, and

wherein the pharmaceutical composition comprises an anti-gpNMB antibody or its fragment or a derivative thereof that binds specifically to at least one site in a region from V78 to a PKD domain of human gpNMB (glycoprotein nonmetastatic melanoma protein B) having the amino acid sequence of SEQ ID NO 209.

[Claim 2]

The use according to claim 1, wherein the anti-gpNMB antibody which specifically:

(i) binds to a region containing amino acid residue(s) D287 and/or H301 of human gpNMB having the amino acid sequence of SEQ ID NO 209, and optionally also specifically binds to one or more regions selected from a region containing amino acid residue(s) K257 and/or D258, a region containing amino acid residue(s) H268 and/or D269, a region containing amino acid residue K282, a region containing amino acid residue K316, a region containing amino acid residue K186, and a region containing amino acid residue(s) H216 and/or R218 of human gpNMB having the amino acid sequence of SEQ ID NO 209;

(ii) binds to a region containing amino acid residue(s) R214 and/or R215 of human gpNMB having the amino acid sequence of SEQ ID NO 209, and optionally also specifically binds to one or more regions selected from a region containing amino acid residue(s) K257 and/or D258, a region containing amino acid residue(s) H268 and/or D269, a region containing amino acid residue K282, a region containing amino acid residue K316, a region containing amino acid residue K186, and a region containing amino acid residue(s) H216 and/or R218 of human gpNMB having the amino acid sequence of SEQ ID NO 209; and/or

(iii) binds specifically to at least one site in a region from V78 to S92 of human gpNMB having the amino acid sequence of SEQ ID NO 209.

[Claim 3]

The use according to claim 1 or 2, wherein the anti-gpNMB antibody specifically binds to at least one site in a region from V78 to a PKD domain of mouse gpNMB having the amino acid sequence of SEQ ID NO 211.

[Claim 4]

The use according to any one of claims 1 to 3, wherein the anti-gpNMB antibody is ;

(i) a monoclonal antibody or its fragment or a derivative thereof; and/or

(ii) a Fab, scFv, Diabody, Nanobody, VHH, bispecific antibody, or multispecific antibody, or a derivative thereof.

[Claim 5]

The use according to any one of claims 1 to 4, wherein the anti-gpNMB antibody comprises at least a heavy chain variable region comprising:

(1) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 1, or an amino acid sequence derived from SEQ ID NO 1 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 1,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 3, or an amino acid sequence derived from SEQ ID NO 3 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 3, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 5, or an amino acid sequence derived from SEQ ID NO 5 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 75.0 % or more, 83.3 % or more, or 91.6 % or more to the amino acid sequence defined in SEQ ID NO 5, or

(2) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 17, or an amino acid sequence derived from SEQ ID NO 17 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 17,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 19, or an amino acid sequence derived from SEQ ID NO 19 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 19, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 21, or an amino acid sequence derived from SEQ ID NO 21 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 66.6 % or more, 73.3 % or more, 80.0 % or more, 86.6 % or more, or 93.3 % or more to the amino acid sequence defined in SEQ ID NO 21, or

(3) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 33, or an amino acid sequence derived from SEQ ID NO 33 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 33,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 35, or an amino acid sequence derived from SEQ ID NO 35 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 35, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 37, or an amino acid sequence derived from SEQ ID NO 37 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 66.6 % or more, 73.3 % or more, 80.0 % or more, 86.6 % or more, or 93.3 % or more to the amino acid sequence defined in SEQ ID NO 37, or

(4) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 49, or an amino acid sequence derived from SEQ ID NO 49 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 49,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 51, or an amino acid sequence derived from SEQ ID NO 51 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 51, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 53, or an amino acid sequence derived from SEQ ID NO 53 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 68.7 % or more, 75.0 % or more, 81.2 % or more, 87.5 % or more, or 93.7 % or more to the amino acid sequence defined in SEQ ID NO 53, or

(5) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 65, or an amino acid sequence derived from SEQ ID NO 65 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 65,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 67, or an amino acid sequence derived from SEQ ID NO 67 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology

(preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 67, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 69, or an amino acid sequence derived from SEQ ID NO 69 via substitution, deletion, or insertion of any one, two, three, four, or five amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 64.2 % or more, 71.4 % or more, 78.5 % or more, 85.7 % or more, or 92.8 % or more to the amino acid sequence defined in SEQ ID NO 69,

(6) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 81, or an amino acid sequence derived from SEQ ID NO 81 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 81,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 83, or an amino acid sequence derived from SEQ ID NO 83 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 83, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 85, or an amino acid sequence derived from SEQ ID NO 85 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 85, or

(7) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 97, or an amino acid sequence derived from SEQ ID NO 97 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 97,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 99, or an amino acid sequence derived from SEQ ID NO 99 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 99, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 101, or an amino acid sequence derived from SEQ ID NO 101 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more or 80.0 % or more to the amino acid sequence defined in SEQ ID NO 101, or

(8) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 113, or an amino acid sequence derived from SEQ ID NO 113 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a

homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 113,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 115, or an amino acid sequence derived from SEQ ID NO 115 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 115, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 117, or an amino acid sequence derived from SEQ ID NO 117 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 66.6 % or more, 73.3 % or more, 80.0 % or more, 86.6 % or more, or 93.3 % or more to the amino acid sequence defined in SEQ ID NO 117, or

(9) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 129, or an amino acid sequence derived from SEQ ID NO 129 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 129,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 131, or an amino acid sequence derived from SEQ ID NO 131 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 131, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 133, or an amino acid sequence derived from SEQ ID NO 133 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 66.6 % or more, 73.3 % or more, 80.0 % or more, 86.6 % or more, or 93.3 % or more to the amino acid sequence defined in SEQ ID NO 133, or

(10) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 145, or an amino acid sequence derived from SEQ ID NO 145 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 145,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 147, or an amino acid sequence derived from SEQ ID NO 147 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 147, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 149, or an amino acid sequence derived from SEQ ID NO 149 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 66.6 % or more, 73.3 % or more, 80.0 % or more, 86.6 % or more, or 93.3 % or more to the amino acid sequence defined in SEQ ID NO 149, or

(11) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 161, or an amino acid sequence derived from SEQ ID NO 161 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 161,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 163, or an amino acid sequence derived from SEQ ID NO 163 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 163, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 165, or an amino acid sequence derived from SEQ ID NO 165 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 66.6 % or more, 73.3 % or more, 80.0 % or more, 86.6 % or more, or 93.3 % or more to the amino acid sequence defined in SEQ ID NO 165, or

(12) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 255, or an amino acid sequence derived from SEQ ID NO 255 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 255,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 257, or an amino acid sequence derived from SEQ ID NO 257 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 257, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 259, or an amino acid sequence derived from SEQ ID NO 259 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 259, or

(13) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 283, or an amino acid sequence derived from SEQ ID NO 283 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a

homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 283,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 285, or an amino acid sequence derived from SEQ ID NO 285 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 285,

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 287, or an amino acid sequence derived from SEQ ID NO 287 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 66.6 % or more, 73.3 % or more, 80.0 % or more, 86.6 % or more, or 93.3 % or more to the amino acid sequence defined in SEQ ID NO 287, or

(14) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 311, or an amino acid sequence derived from SEQ ID NO 311 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 311,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 313, or an amino acid sequence derived from SEQ ID NO 313 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 313,

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 315, or an amino acid sequence derived from SEQ ID NO 315 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 66.6 % or more, 73.3 % or more, 80.0 % or more, 86.6 % or more, or 93.3 % or more to the amino acid sequence defined in SEQ ID NO 315, or

(15) as a CDR grafting region H1 sequence, the amino acid sequence defined in SEQ ID NO 271, or an amino acid sequence derived from SEQ ID NO 271 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues other than tyrosine at position 27, asparagine at position 32, and tryptophan at position 33,

as a CDR grafting region H2 sequence, the amino acid sequence defined in SEQ ID NO 273, or an amino acid sequence derived from SEQ ID NO 273 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues other than aspartic acid at position 55, phenylalanine at position 57, threonine at position 58, asparagine at position 59, tyrosine at position 60, and asparagine at position 61,

as a CDR grafting region H3 sequence, the amino acid sequence defined in SEQ ID NO 275, or an amino acid sequence defined in SEQ ID NO 275 via substitution, deletion,

or insertion of any one, two, three, four, five, or six amino acid residues other than arginine at position 98, glycine at position 100, and glycine at position 109, or

(16) as a CDR grafting region H1 sequence, the amino acid sequence defined in SEQ ID NO 299, or an amino acid sequence derived from SEQ ID NO 299 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues,

as a CDR grafting region H2 sequence, the amino acid sequence defined in SEQ ID NO 301, or an amino acid sequence derived from SEQ ID NO 301 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues other than aspartic acid at position 52, tryptophan at position 54, aspartic acid at position 58, and proline at position 63,

as a CDR grafting region H3 sequence, the amino acid sequence defined in SEQ ID NO 303, or an amino acid sequence derived from SEQ ID NO 303 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues other than arginine at position 99, threonine at position 100, tyrosine at position 102, tyrosine at position 105, tyrosine at position 107, and methionine at position 110, or

(17) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 177, or an amino acid sequence derived from SEQ ID NO 177 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 177,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 179, or an amino acid sequence derived from SEQ ID NO 179 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 179, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 181, or an amino acid sequence derived from SEQ ID NO 181 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 181, or

(18) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 330, or an amino acid sequence derived from SEQ ID NO 330 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 330,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 331, or an amino acid sequence derived from SEQ ID NO 331 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 331, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 332, or an amino acid sequence derived from SEQ ID NO 332 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 332, or

(19) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 337, or an amino acid sequence derived from SEQ ID NO 337 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 337,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 338, or an amino acid sequence derived from SEQ ID NO 338 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 338, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 339, or an amino acid sequence derived from SEQ ID NO 339 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 339, or

(20) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 344, or an amino acid sequence derived from SEQ ID NO 344 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 344,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 345, or an amino acid sequence derived from SEQ ID NO 345 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 345, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 346, or an amino acid sequence derived from SEQ ID NO 346 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 346, or

(21) as a CDR grafting region H1 sequence, the amino acid sequence defined in SEQ ID NO 327, or an amino acid sequence derived from SEQ ID NO 327 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 327,

as a CDR grafting region H2 sequence, the amino acid sequence defined in SEQ ID NO 328, or an amino acid sequence derived from SEQ ID NO 328 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 64.7 % or more, 70.5 % or more, 76.4 % or more, 82.3 % or more, 88.2 % or more, or 94.1 % or more to the amino acid sequence defined in SEQ ID NO 328,

as a CDR grafting region H3 sequence, the amino acid sequence defined in SEQ ID NO 329, or an amino acid sequence derived from SEQ ID NO 329 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 329, or

(22) as a CDR grafting region H1 sequence, the amino acid sequence defined in SEQ ID NO 334, or an amino acid sequence derived from SEQ ID NO 334 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 334,

as a CDR grafting region H2 sequence, the amino acid sequence defined in SEQ ID NO 335, or an amino acid sequence derived from SEQ ID NO 335 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 64.7 % or more, 70.5 % or more, 76.4 % or more, 82.3 % or more, 88.2 % or more, or 94.1 % or more to the amino acid sequence defined in SEQ ID NO 335,

as a CDR grafting region H3 sequence, the amino acid sequence defined in SEQ ID NO 336, or an amino acid sequence derived from SEQ ID NO 336 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 336, or

(23) as a CDR grafting region H1 sequence, the amino acid sequence defined in SEQ ID NO 341, or an amino acid sequence derived from SEQ ID NO 341 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 341,

as a CDR grafting region H2 sequence, the amino acid sequence defined in SEQ ID NO 342, or an amino acid sequence derived from SEQ ID NO 342 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 64.7 % or more, 70.5 % or more, 76.4 % or more, 82.3 % or more, 88.2 % or more, or 94.1 % or more to the amino acid sequence defined in SEQ ID NO 342,

as a CDR grafting region H3 sequence, the amino acid sequence defined in SEQ ID NO 343, or an amino acid sequence derived from SEQ ID NO 343 via substitution,

deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 343;

or which comprises at least a heavy chain variable region comprising:

(1) the amino acid sequence defined in SEQ ID NO 13, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 13, or

(2) the amino acid sequence defined in SEQ ID NO 29, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 29, or

(3) the amino acid sequence defined in SEQ ID NO 45, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 45, or

(4) the amino acid sequence defined in SEQ ID NO 61, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 61, or

(5) the amino acid sequence defined in SEQ ID NO 77, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 77, or

(6) the amino acid sequence defined in SEQ ID NO 93, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 93, or

(7) the amino acid sequence defined in SEQ ID NO 109, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 109, or

(8) the amino acid sequence defined in SEQ ID NO 125, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 125, or

(9) the amino acid sequence defined in SEQ ID NO 141, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 141, or

(10) the amino acid sequence defined in SEQ ID NO 157, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 157, or

(11) the amino acid sequence defined in SEQ ID NO 173, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 173, or

(12) the amino acid sequence defined in SEQ ID NO 267, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 267, or

(13) the amino acid sequence defined in SEQ ID NO 295, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 295, or
(14) the amino acid sequence defined in SEQ ID NO 323, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 323, or
(17) the amino acid sequence defined in SEQ ID NO 189, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 189, or
(18) the amino acid sequence defined in SEQ ID NO 333, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 333, or
(19) the amino acid sequence defined in SEQ ID NO 340, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 340, or
(20) the amino acid sequence defined in SEQ ID NO 347, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 347: and

optionally wherein:

(i) the heavy chain variable region comprises, as a framework sequence, a framework sequence of a class of human immunoglobulin; and/or
(ii) the antibody, fragment, or derivative further comprises a heavy chain constant region having an amino acid sequence of a heavy chain constant region in a class of human immunoglobulin.

[Claim 6]

The use according to any one of claims 1 to 8, wherein the anti-gpNMB antibody comprises at least a light chain variable region comprising:

(1) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 7, or an amino acid sequence derived from SEQ ID NO 7 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 7,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 9, or an amino acid sequence derived from SEQ ID NO 9 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 9, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 11, or an amino acid sequence derived from SEQ ID NO 11 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology

(preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 11, or

(2) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 23, or an amino acid sequence derived from SEQ ID NO 23 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more or 80.0 % or more to the amino acid sequence defined in SEQ ID NO 23,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 25, or an amino acid sequence derived from SEQ ID NO 25 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 25, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 27, or an amino acid sequence derived from SEQ ID NO 27 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 27, or

(3) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 39, or an amino acid sequence derived from SEQ ID NO 39 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more or 80.0 % or more to the amino acid sequence defined in SEQ ID NO 39,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 41, or an amino acid sequence derived from SEQ ID NO 41 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 41, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 43, or an amino acid sequence derived from SEQ ID NO 43 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 43, or

(4) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 55, or an amino acid sequence derived from SEQ ID NO 55 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 55,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 57, or an amino acid sequence derived from SEQ ID NO 57 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 57, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 59, or an amino acid sequence derived from SEQ ID NO 59 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 59, or

(5) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 71, or an amino acid sequence derived from SEQ ID NO 71 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more or 80.0 % or more to the amino acid sequence defined in SEQ ID NO 71,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 73, or an amino acid sequence derived from SEQ ID NO 73 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 73, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 75, or an amino acid sequence derived from SEQ ID NO 75 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 75, or

(6) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 87, or an amino acid sequence derived from SEQ ID NO 87 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 87,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 89, or an amino acid sequence derived from SEQ ID NO 89 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 89, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 91, or an amino acid sequence derived from SEQ ID NO 91 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 91, or

(7) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 103, or an amino acid sequence derived from SEQ ID NO 103 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 103,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 105, or an amino acid sequence derived from SEQ ID NO 105 via substitution, deletion, or insertion

of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 105, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 107, or an amino acid sequence derived from SEQ ID NO 107 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 107, or

(8) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 119, or an amino acid sequence derived from SEQ ID NO 119 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 119,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 121, or an amino acid sequence derived from SEQ ID NO 121 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 121, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 123, or an amino acid sequence derived from SEQ ID NO 123 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 123, or

(9) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 135, or an amino acid sequence derived from SEQ ID NO 135 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 135,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 137, or an amino acid sequence derived from SEQ ID NO 137 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 137, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 139, or an amino acid sequence derived from SEQ ID NO 139 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 139, or

(10) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 151, or an amino acid sequence derived from SEQ ID NO 151 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 151,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 153, or an amino acid sequence derived from SEQ ID NO 153 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 153, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 155, or an amino acid sequence derived from SEQ ID NO 155 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 155, or

(11) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 167, or an amino acid sequence derived from SEQ ID NO 167 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 167,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 169, or an amino acid sequence derived from SEQ ID NO 169 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 169, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 171, or an amino acid sequence derived from SEQ ID NO 171 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 171, or

(12) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 261, or an amino acid sequence derived from SEQ ID NO 261 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 261,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 263, or an amino acid sequence derived from SEQ ID NO 263 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 263, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 265, or an amino acid sequence derived from SEQ ID NO 265 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 265, or

(13) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 289, or an amino acid sequence derived from SEQ ID NO 289 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology

(preferably an identity) of 60.0 % or more or 80.0 % or more to the amino acid sequence defined in SEQ ID NO 289,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 291, or an amino acid sequence derived from SEQ ID NO 291 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 291, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 293, or an amino acid sequence derived from SEQ ID NO 293 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 293, or

(14) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 317, or an amino acid sequence derived from SEQ ID NO 317 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 317,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 319, or an amino acid sequence derived from SEQ ID NO 319 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 319, and

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 321, or an amino acid sequence derived from SEQ ID NO 321 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 321, or

(15) as a CDR grafting region L1 sequence, the amino acid sequence defined in SEQ ID NO 277, or an amino acid sequence defined in SEQ ID NO 277 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues other than isoleucine at position 29, tyrosine at position 31, and histidine at position 33,

as a CDR grafting region L2 sequence, the amino acid sequence defined in SEQ ID NO 279, or an amino acid sequence defined in SEQ ID NO 279 via substitution, deletion, or insertion of any one or two amino acid residue other than threonine at position 50,

as a CDR grafting region L3 sequence, the amino acid sequence defined in SEQ ID NO 281, or an amino acid sequence defined in SEQ ID NO 281 via substitution, deletion, or insertion of any one, two, or three amino acid residues other than histidine at position 88, glutamine at position 89, tryptophan at position 90, serine at position 92, tyrosine at position 93, proline at position 94, and cysteine at position 95, or

(16) as a CDR grafting region L1 sequence, the amino acid sequence defined in SEQ ID NO 305, or an amino acid sequence defined in SEQ ID NO 305 via substitution, deletion,

or insertion of any one, two, three, four, five, or six amino acid residues other than leucine at position 31, tyrosine at position 37 and glutamic acid at position 39,

as a CDR grafting region L2 sequence, the amino acid sequence defined in SEQ ID NO 307, or an amino acid sequence defined in SEQ ID NO 307 via substitution, deletion, or insertion of any one or two amino acid residue other than lysine at position 55,

as a CDR grafting region L3 sequence, the amino acid sequence defined in SEQ ID NO 309, or an amino acid sequence defined in SEQ ID NO 309 via substitution, deletion, or insertion of any one, two, or three amino acid residues other than phenylalanine at position 94, or

(17) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 183, or an amino acid sequence derived from SEQ ID NO 183 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 183,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 185, or an amino acid sequence derived from SEQ ID NO 185 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 185,

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 187, or an amino acid sequence derived from SEQ ID NO 187 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 187, or

(18) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 351, or an amino acid sequence derived from SEQ ID NO 351 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 351,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 352, or an amino acid sequence derived from SEQ ID NO 352 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 352,

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 353, or an amino acid sequence derived from SEQ ID NO 353 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 353, or

(19) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 358, or an amino acid sequence derived from SEQ ID NO 358 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology

(preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 358,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 359, or an amino acid sequence derived from SEQ ID NO 359 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 359,

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 360, or an amino acid sequence derived from SEQ ID NO 360 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 360, or

(20) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 365, or an amino acid sequence derived from SEQ ID NO 365 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 365,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 366, or an amino acid sequence derived from SEQ ID NO 366 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 366,

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 367, or an amino acid sequence derived from SEQ ID NO 367 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 367, or

(21) as a CDR grafting region L1 sequence, the amino acid sequence defined in SEQ ID NO 348, or an amino acid sequence derived from SEQ ID NO 348 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 348,

as a CDR grafting region L2 sequence, the amino acid sequence defined in SEQ ID NO 349, or an amino acid sequence derived from SEQ ID NO 349 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 349,

as a CDR grafting region L3 sequence, the amino acid sequence defined in SEQ ID NO 350, or an amino acid sequence derived from SEQ ID NO 350 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 350, or

(22) as a CDR grafting region L1 sequence, the amino acid sequence defined in SEQ ID NO 355, or an amino acid sequence derived from SEQ ID NO 355 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 355,

as a CDR grafting region L2 sequence, the amino acid sequence defined in SEQ ID NO 356, or an amino acid sequence derived from SEQ ID NO 356 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 356,

as a CDR grafting region L3 sequence, the amino acid sequence defined in SEQ ID NO 357, or an amino acid sequence derived from SEQ ID NO 357 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 357, or

(23) as a CDR grafting region L1 sequence, the amino acid sequence defined in SEQ ID NO 362, or an amino acid sequence derived from SEQ ID NO 362 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 362,

as a CDR grafting region L2 sequence, the amino acid sequence defined in SEQ ID NO 363, or an amino acid sequence derived from SEQ ID NO 363 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 363,

as a CDR grafting region L3 sequence, the amino acid sequence defined in SEQ ID NO 364, or an amino acid sequence derived from SEQ ID NO 364 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 364;

or which comprises at least a light chain variable region comprising:

(1) the amino acid sequence defined in SEQ ID NO 15, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 15, or

(2) the amino acid sequence defined in SEQ ID NO 31, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 31, or

(3) the amino acid sequence defined in SEQ ID NO 47, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 47, or

(4) the amino acid sequence defined in SEQ ID NO 63, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 63, or

(5) the amino acid sequence defined in SEQ ID NO 79, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 79, or

(6) the amino acid sequence defined in SEQ ID NO 95, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 95, or

(7) the amino acid sequence defined in SEQ ID NO 111, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 111, or

(8) the amino acid sequence defined in SEQ ID NO 127, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 127, or

(9) the amino acid sequence defined in SEQ ID NO 143, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 143, or

(10) the amino acid sequence defined in SEQ ID NO 159, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 159, or

(11) the amino acid sequence defined in SEQ ID NO 175, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 175, or

(12) the amino acid sequence defined in SEQ ID NO 269, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 269, or

(13) the amino acid sequence defined in SEQ ID NO 297, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 297, or

(14) the amino acid sequence defined in SEQ ID NO 325, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 325, or

(17) the amino acid sequence defined in SEQ ID NO 191, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 191, or

(18) the amino acid sequence defined in SEQ ID NO 354, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 354, or

(19) the amino acid sequence defined in SEQ ID NO 361, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 361, or
(20) the amino acid sequence defined in SEQ ID NO 368, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 368;

and optionally wherein:

(i) the light chain variable region comprises, as a framework sequence, a framework sequence of a class of human immunoglobulin: and/or
(ii) the antibody, fragment, or derivative further comprises a light chain constant region having an amino acid sequence of a light chain constant region in a class of human immunoglobulin.

[Claim 7] Use of a pharmaceutical composition in the manufacture of a medicament for removing disease-related cells, wherein the pharmaceutical composition comprises an anti-gpNMB antibody or its fragment or a derivative thereof that binds to at least one site in a region from V78 to a PKD domain of human gpNMB (glycoprotein nonmetastatic melanoma protein B) having the amino acid sequence of SEQ ID NO 209 competitively with an anti-gpNMB antibody or its fragment or a derivative thereof according to any one of claims 1 to 6.

[Claim 8]

Use of a pharmaceutical composition in the manufacture of a medicament for removing disease-related cells, wherein the pharmaceutical composition comprises:

a nucleic acid molecule having a polynucleotide sequence encoding an anti-gpNMB antibody or its fragment or a derivative thereof according to any one of claims 1 to 6; and/or

a cloning vector or expression vector carrying at least one of the nucleic acid molecule; and/or

a recombinant cell into which the vector has been introduced.

[Claim 9]

The use according to any one of claims 1 to 8, wherein the disease is selected from obesity, diabetes, arteriosclerosis, fibrosis, cancer, metabolic disease, circulatory disease, lysosomal stress-associated disease (e.g., lysosome disease), autoimmune disease (e.g., multiple sclerosis), neuropathic pain, fibromyalgia, and glioblastoma.

[Claim 10]

The use according to any one of claims 1 to 9, for used in treating or preventing a disease by removing disease-related cells.

[Claim 11]

An anti-gpNMB antibody or its fragment or a derivative thereof that binds specifically to at least one site in a region from V78 to S92 of human gpNMB (glycoprotein nonmetastatic melanoma protein B) having the amino acid sequence of SEQ ID NO 209.

[Claim 12]

The anti-gpNMB antibody or its fragment or a derivative thereof according to claim 11, which:

a) binds specifically to a region containing amino acid residue K186 of human gpNMB having the amino acid sequence of SEQ ID NO 209, and/or

b) binds specifically to at least one site in a region from V78 to S92 of mouse gpNMB having the amino acid sequence of SEQ ID NO 211.

[Claim 13]

The anti-gpNMB antibody or its fragment or a derivative thereof according to claim 11 or 12, which is:

(i) a monoclonal antibody or its fragment or a derivative thereof, and/or

(ii) a Fab, scFv, Diabody, Nanobody, VHH, bispecific antibody, or multispecific antibody, or a derivative thereof.

[Claim 14]

The anti-gpNMB antibody or its fragment or a derivative thereof according to any one of claims 11 to 13, which comprises at least a heavy chain variable region comprising:

(17) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 177, or an amino acid sequence derived from SEQ ID NO 177 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 177,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 179, or an amino acid sequence derived from SEQ ID NO 179 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 179, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 181, or an amino acid sequence derived from SEQ ID NO 181 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 181, or

(18) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 330, or an amino acid sequence derived from SEQ ID NO 330 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 330,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 331, or an amino acid sequence derived from SEQ ID NO 331 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 331, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 332, or an amino acid sequence derived from SEQ ID NO 332 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 332, or

(19) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 337, or an amino acid sequence derived from SEQ ID NO 337 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 337,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 338, or an amino acid sequence derived from SEQ ID NO 338 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 338, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 339, or an amino acid sequence derived from SEQ ID NO 339 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 339, or

(20) as a CDR-H1 sequence, the amino acid sequence defined in SEQ ID NO 344, or an amino acid sequence derived from SEQ ID NO 344 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 344,

as a CDR-H2 sequence, the amino acid sequence defined in SEQ ID NO 345, or an amino acid sequence derived from SEQ ID NO 345 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 345, and

as a CDR-H3 sequence, the amino acid sequence defined in SEQ ID NO 346, or an amino acid sequence derived from SEQ ID NO 346 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 62.5 % or more, 75.0 % or more, or 87.5 % or more to the amino acid sequence defined in SEQ ID NO 346, or

(21) as a CDR grafting region H1 sequence, the amino acid sequence defined in SEQ ID NO 327, or an amino acid sequence derived from SEQ ID NO 327 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 327,

as a CDR grafting region H2 sequence, the amino acid sequence defined in SEQ ID NO 328, or an amino acid sequence derived from SEQ ID NO 328 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 64.7 % or more, 70.5 % or more, 76.4 % or more, 82.3 % or more, 88.2 % or more, or 94.1 % or more to the amino acid sequence defined in SEQ ID NO 328,

as a CDR grafting region H3 sequence, the amino acid sequence defined in SEQ ID NO 329, or an amino acid sequence derived from SEQ ID NO 329 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 329, or

(22) as a CDR grafting region H1 sequence, the amino acid sequence defined in SEQ ID NO 334, or an amino acid sequence derived from SEQ ID NO 334 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 334,

as a CDR grafting region H2 sequence, the amino acid sequence defined in SEQ ID NO 335, or an amino acid sequence derived from SEQ ID NO 335 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 64.7 % or more, 70.5 % or more, 76.4 % or more, 82.3 % or more, 88.2 % or more, or 94.1 % or more to the amino acid sequence defined in SEQ ID NO 335,

as a CDR grafting region H3 sequence, the amino acid sequence defined in SEQ ID NO 336, or an amino acid sequence derived from SEQ ID NO 336 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 336, or

(23) as a CDR grafting region H1 sequence, the amino acid sequence defined in SEQ ID NO 341, or an amino acid sequence derived from SEQ ID NO 341 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid

sequence having a homology (preferably an identity) of 60.0 % or more, 70.0 % or more, 80.0 % or more, or 90.0 % or more to the amino acid sequence defined in SEQ ID NO 341,

as a CDR grafting region H2 sequence, the amino acid sequence defined in SEQ ID NO 342, or an amino acid sequence derived from SEQ ID NO 342 via substitution, deletion, or insertion of any one, two, three, four, five, or six amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 64.7 % or more, 70.5 % or more, 76.4 % or more, 82.3 % or more, 88.2 % or more, or 94.1 % or more to the amino acid sequence defined in SEQ ID NO 342,

as a CDR grafting region H3 sequence, the amino acid sequence defined in SEQ ID NO 343, or an amino acid sequence derived from SEQ ID NO 343 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 343; or which comprises at least a heavy chain variable region comprising:

(17) the amino acid sequence defined in SEQ ID NO 189, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 189, or

(18) the amino acid sequence defined in SEQ ID NO 333, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 333, or

(19) the amino acid sequence defined in SEQ ID NO 340, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 340, or

(20) the amino acid sequence defined in SEQ ID NO 347, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 347: and

optionally wherein:

(i) the heavy chain variable region comprises, as a framework sequence, a framework sequence of a class of human immunoglobulin; and/or

(ii) the antibody, fragment, or derivative further comprises a heavy chain constant region having an amino acid sequence of a heavy chain constant region in a class of human immunoglobulin.

[Claim 15]

The anti-gpNMB antibody or its fragment or a derivative thereof according to any one of claims 11 to 14, which comprises at least a light chain variable region comprising:

(17) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 183, or an amino acid sequence derived from SEQ ID NO 183 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology

(preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 183,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 185, or an amino acid sequence derived from SEQ ID NO 185 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 185,

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 187, or an amino acid sequence derived from SEQ ID NO 187 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 187, or

(18) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 351, or an amino acid sequence derived from SEQ ID NO 351 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 351,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 352, or an amino acid sequence derived from SEQ ID NO 352 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 352,

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 353, or an amino acid sequence derived from SEQ ID NO 353 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 353, or

(19) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 358, or an amino acid sequence derived from SEQ ID NO 358 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 358,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 359, or an amino acid sequence derived from SEQ ID NO 359 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 359,

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 360, or an amino acid sequence derived from SEQ ID NO 360 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 360, or

(20) as a CDR-L1 sequence, the amino acid sequence defined in SEQ ID NO 365, or an amino acid sequence derived from SEQ ID NO 365 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more or 83.3 % or more to the amino acid sequence defined in SEQ ID NO 365,

as a CDR-L2 sequence, the amino acid sequence defined in SEQ ID NO 366, or an amino acid sequence derived from SEQ ID NO 366 via substitution, deletion, or insertion of any one amino acid residue, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more to the amino acid sequence defined in SEQ ID NO 366,

as a CDR-L3 sequence, the amino acid sequence defined in SEQ ID NO 367, or an amino acid sequence derived from SEQ ID NO 367 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 367, or

(21) as a CDR grafting region L1 sequence, the amino acid sequence defined in SEQ ID NO 348, or an amino acid sequence derived from SEQ ID NO 348 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 348,

as a CDR grafting region L2 sequence, the amino acid sequence defined in SEQ ID NO 349, or an amino acid sequence derived from SEQ ID NO 349 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 349,

as a CDR grafting region L3 sequence, the amino acid sequence defined in SEQ ID NO 350, or an amino acid sequence derived from SEQ ID NO 350 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 350, or

(22) as a CDR grafting region L1 sequence, the amino acid sequence defined in SEQ ID NO 355, or an amino acid sequence derived from SEQ ID NO 355 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 355,

as a CDR grafting region L2 sequence, the amino acid sequence defined in SEQ ID NO 356, or an amino acid sequence derived from SEQ ID NO 356 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 356,

as a CDR grafting region L3 sequence, the amino acid sequence defined in SEQ ID NO 357, or an amino acid sequence derived from SEQ ID NO 357 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 357, or

(23) as a CDR grafting region L1 sequence, the amino acid sequence defined in SEQ ID NO 362, or an amino acid sequence derived from SEQ ID NO 362 via substitution, deletion, or insertion of any one, two, three, or four amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 63.6 % or more, 72.7 % or more, 81.8 % or more, or 90.9 % or more to the amino acid sequence defined in SEQ ID NO 362,

as a CDR grafting region L2 sequence, the amino acid sequence defined in SEQ ID NO 363, or an amino acid sequence derived from SEQ ID NO 363 via substitution, deletion, or insertion of any one or two amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 71.4 % or more or 85.7 % or more to the amino acid sequence defined in SEQ ID NO 363,

as a CDR grafting region L3 sequence, the amino acid sequence defined in SEQ ID NO 364, or an amino acid sequence derived from SEQ ID NO 364 via substitution, deletion, or insertion of any one, two, or three amino acid residues, or an amino acid sequence having a homology (preferably an identity) of 66.6 % or more, 77.7 % or more, or 88.8 % or more to the amino acid sequence defined in SEQ ID NO 364; or which comprises at least a light chain variable region comprising:

(17) the amino acid sequence defined in SEQ ID NO 191, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 191, or

(18) the amino acid sequence defined in SEQ ID NO 354, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 354, or

(19) the amino acid sequence defined in SEQ ID NO 361, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 361, or

(20) the amino acid sequence defined in SEQ ID NO 368, or an amino acid sequence having a homology of 60 % or more to the amino acid sequence defined in SEQ ID NO 368; and

optionally wherein:

(i) the light chain variable region comprises, as a framework sequence, a framework sequence of a class of human immunoglobulin, and/or

(ii) the antibody, fragment, or derivative further comprises a light chain constant region having an amino acid sequence of a light chain constant region in a class of human immunoglobulin.