CLAIMS

1. An antibody or a fragment or derivative thereof which is capable of binding to a mucin protein and which comprises at least a portion of the heavy chain variable region which comprises a proline residue at amino acid position 28 according to the Kabat numbering.

2. The antibody according to claim 1, having the following characteristics:

   (a) it specifically binds a glycosylated MUC1 tumor epitope, and

   (b) it comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 16 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 28;

   or it is a functional fragment or derivative of the antibody having the characteristics (a) and (b) said functional fragment or derivative showing cross-specificity with an antibody comprising the amino acid sequence of SEQ ID NO: 16 and SEQ ID NO: 28.

3. The antibody or fragment or derivative thereof according to claim 1, having one or more of the following characteristics:

   (a) the specific binding to its epitope is dependent on the conformation and/or the glycosylation pattern of the epitope;

   (b) it is capable of specifically binding a peptide comprising the amino acid sequence PDTR, which preferably is glycosylated at the threonine residue with N-acetyl galactosamine (Tn) or galactose ß1-3 N-acetyl galactosamine (TF);

   (c) it is capable of specifically binding to MUC1, in particular to at least a portion of the glycosylated extracellular tandem repeats of tumor-derived MUC1;

   (d) it specifically binds a glycosylated MUC1 tumor epitope such that the strength of the bond is increased at least by a factor 20 in comparison with the bond to the non-glycosylated peptide of identical length and identical peptide sequence;

   (e) it is engineered, preferably humanized;

   (f) it comprises at least one complementarity determining region, preferably at least two, selected from the group consisting of

(i) CDR1 having the amino acid sequence of SEQ ID NO: 1,

(ii) CDR2 having the amino acid sequence of SEQ ID NO: 3, and

(iii) CDR3 having the amino acid sequence of SEQ ID NO: 5;

(g) it comprises the antibody framework regions selected from the following:

(i) FRH1, FRH2, FRH3 and FRH4 for the variable heavy chain VH have the following amino acid sequences, the amino acid position corresponding to the numeration according to Kabat:

for FRH1 (SEQ ID NO: 7)

Pos.	Amino acid
1	E
2	V
3	Q or K
4	L
5	V
6	E
7	S
8	G
9	G
10	G
11	L
12	V
13	Q
14	P

15	G
16	G
17	S
18	L or M
19	R
20	L
21	S
22	C
23	A or V
24	A
25	S
26	G
27	F
28	P
29	F
30	S

for FRH2 (SEQ ID NO: 9)

Pos.	Amino acid
36	W
37	V
38	R

39	Q
40	A or S
41	P
42	G or E
43	K
44	G
45	L
46	E
47	W
48	V
49	G or A

for FRH3 (SEQ ID NO: 11)

Pos.	Amino acid
66	R
67	F
68	T
69	I
70	S
71	R
72	D
73	D

74	S
75	K
76	N or S
77	S
78	L or V
79	Y
80	L
81	Q
82	M
82a	N
82b	S
82c	L
83	K
84	T
85	E
86	D
87	T
88	A
89	V
90	Y
91	Y
92	C
93	T or A

94	R

for FRH4 (SEQ ID NO: 13)

Pos.	Amino acid
103	W
104	G
105	Q
106	G
107	T
108	L
109	V or L
110	T
111	V
112	S
113	S

(ii) and optionally FRL1, FRL2, FRL3 and FRL4 for the light chain variable region VL have the following amino acid sequences, the amino acid position corresponding to the numeration according to Kabat:

for FRL1 (SEQ ID NO: 23)

Pos.	Amino acid
1	D

2	I
3	V
4	M
5	T
6	Q
7	S
8	P
9	L
10	S
11	L or N
12	P
13	V
14	T
15	P
16	G
17	E or D
18	P
19	A
20	S
21	I
22	S
23	C

for FRL2 (SEQ ID NO: 24)

Pos.	Amino acid
35	W
36	Y
37	L
38	Q
39	K
40	P
41	G
42	Q
43	S
44	P
45	Q
46	L
47	L
48	I
49	Y

for FRL3 (SEQ ID NO: 25)

Pos.	Amino acid
57	G

58	V
59	P
60	D
61	R
62	F
63	S
64	G
65	S
66	G
67	S
68	G
69	T
70	D
71	F
72	T
73	L
74	K or R
75	I
76	S
77	R
78	V
79	E
80	A

81	E
82	D
83	V
84	G
85	V
86	Y
87	Y
88	C

for FRL4 (SEQ ID NO: 26)

Pos.	Amino acid
98	R
99	G
100	Q or G
101	G
102	T
103	K
104	V
105	E
106	I
107	K
108	R

(h) it comprises a framework region 1 comprising the amino acid sequence of SEQ ID NO: 7, in particular SEQ ID NO: 8;

(i) it comprises a heavy chain variable region of an antibody comprising the amino acid sequence of SEQ ID NO: 15, preferably SEQ ID NO: 16;

(j) it comprises a light chain variable region of an antibody comprising the amino acid sequence of SEQ ID NO: 27, preferably SEQ ID NO: 28;

(k) it comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 16 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 28 or is a functional fragment or derivative thereof;

(l) it shows cross-specificity with the antibody Pankomab comprising the amino acid sequences of SEQ ID NO: 29 as heavy chain variable region and SEQ ID NO: 30 as light chain variable region; and/or

(m) it shows cross-specificity with the antibody comprising the amino acid sequences of SEQ ID NO: 16 as heavy chain variable region and SEQ ID NO: 28 as light chain variable region.

4. A nucleic acid encoding the antibody or fragment or derivative thereof according to any one of claims 1 to 3.

5. An expression cassette or vector comprising the nucleic acid according to claim 4 and a promoter operatively connected with said nucleic acid.

6. A host cell comprising the nucleic acid according to claim 4 or the expression cassette or vector according to claim 5.

7. A composition comprising the antibody or fragment or derivative thereof according to any one of claims 1 to 3, the nucleic acid according to claim 4, the expression cassette or vector according to claim 5, or the host cell according to claim 6.

8. The composition according to claim 7 being a pharmaceutical composition which preferably further comprises one or more components selected from the group consisting of solvents, diluents, and excipients.

9. The antibody or fragment or derivative thereof according to any one of claims 1 to 3, the nucleic acid according to claim 4, the expression cassette or vector according to claim 5, the host cell according to claim 6, or the composition according to claim 7 or 8 for use in medicine.

10. The antibody or fragment or derivative thereof according to any one of claims 1 to 3, the nucleic acid according to claim 4, the expression cassette or vector according to claim 5, the host cell according to claim 6, or the composition according to claim 7 or 8 for use in the treatment, prognosis, diagnosis and/or monitoring of cancer, **wherein** the cancer preferably is selected from the group consisting of cancer of the colon, stomach, liver, pancreas, kidney, blood, lung, and ovary.

11. A method for improving the antigen binding and/or recognition of an antibody or a fragment or derivative thereof which is capable of binding to a mucin protein and which comprises at least a portion of the heavy chain variable region, comprising the step of providing a proline residue at position 28 of the heavy chain variable region, according to the Kabat numbering.

12. The method according to claim 11, having at least one or more of the following characteristics:

    (a) the amino acid residue in position 28 is obtained by introducing a mutation into the nucleic acid coding for the antibody or fragment or derivative thereof, wherein the mutation is introduced in the codon coding for said amino acid residue; and/or

    (b) improving the antigen binding and/or antigen recognition includes enhancing the affinity of the antibody or fragment or derivative thereof to its antigen and/or increasing the specificity of the antibody or fragment or derivative thereof towards its antigen.

13. The method according to claim 11 or 12, **wherein** the antibody or fragment or derivative thereof has one or more of the following characteristics:

    (a) the specific binding to its epitope is dependent on the conformation and/or the glycosylation pattern of the epitope;

    (b) it is capable of specifically binding a peptide comprising the amino acid sequence PDTR, which preferably is glycosylated at the threonine residue with N-acetyl galactosamine (Tn) or galactose ß1-3 N-acetyl galactosamine (TF);

    (c) it is capable of specifically binding to MUC1, in particular to at least a portion of the glycosylated extracellular tandem repeats of tumor-derived MUC1;

    (d) it specifically binds a glycosylated MUC1 tumor epitope such that the strength of the bond is increased at least by a factor 20 in comparison with the bond to

the non-glycosylated peptide of identical length and identical peptide sequence;

(e) it is engineered, preferably humanized;

(f) it comprises at least one complementarity determining region selected from the group consisting of

(i) CDR1 having the amino acid sequence of SEQ ID NO: 1,

(ii) CDR2 having the amino acid sequence of SEQ ID NO: 3, and

(iii) CDR3 having the amino acid sequence of SEQ ID NO: 5;

(g) it comprises antibody framework regions selected from the following

(i) FRH1, FRH2, FRH3 and FRH4 for the variable heavy chain VH have the following amino acid sequences, the amino acid position corresponding to the numeration according to Kabat:

for FRH1 (SEQ ID NO: 33)

Pos.	Amino acid
1	E
2	V
3	Q or K
4	L
5	V
6	E
7	S
8	G
9	G
10	G

11	L
12	V
13	Q
14	P
15	G
16	G
17	S
18	L or M
19	R
20	L
21	S
22	C
23	A or V
24	A
25	S
26	G
27	F
28	T
29	F
30	S

for FRH2 (SEQ ID NO: 9)

Pos.	Amino

	acid
36	W
37	V
38	R
39	Q
40	A or S
41	P
42	G or E
43	K
44	G
45	L
46	E
47	W
48	V
49	G or A

for FRH3 (SEQ ID NO: 11)

Pos.	Amino acid
66	R
67	F
68	T
69	I

70	S
71	R
72	D
73	D
74	S
75	K
76	N or S
77	S
78	L or V
79	Y
80	L
81	Q
82	M
82a	N
82b	S
82c	L
83	K
84	T
85	E
86	D
87	T
88	A
89	V

90	Y
91	Y
92	C
93	T or A
94	R

for FRH4 (SEQ ID NO: 13)

Pos.	Amino acid
103	W
104	G
105	Q
106	G
107	T
108	L
109	V or L
110	T
111	V
112	S
113	S

(ii) and optionally FRL1, FRL2, FRL3 and FRL4 for the light chain variable region VL have the following amino acid sequences, the amino acid position corresponding to the numeration according to Kabat:

for FRL1 (SEQ ID NO: 23)

Pos.	Amino acid
1	D
2	I
3	V
4	M
5	T
6	Q
7	S
8	P
9	L
10	S
11	L or N
12	P
13	V
14	T
15	P
16	G
17	E or D
18	P
19	A
20	S

21	I
22	S
23	C

for FRL2 (SEQ ID NO: 24)

Pos.	Amino acid
35	W
36	Y
37	L
38	Q
39	K
40	P
41	G
42	Q
43	S
44	P
45	Q
46	L
47	L
48	I
49	Y

for FRL3 (SEQ ID NO: 25)

Pos.	Amino acid
57	G
58	V
59	P
60	D
61	R
62	F
63	S
64	G
65	S
66	G
67	S
68	G
69	T
70	D
71	F
72	T
73	L
74	K or R
75	I
76	S

77	R
78	V
79	E
80	A
81	E
82	D
83	V
84	G
85	V
86	Y
87	Y
88	C

for FRL4 (SEQ ID NO: 26)

Pos.	Amino acid
98	F
99	G
100	Q or G
101	G
102	T
103	K
104	V

105	E
106	I
107	K
108	R

(h) it comprises a framework region 1 comprising the amino acid sequence of SEQ ID NO: 33 or 34;

(i) it comprises a heavy chain variable region of an antibody comprising the amino acid sequence of SEQ ID NO: 38 or 29;

(j) it comprises a light chain variable region of an antibody comprising the amino acid sequence of SEQ ID NO: 27 or 30;

(k) it comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 38 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 27 or is a functional fragment or derivative thereof;

(l) it shows cross-specificity with the antibody Pankomab comprising the amino acid sequence of SEQ ID NO: 29 (heavy chain variable region) and SEQ ID NO: 30 (light chain variable region); and/or

(m) it shows cross specificity with the antibody comprising the amino acid sequences of SEQ ID NO: 16 as heavy chain variable region and SEQ ID NO: 28 as light chain variable region.

14. A method for preparing a nucleic acid according to claim 4, comprising the steps of

(a) providing a nucleic acid comprising the nucleic acid sequence coding for an antibody or a fragment or derivative thereof which is capable of binding to MUC1 and which comprises a heavy chain variable region, wherein the heavy chain variable region does not comprise a proline residue at amino acid position 28 according to the Kabat numbering; and

(b) introducing a mutation into the codon coding for amino acid number 28, according to the Kabat numbering, of the heavy chain variable region so that said codon codes for a proline residue.

15. The antibody or fragment or derivative thereof according to any one of claim 1 to 3, having a glycosylation pattern which has one or more of the following characteristics:

(a) it is a human glycosylation pattern;

(b) it enhances the activity of the antibody, in particular its binding affinity to its specific epitope, its binding affinity to one or more of its downstream receptors such as Fc receptors, its complement dependent cytotoxicity (CDC), and/or its antibody-dependent cell-mediated cytotoxicity (ADCC); and/or

(c) it is a glycosylation pattern as obtained when expressing the antibody or fragment or derivative thereof in a cell line selected from the group consisting of K562, KG1, MUTZ-3, NM-F9 [DSM ACC2606], NM-D4 [DSM ACC2605], NM-H9D8 [DSM ACC 2806], NM-H9D8-E6 [DSM ACC 2807], NM H9D8-E6Q12 [DSM ACC 2856], and GT-2X [DSM ACC 2858].

CLAIMS

1. An invention not claimed in any divisional application.