CLAIMS

1. A protein binding to Glycoprotein A repetitions predominant (GARP) in the presence of TGF-ß.

2. The protein according to claim **1** binding to GARP only in the presence of TGF-ß.

3. The protein according to claim **1** or **2**, binding to GARP when GARP is complexed to TGF-ß.

4. The protein according to any one of claims **1** to **2**, which binds to a complex of GARP and TGF-ß.

5. The protein according to any one of claims **1** to **4** inhibiting TGF-ß signaling.

6. The protein according to any one of claims **1** to **5**, being an antibody molecule selected from the group consisting of a whole antibody, a humanized antibody, a single chain antibody, a dimeric single chain antibody, a Fv, a Fab, a F(ab)'2, a defucosylated antibody, a bi-specific antibody, a diabody, a triabody, a tetrabody; or an antibody fragment selected from the group consisting of a unibody, a domain antibody, and a nanobody; or an antibody mimetic selected from the group consisting of an affibody, an affilin, an affitin, an adnectin, an atrimer, an evasin, a DARPin, an anticalin, an avimer, a fynomer, a versabody and a duocalin.

7. The protein according to any one of claims **1** to **6,** wherein said protein is an antibody or antigen binding fragment thereof that binds to a conformational epitope comprising one or more amino acids of GARP or an epitope of GARP modified as a result of GARP being complexed with latent TGF-ß.

8. The protein according to any one of claims **1** to **7**, wherein the variable region of the heavy chain comprises at least one of the following CDRs:

VH-CDR1: GFSLTGYGIN (SEQ ID NO: 2) or GYGIN (SEQ ID NO: 52);
VH-CDR2: MIWSDGSTDYNSVLTS (SEQ ID NO: 3); and
VH-CDR3: DRNYYDYDGAMDY (SEQ ID NO: 4),

or any CDR having an amino acid sequence that shares at least 60% of identity with SEQ ID NO: 2-4 or 52;

or wherein the variable region of the light chain comprises at least one of the following CDRs:

VL-CDR1: KASDHIKNWLA (SEQ ID NO: 5);

VL-CDR2: GATSLEA (SEQ ID NO: 6); and

VL-CDR3: QQYWSTPWT (SEQ ID NO: 7),

or any CDR having an amino acid sequence that shares at least 60% of identity with SEQ ID NO: 5-7;

or the variable region of the heavy chain comprises at least one of the following CDRs:

VH-CDR1: SYYID (SEQ ID NO: 13);

VH-CDR2: RIDPEDGGTKYAQKFQG (SEQ ID NO: 14);

VH-CDR3: or NEWETVVVGDLMYEYEY (SEQ ID NO: 15),

or any CDR having an amino acid sequence that shares at least 60% of identity with SEQ ID NO: 13-15;

or wherein the variable region of the light chain comprises at least one of the following CDRs:

VL-CDR1: QASQX_1I X_2S X_3LA (SEQ ID NO: 16), wherein X_1 is S or T, X_2 is S or V, X_3 is Y or F;

VL-CDR2: $X_1X_2SX_3X_4X_5$T (SEQ ID NO: 17), wherein X_1 is G or R; X_2 is A or T; X_3 is R or I; X_4 is L or P; X_5 is Q or K;

VL-CDR3: QQYX_1SX_2PX_3T, wherein X_1 is D, A, Y or V; X_2 is A, L or V; X_3 is V or P (SEQ ID NO: 18);

or any CDR having an amino acid sequence that shares at least 60% of identity with SEQ ID NO: 16-18.

9. The protein according to any one of claims **1** to **8**, wherein the variable region of the heavy chain comprises at least one of the following CDRs:

VH-CDR1: GFSLTGYGIN (SEQ ID NO: 2) or GYGIN (SEQ ID NO: 52);

VH-CDR2: MIWSDGSTDYNSVLTS (SEQ ID NO: 3); and

VH-CDR3: DRNYYDYDGAMDY (SEQ ID NO: 4),
or any CDR having an amino acid sequence that shares at least 60% of identity with SEQ ID NO: 2-4 or 52
and the variable region of the light chain comprises at least one of the following CDRs:
VL-CDR1: KASDHIKNWLA (SEQ ID NO: 5);
VL-CDR2: GATSLEA (SEQ ID NO: 6); and
VL-CDR3: QQYWSTPWT (SEQ ID NO: 7),
or any CDR having an amino acid sequence that shares at least 60% of identity with SEQ ID NO: 5-7
or the variable region of the heavy chain comprises at least one of the following CDRs:
VH-CDR1: SYYID (SEQ ID NO: 13);
VH-CDR2: RIDPEDGGTKYAQKFQG (SEQ ID NO: 14);
VH-CDR3: or NEWETVVVGDLMYEYEY (SEQ ID NO: 15);
or any CDR having an amino acid sequence that shares at least 60% of identity with SEQ ID NO: 13-15,

and the variable region of the light chain comprises at least one of the following CDRs:
VL-CDR1: QASQX_1I X_2S X_3LA (SEQ ID NO: 16), wherein X_1 is S or T, X_2 is S or V, X_3 is Y or F;
VL-CDR2: $X_1X_2SX_3X_4X_5$T (SEQ ID NO: 17), wherein X_1 is G or R; X_2 is A or T; X_3 is R or I; X_4 is L or P; X_5 is Q or K;
VL-CDR3: QQYX_1SX_2PX_3T, wherein X_1 is D, A, Y or V; X_2 is A, L or V; X_3 is V or P (SEQ ID NO: 18);
or any CDR having an amino acid sequence that shares at least 60% of identity with SEQ ID NO: 16-18.

10. The protein according to any one of claims **1** to **9**, wherein the variable region of the heavy chain comprises the following CDRs: GFSLTGYGIN (SEQ ID NO: 2), MIWSDGSTDYNSVLTS (SEQ ID NO: 3), DRNYYDYDGAMDY (SEQ ID NO: 4), and the variable region of the light chain comprises the following CDRs:

KASDHIKNWLA (SEQ ID NO: 5), GATSLEA (SEQ ID NO: 6), QQYWSTPWT (SEQ ID NO: 7), or any CDR having an amino acid sequence that shares at least 60% of identity with said SEQ ID NO: 2-7;

or wherein the variable region of the heavy chain comprises the following CDRs: GYGIN (SEQ ID NO: 52), MIWSDGSTDYNSVLTS (SEQ ID NO: 3), DRNYYDYDGAMDY (SEQ ID NO: 4), and the variable region of the light chain comprises the following CDRs: KASDHIKNWLA (SEQ ID NO: 5), GATSLEA (SEQ ID NO: 6), QQYWSTPWT (SEQ ID NO: 7), or any CDR having an amino acid sequence that shares at least 60% of identity with said SEQ ID NO: 52 and 3-7;

or wherein the variable region of the heavy chain comprises the following CDRs: SYYID (SEQ ID NO: 13), RIDPEDGGTKYAQKFQG (SEQ ID NO: 14), or NEWETVVVGDLMYEYEY (SEQ ID NO: 15); and the variable region of the light chain comprises the following CDRs: QASQX_1I X_2S X_3LA (SEQ ID NO: 16), wherein X_1 is S or T, X_2 is S or V, X_3 is Y or F; $X_1X_2SX_3X_4X_5$T (SEQ ID NO: 17), wherein X_1 is G or R; X_2 is A or T; X_3 is R or I; X_4 is L or P; X_5 is Q or K; QQYX_1SX_2PX_3T, wherein X_1 is D, A, Y or V; X_2 is A, L or V; X_3 is V or P (SEQ ID NO: 18); or any CDR having an amino acid sequence that shares at least 60% of identity with said SEQ ID NO: 16-18.

11. The protein according to any one of claims **1** to **10**, wherein the amino acid sequence encoding the heavy chain variable region is SEQ ID NO: 8 or SEQ ID NO: 50 and the amino acid sequence encoding the light chain variable region is SEQ ID NO: 9 or SEQ ID NO: 51, or the amino acid sequence encoding the heavy chain variable region is SEQ ID NO: 34 and the amino acid sequence encoding the light chain variable region is one of SEQ ID NO: 35-39 or any sequence having an amino acid sequence that shares at least 60% of identity with said SEQ ID NO: 8-9, 50-51 or 34-39.

12. The protein according to any one of claims **1** to **11** binding to an epitope on the polypeptide having the amino acid sequence SEQ ID No: 1 recognized by an antibody comprising a heavy chain variable region as set forth in SEQ ID NO: 8

~~or in SEQ ID NO: 50 and a light chain variable region as set forth in SEQ ID NO: 9 or in SEQ ID NO: 51, or by an antibody comprising a heavy chain variable region as set forth in SEQ ID NO: 34 and one of the light chain variable region as set forth in SEQ ID NO: 35-39.~~

~~**13.** An antibody or antigen binding fragment produced by a hybridoma registered under the accession number LMBP 10246CB on May 30, 2013.~~

~~**14.** A hybridoma cell line producing an antibody against GARP registered under the accession number LMBP 10246CB on May 30, 2013.~~

~~**15.** A pharmaceutical composition comprising the protein according to any one of claims **1** to **14** and a pharmaceutically acceptable excipient.~~

~~**16.** The pharmaceutical composition according to claim **15** for treating a TGF-ß related disorder in a subject in need thereof.~~

~~**17.** The pharmaceutical composition according to claim **16,** wherein the TGF-ß related disorder is selected from the group consisting of inflammatory diseases, chronic infection, cancer, fibrosis, cardiovascular diseases, cerebrovascular disease (e.g. ischemic stroke), and neurodegenerative diseases.~~

~~**18.** The pharmaceutical composition according to any one of claim **15** to **17**, wherein said pharmaceutical composition is to be administered in combination with another treatment for cancer or another immunotherapeutic agent such as a tumor vaccine or an immunostimulatory antibody.~~

~~**19.** The pharmaceutical composition according to claim **15** or **16**, wherein said pharmaceutical composition is to be administered as an immunostimulatory antibody for treatment of cancer patients.~~

1. An antibody that binds to a complex of human Glycoprotein A repetitions predominant (hGARP) and latent TGF-ß1, wherein the antibody binds to an epitope which comprises the residues Y137, S138 and G139 of the hGARP amino acid

sequence of SEQ ID NO:1, and wherein the antibody is a monoclonal IgG antibody comprising

heavy chains each comprising a variable region comprising the following CDRs:

a VH-CDR1 having an amino acid sequence of: SYYID (SEQ ID NO:13);

a VH-CDR2 having an amino acid sequence of: RIDPEDGGTKYAQKFQG (SEQ ID NO:14) or any amino acid sequence having a single amino acid replacement substitution to the sequence SEQ ID NO:14;

a VH-CDR3 having an amino acid sequence of: NEWETVVVGDLMYEYEY (SEQ ID NO:15) or any amino acid sequence having a single amino acid replacement substitution to the sequence SEQ ID NO:15, and

light chains each comprising a variable region comprising the following CDRs:

a VL-CDR1 having an amino acid sequence of: QASQSISSYLA (SEQ ID NO:31);

a VL-CDR2 having an amino acid sequence of: GASRLKT (SEQ ID NO:32);

a VL-CDR3: having an amino acid sequence of QQYASVPVT (SEQ ID NO:33).

2. The antibody of claim 1, wherein the antibody is a humanized antibody.

3. The antibody of claim 1, wherein the antibody comprises a CH1 domain, hinge region, CH2 domain, and CH3 domain of a human IgG4.