Binding molecules for BCMA and CD3

The present invention relates generally to a binding molecule which is at least bispecific comprising a first and a second binding domain, wherein the first binding domain is capable of binding to BCMA, and the second binding domain is capable of binding to the T cell CD3 receptor complex. Moreover, the invention provides a nucleic acid sequence encoding the binding molecule, a vector comprising said nucleic acid sequence and a host cell transformed or transfected with said vector. Furthermore, the invention provides a process for the production of the binding molecule of the invention, a medical use of said binding molecule and a kit comprising said binding molecule.

Background

BCMA (B-cell maturation antigen, TNFRSF17, CD269) is a transmembrane protein belonging to the TNF receptor super family. BCMA is originally reported as an integral membrane protein in the Golgi apparatus of human mature B lymphocytes, i.e., as an intracellular protein (Gras et al., (1995) International Immunol 7(7):1093-1105) showing that BCMA seems to have an important role during B-cell development and homeostasis. The finding of Gras et al. might be associated with the fact that the BCMA protein that was described in Gras et al. is, because of a chromosomal translocation, a fusion protein between BCMA and IL-2. Meanwhile BCMA is, however, established to be a B-cell marker that is essential for B-cell development and homeostasis (Schliemann et al., (2001) Science 293 (5537):2111-2114) due to its presumably essential interaction with its ligands BAFF (B cell activating factor), also designated as TALL-1 or TNFSF13B, and APRIL (A proliferation-inducing ligand).

BCMA expression is restricted to the B-cell lineage and mainly present on plasma cells and plasmablasts and to some extent on memory B-cells, but virtually absent on peripheral and naive B-cells. BCMA is also expressed on multiple myeloma (MM) cells. Together with its family members transmembrane activator and cyclophylin ligand interactor (TACI) and B cell activation factor of TNF family receptor (BAFF-R), BCMA regulates different aspects of humoral immunity, B-cell development and homeostasis. Expression of BCMA appears rather late in B-cell differentiation and contributes to the long term survival of plasmablasts and plasma cells in the

antagonizing both BCMA and TACI might be beneficial in the treatment of plasma cell disorders. In addition, BCMA-specific antibodies that cross react with TACI have been described (WO 02/066516).

Human Genome Sciences and GlaxoSmithKline have developed an antibody targeting BAFF which is called Belimumab. Belimumab blocks the binding of soluble BAFF to its receptors BAFF-R, BCMA and TACI on B cells. Belimumab does not bind B cells directly, but by binding BAFF, belimumab inhibits the survival of B cells, including autoreactive B cells, and reduces the differentiation of B cells into immunoglobulin-producing plasma cells.

Nevertheless, despite the fact that BCMA; BAFF-R and TACI, i.e., B cell receptors belonging to the TNF receptor super family, and their ligands BAFF and APRIL are subject to therapies in fighting against cancer and/or autoimmune disorders, there is still a need for having available further options for the treatment of such medical conditions.

Accordingly, there is provided herewith means and methods in the form of a binding molecule which is at least bispecific with one binding domain to cytotoxic cells, i.e., cytotoxic T cells, and with a second binding domain to BCMA.

Aspects of the invention are provided in the independent claims. Some optional features of the invention are provided in the dependent claims.

Thus, in a first aspect the present disclosure provides a binding molecule which is at least bispecific comprising a first and a second binding domain, wherein

(a) the first binding domain is capable of binding to epitope clusters of BCMA as defined herein; and

(b) the second binding domain is capable of binding to the T cell CD3 receptor complex.

A great number of biological pharmaceuticals, such as antibodies and/or other physiologically active proteins, have been produced in the last decade but their efficient production remains a challenging task. In particular, in antibody preparations therapeutically active doses are often in the order of milligram (mg) per administration. Thus, considerable amounts of antibodies are needed as active ingredients. Technologies that allow efficient production of such antibodies, e.g. in heterologous host cells (such as E.coli, yeast or CHO) will lead to cost reduction of antibody preparations and promise a cheap and moreover stable supply to patients.

During the purification of therapeutic antibodies, impurities such as host cell proteins, host cell DNA, process related contaminants (e.g. endotoxins or viral particles) and product variants must be removed. The purification techniques used must be efficient, cost-effective, reliable, and meet the rigorous purity requirements of the final product. Current purification techniques

5

typically involve multiple chromatographic separations. Chromatography techniques exploit inter alia the chemical and physical properties of proteins to achieve a high degree of purification. These chemical and physical properties include for example the size, isoelectric point, charge distribution, hydrophobic sites etc. The various separation modes of chromatography include: ion-exchange, chromatofocussing, gel filtration (size exclusion), hydrophobic interaction, reverse phase, and affinity chromatography. Ion-exchange chromatography (IEX), including anion-exchange and cation-exchange chromatography separates analytes (e.g. therapeutic proteins) by differences of their net surface charges. IEX is a primary tool for the separation of expressed proteins from cellular debris and other impurities. Today, IEX is one of the most frequently used techniques for purification of proteins, peptides, nucleic acids and other charged biomolecules, offering high resolution and group separations with high loading capacity. The technique is capable of separating molecular species that have only minor differences in their charge properties, for example two proteins differing by one charged amino acid. These features make IEX well suited for capture, intermediate purification or polishing steps in a purification protocol and the technique is used from microscale purification and analysis through to purification of kilograms of product. Ion exchange chromatography separates proteins according to their net charge (which is dependent on the composition of the mobile phase). By adjusting the pH or the ionic concentration of the mobile phase, various protein molecules can be separated. This presupposes, however, that the protein in question (the therapeutic antibody for example) has to tolerate the mentioned changes in the pH or the ionic strength during the IEX-procedure. From this it follows that the more tolerant an antibody behaves at un-physiological pH which is required to run an IEX, the more antibody can be recovered/eluted from the IEX column relative to the total amount of loaded protein.

As mentioned before, BCMA is subject to therapies in fighting against cancer and/or autoimmune disorders, but there is still a need for having available further options for the treatment of such medical conditions that can be produced and purified efficiently.

Accordingly, there is provided herewith means and methods also for the solution of the latter technical problem in the form of binding molecules that are disclosed herein.

Thus, in a further aspect, the present disclosure relates to a binding molecule which is at least bispecific comprising a first and a second binding domain, wherein

(a) the first binding domain is capable of binding to epitope clusters of BCMA as defined herein; and

Elution was carried out by a steadily increasing gradient with elution buffer from zero to 100% over a total volume corresponding to 200 column volumes. The whole run was monitored at 280 (blue line) and 254 nm (red line) optical absorption.

For calculation of protein recovery from the column matrix an amount of 50 µg monomeric BCMA/CD3 bispecific antibody was applied to the Äkta Micro Device without an installed column. The resulting peak area was determined and used as 100% reference for comparison with the peak areas measured in the analytical runs.

When applying the above IEX method, the following results could be obtained for 14 representative binding molecules.

BCMA/CD3 bispecific antibody	***AUC of Main Peak [%]***	***Recovery [%]***
BCMA-54	67	49.4
BCMA-53	52	49.4
BCMA-83	89	70.2
BCMA-62	89	67.0
BCMA-5	92	65.4
BCMA-98	93	73.4
BCMA-71	89	70.2
BCMA-34	91	71.8
BCMA-74	79	65.4
BCMA-20	83	71.8
BCMA-90	86	76.6
BCMA-91	84	59.0
BCMA-30	91	76.6
BCMA-50	92	78.1

Thus, in a preferred embodiment, said binding molecule comprises:

(a) (i) the CDRs as defined in SEQ ID Nos 41 to 46, or (ii) the VH and/or VL as defined in SEQ ID Nos 47 and 48, or (iii) the scFv as defined in SEQ ID No 49, or the bispecific BCMA/CD3 binder as defined in SEQ ID No 50;

In a particular preferred embodiment, said binding molecule comprises or consists of a polypeptide as represented by SEQ ID No: 50, 200, 300, 340, 500, 620, 710, 740, 830, 900, 910 or 980.

In a further preferred embodiment, said binding molecule further comprises at least one protein purification tag such as a GST tag, a FLAG tag, a polyhistidine tag etc. Polyhistidine-tags are preferred. A polyhistidine-tag is typically five or six histidine residues in length, but may be longer. Said protein purification tag may be at the carboxy or amino terminus of the binding molecule. Binding molecules as disclosed herein (e.g. in form of SEQ ID Nos) comprise in a preferred embodiment at least one His-tag that comprises or consists of six histidine residues in length. It is even more preferred that said His-tag is six histidine residues in length and is located at the C-terminus of the disclosed binding molecules. Thus, in a particularly preferred arrangement, said binding molecule comprises or consists of a polypeptide as represented by SEQ ID No: 50, 200, 300, 340, 500, 620, 710, 740, 830, 900, 910 or 980 and additionally of a hexa-histidine-tag (HHHHHH) which is located at its C-terminus. It is also preferred that the protein purification tag (His-tag being more preferred and Hexa-His-tag being most preferred) is linked to the C-terminus of the binding molecule (preferably consisting of or comprising SEQ ID No: 50, 200, 300, 340, 500, 620, 710, 740, 830, 900, 910 or 980) via a peptide bond.

In a less preferred embodiment, said binding molecule comprises or consists of SEQ ID No: 540 or 530 and additionally of a hexa-histidine-tag (HHHHHH) which is located at its C-terminus and is linked to it via a peptide bond.

In a further preferred embodiment, said binding molecule including the above mentioned protein purification tag(s), His-tags being preferred and Hexa-His-tags at the C-terminus being more preferred, is produced in a host cell as defined herein. CHO is thereby a particularly preferred host cell. It is also preferred that the binding molecules are characterized by a % dimer conversion after (i) 7 days in solution at 100 µg/ml which is below 2.9, or (ii) 7 days in solution at 250 µg/ml which is below 3.5.

***

It must be noted that as used herein, the singular forms “a”, “an”, and “the”, include plural references unless the context clearly indicates otherwise. Thus, for example, reference to “a

reagent” includes one or more of such different reagents and reference to “the method” includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

Unless otherwise indicated, the term "at least" preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the disclosure.

The term "and/or" wherever used herein includes the meaning of "and", "or" and "all or any other combination of the elements connected by said term".

The term "about" or "approximately" as used herein means within ±20%, preferably within ±15%, more preferably within ±10%, and most preferably within ±5% of a given value or range.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word “comprise”, and variations such as “comprises” and “comprising”, will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. When used herein the term “comprising” can be substituted with the term “containing” or “including” or sometimes when used herein with the term “having”.

When used herein “consisting of" excludes any element, step, or ingredient not specified in the claim element. When used herein, "consisting essentially of" does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim.

In each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms.

The following description provides exemplary arrangements of the claimed techniques. These are not intended to limit the invention. As mentioned above, aspects of the invention are set out in the appended claims.

***

General description

Epitope clusters 1, 2, 3, 4, 5, 6, 7 are comprised by the extracellular domain of BCMA. The "**BCMA extracellular domain**" or "**BCMA ECD**" refers to a form of BCMA which is essentially free of transmembrane and cytoplasmic domains of BCMA. It will be understood by the skilled artisan that the transmembrane domain identified for the BCMA polypeptide of the present invention is identified pursuant to criteria routinely employed in the art for identifying that type of

Those "**in need of treatment**" include those already with the disorder, as well as those in which the disorder is to be prevented. The term "disease" is any condition that would benefit from treatment with the protein formulation described herein. This includes chronic and acute disorders or diseases including those pathological conditions that predispose the mammal to the disease in question. Non-limiting examples of diseases/disorders to be treated herein include proliferative disease, a tumorous disease, or an immunological disorder.

Preferably, the binding molecule of the invention is for use in the prevention, treatment or amelioration of B cell disorders that correlate with BCMA (over)expression such as plasma cell disorders, and/or autoimmune diseases. The autoimmune disease is, for example, systemic lupus erythematosus or rheumatoid arthritis.

Cytotoxicity mediated by BCMA/CD3 bispecific binding molecules can be measured in various ways. Effector cells can be e.g. stimulated enriched (human) CD8 positive T cells or unstimulated (human) peripheral blood mononuclear cells (PBMC). If the target cells are of macaque origin or express or are transfected with macaque BCMA, the effector cells should also be of macaque origin such as a macaque T cell line, e.g. 4119LnPx. The target cells should express (at least the extracellular domain of) BCMA, e.g. human or macaque BCMA. Target cells can be a cell line (such as CHO) which is stably or transiently transfected with BCMA, e.g. human or macaque BCMA. Alternatively, the target cells can be a BCMA positive natural expresser cell line, such as the human multiple myeloma cell line L363 or NCI-H929. Usually EC50-values are expected to be lower with target cell lines expressing higher levels of BCMA on the cell surface. The effector to target cell (E:T) ratio is usually about 10:1, but can also vary. Cytotoxic activity of BCMA/CD3 bispecific binding molecules can be measured in an 51-chromium release assay (incubation time of about 18 hours) or in a in a FACS-based cytotoxicity assay (incubation time of about 48 hours). Modifications of the assay incubation time (cytotoxic reaction) are also possible. Other methods of measuring cytotoxicity are well-known to the skilled person and comprise MTT or MTS assays, ATP-based assays including bioluminescent assays, the sulforhodamine B (SRB) assay, WST assay, clonogenic assay and the ECIS technology.

The cytotoxic activity mediated by BCMA/CD3 bispecific binding molecules of the present invention is preferably measured in a cell-based cytotoxicity assay. It is represented by the EC_{50} value, which corresponds to the half maximal effective concentration (concentration of the binding molecule which induces a cytotoxic response halfway between the baseline and maximum).

Also provided by the present invention is a method for the treatment or amelioration of B cell disorders that correlate with BCMA (over)expression such as plasma cell disorders, and/or autoimmune diseases, comprising the step of administering to a subject in need thereof the binding molecule of the invention. The autoimmune disease is, for example, systemic lupus erythematosus or rheumatoid arthritis.

In plasma cell disorders, one clone of plasma cells multiplies uncontrollably. As a result, this clone produces vast amounts of a single (monoclonal) antibody known as the M-protein. In some cases, such as with monoclonal gammopathies, the antibody produced is incomplete, consisting of only light chains or heavy chains. These abnormal plasma cells and the antibodies they produce are usually limited to one type.

Preferably, the plasma cell disorder is selected from the group consisting of multiple myeloma, plasmacytoma, plasma cell leukemia, macroglobulinemia, amyloidosis, Waldenstrom's macroglobulinemia , solitary bone plasmacytoma, extramedullary plasmacytoma, osteosclerotic myeloma, heavy chain diseases, monoclonal gammopathy of undetermined significance, and smoldering multiple myeloma.

In another aspect, kits are provided comprising a binding molecule of the invention, a nucleic acid molecule of the invention, a vector of the invention, and/or a host cell of the invention. The kit may comprise one or more vials containing the binding molecule and instructions for use. The kit may also contain means for administering the binding molecule of the present invention such as a syringe, pump, infuser or the like, means for reconstituting the binding molecule of the invention and/or means for diluting the binding molecule of the invention.

In another aspect of the invention, the second binding domain is capable of binding to CD3 epsilon. In still another aspect of the invention, the second binding domain is capable of binding to human CD3 and to macaque CD3, preferably to human CD3 epsilon and to macaque CD3 epsilon. Additionally or alternatively, the second binding domain is capable of binding to *Callithrix jacchus*, *Saguinus oedipus* and/or *Saimiri sciureus* CD3 epsilon. According to these embodiments, one or both binding domains of the binding molecule of the invention are preferably cross-species specific for members of the mammalian order of primates. Cross-species specific CD3 binding domains are, for example, described in WO 2008/119567.

It is particularly preferred for the binding molecule of the present invention that the second binding domain capable of binding to the T cell CD3 receptor complex comprises a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from:

selected from the group consisting of plasma cell disorders, other B cell disorders that correlate with BCMA expression and autoimmune diseases.

17. A method for the treatment or amelioration of a disease selected from the group consisting of plasma cell disorders, other B cell disorders that correlate with BCMA expression and autoimmune diseases, comprising the step of administering to a subject in need thereof the binding molecule according to any one of items 1 to 10, or produced according to the process of item 14.

18. The method according to item 17, wherein the plasma cell disorder is selected from the group consisting of multiple myeloma, plasmacytoma, plasma cell leukemia, macroglobulinemia, amyloidosis, Waldenstrom's macroglobulinemia , solitary bone plasmacytoma, extramedullary plasmacytoma, osteosclerotic myeloma, heavy chain diseases, monoclonal gammopathy of undetermined significance, and smoldering multiple myeloma.

19. The method according to item 17, wherein the autoimmune disease is systemic lupus erythematosus or rheumatoid arthritis.

20. A kit comprising a binding molecule as defined in any one of items 1 to 10, a nucleic acid molecule as defined in item 11, a vector as defined in item 12, or a host cell as defined in item 13.

<u>Third group of binding molecules (C)</u>

The third group of binding molecules of the present invention relates to a binding molecule which is at least bispecific comprising a first and a second binding domain, wherein the first binding domain is capable of binding to epitope cluster 1 and 4 of BCMA, and the second binding domain is capable of binding to the T cell CD3 receptor complex.

Thus, in a first aspect the present invention provides a binding molecule which is at least bispecific comprising a first and a second binding domain, wherein

(a) the first binding domain is capable of binding to epitope cluster 1 (MLQMAGQ) (SEQ ID NO: 1018) and 4 (NASVTNSVKGTNA) (SEQ ID NO: 1019) of BCMA; and

(b) the second binding domain is capable of binding to the T cell CD3 receptor complex; and

16. A pharmaceutical composition comprising a binding molecule according to any one of items 1 to 11, or produced according to the process of item 15.

17. The binding molecule according to any one of items 1 to 11, or produced according to the process of item 15 for use in the prevention, treatment or amelioration of a disease selected from the group consisting of plasma cell disorders, other B cell disorders that correlate with BCMA expression and autoimmune diseases.

18. A method for the treatment or amelioration of a disease selected from the group consisting of plasma cell disorders, other B cell disorders that correlate with BCMA expression and autoimmune diseases, comprising the step of administering to a subject in need thereof the binding molecule according to any one of items 1 to 11, or produced according to the process of item 15.

19. The method according to item 18, wherein the plasma cell disorder is selected from the group consisting of multiple myeloma, plasmacytoma, plasma cell leukemia, macroglobulinemia, amyloidosis, Waldenstrom's macroglobulinemia , solitary bone plasmacytoma, extramedullary plasmacytoma, osteosclerotic myeloma, heavy chain diseases, monoclonal gammopathy of undetermined significance, and smoldering multiple myeloma.

20. The method according to item 18, wherein the autoimmune disease is systemic lupus erythematosus.

21. A kit comprising a binding molecule as defined in any one of items 1 to 11, a nucleic acid molecule as defined in item 12, a vector as defined in item 13, and/or a host cell as defined in item 14.

22. Use of epitope cluster 1 and of epitope cluster 4 of BCMA for the generation of a binding molecule, preferably an antibody, which is capable of binding to BCMA, wherein epitope cluster 1 of BCMA corresponds to amino acid residues 1 to 7 of the sequence as depicted in SEQ ID NO: 1002, and epitope cluster 4 of BCMA corresponds to amino acid residues 42 to 54 of the sequence as depicted in SEQ ID NO: 1002.

21. The method according to item 19, wherein the autoimmune disease is systemic lupus erythematosus.

22. A kit comprising a binding molecule as defined in any one of items 1 to 12, a nucleic acid molecule as defined in item 13, a vector as defined in item 14, or a host cell as defined in item 15.

Fifth group of binding molecules (E)

The fifth group of binding molecules of the present invention relates to a binding molecule comprising at least a first and a second binding domain which is bispecific, wherein the first binding domain of the present invention is capable of binding to epitope cluster 3 of human BCMA, preferably human BCMA ECD. Accordingly, when the respective epitope cluster in the human BCMA protein is exchanged with the respective epitope cluster of a murine BCMA antigen (resulting in a construct comprising human BCMA, wherein human epitope cluster 3 is replaced with murine epitope cluster 3; see SEQ ID NO: 1011), a decrease in the binding of the binding domain will occur. Said decrease is preferably at least 10%, 20%, 30%, 40%, 50%; more preferably at least 60%, 70%, 80%, 90%, 95% or even 100% in comparison to the respective epitope cluster in the human BCMA protein, whereby binding to the respective epitope cluster in the human BCMA protein is set to be 100%. It is envisaged that the aforementioned human BCMA/murine BCMA chimeras are expressed in CHO cells. It is also envisaged that the human BCMA/murine BCMA chimeras are fused with a transmembrane domain and/or cytoplasmic domain of a different membrane-bound protein such as EpCAM; see Figure 2a.

A method to test this loss of binding due to exchange with the respective epitope cluster of a non-human (e.g. murine) BCMA antigen is described in the appended Examples, in particular in Examples E1-3. A further method to determine the contribution of a specific residue of a target antigen to the recognition by a given binding molecule or binding domain is alanine scanning (see e.g. Morrison KL & Weiss GA. Cur Opin Chem Biol. 2001 Jun;5(3):302-7), where each residue to be analyzed is replaced by alanine, e.g. via site-directed mutagenesis. Alanine is used because of its non-bulky, chemically inert, methyl functional group that nevertheless mimics the secondary structure references that many of the other amino acids possess. Sometimes bulky amino acids such as valine or leucine can be used in cases where

monoclonal gammopathy of undetermined significance, and smoldering multiple myeloma.

23. The method according to item 21, wherein the autoimmune disease is systemic lupus erythematosus.

24. A kit comprising a binding molecule as defined in any one of items 1 to 14, a nucleic acid molecule as defined in item 15, a vector as defined in item 16, and/or a host cell as defined in item 17.

25. Use of epitope cluster 3 of BCMA for the generation of a binding molecule, preferably an antibody, which is capable of binding to BCMA, wherein epitope cluster 3 of BCMA corresponds to amino acid residues 24 to 41 of the sequence as depicted in SEQ ID NO: 1002.

26. A method for the generation of an antibody, preferably a bispecific binding molecule, which is capable of binding to BCMA, comprising
    (a) immunizing an animal with a polypeptide comprising epitope cluster 3 of BCMA, wherein epitope cluster 3 of BCMA corresponds to amino acid residues 24 to 41 of the sequence as depicted in SEQ ID NO: 1002,
    (b) obtaining said antibody, and
    (c) optionally converting said antibody into a bispecific binding molecule which is capable of binding to human BCMA and preferably to the T cell CD3 receptor complex.

It should be understood that the inventions herein are not limited to particular methodology, protocols, or reagents, as such can vary. The discussion and examples provided herein are presented for the purpose of describing particular embodiments only and are not intended to limit the scope of the present invention, which is defined solely by the claims.

All publications and patents cited throughout the text of this specification (including all patents, patent applications, scientific publications, manufacturer's specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by

Claims

1. A binding molecule which is at least bispecific comprising
a first and a second binding domain, wherein
(a) the first binding domain is capable of binding to BCMA; and
(b) the second binding domain is capable of binding to the T cell CD3 receptor complex; and comprising

at least one protein purification tag which is a GST tag, a FLAG tag or a polyhistidine tag, wherein the polyhistidine tag is (a) six histidine residues in length or longer and/or (b) at the carboxy or amino terminus of the binding molecule;

wherein the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of:

(1) CDR-H1 as depicted in SEQ ID NO: 1, CDR-H2 as depicted in SEQ ID NO: 2, CDR-H3 as depicted in SEQ ID NO: 3, CDR-L1 as depicted in SEQ ID NO: 4, CDR-L2 as depicted in SEQ ID NO: 5 and CDR-L3 as depicted in SEQ ID NO: 6;

(2) CDR-H1 as depicted in SEQ ID NO: 11, CDR-H2 as depicted in SEQ ID NO: 12, CDR-H3 as depicted in SEQ ID NO: 13, CDR-L1 as depicted in SEQ ID NO: 14, CDR-L2 as depicted in SEQ ID NO: 15 and CDR-L3 as depicted in SEQ ID NO: 16;

(3) CDR-H1 as depicted in SEQ ID NO: 21, CDR-H2 as depicted in SEQ ID NO: 22, CDR-H3 as depicted in SEQ ID NO: 23, CDR-L1 as depicted in SEQ ID NO: 24, CDR-L2 as depicted in SEQ ID NO: 25 and CDR-L3 as depicted in SEQ ID NO: 26;

(4) CDR-H1 as depicted in SEQ ID NO: 31, CDR-H2 as depicted in SEQ ID NO: 32, CDR-H3 as depicted in SEQ ID NO: 33, CDR-L1 as depicted in SEQ ID NO: 34, CDR-L2 as depicted in SEQ ID NO: 35 and CDR-L3 as depicted in SEQ ID NO: 36;

(5) CDR-H1 as depicted in SEQ ID NO: 41, CDR-H2 as depicted in SEQ ID NO: 42, CDR-H3 as depicted in SEQ ID NO: 43, CDR-L1 as depicted in SEQ ID NO: 44, CDR-L2 as depicted in SEQ ID NO: 45 and CDR-L3 as depicted in SEQ ID NO: 46;

(6) CDR-H1 as depicted in SEQ ID NO: 51, CDR-H2 as depicted in SEQ ID NO: 52, CDR-H3 as depicted in SEQ ID NO: 53, CDR-L1 as depicted in SEQ ID NO: 54, CDR-L2 as depicted in SEQ ID NO: 55 and CDR-L3 as depicted in SEQ ID NO: 56;

(7) CDR-H1 as depicted in SEQ ID NO: 61, CDR-H2 as depicted in SEQ ID NO: 62, CDR-H3 as depicted in SEQ ID NO: 63, CDR-L1 as depicted in SEQ ID NO: 64, CDR-L2 as depicted in SEQ ID NO: 65 and CDR-L3 as depicted in SEQ ID NO: 66;

(8) CDR-H1 as depicted in SEQ ID NO: 71, CDR-H2 as depicted in SEQ ID NO: 72, CDR-H3 as depicted in SEQ ID NO: 73, CDR-L1 as depicted in SEQ ID NO: 74, CDR-L2 as depicted in SEQ ID NO: 75 and CDR-L3 as depicted in SEQ ID NO: 76;

(9) CDR-H1 as depicted in SEQ ID NO: 161, CDR-H2 as depicted in SEQ ID NO: 162, CDR-H3 as depicted in SEQ ID NO: 163, CDR-L1 as depicted in SEQ ID NO: 164, CDR-L2 as depicted in SEQ ID NO: 165 and CDR-L3 as depicted in SEQ ID NO: 166;

(10) CDR-H1 as depicted in SEQ ID NO: 171, CDR-H2 as depicted in SEQ ID NO: 172, CDR-H3 as depicted in SEQ ID NO: 173, CDR-L1 as depicted in SEQ ID NO: 174, CDR-L2 as depicted in SEQ ID NO: 175 and CDR-L3 as depicted in SEQ ID NO: 176;

(11) CDR-H1 as depicted in SEQ ID NO: 181, CDR-H2 as depicted in SEQ ID NO: 182, CDR-H3 as depicted in SEQ ID NO: 183, CDR-L1 as depicted in SEQ ID NO: 184, CDR-L2 as depicted in SEQ ID NO: 185 and CDR-L3 as depicted in SEQ ID NO: 186;

(12) CDR-H1 as depicted in SEQ ID NO: 191, CDR-H2 as depicted in SEQ ID NO: 192, CDR-H3 as depicted in SEQ ID NO: 193, CDR-L1 as depicted in SEQ ID NO: 194, CDR-L2 as depicted in SEQ ID NO: 195 and CDR-L3 as depicted in SEQ ID NO: 196;

(13) CDR-H1 as depicted in SEQ ID NO: 201, CDR-H2 as depicted in SEQ ID NO: 202, CDR-H3 as depicted in SEQ ID NO: 203, CDR-L1 as depicted in SEQ ID NO: 204, CDR-L2 as depicted in SEQ ID NO: 205 and CDR-L3 as depicted in SEQ ID NO: 206;

(14) CDR-H1 as depicted in SEQ ID NO: 211, CDR-H2 as depicted in SEQ ID NO: 212, CDR-H3 as depicted in SEQ ID NO: 213, CDR-L1 as depicted in SEQ ID NO:214 , CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216;

(15) CDR-H1 as depicted in SEQ ID NO: 221, CDR-H2 as depicted in SEQ ID NO: 222, CDR-H3 as depicted in SEQ ID NO: 223, CDR-L1 as depicted in SEQ ID NO: 224, CDR-L2 as depicted in SEQ ID NO: 225 and CDR-L3 as depicted in SEQ ID NO: 226;

(16) CDR-H1 as depicted in SEQ ID NO: 311, CDR-H2 as depicted in SEQ ID NO: 312, CDR-H3 as depicted in SEQ ID NO: 313, CDR-L1 as depicted in SEQ ID NO: 314, CDR-L2 as depicted in SEQ ID NO: 315 and CDR-L3 as depicted in SEQ ID NO: 316;

(17) CDR-H1 as depicted in SEQ ID NO: 321, CDR-H2 as depicted in SEQ ID NO: 322, CDR-H3 as depicted in SEQ ID NO: 323, CDR-L1 as depicted in SEQ ID NO: 324, CDR-L2 as depicted in SEQ ID NO: 325 and CDR-L3 as depicted in SEQ ID NO: 326;

(18) CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, CDR-H3 as depicted in SEQ ID NO: 333, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336;

(19) CDR-H1 as depicted in SEQ ID NO: 341, CDR-H2 as depicted in SEQ ID NO: 342, CDR-H3 as depicted in SEQ ID NO: 343, CDR-L1 as depicted in SEQ ID NO: 344, CDR-L2 as depicted in SEQ ID NO: 345 and CDR-L3 as depicted in SEQ ID NO: 346;

(20) CDR-H1 as depicted in SEQ ID NO: 351, CDR-H2 as depicted in SEQ ID NO: 352, CDR-H3 as depicted in SEQ ID NO: 353, CDR-L1 as depicted in SEQ ID NO: 354, CDR-L2 as depicted in SEQ ID NO: 355 and CDR-L3 as depicted in SEQ ID NO: 356;

(21) CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, CDR-H3 as depicted in SEQ ID NO: 363, CDR-L1 as depicted in SEQ ID NO: 364, CDR-L2 as depicted in SEQ ID NO: 365 and CDR-L3 as depicted in SEQ ID NO: 366;

(22) CDR-H1 as depicted in SEQ ID NO: 371, CDR-H2 as depicted in SEQ ID NO: 372, CDR-H3 as depicted in SEQ ID NO: 373, CDR-L1 as depicted in SEQ ID NO: 374, CDR-L2 as depicted in SEQ ID NO: 375 and CDR-L3 as depicted in SEQ ID NO: 376;

(23) CDR-H1 as depicted in SEQ ID NO: 381, CDR-H2 as depicted in SEQ ID NO: 382, CDR-H3 as depicted in SEQ ID NO: 383, CDR-L1 as depicted in SEQ ID NO: 384, CDR-L2 as depicted in SEQ ID NO: 385 and CDR-L3 as depicted in SEQ ID NO: 386;

(24) CDR-H1 as depicted in SEQ ID NO: 581, CDR-H2 as depicted in SEQ ID NO: 582, CDR-H3 as depicted in SEQ ID NO: 583, CDR-L1 as depicted in SEQ ID NO: 584, CDR-L2 as depicted in SEQ ID NO: 585 and CDR-L3 as depicted in SEQ ID NO: 586;

(25) CDR-H1 as depicted in SEQ ID NO: 591, CDR-H2 as depicted in SEQ ID NO: 592, CDR-H3 as depicted in SEQ ID NO: 593, CDR-L1 as depicted in SEQ ID NO: 594, CDR-L2 as depicted in SEQ ID NO: 595 and CDR-L3 as depicted in SEQ ID NO: 596;

(26) CDR-H1 as depicted in SEQ ID NO: 601, CDR-H2 as depicted in SEQ ID NO: 602, CDR-H3 as depicted in SEQ ID NO: 603, CDR-L1 as depicted in SEQ ID NO: 604, CDR-L2 as depicted in SEQ ID NO: 605 and CDR-L3 as depicted in SEQ ID NO: 606;

(27) CDR-H1 as depicted in SEQ ID NO: 611, CDR-H2 as depicted in SEQ ID NO: 612, CDR-H3 as depicted in SEQ ID NO: 613, CDR-L1 as depicted in SEQ ID NO: 614, CDR-L2 as depicted in SEQ ID NO: 615 and CDR-L3 as depicted in SEQ ID NO: 616;

(28) CDR-H1 as depicted in SEQ ID NO: 621, CDR-H2 as depicted in SEQ ID NO: 622, CDR-H3 as depicted in SEQ ID NO: 623, CDR-L1 as depicted in SEQ ID NO: 624, CDR-L2 as depicted in SEQ ID NO: 625 and CDR-L3 as depicted in SEQ ID NO: 626;

(29) CDR-H1 as depicted in SEQ ID NO: 631, CDR-H2 as depicted in SEQ ID NO: 632, CDR-H3 as depicted in SEQ ID NO: 633, CDR-L1 as depicted in SEQ ID NO: 634, CDR-L2 as depicted in SEQ ID NO: 635 and CDR-L3 as depicted in SEQ ID NO: 636;

(30) CDR-H1 as depicted in SEQ ID NO: 641, CDR-H2 as depicted in SEQ ID NO: 642, CDR-H3 as depicted in SEQ ID NO: 643, CDR-L1 as depicted in SEQ ID NO: 644, CDR-L2 as depicted in SEQ ID NO: 645 and CDR-L3 as depicted in SEQ ID NO: 646;

(31) CDR-H1 as depicted in SEQ ID NO: 651, CDR-H2 as depicted in SEQ ID NO: 652, CDR-H3 as depicted in SEQ ID NO: 653, CDR-L1 as depicted in SEQ ID NO: 654, CDR-L2 as depicted in SEQ ID NO: 655 and CDR-L3 as depicted in SEQ ID NO: 656;

(32) CDR-H1 as depicted in SEQ ID NO: 661, CDR-H2 as depicted in SEQ ID NO: 662, CDR-H3 as depicted in SEQ ID NO: 663, CDR-L1 as depicted in SEQ ID NO: 664, CDR-L2 as depicted in SEQ ID NO: 665 and CDR-L3 as depicted in SEQ ID NO: 666;

(33) CDR-H1 as depicted in SEQ ID NO: 671, CDR-H2 as depicted in SEQ ID NO: 672, CDR-H3 as depicted in SEQ ID NO: 673, CDR-L1 as depicted in SEQ ID NO: 674, CDR-L2 as depicted in SEQ ID NO: 675 and CDR-L3 as depicted in SEQ ID NO: 676;

(34) CDR-H1 as depicted in SEQ ID NO: 681, CDR-H2 as depicted in SEQ ID NO: 682, CDR-H3 as depicted in SEQ ID NO: 683, CDR-L1 as depicted in SEQ ID NO: 684, CDR-L2 as depicted in SEQ ID NO: 685 and CDR-L3 as depicted in SEQ ID NO: 686;

(35) CDR-H1 as depicted in SEQ ID NO: 691, CDR-H2 as depicted in SEQ ID NO: 692, CDR-H3 as depicted in SEQ ID NO: 693, CDR-L1 as depicted in SEQ ID NO: 694, CDR-L2 as depicted in SEQ ID NO: 695 and CDR-L3 as depicted in SEQ ID NO: 696;

(36) CDR-H1 as depicted in SEQ ID NO: 701, CDR-H2 as depicted in SEQ ID NO: 702, CDR-H3 as depicted in SEQ ID NO: 703, CDR-L1 as depicted in SEQ ID NO: 704, CDR-L2 as depicted in SEQ ID NO: 705 and CDR-L3 as depicted in SEQ ID NO: 706;

(37) CDR-H1 as depicted in SEQ ID NO: 711, CDR-H2 as depicted in SEQ ID NO: 712, CDR-H3 as depicted in SEQ ID NO: 713, CDR-L1 as depicted in SEQ ID NO: 714, CDR-L2 as depicted in SEQ ID NO: 715 and CDR-L3 as depicted in SEQ ID NO: 716;

(38) CDR-H1 as depicted in SEQ ID NO: 721, CDR-H2 as depicted in SEQ ID NO: 722, CDR-H3 as depicted in SEQ ID NO: 723, CDR-L1 as depicted in SEQ ID NO: 724, CDR-L2 as depicted in SEQ ID NO: 725 and CDR-L3 as depicted in SEQ ID NO: 726;

(39) CDR-H1 as depicted in SEQ ID NO: 731, CDR-H2 as depicted in SEQ ID NO: 732, CDR-H3 as depicted in SEQ ID NO: 733, CDR-L1 as depicted in SEQ ID NO: 734, CDR-L2 as depicted in SEQ ID NO: 735 and CDR-L3 as depicted in SEQ ID NO: 736;

(40) CDR-H1 as depicted in SEQ ID NO: 741, CDR-H2 as depicted in SEQ ID NO: 742, CDR-H3 as depicted in SEQ ID NO: 743, CDR-L1 as depicted in SEQ ID NO: 744, CDR-L2 as depicted in SEQ ID NO: 745 and CDR-L3 as depicted in SEQ ID NO: 746;

(41) CDR-H1 as depicted in SEQ ID NO: 751, CDR-H2 as depicted in SEQ ID NO: 752, CDR-H3 as depicted in SEQ ID NO: 753, CDR-L1 as depicted in SEQ ID NO: 754, CDR-L2 as depicted in SEQ ID NO: 755 and CDR-L3 as depicted in SEQ ID NO: 756;

(42) CDR-H1 as depicted in SEQ ID NO: 761, CDR-H2 as depicted in SEQ ID NO: 762, CDR-H3 as depicted in SEQ ID NO: 763, CDR-L1 as depicted in SEQ ID NO: 764, CDR-L2 as depicted in SEQ ID NO: 765 and CDR-L3 as depicted in SEQ ID NO: 766;

(43) CDR-H1 as depicted in SEQ ID NO: 771, CDR-H2 as depicted in SEQ ID NO: 772, CDR-H3 as depicted in SEQ ID NO: 773, CDR-L1 as depicted in SEQ ID NO: 774, CDR-L2 as depicted in SEQ ID NO: 775 and CDR-L3 as depicted in SEQ ID NO: 776;

(44) CDR-H1 as depicted in SEQ ID NO: 781, CDR-H2 as depicted in SEQ ID NO: 782, CDR-H3 as depicted in SEQ ID NO: 783, CDR-L1 as depicted in SEQ ID NO: 784, CDR-L2 as depicted in SEQ ID NO: 785 and CDR-L3 as depicted in SEQ ID NO: 786;

(45) CDR-H1 as depicted in SEQ ID NO: 791, CDR-H2 as depicted in SEQ ID NO: 792, CDR-H3 as depicted in SEQ ID NO: 793, CDR-L1 as depicted in SEQ ID NO: 794, CDR-L2 as depicted in SEQ ID NO: 795 and CDR-L3 as depicted in SEQ ID NO: 796;

(46) CDR-H1 as depicted in SEQ ID NO: 801, CDR-H2 as depicted in SEQ ID NO: 802, CDR-H3 as depicted in SEQ ID NO: 803, CDR-L1 as depicted in SEQ ID NO: 804, CDR-L2 as depicted in SEQ ID NO: 805 and CDR-L3 as depicted in SEQ ID NO: 806;

(47) CDR-H1 as depicted in SEQ ID NO: 811, CDR-H2 as depicted in SEQ ID NO: 812, CDR-H3 as depicted in SEQ ID NO: 813, CDR-L1 as depicted in SEQ ID NO: 814, CDR-L2 as depicted in SEQ ID NO: 815 and CDR-L3 as depicted in SEQ ID NO: 816;

(48) CDR-H1 as depicted in SEQ ID NO: 821, CDR-H2 as depicted in SEQ ID NO: 822, CDR-H3 as depicted in SEQ ID NO: 823, CDR-L1 as depicted in SEQ ID NO: 824, CDR-L2 as depicted in SEQ ID NO: 825 and CDR-L3 as depicted in SEQ ID NO: 826;

(49) CDR-H1 as depicted in SEQ ID NO: 831, CDR-H2 as depicted in SEQ ID NO: 832, CDR-H3 as depicted in SEQ ID NO: 833, CDR-L1 as depicted in SEQ ID NO: 834, CDR-L2 as depicted in SEQ ID NO: 835 and CDR-L3 as depicted in SEQ ID NO: 836;

(50) CDR-H1 as depicted in SEQ ID NO: 961, CDR-H2 as depicted in SEQ ID NO: 962, CDR-H3 as depicted in SEQ ID NO: 963, CDR-L1 as depicted in SEQ ID NO: 964, CDR-L2 as depicted in SEQ ID NO: 965 and CDR-L3 as depicted in SEQ ID NO: 966;

(51) CDR-H1 as depicted in SEQ ID NO: 971, CDR-H2 as depicted in SEQ ID NO: 972, CDR-H3 as depicted in SEQ ID NO: 973, CDR-L1 as depicted in SEQ ID NO: 974, CDR-L2 as depicted in SEQ ID NO: 975 and CDR-L3 as depicted in SEQ ID NO: 976;

(52) CDR-H1 as depicted in SEQ ID NO: 981, CDR-H2 as depicted in SEQ ID NO: 982, CDR-H3 as depicted in SEQ ID NO: 983, CDR-L1 as depicted in SEQ ID NO: 984, CDR-L2 as depicted in SEQ ID NO: 985 and CDR-L3 as depicted in SEQ ID NO: 986; and

(53) CDR-H1 as depicted in SEQ ID NO: 991, CDR-H2 as depicted in SEQ ID NO: 992, CDR-H3 as depicted in SEQ ID NO: 993, CDR-L1 as depicted in SEQ ID NO: 994, CDR-L2 as depicted in SEQ ID NO: 995 and CDR-L3 as depicted in SEQ ID NO: 996.

2. The binding molecule according to claim 1, wherein the first binding domain is further capable of binding to macaque BCMA.

3. The binding molecule according to any one of the preceding claims, wherein the second binding domain is capable of binding to CD3 epsilon.

4. The binding molecule according to any one of the preceding claims, wherein the second binding domain is capable of binding to human CD3 and to macaque CD3.

5. The binding molecule according to any one of the preceding claims, wherein the second binding domain is derived from an antibody.

6. The binding molecule according to claim 5, which is selected from the group consisting of $(scFv)_2$, $(single\ domain\ mAb)_2$, scFv-single domain mAb, diabodies and oligomers thereof.

7. The binding molecule according to any one of the preceding claims, wherein the first binding domain comprises a VH region selected from the group consisting of a VH region as depicted in SEQ ID NO: 7, SEQ ID NO: 17, SEQ ID NO: 27, SEQ ID NO: 37, SEQ ID NO: 47, SEQ ID NO: 57, SEQ ID NO: 67, SEQ ID NO: 77, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637, SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737, SEQ ID NO: 747, SEQ ID NO: 757, SEQ ID NO: 767, SEQ ID NO: 777, SEQ ID NO: 787, SEQ ID NO: 797, SEQ ID NO: 807, SEQ ID NO: 817, SEQ ID NO: 827, SEQ ID NO: 837, SEQ ID NO: 967, SEQ ID NO: 977, SEQ ID NO: 987, and SEQ ID NO: 997.

8. The binding molecule according to any one of the preceding claims, wherein the first binding domain comprises a VL region selected from the group consisting of a VL region as depicted in SEQ ID in SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 28, SEQ ID NO: 38, SEQ ID NO: 48, SEQ ID NO: 58, SEQ ID NO: 68, SEQ ID NO: 78, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 588, SEQ ID NO: 598, SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 748, SEQ ID NO: 758, SEQ ID NO: 768, SEQ ID NO: 778, SEQ ID NO: 788,

SEQ ID NO: 798, SEQ ID NO: 808, SEQ ID NO: 818, SEQ ID NO: 828, SEQ ID NO: 838, SEQ ID NO: 968, SEQ ID NO: 978, SEQ ID NO: 988, and SEQ ID NO: 998.

9. The binding molecule according to any one of the preceding claims, wherein the first binding domain comprises a VH region and a VL region selected from the group consisting of:

(1) a VH region as depicted in SEQ ID NO: 7, and a VL region as depicted in SEQ ID NO: 8;
(2) a VH region as depicted in SEQ ID NO: 17, and a VL region as depicted in SEQ ID NO: 18;
(3) a VH region as depicted in SEQ ID NO: 27, and a VL region as depicted in SEQ ID NO: 28;
(4) a VH region as depicted in SEQ ID NO: 37, and a VL region as depicted in SEQ ID NO: 38;
(5) a VH region as depicted in SEQ ID NO: 47, and a VL region as depicted in SEQ ID NO: 48;
(6) a VH region as depicted in SEQ ID NO: 57, and a VL region as depicted in SEQ ID NO: 58;
(7) a VH region as depicted in SEQ ID NO: 67, and a VL region as depicted in SEQ ID NO: 68;
(8) a VH region as depicted in SEQ ID NO: 77, and a VL region as depicted in SEQ ID NO: 78;
(9) a VH region as depicted in SEQ ID NO: 167, and a VL region as depicted in SEQ ID NO: 168;
(10) a VH region as depicted in SEQ ID NO: 177, and a VL region as depicted in SEQ ID NO: 178;
(11) a VH region as depicted in SEQ ID NO: 187, and a VL region as depicted in SEQ ID NO: 188;
(12) a VH region as depicted in SEQ ID NO: 197, and a VL region as depicted in SEQ ID NO: 198;
(13) a VH region as depicted in SEQ ID NO: 207, and a VL region as depicted in SEQ ID NO: 208;
(14) a VH region as depicted in SEQ ID NO: 217, and a VL region as depicted in SEQ ID NO: 218;
(15) a VH region as depicted in SEQ ID NO: 227, and a VL region as depicted in SEQ ID NO: 228;

(16) a VH region as depicted in SEQ ID NO: 317, and a VL region as depicted in SEQ ID NO: 318;

(17) a VH region as depicted in SEQ ID NO: 327, and a VL region as depicted in SEQ ID NO: 328;

(18) a VH region as depicted in SEQ ID NO: 337, and a VL region as depicted in SEQ ID NO: 338;

(19) a VH region as depicted in SEQ ID NO: 347, and a VL region as depicted in SEQ ID NO: 348;

(20) a VH region as depicted in SEQ ID NO: 357, and a VL region as depicted in SEQ ID NO: 358;

(21) a VH region as depicted in SEQ ID NO: 367, and a VL region as depicted in SEQ ID NO: 368;

(22) a VH region as depicted in SEQ ID NO: 377, and a VL region as depicted in SEQ ID NO: 378;

(23) a VH region as depicted in SEQ ID NO: 387, and a VL region as depicted in SEQ ID NO: 388;

(24) a VH region as depicted in SEQ ID NO: 587, and a VL region as depicted in SEQ ID NO: 588;

(25) a VH region as depicted in SEQ ID NO: 597, and a VL region as depicted in SEQ ID NO: 598;

(26) a VH region as depicted in SEQ ID NO: 607, and a VL region as depicted in SEQ ID NO: 608;

(27) a VH region as depicted in SEQ ID NO: 617, and a VL region as depicted in SEQ ID NO: 618;

(28) a VH region as depicted in SEQ ID NO: 627, and a VL region as depicted in SEQ ID NO: 628;

(29) a VH region as depicted in SEQ ID NO: 637, and a VL region as depicted in SEQ ID NO: 638;

(30) a VH region as depicted in SEQ ID NO: 647, and a VL region as depicted in SEQ ID NO: 648;

(31) a VH region as depicted in SEQ ID NO: 657, and a VL region as depicted in SEQ ID NO: 658;

(32) a VH region as depicted in SEQ ID NO: 667, and a VL region as depicted in SEQ ID NO: 668;

(33) a VH region as depicted in SEQ ID NO: 677, and a VL region as depicted in SEQ ID NO: 678;

(34) a VH region as depicted in SEQ ID NO: 687, and a VL region as depicted in SEQ ID NO: 688;

(35) a VH region as depicted in SEQ ID NO: 697, and a VL region as depicted in SEQ ID NO: 698;

(36) a VH region as depicted in SEQ ID NO: 707, and a VL region as depicted in SEQ ID NO: 708;

(37) a VH region as depicted in SEQ ID NO: 717, and a VL region as depicted in SEQ ID NO: 718;

(38) a VH region as depicted in SEQ ID NO: 727, and a VL region as depicted in SEQ ID NO: 728;

(39) a VH region as depicted in SEQ ID NO: 737, and a VL region as depicted in SEQ ID NO: 738;

(40) a VH region as depicted in SEQ ID NO: 747, and a VL region as depicted in SEQ ID NO: 748;

(41) a VH region as depicted in SEQ ID NO: 757, and a VL region as depicted in SEQ ID NO: 758;

(42) a VH region as depicted in SEQ ID NO: 767, and a VL region as depicted in SEQ ID NO: 768;

(43) a VH region as depicted in SEQ ID NO: 777, and a VL region as depicted in SEQ ID NO: 778;

(44) a VH region as depicted in SEQ ID NO: 787, and a VL region as depicted in SEQ ID NO: 788;

(45) a VH region as depicted in SEQ ID NO: 797, and a VL region as depicted in SEQ ID NO: 798;

(46) a VH region as depicted in SEQ ID NO: 807, and a VL region as depicted in SEQ ID NO: 808;

(47) a VH region as depicted in SEQ ID NO: 817, and a VL region as depicted in SEQ ID NO: 818;

(48) a VH region as depicted in SEQ ID NO: 827, and a VL region as depicted in SEQ ID NO: 828;

(49) a VH region as depicted in SEQ ID NO: 837, and a VL region as depicted in SEQ ID NO: 838;

(50) a VH region as depicted in SEQ ID NO: 967, and a VL region as depicted in SEQ ID NO: 968;

(51) a VH region as depicted in SEQ ID NO: 977, and a VL region as depicted in SEQ ID NO: 978;

(52) a VH region as depicted in SEQ ID NO: 987, and a VL region as depicted in SEQ ID NO: 988; and

(53) a VH region as depicted in SEQ ID NO: 997, and a VL region as depicted in SEQ ID NO: 998.

10. The binding molecule according to claim 9, wherein the first binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 19, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 49, SEQ ID NO: 59, SEQ ID NO: 69, SEQ ID NO: 79, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, SEQ ID NO: 229, SEQ ID NO: 319, SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, SEQ ID NO: 389, SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 749, SEQ ID NO: 759, SEQ ID NO: 769, SEQ ID NO: 779, SEQ ID NO: 789, SEQ ID NO: 799, SEQ ID NO: 809, SEQ ID NO: 819, SEQ ID NO: 829, SEQ ID NO: 839, SEQ ID NO: 969, SEQ ID NO: 979, SEQ ID NO: 989, and SEQ ID NO: 999.

11. The binding molecule according to any one of the previous claims having the amino acid sequence shown in SEQ ID NO:340 or SEQ ID NO: 980.

12 The binding molecule according to claim 11, further comprising a polyhistidine tag.

13. The binding molecule according to claim 12, wherein the polyhistidine tag is a hexa-histidine-tag (HHHHHH) located at the C-terminus and linked via a peptide bond.

14. A nucleic acid sequence encoding a binding molecule as defined in any one of claims 1 to 13.

15. A vector comprising a nucleic acid sequence as defined in claim 14.

16. A host cell transformed or transfected with the nucleic acid sequence as defined in claim 14 or with the vector as defined in claim 15.

17. A process for the production of a binding molecule according to any one of claims 1 to 13, said process comprising culturing a host cell as defined in claim 16 under conditions allowing the expression of the binding molecule as defined in any one of claims 1 to 13 and recovering the produced binding molecule from the culture.

18. A pharmaceutical composition comprising a binding molecule according to any one of claims 1 to 13, or produced according to the process of claim 17.

19. The binding molecule according to any one of claims 1 to 13, for use in the prevention, treatment or amelioration of a disease selected from the group consisting of plasma cell disorders, other B cell disorders that correlate with BCMA expression and autoimmune diseases.

20. The use of the binding molecule according to any one of claims 1 to 13, in the manufacture of a medicament for the treatment or amelioration of a disease selected from the group consisting of plasma cell disorders, other B cell disorders that correlate with BCMA expression and autoimmune diseases.

21. The use according to claim 20, wherein the plasma cell disorder is selected from the group consisting of multiple myeloma, plasmacytoma, plasma cell leukemia, macroglobulinemia, amyloidosis, Waldenstrom's macroglobulinemia , solitary bone plasmacytoma, extramedullary plasmacytoma, osteosclerotic myeloma, heavy chain diseases, monoclonal gammopathy of undetermined significance, and smoldering multiple myeloma.

22. The use according to claim 20, wherein the autoimmune disease is systemic lupus erythematosus.

23. A kit comprising a binding molecule as defined in any one of claims 1 to 13, a nucleic acid molecule as defined in claim 14, a vector as defined in claim 15, and/or a host cell as defined in claim 16.