Method for the production and selection of molecules comprising at least two different entities and uses thereof

Herein is reported a method for producing and selecting molecules formed by the combination of two different entities, such as binding entities, effector entities, or payloads, by using a transpeptidase, such as sortase A, wherein the at least two different entities are joined in vivo. This has been achieved by adding an endoplasmic reticulum retention signal to the sortase and to one of the entities.

Background of the Invention

Over the past years, a wide variety of specific therapeutic proteins, including antibodies, antibody fragments, and ligands for cell surface receptors have been developed and clinically tested. Exemplary proteins are antibodies, Fc-region conjugates, or targeted delivery vehicles. Some of these therapeutic proteins have been conjugated to several classes of therapeutic toxins such as small molecule drugs, enzymes, radioisotopes, protein toxins, and other toxins for specific delivery to patients.

Effective delivery to the site of disease is a prerequisite for high efficacy and low toxicity of any therapeutic molecule. For example, antibodies can participate in this context. If the antibody is not the therapeutic principle by itself, conjugation of an effector molecule to an antibody makes it possible to achieve precise localization of the drug at the desired site within the human body. This increases the effective drug concentration within this target area, thereby optimizing the therapeutic efficacy of the agent. Furthermore, with targeted delivery, the clinician may be able to lower the overall dose of the therapeutic agent and, thus, minimize systemic exposure - something that is particularly relevant if the drug payload has associated toxicities or if it is to be used in the treatment of chronic conditions (see e.g. McCarron, P.A., et al., Mol. Interventions 5 (2005) 368-380).

In WO 2010087994 methods for ligation and uses thereof are reported. Recombinant approaches to IgG-like bispecific antibodies are reported by Marvin, J.S., et al. (Acta Pharmacol. Sinica 26 (2005) 649-658). Levary, D.A., et al. (PLoS one, 6 (2011) e18342.1-e18342.6) report protein-protein fusion catalyzed by sortase A. In WO 2013/003555 the use of sortases to install click chemistry handles for protein ligation is reported.

Strijbis, K. et al (Traffic 13 (2012) 780-789) report protein ligation in living cells using sortase. It has been stated by them that the Ca^{2+}-dependent S. aureus sortase A is not functional intracellularly, but that the Ca^{2+}-independent S. pyogenes sortase A is functional in the cytosol and endoplasmic reticulum (ER) lumen of both Saccharomyces cerevisiae and mammalian HEK293T cells.

Summary

Herein is reported a method for producing in vivo intracellularly an enzyme – catalyzed (i.e. enzymatic) conjugate of a first polypeptide domain with a second polypeptide domain by using the Ca^{2+}-dependent enzyme sortase A of Staphylococcus aureus (S. aureus), whereby one of the polypeptide domains and the soluble sortase A enzyme contain an endoplasmic reticulum retention signal sequence.

This technology is especially suited for the rapid generation e.g. of a library of combinations of a first group of polypeptide domains (e.g. a first group of binding domains such as cognate pairs of antibody variable domains) and a second group of polypeptide domains (e.g. a second group of binding domains such as cognate pairs of antibody variable domains but directed against other epitopes/antigens as those of the first group, or a group of payload molecules). This library can be easily generated e.g. by transient transfection in HEK cells and the resulting combinations can be screened thereafter e.g. for the intended biological effect or intended properties.

There is provided a method for producing a polypeptide comprising at least two polypeptide domains comprising the step of

- cultivating a cell comprising

  a) a nucleic acid encoding a soluble sortase A with a C-terminal endoplasmic reticulum retention signal,

  b) a nucleic acid encoding a first polypeptide domain comprising at its C-terminus or in its C-terminal region a sortase motif followed by an endoplasmic reticulum retention signal, and

  c) a nucleic acid encoding a second polypeptide domain comprising at its N-terminus an oligoglycine motif of at least two glycine residues,

whereby the cell secretes the sortase A(-mediated/-catalyzed) conjugate of the first polypeptide domain and the second polypeptide domain,

thereby producing a polypeptide comprising at least two polypeptide domains.

There is also provided a method for producing a multispecific binder comprising at least two binding entities comprising the step of

- cultivating a cell comprising

  a) a nucleic acid encoding a soluble sortase A with a C-terminal endoplasmic reticulum retention signal,

  b) a nucleic acid encoding a first binding entity comprising at its C-terminus or in its C-terminal region a sortase motif followed by an endoplasmic reticulum retention signal, and

  c) a nucleic acid encoding a second binding entity comprising at its N-terminus at least a diglycine,

whereby the cell secretes the sortase A(-mediated/catalyzed) conjugate of the first binding entity and the second binding entity,

whereby the first binding entity specifically binds to a first antigen or target and the second binding entity specifically binds to a second antigen or target,

thereby producing a multispecific binder comprising at least two binding entities.

In one aspect, there is provided a method for producing a multispecific binder comprising at least two binding entities comprising the step of

- cultivating a HEK cell comprising

  a) a nucleic acid encoding a soluble S. aureus sortase A with a C-terminal endoplasmic reticulum retention signal,

  b) a nucleic acid encoding a first binding entity comprising at its C-terminus a sortase motif followed by an endoplasmic reticulum retention signal, and

  c) a nucleic acid encoding a second binding entity comprising at its N-terminus at least a diglycine,

whereby the HEK cell secretes the sortase A conjugate of the first binding entity and the second binding entity,

whereby the first binding entity specifically binds to a first antigen or target and the second binding entity specifically binds to a second antigen or target,

thereby producing a multispecific binder comprising at least two binding entities.

The sortase A may be the sortase A of Staphylococcus aureus (S. aureus). In one embodiment the nucleic acid encoding a (soluble) sortase A with a C-terminal endoplasmic reticulum retention signal encodes an amino acid sequence of SEQ ID NO: 51 or SEQ ID NO: 52.

Herein is reported a method for providing tailor-made, highly specific therapeutic molecules for the treatment of a disease, such as cancer or a viral infection, in a patient in need of a treatment, whereby the therapeutic molecule is adapted to the characteristics of the disease of the patient and/or to the genotype/phenotype of the patient.

Such adaptation is achieved by making a tailor-made molecule taking into account the genotype/phenotype of the disease harboring/affected cells of the patient.

In a first step the genotype/phenotype of the cells (e.g. the presence and number/quantity of disease-specific cell surface molecules) that are intended to be targeted with the therapeutic molecule is determined. This can be achieved, e.g. by cell imaging techniques such as immunohistochemical staining (IHC, immunohistochemistry) of patient's cells derived e.g. from blood and/or biopsied material using fluorescently labeled monospecific (therapeutic or diagnostic) antibodies. Alternatively the genotype/phenotype of the cells can be analyzed after staining with labeled therapeutic or diagnostic antibodies using FACS-based methods. In vivo imaging techniques including optical imaging, molecular imaging, fluorescence imaging, bioluminescence Imaging, MRI, PET, SPECT, CT, and intravital microscopy may be used also for determination of the genotype/phenotype of disease-related cells of a patient. Depending on the determined genotype/phenotype of the disease-related cells of a patient a tailor-made combination of targeting/binding entities can be/is chosen and are combined in a therapeutic molecule. Such a therapeutic molecule may be for example a bispecific antibody.

Such tailor-made therapeutic molecules i) will be highly specific, ii) will have a good therapeutic efficacy, and iii) will induce fewer and/or less severe side effects compared to conventionally chosen therapeutics. This can be achieved by endowing the therapeutic molecule with improved targeting and/or improved tailor-made delivery properties, e.g. for delivery of a therapeutic payload to its intended site of action.

The improved delivery of the therapeutic molecule to its site of action, such as e.g. a cancer cell, can be achieved by a higher/increased selectivity and/or specificity for the targeted therapeutic molecule compared to conventionally chosen therapeutic molecules. The therapeutic molecule comprises at least two entities that specifically bind to or can be bound by different proteins (e.g. two different cell surface markers).

The increased selectivity and/or specificity of the tailor-made therapeutic molecule can be achieved by the simultaneous binding of both targeting entities to their respective targets/epitopes or by the simultaneous binding of both polypeptide domains by its interaction partner, or by mixtures thereof.

Especially suited is the combination of two binding entities having a low to medium affinity for their respective targets/epitopes. Additionally, off-target binding is greatly reduced or can even be eliminated totally.

It has been found that with the method as reported herein it is possible to tailor-make e.g. bispecific binders such as e.g. bispecific antibodies specifically directed to two surface markers found on the surface of a cell, such as a cancer cell. As the binding specificities are individually provided by the starting components it is possible to tailor-make a multispecific targeting and binding molecule simply by determining the surface markers present on a cell, e.g. on a cancer cell, and conjugating the respective antibody fragments that specifically bind to these surface markers or their respective ligands by an enzymatic procedure. As the enzymatic conjugation is performed by the enzyme sortase A, in one embodiment by the sortase A of S. aureus, the resulting bispecific binder (bispecific antibody) is characterized by the presence of the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue).

There is also provided a method for selecting a multispecific binder that specifically binds to two different epitopes or antigens comprising the step of

- selecting from a multitude of multispecific binders comprising different combinations of a first binding entity and a second binding entity a multispecific binder that specifically binds to two different epitopes or antigens.

In another aspect, there is provided a method for selecting a multispecific binder that specifically binds to two different epitopes or antigens comprising the step of

- selecting from a multitude of multispecific binders comprising different combinations of a first binding entity and a second binding entity a multispecific binder that specifically binds to two different epitopes or antigens,

wherein the members of the multitude of multispecific binders are each obtained by a method as defined herein.

There is also provided a method for selecting a bispecific antibody comprising the following steps

(i) determining the cell surface makers present in a cell containing sample and selecting thereof at least a first surface marker and a second surface marker,

(ii) transfecting a cell with (a) a nucleic acid encoding an antibody Fab, or scFab fragment, or an scFv antibody comprising within the 20 (twenty) C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) followed by an endoplasmic reticulum retention signal KDEL (SEQ ID NO: 02), whereby the Fab, or scFab fragment, or scFv antibody specifically binds to the first surface marker or its ligand, (b) a nucleic acid encoding a one-

armed antibody fragment comprising a full length antibody heavy chain, a full length antibody light chain, and an antibody heavy chain Fc-region polypeptide, whereby the full length antibody heavy chain and the full length antibody light chain are cognate antibody chains complementary to each other and the pair of variable domains (VH and VL) thereof forms an antigen binding site that specifically binds to the second surface marker or its ligand, whereby the full length antibody heavy chain and the antibody heavy chain Fc-region polypeptide are covalently linked to each other via one or more disulfide bonds forming an antibody hinge region, and whereby the antibody heavy chain Fc-region polypeptide has an oligoglycine G_m (m = 2, or 3, or 4, or 5) amino acid sequence at its N-terminus, and (c) a nucleic acid encoding a soluble sortase A with a C-terminal endoplasmic reticulum retention signal,

and thereby producing the bispecific antibody.

In another aspect, there is provided a method for producing a bispecific antibody comprising the following steps

(i) determining the cell surface makers present in a cell containing sample and selecting thereof at least a first surface marker and a second surface marker,

(ii) transfecting a cell with (a) a nucleic acid encoding an antibody Fab fragment, or an antibody scFab, or a scFv antibody comprising within the 20 C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) followed by an endoplasmic reticulum retention signal KDEL (SEQ ID NO: 02), whereby the Fab fragment or scFv antibody specifically binds to the first surface marker or its ligand, (b) a nucleic acid encoding an one-armed antibody fragment comprising a full length antibody heavy chain, a full length antibody light chain, and an antibody heavy chain Fc-region polypeptide, whereby the full length antibody heavy chain and the full length antibody light chain are cognate antibody chains complementary to each other and the pair of variable domains (VH and VL) thereof forms an antigen binding site that specifically binds to the second surface marker or its ligand, whereby the full length antibody heavy chain and the antibody heavy chain Fc-region polypeptide are covalently linked to each other via one or more disulfide bonds forming an antibody hinge

region, and whereby the antibody heavy chain Fc-region polypeptide has an oligoglycine G_m (m = 2, or 3, or 4, or 5) amino acid sequence at its N-terminus, and (c) a nucleic acid encoding a soluble S. aureus sortase A with a C-terminal endoplasmic reticulum retention signal,

and thereby producing the bispecific antibody.

There is also provided a method for determining a combination of antigen binding sites comprising the following steps:

(i) determining the binding specificity and/or selectivity and/or affinity and/or effector function and/or in vivo half-life of a multitude of bispecific antibodies prepared by combining (a) each member of a first multitude of antibody Fab, or scFab fragments, or scFv antibody fragments whereby each member comprises within the 20 C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) followed by an endoplasmic reticulum retention signal KDEL (SEQ ID NO: 02), whereby the Fab, or scFab fragment, or scFv antibody specifically binds to a first epitope or antigen, with (b) each member of a multitude of one-armed antibody fragments comprising a full length antibody heavy chain, a full length antibody light chain, and an antibody heavy chain Fc-region polypeptide, whereby the full length antibody heavy chain and the full length antibody light chain are cognate antibody chains complementary to each other and the pair of variable domains (VH and VL) thereof forms an antigen binding site that specifically binds to a second epitope or antigen, whereby the full length antibody heavy chain and the antibody heavy chain Fc-region polypeptide are covalently linked to each other via one or more disulfide bonds forming an antibody hinge region, and whereby

the antibody heavy chain Fc-region polypeptide has an oligoglycine G_m (m = 2, or 3, or 4, or 5) amino acid sequence at its N-terminus, covalently by a sortase A catalyzed enzymatic reaction,

and

(ii) choosing the bispecific antibody with suitable binding specificity and/or selectivity and/or affinity and/or effector function and/or in vivo half-life and thereby determining a combination of antigen binding sites.

In another aspect, there is provided a method for determining a combination of antigen binding sites comprising the following steps

(i) determining a characteristic selected from the group consisting of binding specificity, selectivity, affinity, effector function, in vivo half-life and combinations thereof of a multitude of bispecific antibodies prepared by combining (a) each member of a first multitude of antibody Fab fragments or scFv antibody fragments whereby each member comprises within the 20 C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) followed by an endoplasmic reticulum retention signal KDEL (SEQ ID NO: 02), whereby the Fab fragment or scFv antibody specifically binds to a first epitope or antigen, with (b) each member of a multitude of one-armed antibody fragments comprising a full length antibody heavy chain, a full length antibody light chain, and an antibody heavy chain Fc-region polypeptide, whereby the full length antibody heavy chain and the full length antibody light chain are cognate antibody chains complementary to each other and the pair of variable domains (VH and VL) thereof forms an antigen binding site that specifically binds to a second epitope or antigen, whereby the full length antibody heavy chain and the antibody heavy chain Fc-region polypeptide are covalently linked to each other via one or more disulfide bonds forming an antibody hinge region, and whereby the antibody heavy chain Fc-region polypeptide has an oligoglycine G_m (m = 2, or 3, or 4, or 5) amino acid sequence at its N-terminus, via a S.aureus sortase A-mediated intracellular enzymatic coupling reaction,

and

(ii) choosing the bispecific antibody with the suitable characteristic selected from the group consisting of binding specificity, selectivity, affinity, effector function, in vivo half-life and combinations thereof, and thereby determining a combination of antigen binding sites.

The sortase A may be the sortase A of Staphylococcus aureus (S. aureus). In one embodiment the nucleic acid encoding a (soluble) sortase A with a C-terminal endoplasmic reticulum retention signal encodes an amino acid sequence of SEQ ID NO: 51 or SEQ ID NO: 52.

There is provided a bispecific antibody obtained by a method as reported herein.

There is provided a bispecific antibody comprising the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) in one of its heavy chains.

The following embodiments as reported herein are given.

In one embodiment the members of the multitude of multispecific binders are each obtained by a method as reported herein.

In one embodiment a multispecific binder is selected based on its binding specificity and/or selectivity and/or affinity and/or effector function and/or in vivo half-life.

In one embodiment the binding entity is a cognate pair of an antibody heavy chain variable domain and an antibody light chain variable domain.

In one embodiment the multispecific binder is a bispecific antibody comprising two or four binding entities.

In one embodiment the first polypeptide domain and the second polypeptide domain are selected independently of each other from full length antibody, scFv, scFab, antibody heavy chain, antibody light chain, antibody heavy chain Fc-region fragment, pair of antibody light chain variable domain and antibody heavy chain

variable domain, antigen binding antibody fragments, VH, VL, CH1, CH2, CH3, CH4, CL, antibody hinge region, cytokine, receptor, receptor ligand, detectable label, tag, and partner of a binding pair.

In one embodiment the endoplasmic reticulum retention signal is selected from SEQ ID NO: 02 (KDEL), SEQ ID NO: 03 (HDEL), or SEQ ID NO: 04 (SFIXXXXMP).

In one embodiment the sortase motif is LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue).

In one embodiment the first binding domain or the first binding entity has within the 20 C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue).

In one embodiment the cell is a mammalian cell or a yeast cell. In one embodiment the mammalian cell is selected from a HEK cell, a CHO cell, or a BHK cell.

In one embodiment the Fc-region comprises a mutation of the naturally occurring amino acid residue at position 329 and at least one further mutation of at least one amino acid residue selected from the group comprising amino acid residues at position 228, 233, 234, 235, 236, 237, 297, 318, 320, 322 and 331 to a different residue, wherein the residues in the Fc-region are numbered according to the EU index of Kabat. The change of these specific amino acid residues results in an altering of the effector function of the Fc-region compared to the non-modified (wild-type) Fc-region.

In one embodiment the binding entity is selected from (or the first binding entity and the second binding entity are selected independently of each other from) the group of a darpin domain based binding entity, an anticalin domain based binding entity, a T-cell receptor fragment like scTCR domain based binding entity, a camel VH domain based binding entity, a tenth fibronectin 3 domain based binding entity, a tenascin domain based binding entity, a cadherin domain based binding entity, an ICAM domain based binding entity, a titin domain based binding entity, a GCSF-R domain based binding entity, a cytokine receptor domain based binding entity, a glycosidase inhibitor domain based binding entity, a superoxide dismutase domain based binding entity, or antibody fragments like Fab, or scFab, or scFv fragment.

In one embodiment the first polypeptide domain comprises i) the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) in its C-terminal amino acid sequence region (i.e. within the twenty C-terminal amino acid residues) and ii) the endoplasmic reticulum retention signal KDEL (SEQ ID NO: 02) at its C-terminus, and the second polypeptide domain comprises an oligoglycine G_m (m = 2, or 3, or 4, or 5) at its N-terminus.

In one embodiment the second polypeptide domain or the second binding entity comprises an oligoglycine G_m (m = 2, or 3, or 4, or 5) amino acid sequence at its N-terminus.

The present disclosure may relate to a pharmaceutical formulation comprising a multispecific binder as reported herein.

The present disclosure may relate to use of a multispecific binder as reported herein in the manufacture of a medicament.

In one embodiment the medicament is for the treatment of cancer.

The present disclosure may relate to a method of treating an individual having cancer comprising administering to the individual an effective amount of a multispecific binder as reported herein.

The present disclosure may relate to a method for destroying cancer cells in an individual comprising administering to the individual an effective amount of a multispecific binder as reported herein.

There is provided a pharmaceutical formulation comprising a bispecific antibody as reported herein.

There is provided use of a bispecific antibody as reported herein in the manufacture of a medicament.

In one embodiment the medicament is for the treatment of cancer.

The present disclosure may relate to a method of treating an individual having cancer comprising administering to the individual an effective amount of a bispecific antibody as reported herein.

The present disclosure may relate to a method for destroying cancer cells in an individual comprising administering to the individual an effective amount of a

bispecific antibody as reported herein. In one embodiment, the Fc-region is a human Fc-region or a variant thereof.

In one embodiment the human antibody Fc-region is of human IgG1 subclass, or of human IgG2 subclass, or of human IgG3 subclass, or of human IgG4 subclass.

In one embodiment the antibody Fc-region is a human antibody Fc-region of the human IgG1 subclass, or of the human IgG4 subclass.

In one embodiment the human antibody Fc-region comprises a mutation of the naturally occurring amino acid residue at least at one of the following amino acid positions 228, 233, 234, 235, 236, 237, 297, 318, 320, 322, 329, and/or 331 to a different residue, wherein the residues in the antibody Fc-region are numbered according to the EU index of Kabat.

In one embodiment the human antibody Fc-region comprises a mutation of the naturally occurring amino acid residue at position 329 and at least one further mutation of at least one amino acid residue selected from the group comprising amino acid residues at position 228, 233, 234, 235, 236, 237, 297, 318, 320, 322 and 331 to a different residue, wherein the residues in the Fc-region are numbered according to the EU index of Kabat. The change of these specific amino acid residues results in an altering of the effector function of the Fc-region compared to the non-modified (wild-type) Fc-region.

In one embodiment the human antibody Fc-region has a reduced affinity to the human FcγRIIIA, and/or FcγRIIA, and/or FcγRI compared to a conjugate comprising the corresponding wild-type IgG Fc-region.

In one embodiment the amino acid residue at position 329 in the human antibody Fc-region is substituted with glycine, or arginine, or an amino acid residue large enough to destroy the proline sandwich within the Fc-region.

In one embodiment the mutation in the human antibody Fc-region of the naturally occurring amino acid residue is at least one of S228P, E233P, L234A, L235A, L235E, N297A, N297D, P329G, and/or P331S.

In one embodiment the mutation is L234A and L235A if the antibody Fc-region is of human IgG1 subclass, or S228P and L235E if the antibody Fc-region is of human IgG4 subclass.

In one embodiment the antibody Fc-region comprises the mutation P329G.

In one embodiment the antibody Fc-region comprises the mutation T366W in the first heavy chain Fc-region polypeptide and the mutations T366S, L368A and Y407V in the second heavy chain Fc-region polypeptide, wherein the numbering is according to the EU index of Kabat.

In one embodiment the antibody Fc-region comprises the mutation S354C in the first heavy chain Fc-region polypeptide and the mutation Y349C in the second heavy chain Fc-region polypeptide.

Description of the Figures

Figure 1 Plasmid map of the expression plasmid for the soluble sortase A comprising an endoplasmic retention signal at its C-terminus.

Figure 2 Coomassie stained SDS-gel, reducing conditions; culture supernatants of HEK293 cells transfected with scFab-GS-His6-GS-LPETGGS-KDEL (lane 1), scFab-GS-His6-GAPPPS-LPETGGS-KDEL (lane 2), $(GGGGS)_2$ – scFab (lane 3), soluble sortase A-KDEL (lane 4), combination 1+3+4 (plasmid ratios 2.5 : 5 : 1) (lane 5), combination 2+3+4 (plasmid ratio 2 : 8 : 1) (lane 6); scFab-GS-His6-GS-LPETGGS-KDEL and scFab-GS-His6-GAPPPS-LPETGGS-KDEL are retained mostly intracellularly, $(GGGGS)_2$-scFab is expressed and secreted into the medium (about 50kDa), for the combination a band at about 100 kDa of the enzymatic conjugate can be seen.

Figure 3 Coomassie stained SDS-gel, reducing conditions; cell lysates (left) of HEK293 cells transfected with scFab-GS-His6-GS-LPETGGS-KDEL (lane 1), scFab-GS-His6-GAPPPS-LPETGGS-KDEL (lane 2), $(GGGGS)_2$ – scFab (lane 3), soluble sortase A-KDEL (lane 4), combination 1+3+4 (plasmid ratio 2.5 : 5 : 1) (lane 5), combination 2+3+4 (plasmid ratio 2 : 8 : 1) (lane 6); scFab-GS-His6-GS-LPETGGS-KDEL and scFab-GS-His6-GAPPPS-LPETGGS-KDEL are retained mostly intracellularly.

Figure 4 Western blot analysis of an SDS gel using the identical samples and performed under identical conditions as the gels from Figures 2 and 3; the scFab-LPXTG molecules and the conjugation product are detected with an anti-His-tag antibody (PentaHis-AK

(Qiagen)); for the combination a band at about 100 kDa of the enzymatic conjugate can be seen.

Detailed Description of embodiments of the Invention

I. DEFINITIONS

In the present specification and claims the numbering of the residues in an immunoglobulin heavy chain Fc-region is that of the EU index of Kabat (Kabat, E.A., et al., Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, National Institutes of Health, Bethesda, MD (1991), NIH Publication 91-3242, expressly incorporated herein by reference).

The term "alteration" denotes the mutation, addition, or deletion of one or more amino acid residues in a parent amino acid sequence.

The term "tag" denotes a sequence of amino acid residues connected to each other via peptide bonds that has specific binding properties. In one embodiment the tag is an affinity or purification tag. In one embodiment the tag is selected from Arg-tag, His-tag, Flag-tag, 3xFlag-tag, Strep-tag, Nano-tag, SBP-tag, c-myc-tag, S-tag, calmodulin-binding-peptide, cellulose-binding-domain, chitin-binding-domain, GST-tag, or MBP-tag. In one embodiment the tag is selected from SEQ ID NO: 05 (RRRRR), or SEQ ID NO: 06 (RRRRRR), or SEQ ID NO: 07 (HHHHHH), or SEQ ID NO: 08 (KDHLIHNVHKEFHAHAHNK), or SEQ ID NO: 09 (DYKDDDDK), or SEQ ID NO: 10 (DYKDHDGDYKDHDIDYKDDDDK), or SEQ ID NO: 11 (AWRHPQFGG), or SEQ ID NO: 12 (WSHPQFEK), or SEQ ID NO: 13 (MDVEAWLGAR), or SEQ ID NO: 14 (MDVEAWLGARVPLVET), or SEQ ID NO: 15 (MDEKTTGWRGGHVVEGLAGELEQLRARLEHHPQGQREP), or SEQ ID NO: 16 (EQKLISEEDL), or SEQ ID NO: 17 (KETAAAKFERQHMDS), or SEQ ID NO: 18 (KRRWKKNFIAVSAANRFKKISSSGAL), or SEQ ID NO: 19 (cellulose binding domain), or SEQ ID NO: 20 (cellulose binding domain), or SEQ ID NO: 21 (TNPGVSAWQVNTAYTAGQLVTYNGKTYKCLQPHTSLAGWEP SNVPALWQLQ), or SEQ ID NO: 22 (GST-tag), or SEQ ID NO: 23 (MBP-tag).

The term "antigen binding antibody fragment" denotes a molecule other than a full length antibody that comprises a portion of a full length antibody that binds the antigen to which the intact antibody binds. Examples of antibody fragments include but are not limited to Fv, scFv, Fab, scFab, Fab', Fab'-SH, $F(ab')_2$, diabodies, linear

antibodies, single-chain antibody molecules (e.g. scFv), and multispecific antibodies formed from antibody fragments.

Antibody fragments include, but are not limited to, Fab, Fab', Fab'-SH, $F(ab')_2$, Fv, and scFv fragments, and other fragments described below. For a review of certain antibody fragments, see Hudson, P.J., et al., Nat. Med. 9 (2003) 129-134. For a review of scFv fragments, see, e.g., Plueckthun, A., In: The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore (eds.), Springer-Verlag, New York (1994), pp. 269-315; see also WO 93/16185; US 5,571,894 and US 5,587,458. For discussion of Fab and $F(ab')_2$ fragments comprising salvage receptor binding epitope residues and having increased in vivo half-life, see US 5,869,046.

Antibody fragments can be made by various techniques, including but not limited to proteolytic digestion or cleavage of an intact antibody as well as production by recombinant host cells (e.g. E. coli or phage or eukaryotic cells), as described herein.

The term "bispecific antibody" denotes an antigen binding molecule that can specifically bind to a first antigen or epitope and to a second antigen or epitope, whereby the first antigen or epitope is different from the second antigen or epitope.

Bispecific antibody formats are described e.g. in WO 2009/080251, WO 2009/080252, WO 2009/080253, WO 2009/080254, WO 2010/112193, WO 2010/115589, WO 2010/136172, WO 2010/145792, and WO 2010/145793.

The term "class" of an antibody denotes the type of constant domain or constant region possessed by its heavy chain. There are five major classes of antibodies in humans: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2. The gene segments encoding the heavy chain constant domains that correspond to the different classes of immunoglobulins are called α, δ, ε, γ, and μ, respectively. In addition, there are two classes of light chains present in antibodies of human origin: kappa and lambda which can form intact antibodies in combination with their cognate heavy chain partners. The genes encoding the kappa or lambda light chains are called κ and λ, respectively.

The term "effector function" denotes those biological activities attributable to the Fc-region of an antibody, which vary with the antibody class and/or subclass.

Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity (CDC); Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); antibody-dependent cellular phagocytosis (ADCP); down regulation of cell surface receptors (e.g. B-cell receptor); and B-cell activation. Such function can be effected by, for example, binding of an Fc-region to an Fc receptor on an immune cell with phagocytic or lytic activity, or by binding of an Fc-region to components of the complement system.

An "effective amount" of an agent, e.g., a pharmaceutical formulation, refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic or prophylactic result.

The term "Fc-region" denotes the C-terminal region of an immunoglobulin. The Fc-region is a dimeric molecule comprising two disulfide-linked antibody heavy chain fragments (heavy chain Fc-region polypeptide chains). An Fc-region can be generated by papain digestion, or IdeS digestion, or trypsin digestion of an intact (full length) antibody or can be produced recombinantly.

The Fc-region obtainable from a full length antibody or immunoglobulin comprises at least residues 226 (Cys) to the C-terminus of the full length heavy chain and, thus, comprises a part of the hinge region and two or three constant region domains, i.e. a CH2 domain, a CH3 domain, and an additional/extra CH4 domain in case of IgE and IgM class antibodies. It is known from US 5,648,260 and US 5,624,821 that the modification of defined amino acid residues in the Fc-region results in phenotypic effects.

The formation of the dimeric Fc-region comprising two identical or non-identical antibody heavy chain fragments is mediated by the non-covalent dimerization of the comprised CH3 domains (for involved amino acid residues see e.g. Dall'Acqua, Biochem. 37 (1998) 9266-9273). The Fc-region is covalently stabilized by the formation of disulfide bonds in the hinge region (see e.g. Huber, et al., Nature 264 (1976) 415-420; Thies, et al., J. Mol. Biol. 293 (1999) 67-79). The introduction of amino acid residue changes within the CH3 domain in order to disrupt the dimerization of CH3-CH3 domain interactions do not adversely affect the neonatal Fc receptor (FcRn) binding due to the location of the residues involved in CH3-CH3-domain dimerization which are located on the inner interface of the CH3 domains, whereas the residues involved in Fc-region-FcRn interaction are located on the outside of the CH2-CH3 domains.

The residues associated with effector functions of an Fc-region are located in the hinge region, the CH2, and/or the CH3 domains as determined for a full length antibody molecule. The Fc-region associated/mediated functions are:

(i) antibody-dependent cellular cytotoxicity (ADCC),
(ii) complement (C1q) binding, activation and complement-dependent cytotoxicity (CDC),
(iii) antibody-dependent cellular phagocytosis (ADCP)
(iv) phagocytosis/clearance of antigen-antibody complexes (immune complexes),
(v) cytokine release in some instances, and
(vi) half-life/clearance rate of antibody and antigen-antibody complexes.

The Fc-region-associated effector functions are triggered/initiated by the interaction of the Fc-region with effector function specific molecules or receptors. Predominantly antibodies of the IgG1 subclass can effect receptor activation, whereas antibodies of the IgG2 and IgG4 subclasses do not have effector function or have limited effector function.

The effector function eliciting receptors are the Fc receptor types (and sub-types) FcγRI, FcγRII and FcγRIII. The effector functions associated with an IgG1 subclass can be reduced by introducing specific amino acid changes in the lower hinge region, such as L234A and/or L235A, which are involved in FcγR and C1q binding. Also certain amino acid residues, especially located in the CH2 and/or CH3 domains, are associated with the control of the circulation half-life of an antibody molecule or an Fc-region fusion polypeptide in the blood stream. The circulation half-life is determined by the binding of the Fc-region to the neonatal Fc receptor (FcRn).

The term "human Fc-region" denotes the C-terminal region of an immunoglobulin heavy chain of human origin that contains at least a part of the hinge region, the CH2 domain and the CH3 domain. In one embodiment, a human IgG antibody heavy chain Fc-region extends from about Glu216, or from about Cys226, or from about Pro230, to the carboxyl-terminus of the heavy chain. However, the C-terminal lysine (Lys447) of the antibody Fc-region may or may not be present.

A polypeptide chain of a wild-type human Fc-region of the IgG1 subclass has the following amino acid sequence:

CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI
AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK (SEQ ID NO: 24).

A polypeptide chain of a wild-type human Fc-region of the IgG4 subclass has the following amino acid sequence:

CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNW
YVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
GLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVM
HEALHNHYTQKSLSLSLGK (SEQ ID NO: 25).

The term "full length antibody" denotes an antibody having a structure and amino acid sequence substantially identical to a native antibody structure as well as polypeptides that comprise the Fc-region as reported herein.

The term "full length antibody heavy chain" denotes a polypeptide comprising in N- to C-terminal direction an antibody variable domain, a first constant domain, an antibody heavy chain hinge region, a second constant domain, and a third constant domain, and in some instances a fourth constant domain.

The term "antibody heavy chain Fc-region" denotes a polypeptide comprising an antibody heavy chain hinge region, a first constant domain (normally the CH2 domain), and a second constant domain (normally the CH3 domain).

The term "CH2 domain" denotes the part of an antibody heavy chain polypeptide that extends approximately from EU position 231 to EU position 340 (EU numbering system according to Kabat). In one embodiment a CH2 domain has the amino acid sequence of SEQ ID NO: 26 (APELLGGPSVFLFPPKPKDTLMISRTPEVTCVWDVSHEDPEVKFNWYVDG
VEVHNAKTKPREEQESTYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAK). The CH2 domain is unique in that it is not closely paired with another domain. Rather, two N-linked branched carbohydrate chains are interposed

between the two CH2 domains of an intact native Fc-region. It has been speculated that the carbohydrate may provide a substitute for the domain-domain pairing and help stabilize the CH2 domain. Burton, Mol. Immunol. 22 (1985) 161-206.

The term "CH3 domain" denotes the part of an antibody heavy chain polypeptide that extends approximately from EU position 341 to EU position 446. In one embodiment the CH3 domain has the amino acid sequence of SEQ ID NO: 27 (GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPG).

The term "full length antibody light chain" denotes a polypeptide comprising in N- to C-terminal direction an antibody variable domain and a constant domain.

The term "hinge region" denotes the part of an antibody heavy chain polypeptide that joins in a wild-type antibody heavy chain the CH1 domain and the CH2 domains, e. g. from about position 216 to about position 230 according to the EU number system of Kabat, or from about position 226 to about position 230 according to the EU number system of Kabat. The hinge regions of other IgG subclasses can be determined by aligning with the hinge-region cysteine residues of the IgG1 subclass sequence.

The hinge region is normally a dimer consisting of two polypeptides with identical amino acid sequence. The hinge region generally comprises about 25 amino acid residues and is flexible allowing the antigen binding regions to move independently of each other. The hinge region can be subdivided into three subdomains: the upper, the middle, and the lower hinge region (see e.g. Roux, et al., J. Immunol. 161 (1998) 4083).

The term "lower hinge region" of an Fc-region denotes the stretch of amino acid residues immediately C-terminal to the middle (central) hinge region, i.e. residues 233 to 239 of the Fc-region according to the EU numbering of Kabat.

The term "wild-type Fc-region" denotes an amino acid sequence identical to the amino acid sequence of an Fc-region found in nature. Wild-type human Fc-regions include a native human IgG1 Fc-region (non-A and A allotypes), native human IgG2 Fc-region, native human IgG3 Fc-region, and native human IgG4 Fc-region as well as naturally occurring variants thereof.

The term "individual" or "subject" denotes a mammal. Mammals include, but are not limited to, domesticated animals (e.g. cows, sheep, cats, dogs, and horses), primates (e.g., humans and non-human primates such as monkeys), rabbits, and rodents (e.g., mice, rats, and hamsters). In certain embodiments, the individual or subject is a human.

"Percent (%) amino acid sequence identity" with respect to a reference polypeptide sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Sequence alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc., and the source code has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available from Genentech, Inc., South San Francisco, California, or may be compiled from the source code. The ALIGN-2 program should be compiled for use on a UNIX operating system, including digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

The term "pharmaceutical formulation" refers to a preparation which is in such a form as to permit the biological activity of an active ingredient contained therein to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the formulation would be administered.

A "pharmaceutically acceptable carrier" refers to an ingredient in a pharmaceutical formulation, other than an active ingredient, which is nontoxic to a subject. A pharmaceutically acceptable carrier includes, but is not limited to, a buffer, excipient, stabilizer, or preservative.

The term "phenotype of a patient" denotes the composition of cell surface molecules/receptors in a kind of cells from a patient. The composition can be a qualitative as well as a quantitative composition. The cells for which the genotype is determined/given can be a single cell or a sample comprising cells.

The term "position" denotes the location of an amino acid residue in the amino acid sequence of a polypeptide. Positions may be numbered sequentially, or according to an established format, for example the EU index of Kabat for antibody numbering.

The term "receptor" denotes a polypeptide capable of binding at least one ligand. In one embodiment the receptor is a cell-surface receptor having an extracellular ligand-binding domain and, optionally, other domains (e.g. transmembrane domain, intracellular domain and/or membrane anchor). The receptor to be evaluated in the assay described herein may be an intact receptor or a fragment or derivative thereof (e.g. a fusion protein comprising the binding domain of the receptor fused to one or more heterologous polypeptides). Moreover, the receptor to be evaluated for its binding properties may be present in a cell or isolated and optionally coated on an assay plate or some other solid phase.

As used herein, "treatment" (and grammatical variations thereof such as "treat" or "treating") refers to clinical intervention in an attempt to alter the natural course of the individual being treated, and can be performed either for prophylaxis or during the course of clinical pathology. Desirable effects of treatment include, but are not limited to, preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis. In some embodiments, antibodies of the invention are used to delay development of a disease or to slow the progression of a disease.

II. Tailor-made molecules comprising a first and a second polypeptide domain

It has been found that by using a modular approach as reported herein tailor-made therapeutic polypeptides can be provided. These polypeptides are tailor-made with respect to the polypeptide domains from which they are formed.

With this tailor-made generation of therapeutics by combining two polypeptide domains, different modes of action can be combined, such as dual targeting (combination of two binding entities, bispecific or multispecific binder), targeting and payload delivery (combination of binding entity (targeting) and effector entity (payload), such as antibody-conjugates), or combined receptor inhibition (combination of two receptors and/or ligands). The resulting therapeutics are single therapeutic molecules simultaneously performing the modes of action of the individual polypeptide domains. Therewith, e.g., additive/synergistic effect is expected in comparison to single domain therapeutic molecules.

By using already available therapeutic entities, such as those e.g. derived from therapeutic antibodies, a fast and easy production of multi-domain therapeutic molecule can be achieved.

For example, avidity engineered binding molecules/antibodies can bind to two or more cell surface markers present on a single cell. This binding is only avid if all/both binding entities simultaneously bind to the cell. For this purpose low to medium, low to high, or medium to high affine antibodies are especially suited. This allows also on the other hand to exclude less specific combinations of binding specificities during a screening process.

With such an approach the generation of tailor-made and, thus, highly efficacious therapeutic molecules is possible. These molecules will have fewer or less severe/reduced side effects because of their improved properties, such as targeted delivery (e.g. payload for tumor cells) and improved targeting to target cells based on higher selectivity and specificity of the targeting component (comprising at least two binding molecules).

The higher selectivity and specificity of a multispecific binder is effected by the simultaneous binding (avidity) of the combination of two „low affinity" binders, which reduces or prevents altogether potential „off-target" binding.

Methods as reported herein

One aspect as reported herein is a method for producing a polypeptide comprising at least two polypeptide domains comprising the step of

- cultivating a cell comprising

  a) a nucleic acid encoding a soluble sortase A with a C-terminal endoplasmic reticulum retention signal,

  b) a nucleic acid encoding a first polypeptide domain comprising at its C-terminus or in its C-terminal region a sortase motif followed by an endoplasmic reticulum retention signal, and

  c) a nucleic acid encoding a second polypeptide domain comprising at its N-terminus at least a diglycine motif,

whereby the cell secretes the sortase A(-ligated) conjugate of the first polypeptide domain and the second polypeptide domain,

thereby producing a polypeptide comprising at least two polypeptide domains.

One aspect as reported herein is a method for producing a multispecific binder comprising at least two binding entities comprising the step of

- cultivating a cell comprising

  a) a nucleic acid encoding a soluble sortase A with a C-terminal endoplasmic reticulum retention signal,

b) a nucleic acid encoding a first binding entity comprising at its C-terminus or in its C-terminal region a sortase motif followed by an endoplasmic reticulum retention signal, and

c) a nucleic acid encoding a second binding entity comprising at its N-terminus at least a diglycine motif,

whereby the cell secretes the sortase A(-ligated) conjugate of the first binding entity and the second binding entity,

whereby the first binding entity specifically binds to a first antigen or target and the second binding entity specifically binds to a second antigen or target,

thereby producing a multispecific binder comprising at least two binding entities.

One aspect as reported herein is a method for selecting a multispecific binder that specifically binds to two different epitopes or antigens comprising the step of

- selecting from a multitude of multispecific binders comprising different combinations of a first binding entity and a second binding entity a multispecific binder that specifically binds to two different epitopes or antigens.

One aspect as reported herein is a method for selecting a bispecific antibody comprising the following steps

(i) determining the cell surface makers present in a cell-containing sample and selecting thereof at least a first surface marker and a second surface marker,

(ii) transfecting a cell with (a) a nucleic acid encoding an antibody Fab fragment, or an antibody scFab, or a scFv antibody comprising within the 20 C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) followed by an endoplasmic reticulum retention signal KDEL (SEQ ID NO: 02), whereby the Fab fragment, or the scFab fragment, or the scFv antibody specifically binds to the first surface marker or its ligand, (b) a nucleic acid encoding a one-armed antibody fragment comprising a full length antibody heavy chain, a full length antibody light chain, and an antibody

heavy chain Fc-region polypeptide, whereby the full length antibody heavy chain and the full length antibody light chain are cognate antibody chains complementary to each other and the pair of variable domains (VH and VL) thereof forms an antigen binding site that specifically binds to the second surface marker or its ligand, whereby the full length antibody heavy chain and the antibody heavy chain Fc-region polypeptide are covalently linked to each other via one or more disulfide bonds forming an antibody hinge region, and whereby the antibody heavy chain Fc-region polypeptide has an oligoglycine G_m (m = 2, or 3, or 4, or 5) amino acid sequence at its N-terminus, and (c) a nucleic acid encoding a soluble sortase A with a C-terminal endoplasmic reticulum retention signal,

and thereby producing the bispecific antibody.

One aspect as reported herein is a method for determining a combination of antigen binding sites comprising the following steps

(i) determining the binding specificity and/or selectivity and/or affinity and/or effector function and/or in vivo half-life of a multitude of bispecific antibodies prepared by combining (a) each member of a first multitude of antibody Fab fragments, or antibody scFab fragments, or scFv antibody fragments whereby each member comprises within the 20 C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) followed by an endoplasmic reticulum retention signal KDEL (SEQ ID NO: 02), whereby the Fab fragment, or the scFab fragment, or the scFv antibody specifically binds to a first epitope or antigen, with (b) each member of a multitude of one-armed antibody fragments comprising a full length antibody heavy chain, a full length antibody light chain, and an antibody heavy chain Fc-region polypeptide, whereby the full length antibody heavy chain and the full length antibody light chain are cognate antibody chains complementary to each other and the pair of variable domains (VH and VL) thereof forms an antigen binding site that specifically binds to a second epitope or antigen, whereby the full length antibody heavy chain and the antibody heavy chain Fc-region polypeptide are covalently linked to each other via one or more disulfide bonds forming an antibody hinge region, and whereby the antibody heavy chain Fc-

region polypeptide has an oligoglycine G_m (m = 2, or 3, or 4, or 5) amino acid sequence at its N-terminus, using a sortase A-mediated enzymatic coupling reaction,

and

(ii) choosing the bispecific antibody with suitable binding specificity and/or selectivity and/or affinity and/or effector function and/or in vivo half-life and thereby determining a combination of antigen binding sites.

In the following embodiments of all methods as reported herein are given.

In one embodiment of all aspects is the sortase A the sortase A of Staphylococcus aureus (S. aureus). In one embodiment the nucleic acid encoding a (soluble) sortase A with a C-terminal endoplasmic reticulum retention signal encodes an amino acid sequence of SEQ ID NO: 51 or SEQ ID NO: 52.

In one embodiment the members of the multitude of multispecific binders are each obtained by a method as reported herein.

In one embodiment a multispecific binder is selected based on its binding specificity and/or selectivity and/or affinity and/or effector function and/or in vivo half-life.

In one embodiment the binding entity is a cognate pair of an antibody heavy chain variable domain and an antibody light chain variable domain.

In one embodiment the multispecific binder is a bispecific antibody comprising two or four binding entities.

In one embodiment the first polypeptide domain and the second polypeptide domain are selected independently of each other from full length antibody, scFv, scFab, antibody heavy chain, antibody light chain, antibody heavy chain Fc-region fragment, pair of antibody light chain variable domain and antibody heavy chain variable domain, antigen binding antibody fragments, VH, VL, CH1, CH2, CH3, CH4, CL, antibody hinge region, cytokine, receptor, receptor ligand, detectable label, tag, and partner of a binding pair.

In one embodiment the endoplasmic reticulum retention signal is selected from SEQ ID NO: 02 (KDEL), SEQ ID NO: 03 (HDEL), or SEQ ID NO: 04 (SFIXXXXMP).

In one embodiment the sortase motif is LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue).

In one embodiment the first binding domain or the first binding entity comprises or has within the 20 C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue).

In one embodiment the cell is a mammalian cell or a yeast cell. In one embodiment the mammalian cell is selected from a HEK cell, a CHO cell, or a BHK cell.

In one embodiment the Fc-region comprises a mutation of the naturally occurring amino acid residue at position 329 and at least one further mutation of at least one amino acid residue selected from the group comprising amino acid residues at position 228, 233, 234, 235, 236, 237, 297, 318, 320, 322 and 331 to a different residue, wherein the residues in the Fc-region are numbered according to the EU index of Kabat. The change of these specific amino acid residues results in an altering of the effector function of the Fc-region compared to the non-modified (wild-type) Fc-region.

In one embodiment the binding entity is selected from (or the first binding entity and the second binding entity are selected independently of each other from) the group of a darpin domain based binding entity, an anticalin domain based binding entity, a T-cell receptor fragment like scTCR domain based binding entity, a camel VH domain based binding entity, a tenth fibronectin 3 domain based binding entity, a tenascin domain based binding entity, a cadherin domain based binding entity, an ICAM domain based binding entity, a titin domain based binding entity, a GCSF-R domain based binding entity, a cytokine receptor domain based binding entity, a glycosidase inhibitor domain based binding entity, a superoxide dismutase domain based binding entity, or antibody fragments like Fab, or scFab, or scFv fragment.

In one embodiment the first polypeptide domain comprises i) the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) in its C-terminal amino acid sequence region (i.e. within the twenty C-terminal amino acid residues) and ii) the endoplasmic reticulum retention signal KDEL (SEQ ID

NO: 02) at its C-terminus, and the second polypeptide domain comprises an oligoglycine G_m (m = 2, or 3, or 4, or 5) at its N-terminus.

In one embodiment the second polypeptide domain or the second binding entity comprises an oligoglycine G_m (m = 2, or 3, or 4, or 5) amino acid sequence at its N-terminus.

In one embodiment the human antibody Fc-region is of human IgG1 subclass, or of human IgG2 subclass, or of human IgG3 subclass, or of human IgG4 subclass.

In one embodiment the antibody Fc-region is a human antibody Fc-region of the human IgG1 subclass, or of the human IgG4 subclass.

In one embodiment the human antibody Fc-region comprises a mutation of the naturally occurring amino acid residue at least at one of the following amino acid positions 228, 233, 234, 235, 236, 237, 297, 318, 320, 322, 329, and/or 331 to a different residue, wherein the residues in the antibody Fc-region are numbered according to the EU index of Kabat.

In one embodiment the human antibody Fc-region comprises a mutation of the naturally occurring amino acid residue at position 329 and at least one further mutation of at least one amino acid residue selected from the group comprising amino acid residues at position 228, 233, 234, 235, 236, 237, 297, 318, 320, 322 and 331 to a different residue, wherein the residues in the Fc-region are numbered according to the EU index of Kabat. The change of these specific amino acid residues results in an altering of the effector function of the Fc-region compared to the non-modified (wild-type) Fc-region.

In one embodiment the human antibody Fc-region has a reduced affinity to the human FcγRIIIA, and/or FcγRIIA, and/or FcγRI compared to a conjugate comprising the corresponding wild-type IgG Fc-region.

In one embodiment the amino acid residue at position 329 in the human antibody Fc-region is substituted with glycine, or arginine, or an amino acid residue large enough to destroy the proline sandwich within the Fc-region.

In one embodiment the mutation in the human antibody Fc-region of the naturally occurring amino acid residue is at least one of S228P, E233P, L234A, L235A, L235E, N297A, N297D, P329G, and/or P331S.

In one embodiment the mutation is L234A and L235A if the antibody Fc-region is of human IgG1 subclass, or S228P and L235E if the antibody Fc-region is of human IgG4 subclass.

In one embodiment the antibody Fc-region comprises the mutation P329G.

In one embodiment the antibody Fc-region comprises the mutation T366W in the first heavy chain Fc-region polypeptide and the mutations T366S, L368A and Y407V in the second heavy chain Fc-region polypeptide, wherein the numbering is according to the EU index of Kabat.

In one embodiment the antibody Fc-region comprises the mutation S354C in the first heavy chain Fc-region polypeptide and the mutation Y349C in the second heavy chain Fc-region polypeptide.

In one embodiment the antibody Fc-region comprises besides a mutation of the amino acid residue proline at position 329 at least one further addition, mutation, or deletion of an amino acid residue in the Fc-region that is correlated with increased stability of the antibody Fc-region conjugate.

In one embodiment the further addition, mutation, or deletion of an amino acid residue in the Fc-region is at position 228 and/or 235 of the Fc-region if the Fc-region is of IgG4 subclass. In one embodiment the amino acid residue serine at position 228 and/or the amino acid residue leucine at position 235 is/are substituted by another amino acid. In one embodiment the antibody Fc-region conjugate comprises a proline residue at position 228 (mutation of the serine residue to a proline residue). In one embodiment the antibody Fc-region conjugate comprises a glutamic acid residue at position 235 (mutation of the leucine residue to a glutamic acid residue).

In one embodiment the Fc-region comprises three amino acid mutations. In one embodiment the three amino acid mutations are P329G, S228P and L235E mutation (P329G SPLE).

In one embodiment the further addition, mutation, or deletion of an amino acid residue in the Fc-region is at position 234 and/or 235 of the Fc-region if the Fc-region is of IgG1 subclass. In one embodiment the amino acid residue leucine at position 234 and/or the amino acid residue leucine at position 235 is/are mutated to another amino acid.

In one embodiment the Fc-region comprises an amino acid mutation at position 234, wherein the leucine amino acid residue is mutated to an alanine amino acid residue.

In one embodiment the Fc-region comprises an amino acid mutation at position 235, wherein the leucine amino acid residue is mutated to an alanine amino acid residue.

In one embodiment the Fc-region comprises an amino acid mutation at position 329, wherein the proline amino acid residue is mutated to a glycine amino acid residue, an amino acid mutation at position 234, wherein the leucine amino acid residue is mutated to an alanine amino acid residue, and an amino acid mutation at position 235, wherein the leucine amino acid residue is mutated to an alanine amino acid residue.

Fc-region variants with increased affinity for FcRn have longer serum half-lives, and such molecules will have useful applications in methods of treating mammals where long systemic half-life of the administered antibody or Fc-region conjugate is desired, e.g., to treat a chronic disease or disorder.

Antibody Fc-region conjugates with decreased FcRn binding affinity have shorter serum half-lives, and such molecules will have useful applications in methods of treating mammals where a shorter systemic half-life of the administered antibody Fc-region conjugate is desired, e.g. to avoid toxic side effects or for in vivo diagnostic imaging applications. Fc-region fusion polypeptides or conjugates with decreased FcRn binding affinity are less likely to cross the placenta, and thus may be utilized in the treatment of diseases or disorders in pregnant women.

An Fc-region with altered binding affinity for FcRn is in one embodiment an Fc-region with an amino acid alteration at one or more of the amino acid positions 238, 252, 253, 254, 255, 256, 265, 272, 286, 288, 303, 305, 307, 309, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 386, 388, 400, 413, 415, 424, 433, 434, 435, 436, 439, and/or 447.

The Fc-region is in one embodiment an Fc-region with one or more amino acid alterations at the amino acid positions 252, 253, 254, 255, 288, 309, 386, 388, 400, 415, 433, 435, 436, 439, and/or 447.

An Fc-region which display increased binding to FcRn comprises in one embodiment one or more amino acid alterations at the amino acid positions 238, 256, 265, 272, 286, 303, 305, 307, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 413, 424, and/or 434.

In one embodiment the Fc-region is an Fc-region of the IgG1 subclass and comprises the amino acid mutations P329G, and/or L234A and L235A.

In one embodiment the Fc-region is an Fc-region of the IgG4 subclass and comprises the amino acid mutations P329G, and/or S228P and L235E.

In one embodiment the antibody Fc-region comprises the mutation T366W in the first heavy chain Fc-region polypeptide and the mutations T366S, L368A and Y407V in the second heavy chain Fc-region polypeptide, wherein the numbering is according to the EU index of Kabat.

In one embodiment the antibody Fc-region comprises the mutation S354C in the first heavy chain Fc-region polypeptide and the mutation Y349C in the second heavy chain Fc-region polypeptide.

Enzymatic conjugation using Sortase A

A multi-domain polypeptide can be obtained in vivo by using the enzyme sortase A.

Many gram-positive bacteria use sortase to covalently anchor a variety of surface proteins including virulence factors to their cell wall (peptidoglycan). Sortases are membrane associated enzymes. The wild-type Staphylococcus aureus sortase A (SrtA) is a polypeptide of 206 amino acids with an N-terminal membrane-spanning region. In a first step, sortase A recognizes substrate proteins that contain a LPXTG (SEQ ID NO: 01) amino acid sequence motif and cleaves the amide bond between the Thr and Gly by means of an active-site Cys. This peptide cleaving reaction results in a sortase A-substrate thioester intermediate. In a second step the thioester acyl-enzyme intermediate is resolved by nucleophilic attack of an amino group of an oligoglycine containing second substrate polypeptide (corresponding to the pentaglycine unit of peptidoglycan in S. aureus) leading to a covalently linked cell wall protein and the regeneration of sortase A. In the absence of oligoglycine nucleophiles, the acyl-enzyme intermediate can be hydrolyzed by a water molecule.

Sortase-mediated ligation/conjugation has begun to be applied for a variety of protein engineering and bioconjugation purposes. This new technique enables the introduction of natural and synthetic functionalities into LPXTG-tagged recombinant or chemically synthesized polypeptides. Examples include the covalent attachment of oligoglycine derivatized polymers (e.g. PEG), fluorophores, vitamins (e.g. biotin and folate), lipids, carbohydrates, nucleic acids, synthetic peptides and proteins (e.g. GFP) (Tsukiji, S. and Nagamune, T., ChemBioChem 10 (2009) 787-798; Popp, M.W.-L. and Ploegh, H.L., Angew. Chem. Int. Ed. 50 (2011) 5024-5032).

It has been shown that a triglycine and even a diglycine motif of the amino component is sufficient for the SrtA-mediated ligation step (Clancy, K.W., et al., Peptide Science 94 (2010) 385-396).

For the enzymatic conjugation a soluble truncated sortase A lacking the membrane-spanning region (SrtA; amino acid residues 60-206 of Staphylococcus aureus SrtA) can be used (Ton-That, H., et al., Proc. Natl. Acad. Sci. USA 96 (1999) 12424-12429; Ilangovan, H., et al., Proc. Natl. Acad. Sci. USA 98 (2001) 6056-6061).

Any polypeptide domain comprising an oligoglycine motif at least at one of its N-termini (G_m, m = 2, or 3, or 4, or 5) can be expressed und purified from the supernatant of eukaryotic cells (e.g. HEK293 cells, CHO cells).

A binding entity (e.g. a single chain antigen binding polypeptide such as a scFv, a scFab, or a darpin, or a multi chain antigen binding polypeptide such as a dsFv or a Fab) comprising the SrtA recognition motif at the C-terminus of one polypeptide chain can be expressed und purified from the supernatant of eukaryotic cells (e.g. HEK293 cells, CHO cells).

The "Combimatrix" approach

It is desirable to combine a first binding entity, such as an antibody Fab fragment, with another specific binding entity, such as a second antibody Fab fragment or a one-armed antibody fragment comprising a full length heavy chain and its cognate full length light chain and a disulfide linked heavy chain Fc-region polypeptide. In addition it is possible to screen, whether a first binding entity shows better properties when linking it to a number of different other binding entities. Using a so-called Combimatrix approach, a multitude of combinations of binding entities can be addressed in an easy way. It has to be pointed out that the second binding

entities can either bind to different targets/epitopes/antigens, or can bind to the same antigen but to different epitopes, or can bind to the same epitope but be different variants of a single binding entity (e.g. humanization candidates).

In this scenario, an automated platform process can be performed. Any platform that uses e.g. 96-well plates or other high throughput formats is suitable, such as an Eppendorf epMotion 5075vac pipetting robot.

First, cloning of the binding entity encoding constructs is performed. The plasmids with the binding entity encoding nucleic acids are usually obtained by gene synthesis or PCR amplification, whereby the C-terminal region of one encoded binding entity contains a sortase-motif, and an endoplasmic reticulum retention signal, and the N-terminal region of the respective other binding entity comprises an N-terminal oligoglycine motif comprising/of at least two consecutive glycine residues (diglycine). The plasmids are individually transferred into a separate well of a multi-well plate (a whole plate can be loaded). Thereafter, the plasmids are digested with a restriction enzyme mix that cuts out the binding entity-coding region. It is desirable to design all gene syntheses and/or PCR primers in a way that only one restriction enzyme mix is needed for all plasmids. Afterwards, an optional cleaning step yields purified DNA fragments. These fragments are ligated into a plasmid backbone that had been cut out of an acceptor vector with the same restriction mix as mentioned above. Alternatively, the cloning procedure can be performed by a SLIC-mediated cloning step. After ligation, the automated platforms transfers all ligation mixes into a further multi-well plate with competent E. coli cells (e.g. Top10 Multi Shot, Invitrogen), and a transformation reaction is performed. The cells are cultivated to the desired density. From an aliquot of the cultivation mixture glycerol stocks can be obtained. From the culture plasmid is isolated (e.g. using a plasmid isolation mini kit (e.g. NucleoSpin 96 Plasmid, Macherey& Nagel)). Plasmid identity is verified by digesting an aliquot with an appropriate restriction mix and SDS-gel electrophoresis (e.g. E-Gel 48, Invitrogen). Afterwards a new plate can be loaded with an aliquot of the plasmid for performing a control sequencing reaction.

In the next step the binding entities are expressed. To this end, HEK cells are seeded onto a multi-well plate (e.g. a 48-well-plate) and are transfected with the respective isolated plasmid combinations (containing the binding entity-coding regions in appropriate backbone vectors) together with a plasmid encoding soluble sortase bearing a C-terminal endoplasmic retention signal. Thus, HEK cells are co-

transfected with three expression plasmids: i) a plasmid encoding a binding entity that has a C-terminal His-tag, sortase motif and endoplasmic retention signal (in N-terminal to C-terminal direction), ii) a plasmid encoding a binding entity that has an N-terminal oligo glycine motif of at least two glycine residues and iii) a plasmid encoding soluble sortase that has a C-terminal endoplasmic retention signal. Transfected HEK cells are cultivated for several days and subsequently culture supernatants are harvested (e.g. by filtrating through a 1.2 µm and a 0.22 µm filter plate by using a vacuum station). Titers can be monitored by performing e.g. an ELISA.

The binding entities are linked to the each other using a sortase-mediated transpeptidation reaction during the expression in vivo. This is achieved as the binding domain comprising the C-terminal sortase recognition motif comprises an endoplasmic reticulum retention signal. The soluble sortase employed comprises the same endoplasmic reticulum retention signal at its C-terminus. Thus, both molecules are almost completely retained in the endoplasmic reticulum. Upon entry of the second polypeptide domain into the endoplasmic reticulum the enzymatic conjugation reaction takes place and the enzymatic conjugate, which is devoid of the endoplasmic reticulum retention signal, which is removed during the enzymatic transpeptidation reaction, is secreted into the cultivation medium. The conjugates can be harvested from the cultivation medium by using a His-tag selection procedure (the culture supernatant is applied onto e.g. His MultiTrap HP plates (GE Healthcare) and filtrated, whereby all molecules that comprise a His-tag are bound to the matrix (i.e. the conjugates) and can be eluted after washing with an appropriate elution buffer, while all other molecules will not bind to the chromatography material.

The multispecific binding molecules can be made using the Combimatrix approach, see the following Table below).

	1	2	3	4	5	6	7	8	9	10	11
A	1A	2A	3A	4A	5A	6A	7A	8A	9A	10A	11A
B	1B	...	...	...	...	...	...	...	...	...	...
C	1C	...	...	...	...	...	...	...	...	...	...
D	1D	...	...	...	...	...	...	...	...	...	...
E	1E	...	...	...	...	...	...	...	...	...	...
F	1F	...	...	...	...	...	...	...	...	...	...
G	1G	...	...	...	...	...	...	...	...	...	11G

The wells of the first column of a multi-well plate denote different plasmids encoding first binding entities comprising a C-terminal sortase motif (designated in arabic numbers, e.g. 1 to 11 for a 96-well plate). The wells of the first row of the same plate denote different plasmids encoding second binding entities comprising an oligoglycine at the N-terminus/in the N-terminal region (excluding the first row, designated in letters, e.g. A to G). Thereafter all plasmids encoding a first binding entity of the first row are combined with all plasmids encoding a second binding entity of the first column (e.g. resulting in 77 combinations in a 96-well plate), designated by a combination of number and letter (e.g. 1A to 11G). In addition, plasmid encoding sortase is added to all wells. All combinations are co-transfected into HEK cells and thereby expressed and conjugated in vivo by the sortase A comprising an endoplasmic reticulum retention signal. After the enzymatic in vivo conjugation has been performed, an optional purification step can be performed. The multispecific binding molecules are then ready for evaluation in biochemical or cell-based assays.

III. RECOMBINANT METHODS

Suitable host cells for cloning and/or expression/secretion of polypeptide-encoding vectors include prokaryotic and eukaryotic cells described herein. For example, polypeptides may be produced in bacteria, in particular when glycosylation and Fc effector function are not needed (see, e.g., US 5,648,237, US 5,789,199, and US 5,840,523, Charlton, Methods in Molecular Biology 248 (2003) 245-254 (B.K.C. Lo, (ed.), Humana Press, Totowa, NJ), describing expression of antibody fragments in *E. coli*.). After expression, the polypeptide may be isolated from the bacterial cell paste in a soluble fraction or may be isolated from the insoluble

fraction, so-called inclusion bodies which can be solubilized and the polypeptide be refolded to bioactive forms. Thereafter the polypeptide can be further purified.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeasts are suitable cloning or expression hosts for polypeptide-encoding vectors, including fungi and yeast strains whose glycosylation pathways have been "humanized", resulting in the production of a polypeptide with a partially or fully human glycosylation pattern (see e.g. Gerngross, Nat. Biotech. 22 (2004) 1409-1414, and Li, et al., Nat. Biotech. 24 (2006) 210-215).

Suitable host cells for the expression of glycosylated polypeptides are also derived from multicellular organisms (invertebrates and vertebrates). Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains have been identified which may be used in conjunction with insect cells, particularly for transfection of Spodoptera frugiperda cells.

Plant cell cultures can also be utilized as hosts (see, e.g., US 5,959,177, US 6,040,498, US 6,420,548, US 7,125,978, and US 6,417,429 (describing PLANTIBODIES^{TM} technology for producing antibodies in transgenic plants)).

Vertebrate cells may also be used as hosts. For example, mammalian cell lines that are adapted to grow in suspension culture may be useful. Other examples of useful mammalian host cell lines are the COS-7 cell line (monkey kidney CV1 cell transformed by SV40; the HEK293 cell line (human embryonic kidney) BHK cell line (baby hamster kidney); the TM4 mouse sertoli cell line (TM4 cells as described, e.g., in Mather, Biol. Reprod. 23 (1980) 243-251); the CV1 cell line (monkey kidney cell); the VERO-76 cell line (African green monkey kidney cell); the HELA cell line (human cervical carcinoma cell); the MDCK cell line (canine kidney cell); the BRL-3A cell line (buffalo rat liver cell); the W138 cell line (human lung cell); the HepG2 cell line (human liver cell); the MMT 060562 cell line (mouse mammary tumor cell); the TRI cell line, as described, e.g., in Mather, et al., Annals N.Y. Acad. Sci. 383 (1982) 44-68; the MRC5 cell line; and FS4 cell-s line. Other useful mammalian host cell lines include the CHO cell line (Chinese hamster ovary cell), including DHFR negative CHO cell lines (Urlaub, et al., Proc. Natl. Acad. Sci. USA 77 (1980) 4216), and myeloma cell lines such as Y0, NS0 and Sp2/0 cell line. For a review of certain mammalian host cell lines suitable for polypeptide production, see, e.g., Yazaki, and Wu, Methods in Molecular Biology,

Antibody Engineering 248 (2004) 255-268 (B.K.C. Lo, (ed.), Humana Press, Totowa, NJ).

IV. Methods and Compositions for Diagnostics and Detection

In certain embodiments, any of the bispecific antibodies provided herein is useful for detecting the presence of one or both antigens in a biological sample. The term "detecting" as used herein encompasses quantitative or qualitative detection. In certain embodiments, a biological sample comprises a cell or tissue, such as biopsies of cancer cells.

In one embodiment, a bispecific antibody for use in a method of diagnosis or detection is provided. In a further aspect, a method of detecting the presence of cancer cells in a biological sample is provided. In certain embodiments, the method comprises contacting the biological sample with a bispecific antibody as described herein under conditions permissive for binding of the bispecific antibody to its antigen or antigens, and detecting whether a complex is formed between the bispecific antibody and its antigen or antigens. Such method may be an *in vitro* or *in vivo* method.

Exemplary disorders that may be diagnosed using an antibody of the invention include cancer.

In certain embodiments, labeled bispecific antibodies are provided. Labels include, but are not limited to, labels or moieties that are detected directly (such as fluorescent, chromophoric, electron-dense, chemiluminescent, and radioactive labels), as well as moieties, such as enzymes or ligands, that are detected indirectly, e.g., through an enzymatic reaction or molecular interaction. Exemplary labels include, but are not limited to, the radioisotopes ^{32}P, ^{14}C, ^{125}I, ^{3}H, and ^{131}I, fluorophores such as rare earth chelates or fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, luceriferases, e.g., firefly luciferase and bacterial luciferase (US 4,737,456), luciferin, 2,3-dihydrophthalazinediones, horseradish peroxidase (HRP), alkaline phosphatase, β-galactosidase, glucoamylase, lysozyme, saccharide oxidases, e.g., glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase, heterocyclic oxidases such as uricase and xanthine oxidase, coupled with an enzyme that employs hydrogen peroxide to oxidize a dye precursor such as HRP, lactoperoxidase, or microperoxidase, biotin/avidin, spin labels, bacteriophage labels, stable free radicals, and the like.

V. Pharmaceutical Formulations

Pharmaceutical formulations of a bispecific antibody as described herein are prepared by mixing such antibody having the desired degree of purity with one or more optional pharmaceutically acceptable carriers (Remington's Pharmaceutical Sciences, 16th edition, Osol, A. (ed.), (1980)), in the form of lyophilized formulations or aqueous solutions. Pharmaceutically acceptable carriers are generally nontoxic to recipients at the dosages and concentrations employed, and include, but are not limited to: buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyl dimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride; benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as poly (vinylpyrrolidone); amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.* Zn-protein complexes); and/or non-ionic surfactants such as polyethylene glycol (PEG). Exemplary pharmaceutically acceptable carriers herein further include interstitial drug dispersion agents such as soluble neutral-active hyaluronidase glycoproteins (sHASEGP), for example, human soluble PH-20 hyaluronidase glycoproteins, such as rhuPH20 (HYLENEX®, Baxter International, Inc.). Certain exemplary sHASEGPs and methods of use, including rhuPH20, are described in US 2005/0260186 and US 2006/0104968. In one aspect, a sHASEGP is combined with one or more additional glycosaminoglycanases such as chondroitinases.

Exemplary lyophilized antibody formulations are described in US 6,267,958. Aqueous antibody formulations include those described in US 6,171,586 and WO 2006/044908, the latter formulations including a histidine-acetate buffer.

The formulation herein may also contain more than one active ingredients as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Such active

ingredients are suitably present in combination in amounts that are effective for the purpose intended.

Active ingredients may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methyl methacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Osol, A. (ed.) (1980).

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.* films, or microcapsules.

The formulations to be used for *in vivo* administration are generally sterile. Sterility may be readily accomplished, e.g., by filtration through sterile filtration membranes.

VI. Therapeutic Methods and Compositions

Any of the bispecific antibodies provided herein may be used in therapeutic methods.

In one aspect, a bispecific antibody for use as a medicament is provided. In further aspects, a bispecific antibody for use in treating cancer is provided. In certain embodiments, a bispecific antibody for use in a method of treatment is provided. In certain embodiments, the invention provides a bispecific antibody for use in a method of treating an individual having cancer comprising administering to the individual an effective amount of the bispecific antibody. In one such embodiment, the method further comprises administering to the individual an effective amount of at least one additional therapeutic agent, e.g., as described below. In further embodiments, the invention provides a bispecific antibody for use in removing/killing/lysing cancer cells. In certain embodiments, the invention provides a bispecific antibody for use in a method for removing/killing/lysing cancer cells in an individual comprising administering to the individual an effective of the bispecific antibody to remove/kill/lyse cancer cells. An "individual" according to any of the above embodiments can be a human.

In a further aspect, the invention provides for the use of a bispecific antibody in the manufacture or preparation of a medicament. In one embodiment, the medicament is for treatment of cancer. In a further embodiment, the medicament is for use in a method of treating cancer comprising administering to an individual having cancer an effective amount of the medicament. In one such embodiment, the method further comprises administering to the individual an effective amount of at least one additional therapeutic agent, e.g., as described below. In a further embodiment, the medicament is for removing/killing/lysing cancer cells. In a further embodiment, the medicament is for use in a method of removing/killing/lysing cancer cells in an individual comprising administering to the individual an amount effective of the medicament to remove/kill/lyse cancer cells. An "individual" according to any of the above embodiments may be a human.

In a further aspect, the invention provides a method for treating cancer. In one embodiment, the method comprises administering to an individual having cancer an effective amount of a bispecific antibody. In one such embodiment, the method further comprises administering to the individual an effective amount of at least one additional therapeutic agent, as described below. An "individual" according to any of the above embodiments may be a human.

In a further aspect, the invention provides a method for removing/killing/lysing cancer cells in an individual. In one embodiment, the method comprises administering to the individual an effective amount of the bispecific antibody to remove/kill/lyse cancer cells. In one embodiment, an "individual" is a human.

In a further aspect, the invention provides pharmaceutical formulations comprising any of the bispecific antibodies provided herein, e.g., for use in any of the above therapeutic methods. In one embodiment, a pharmaceutical formulation comprises any of the bispecific antibodies provided herein and a pharmaceutically acceptable carrier. In another embodiment, a pharmaceutical formulation comprises any of the bispecific antibodies provided herein and at least one additional therapeutic agent, e.g., as described below.

Antibodies of the invention can be used either alone or in combination with other agents in a therapy. For instance, an antibody of the invention may be co-administered with at least one additional therapeutic agent. In certain embodiments, an additional therapeutic agent is a cytotoxic agent or a chemotherapeutic agent.

Such combination therapies noted above encompass combined administration (where two or more therapeutic agents are included in the same or separate formulations), and separate administration, in which case, administration of the antibody of the invention can occur prior to, simultaneously with, and/or following, the administration of the additional therapeutic agent and/or adjuvant. Antibodies of the invention can also be used in combination with radiation therapy.

An antibody of the invention (and any additional therapeutic agent) can be administered by any suitable means, including parenteral, intrapulmonary, and intranasal, and, if desired for local treatment, intralesional administration. Parenteral infusions include intramuscular, intravenous, intraarterial, intraperitoneal, intradermal, or subcutaneous administration. Dosing can be by any suitable route, e.g. by injections, such as intravenous or subcutaneous injections, depending in part on whether the administration is brief or chronic. Various dosing schedules including but not limited to single or multiple administrations over various points in time, bolus administration, and pulse infusion are contemplated herein.

Antibodies of the invention would be formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the particular disorder being treated, the particular mammal being treated, the clinical condition of the individual patient, the cause of the disorder, the site of delivery of the agent, the method of administration, the scheduling of administration, and other factors known to medical practitioners. The antibody need not be, but is optionally, formulated with one or more agents currently used to prevent or treat the disorder in question. The effective amount of such other agents depends on the amount of antibody present in the formulation, the type of disorder or treatment, and other factors discussed above. These are generally used in the same dosages and with administration routes as described herein, or about from 1 to 99% of the dosages described herein, or in any dosage and by any route that is empirically/clinically determined to be appropriate.

For the prevention or treatment of disease, the appropriate dosage of an antibody of the invention (when used alone or in combination with one or more other additional therapeutic agents) will depend on the type of disease to be treated, the type of antibody, the severity and course of the disease, whether the antibody is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, and the discretion of the attending

physician. The antibody is suitably administered to the patient at one time or over a series of treatments. Depending on the type and severity of the disease, about 1 μg/kg to 15 mg/kg (e.g. 0.5 mg/kg - 10 mg/kg) of antibody can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. One typical daily dosage might range from about 1 μg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment would generally be sustained until a desired suppression of disease symptoms occurs. One exemplary dosage of the antibody would be in the range from about 0.05 mg/kg to about 10 mg/kg. Thus, one or more doses of about 0.5 mg/kg, 2.0 mg/kg, 4.0 mg/kg or 10 mg/kg (or any combination thereof) may be administered to the patient. Such doses may be administered intermittently, e.g. every week or every three weeks (*e.g.* such that the patient receives from about two to about twenty, or *e.g.* about six doses of the antibody). An initial higher loading dose, followed by one or more lower doses may be administered. However, other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays.

It is understood that any of the above formulations or therapeutic methods may be carried out using an immunoconjugate of the invention in place of or in addition to a bispecific antibody.

VII. Articles of Manufacture

In another aspect of the invention, an article of manufacture containing materials useful for the treatment, prevention and/or diagnosis of the disorders described above is provided. The article of manufacture comprises a container and a label or package insert on, or associated with, the container. Suitable containers include, for example, bottles, vials, syringes, IV solution bags, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is by itself or combined with another composition effective for treating, preventing and/or diagnosing the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). At least one active agent in the composition is an antibody of the invention. The label or package insert indicates that the composition is used for treating the condition of choice. Moreover, the article of manufacture may comprise (a) a first container with a composition contained therein, wherein the composition comprises an antibody of

the invention; and (b) a second container with a composition contained therein, wherein the composition comprises a further cytotoxic or otherwise therapeutic agent. The article of manufacture in this embodiment of the invention may further comprise a package insert indicating that the compositions can be used to treat a particular condition. Alternatively, or additionally, the article of manufacture may further comprise a second (or third) container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

It is understood that any of the above articles of manufacture may include an immunoconjugate of the invention in place of or in addition to a bispecific antibody.

Examples

The following examples are examples of methods and compositions of the invention. It is understood that various other embodiments may be practiced, given the general description provided above.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, the descriptions and examples should not be construed as limiting the scope of the invention.

Materials and Methods

Recombinant DNA techniques

Standard methods were used to manipulate DNA as described in Sambrook, J. et al., Molecular cloning: A laboratory manual; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989. The molecular biological reagents were used according to the manufacturer's instructions.

Gene and oligonucleotide synthesis

Desired gene segments were prepared by chemical synthesis at Geneart GmbH (Regensburg, Germany). The synthesized gene fragments were cloned into an E. coli plasmid for propagation/amplification. The DNA sequences of subcloned gene fragments were verified by DNA sequencing. Alternatively, short synthetic DNA

fragments were assembled by annealing chemically synthesized oligonucleotides or via PCR. The respective oligonucleotides were prepared by metabion GmbH (Planegg-Martinsried, Germany)

Protein determination

The protein concentration of purified polypeptides was determined by determining the optical density (OD) at 280 nm, using the molar extinction coefficient calculated on the basis of the amino acid sequence of the polypeptide.

Example 1

Generation of expression plasmids for antibodies and antibody fragments including single chain Fab antibody fragments

Desired proteins were expressed by transient transfection of human embryonic kidney cells (HEK 293). For the expression of a desired gene/protein (e.g. full length antibody heavy chain, full length antibody light chain, scFab fragments or an Fc-chain containing an oligoglycine at its N-terminus) a transcription unit comprising the following functional elements was used:

- the immediate early enhancer and promoter from the human cytomegalovirus (P-CMV) including intron A,
- a human heavy chain immunoglobulin 5'-untranslated region (5'UTR),
- a murine immunoglobulin heavy chain signal sequence (SS),
- a gene/protein to be expressed, and
- the bovine growth hormone polyadenylation sequence (BGH pA).

In addition to the expression unit/cassette including the desired gene to be expressed the basic/standard mammalian expression plasmid contains

- an origin of replication from the vector pUC18 which allows replication of this plasmid in E. coli, and
- a beta-lactamase gene which confers ampicillin resistance in E. coli.

a) Generation of an expression plasmid for a single chain Fab fragment (scFab) with C-terminal His-tag, Sortase motif, and ER retention signal

The scFab encoding fusion gene comprising a C-terminal His-tag, followed by a sortase recognition motif and an endoplasmic retention (ER) signal was assembled by fusing a DNA fragment coding for the respective sequence elements (His6-tag

(HHHHHH, SEQ ID NO: 07), sortase motif (LPETGGS, SEQ ID NO: 28), and ER retention signal (KDEL, SEQ ID NO: 02), separated each by a short GS sequence element (GSHHHHHHGSLPETGGSKDEL (SEQ ID NO: 29) to a rat-human chimeric single chain Fab molecule (Vkappa-huCkappa-linker-Vheavy-huCH1).

The expression plasmid for the transient expression of a scFab fragment with a C-terminal His-tag, sortase motif and ER retention signal fusion protein in HEK293 cells comprised besides the scFab fragment with C-terminal His-tag, sortase motif and ER retention signal expression cassette, an origin of replication from the vector pUC18, which allows replication of this plasmid in E. coli, and a beta-lactamase gene which confers ampicillin resistance in E. coli. The transcription unit of the scFab fragment with C-terminal His-tag, sortase motif and ER retention signal fusion gene comprises the following functional elements:

- the immediate early enhancer and promoter from the human cytomegalovirus (P-CMV) including intron A,
- a human heavy chain immunoglobulin 5'-untranslated region (5'UTR),
- a murine immunoglobulin heavy chain signal sequence,
- a scFab (Vkappa-huCkappa-linker-Vheavy-huCH1) encoding nucleic acid,
- a His-tag encoding nucleic acid,
- a sortase recognition motif encoding nucleic acid,
- an ER retention signal encoding nucleic acid, and
- the bovine growth hormone polyadenylation sequence (BGH pA).

The amino acid sequence of the mature scFab fragment of anti-transferrin receptor antibody 3D8 with C-terminal His-tag, sortase motif, and ER retention signal fusion protein is

DIQMTQSPASLSASLEEIVTITCQASQDIGNWLAWYQQKPGKSPQLLIYGAT
SLADGVPSRFSGSRSGTQFSLKISRVQVEDIGIYYCLQAYNTPWTFGGGTKV
EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT
KSFNRGECGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGEVQLVESGG
GLVQPGNSLTLSCVASGFTFSNYGMHWIRQAPKKGLEWIAMIYYDSSKMN
YADTVKGRFTISRDNSKNTLYLEMNSLRSEDTAMYYCAVPTSHYVVDVW
GQGVSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCGSHHHHHHGSLPETGGSKDEL (SEQ ID NO: 30).

b) Generation of the expression plasmid for a single chain Fab fragment (scFab) with N-terminal glycine-serine motif

The scFab fusion gene comprising an N-terminal glycine-serine motif was assembled by fusing a DNA fragment coding for the respective sequence element ($(G_4S)_2$, SEQ ID NO: 31) to a rat-human chimeric single chain Fab molecule (Vkappa-huCkappa-linker-Vheavy-huCH1).

The expression plasmid for the transient expression of a scFab fragment with an N-terminal glycine-serine motif in HEK293 cells comprised besides the scFab fragment with an N-terminal glycine-serine motif expression cassette an origin of replication from the vector pUC18, which allows replication of this plasmid in E. coli, and a beta-lactamase gene which confers ampicillin resistance in E. coli. The transcription unit of the scFab fragment with an N-terminal glycine-serine motif fusion gene comprises the following functional elements:

- the immediate early enhancer and promoter from the human cytomegalovirus (P-CMV) including intron A,
- a human heavy chain immunoglobulin 5'-untranslated region (5'UTR),
- a murine immunoglobulin heavy chain signal sequence,
- a $(G_4S)_2$ motif encoding nucleic acid,
- a scFab (Vkappa-huCkappa-linker-Vheavy-huCH1) encoding nucleic acid, and
- the bovine growth hormone polyadenylation sequence (BGH pA).

The amino acid sequence of the mature scFab fragment of anti-transferrin receptor antibody 3D8 with N-terminal glycine-serine motif is

GGGGSGGGGSDIQMTQSPASLSASLEEIVTITCQASQDIGNWLAWYQQKPG
KSPQLLIYGATSLADGVPSRFSGSRSGTQFSLKISRVQVEDIGIYYCLQAYNT
PWTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE
VTHQGLSSPVTKSFNRGECGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS
GGEVQLVESGGGLVQPGNSLTLSCVASGFTFSNYGMHWIRQAPKKGLEWI
AMIYYDSSKMNYADTVKGRFTISRDNSKNTLYLEMNSLRSEDTAMYYCA
VPTSHYVVDVWGQGVSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSC (SEQ ID NO: 32).

c) Generation of the expression plasmid for an antibody Fc-region fragment (FC) with N-terminal triple glycine motif

The FC fusion gene comprising an N-terminal triple glycine motif was assembled by fusing a DNA fragment coding for the respective sequence element (GGG, SEQ ID NO: 33) to a human antibody heavy chain Fc-region molecule.

The expression plasmid for the transient expression of an antibody Fc-region fragment with N-terminal triple glycine motif in HEK293 cells comprised besides the antibody heavy chain Fc-region with N-terminal triple glycine motif expression cassette an origin of replication from the vector pUC18, which allows replication of this plasmid in E. coli, and a beta-lactamase gene which confers ampicillin resistance in E. coli. The transcription unit of the antibody Fc-region fragment (FC) with N-terminal triple glycine motif fusion gene comprises the following functional elements:

- the immediate early enhancer and promoter from the human cytomegalovirus (P-CMV) including intron A,
- a human heavy chain immunoglobulin 5'-untranslated region (5'UTR),
- a murine immunoglobulin heavy chain signal sequence,
- a GGG encoding nucleic acid,
- an Fc-region encoding nucleic acid, and
- the bovine growth hormone polyadenylation sequence (BGH pA).

The amino acid sequence of the mature antibody Fc-region fragment with N-terminal triple glycine motif is

GGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 34).

d) Expression plasmid for an antibody heavy and light chains

Expression plasmids coding for the following polypeptides/proteins were constructed according to the methods as outlined before:

- Pertuzumab heavy chain variable domain combined with a human heavy chain constant region of the subclass IgG1 containing a T366W mutation:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEW
VADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYY
CARNLGPSFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL
GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK (SEQ ID NO: 35).

- Pertuzumab light chain variable domain combined with a human kappa light chain constant region:

DIQMTQSPSSLSASVGDRVTITCKASQDVSIGVAWYQQKPGKAPKLLIY
SASYRYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYIYPYTFG
QGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV
THQGLSSPVTKSFNRGEC (SEQ ID NO: 36).

- Trastuzumab heavy chain variable domain combined with a human heavy chain constant region of the subclass IgG1 containing a T366S, L368A, and Y407V mutation:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK (SEQ ID NO: 37).

- Trastuzumab light chain variable domain combined with a human kappa light chain constant region:

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI
YSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTF
GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE
VTHQGLSSPVTKSFNRGEC (SEQ ID NO: 38).

- antibody VH-CH1 fragment comprising a Pertuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal GGGSHHHHHHGSLPETGGSKDEL amino acid sequence:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEW
VADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYY
CARNLGPSFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL
GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
SLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSHHHHHHGSLPETGGS
KDEL (SEQ ID NO: 39).

- antibody VH-CH1 fragment comprising a Pertuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal GSHHHHHHGSLPETGGSKDEL sequence:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEW
VADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYY
CARNLGPSFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL
GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
SLGTQTYICNVNHKPSNTKVDKKVEPKSCGSHHHHHHGSLPETGGSKD
EL (SEQ ID NO: 40).

- antibody VH-CH1 fragment comprising a Pertuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal HHHHHHGSLPETGGSKDEL sequence:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEW
VADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYY
CARNLGPSFYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL
GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
SLGTQTYICNVNHKPSNTKVDKKVEPKSCHHHHHHGSLPETGGSKDEL
(SEQ ID NO: 41).

- antibody VH-CH1 fragment comprising a Trastuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal GGGSHHHHHHGSLPETGGSGSKDEL sequence:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSHHHHHHGSLPETG
GSGSKDEL (SEQ ID NO: 42).

- antibody VH-CH1 fragment comprising a Trastuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal GSHHHHHHGSLPETGGSGSKDEL sequence:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGSHHHHHHGSLPETGGS
GSKDEL (SEQ ID NO: 43).

- antibody VH-CH1 fragment comprising a Trastuzumab heavy chain variable domain and a human heavy chain constant region 1 (CH1) of the subclass IgG1 containing a C-terminal HHHHHHGSLPETGGSGSKDEL sequence:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCHHHHHHGSLPETGGSGS
KDEL (SEQ ID NO: 44).

- heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366S, L368A, and Y407V mutation containing an N-terminal GGGDKTHTCPPC sequence:

GGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD

WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKN
QVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID
NO: 45).

- heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366S, L368A, and Y407V mutation containing an N-terminal GGHTCPPC sequence:

GGHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSC
AVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 46).

- heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366S, L368A, and Y407V mutation containing an N-terminal GGCPPC sequence:

GGCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSRDELTKNQVSLSCA
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 47).

- heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366W mutation containing an N-terminal GGGDKTHTCPPC sequence:

GGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTK
NQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID
NO: 48).

- heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366W mutations containing an N-terminal GGHTCPPC sequence:

GGHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLW

CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 49).

- heavy chain Fc-region polypeptide (human IgG1(CH2-CH3)) with T366W mutation containing an N-terminal GGCPPC sequence:

GGCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 50).

Example 2

Generation of an expression plasmid for soluble S. aureus sortase A with C-terminal ER retention signal

The sortase fusion gene comprising a C-terminal ER retention signal was assembled by fusing a DNA fragment coding for an ER retention signal (KDEL) to an N-terminally truncated Staphylococcus aureus sortase A (60-206) molecule (SrtA-KDEL).

The expression plasmid for the transient expression of soluble sortase with ER retention signal in HEK293 cells comprised besides the soluble sortase with ER retention signal expression cassette an origin of replication from the vector pUC18, which allows replication of this plasmid in E. coli, and a beta-lactamase gene which confers ampicillin resistance in E. coli. The transcription unit of the soluble sortase with ER retention signal comprises the following functional elements:

- the immediate early enhancer and promoter from the human cytomegalovirus (P-CMV) including intron A,
- a human heavy chain immunoglobulin 5'-untranslated region (5'UTR),
- a murine immunoglobulin heavy chain signal sequence,
- an N-terminally truncated S. aureus sortase A encoding nucleic acid,
- an ER retention signal encoding nucleic acid, and
- the bovine growth hormone polyadenylation sequence (BGH pA).

As the C-terminal amino acid residue of the N-terminally truncated S. aureus sortase A is already a lysine (K) only the amino acid sequence DEL had to be fused at the C-terminus of the enzyme in order to establish a functional ER retention

signal (KDEL).

The amino acid sequence of the mature soluble sortase with ER retention signal (KDEL) is

QAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLD DQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDV KPTDVGVLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEVKDEL (SEQ ID NO: 51).

The amino acid sequence of the mature soluble sortase with GSKDEL endoplasmic reticulum retention signal is

QAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLD DQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDV KPTDVGVLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEVKGSKDE L (SEQ ID NO: 52).

Example 3

Transient expression, purification and analytical characterization of the conjugates generated in vivo by sortase-mediated transpeptidation

The conjugates were generated in vivo in transiently transfected HEK293 cells (human embryonic kidney cell line 293-derived) cultivated in F17 Medium (Invitrogen Corp.). For transfection "293-Free" Transfection Reagent (Novagen) was used. The N- and C-terminally extended scFab molecules as described above as well as the soluble sortase each were expressed from individual expression plasmids. Transfections were performed as specified in the manufacturer's instructions. Fusion protein-containing cell culture supernatants were harvested three to seven (3-7) days after transfection. Supernatants were stored at reduced temperature (e.g. -80°C) until purification.

General information regarding the recombinant expression of human immunoglobulins in e.g. HEK293 cells is given in: Meissner, P. et al., Biotechnol. Bioeng. 75 (2001) 197-203.

The culture supernatants were filtered and subsequently purified by Ni^{2+}-ion affinity chromatography. The secreted proteins comprising a His-tag were captured by affinity chromatography using Ni Sepharose™ high performance His-Trap HP (GE Healthcare). Unbound proteins were removed by washing with 10 mM Tris

buffer pH 7.5 containing 500 mM NaCl and 30 mM imidazole. The bound His-tag containing proteins were eluted with 10 mM Tris buffer pH 7.5 containing 500 mM NaCl and 500 mM imidazole. Size exclusion chromatography on Superdex 200™ (GE Healthcare) was used as second purification step. The size exclusion chromatography was performed in 20 mM histidine buffer, 0.14 M NaCl, pH 6.0. The recovered proteins were dialyzed into 10 mM histidine buffer pH 6.0 containing 140 mM NaCl, and stored at -80 °C.

The protein concentration of the proteins was determined by measuring the optical density (OD) at 280 nm, using the molar extinction coefficient calculated on the basis of the amino acid sequence. Purity was analyzed by SDS-PAGE in the presence and absence of a reducing agent (5 mM 1,4-dithiotreitol) and staining with Coomassie brilliant blue. Aggregate content of the Fc-fusion protein preparations was determined by high-performance SEC using a SK3000SWxl analytical size-exclusion column (Tosohaas, Stuttgart, Germany). The integrity of the amino acid backbone of reduced Fc fusion proteins were verified by Nano Electrospray QTOF mass spectrometry after removal of N-glycans by enzymatic treatment with peptide-N-glycosidase F (Roche Applied Science).

Patent Claims

1. A method for producing a multispecific binder comprising at least two binding entities comprising the step of

- cultivating a HEK cell comprising

a) a nucleic acid encoding a soluble S. aureus sortase A with a C-terminal endoplasmic reticulum retention signal,

b) a nucleic acid encoding a first binding entity comprising at its C-terminus a sortase motif followed by an endoplasmic reticulum retention signal, and

c) a nucleic acid encoding a second binding entity comprising at its N-terminus at least a diglycine,

whereby the HEK cell secretes the sortase A conjugate of the first binding entity and the second binding entity,

whereby the first binding entity specifically binds to a first antigen or target and the second binding entity specifically binds to a second antigen or target,

thereby producing a multispecific binder comprising at least two binding entities.

2. A method for selecting a multispecific binder that specifically binds to two different epitopes or antigens comprising the step of

- selecting from a multitude of multispecific binders comprising different combinations of a first binding entity and a second binding entity a multispecific binder that specifically binds to two different epitopes or antigens,

wherein the members of the multitude of multispecific binders are each obtained by a method according to claim 1.

3. The method according to claim 2, characterized in that a multispecific binder is selected based on a characteristic selected from the group consisting of its binding specificity, selectivity, affinity, effector function, in vivo half-life and combinations thereof.

4. The method according to any one of claims 1 to 3, characterized in that the binding entity is a cognate pair of an antibody heavy chain variable domain and an antibody light chain variable domain.

5. The method according to any one of claims 1 to 4, characterized in that the multispecific binder is a bispecific antibody comprising two or four binding entities.

6. The method according to any one of claims 1 to 5, characterized in that the endoplasmic reticulum retention signal is selected from SEQ ID NO: 02 (KDEL), SEQ ID NO: 03 (HDEL), or SEQ ID NO: 04 (SFIXXXXMP).

7. The method according to any one of claims 1 to 6, characterized in that the sortase motif is LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue).

8. The method according to any one of claims 1 to 7, characterized in that the first binding domain or the first binding entity has within the 20 C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue).

9. A method for producing a bispecific antibody comprising the following steps

(i) determining the cell surface makers present in a cell containing sample and selecting thereof at least a first surface marker and a second surface marker,

(ii) transfecting a cell with (a) a nucleic acid encoding an antibody Fab fragment, or an antibody scFab, or a scFv antibody comprising within the 20 C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) followed by an endoplasmic reticulum retention signal KDEL (SEQ ID NO: 02), whereby the Fab fragment or scFv antibody specifically binds to the first surface marker or its ligand, (b) a nucleic acid encoding an one-armed antibody fragment comprising a full length antibody heavy chain, a full length antibody light chain, and an antibody heavy chain Fc-region polypeptide, whereby the full length antibody heavy chain and the full length antibody light chain are cognate antibody chains complementary to each other and the pair of variable domains (VH and VL) thereof forms an antigen binding site that specifically binds to the second surface marker or its ligand, whereby the full length antibody heavy chain and

the antibody heavy chain Fc-region polypeptide are covalently linked to each other via one or more disulfide bonds forming an antibody hinge region, and whereby the antibody heavy chain Fc-region polypeptide has an oligoglycine G_m (m = 2, or 3, or 4, or 5) amino acid sequence at its N-terminus, and (c) a nucleic acid encoding a soluble S. aureus sortase A with a C-terminal endoplasmic reticulum retention signal,

and thereby producing the bispecific antibody.

10. A method for determining a combination of antigen binding sites comprising the following steps

(i) determining a characteristic selected from the group consisting of binding specificity, selectivity, affinity, effector function, in vivo half-life and combinations thereof of a multitude of bispecific antibodies prepared by combining (a) each member of a first multitude of antibody Fab fragments or scFv antibody fragments whereby each member comprises within the 20 C-terminal amino acid residues the amino acid sequence LPXTG (SEQ ID NO: 01, wherein X can be any amino acid residue) followed by an endoplasmic reticulum retention signal KDEL (SEQ ID NO: 02), whereby the Fab fragment or scFv antibody specifically binds to a first epitope or antigen, with (b) each member of a multitude of one-armed antibody fragments comprising a full length antibody heavy chain, a full length antibody light chain, and an antibody heavy chain Fc-region polypeptide, whereby the full length antibody heavy chain and the full length antibody light chain are cognate antibody chains complementary to each other and the pair of variable domains (VH and VL) thereof forms an antigen binding site that specifically binds to a second epitope or antigen, whereby the full length antibody heavy chain and the antibody heavy chain Fc-region polypeptide are covalently linked to each other via one or more disulfide bonds forming an antibody hinge region, and whereby the antibody heavy chain Fc-region polypeptide has an oligoglycine G_m (m = 2, or 3, or 4, or 5) amino acid sequence at its N-terminus, via a S.aureus sortase A-mediated intracellular enzymatic coupling reaction,

and

(ii) choosing the bispecific antibody with the suitable characteristic selected from the group consisting of binding specificity, selectivity, affinity, effector function, in vivo half-life and combinations thereof, and thereby determining a combination of antigen binding sites.

11. The method according to any one of claims 5 to 9, characterized in that Fc-region comprises a mutation of the naturally occurring amino acid residue at position 329 and at least one further mutation of at least one amino acid residue selected from the group comprising amino acid residues at position 228, 233, 234, 235, 236, 237, 297, 318, 320, 322 and 331 to a different residue, wherein the residues in the Fc-region are numbered according to the EU index of Kabat.