Dual Antigen-Induced Bipartite Functional Complementation

The present invention relates to a set of polypeptides and its uses. In particular, the present invention relates to a set of polypeptides whereby this set comprises two polypeptides each of which comprises a targeting moiety "T" binding to an antigen "A" and a fragment of "F" of a functional domain, wherein said two polypeptides are not associated with each other in absence of a substrate that has "A" at (on) its surface and wherein, upon dimerization of "F", the resulting dimer becomes functional. Furthermore, medical and diagnostic uses of said set are described. Moreover, the present invention relates to nucleic acid molecule(s) encoding said set of polypeptides. The present invention also relates to a vector comprising the nucleotide sequence of nucleic acid molecule(s) encoding said set of polypeptides. Furthermore, the present invention relates to pharmaceutical compositions comprising said set of polypeptides. Moreover, the present invention relates to a kit comprising said set of polypeptides.

The last years have seen a number of landmark papers reporting outstanding efficacy of bispecific antibody constructs for immune therapy of tumours *in vitro* and in pre-clinical and early clinical trials. Today, a substantial number of different bispecific constructs are available that differ in size, composition, pharmacokinetics and ability to directly eliminate neoplastic cells or to engage immune effector cells for tumour cell lysis.

Antibody-based cancer immune strategies are highly promising therapeutic options due to their excellent sensitivity and specificity towards target structures.

The modular structural and functional organisation of antibodies allows extensive manipulation by genetic engineering. Different immunoglobulin-like domains can be separated and/or joined without losing specific domain-associated functional features. Moreover, they can be combined and linked with heterologous protein domains but also with non-peptidic moieties. It is therefore possible to develop fusion constructs in a rational way devoid of the natural limitations of conventional antibodies.

Antibody- based fusion proteins can be generated with novel biological and/or pharmaceutical properties. There are promising efforts to modify the capability of the Fc domain to elicit ADCC (antibody dependent cell mediated cytotoxicity) and CDC (complement-dependent cytotoxicity) by mutagenesis, dependent on the intended application, either to reduce side effects (inhibitory mutations) or to enhance therapeutic efficacy (activating mutations). New applications that become possible by genetic engineering are even more variate when the antigen binding domain of antibodies is considered.

The antigen recognizing variable domains of the heavy (V_H) and light chain (V_L) of an antibody can be joined by a peptide linker via genetic engineering while preserving the antigen binding capability. Such antigen binding single chain variable fragments (scFvs) can be used as small antibody surrogates with high tissue penetrating capability and low serum retention time for clinical imaging procedures and radiotherapy and other applications. Importantly, these scFv moieties can be easily employed as antigen specific modules in the development of novel recombinant therapeutics.

Recent reports indicate a tremendous potential of recombinant bispecific antibodies in anti-tumour therapy. Such bispecific antibodies recognise two antigens, one of which is expressed by the tumour, whereas the other is usually found on an immune cell. Most bispecific antibodies in anti-tumour therapy target a tumour-associated lineage marker on the one hand and CD3ε, an invariant molecule of the T-cell receptor/CD3 complex on the other hand, thus recruiting T cells to destroy the tumour [Müller and Kontermann, Bispecific antibodies for cancer immunotherapy: Current perspectives. BioDrugs 2010, 24(2):89-98].

Despite the extensive options for manipulating antibody structure and function, the therapeutic efficacy of such antibody-based reagents is limited by the nature of the addressed antigen, the accessibility of the antigen in tumour and tumour-associated tissues and the aptitude of the antibody to elicit or mediate the desired cell death inducing function.

For example, when patients are treated with bispecific constructs directed against antigens also expressed on tissues with vital functions, severe side effects are observed. This is a severe problem, since, with the exception of an unknown number of individually mutated cell surface molecules and the monoclonal B- or T- cell receptor in case of lymphomas, tumour specific antigens that discriminate a transformed cell from its healthy progenitor are

not available.

Since therapeutic concepts based on the use of bispecific antibodies usually rely on the recruitment of effector cells, it appears that the more effective the tool (bispecific construct), the more likely side effects do occur, and even minute expression of antigen on non-transformed tissue can cause uncontrollable off-target effects.

In 2008, SCIENCE published the first report on the clinical efficacy of the single-chain bispecific T cell engaging (BiTE) antibody MT103/blinatumomab; it induces remissions in about 80% of lymphoma patients relapsed or refractory to standard immune-chemotherapy at serum levels about 5 orders of magnitude lower than serum levels reported for the monoclonal antibody rituximab (Bargou, R. et al Science 321, 974-977, 2008). This publication and subsequent reports on confirmatory phase II trials in acute lymphatic leukemia (ALL) ushered in a new era of bispecific antibodies, until then in grave demise for almost two decades due to systemic toxicity and little or no therapeutic activity. Mainly in the wake of that SCIENCE paper, bispecific antibodies became a burgeoning field again in which more than 35 different formats were counted (Reichert, *Drug Discov Today.* 17 (2012) 954-963). These formats differ in size and are optimized for affinity to the antigen, stability, ability to recruit effector cells (mostly T cells) and pharmacokinetics. Affinity or avidity of the constructs are manipulated by affinity maturation using diverse techniques or simply by joining multiple scFv domains in line in order to create a multivalent construct. Even trispecific antibodies are reported that are designed to display enhance binding capabilities by addressing two instead of one target molecule. Stability of the formats can be optimized by adding immunoglobulin-like domains in order to mimic naturally occurring antibodies and to simultaneously enhance pharmacokinetic properties like prolonged half life in serum and protection from proteolytic digestion by proteases. Moreover, stability of the formats can be enhanced by optimizing the production. Since linker sequences which are utilized to covalently join scFv domains often leads to aggregates, production lines have been established that first produce two or three polypeptides that can be easily reassembled in order to generate a functional drug. Such techniques utilize directed disulphid-bridges or crosslinking reagents to covalently join two different polypeptides. Other techniques make use of hetero- or homo-dimerization domains like leucine-zipper domains, Fc-domains and others like knob into hole technologies (see, for example, WO 2007/062466). Moreover, V_H and V_L interactions, which can be stabilized by the binding of the antigen, have been used in

so called open-sandwich immunoassays for the detection of the antigen (Ueda, Nature Biotechnology 14 (1996), 1714-1718; Ohmuro-Matsuyama (2012) Detection of Protein Phosphorylation by

Open-Sandwich Immunoassay, Integrative Proteomics, Dr. Hon-Chiu Leung (Ed.), ISBN: 978-953-51-0070-6; WO 2004/016782/EP-A1 1536005.)

However, bi/tri-specific and bi-or multivalent constructs described in the art have disadvantages. First, the absence of truly specific tumor antigens that can be addressed as target molecule. In fact, the more potent the bispecific antibody format, the more severe are collateral damages, because the target antigens addressed so far are differentiation antigens shared by tumours and non-maligant cells. In consequence, bi- or tri-specific formats of the prior art cannot discriminate malignant from non-malignant cells. In this respect, tri-specific constructs, developed for high avidity binding to target cells, may turn out to confer a high degree of off-target effects because binding of one target molecule in general suffice to recruit immune cells for destruction of a cell which express either target molecule. Thus, tri-specific construct enhance avidity on the cost of specificity. Recent multi-parameter analyses indicate that tumor cells can be distinguished from their respective non-transformed tissues of origin because of the expression of aberrant antigen signatures. Today, these findings constitute an integral part of the World Health Organization (WHO) classification system of hematopoietic neoplasms, and also hold true for cancer and cancer stem or cancer initiating cells of other provenance. Thus, it would be advantageous to target cells that simultaneously express a combination of antigens that together signify a malignant state. None of the antibodies disclosed by prior art is able to discriminate between cells that express a combination of target antigens from single antigen positive cells. Second, a major problem of bi-specific antibody technologies using, for example, complete CD3 modules (e.g. a anti Cd3 scFv) is the inherent ability of these proteins to stimulate or pre-stimulate T cells irrespective of binding to the target antigen on target cells and many side effects observed so far appear to be associated with errant T cell function.

Thus, there is a need in the art for more specific treatment options in cancer treatment, in particular there is a need for improved ways to identify and/or eliminate cancer cells with higher specificity and reduce side-effects.

Similar needs exist in the field of allogeneic stem cell transplantation, i.e. the transplantation

of stem cells obtained from another person to a patient. A patient suffering from relapsed or refractory leukaemia or another haematological disease may be treated by chemotherapy/irradiation (to eliminate the malignant haematopoietic cells) in combination with a transplantation of healthy haematopoietic cells from a donor. If elimination of malignant cells is incomplete, the tumour may grow back from the surviving malignant recipient cells despite the presence of healthy cells provided by the transplantation. As a result, survival rates among patients undergoing tumour treatment and allogeneic transplantation are significantly reduced.

However, it is difficult to eliminate (and, similarly, to identify) the surviving malignant cells with high specificity, and thus despite various attempts, good solutions to this problem have not been found. Accordingly, there exists a need in the art to provide improved ways to specifically identify and/or eliminate such malignant recipient cells with minimal side effects on other cells.

The graft (allogenic stem cells), given shortly after the conditioning therapy (radiation/chemotherapy) can replace and reconstitute hematopoiesis. The graft is harvested from either bone marrow or from stimulated peripheral blood cells and contains about one percent of hematopoetic stem cells which are the source of newly built blood cells. In addition, the graft normally contains a huge number of immune cells, especially T lymphocytes, that are part of the adoptive immune system and thet can be very beneficial in cases where these T cells mount an immune attack against leukemic cells. This situation is well described and known as graft versus leukemia effect. On the other side, an errant immune response which directs T cells against the patient, known as graft versus host disease, is also frequently observed.

To minimize graft versus host disease, grafts are usually selected on the basis of HLA (human leukocyte antigen) or MHC (major histocompatibility complex). The closer the antigens between donor and recipient match the lower is the probability of severe graft versus host disease. However, for many patients, a full matched graft cannot be found. In these cases, a bone marrow or peripheral blood stem cells are utilized that differ in one or even more HLA molecules. These clinical situation requires a strict immunosuppressive regimen after transplantation to keep the T cell system strictly under control.

It is therefore one object of the present invention to provide for improved ways to

specifically identify and/or eliminate specific kinds of cells. Moreover, it is an object of the present invention to provide for improved ways to specifically identify and/or eliminate cells that have a specific combination of two specific antigens at their cell surface. Furthermore, it is an object of the present invention to provide for improved ways to specifically identify and/or eliminate cancerous cells. Furthermore, it is an object of the present invention to provide for improved ways to specifically identify and/or eliminate cells that (1) are of a certain origin (such as, in the situation of a tissue or cell transplantation, cells originating from the recipient or from the donor) and that (2) belong to a specific cell type or cell lineage (such as haematopoietic cells).

Summary

In one aspect, there is provided a set of polypeptides comprising:

a first polypeptide P1 comprising

(i) a targeting moiety T1,

wherein said targeting moiety T1 specifically binds to an antigen A1, and

(ii) a fragment F1 of a functional domain F,

wherein neither said fragment F1 by itself nor said polypeptide P1 by itself is functional with respect to the function of said domain F,

and

a second polypeptide P2 comprising

(i) a targeting moiety T2,

wherein said targeting moiety T2 specifically binds to an antigen A2, and

(ii) a fragment F2 of said functional domain F,

wherein neither said fragment F2 by itself nor said polypeptide P2 by itself is functional with respect to the function of said domain F,

wherein said antigen A1 is different from said antigen A2,

wherein said polypeptide P1 and said polypeptide P2 are not associated with each other in the absence of a substrate that has both antigens A1 and A2 at its surface, and

wherein, upon dimerization of said fragment F1 of said polypeptide P1 with said fragment F2 of said polypeptide P2, the resulting dimer is functional with respect to the function of said domain F.

In another aspect, there is provided a nucleic acid molecule or a set of nucleic acid molecules

encoding the set of polypeptides or one of the polypeptides of the set of polypeptides as defined herein.

In another aspect, there is provided a pharmaceutical composition comprising either the set of polypeptides as defined herein or the nucleic acid molecule/set of nucleic acid molecules as defined herein, said pharmaceutical composition further comprises a pharmaceutically acceptable carrier.

In another aspect, there is provided a kit comprising the set of polypeptides as defined herein or the nucleic acid molecule or the set of nucleic acid molecules as defined herein.

Detailed Description

The objects of the present invention are solved by a set of polypeptides comprising:

a first polypeptide P1 comprising

(i) a targeting moiety T1,

wherein said targeting moiety T1 specifically binds to an antigen A1, and

(ii) a fragment F1 of a functional domain F,

wherein neither said fragment F1 by itself nor said polypeptide P1 by itself is functional with respect to the function of said domain F,

and

a second polypeptide P2 comprising

(i) a targeting moiety T2,

wherein said targeting moiety T2 specifically binds to an antigen A2, and

(ii) a fragment F2 of said functional domain F,

wherein neither said fragment F2 by itself nor said polypeptide P2 by itself is functional with respect to the function of said domain F,

wherein said antigen A1 is different from said antigen A2,

wherein said polypeptide P1 and said polypeptide P2 are not associated with each other in the absence of a substrate that has both antigens A1 and A2 at or on its surface, more specifically a cell that carries both antigens A1 and A2 at or on its cell surface, and

wherein, upon dimerization of said fragment F1 of said polypeptide P1 with said fragment F2 of said polypeptide P2, the resulting dimer is functional with respect to the function of said domain F.

The objects of the present invention are also solved by a set of polypeptides comprising:

a first polypeptide P1 comprising

(i) a targeting moiety T1,

wherein said targeting moiety T1 specifically binds to an antigen A1, and

(ii) a fragment F1 of a functional domain F,

wherein neither said fragment F1 by itself nor said polypeptide P1 by itself is functional with respect to the function of said domain F,

and

a second polypeptide P2 comprising

(i) a targeting moiety T2,

wherein said targeting moiety T2 specifically binds to an antigen A2, and

(ii) a fragment F2 of said functional domain F,

wherein neither said fragment F2 by itself nor said polypeptide P2 by itself is functional with respect to the function of said domain F,

wherein said antigen A1 is different from said antigen A2,

wherein

(a) said fragment F1 comprises a V_L domain of an antibody and said fragment F2 comprises a V_H domain of the same antibody; or wherein said fragment F1 comprises a V_H domain of an antibody and said fragment F2 comprises a V_L domain of the same antibody; or

(b) said fragment F1 comprises a V_L domain of an antibody and said fragment F2 comprises a V_H domain of the same antibody; or wherein said fragment F1 comprises a V_H domain of an antibody and said fragment F2 comprises a V_L domain of the same antibody; and

wherein said polypeptide P1 and said polypeptide P2 are not associated with each other in the absence of a substrate that has both antigens A1 and A2 at or on its surface, more specifically a cell that carries both antigens A1 and A2 at or on its cell surface, and

wherein, upon dimerization of said fragment F1 of said polypeptide P1 with said fragment F2 of said polypeptide P2, the resulting dimer is functional with respect to the function of said domain F.

The objects of the present invention are also solved by a set of polypeptides comprising:

a first polypeptide P1 comprising

(i) a targeting moiety T1,

wherein said targeting moiety T1 specifically binds to an antigen A1, and

(ii) a fragment F1 of a functional domain F,

wherein neither said fragment F1 by itself nor said polypeptide P1 by itself is functional with respect to the function of said domain F,

and

a second polypeptide P2 comprising

(i) a targeting moiety T2,

wherein said targeting moiety T2 specifically binds to an antigen A2, and

(ii) a fragment F2 of said functional domain F,

wherein neither said fragment F2 by itself nor said polypeptide P2 by itself is functional with respect to the function of said domain F,

wherein said antigen A1 is different from said antigen A2,

wherein

(c) said fragment F1 comprises a V_L domain of an antibody and said fragment F2 comprises a V_H domain of the same antibody; or wherein said fragment F1 comprises a V_H domain of an antibody and said fragment F2 comprises a V_L domain of the same antibody;

(d) said polypeptide P1 and said polypeptide P2 are not associated with each other in the absence of a substrate that has both antigens A1 and A2 at its surface, more specifically a cell that carries both antigens A1 and A2 at its cell surface; or

(e) said fragment F1 comprises a V_L domain of an antibody and said fragment F2 comprises a V_H domain of the same antibody; or wherein said fragment F1 comprises a V_H domain of an antibody and said fragment F2 comprises a V_L domain of the same antibody; and

wherein said polypeptide P1 and said polypeptide P2 are not associated with each other in the absence of a substrate that has both antigens A1 and A2 at its surface, more specifically a cell that carries both antigens A1 and A2 at its cell surface, and

wherein, upon dimerization of said fragment F1 of said polypeptide P1 with said fragment F2 of said polypeptide P2, the resulting dimer is functional with respect to the function of said domain F, and wherein said polypeptides P1 and P2, in particular said fragments F1 and F2, have, in the absence of a substrate or cell, with each other a dissociation constant K_D in the range of 10^{-8} M to 10^{-2} M.

The present invention further refers to the following items:

1. A set of polypeptides comprising:

a first polypeptide P1 comprising

(i) a targeting moiety T1,

wherein said targeting moiety T1 specifically binds to an antigen A1, and

(ii) a fragment F1 of a functional domain F,

wherein neither said fragment F1 by itself nor said polypeptide P1 by itself is functional with respect to the function of said domain F,

and

a second polypeptide P2 comprising

(i) a targeting moiety T2,

wherein said targeting moiety T2 specifically binds to an antigen A2, and

(ii) a fragment F2 of said functional domain F,

wherein neither said fragment F2 by itself nor said polypeptide P2 by itself is functional with respect to the function of said domain F,

wherein said antigen A1 is different from said antigen A2,

wherein said polypeptide P1 and said polypeptide P2 are not associated with each other in the absence of a substrate that has both antigens A1 and A2 at its surface, more specifically a cell that carries both antigens A1 and A2 at its cell surface, and

wherein, upon dimerization of said fragment F1 of said polypeptide P1 with said fragment F2 of said polypeptide P2, the resulting dimer is functional with respect to the function of said domain F.

2. The set of polypeptides according to item 1, wherein a cell carrying both antigens A1 and A2 at its cell surface induces dimerization of the fragment F1 of said polypeptide P1 with the fragment F2 of said polypeptide P2, whereas a cell which does not carry both antigens A1 and A2 at its cell surface does not induce dimerization of the fragment F1 of said polypeptide P1 with the fragment F2 of said polypeptide P2.

3. The set of polypeptides according to item 1 or 2, wherein said targeting moiety T1 comprises an immunoglobulin module, preferably an immunoglobulin module I1 comprising a V_L domain linked to a V_H domain, more preferably an immunoglobulin module I1 that comprises a scFv (single-chain variant fragment) of an antibody, or an

immunoglobulin module comprising a variable domain V_HH of a llama antibody, camel antibody or shark antibody,

and/or said targeting moiety T2 comprises an immunoglobulin module, preferably an immunoglobulin module I2 comprising a V_L domain linked to a V_H domain, more preferably an immunoglobulin module I2 that comprises a scFv (single-chain variant fragment) of an antibody, or an immunoglobulin module comprising a variable domain V_HH of a llama antibody, camel antibody or shark antibody,

or wherein said targeting moiety T1 and/or said targeting moiety T2 comprises an aptamer or a natural ligand of said antigen A1 or antigen A2, respectively

4. The set of polypeptides according to any of the preceding items, wherein said antigen A1 and/or said antigen A2 is an antigen expressed on the surface of cells of a tumour or on the surface of progenitor/precursor cells of a tumour, preferably an antigen expressed on the surface of cells of a haematologic tumour or an antigen expressed on the surface of cells of a non-haematologic tumour.

5. The set of polypeptides according to any of the preceding items, wherein the combination of antigen A1 and antigen A2 is only found on cancerous cells, and not on cells that are not cancerous, and wherein, preferably, the combination of antigen A1 and antigen A2 is specific for cancerous cells of a certain type of cancer.

6. The set of polypeptides according to any of the preceding items, wherein said antigen A1 is an MHC antigen, preferably an allelic variant of any of HLA-A, HLA-B, HLA-C, HLA-DQ, HLA-DR, or HLA-DM, more preferably an allelic variant of an MHC class I molecule, more preferably an allelic variant selected from the group consisting of HLA-A1, HLA-A2, HLA-A3, HLA-A25, HLA-B7, HLA-B8, HLA-B35, HLA-B44, HLA-Cw3, HLA-Cw4, and HLA-Cw7, and/or said antigen A2 is an antigen that is specific for a certain cell type or cell lineage.

7. The set of polypeptides according to any of the preceding items, wherein said functional domain F is an immunoglobulin module, preferably a scFv (single-chain variant fragment) of an antibody, or a fluorescent molecule, preferably GFP or a GFP variant, or a molecule capable of mediating bioluminescence, preferably *Gaussia* luciferase.

8. The set of polypeptides according to any of the preceding items, wherein said functional domain F is a domain that specifically binds to a carrier molecule, preferably a carrier molecule that is a peptide or a carbohydrate molecule, or an affinity tag, preferably an affinity tag selected from the group consisting of a FLAG-tag, a myc-tag, a glutathione-S-transferase(GST)-tag, a hemagglutinin(HA)-tag, a polyhistidine(His)-tag and a maltose binding protein(MBP)-tag.

9. The set of polypeptides according to any of the preceding items, wherein said functional domain F is a domain that specifically binds to a radioactive compound, a domain that specifically binds to a toxin molecule that by itself is not capable of penetrating through the cell membrane of a human cell and that is internalized into a human cell upon association with the cell membrane of said cell, a domain that specifically binds to a fluorescent molecule, or a domain that specifically binds to a molecule capable of mediating bioluminescence.

10. The set of polypeptides according to any of the preceding items, wherein said fragment F1 comprises a V_L domain of an antibody and said fragment F2 comprises a V_H domain of the same antibody, wherein, preferably, said antibody is an anti-CD3 antibody, or wherein said fragment F1 comprises a V_H domain of an antibody and said fragment F2 comprises a V_L domain of the same antibody, wherein, preferably, said antibody is an anti-CD3 antibody.

11. The set of polypeptides according to any of the preceding items for use in the treatment of a patient who is suffering from a tumour or for diagnostic use in a patient who is suffering from a tumour, preferably for use in the treatment of a patient who is suffering from a tumour and undergoing allogeneic tissue or cell transplantation or meant to undergo such transplantation or for diagnostic use in a patient who is suffering from a tumour and undergoing or meant to undergo allogeneic tissue or cell transplantation, wherein, preferably, said set of polypeptides is administered to said patient.

12. A nucleic acid molecule or a set of nucleic acid molecules encoding the set of polypeptides or one of the polypeptides of the set of polypeptides according to any of the preceding items.

13. A vector comprising the nucleotide sequence of the nucleic acid molecule according to item 12 or the sequence of one of the nucleic acid molecules of the set of nucleic acid molecules according to item 12.

14. A pharmaceutical composition comprising either the set of polypeptides according to any of items 1 to 11 or the nucleic acid molecule/set of nucleic acid molecules according to item 12 or the vector according to item 13, wherein, preferably, said pharmaceutical composition further comprises a pharmaceutically acceptable carrier.

15. A kit comprising the set of polypeptides according to any of items 1-11.

Preferably, said antigen A1 is a cell surface molecule. Preferably, said antigen A2 is a cell surface molecule. Preferably, said antigen A1 is specific for the malignant state of a cell. Preferably, said antigen A2 is specific for a certain cell type or cell lineage or for the malignant state of a cell. Preferably, said antigen A1 is specific for a malignant cell type. Preferably, said antigen A2 is specific for a malignant cell type.

In one aspect, the present invention relates to the set of polypeptides as defined and described herein, wherein, however, the antigen A1 is the same as the antigen A2. Hence, in such a set of polypeptides P1 and P2, the F1 fragment may be linked to the targeting moiety T1 and the F2 fragment may be linked to the targeting moiety T2, whereas both T1 and T2 specifically bind to the same antigen. In this context, the epitope on antigen A1, to which the targeting moiety T1 binds, may be the same or a different epitope as the epitope on the antigen A2, to which the targeting moiety T2 binds. In case the epitope on antigen A1 is the same as the epitope on the antigen A2, polypeptide P1 may comprise a targeting moiety which is identical to the targeting moiety comprised in P2. Also this aspect of the invention is based on the advantage that the set of polypeptides P1 and P2 with the disrupted F domain displays no off target effects (for example no pre-activation of CD3-displaying T cells and, hence, less toxic properties and/or side effects, for example as compared to conventional bispecific antibodies).

In one embodiment, said fragment F1 and said fragment F2 together are said functional domain F.

In one embodiment, said polypeptide P1 and said polypeptide P2 are not covalently linked to each other in the absence of a substrate that has both antigens A1 and A2 at its surface, more

specifically a cell that carries both antigens A1 and A2 at its cell surface.

In one embodiment, said polypeptide P1 and said polypeptide P2 are not covalently linked to each other.

Said polypeptide P1 and polypeptide P2 and/or, in particular, said fragment F1 and fragment F2 as comprised therein, more particular the V_H and V_L which may be comprised therein, are not associated with each other, in particular when administered to a subject in need of medical intervention. i.e. in need of therapy and/or diagnosis. Accordingly, the pharmaceutical or diagnostic means provided herein comprise the two polypeptides P1 and P2 as comprised in the herein defined "set of polypeptides" in non-associated form. The association of said two polypeptides take place in vivo under the presence of said substrate or cell. Under the presence of said substrate or cell, the association of said two polypeptides may be (further) stabilized by a stabilizing agent (for example an antigen, like, for example, CD3, HIS or DIG as described herein). Preferably, they are not associated with each other in the absence of said substrate or cell and/or do not dimerizise in the absence of said substrate or cell. More preferably, they are not associated with each other in the absence of said substrate or cell and/or do not dimerizise in the absence of said substrate or cell even if an agent is present which stabilizes association and/or dimerization of polypeptide P1 and polypeptide P2 and/or, in particular, fragment F1 and fragment F2, i.e. even if said polypeptide P1 and polypeptide P2 and/or, in particular, said fragment F1 and fragment F2 is present in an stabilizing agent/P1(F1)/P2(F2)-trimeric complex (for example in an antigen/VH/VL-trimeric complex).

In one specific embodiment, said polypeptide P1 and polypeptide P2 and/or, in particular, said fragment F1 and fragment F2 as comprised therein, more particular the V_H and V_L which may be comprised therein, are associated with each other and/or dimerizise into a three-part-complex-formation, preferably by an interaction mediated by an agent which stabilizes association and/or dimerization of polypeptide P1 and polypeptide P2 and/or, in particular, fragment F1 and fragment F2 (for example by an antigen-mediated interaction). Most preferably, however, this association and/or dimerization only occurs in the presence of said substrate or cell.

The affinity strength with which, for example, leucine-zippers and/or constant domains, like immunoglobulin CH3 or Fc fragments, hetero- and homodimerize is estimated to be at a

dissociation constant K_D in the range of ~ 10^{-8} to 10^{-11} M (see, for example, Zhu (1997) Protein Sci. 6, 781-8; Plückthun (1997) Immunotech. 3, 83-105). This K_D range is clearly below the K_D with which, in the absence of said substrate or cell, association and/or dimerization of said polypeptides P1 and P2, in particular of said fragments F1 and F2, of this invention might occur. Hence, in one embodiment, polypeptide P1 and polypeptide P2 and/or, in particular, fragment F1 and fragment F2 as comprised therein, more particular the V_H and V_L which may be comprised therein, associate with each other and/or dimerizise in the absence of said substrate or cell only with a K_D which is above the K_D of, for example, hetero- and homodimerization of leucine-zippers and/or constant domains, like immunoglobulin CH3 or Fc fragments. In the presence of said substrate or cell, it is envisaged that polypeptide P1 and polypeptide P2 and/or, in particular, fragment F1 and fragment F2 as comprised therein, more particular the V_H and V_L which may be comprised therein, associate with each other and/or dimerizise with a K_D which is in the range of the K_D of, for example, hetero- and homodimerization of leucine-zippers and/or constant domains, like immunoglobulin CH3 or Fc fragments, or even below this range.

The interaction strength of, for example, isolated VH and VL domains in general is of low affinity. Using calorimetric, fluorometric or ultraviolet difference spectroscopy and/or circular dichroisma techniques, dissociation constants K_D of 10^{-9} to 10^{-6} M have been determined (see, for example, Wörn JMB (2001) 305, 989-1010; Plückthun (1992) Immunological Reviews No 130). Using surface plasmon resonance techniques (SPR biosensor BIAcore or BIAcore 2000, Pharmacia) and an anti HEL-Antibody system (anti-hen egg lysozyme antibody HyHEL-10), Ueda (loc. cit.) and Ohmuro-Matsuyama (loc. cit.) found that isolated VH and VL domains do not dimerize at all ($K_a < 10^5$/M, below detection limit). However, association of the VH and VL peptides was significantly enhanced in the presence of cognate antigens (Ka ~ 10^9/M) with a remarkable reduction of the dissociation rate of the antigen/VH/VL-trimeric complex with a calculated $K_d \sim 2.73 \times 10^{-5} \pm 1.43 \times 10^{-6}$ /s at 1.4 μM of the antigen. Hence, it is particularly envisaged in the context of this invention that the K_D with which, in the absence of said substrate or cell, association and/or dimerization of said polypeptides P1 and P2, in particular of said fragments F1 and F2, of this invention might occur is only at, or even above, the K_D or range of K_D of isolated VH and VL domains, for example as has been estimated in the context of Wörn (loc. cit.), Plückthun (1992; loc. cit.), Ueda (loc. cit.) and Ohmuro-Matsuyama (loc. cit.), in particular above the K_D or range of K_D of the antigen/VH/VL-trimeric complex as has been estimated

in the context of Wörn (loc. cit.), Plückthun (1992;loc. cit.), Ueda (loc. cit.) and Ohmuro-Matsuyama (loc. cit.). In the presence of said substrate or cell, it is envisaged that polypeptide P1 and polypeptide P2 and/or, in particular, fragment F1 and fragment F2 as comprised therein, more particular the V_H and V_L which may be comprised therein, associate with each other and/or dimerizise with a K_D which is (far) below the K_D or range of K_D of isolated VH and VL domains, for example as has been estimated in the context of Wörn (loc. cit.), Plückthun (1992;loc. cit.), Ueda (loc. cit.) and Ohmuro-Matsuyama (loc. cit.), preferably at, or even below, the K_D or range of K_D of the antigen/VH/VL-trimeric complex as has been estimated in the context of Plückthun (loc. cit.), Ueda (loc. cit.) and Ohmuro-Matsuyama (loc. cit.)

In one aspect, polypeptide P1 and polypeptide P2 and/or, in particular, fragment F1 and fragment F2 as comprised therein, more particular the V_H and V_L which may be comprised therein, are not associated in the absence of said substrate or cell and/or do not dimerizise in the absence of said substrate or cell. If at all, they associate with each other and/or dimerizise in the absence of said substrate or cell only with a K_D above 10^{-8} M, preferably above 10^{-6} M, more preferably above 10^{-5} M and more preferably above 10^{-4}M. In another aspect, if at all, they associate with each other and /or dimerizise in the absence of said substrate or cell only with a K_D in the range of 10^{-8} M to 10^{-2} M, preferably 10^{-7} M to 10^{-3} M, more preferably 10^{-6} M to 10^{-3} M and even more preferably 10^{-5} M to 10^{-3} M. I another aspect, polypeptide P1 and polypeptide P2 and/or, in particular, fragment F1 and fragment F2 as comprised therein, more particular the V_H and V_L which may be comprised therein, are associated in the presence of said substrate or cell and/or dimerizise in the presence of said substrate or cell. In particular, they associate with each other and /or dimerizise in the presence of said substrate or cell with a K_D below 10^{-6} M, preferably below 10^{-7} M, more preferably below 10^{-8} M and more preferably below 10^{-9}M. They may also associate with each other and/or may dimerizise in the presence of said substrate or cell with a K_D in the range of 10^{-11} M to 10^{-6} M, more preferably 10^{-11} M to 10^{-7} M and even more preferably 10^{-11} M to 10^{-8} M.

In a preferred embodiment, the above even applies in case an agent is present which stabilizes association and/or dimerization of polypeptide P1 and polypeptide P2 and/or, in particular, fragment F1 and fragment F2. For example, such an stabilizing agent in accordance with this invention may be an antigen, like, for example, CD3, HIS or DIG as

described herein, capable to bind to the domain F which, for example, may comprise a V_H and aV_L of an antibody (F1 and F2, respectively, or F2 and F3, respectively).

Being "present", in the context of this invention and, in particular, in the context of the above (i.e. with respect to said agent and/or said substrate or cell and/or said antigens A1 and A2), particularly means being present at a concentration in a range of 0.01 μM to 1 mM, in a range of 0.1 to 500 μM, in a range of 0.1 to 300 μM, in a range of 0.1 to 100 μM, in a range of 1 to 500 μM, in a range of 10 to 500 μM. Being "absent", in the context of this invention and, in particular, in the context of above (i.e. with respect to said agent and/or said substrate or cell and/or said antigens A1 and A2), particularly means being present at a concentration below the above ranges or below 1 mM, 500 μM, 300 μM, 100 μM, 10 μM, 1 μM, 0.1 μM, 0.01 μM, 0.001 μM or 1 nM wherein the lower values are preferred.

The person skilled in the art is readily in the position to measure the K_D of dimerization, in particular, of P1 and P2, more particular of F1 and F2 as comprised therein, more particular of the V_H and V_L which may be comprised therein. Examples of respective measuring methods are x-ray crystallography; nuclear magnet resonance (NMR); isothermal calorimetry (ITC); cryo-electro microscopy (CEM); mass spectrometry (MS); surface Plasmon resonance (SPR). Such methods are, for example, described in Protein Surface Recognition: Approaches for Drug Discovery: Approaches for the Inhibition of Protein-Protein Interactions for Drug Discovery (Eds: Ernest Giralt, Mark Peczuh, Xavier Salvatella John Wiley & Sons; 12. November 2010). Further examples of respective measuring methods are circular Dichroism Analysis; small Zone Gel Filtratoion Chromatography; Fluorescence Gel Retardation; Sedimentation Equilibrium; Fluorescence Polarization Assay; Blot Overlay or Far Western Blot Analysis; Affinity Capillary Electrophoresis Analysis; Fluorescence Resonance Energy Transfer (FRET); such methods are, for example described in Protein'Protein Interactions: Methods and Applications: 261 (Methods in Molecular Biology); Haian Fu (Editor); Humana Press; 1 (23. März 2004). A preferred method to measure the K_D in accordance with this invention is Fluorescence Correlation Spectroscopy (FCS). This method is, for example, described in Douglas Magde (Physical Review Letters 29, 11, 1972, S. 705–708).

In one particular aspect, the K_Ds referred to herein (i) apply to, (ii) are at or (iii) are to be measured at a temperature of 4 to 38 °C, preferably 4 to 20 °C (for example 10°C) or 20 to 38 °C (for example 30°C), and/or a pH of 4,5 to 8 (for example a pH of 7),

"Not associated" in the context of the present invention particularly means not functionally associated with respect of the function of the domain F, i.e. not allowing F1 and F2 to form a functional F. Hence, in one aspect of the invention, P1 and P2 may be bound to each other (for example covalently) as far as no functional domain F is formed by F1 and F2. It is, however, preferred that P1 and P2 are separated.

In one embodiment, said antigen A1 and/or said antigen A2 is a molecule.

In one embodiment, said antigen A1 and/or said antigen A2 is proteinaceous.

In one embodiment, said antigen A1 and/or said antigen A2 is non-proteinaceous.

In one embodiment, said targeting moiety T1 binds non-covalently to said antigen A1.

In one embodiment, said targeting moiety T2 binds non-covalently to said antigen A2.

In one embodiment, a substrate having both antigens A1 and A2 at its surface induces dimerization of the fragment F1 of said polypeptide P1 with the fragment F2 of said polypeptide P2, whereas a substrate which does not have both antigens A1 and A2 at its cell surface does not induce dimerization of the fragment F1 of said polypeptide P1 with the fragment F2 of said polypeptide P2.

In one embodiment, a cell carrying both antigens A1 and A2 at its cell surface induces dimerization of the fragment F1 of said polypeptide P1 with the fragment F2 of said polypeptide P2, whereas a cell which does not carry both antigens A1 and A2 at its cell surface does not induce dimerization of the fragment F1 of said polypeptide P1 with the fragment F2 of said polypeptide P2. In this context "induces dimerization" particularly means "allows juxtaposition and subsequent dimerization".

In one embodiment, said targeting moiety T1 comprises an immunoglobulin module and/or said targeting moiety T2 comprises an immunoglobulin module.

In one embodiment, said targeting moiety T1 comprises an immunoglobulin module I1 which comprises a V_L domain linked to a V_H domain, preferably an immunoglobulin module I1 that comprises a scFv (single-chain variant fragment) of an antibody, a Fab or a $F(ab')_2$ (for example with additional parts of, for example, an Fc domain) of an antibody or a complete antibody.

and/or said targeting moiety T2 comprises an immunoglobulin module I2 which comprises a V_L domain linked to a V_H domain, preferably an immunoglobulin module I2 that comprises a scFv (single-chain variant fragment) of an antibody a Fab or a $F(ab')_2$ (for example with additional parts of, for example, an Fc domain) of an antibody or a complete antibody.

In one embodiment, said targeting moiety T1 and/or said targeting moiety T2 comprises an immunoglobulin module which comprises a variable domain V_HH of a llama antibody, a camel antibody, or a shark antibody.

In one embodiment, said targeting moiety T1 and/or said targeting moiety T2 is an aptamer, or a natural ligand of said antigen A1 or antigen A2, respectively.

In one embodiment, said targeting moiety T1 and/or said targeting moiety T2 comprises a Fv or scFv ((single-chain) variant fragment) of an antibody.

In one embodiment, the immunoglobulin module comprised in the targeting moiety T1 and T2 comprises a V domain selected from the group consisting of:

(i) a V domain of an anti-HLA-A2 antibody comprising a V_L domain comprising SEQ ID NOS: 78 and 79 (CDRs 1 and 3) and DAS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 75-77 (CDRs 1-3);

(ii) a V domain of an anti-HLA-Cw6 antibody comprising a V_L domain comprising SEQ ID NOS: 83 and 84 (CDRs 1 and 3) and DDS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 80-82 (CDRs 1-3);

(iii) a V domain of an anti-EpCAM antibody comprising a V_L domain comprising SEQ ID NOS: 88 and 89 (CDRs 1 and 3) and WAS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 85-87 (CDRs 1-3);

(iv) a V domain of an anti-Her2 antibody comprising a V_L domain comprising SEQ ID NOS: 93 and 94 (CDRs 1 and 3) and SAS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 90-92 (CDRs 1-3);

(v) a V domain of an anti-EGFR1 antibody comprising a V_L domain comprising SEQ ID NOS: 98 and 99 (CDRs 1 and 3) and DAS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 95-97 (CDRs 1-3);

(vi) a V domain of an anti-CEA antibody comprising a V_L domain comprising SEQ ID NOS: 103 and 104 (CDRs 1 and 3) and SAS (CDR 2) and/or a V_H domain comprising SEQ ID NOS:100-102 (CDRs 1-3);

(vii) a V domain of an anti-CD45 antibody comprising a V_L domain comprising SEQ ID NOS: 107 and 108 (CDRs 1 and 3) and LAS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 105 and 106 (CDRs 1 and 2) and CDR3 or SEQ ID NOS:132-134 (CDRs 1-3);

(viii) a V domain of an anti-CD138 antibody comprising a V_L domain comprising SEQ ID NOS: 112 and 113 (CDRs and 1 and 3) and YTS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 109-111 (CDRs 1-3); and

(ix) a V domain of an anti-CD19 antibody comprising a V_L domain comprising SEQ ID NOS: 158 and 159 (CDRs 1 and 3) and DAS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 155-157 (CDRs 1-3).

In a further, preferred, embodiment, the immunoglobulin module comprised in the targeting moiety T1 and/or T2 comprises a V domain selected from the group consisting of:

(i) a V domain of an anti-HLA-A2 antibody comprising a V_L domain comprising SEQ ID NO: 52 and/or a V_H domain comprising SEQ ID NO: 51;

(ii) a V domain of an anti-HLA-Cw6 antibody comprising a V_L domain comprising SEQ ID NO: 54 and/or a V_H domain comprising SEQ ID NO: 53;

(iii) a V domain of an anti-EpCAM antibody comprising a V_L domain comprising SEQ ID NO: 56 and/or a V_H domain comprising SEQ ID NO: 55;

(iv) a V domain of an anti-Her2 antibody comprising a V_L domain comprising SEQ ID NO: 58 and/or a V_H domain comprising SEQ ID NO: 57;

(v) a V domain of an anti-EGFR1 antibody comprising a V_L domain comprising SEQ ID NO: 60 and/or a V_H domain comprising SEQ ID NO: 59;

(vi) a V domain of an anti-CEA antibody comprising a V_L domain comprising SEQ ID NO: 62 and/or a V_H domain comprising SEQ ID NO: 61;

(vii) a V domain of an anti-CD45 antibody comprising a V_L domain comprising SEQ ID NO: 64 and/or a V_H domain comprising SEQ ID NO: 63; and

(viii) a V domain of an anti-CD138 antibody comprising a V_L domain comprising SEQ ID NO: 66 and/or a V_H domain comprising SEQ ID NOS: 65;

(ix) a V domain of an anti-CD19 antibody comprising a V_L domain comprising SEQ ID NO: 153 and/or a V_H domain comprising SEQ ID NO: 152.

In a further, preferred, embodiment, the immunoglobulin module comprised in the targeting moiety T1 and/or T2 comprises a V domain comprising any one of SEQ ID NOS: 67-74 and 154.

In one embodiment, polypeptide P1 has the general structure F1-T1 and/or polypeptide P2 has the general structure F2-T2. The F fragment and T moieties may be separated by a linker (e.g. F1-linker-T1 and/or F2-linker-T2) and/or flanked by (an) additional amino acid stretche(s) 1 and/or 2 (stretch-F1-(linker)-T1-stretch2 and/or stretch1-F2-(linker)-T2-stretch2). It is preferred that the above general structure is from the N terminus to the C terminus of the polypeptides, i.e. N-F1-T1-C and/or N-F2-T2-C, N-F1-linker-T1-C and/or N-F2-linker-T2-C and N-stretch1-F1-(linker)-T1-stretch2-C and/or N-stretch1-F2-(linker)-T2-stretch2-C. In case the targeting moiety is or comprises an immunoglobulin module I, like an Fv or scFv, polypeptide P1 may have the general structure F1-VH1-VL1 and/or polypeptide P2 may have the general structure F2-VH2-VL2 or polypeptide P1 may have the general structure F1-VL1-VH1 and/or polypeptide P2 may have the general structure F2-VL2-VH2. Also in these cases the F fragment and T moieties may be separated by a linker (e.g. F1-linker-VH/VL1-VL/VH1 and/or F2-linker-VH/VL2-VL/VH2) and/or flanked by (an) additional amino acid stretche(s) 1 and/or 2 (stretch1-F1-(linker)-VH/VL1-VL/VH1-stretch2 and/or stretch1-F2-(linker)-VH/VL2-VL/VH2-stretch2). Also in this case, it is preferred that the above general structure is from the N terminus to the C terminus of the polypeptides, i.e. N-F1-VH/VL1-VL/VH1-C and/or N-F2-VH/VL2-VL/VH2-C, N-F1-linker-VH/VL1-VL/VH1-C and/or N-F2-linker-VH/VL2-VL/VH2-C and N-stretch1-F1-(linker)-VH/VL1-VL/VH1-stretch2-C and/or N-stretch1-F2-(linker)-VH/VL2-VL/VH2-stretch2-C. There may also a linker be present between VH and VL or VL and VH.

The above described linker, in particular the between the V domains, may comprise 1 to 25 amino acids, preferably 12 to 20 amino acids, preferably 12 to 16 or 15 to 20 amino acids. The above described linker may comprise one or more (G_3S) and/or (G_4S) motives, in particular 1, 2, 3, 4, 5 or 6 (G_3S) and/or (G_4S) motives, preferably 3 or 4 (G_3S) and/or (G_4S) motives, more preferably 3 or 4 (G_4S) motives.

In one embodiment, said immunoglobulin module I1 and said fragment F1 are separated by a linker comprising 1 to 12, preferably 3 to 12, amino acids, and/or said immunoglobulin module I2 and said fragment F2 are separated by a linker comprising 1 to 12, preferably 3 to

12, amino acids.

In one embodiment, the V_L domain of I1 is linked to the V_H domain of I1 by a linker comprising 12 to 25 amino acids, preferably a linker with the sequence $(G_3S)_3$ or $(G_3S)_4$ or $(G_4S)_3$ or $(G_4S)_4$ and/or the V_L domain of I2 is linked to the V_H domain of I2 by a linker comprising 12 to 25 amino acids, preferably a linker with the sequence $(G_3S)_3$ or $(G_3S)_4$ or $(G_4S)_3$ or $(G_4S)_4$.

As mentioned, the linker as describe above may comprise (G_3S) and/or (G_4S) motives. Alternative linkers may consist of or comprise the GEGTSTGSGGSGGSGGAD motive. The person skilled in the art can without further ado find and use further (peptide) linker known in the art.

The said additional amino acid stretches 1 and/or 2 may consist of or comprise 1 to 200, 1 to 100, 1 to 70, 1 to 65, 1 to 50, 1 to 25 or 1 to 20 amino acids.

In one embodiment, said antigen A1 and/or said antigen A2 is an antigen expressed on the surface of cells of a tumour or on the surface of progenitor/precursor cells of a tumour, preferably an antigen expressed on the surface of cells of a haematologic tumour, more preferably an antigen expressed on the surface of cells selected from the group consisting of acute myeloic leukemia cells, chronic myeloic leukemia cells, acute lymphatic leukemia cells, chronic lymphatic leukemia cells, lymphoma cells, myeloproliferative syndrome cells, myelodysplastic cells, more preferably myeloma cells, or said antigen A1 and/or said antigen A2 is an antigen expressed on the surface of cells of a non-haematologic tumour, preferably a cell selected from the group consisting of renal cell carcinoma cells, bladder cancer cells, lung cancer cells, mesothelioma cells, prostate cancer cells, brain cancer cells, bone cancer cells, sarcoma cells, soft tissue cancer cells, ovarian cancer cells, cervix cancer cells, breast cancer cells, endometrial cancer cells, uterine cancer cells, germ cell tumour cells, anal cancer cells, rectal carcinoma cells, colon carcinoma cells, small intestine carcinoma cells, gastric carcinoma cells, gastrointestinal stroma tumour cells, liver carcinoma cells, pancreas carcinoma cells, bile duct carcinoma cells, gall bladder carcinoma cells, head and neck cancer cells, hypopharyngeal cancer cells, laryngeal cancer cells, cells of a cancer of the esophagus, skin cancer cells, preferably melanoma cells, cells of a childhood cancer, cells of an endocrine tumour, cells of a carcinoid tumour, thymoma cells, thyroid cancer cells, cells of an islet cell tumour, cells of an adrenal cell tumour, cells of a neuroendocrine tumour and

cells of a cancer of unknown primary (cancer of unknown primary origin). Detailed information on such cancers can be found in the relevant literature, such as "Cancer Medicine", JF Holland, E Frei (editors), Mcgraw-Hill Professional, 8th edition (2010) and references cited therein.

In one embodiment, the combination of antigen A1 and antigen A2 is only found on blood cells or precursor cells of blood cells, preferably on only one type of blood cells.

In one embodiment, the combination of antigen A1 and antigen A2 is only found on target, in particular, cancerous cells, and not (or only to a negligible extent) on cells that are not target cells, in particular, that are not cancerous. In a preferred embodiment, the combination of antigen A1 and antigen A2 is specific for cancerous cells of a certain type of cancer.

In one embodiment, the combination of antigen A1 and antigen A2 distinguishes a certain kind of cells, preferably a certain type of cancer cells, from any other cells.

"Certain type of cancer" in this context may mean type of cancer characterized by the same organ in which the cancer is formed or, preferred, type cancer characterized by the same pair of (aberrant) antigens A1 and A2.

In one embodiment, the combination of antigen A1 and antigen A2 is found on progenitor/precursor cells that are progenitor/precursor cells of a tumour and not on progenitor/precursor cells that are not progenitor/precursor cells of a tumour.

In one embodiment, said antigen A1 is an antigen that is specific for the malignant state of a cell and said antigen A2 is an antigen that is specific for the cell type or cell lineage of said cell.

In one embodiment,

a) antigen A1 is EpCAM (epithelial cell adhesion molecule) and antigen A2 is CD10 (cluster of differentiation 10), HER2/neu (human epidermal growth factor receptor 2), VEGF-R (vascular endothelial growth factor receptor), EGFR (epidermal growth factor receptor; also called HER1 (human epidermal growth factor receptor 1) or ErbB1) or MDR (multidrug resistance protein), or

b) antigen A1 is MCSP (melanoma-associated chondroitin sulfate proteoglycan) and antigen A2 is melanoferrin or EpCAM, or

c) antigen A1 is CA125 (cancer antigen 125/carbohydrate antigen 125) and antigen A2

is CD227 (PEM (polymorphic epithelial mucin) or MUC1 (mucin-1)), or

d) antigen A1 is CD56 and antigen A2 is CD140b (PDGFRβ (platelet-derived growth factor receptor beta)) or GD3 ganglioside, or

e) antigen A1 is EGFR and antigen 2 is HER2, or

f) antigen A1 is PSMA (prostate-specific membrane antigen) and antigen 2 is HER2, or

g) antigen 1 is Sialyl Lewis and antigen 2 is EGFR, or

h) antigen 1 is CD44 and antigen 2 is ESA (epithelial surface antigen) (CD326, EpCAM), CD24, CD133, MDR (multidrug resistance protein) or CD117, or

i) antigen 1 is CD34 and antigen 2 is CD19, CD79a, CD2, CD7, HLA-DR (human leukocyte antigen DR), CD13, CD117, CD33 or CD15, or

j) antigen 1 is CD33 and antigen 2 is CD19, CD79a, CD2, CD7, HLA-DR (human leukocyte antigen DR), CD13, CD117 or CD15, or

k) antigen 1 is MUC1 and antigen 2 is CD10, CEA or CD57, or

l) antigen 1 is CD38 and antigen 2 is CD138, or

m) antigen 1 is CD 24 and antigen 2 is CD29 or CD49f, or

n) antigen 1 is carbonic anhydrase IX and antigen 2 is aquaporin, preferably aquaporin-2.

In one embodiment, said antigen A1 and/or said antigen A2 is selected from the group consisting of HLA-A (HLA-A major histocompatibility complex, class I, A [Homo sapiens]; Gene ID: 3105 updated on 13-Jan-2013; DAQB-90C11.16-002; Chromosome: 6; NC_000006.11 (29910247..29913661); for HLA-A2: 1. mRNA = LOCUS NM_001242758 = Version NM_001242758.1 GI:337752169 = GenBank: AY191309.1 PRI 13-JAN-2013; 2. Protein = P79495 [UniParc]. Last modified May 1, 1997. Version 1.; for HLA-Cw6: mRNA = LOCUS HUMMHCCW6A = GenBank: VERSION M28160.1 GI:531197PRI (18-AUG-1994); Protein = Q29963 [UniParc]. Last modified August 22, 2003. Version 2.); EpCAM (EPCAM epithelial cell adhesion molecule [Homo sapiens]; also known as ESA; KSA; M4S1; MK-1; DIAR5; EGP-2; EGP40; KS1/4; MIC18; TROP1; EGP314; HNPCC8; TACSTD1.; Gene ID: 4072, updated on 6-Jan-2013; mRNA = VERSION NM_002354.2 GI:218505669PRI 06-JAN-2013; Protein = P16422 [UniParc]. last modified November 13, 2007. Version 2.); CD45 (PTPRC protein tyrosine phosphatase, receptor type, C [Homo sapiens]; also known asLCA; LY5; B220; CD45; L-CA; T200; CD45R; GP180; Gene ID: 5788, updated on 13-Jan-2013; mRNA = VERSION NM_002838.4 GI:392307006 PRI 13-JAN-2013; Protein = P08575-1 = Isoform 1, Last modified July 19, 2003. Version 2.;

Protein = P08575-2 = Isoform 2); Her2 (ERBB2 v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) [Homo sapiens]; also known asNEU; NGL; HER2; TKR1; CD340; HER-2; MLN 19; HER-2/neu; gene ID: 2064, updated on 13-Jan-2013; mRNA transcript variant 1 = VERSION NM_004448.2 GI:54792095, PRI 06-JAN-2013; mRNA transcript variant 2 = VERSION NM_001005862.1 GI:54792097, PRI 06-JAN-2013; Protein = P04626-1 = Isoform 1 , Last modified August 13, 1987. Version 1.; Protein = P04626-2= Isoform 2; Protein = P04626-3= Isoform 3; Protein = P04626-4= Isoform 4); EGFR (EGFR epidermal growth factor receptor [Homo sapiens]; also known asERBB; HER1; mENA; ERBB1; PIG61; Gene ID: 1956, updated on 13-Jan-2013; mRNA transcript variant 1 = VERSION NM_005228.3 GI:41327737, PRI 13-JAN-2013; mRNA transcript variant 2 = VERSION NM_201282.1 GI:41327731, PRI 13-JAN-2013; mRNA transcript variant 3 = VERSION NM_201283.1 GI:41327733, PRI 13-JAN-2013; mRNA transcript variant 4 = VERSION NM_201284.1 GI:41327735, PRI 13-JAN-2013; Protein = P00533-1 = Isoform 1, Last modified November 1, 1997. Version 2.; Protein = P00533-2 = Isoform 2; Protein = P00533-3 = Isoform 3; Protein = P00533-4 = Isoform 4); CD138 (SDC1 syndecan 1 [Homo sapiens]; Gene ID: 6382, updated on 6-Jan-2013; mRNA transcript variant 1 = VERSION NM_001006946.1 GI:55749479, PRI 06-JAN-2013; mRNA transcript variant 2 = VERSION NM_002997.4 GI:55925657, PRI 06-JAN-2013; Protein = P18827 [UniParc]. Last modified May 5, 2009. Version 3.); CEA (CEACAM5 carcinoembryonic antigen-related cell adhesion molecule 5 [Homo sapiens]; also known asCEA; CD66e; Gene ID: 1048, updated on 13-Jan-2013; mRNA = VERSION NM_004363.2 GI:98986444, PRI 13-JAN-2013; P06731, Last modified January 11, 2011. Version 3.); and CD19 (CD19 CD19 molecule [Homo sapiens]; also known asB4; CVID3; Gene ID: 930, updated on 5-Jan-2013; mRNA transcript 1 = VERSION NM_001178098.1 GI:296010920, PRI 06-JAN-2013; mRNA transcript 2 = VERSION NM_001770.5 GI:296010919, PRI 06-JAN-2013; Protein = P15391 [UniParc]. Last modified November 13, 2007. Version 6).

In one embodiment, said antigen A1 and/or said antigen A2 is an MHC antigen, preferably an allelic variant of any of HLA-A, HLA-B, HLA-C, HLA-DQ, HLA-DR, or HLA-DM, more preferably an allelic variant of an MHC class I molecule, more preferably an allelic variant selected from the group consisting of HLA-A1, HLA-A2, HLA-A3, HLA-A25, HLA-B7, HLA-B8, HLA-B35, HLA-B44, HLA-Cw3, HLA-Cw4, HLA-Cw6, and HLA-Cw7.

In one embodiment, said antigen A1 is HLA-A2.

In one embodiment, said antigen A1 and/or said antigen A2 is selected from the group consisting of CD45, aquaporin, preferably aquaporin-2, scavenger receptor class B member 1 (SCARB1), CD34, CD33, CD138, CD15, CD1a, CD2, CD3, CD4, CD5, CD8, CD20, CD23, CD31, CD43, CD56, CD57, CD68, CD79a, CD146, synaptophysin, CD56, CD57, nicotinic acetylcholine receptor, muscle-specific kinase (MUSK), voltage-gated calcium channel (P/Q-type), voltage-gated potassium channel (VGKC), N-methyl-D-aspartate receptor (NMDA), TSH (thyroid stimulating hormone) receptor, amphiphysin, HepPar-1, ganglioside GQ1B, ganglioside GD3, ganglioside GM1 and glycophorin-A.

In a preferred embodiment, said antigen A1 is an MHC antigen and said antigen A2 is an antigen that is specific for a certain cell type or cell lineage.

In one embodiment, said functional domain F is an immunoglobulin module, preferably a scFv (single-chain variant fragment) of an antibody more preferably a Fv (variant fragment) of an antibody, or a fluorescent molecule, preferably a bimolecular fluorescence complementation molecule, more preferably GFP or a GFP variant, or a molecule capable of mediating bioluminescence, preferably a luciferase molecule, more preferably *Gaussia* luciferase.

In one embodiment, said functional domain F is a Fv (variant fragment) of an antibody.

In one embodiment, said functional domain F specifically binds or is capable of specifically binding to an antigen. In a specific aspect, said antigen may be an antigen that is present on cells of the human immune system. In a preferred embodiment, said binding activates said cells of the human immune system.

In one embodiment, said functional domain F is a T cell engaging domain, preferably a T cell engaging domain specifically binding to CD2, CD3, CD5, T cell receptor or CD28, more preferably a T cell engaging domain specifically binding to CD3ε, an NK cell (natural killer cell) engaging domain, preferably a NK cell engaging domain specifically binding to CD1a, CD16a or CD56, a domain engaging macrophage cells, preferably a domain engaging macrophage cells specifically binding to CD16a, CD32a, CD32b, CD89 or CD64, a monocyte engaging domain, preferably a monocyte engaging domain specifically binding to CD32a, CD32b, CD64 or CD89, a granulocyte engaging domain, preferably a granulocyte

engaging domain specifically binding to CD16b, CD32a, CD32b, CD64, or CD89, a domain engaging neutrophil granulocytes, preferably a domain engaging neutrophil granulocytes that specifically binds to CD89 (FcαRI), or a domain engaging activated neutrophil granulocytes, monocytes and/or macrophages, preferably a domain engaging activated neutrophil granulocytes, monocytes and/or macrophages that specifically binds to CD64 (FcγRI).

In one embodiment, said functional domain F is a domain that specifically binds to an antigen linked to a diagnostic or therapeutic compound.

In one embodiment, said functional domain F is a domain that specifically binds to a carrier molecule or an affinity tag. Preferably, said carrier molecule is linked to a diagnostic or therapeutic compound. Preferably, said affinity tag is linked to a diagnostic or therapeutic compound.

Preferably, said affinity tag is selected from the group consisting of a FLAG-tag, a myc-tag, a glutathione-S-transferase(GST)-tag, a hemagglutinin(HA)-tag, a polyhistidine(His)-tag, a digoxigenin (DIG)-tag and a maltose binding protein(MBP)-tag.

Preferably, said carrier molecule is a peptide or a carbohydrate molecule. In a preferred embodiment, said functional domain F is a domain that specifically binds to a carrier molecule, preferably a carrier molecule linked to a diagnostic or therapeutic compound, wherein said carrier molecule is selected from the group consisting of gelatine, inulin, dextrane and hydroxyethyl starch.

In one embodiment, said therapeutic compound is a radioactive compound, preferably a radioactive compound comprising ^{90}Y, ^{177}Lu, ^{131}I, ^{32}P, ^{10}B, or ^{213}Bi. In one embodiment, said therapeutic compound is a toxin. Preferably, said toxin is selected from the group consisting of *B. anthracis* edema factor, *B. anthracis* lethal factor, *C. perfringens* iota toxin, *C. botulinum C2 toxin, C. difficile ADP-ribosyltransferase, C. diphtheriae diphteria toxin fragment A*, *Burgholderia* sp. shiga toxin (subunit A), *Clostridium perfringens* str. 13 toxin pfoA perfringolysin O, Ricin A chain, plant RIP bouganin, Human RNASE3 ribonuclease (RNase A family, 3) and anthrax lethal factor endopeptidase. A further non-limiting example of a toxin in accordance with this invention is a toxin being or comprising an amino acid sequence selected from the group consisting of SEQ ID NOS 160 to 168.

In one embodiment, said diagnostic compound is a radioactive compound, preferably a

radioactive compound comprising ^{99m}Tc, ^{111}In, ^{82}Rb or ^{201}Tl. In one embodiment, said diagnostic compound is a fluorescent compound, preferably GFP, a GFP variant, or a fluorescent small-molecule compound such as FITC (fluorescein isothiocyanate), PE (phycoerythrin), an alexa fluor dye (such as AlexaFluor488 or related dyes) or a cyanine dye (such as Cy3 (Indocarbocyanine) or Cy5 (Indodicarbocyanine) or related dyes), In one embodiment, said diagnostic compound is a molecule capable of mediating bioluminescence, preferably a luciferase molecule, more preferably *Gaussia* luciferase.

In one embodiment, said fragment F1 comprises a V_L domain of an antibody and said fragment F2 comprises a V_H domain of the same antibody, wherein, preferably, said antibody is an anti-CD3 antibody, more preferably an anti-CD3ε antibody, or an anti-His or anti-DIG antibody or said fragment F1 comprises a V_H domain of an antibody and said fragment F2 comprises a V_L domain of the same antibody, wherein, preferably, said antibody is an anti-CD3 antibody, more preferably an anti-CD3ε antibody, or an anti-His or anti-DIG antibody.

In another embodiment, the V_L and V_H domains as comprised in the F1 and F2 fragment, respectively, or in the F2 and F1 fragment, respectively may also of two different antibodies, either specific for the same Antigen (and for the same or a different epitope) or for different Antigen. This is, for example, envisaged to be employed where new specifications are to be created (for example in phage-display approaches).

In another embodiment, the immunoglobulin module comprised in the F domain comprises a V domain selected from the group consisting of:

(i) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NOS: 18-20 (CDRs 1-3) and/or a V_H domain comprising SEQ ID NOS: 15-17 (CDRs 1-3);

(ii) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NOS: 24-26 (CDRs 1-3) and/or a V_H domain comprising SEQ ID NOS: 21-23 (CDRs 1-3);

(iii) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NOS: 30-32 (CDRs 1-3) and/or a V_H domain comprising SEQ ID NOS: 27-29 (CDRs 1-3);

(iv) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NOS: 36 and 37 (CDRs 1 and 3) and DTS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 33-35 (CDRs 1-3);

(v) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NOS: 41 and 42 (CDRs 1 and 3) and YTN (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 38-40 (CDRs1-3); and

(vi) a V domain of an anti-His antibody comprising a V_L domain comprising SEQ ID NOS: 46 and 47 (CDRs 1 and 3) and KVS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 43-45 (CDRs 1-3);

(vii) a V domain of an anti-DIG antibody comprising a V_L domain comprising SEQ ID NOS: 50 and 131 (CDRs 1 and 3) and YSS (CDR 2) and/or a V_H domain comprising SEQ ID NOS: 48 and 49 (CDRs 1 and 2) and A (CDR 3).

In another, preferred embodiment, the immunoglobulin module comprised in the F domain comprises a V domain selected from the group consisting of:

(i) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NO: 2 and/or a V_H domain comprising SEQ ID NO: 1;

(ii) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NO: 4 and/or a V_H domain comprising SEQ ID NO: 3;

(iii) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NO: 6 and/or a V_H domain comprising SEQ ID NO: 5;

(iv) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NO: 8 and/or a V_H domain comprising SEQ ID NO: 7;

(v) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NO: 10 and/or a V_H domain comprising SEQ ID NO: 9; and

(vi) a V domain of an anti-His antibody comprising a V_L domain comprising SEQ ID NO: 12 and/or a V_H domain comprising SEQ ID NO: 11;

(vii) a V domain of an anti-DIG antibody comprising a V_L domain comprising SEQ ID NO: 14 and/or a V_H domain comprising SEQ ID NO: 30.

In one embodiment, said functional domain F is a domain that specifically binds to a toxin molecule, preferably a toxin molecule that by itself is not capable of penetrating through the cell membrane of a human cell and that, preferably, is internalized into a human cell upon

association with the cell membrane of said cell, wherein, preferably, said association with the cell membrane of said cell is mediated by specifically binding to a heterodimer formed from two molecules, preferably two molecules associated with said cell membrane, wherein, preferably, said two molecules are the polypeptides P1 and P2 as described herein.. In one embodiment, said functional domain F is a domain that specifically binds to the A-component (active component) of a bacterial two-component A-B toxin. In one embodiment said functional domain F is a domain that specifically binds to a toxin selected from the group consisting of *B. anthracis* edema factor, *B. anthracis* lethal factor, *C. perfringens* iota toxin, *C. botulinum* C2 toxin, *C. difficile* ADP-ribosyltransferase, *C. diphtheriae* diphteria toxin fragment A, *Burgholderia* sp. shiga toxin (subunit A), *Clostridium perfringens* str. 13 toxin pfoA perfringolysin O, Ricin A chain, plant RIP bouganin, Human RNASE3 ribonuclease (RNase A family, 3) and anthrax lethal factor endopeptidase. A further non-limiting example of a toxin in accordance with this invention is a toxin being or comprising an amino acid sequence selected from the group consisting of SEQ ID NOS 160 to 168.

In one embodiment, said functional domain F is a domain that specifically binds to a fluorescent molecule, preferably a fluorescent molecule that by itself is not capable of penetrating through the cell membrane of a human cell. Preferably, said fluorescent molecule is GFP or a GFP variant or a molecule that is or comprises a fluorescent small-molecule compound such as FITC (fluorescein isothiocyanate), PE (phycoerythrin), an alexa fluor dye (such as AlexaFluor488 or related dyes) or a cyanine dye (such as Cy3 (Indocarbocyanine) or Cy5 (Indodicarbocyanine) or related dyes).

In one embodiment, said functional domain F is a domain that specifically binds to a molecule capable of mediating bioluminescence, preferably to a luciferase molecule, more preferably to *Gaussia* luciferase.

In one embodiment, said functional domain F is a fluorescent molecule, preferably a bimolecular fluorescence complementation molecule, more preferably GFP or a GFP variant, such as YFP, CFP, Venus, or Cerulean.

Examples of particular polypeptides P1 or P2 comprised in the set of polypeptides according to this invention are polypeptides comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 114-129 and 197.

In general, the present invention relates to the treatment or elimination of any undesired cell

population and the treatment or prevention of any disorder or disease which comes along with this undesired cell population. For this purpose, the set of polypeptides of this invention is to be used.

In one embodiment, said set of polypeptides is a set of polypeptides for use in the treatment of a patient who is suffering from a tumour or cancer or for diagnostic use in a patient who is suffering from a tumour or cancer, preferably for use in the treatment of a patient who is suffering from a tumour or cancer and undergoing allogeneic tissue or cell transplantation or meant to undergo such transplantation, or for diagnostic use in a patient who is suffering from a tumour or cancer and undergoing or meant to undergo allogeneic tissue or cell transplantation, wherein, preferably, said set of polypeptides is administered to said patient.

Examples of tumours to be treated or diagnosed are those for which the tumour or cancer cells are described herein above with respect to the antigens A1 and/or A2.

In one embodiment, said treatment involves the elimination of recipient tissue/cells of a certain cell type, preferably a cancerous cell type, or recipient precursor cells giving rise to a certain cell type, preferably to a cancerous cell type, optionally after or in parallel to transplantation to the recipient of donor tissue/cells of said same cell type or donor precursor cells giving rise to said same cell type.

In one embodiment, the set of polypeptides of the invention is for use in an allogeneic transplantation setting for haematopoietic neoplasias, for example, with mismatched HLA antigens, in particular for use in therapeutically exploiting this mismatch situation. In this exemplary situation, the dual information of recipient HLA haplotype ($HLA_{patient}$) and haematopoietic lineage origin (CD45) is displayed exclusively on leukemic blasts and other haematopoietic cells of the patient. All other cells of recipient origine express the recipient haplotype but not the hematopoietic lineage antigen CD45 (e.g. recipient non-hematopoietic cells are positive for HLA-A2 but negative for CD45). Likewise, all donor hematopoietic cells express donor HLA haplotype molecules that means that they are CD45 positive but HLA-A2 negative in the situation a mismatch transplantation where the patient but not the donor is positive for HLA-A2. Consequently, the present invention also relates to bimolecular and complementing single-chain antibody constructs directed against HLA-A2, in cases where the patient but not the donor is HLA-A2 positive, and a second construct specific for the haematopoietic lineage marker CD45 to specifically target all hematopoietic

cells of the patient including all hematologic neoplasms. Hence, the first polypeptide P1 may comprise a single-chain variable fragment antibody construct directed against the HLA of the patient (targeting moiety T1) fused to the V_L fragment of F1 antiCD3 (for example, fragment F1). The second polypeptide P2 may comprise a single-chain variable fragment construct specific for a haematopoietic lineage marker (for example, CD45; targeting moiety T2), fused to the V_H split-fragment of F2 anti CD3-Fv (fragment F2).

In one embodiment, said elimination involves the destroying of said recipient tissue/cells or said recipient precursor cells by cells of the immune system, by a toxin or by a radioactive compound.

In one embodiment, said set of polypeptides is a set of polypeptides for diagnostic use in a patient undergoing allogeneic tissue or cell transplantation, wherein, preferably, said patient is a patient suffering from a tumour.

In one embodiment, said diagnostic use involves the specific detection of recipient cells of a certain cell type or cell lineage among recipient cells of different cell type or cell lineage and donor cells of the same or different type or cell lineage.

In one embodiment, said diagnostic use involves the specific detection of recipient cells that are malignant cells among recipient cells that are not malignant and among donor cells. In one embodiment, said set of polypeptides is administered to a patient.

Preferably, said patient is a mammal, more preferably a human being.

In one embodiment, said administration occurs by bolus administration or by continuous administration.

In one embodiment, the polypeptides P1 and P2 of said set of polypeptides are administered in parallel. In another embodiment, the polypeptides P1 and P2 of said set of polypeptides are administered sequentially.

In one embodiment, one of the polypeptides P1 or P2 of said set of polypeptides is administered by bolus administration, whereas the other one is administered by continuous administration.

In one embodiment, the amount of polypeptide administered is in the range of from

0.5 $\mu g/m^2$ per day to 500 $\mu g/m^2$ per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2, preferably in the range of from 5 $\mu g/m^2$ per day to 200 $\mu g/m^2$ per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2, more preferably in the range of from 10 $\mu g/m^2$ per day to 80 $\mu g/m^2$ per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2.

In one embodiment, the amount of polypeptide administered is in the range of from 0.05 $\mu g/m^2$ per day to 0.5 $\mu g/m^2$ per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2.

In one embodiment, the amount of polypeptide P1 administered is different from the amount of polypeptide P2 administered.

In one embodiment, the amount of polypeptide administered is in the range of from 0.5 $\mu g/m^2$ per day to 50 $\mu g/m^2$ per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2. In one embodiment, the amount of polypeptide administered is in the range of from 50 $\mu g/m^2$ per day to 100 $\mu g/m^2$ per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2. In one embodiment, the amount of polypeptide administered is in the range of from 100 $\mu g/m^2$ per day to 200 $\mu g/m^2$ per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2. In one embodiment, the amount of polypeptide administered is in the range of from 200 $\mu g/m^2$ per day to 300 $\mu g/m^2$ per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2. In one embodiment, the amount of polypeptide administered is in the range of from 300 $\mu g/m^2$ per day to 400 $\mu g/m^2$ per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2. In one embodiment, the amount of polypeptide administered is in the range of from 400 $\mu g/m^2$ per day to 500 $\mu g/m^2$ per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2. In one embodiment, the amount of polypeptide administered is in the range of from 500 $\mu g/m^2$ per day to 1 mg/m^2 per day for the polypeptide P1 or for the polypeptide P2 or for each of the polypeptides P1 and P2.

Further reference points for deriving the amounts of the polypeptides P1 and P2 to be administered can also be obtained by consulting studies carried out with bispecific antibody constructs (e.g. Bargou R et al., Tumor regression in cancer patients by very low doses of a

T cell-engaging antibody. Science. 2008; 321(5891):974-7; and Topp MS et al. Targeted therapy with the T-cell-engaging antibody blinatumomab of chemotherapy-refractory minimal residual disease in B-lineage acute lymphoblastic leukemia patients results in high response rate and prolonged leukemia-free survival. J Clin Oncol. 2011, 29:2493-8).

In one embodiment, said administration occurs continuously for at least 12 hours or for at least 1 day or for at least 2 days or for at least 3 days or for at least 4 days or for at least 5 days or for at least 6 days or for at least 7 days or for at least 8 days or for at least 9 days or for at least 10 days or for at least 11 days or for at least 12 days or for at least 13 days or for at least 14 days or for at least 15 days or for at least 16 days or for at least 17 days or for at least 18 days or for at least 19 days or for at least 20 days or for at least 21 days or for at least 22 days or for at least 23 days or for at least 24 days or for at least 25 days or for at least 26 days or for at least 27 days or for at least 28 days or for at least 29 days or for at least 30 days or for at least 5 weeks or for at least 6 weeks.

In one embodiment, said administration of said set of polypeptides or of one of the polypeptides of said set of polypeptides occurs intravenously, preferably by intravenous injection.

In one embodiment, said administration of said set of polypeptides or of one of the polypeptides of said set of polypeptides occurs subcutaneously, preferably by subcutaneous injection.

In one embodiment, said set of polypeptides is administered in combination with one or more drugs selected from the group consisting of an immunomodulatory drug, and/or a steroid, preferably prednisolone or prednisone.

In one embodiment, said set of polypeptides is administered in combination with a radioactive compound, preferably a radioactive compound linked to an antigen, a carrier molecule or an affinity tag, wherein said radioactive compound, said antigen, said carrier molecule or said affinity tag is specifically bound by said functional domain F.

In one embodiment, said set of polypeptides is administered in combination with a toxin, preferably a toxin linked to an antigen, a carrier molecule or an affinity tag, wherein said toxin, said antigen, said carrier molecule or said affinity tag is specifically bound by said functional domain F.

In one embodiment, said set of polypeptides is administered in combination with a fluorescent molecule, preferably a fluorescent molecule linked to an antigen, a carrier molecule or an affinity tag, wherein said fluorophore, said antigen, said carrier molecule or said affinity tag is specifically bound by said functional domain F.

In one embodiment, said functional domain F is a domain that specifically binds to an antigen which is not recognized as foreign by the immune system of said patient to whom said set of polypeptides is administered.

In one embodiment two sets of polypeptides as described above (a first set of polypeptides and a second set of polypeptides) are administered simultaneously or sequentially. In one preferred embodiment, said first set of polypeptides has different fragments F1 and F2 than said second set of polypeptides. In one preferred embodiment, said first set of polypeptides has the same fragments F1 and F2 as said second set of polypeptides. In one preferred embodiment, the targeting moieties T1 and T2 of said first set of polypeptides bind to the same antigens as the targeting moieties T1 and T2, respectively, of said second set of polypeptides. In one preferred embodiment, the targeting moieties T1 and T2 of said first set of polypeptides bind to different antigens than the targeting moieties T1 and T2 of said second set of polypeptides.

In one embodiment, said patient has undergone cancer treatment before treatment with said set of polypeptides, said cancer treatment preferably being chemotherapy, radiation therapy or operative removal of the tumour, or undergoes cancer treatment parallel to treatment with said set of polypeptides, said cancer treatment preferably being chemotherapy, radiation therapy or operative removal of the tumour.

In one embodiment, said set of polypeptides or one of the polypeptides of said set of polypeptides has been produced by means of a prokaryotic or eukaryotic expression system or by de novo peptide synthesis.

In one embodiment, said set of polypeptides or one of the polypeptides of said set of polypeptides is generated inside said patient by protein expression from a nucleic acid introduced into said patient.

Many patients suffer from allergic or auto-immune diseases. In many of these cases, a clonal B cell population produce an errant antibody that reacts with antigens expressed by the

patients' tissues or complex with an allergen, causing anaphylactic reactions. In both cases, it is desirable to specifically eliminate the errant B cell clone.

To this end, one may modify the combinatorial system in a way so that one arm (P1 or P2, in particular T1 or T2) recognizes a B cell associated antigen (e.g. CD19, CD20, CD38 or CD138) and the other arm (P2 or P1, in particular T2 or T1, respectively) is the allergen or the substrate bound by the antibody that causes the autoimmune disease. When these two constructs bind to a B cell that is CD19 (CD20, CD38 or CD138) positive and simultaneously displays the clonotypic antibody on the surface, the attached anti-CD3 VH and VL can interact and reconstitute the CD3 binding site exactly on the B cell. This allergen-specific or antigen-specific assembly will ultimately result in the clonal depletion of the Target B cells.

Hence, in accordance with this invention, any of said antigens A1 and A2 may also be a clonotypic antibody on the surface of a B cell, in particular a B cell that causes an autoimmune disorder.

In this context, for example, one of said antigens A1 and A2 may be CD19 and the other one may be a clonotypic antibody on the surface of a B cell, in particular a B cell that causes an autoimmune disorder.

In accordance with this aspect of the invention, any one of said targeting moiety T1 and T2 may comprise an allergen or substrate which binds to the clonotypic antibody on the surface of the B cell and/or which is, upon binding to the clonotypic antibody, capable to cause an autoimmune disorder. Non-limiting examples of an allergen comprised in any one of said targeting moiety T1 and T2 are hair allergens, like, for example, dog-hair, cat-hair (e.g. Fel d 1, Feld d1A, Feld d1B) or guinea-pig-hair allergens, or pollen allergens, like, for example, birch, grass, pollen allergens. Further non-limiting examples are mite allergens (for example Tyr p 2, Der P1, Der f 2), cat allergens (for example Fel d 1, Feld d1A, Feld d1B), peanut allergens (for example Conglutin-7), rot fungus allergens (for example Alt a 1), dog allergens (for example Can f 1), sprue wheat allergens (for example Alpha/beta-gliadin), german cockroach allergens (for example Bla g 1.02 variant allergen), birch tree or (major) pollen allergens (for example Cyn d 1, Pha a 1, Dac g 3, Phl p 2, Phl p 1, Profilin, Bet v 1-L, Bet v 1-A), major apple allergens (for example Mal d 1), cow's milk allergens (for example alpha-lactalbumin, alpha-S1-casein), chicken egg allergens (for example lysozyme C,

ovalbumin) and Horse allergens (for example latherin, Equ c 1), and the like. A further non-limiting and preferred example of an allergen comprised in any one of said targeting moiety T1 and T2 is the antigen for human myeloma cell line U266 antibody IgE-ND. A further non-limiting and preferred example of an allergen comprised in any one of said targeting moiety T1 and T2 is an allergen being or comprising an amino acid sequence selected from the group consisting of SEQ ID NOS 169 to 195.

In this context, the inventions also relates to the set of polypeptides as described herein, and, in particular in the above aspect, for use in treating or preventing a disorder selected from the group consisting of

(i) an autoimmune disorder; and
(ii) a hypersensitivity disorder.

Non-limiting examples of an autoimmune disorder to be treated or prevented in accordance with this invention are selected from the group consisting of

(i) allergic disorders;
(ii) Multiple Sclerosis;
(iii) Psoriasis;
(iv) Systemic Lupus Erythematosus;
(v) Sjögren's syndrome;
(vi) Rheumatoid Arthritis;
(vii) Idiopathic Thrombocytopenic Purpura;
(viii) Diabetes;
(xi) Vasculitis;
(x) Crohn's disease; and
(xi) Amyloidosis.

Non-limiting examples of a hypersensitivity disorder to be treated or prevented in accordance with this invention are selected from the group consisting of allergies (type I hypersensitivity reaction according to Coombs and Gell classification), an antibody dependent cytotoxic reaction (type II hypersensitivity reaction), a immune complex disease (type III hypersensitivity reaction), delayed type hypersensitivity (type IV hypersensitivity reaction) and a receptor mediated autoimmune disease (type V hypersensitivity reaction).

In a preferred embodiment, said autoimmune or hypersensitivity disorder comes along with or is triggered by allogenic stem cell transplantation (i.e. any of type I to type V hypersensitivity disorder according to the Coombs and Gell classification).

Many cells which are infected by a pathogen (for example a virus, like, for example, HIV, EBV, CMV) express pathogen-encoded proteins on their cell surface. Hence, in accordance with this invention, any of said antigens A1 and A2 may also be such a pathogen-encoded protein, like, for example, a HIV, EBV or CMV protein on the surface of a cell. In this context, the inventions also relates to the set of polypeptides as described herein for use in treating or preventing an infectious disease, for example a viral infectious disease. Particular examples of pathogen-encoded proteins can be derived from http://www.uniprot.org/uniprot/ and are HIV gp120 (Q78706); EBV LMP-2 (P13285); CMV gB (P06473); HBV HBS (Q9JG36); HCV E1 (C4B751); HCV E2 (Q6TRB1); Human adenovirus C serotype 2 HAdV-2 (P03276) .

The objects of the present invention are also solved by a nucleic acid molecule or a set of nucleic acid molecules encoding the set of polypeptides or one of the polypeptides of the set of polypeptides as defined in the embodiments above, wherein, preferably, said nucleic acid molecule or the nucleic acid molecules of said set of nucleic acid molecules comprises an export signal that mediates secretion of the encoded polypeptide(s) by a bacterial or eukaryotic cell.

A non-limiting example of the nucleic acid molecule or set of nucleic acid molecules according to this invention comprises one or more of the nucleotide sequences as depicted in any one of SEQ ID NOS: 135-150 and 196.

The objects of the present invention are also solved by a vector comprising the nucleotide sequence of the nucleic acid molecule as defined above or the sequence of one of the nucleic acid molecules of the set of nucleic acid molecules as defined above.

The objects of the present invention are also solved by a cell comprising said nucleic acid/set of nucleic acids or said vector.

The objects of the present invention are also solved by a pharmaceutical composition comprising either the set of polypeptides as defined above or the nucleic acid molecule/set of

nucleic acid molecules as defined above or the vector as defined above, wherein, preferably, said pharmaceutical composition further comprises a pharmaceutically acceptable carrier.

The objects of the present invention are also solved by a kit comprising the set of polypeptides as defined above and/or the nucleic acid molecule or the set of nucleic acid molecules according the invention and/or the vector according the invention.

In one embodiment, the polypeptides of said set of polypeptides comprised by said kit are contained in a single vial.

In one preferred embodiment, the polypeptides of said set of polypeptides comprised by said kit are contained in separate vials.

In one embodiment, one or more of the polypeptides of said set of polypeptides comprised by said kit are freeze-dried.

In one embodiment, one or more of the polypeptides of said set of polypeptides comprised by said kit are in solution.

The objects of the present invention are also solved by a method for treatment of a patient who is suffering from a

(i) tumour or cancer and/or who is undergoing allogeneic cell or tissue transplantation;
(ii) an autoimmune disorder; or
(iii) a hypersensitivity disorder.

Said method may comprise the steps:

- obtaining a set of polypeptides, said set of polypeptides comprising

a first polypeptide P1 comprising

(i) a targeting moiety T1,

wherein said targeting moiety T1 specifically binds to an antigen A1, and

(ii) a fragment F1 of a functional domain F,

wherein neither said fragment F1 by itself nor said polypeptide P1 by itself is functional with respect to the function of said domain F,

and

a second polypeptide P2 comprising

(i) a targeting moiety T2,

wherein said targeting moiety T2 specifically binds to an antigen A2, said

antigen A2 being a cell surface molecule that is specific for a certain cell type or cell lineage, and

(ii) a fragment F2 of said functional domain F,

wherein neither said fragment F2 by itself nor said polypeptide P2 by itself is functional with respect to the function of said domain F,

wherein said antigen A1 is different from said antigen A2,

wherein said polypeptide P1 and said polypeptide P2 are not associated with each other in the absence of a substrate that has both antigens A1 and A2 at its surface, more specifically a cell that carries both antigens A1 and A2 at its cell surface, and

wherein, upon dimerization of said fragment F1 of said polypeptide P1 with said fragment F2 of said polypeptide P2, the resulting dimer is functional with respect to the function of said domain F,

- administering said set of polypeptides to said patient.

In such method of treatment, said set of polypeptides is as defined in the embodiments above.

The objects of the present invention are also solved by a method of using the set of polypeptides as described above for treatment of a patient undergoing cell or tissue transplantation.

The objects of the present invention are also solved by the use of a set of proteins as defined in the embodiments above for the manufacture of a medicament for the treatment of a patient suffering from the above defined and described diseases a disorder or, for example, a patient suffering from cancer and/or undergoing cell or tissue transplantation.

As used herein, the term "polypeptide" refers to a linear molecular chain of amino acids containing more than 30 amino acids. Optionally, a polypeptide may include one or more disulfide bonds or be chemically modified. Moreover, optionally a non-proteinaceous element (such as a fluorophore, RNA-aptamer, DNA-aptamer, or small molecule) may be attached to said linear molecular chain of amino acids. Such polypeptides can be produced by any known method. The polypeptide can for example be generated by expression from a nucleic acid coding for said polypeptide, or can be synthesized by solid phase synthesis methods, or be produced by conjugation or linkage of existing molecules, e.g., by chemical linkage.

The term "polypeptide P1" is used to refer to a polypeptide comprising (i) a targeting moiety, wherein said targeting moiety specifically binds to an antigen, and (ii) a fragment of a functional domain, wherein neither said fragment by itself nor said polypeptide P1 by itself is functional with respect to the function of said functional domain. The term "polypeptide P2" is used to refer to a polypeptide comprising (i) a targeting moiety, wherein said targeting moiety specifically binds to an antigen, and (ii) a fragment of a functional domain, wherein neither said fragment by itself nor said polypeptide P2 by itself is functional with respect to the function of said functional domain.

The term "domain", as used herein, refers to a linear molecular chain of amino acids that includes the amino acid sequence of an entire polypeptide or a portion of a polypeptide. Optionally, a domain may include one or more disulfide bonds or be chemically modified. Moreover, optionally a domain may comprise a non-proteinaceous element (such as a fluorophore). In one embodiment, however, the term "domain" does not comprise compounds that are chemically modified or comprise non-proteinaceous element(s).

A "functional domain", as used herein, is a domain that is capable of fulfilling a certain function, such as specific binding to a certain binding partner or antigen, specific activation of a certain receptor, mediation of toxic effects, or fluorescence upon excitation with light of an appropriate wavelength.
The term "functional domain F" is preferably meant to also include compounds that are non-proteinaceous. In one embodiment, however, it refers to a proteinaceous compound or a functional part thereof.

The term "a fragment of a domain", as used herein, refers to a linear molecular chain of amino acids that corresponds to a part of a domain, but not the entire domain. Optionally, a fragment of a domain may include one or more disulfide bonds or be chemically modified. Moreover, optionally a domain may comprise a non-proteinaceous element or part of such a non-proteinaceous element.
The term "fragment F1" is used to refer to a fragment of a functional domain. The term "fragment F2" is used to refer to a fragment of a functional domain.

The pairwise abbreviations P1, P2; T1, T2; F1, F2; A1, A2; and I1, I2, as used herein, are meant to designate different polypeptides, targeting moieties, fragments, antigens, and immunoglobulin modules, respectively. They are synonymous to first polypeptide, second

polypeptide; first targeting moiety, second targeting moiety; first fragment, second fragment; first antigen, second antigen; and first immunoglobulin module, second immunoglobulin module, respectively.

The term "moiety", as used herein, refers to a linear molecular chain of amino acids that includes the amino acid sequence of an entire polypeptide or a portion of a polypeptide. Optionally, a moiety may include one or more disulfide bonds or be chemically modified. Moreover, optionally a moiety may comprise a non-proteinaceous element (such as an oligonucleotide). In one embodiment, however, the term "moiety" does not comprise compounds that are chemically modified or comprise non-proteinaceous element(s).
The term "targeting moiety T1" is used to refer to a moiety that specifically binds to an antigen, for example antigen A1. The term "targeting moiety T2" is used to refer to a moiety that specifically binds to an antigen, for example antigen A2.

As used herein, a "linker" is a sequence of amino acids within a polypeptide that connects two parts of said polypeptide or two domains comprised by said polypeptide.

The term "nucleic acid molecule", as used by the present invention, defines a linear molecular chain consisting of more than 30 nucleotides. The term includes DNA, such as cDNA or genomic DNA, and RNA.

The term "construct", as used herein, refers to a nucleic acid molecule comprising one or more recombinant nucleotide sequences. The term also includes polypeptides that are expressed from a recombinant nucleotide sequence or that are artificially made or recombinant molecules that comprise two or more amino acid sequences that are not naturally found within the same protein.

The term "specifically binds to" or "specifically binds", as used by the present invention in the context of a molecule or domain that specifically binds to an interaction partner or antigen or that specifically binds an interaction partner or antigen, means that a molecule or domain binds to said interaction partner or antigen, preferably by non-covalent binding, or is capable of binding said interaction partner or antigen, preferably by non-covalent binding, and does not or essentially not cross-react with any other interaction partner or antigen with a structure similar to that of the interaction partner or antigen.
In the context of a targeting moiety (such as targeting moiety T1 or T2) specifically binding to an antigen (such as antigen A1 or A2), the term "specifically binds to" is meant to refer to

a situation where either said targeting moiety is capable of specifically binding to said antigen, or where it actually binds thereto.

In the context of a T cell engaging domain, an NK cell engaging domain, domain engaging macrophage cells, a monocyte engaging domain, a granulocyte engaging domain, a domain engaging neutrophil granulocytes, or a domain engaging activated neutrophil granulocytes, monocytes and/or macrophages, the term "specifically binding to" an antigen or molecule or "specifically binds to" an antigen or molecule is meant to refer to a situation where either the respective domain is capable of specifically binding to said antigen or molecule, or where it actually binds thereto.

In the context of a functional domain being a domain that "specifically binds to" an antigen, a molecule, a compound, a carrier molecule or an affinity tag, the term "specifically binds to" is meant to refer to a situation where either said functional domain is capable of specifically binding to said antigen, molecule, compound, carrier molecule or affinity tag, or where it actually binds thereto.

In the context of a toxin, fluorophore, antigen, carrier molecule or affinity tag being "specifically bound by" a functional domain, this is meant to refer to a situation where either said functional domain is capable of specifically binding to said toxin, fluorophore, antigen, carrier molecule or affinity tag, or where it actually binds thereto.

As used in the present application, a molecule or antigen is "specific for a certain cell type or cell lineage" if it is expressed by said cell type/cells of said cell lineage, but not (or only to a negligible extent) by other cell types or cells of other cell lineage. In some embodiments, a molecule or antigen is "specific for a certain cell type or cell lineage" if it is expressed by said cell type/cells of said cell lineage, and not more than a few other cell types or cells of other cell lineage besides said cell type/cells of said cell lineage express said antigen as well, while most other cell types or cells of other cell lineage besides said cell type/cells of said cell lineage do not express said antigen (or only to a negligible extent). The term "specific for a certain cell type or cell lineage" may also mean that said molecule or antigen is expressed by said cell type/cells of said cell lineage at a higher rate or at a higher proportion or amount than by other cell types/cells of other cell lineages, in the sense that there may be a small but detectable expression of said molecule also in other cell types/cells of other cell lineages. The term "marker", as used herein in the context of a marker for a certain cell type or cell lineage, can refer to a molecule or antigen that is specific for a cell type or cells of a cell lineage, respectively, as described above.

As used herein, the term "aptamer" refers to a small compound composed of oligonucleic acid (such as RNA or DNA) or peptidic or non-peptidic molecule that binds to a specific target molecule with high affinity.

As used herein, the term "carrier molecule" refers to a molecule or part of a molecule that is not recognized as foreign by the immune system of a patient to whom the set of polypeptides according to the invention is administered or that causes no or only a weak immune reaction by a patient to whom the set of polypeptides according to the invention is administered. Preferably, such a "carrier molecule" is being bound by or capable of being bound by another molecule, such as an antibody. In some embodiments, a "carrier molecule" is a molecule or part of a molecule that In certain embodiments, the carrier molecule is attached covalently or non-covalently to a second molecule or part of a second molecule, for example a fluorophore or toxin.

The term "MHC" refers to the Major Histocompatibility Complex, which is a set of genes encoding a group of molecules comprising cell-surface molecules that are required for antigen presentation to T-cells and that are also responsible for rapid graft rejections. In humans, the MHC includes the genes HLA-A, HLA-B, HLA-C, HLA-DP, HLA-HQ, and HLA-DR. In the present application, the term is used to refer to the genes of the Major Histocompatibility Complex as well to the gene products encoded by these genes. The term "HLA" refers to Human Leukocyte Antigens. As used herein, "HLA" is the human form of "MHC".

The term "allelic variant", as used herein, denotes any of two or more alternative forms of a gene occupying the same chromosomal locus. For example, HLA-A1, HLA-A2, and HLA-A3 are three of the allelic variants of HLA-A. The term allelic variant is also used herein to denote a protein encoded by an allelic variant of a gene.

The term "antigen", as used herein, refers to a molecule known to be specifically bound by or capable of being specifically bound by an antibody or the antigen-binding part of an antibody. In its broadest meaning, "antigen A1" refers to an antigen as defined above. In its broadest meaning "antigen A2" refers to an antigen as defined above. The designations "antigen A1" and "antigen A2" have been chosen in order to allow for distinction between "antigen A1" and "antigen A2". An "MHC antigen" is an antigen that is also a molecule belonging to the major histocompatibility complex. MHC antigens include MHC class I

antigens (in humans, the antigens HLA-A, -B, and -C) and MHC class II antigens (in humans, the antigens HLA-DP, -DQ, and -DR). The phrase that a cell "carries an antigen" or "carries an antigen at its cell surface" is meant to refer to a situation where a cell expresses an antigen that is present at the cell surface of said cell and accessible for an antibody from outside said cell. The phrase that a substrate "has an antigen at its surface" is meant to refer to a situation where said antigen is present at the surface of said substrate and accessible for an antibody applied to said substrate.

The term "an antigen that is specific for the malignant state of a cell", as used herein, refers to an antigen that a malignant cell of a certain cell type (such as a malignant B-cell tumour cell) carries at its cell surface, but that a cell of the same cell type that is not malignant (such as a non malignant B-cell) does not (or only to a negligible extent) carry at its cell surface.

The term "an antigen/molecule that is specific for a malignant cell type", as used herein, refers to an antigen/molecule that a malignant cell of a certain cell type (such as malignant B-cell tumour cell) carries at its cell surface, but that a cell of the same cell type that is not malignant (such as a non malignant B-cell) or cells of other cell types (such as T-cells or hepatocytes) do not (or only to a negligible extent) carry at their cell surface. In some embodiments, the term "an antigen/molecule that is specific for a malignant cell type" refers to an antigen/molecule that a malignant cell of a certain cell type (such as malignant B-cell tumour cell) carries at its cell surface, but that a cell of the same cell type that is not malignant (such as a non malignant B-cell) does not (or only to a negligible extent) carry at its cell surface, and that only cells of a few other cell types besides that certain cell type carry at their cell surface, while cells of most other cell types do not (or only to a negligible extent). The term "an antigen/molecule that is specific for a malignant cell type" may also mean that said antigen/molecule is expressed by said malignant cell of a certain cell type at a higher rate or at a higher proportion or amount than by a cell of the same cell type that is not malignant, in the sense that there may be a small but detectable expression of said molecule also in a cell of the same cell type that is not malignant. The term "marker", as used herein in the context of a marker for the malignant state of a certain cell or for a malignant cell type, can refer to a molecule or antigen that is specific for the malignant state of a certain cell or for a malignant cell type, respectively, as described above.

The term "immunoglobulin domain", as used herein, refers to a domain that essentially consists of a globular region of an antibody chain. Immunoglobulin domains are characterized in that they retain the immunoglobulin fold characteristic of antibody

molecules. Immunoglobulins, such as IgG, IgE, or IgM, are composed of a varying number of heavy and light chains. Each heavy and light chain contains a constant region and a variable region. Each light chain variable region (V_L) and each heavy chain variable region (V_H) contains three hypervariable regions, also called "complementarity-determining regions" or "CDRs". The CDRs are primarily responsible for binding of the immunoglobulin to an antigen.

The terms "V_H" or "V_H domain" are used interchangeably and refer to the variable region of an immunoglobulin heavy chain of an antibody. The terms "V_L" or "V_L domain" are used interchangeably and refer to the variable region of an immunoglobulin light chain of an antibody.

The term "immunoglobulin module", as used herein, refers to a molecule, part of a molecule or molecular assembly which comprises one or more, preferably two or more, immunoglobulin domains and which is capable of binding to an antigen. Preferably, an "immunoglobulin module" comprises a linear molecular chain of amino acids that includes the amino acid sequence of one or more, preferably two or more, immunoglobulin domains. Optionally, an "immunoglobulin module" comprises one ore more, preferably two or more, disulfide bonds. Included in the term "immunoglobulin module" are molecules or parts of a molecule that comprise or consist of a "single-chain variant fragment" of an antibody. Included in the term "immunoglobulin module" are also molecules or parts of a molecule that comprise or consist of a V_HH domain of a llama antibody, a camel antibody, or a shark antibody.

The term "immunoglobulin module I1" is used to refer to an immunoglobulin module comprising a V_L domain linked to a V_H domain. Preferably, said V_L domain and said V_H domain of said immunoglobulin module I1 are derived from the same antibody. Preferably, said V_L domain and said V_H domain of said immunoglobulin module I1 form a dimer. Preferably, said dimer is capable of specifically binding to an antigen. Said antigen may be, for example, the antigen A1. In one embodiment, said "immunoglobulin module I1" comprises a "single-chain variant fragment" of an antibody that is capable of specifically binding to an antigen, for example the antigen A1.

The term "immunoglobulin module I2" is used to refer to an immunoglobulin module comprising a V_L domain linked to a V_H domain. Preferably, said V_L domain and said V_H domain of said immunoglobulin module I2 are derived from the same antibody. Preferably, said V_L domain and said V_H domain of said immunoglobulin module I2 form a dimer. Preferably, said dimer is capable of specifically binding to an antigen. Said antigen may be,

for example, the antigen A2. In one embodiment, said "immunoglobulin module I2" comprises a "single-chain variant fragment" of an antibody that is capable of specifically binding to an antigen, for example the antigen A2.
Within a construct of an immunoglobulin module comprising a V_L domain linked to a V_H domain, the V_L domain may be positioned N- or C-terminally of the corresponding V_H domain. The skilled person is able to determine which arrangement of the V_H and V_L domains is more suitable for a specific single-chain variant fragment domain.

The terms "Fv" and "variant fragment", as used herein, refers to a fragment of an antibody that is the minimum antibody fragment which contains a complete antigen recognition and binding site. This region consists of a dimer of one heavy and one light chain variable region in a tight, non-covalent association (V_H-V_L dimer). In this configuration, the V_H and V_L domain together define an antigen binding site with antigen binding specificity on the surface of the V_H-V_L dimer.

The terms "scFv", "single chain Fv", and "single-chain variant fragment" are used interchangeably and are meant to designate an antibody or portion of an antibody in which the variable region of the heavy chain (V_H) and the variable region of the light chain (V_L) of a traditional two chain antibody have been joined to form one chain. Typically, a linker is inserted between the two chains to allow for proper folding and creation of an active binding site.

The term "llama antibody", as used herein, refers to an antibody or part of an antibody derived from llama. The term "camel antibody", as used herein, refers to an antibody or part of an antibody derived from camel. The term "shark antibody", as used herein, refers to an antibody or part of an antibody derived from shark. Llama, camel and shark antibodies have an antigen binding moiety that is built up by one single domain, V_HH, (rather than a V_H and a V_L chain).

The expression "T cell engaging domain", as used herein, is meant to refer to a domain that specifically binds to an antigen that is present on the cell surface of T cells. Preferably, binding of said T cell engaging domain to said antigen activates said T cell. Similarly, the expression "NK cell engaging domain" refers to a domain that specifically binds to an antigen that is present on the cell surface of Natural Killer cells. Preferably, binding of said NK cell engaging domain to said antigen activates said Natural Killer cells. The expression

"domain engaging macrophage cells" refers to a domain that specifically binds to an antigen that is present on the cell surface of macrophage cells. Preferably, binding of said domain engaging macrophage cells to said antigen activates said macrophage cells. The expression "monocyte engaging domain" refers to a domain that specifically binds to an antigen that is present on the cell surface of monocytes. Preferably, binding of said monocyte engaging domain to said antigen activates said monocytes. The expression "granulocyte engaging domain" refers to a domain that specifically binds to an antigen that is present on the cell surface of granulocytes. Preferably, binding of said granulocyte engaging domain to said antigen activates said granuloctyes. The expression "domain engaging neutrophil granulocytes" refers to a domain that specifically binds to an antigen that is present on the cell surface of neutrophil granulocytes. Preferably, binding of said domain engaging neutrophil granulocytes to said antigen activates said neutrophil granuloctyes. The expression "domain engaging activated neutrophil granulocytes, monocytes and/or macrophages" refers to a domain that specifically binds to an antigen that is present on the cell surface of activated neutrophil granulocytes, monocytes and/or macrophages. Preferably, binding of said domain engaging activated neutrophil granulocytes, monocytes and/or macrophages to said antigen activates said monocytes and/or macrophages.

The term "molecule capable of mediating bioluminescence", as used herein, refers to a molecule (or functional part of a molecule) that has an enzymatic activity which in the presence of the appropriate substrate(s) catalyzes a reaction that causes bioluminescence. The term includes luciferases, such as the luciferases of firefly or *Gaussia*.

The term "GFP variant", as used herein, refers to a molecule that has an amino acid sequence derived from the amino acid sequence of green fluorescent protein from *Aequorea victoria* by introducing alterations resulting in greater fluorescence or fluoresce in different colors. The term is meant to include, among others, YFP (yellow fluorescent protein), CFP (cyan fluorescent protein), Venus (Nagai T et al., A variant of yellow fluorescent protein with fast and efficient maturation for cell-biological applications. Nat Biotechnol. 2002 Jan;20(1):87-90), Cerulean (Enhanced CFP with S72A, Y145A and H148D substitutions).
"Enhanced GFP" (and, analogously, "enhanced YFP", "enhanced CFP") refers to a GFP (YFP, CFP) which has been "humanized", as reported in Kain et al. (1995) Biotechniques 19(4):650-55. "Humanized" refers to changes made to the GFP (YFP, CFP) nucleic acid sequence to optimize the codons for expression of the protein in human cells.

The term "bimolecular fluorescence complementation molecule", as used herein, refers to a fluorescent molecule that can be provided as two fragments which by themselves are not fluorescent, but which upon heterodimerization between the two fragments form a dimer that is capable of fluorescence.

The term "therapeutic compound", as used herein, refers to a compound suited for preventing, treating, alleviating or curing a disease or disease state. Preferably, a "therapeutic compound" is a compound that, upon entry into a cell, is capable of causing the death of that cell. In some embodiments, a therapeutic compound can be a chemical or radioactive compound that damages vital cellular structures or interrupts vital cellular processes.

The term "diagnostic compound", as used herein, refers to a compound that can be detected by common detection methods, such as methods used in the clinic or in biochemical or medical diagnostic laboratories, for example a fluorescent compound, a radioactive compound, or a molecule mediating bioluminescence.

The term "progenitor/precursor cells" is meant to refer to immature, undifferentiated or partially differentiated cells that are typically found in post-natal animals/humans and have the potential to differentiate into a specific cell type or into specific cell types. The term "progenitor/precursor cells of a tumour" designates progenitor/precursor cells with altered properties (e.g. regarding their proliferation behaviour or gene expression pattern) that give rise to tumour cells. Examples for such progenitor/precursor cells of a tumour are e.g. leukemic precursor or progenitor cells.

The term "cancer", as used herein, refers to a malignant cell, group of cells, or malignant neoplasia. The term is meant to comprise carcinomas, sarcomas, lymphomas, leukemias, germ cell tumours, and blastomas. A "cancerous cell" is a cell that is part of or derived from a cancer. The term "tumour" is used interchangeably with the term "cancer".

As used herein, the term "haematologic tumour" refers to a cancer of the blood or blood building system (such as bone marrow cells, blood-building cells, and precursor cells of mature blood cells). In some embodiments, the term "haematologic tumour" refers to a haematologic neoplasia. As used herein, the term "non-haematologic tumour" refers to a tumour that is not a haematologic tumour.

The term "a patient who is undergoing allogeneic tissue or cell transplantation", as used

herein, refers to a situation where a patient receives or has received transplanted cells or transplanted tissue that has/have been obtained from another person. A preferred situation as to this aspect is the situation with mismatched HLA antigens. The unit "$\mu g/m^2$", as used herein in the context of an amount of a polypeptide administered, refers to a certain amount of polypeptide per square meter of body surface of the patient to whom said polypeptide is administered (the peptide may be administered by any adequate route of administration, such as by intravenous or subcutaneous injection). For example, the expression "The amount of polypeptide administered is 50 $\mu g/m^2$ per day for the polypeptide P1." is meant to refer to a situation where the amount of polypeptide P1 administered per day is 50 µg per square meter of body surface of the patient to whom the polypeptide P1 is administered. In the case of a patient having a body surface of 2 m^2 this would mean that 100 µg of polypeptide P1 are administered per day.

The present inventors have surprisingly found that with a set of polypeptides according to the invention the above-indicated problems of the prior art can be overcome and the above-described objects can be accomplished. Moreover, the present inventors have surprisingly found that with a set of polypeptides according to the invention, cells with a specific combination of two antigens can be identified and/or eliminated with high specificity and reduced side-effects.

It is one advantage of the combinatorial strategy of the invention that no preformed F units (for example anti-CD3 units) are used. The F1 and CD3 V_H and V_L) do not heterodimerize per se, not even in the presence of an agent which stabilizes their dimerization (for example an antigen capable to bind to the domain F, like for example, CD3, HIS or DIG), and thus do not result in a functional F domain (for example do not stimulate T cells). Exclusively in situations where both complementary constructs P1 and P2 simultaneously bind on the surface of a given cell, the two components F1 and F2 reconstitute the F domain (for example, the CD3 binding site). Thus, function of the F domain (for example T cell activation) takes place precisely where needed but not systemically. Hence, it can be assumed that the combinatorial strategy of the invention has less toxic effects, for example as compared to normal bispecific antibody strategies. This is also evidenced by the appended examples, in particular by the in vivo model for allogeneic transplantation, where HLA-A2 positive mice did not suffer any clinical effects after infusion of HLA-A2 reactive constructs.

In particular, to tag cells that express a predefined antigen signature, two single-chain

polypeptides were designed as parts of the final bipartite (bi-molecular) construct (bi-moleculer/trispecific antibody construct), each composed of an antigen-binding single-chain variable fragment (scFv) and either the variable light (VL) or variable heavy chain (VH) domain of an antibody. When these two hybrid fragments bind their respective antigens on the surface of a single cell, the VL and VH domains interact with each other to reconstitute the original antigen binding site and thus fulfill the desired requirements.

As mentioned, it is one advantage of the set of polypeptides of the invention that binding of both target antigens on the cell surface is requisite for functional heterodimerization. Self-assembly of the two complementary parts and subsequent T cell stimulation after binding of only one arm to its antigen can be ruled out, thus corroborating published data showing that V_H or V_L binding by itself is of low affinity and that V_H/V_L heterodimers tend to dissociate rapidly in the absence of antigen (Colman, 1987, *Nature* 326, 358-363; Amit, 1986, *Science* 233, 747-753; Law, 2002, Int Immunol 14, 389-400; Ueda, 1996, Nat Biotechnol 14, 1714-1718).

In contrast to the homo- or hetero-dimerization domains well known in the art (leucine-zipper, Fc-domains, knob in the hole etc), VH and HL interactions are of low affinity. However, it has been shown that VH/VL interaction can be stabilized after binding to the specific antigen. Without being bound by theory, VH/VL interaction in accordance with this invention takes place only in situations after both fragments have previously bound to their cognate target antigens, for example on the surface of a target cell. Also without being bound by theory, after simultaneous on-target binding, the constructs are brought into close proximity so that they can form a trimeric complex with the antigen. The thus on-target complemented trispecific heterodimer of the invention is functional with respect to the function of the domain F, for example, engages and stimulates T cells for tumor cell destruction if anti CD3 is reconstituted.

Beside one advantage of the constructs of the invention P1 and P2, e.g. the combinatorial nature of the immune response elicited, it was surprisingly found in the context of this invention that the bi-molecular construct with the disrupted F domain, for example scFv-anti CD3, displays no off target effects.

The set of polypeptides according to this invention, in particular the polypeptides P1 and P2 comprised therein, have the further advantage to be more stable and/ or have an improved

shelf life (in particular at 4°C) as compared to conventional bispecific constructs like BiTE constructs. These conventional bispecific constructs tend to aggregate (in particular at 4°C).

It is envisaged that the polypeptides of this invention P1 and P2, more particular of F1 and F2 as comprised therein, more particular of the V_H and V_L which may be comprised therein, due to their hydrophobic interface, are capable to bind albumin. This leads to an improved retention time; i.e. longer bioavailability in vivo but also in vitro, like, for example, in serum or blood samples.

The set of polypeptides according to the present invention comprises a first polypeptide P1 and a second polypeptide P2. The first polypeptide P1 comprises a first targeting moiety T1 (which is capable of specifically binding to an antigen A1) fused to a first fragment F1 of a functional domain F (see Figure 1A, top). The second polypeptide P2 comprises a second targeting moiety T2 (which is capable of specifically binding to an antigen A2) linked to a second fragment F2 of the functional domain F (see Figure 1A, bottom). Importantly, the fragments F1 resp. F2 of the functional domain are non-toxic by their own and unable to exert any biological function unless there is partnering between the two polypeptides P1 and P2. When both polypeptides P1 and P2 simultaneously bind to their antigens on the surface of a single cell that expresses both antigens A1 and A2, the fragments F1 and F2 of the functional domain F are brought together in close proximity, they hetero-dimerize and thus complement the desired biological function (see Figure 1B). On the other hand, a cell that expresses either only antigen A1 (Figure 1C) or only antigen A2 (Figure 1D) or none of the antigens does not cause complementation of the biological function. Thus, the biological function is achieved with high specificity only in the presence of cells having both antigens A1 and A2 at their cell surface upon simultaneous binding of both polypeptides P1 and P2 to such a cell. Depending on the nature of the functional domain F, different objects, such as specific identification/detection or elimination of cells that express both antigens A1 and A2, can be accomplished.

In one exemplary embodiment, this inventive principle is applied for the specific elimination of tumour cells:

Novel histopathological and flow cytometry analyses have revealed that tumour cells can be detected and distinguished from their non-transformed counterparts not by single surface markers but by the expression of aberrant antigen combinations/profiles, as is known for

haematopoietic neoplasias and cancer and cancer stem cells of various other provenience. Thus, while a single antigen may not be sufficient to specifically identify a certain tumour cell, a specific combination of two antigens may allow discriminating the tumour cell from any other type of cell.

For example, the set of polypeptides according to the invention may be used to specifically eliminate cancer cells characterized by the simultaneous expression of the antigens CD33 and CD19 at their cell surface. This combination of antigens is found on certain types of acute leukemia cells and distinguishes these cells from any other cells (such as non-malignant cells), which may carry either CD33 or CD19 at their cell surface, but do not carry both CD33 and CD19 at their cell surface (Ossenkoppele et al., Review of the relevance of aberrant antigen expression by flow cytometry in myeloid neoplasms. Br J Haematol 2011, 153(4):421-36).

To specifically eliminate these leukemic cells carrying both CD33 and CD19 at their cell surface, the first targeting moiety T1 of the first polypeptide P1 may be a single chain variable Fragment (scFv) specific for CD33. As fragment F1 of the functional domain F, the light chain variable domain V_L of an anti CD3 antibody may be chosen. The second targeting moiety T2 of the second polypeptide P2 may be a scFv specific for CD19. As the fragment F2 of the functional domain F the heavy chain variable domain V_H of that anti CD3 antibody may be chosen. The light chain variable domain V_L and the heavy chain variable domain V_H of the anti CD3 antibody are each non-toxic by their own. They are also unable to exert their biological function (i.e. to effectively bind the CD3 antigen) unless there is partnering between the polypeptides P1 and P2.

In the presence of a leukemic cell having both CD33 and CD19 at its cell surface, both polypeptides P1 and P2 simultaneously bind to that cell. As a consequence, the fragments F1 and F2 of the functional group F (i.e. the heavy and light chain of the Fv anti CD3 variable domain of that anti-CD3 antibody) are brought together in close proximity, they hetero-dimerize and thus complement the desired biological function, enabling the dimer of P1 and P2 to specifically bind to CD3.

CD3 is a cell surface molecule that is present on the surface of T cells. The molecule is part of the T cell signaling complex, and cross- linking of CD3 molecules on the surface of a T cell after binding of a CD3-specific antibody leads to activation of the T cell. By engaging

CD3 antigens on the surface of T cells, heterodimers of polypeptides P1 and P2 are capable of recruiting T cells and activating them. As a result, typical effector mechanisms of a cytotoxic T cell response are elicited, leading to cell lysis: release of lytic granules containing the cytotoxic proteins perforin, granzymes, and granulysin. Perforin forms pores into the membrane of the target cell through which the granzymes can enter and induce apoptosis. These effects lead to specific destruction of leukemic cells that carry both CD33 and the CD19 antigen at their cell surface.

Other cells than the leukemic cells do not have both the CD33 and CD19 antigen at their cell surface. Therefore, they cannot recruit both polypeptides P1 and P2, and no complementation of the CD3 binding capability and engagement of CD3 positive T lymphocytes is achieved. Consequently, other cells besides the leukemic cells are unaffected, and destruction of the malignant cells with exquisite specificity is achieved.

This is in stark contrast to conventional bispecific antibodies. A conventional bispecific construct that engages T cells and has specificity for cells expressing CD33 would mediate the destruction of all CD33 positive cells. Since CD33 is myeloid lineage marker which is expressed on many myeloid cells and myeloid progenitor cells, the destruction of these cells would result in long lasting aplasia and probably death of the patient. A conventional bispecific construct that engages T cells and has specificity for CD19 positive cells would lead to the elimination of all cells carrying the CD19 antigen at their cell surface. CD19 is expressed on a significant subset of B-lymphocytes. Destruction of these cells would lead to a severe defect of the immune system. Thus, besides eliminating leukemic cells that simultaneously express CD33 and CD19 on the surface, the application of conventional bispecific antibodies with specificity for CD33 and CD19 would lead to elimination of myeloid cells and a substantial subset of B-lymphocytes.

Thus, while conventional bispecific antibodies recognize only one antigen on the cell to be eliminated, effector activation according to the present invention requires the simultaneous recognition of two specific antigens on the surface of the cell to be identified/eliminated. In consequence, the present invention achieves significantly improved specificity and reduced side effects.

It is clear to a person of skill in the art that, within the principle of the present invention, diverse variations to the exemplary embodiment described above are possible.

For example, the approach described in the above exemplary embodiment can easily be adapted for the identification/elimination of other types of tumour cells besides CD33 and CD19 positive acute leukemia cells simply by choosing appropriate targeting moieties T1 and T2 that specifically bind to antigens A1 and A2, respectively, that are present simultaneously on the cells to be identified/eliminated, but not present simultaneously on other cell types. As quoted above, many if not all cancer cells (but also progenitor/precursor cells of cancer cells) express a number of cell surface molecules which per se are widely expressed on normal tissues, but are indicative for the malignant phenotype if expressed in a non-physiological combination. For example, CD34 is a marker for haematopoietic stem cells and CD7 can be detected on a subset of lymphoid cells. The combination of CD34 and CD7, however, is strongly associated with malignancy, and aberrant co-expression of the two antigens can be detected on a substantial proportion of acute myelogenous leukemias (Ossenkoppele et al., Review of the relevance of aberrant antigen expression by flow cytometry in myeloid neoplasms. Br J Haematol 2011, 153(4):421-36.). Similarly, aberrant co-expression of CD44 and CD117 has been described for ovarian cancer stem cells, CD44 and CD24 for pancreas cancer initiating cells und the combination of EpCAM and CD44 in colon and breast cancer stem cells (Natasha Y. Frank, Tobias Schatton, Markus H. Frank; The therapeutic promise of the cancer stem cell concept. J Clin Invest. 2010; 120:41–50). Expression of CD24 and CD29, as well as CD24 and CD49f has been found to be specific for breast carcinoma (Vassilopoulos A et al. Identification and characterization of cancer initiating cells from BRCA1 related mammary tumours using markers for normal mammary stem cells. *Int J Biol Sci* 2008; 4:133-142). Moreover, combinations with highly expressed antigen levels are indicative for a number of malignancies, like CD38 and CD138 for myeloma.

In addition to the cancer-specific antigen combinations listed above and those known from the scientific literature, additional combinations of two antigens that are expressed simultaneously on specific tumour cells but not on other cells can be derived in a straight-forward manner by the person of skill in the art.

Firstly, the skilled person may arrive at an antigen combination that is specific for a certain cancer by combining an antigen that is specific for the malignant state of the respective cell type with an appropriate cell type marker or cell lineage marker. For example, carbonic anhydrase IX is a marker strongly associated with renal cell carcinoma and metastases of

renal cell carcinoma and thus represents a marker for the malignant state of renal cells. This membrane located marker, however, is also expressed on normal cells of the intestinal tract. By selecting as second antigen a renal lineage marker like aquaporin, the resulting combination of two antigens is specific for renal cell carcinoma cells and cells resulting from metastasis of renal cell carcinoma, while neither non-malignant kidney cells (which do not express carbonic anhydrase IX) nor cells from the intestinal tract (which do not express aquaporins) are characterized by the selected pair of antigens.

Detailed information on markers for the malignant state of various cell types and on markers for numerous cell types or cell lineages is available from the literature and web-based resources (see below for details) or can be obtained by straight-forward experimentation (see below).

Examples for markers for the malignant state of a cell include: E-cadherin for epithelial cells and ductal-type breast carcinoma cells; Ca-125 for Epitheloid malignancies and ovary cancer cells, adenocarcinoma cells and breast cancer cells; Her-2/neu for breast cancer cells; gross cystic disease fluid protein (BRST-2 protein) for breast cancer cells; BCA-225 (breast carcinoma associated glycoprotein) for lung and breast cancer cells; CA 19-9 (carbohydrate antigen 19-9) for pancreas, bile duct and intestinal tract cancer cells; CEA for colorectal cancer cells; CD117 (c-kit) for gist (gastrointestinal stromal tumour) cells (and myeloid and mast cells); CD30 for Reed-Sternberg cells (and Ki-1 activated T-cells and B-cells); Epithelial antigen (BER-EP4), Epithelial membrane antigen, and Epithelial Related Antigen (MOC-31) for epithelial cancer cells; Epidermal growth factor receptor (HER1) for cells of various cancers; Platelet derived growth factor receptor (PDGFR) alpha for cells of various cancers; Melanoma associated marker/Mart 1/Melan-A for melanoma cells; CD133 for cancer stem cell populations and others; TAG 72 (tumour associated gp 72) for adenocarcinoma cells.

Further examples for markers for a malignant state of a cell/cells include: EpCAM, CD19, HER-2, HER-3, HER-4, PSMA, MUC-1 (mucin), MUC2, MUC3, MUC4, MUC5AC, MUC5B, MUC7, Lewis-Y, CD20, CD33, CD44v6, Wue-1, Plasma Cell Antigen, (membrane-bound) IgE, Melanoma Chondroitin Sulfate Proteoglycan (MCSP), STEAP, mesothelin, Prostate Stem Cell Antigen (PSCA), sTn (sialylated Tn antigen), FAP (fibroblast activation antigen), EGFRvIII, Igα, Igβ, MT-MMPs, Cora antigen, EphA2, L6 and CO-29, CCR5, βHCG, ganglioside GD3, 9-O-Acetyl-GD3, GM2, Globo H, fucosyl GM1, Poly SA,

GD2, Carboanhydrase IX (MN/CA IX), Sonic Hedgehog (Shh), CCR8, TNF-alpha precursor, A33 Antigen, Ly-6, desmoglein 4, E-cadherin neoepitope, Fetal Acetylcholine Receptor, CD25, Muellerian inhibitor Substance (MIS) Receptor type II, endosialin, SAS, CD63, TF-antigen, CD7, CD22, Igα(CD79a), Igβ (CD79b), G250, gp100, F19-antigen and EphA2.

Examples for antigens that are specific for a certain cell type/cell lineage or for a few cell types/cell lineages (cell type markers/cell lineage markers) include: CD45 for hematopoietic cells; CD34 for endothelial cells, stem cells, and stromal cells; CD33 for myeloid cells; CD138 for plasma cells and a subset of epithelial cells; CD15 for epithelial, myeloid, and Reed-Sternberg cells; CD1a for cortical thymocytes and Langerhans cells; CD2 for thymic cells, T-cells, and Natural Killer (NK) cells; CD3 for T-cells; CD4 for helper T-cells; CD5 for T-cells, a subset of B-cells, and thymic carcinoma cells; CD8 for cytotoxic T-cells; CD20 for B-cells; CD23 for activated B-cells; CD31 for endothelial cells; CD43 for T-cells, myeloid cells, a subset of B-cells, histiocytes, and plasma cells; CD56 for NK cells; CD57 for neuroendocrine cells, and NK cells; CD68 for macrophages; CD79a for B-cells and plasma cells; CD146 for the endothelial cell lineage; surfactant proteins for lung cells; synaptophysin, CD56 or CD57 for neuroendocrine cells; nicotinic acetylcholine receptor or muscle-specific kinase (MUSK) for muscle cells; voltage-gated calcium channel (P/Q-type) or voltage-gated potassium channel (VGKC) or N-methyl-D-aspartate receptor (NMDA) for muscle cells and neurons; TSH (thyroid stimulating hormone) receptor for thyreoid gland; amphiphysin for muscle cells; HepPar-1 for hepatocytes; ganglioside GQ1B, GD3 or GM1 for neuronal cells; and glycophorin-A for cells of the erythropoietic cell lineage.

It should be noted that there are situations where it may be advantageous to rely for the purposes of the present invention on an antigen with a less than perfect specificity for the cell type or cell lineage of interest. For example in situations where no antigen is known that is found exclusively on the cell type/cell lineage of interest and not on any other cell types/lineages or in situations where it is not possible to confirm the exclusive specificity of an antigen, also antigens that are present on one or more other cell types/cell lineages besides the cell type/cell lineage of interest may be considered. Similar consideration apply for markers for the malignant state of a cell, or even for the specificity of the combination of two antigens. Thus, there are for example situations where for the purposes of the present invention a combination of two antigens is selected that is specific not only for the cells of

interest, but also for one or more (a few) other cell types/cell lineages/kinds of malignant cells.

Secondly, the skilled person may arrive at an antigen combination that is specific for a certain cancer by straightforward experimentation. This may comprise the steps of (1) determining the surface antigens on the tumour cells to be eliminated and (2) identifying among these tumour cell surface antigens two antigens that are not present simultaneously on other cell types (or, in some embodiments, present on only a few other cell types).

Often, experimentation may not be necessary to determine the surface antigens on tumour cells to be eliminated, because such information may already be available for the respective type of cancer from the printed literature (see, e.g. David J. Dabbs, Diagnostic immunohistochemistry, Churchill Livingstone, 3rd edition (2010); or F Lin and J Prichard, Handbook of Practical Immunohistochemistry: Frequently Asked Questions, Springer, New York, 1st edition (2011)). Even more extensive information is available through web-based resources. For example, the Cancer Genome Anatomy Project (CGAP) of the U.S. National Cancer Institute (NCI) has systematically determined the gene expression profiles of various normal, precancer, and cancer cells (Strausberg RL. The Cancer Genome Anatomy Project: building a new information and technology platform for cancer research. In: Molecular Pathology of Early Cancer, 1999, (Srivastava, S., Henson, D.E., Gazdar, A., eds. IOS Press), pp. 365-370). The resources generated by the CGAP initiative are freely available (http://cgap.nci.nih.gov/) and include access to all CGAP data and the necessary analysis tools. Similarly, the Cancer Genome Characterization Initiative (CGCI) of the National Cancer Institute focuses on tools for characterizing the genomic changes involved in different tumours, for example genomic characterization methods including exome and transcriptome analysis using second generation sequencing. The data generated by CGCI is available through a publicly accessible database (http://cgap.nci.nih.gov/cgci.html). Thus, in many cases information about the presence or absence of various known cell surface proteins on the tumour cells of interest can be derived by simply checking these publicly accessible databases. If desired, this information may then be verified in a second step by immunocytochemical/immunohistochemical analysis of tumour cells/tissue according to the methods described below.

If there is no information available on the proteins expressed by the tumour cells/tissue of interest, the skilled person can carry out a characterization of the antigens on the tumour

cells/tissue by immunocytochemical/immunohistochemical methods with a panel of antibodies (see, e.g., "Handbook of Practical Immunohistochemistry: Frequently Asked Questions" by F Lin and J Prichard, Springer New York, 1st edition (2011); or "Using Antibodies: A Laboratory Manual" by E Harlow and D Lane, Cold Spring Harbor Laboratory Press (1998)). In brief, a histological preparation or cells isolated from the tumour are incubated with a first antibody directed at a potential surface antigen and, after a washing step, incubation of a second antibody directed against the Fc domain of the first antibody. This second antibody is labelled with a fluorophore or an enzyme like HRP (horse radish peroxidase), in order to visualize expression of the targeted antigen. Panels of antibodies that can be used for high throughput antigen profiling purposes of cell surface antigens are commercially available from numerous manufacturers.

In addition, tools specifically dedicated to high throughput proteomic cell characterization to identify and analyze cell surface protein expression are commercially available, such as the FACS (Fluorescence-activated cell sorting)-based high throughput array technology BD FACS™ CAP (Combinational Antibody Profile) of Becton, Dickinson & Company.

The immunocytochemical/immunohistochemical/proteomic analysis described above may be preceded (or, in some cases, replaced) by genome-wide gene expression profiling of tumour cells or by mass spectrometric analysis of the proteins expressed by the tumour cells/tissue of interest. For example, genome-wide gene expression profiling of tumour cells can be carried out to check for the expression of various cell surface molecules, and the presence of such antigens on the cell surface of the tumour cells may then be confirmed through antibody-based staining methods as described above.

Further information about approaches to characterize the surface antigens of (cancer) cells is available in the relevant scientific literature (e.g. Zhou J, Belov L, Huang PY, Shin JS, Solomon MJ, Chapuis PH, Bokey L, Chan C, Clarke C, Clarke SJ, Christopherson RI. Surface antigen profiling of colorectal cancer using antibody microarrays with fluorescence multiplexing. J Immunol Methods. 2010;355:40-51; or Carter P, Smith L, Ryan M. Identification and validation of cell surface antigens for antibody targeting in oncology. Endocr Relat Cancer. 2004;11:659-87).

In a next step, the skilled person may identify among the cell surface antigens of the tumour cells a combination of two antigens which is not expressed simultaneously on other cell types.

Often, already the literature or publicly available databases may provide detailed information about the presence or absence of antigens from other cell types:

The expression of various cell surface molecules on diverse cell types has been studied systematically by researchers in the past decades by immunophenotyping and gene expression profiling of almost any cell type of the body. For example, detailed information on the expression of more than 360 "cluster of differentiation" antigens (or CD antigens) is available in print (e.g. "Leukocyte and Stromal Cell Molecules: The CD Markers" by Zola H, Swart B, Nicholson I, and Voss E; John Wiley & Sons, 1st ed. (2007)) and in online depositories (e.g. www.hcdm.org/MoleculeInformation/tabid/54/Default.aspx), and includes information on tissue distribution and expression levels of antigens, as well as information about antigen reactive antibodies and the epitopes these antibodies bind to.

Moreover, there are publicly available databases which provide access to a large amount of genomic data generated by the scientific community. For example, the Gene Expression Omnibus (GEO) platform of the National Center for Biotechnology Information (NCBI) of the United States (Barrett T et al., NCBI GEO: archive for functional genomics data sets--10 years on. Nucleic Acids Res. 2011;39(Database issue):D1005-10) archives and gives access to an enormous collection of microarray, next-generation sequencing, and other forms of high-throughput functional genomic data, and further provides web-based interfaces and applications for easy access to this information (http://www.ncbi.nlm.nih.gov/geo/).

Once a pair of two antigens has been identified through these resources that appears to be absent from other cell types besides the tumour cells of interest, a person skilled in the art can easily validate the suitability of the antigen combination for further development of P1 and P2-polypeptide constructs. Such validation that the identified combination of two antigens is indeed not expressed simultaneously on other cell types besides the tumour cells can be carried out by immunohistochemical/immunocytochemical analysis of a (optimally large) collection of assorted cell types and/or tissues with antibodies against the two antigens. Cells and tissues of any kind can be obtained from ATCC (American Type Culture Collection), from pathology departments and from tissue banks associated with universities and research institutions. A suitable antigen combination is defined as a pair of antibodies that stains exclusively the tumour cells, but not healthy tissues or healthy cells (i.e. both antibodies of the pair stain the tumour cells, but no other tissues/cells are stained by both antibodies).

It should be noted that, while in many situations the highest degree of specificity (preferably absolute specificity) is of course desirable, there are situations where a lower degree of specificity is acceptable. For example, if the set of polypeptides is used for diagnostic purposes, some degree of crossreactivity with other cell types or tissues may be acceptable (especially in the case of solid tumours, since the additional positional information helps to distinguish tumour cells from crossreacting cells). Moreover, if the set of polypeptides is used for therapeutic purposes, some degree of crossreactivity with other cell types or tissues may also be acceptable, depending on the severity the disease in a treated patient and on the cell types/tissues affected by the crossreactivity. Other situations where a lower degree of specificity may be acceptable may arise in the context of a transplantation setting (see below).

In cases where no hint about a suitable antigen combination can be derived from the literature or public databases, the presence/absence of the cell surface antigens of the tumour cells from other cell types can be checked by straightforward experimentation. To this end, a variety of cell types and/or tissues obtainable from the sources indicated above may be subjected to proteomic cell characterization, immunocytochemical/immunohistochemical analysis and/or gene expression profiling. (It should be noted that such analysis of non-tumour cells/tissues has to be carried out only once in order to obtain data that can be used for the design of various constructs according to the invention that may be adapted to diverse different therapeutic or diagnostic situations.) Upon comparison of the obtained results with the information about cell surface antigens of the tumour cells of interest, a combination of two antigens that is not present on any other cells besides the tumour cells of interest can be easily identified.

A similar systematic approach to identify a pair of two antigens that is specific for tumour cells is also described in a recent publication by Balagurunathan, which relies on genome-wide gene expression profiling followed by immunohistochemistry (Yoganand Balagurunathan, Gene expression profiling-based identification of cell-surface targets for developing multimeric ligands in pancreatic cancer. Mol Cancer Ther 2008;7. 3071-3080). Using DNA microarrays, the authors of that manuscript generated databases of mRNA gene expression profiles for a substantial number of pancreatic cancer specimens and normal tissue samples. The expression data for genes encoding cell-surface molecules were analyzed by a multivariate rule-based computational approach in order to identify gene combinations

that are preferentially expressed on tumour cells but not in normal tissues. Aberrant co-expression of antigens constituting a tumour-specific antigen combination was then confirmed using standard immunohistochemistry techniques on pancreatic tumour tissue and normal tissue microarrays.

Having identified and validated such a combination of antigens that is specific for the tumour cells of interest, the constructs of polypeptide P1 and polypeptide P2 can be engineered by standard protein engineering techniques and methods of molecular biology (see, e.g. G Howard and M Kaser, Making and Using Antibodies: A Practical Handbook, CRC Press, 1st edition (2006); Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York (2001)).

For many cell surface molecules, specific monoclonal antibodies are characterized and therefore readily available. Thus, in many cases the skilled person may have access to hybridoma cells of monoclonal antibodies that are specific for the antigens of the identified combination of antigens. Having the option to choose from a panel of antibodies specific for a given antigen, a person skilled in the art may choose a reactive antibody which binds an epitope close to the membrane, in order to minimize the distance of the antigen expressing cell from the effector cell (Bluemel C, Hausmann S, Fluhr P, Sriskandarajah M, Stallcup WB, Baeuerle PA, Kufer P. Epitope distance to the target cell membrane and antigen size determine the potency of T cell-mediated lysis by BiTE antibodies specific for a large melanoma surface antigen. Cancer Immunol Immunother. 2010 Aug;59(8):1197-209). If no such antibody is available against one or both antigens of the identified combination of antigens, monoclonal antibodies against the antigens can be generated by standard techniques (e.g. G Howard and M Kaser, Making and Using Antibodies: A Practical Handbook, CRC Press, 1st edition (2006)). Moreover, various companies offer full services for the generation of custom-made monoclonal antibodies and hybridoma cells.

DNA or mRNA coding for the variable domains of the monoclonal antibodies of interest can be obtained from hybridomas by PCR amplification or cloning (Orlandi R, Gussow PT, Jones: Cloning immunoglobulin variable domains for expression by the polymerase chain reaction. Proc Natl Acad Sci U S A 1989, 86(10):3833-3837; Wang Z, Raifu M, Howard M, Smith L, Hansen D, Goldsby R, Ratner D: Universal PCR amplification of mouse immunoglobulin gene variable regions: the design of degenerate primers and an assessment of the effect of DNA polymerase 3' to 5'exonuclease activity. J Immunol Methods 2000,

233(1–2):167-177; Essono S, Frobert Y, Grassi J, Cremino C, Boquet D: A general method allowing the design of oligonucleotide primers to amplify the variable regions from immunoglobulin cDNA. J Immunol Methods 2003, 279:251-266; G Howard and M Kaser, Making and Using Antibodies: A Practical Handbook, CRC Press, 1st edition (2006)) or from already established vectors comprising the DNA sequence of the variable fragment of the respective antibody. Often, the sequence can be extracted from public databases, where many sequences are deposited, and then the construct may even be generated by gene synthesis as it is offered by various commercial service providers (e.g. Creative Biolabs, Shirley, USA).

To form the construct of polypeptide P1, the sequence coding for the variable fragment Fv of an antibody specific for the first antigen of the identified pair of antigens (or, optionally, the sequence of a single chain variable fragment derived from that sequence) is used for the first targeting moiety (T1) and linked via a suitable linker (coding, e.g., for less than 12 aa) to a sequence coding for the first fragment F1 of a functional domain (e.g. the V_L domain of an anti CD3 antibody). Likewise, to form the construct of polypeptide P2 the sequence coding for the variable fragment Fv of an antibody specific for the second antigen of the identified pair of antigens (or, optionally, the sequence of a single chain variable fragment derived from that sequence) is used for the second targeting moiety (T2) and linked via a suitable linker to a sequence coding for the second fragment F2 of that functional domain (e.g. the V_H domain of an anti CD3 antibody).

For any construct of a polypeptide P1 or P2 according to the invention, modifications to the construct or to the sequences used for forming the construct are considered in order to adapt the construct to specific needs. For example, a construct can be modified in a way that reduces or abolishes its immunogenicity in humans. In case a sequence is derived from a non-human parent antibody, such as a murine antibody, modifications to the sequence can be carried out that result in a reduced immunogenicity in humans while retaining or substantially retaining the antigen-binding properties of the parent antibody (known to the skilled person as "humanizing" an antibody/construct).

Various modifications of the above-described procedure and adaptions in order to accommodate the embodiments and variations described in this application are evident to the person of skill in the art.

In addition to variations with respect to the antigens that the targeting moieties T1 and T2 specifically bind to, various other modifications are possible. For example, instead of single chain variant fragments (scFv) as targeting moiety T1 and/or T2 other types of monovalent antibodies or antibody-like structures can be employed. For example, an antibody/antibody-like structure derived from a llama, camel or shark antibody can be used. Since llama, camel and shark antibodies have an antigen binding moiety that is built up by one single domain (rather than a V_H and a V_L chain), the resulting polypeptide P1 or P2 is much smaller and may thus better penetrate into tumour tissues.

Furthermore, since many tumour-relevant antigens are cell surface-bound receptors, the single chain Fv of targeting moiety T1 and/or T2 can be replaced by the natural or artificial ligand of such a cell surface-bound receptor. Like antibodies, these natural or artificial ligands confer excellent specificity towards the target receptor. Alternatively, the targeting moiety T1 and/or T2 can be an aptamer.

Moreover, in order to enhance binding affinity of a targeting moiety towards the antigen, the targeting moiety can be multimerized and/or altered by glycosylation or other types of posttranslational or chemical modification or be optimized through site directed mutagenesis or a phage display selection process.

Moreover, the fragments F1 and F2 (i.e. the V_L and V_H fragments of anti CD3 Fv in the above-described exemplary embodiment) can be replaced by fragments of a different functional domain F, resulting in a different biological effect upon complementation of the two fragments. By using fragments of anti CD56, anti CD1a, or anti CD16a, natural killer cells can be recruited and activated. By using fragments of anti CD16, natural killer cells, neutrophil polymorphonuclear leukocytes, monocytes and macrophages can be recruited and activated. By using fragments of anti CD32a, anti CD32b, anti CD89, anti CD16a, or anti CD64, macrophages can be recruited and activated. By using fragments of anti CD32a, anti CD32b, anti CD64, or anti CD89, monocytes can be recruited and activated. By using fragments of anti CD16b, anti CD89, anti CD32a, anti CD32b, or anti CD64, granulocytes can be recruited and activated. Moreover, alternatively to anti CD3, T cells can also be recruited and activated by using fragments of anti CD2, anti CD5, anti CD28, or anti TCR (T cell receptor). Further information or additional options regarding the recruitment and activation of effector cells through antibody binding are available from the published literature, e.g. "Bispecific Antibodies" by Roland E. Kontermann (editor), Springer Berlin

Heidelberg; 1st Edition. (2011).

An additional option is to use a set of polypeptides P1 and P2 with fragments F1 and F2 of a functional domain F that binds an antigen on an effector cell upon complementation of the two fragments, but wherein binding to this antigen of the effector cell does not cause activation of said effector cell. This set of polypeptides ("first set of polypeptides") is then used (e.g. administered to a patient) in combination with a second set of polypeptides with fragments of a functional domain F that upon complementation binds to a second, different antigen on the same effector cell, but wherein again binding to this antigen of the effector cell does not cause activation of the effector cell. The antigens to which the first and the second sets of polypeptides bind are chosen in a way that, while binding of only one of the two antigens on the effector cells does not result in activation of the effector cell, binding of both antigens on the effector cell simultaneously leads to activation of the effector cell. This has the advantages that (1) antigens on effector cells can be used that do not function individually, but require costimulation of a second antigen, and (2) the number of different antigens that dictates the specificity with which a certain cell (such as a cancer cell) is differentiated from other cells can be increased from two (if the first and second set of polypeptides have the same targeting moieties T1 and T2, respectively) to up to four different antigens (if the first and second set of polypeptides have no targeting moiety in common).

Similar effects may be achieved with two sets of polypeptides with different targeting moieties, but the same functional domain: These sets of polypeptides are designed to have a functional domain directed against an effector cell antigen that normally allows each set of polypeptides by itself to activate the effector cell. However, both sets of polypeptides are used in a concentration that is just too low to cause efficient effector cell activation. If both sets of polypeptides are present simultaneously (e.g. upon simultaneous administration to a patient) each set of polypeptides by itself is not capable of activating the effector cell (due to its low concentration), while the combination of both sets of polypeptides is (because the effects of the two sets of polypeptides act synergistically and thus the sum of the effects caused by the two sets of polypeptides is sufficient to activate the effector cell).

As another alternative to recruitment/activation of effector cells, a "pretargeting" approach can be pursued, as it is well established for bispecific antibody constructs (Cancer Imaging and Therapy with Bispecific Antibody Pretargeting. Goldenberg DM, Chatal JF, Barbet J,

Boerman O, Sharkey RM. Update Cancer Ther. 2007 Mar;2(1):19-31). To this end, F1 and F2 are substituted by V_H and V_L fragments of an antibody specific for an antigen, a carrier molecule (i.e. a molecule/part of a molecule that is not recognized as foreign by the immune system of the patient to whom said set of polypeptides is administered or a molecule that causes no or only a weak immune reaction by a patient to whom it is administered) or an affinity tag. Subsequently (or simultaneously) to administering the polypeptides P1 and P2, a therapeutic or diagnostic compound coupled to said antigen, carrier molecule or affinity tag is administered. Only cells which carry both the antigens A1 and A2 at their surface are bound by both polypeptide P1 and polypeptide P2. Consequently, only at these cells functional complementation leads to generation of a binding site capable of recruiting the therapeutic or diagnostic compound through said antigen, carrier molecule or affinity tag. This approach allows exclusive addressing of target cells combined with the possibility of precise administration and dosing of therapeutic compounds like toxins or radioactive substances or diagnostic compounds, while cells that do not express the antigens or do express only one of the antigens are not affected.

A suitable carrier molecule may for example be a peptide or a carbohydrate molecule. Preferably, the carrier molecule may be gelatine, dextrane, or hydroxyethyl starch, which are common plasma expanders that are metabolically inert, remain in the blood and are, if they are small enough, renally eliminated. Alternatively, the carrier molecule may be inulin, a metabolically inert molecule that is used routinely in the clinic for determination of glomerular clearance (and, in addition, antibodies exist that specifically recognize inulin).
A suitable affinity tag may be, for example, a Flag-tag, a myc-tag, a glutathione-S-transferase(GST)-tag, a hemagglutinin(HA)-Tag, a polyhistidine(His)-tag, or a maltose binding protein(MBP)-tag, a digoxigenin(DIG)-tag.

The therapeutic compound coupled to the antigen, carrier molecule or affinity tag may for example be a radioactive compound or a toxin.
Suitable radioactive compounds are for example compounds comprising ^{90}Y, ^{177}Lu, ^{131}I, ^{32}P, ^{10}B, or ^{213}Bi. Recruitment of the antigen, carrier molecule or affinity tag linked to the radioactive compound to cells that express both the first and the second antigen leads to accumulation of radioactivity onto the tumour site, resulting in specific destruction of tumour cells/tissue.
Alternatively, the therapeutic compound coupled to the antigen, carrier molecule or affinity tag may for example be a toxic compound that is not able to cross the cell membrane without

prior binding to the cell surface.

This prerequisite is fulfilled by the A components of classical AB-toxins derived from a number of pathogenic bacteria like *Clostridium perfringens*, *C. botulinum*, *C. difficile*, *B. anthracis* and others. AB-toxins are two-component protein complexes that interfere with internal cell functions. The A component is the "active" component (i.e. it kills a cell upon membrane penetration), but is not able to cross the cell membrane on its own. The B component is the "binding" component that by itself is non-toxic, but is essential for uptake and membrane penetration of component A.

For example, *Bacillus anthracis* protective antigen (PA) is a classical toxin B component which mediates the uptake of the actual anthrax exotoxins edema factor and lethal factor (LF). LF without the PA-component is non-toxic since LF by its own does not penetrate membranes and thus cannot execute its pathogenic capabilities (Pezard C, Berche P, Mock M. "Contribution of individual toxin components to virulence of *Bacillus anthracis*" 1991 Infect. Immun. 59 (10): 3472). However, when bound to cell surface molecules, LF is internalised and highly toxic to the cell.

Upon dimerization of the polypeptides P1 and P2, the function of the functional domain F is reconstituted. Through interaction of the reconstituted functional domain with the antigen, carrier molecule or affinity tag coupled to the toxin, the toxin is recruited to the cell membrane of the target cells, incorporated into the cells and kills the cells.

This principle is easily adapted to the purposes of the invention by the skilled person, since it is already widely used in so called immunotoxins, where a targeting moiety, mostly an antibody-like domain or natural ligand, is coupled to the toxin component (see, e.g., Immunotoxins for targeted cancer therapy. Kreitman RJ, AAPS J. 2006 Aug 18;8(3):E532-51). Examples include immunotoxins based on diphtheria toxin (such as Denileukin diftitox (U.S. trade name Ontak) which has been approved by FDA for the treatment of some T cell lymphomas) or based on *B. anthracis* Lethal Factor (Pastan I, Hassan R, FitzGerald DJ, Kreitman RJ (2007). "Immunotoxin treatment of cancer". Annu. Rev. Med. 58: 221–37).

Suitable A components of AB-toxins may for example be *B. anthracis* edema factor, *B. anthracis* lethal factor, *C. perfringens* iota toxin, *C. botulinum* C2 toxin, *C. difficile* ADP-ribosyltransferase *C. diphtheriae* diphteria toxin fragment A.

Alternatively, the therapeutic compound may for example be a cytotoxic compound that is toxic upon entry into a cell and that is capable of crossing the cell membrane by itself without prior binding to the cell surface. In this case, the antigen, carrier molecule or affinity tag that the therapeutic compound is coupled to is selected such that it prevents the resulting

conjugate (i.e. the therapeutic compound linked to the antigen/carrier molecule/affinity tag) from crossing cell membranes and entering cells without prior binding of the conjugate to the cell surface (a suitable carrier molecule may for example be a hydroxyethyl starch carrier). Thus, such a conjugate does not enter cells without prior binding to their cell surface; once such a conjugate binds to the cell surface, however, it is internalized into the cell and the toxic compound kills the cell. The conjugate does not bind to cells, unless it is recruited in the presence of the inventive set of polypeptides to cells that simultaneously express both antigens A1 and A2 at their cell surface. Such cells bind and recruit both polypeptides P1 and P2, and the reconstituted functional domain specifically binds to and recruits the antigen/carrier molecule/affinity tag which, in turn, results in internalization of the therapeutic compound. In consequence, a specific killing of cells that carry both antigens A1 and A2 at their cell surface is accomplished. Cytotoxic compounds that may be used in this context include e.g. auristatin, ricin, saponin, bryodin 1, bouganin, gelonin, pokeweed antiviral protein (PAP), antifolates, vinca alkaloides, anthracyclines, calicheamicin, ribonuclease, abrin, modeccin, or Listeriolysin O.

The diagnostic compound coupled to the antigen, carrier molecule or affinity tag may for example be a radioactive compound, a fluorophore, or a compound capable of mediating bioluminescence.

Suitable radioactive compounds are for example compounds comprising ^{99m}Tc, ^{111}In, ^{82}Rb or ^{201}Tl. Such compounds are detected by well-known medical imaging procedures in the clinic.

Alternatively, a fluorescent compound may be used as diagnostic compound, such as GFP (green fluorescent protein) or a GFP variant (e.g. BFP (blue fluorescent protein), CFP (cyan fluorescent protein), or YFP (yellow fluorescent protein)), or a fluorescent small-molecule compound like FITC (fluorescein isothiocyanate) or PE (phycoerythrin), alexa fluor dyes (such as AlexaFluor488 and related dyes sold by Molecular Probes, e.g.) or cyanine dyes (such as Cy3 (Indocarbocyanine) or Cy5 (Indodicarbocyanine) or related dyes).

Alternatively, a compound capable of mediating bioluminescence may be used as diagnostic compound, such as a luciferase, for example *Gaussia* luciferase (Chopra A. *Gaussia princeps* luciferase. In: Molecular Imaging and Contrast Agent Database (MICAD) [database online]. Bethesda (MD): National Library of Medicine (US), NCBI; 2004-2012. Available from: http://micad.nih.gov.). The employment of *Gaussia* luciferase for *in vivo* imaging is well established (see, e.g., Santos EB et al. Sensitive *in vivo* imaging of T cells

using a membrane-bound *Gaussia princeps* luciferase. Nat Med. 2009 Mar;15(3):338-44. Epub 2009 Feb 15; or Inoue Y et al. *Gaussia luciferase* for bioluminescence tumor monitoring in comparison with firefly luciferase. Mol Imaging. 2011 Oct 1;10(5):377-85. doi: 10.2310/7290.2010.00057. Epub 2011 Apr 26; see also below for additional details).

Moreover, the fragments F1 and F2 (i.e. the V_L and V_H fragments of anti CD3 Fv in the above-described exemplary embodiment) can be replaced by V_L and V_H fragments of an antibody that is specific for a therapeutic or diagnostic compound (i.e. in this case the functional domain F is capable of directly binding to the therapeutic or diagnostic compound). Here, the same therapeutic and diagnostic compounds as described above in the context of the "pretargeting" approach may be considered.

Furthermore, the fragments F1 and F2 (i.e. the V_L and V_H fragments of anti CD3 Fv in the above-described exemplary embodiment) can be replaced by fragments of a fluorescent or bioluminescent compound that are biologically inactive on their own, but regain their function (i.e. their ability to mediate fluorescence or bioluminescence) upon association of the two fragments and functional complementation, thus allowing for specific identification of cells that carry both the antigens A1 and A2.

A number of fluorescent molecules that may be used in this context are well known and characterized in the art including, but are not limited to, GFP (green fluorescent protein), GFP derivatives (like YFP (yellow fluorescent protein) and CFP (cyan fluorescent protein), Venus (Nagai T et al., A variant of yellow fluorescent protein with fast and efficient maturation for cell-biological applications. Nat Biotechnol. 2002 Jan;20(1):87-90), or Cerulean (Enhanced CFP with S72A, Y145A and H148D substitutions)). For these molecules, split fragments are described that self-assemble in the situation of close proximity in a process called bimolecular fluorescence complementation (BiFC).

For example, GFP, CFP, Venus, Venus with a M153T substitution, or Cerulean may be split after amino acid 155 (i.e., for example, fragment F1 may comprise amino acids 1-155 of GFP, while fragment F2 may comprise amino acids 156-245 of GFP, or vice versa). Alternatively, YFP or Venus may be split after amino acid 173. Further details on split GFP and split GFP variants can be found in Kerppola TK., Visualization of molecular interactions using bimolecular fluorescence complementation analysis: characteristics of protein fragment complementation. Chem Soc Rev. 2009;38:2876-86.

An example for a molecule that mediates bioluminescence and that can be used in this

context is split luciferase. Particularly suited is the luciferase of *Gaussia princeps*, which requires no cofactors to be active and catalyzes the oxidation of the substrate coelenterate luciferin (coelenterazine) in a reaction that emits blue light, or derivatives of *Gaussia* luciferase (Remy I and Michnick S, A highly sensitive protein-protein interaction assay based on *Gaussia* luciferase. Nature Methods - 3, 977 - 979 (2006)). For example, fragment F1 may comprise a fragment from the N-terminus of *Gaussia* luciferase to Gly-93, while fragment F2 may comprise a fragment from Glu-94 to the C-terminus of *Gaussia* luciferase, or vice versa (see Remy I and Michnick S, Nature Methods, 2006 for details). Application of the *Gaussia* split luciferase system *in vivo* has been established (Luker et al., *In vivo* imaging of ligand receptor binding with *Gaussia* luciferase complementation. Nature Medicine 2011, doi:10.1038/nm.2590), allowing for straightforward adaptation to the purposes of the present invention by a skilled person.

Intravital imaging of tumour lesions is of eminent importance in cases, where cancer cells infiltrate tissues and the complete elimination of all transformed cells is prerequisite for cure. A surgeon searching for disseminated cancer cells in the operation site may use split GFP or split GFP derivatives fused to the targeting moieties and a laser assisted Multispectral fluorescence camera system for detection of cells aberrantly expressing an addressed antigen profile, similar to the intraoperative use of fluorescence or bioluminescence that is already exploited in some clinical settings (van Dam GM et al., Intraoperative tumor-specific fluorescence imaging in ovarian cancer by folate receptor-α targeting: first in-human results. Nat Med. 2011 Sep 18;17(10):1315-9; Luker et al., *In vivo* imaging of ligand receptor binding with *Gaussia* luciferase complementation. Nature Medicine 2011, doi:10.1038/nm.2590).

For detection of complemented split luciferase, the application of a substrate for luciferase, which can be luciferin or coelenterazine, is mandatory. Coelenterazine is preferred because coelenterazine emits light independent of ATP and is well established for *in vivo* imaging and *in vivo* applications. A surgeon will be able to visualize cancer cells after having tagged the tumor with polypeptide P1 and P2 and injected a non-toxic amount of coelenterazine intravenously.

In another exemplary embodiment, the inventive principle is applied in the context of a patient who suffers from a haematopoietic tumour and who received a transplantation of healthy haematopoietic cells from another person (the donor). Here, the set of polypeptides according to the invention can be used for the specific elimination (or detection) of

remaining malignant haematopoietic cells of the recipient after transplantation of healthy haematopoietic cells from the donor.

To destroy the malignant haematopoietic cells in a patient suffering from a haematopoietic tumour, the patient may be subjected to chemotherapy and/or radiation therapy. Subsequently, the patient receives a transplantation of healthy haematopoietic cells from a donor.

To minimize the risk of transplant rejection or graft versus host disease, transplantation of tissue/cells (e.g. bone marrow) from a donor who has the same set of MHC (major histocompatibility complex) molecules is usually preferred. However, often no donor with the same set of MHC molecules ("HLA-identical donor") can be identified. Therefore, transplant grafts with one or two mismatches in the set of MHC variants, unrelated cord blood with up to three mismatches, or haploidentical transplantations are increasingly employed. Accordingly, it is common that there is at least one distinctive difference between the set of MHC molecules expressed by the cells of the recipient and the cells of the donor.

In the transplantation according to this exemplary embodiment of the invention, donor cells are used that are distinct from the recipient cells with respect to at least one of their HLA variants. This means that there is at least one "distinguishing antigen" that is present at the cell surface of the recipient cells, but not at the cell surface of the donor cells. For example, the distinguishing antigen may be HLA-A2, if the patient (i.e. the recipient) is HLA-A2 positive, while the donor is HLA-A2 negative.

Despite chemotherapy/radiation therapy, individual malignant haematopoietic cells of the recipient may have escaped eradication. Since the surviving malignant haematopoietic cells are recipient cells, they carry the distinguishing antigen that differentiates recipient cells from donor cells. At the same time, they are cells of haematopoietic lineage origin and thus have markers of this cell lineage, such as CD45, at their cell surface. Leukemic blasts and other haematopoietic cells of the patient are the only cells that simultaneously display the distinguishing antigen (here HLA-A2) and markers of haematopoietic cell lineage (here CD45). The set of polypeptides according to the invention exploits this fact to specifically eliminate these cells.

To this end, the first targeting moiety T1 of the first polypeptide P1 may be a scFv specific for the distinguishing antigen which is present only on recipient cells (here HLA-A2). As

fragment F1 of the functional domain F, the variable region of the light chain (V_L) of a CD3ε-specific antibody may be chosen. The second targeting moiety T2 of the second polypeptide P2 may be a single chain variable Fragment (scFv) specific for CD45. As fragment F2 of the functional domain F, the variable region of the heavy chain (V_H) of said CD3ε-specific antibody may be chosen. (Naturally, it is equally possible to use the variable region of the heavy chain (V_H) of a CD3ε-specific antibody as fragment F1 and the variable region of the light chain (V_L) of said CD3ε-specific antibody as fragment F2. As is evident for a person of skill in the art, this is a general principle, and it is generally possible to switch the fragments used for fragment F1 and fragment F2.) Neither is V_L of the CD3ε-specific antibody capable of engaging CD3ε in the absence of V_H, nor is V_H of the CD3ε-specific antibody capable of engaging CD3ε in the absence of V_L. Accordingly, neither P1 nor P2 is by itself capable of binding to CD3ε.

However, if both the distinguishing antigen (e.g. HLA-A2) and the CD45 antigen are present on one single cell, binding to their respective antigens brings the two polypeptides P1 and P2 into close proximity. As a consequence, the unpaired V_H and V_L domains assemble, resulting in heterodimerization of the polypeptides P1 and P2 and in the formation of a functional variable antibody fragment Fv from the V_H and V_L domains that is capable of binding to CD3ε (see Figure 2).

As a result, T cells are recruited and activated through CD3ε, and the cell carrying both HLA-A2 and CD45 at its cell surface is specifically eliminated by a cytotoxic T cell response.

A person of skill in the art understands that, within the principle of the present invention, diverse variations to this exemplary embodiment are possible.

For example, in polypeptide P2 the scFv fragment recognising the haematopoietic cell lineage marker CD45 can be replaced by a scFv fragment recognising a marker of a different cell lineage or cell type, i.e. the targeting moiety T2 may be a domain that specifically binds an antigen that is specific for a cell lineage other than the haematopoietic cell lineage or for a certain cell type (for a detailed list of various cell lineage markers and cell type markers that may be used in this context see David J. Dabbs, Diagnostic immunohistochemistry, Churchill Livingstone, 3rd edition (2010); or F Lin and J Prichard, Handbook of Practical Immunohistochemistry: Frequently Asked Questions, Springer, New York, 1st edition

(2011)). To adapt the set of polypeptides to an alternative cell lineage marker/cell type marker, it is sufficient to replace the targeting moiety T2 of polypeptide P2 with a targeting moiety that has binding specificity for the desired alternative cell lineage marker/cell type marker.

For example, in the situation of metastatic renal cell carcinoma (RCC), a person skilled in the art might consult the above-cited databases for information on cell surface proteins with restricted expression to kidney cells. Among many other molecules, he will learn that expression of certain members of the aquaporin family is confined to kidney cells and erythrocytes. Having obtained this information, a person skilled in the art will construct a polypeptide P2 recognising an aquaporin family member that is confined to kidney cells and erythrocytes fused to the variable region of the heavy chain (V_H) of a CD3ε-specific antibody. In case that the patient suffering renal cell carcinoma is HLA A2 positive and a kidney transplant from a healthy donor is HLA A2 negative, the clinician treating the patient may utilise the two constructs (anti-aquaporin fused to anti-CD3(V_H) and anti-HLA A2 fused to the light chain (V_L) of said CD3ε-specific antibody). In this case, all cells simultaneously expressing said aquaporin and HLA A2 will be tagged for lysis by T cells which are renal cell carcinoma cells and metastatic tissues. Kidney cells donated by the healthy donor are HLA A2 negative and will not be attacked. Since erythrocytes loose HLA expression along the process of ontogeny and thus do not carry HLA molecules on their surfaces, they will be spared despite expressing large amounts of aquoporins. Again, a conventional, non-complementing bispecific antibody addressing aquaporin would mediate killing of all kidney cells from donor and recipient as well as erythrocytes. A bispecific antibody addressing HLA A2 in a HLA A2 positive patient most likely would be fatal, since every recipient cell except erythrocytes express HLA A2 and can be attacked by the retargeted T cells.

Another example is hepatocellular carcinoma (HCC). Hepatocytes are largely involved in a number of metabolic processes including the trafficking of lipoproteins. To this end, hepatocytes express receptors for high density lipoproteins (HDL) on their surfaces (scavenger receptor class B member 1, SCARB1). Treatment of an HLA A2 positive patient suffering HCC which expresses SCARB1 on the surface of tumor cells and metastases can be accomplished by a Polypeptide P2 construct comprising a scFv domain addressing SCARB1 fused to the variable region of the heavy chain (V_H) of said CD3ε-specific

antibody and a Polypeptide P1 (anti-HLA A2 scFv fused to the light chain (V_L) of said CD3ε-specific antibody) and transplantation of liver cells from a healthy, HLA A2 negative donor. In this case, all hepatocytes and hepatocyte-derived malignant cells expressing both, SCARB1 and HLA A2 will be tagged for lysis by T lymphocytes. Hepatocytes of the donor lacking HLA A2 will be spared as well as normal SCARB1 negative donor cells expressing HLA A2. Since SCARB1 expression is also reported for cells participating in steroid synthesis in the adrenal gland, these cells most likely will also be destroyed by redirected T cells, resulting in Addison's disease.

Various markers that are specific for certain cell types or cell lineages or a few cell types/lineages are known (for a list of examples, see above). More information on lineage markers, differentiation antigens and tissue markers as well as their tissue distribution are easily accessible from published sources (see, e.g. David J. Dabbs, Diagnostic immunohistochemistry, Churchill Livingstone, 3rd edition (2010); or F Lin and J Prichard, Handbook of Practical Immunohistochemistry: Frequently Asked Questions, Springer, New York, 1st edition (2011)) and public databases (such as the Gene Expression Atlas of the European Bioinformatics Institute (EBI), http://www.ebi.ac.uk/gxa/; or the Gene Expression Omnibus (GEO) platform, see above). Moreover, such markers can be identified and/or verified in a straightforward manner by a skilled person using similar methods as described above for the identification of tumour-specific combinations of antigens.

In certain preferred embodiments, an antigen with less than perfect specificity for a certain cell type or cell lineage is used (i.e. an antigen is used that is present on more than one, but preferably only a few, cell types or cell lineages). In some embodiments, an antigen is used that is expressed by said cell type/cell lineage at a higher rate or at a higher proportion or amount than by other cell types/cell lineages, in the sense that there may be a small but detectable expression of said antigen also in other cell types/cell lineages.

The concept can further be adapted to any other HLA haplotype besides HLA-A2 used in the exemplary embodiment above, as long as the recipient cells are positive for this HLA antigen and the donor cells are negative for it. Possible HLA antigens include, among others, HLA A1, HLA A2, HLA A3, HLA A25, HLA B7, HLA B8, HLA B35, HLA B44 and HLA Cw3, HLA Cw4, HLA Cw6, HLA Cw7. To adapt the set of polypeptides to an alternative HLA antigen, it is sufficient to replace the targeting moiety T1 of polypeptide P1 with a targeting moiety that has binding specificity for the desired alternative HLA antigen. By an

appropriate choice of the targeting moiety T1, it is of course also possible to specifically eliminate donor cells.

Moreover, instead of a V_L domain and a V_H domain that upon assembly form a domain capable of binding to CD3ε (i.e. fragment F1 and fragment F2 of polypeptides P1 and P2, respectively), the V_L domain and V_H domain can be replaced with domains/fragments that upon assembly confer a different function to the resulting dimer. In this respect, all the variations described above for the exemplary embodiment relating to the elimination/detection of tumour cells identified by a specific combination of two cell surface antigens are equally applicable. For example, upon assembly the complemented functional domain may mediate binding/activation of other effector cells than T cells, may be adapted to a "pretargeting" approach, may bind a therapeutic or diagnostic compound, or may form a fluorescent molecule/molecule capable of mediating bioluminescence.

The diverse options for the choice of the fragments F1 and F2 and for the choice of the targeting moieties T1 or T2 described above in the exemplary embodiment relating to application of the inventive principle for the specific elimination of tumour cells may of course be considered, as well.

From the described exemplary embodiments and variations, it will be clear to a person of skill in the art that the inventive principle described above can not only be used for the highly specific identification/elimination of tumour cells or of remaining malignant recipient cells after a cell transplantation, but also for the identification/elimination of any other type of cell carrying a specific combination of two antigens that distinguishes it from other types of cells.

In the following, reference is made to the figures:

Figure 1 shows the principle of the invention. Figure 1A: Antigens and design of polypeptides P1 and P2. Figure 1B: If a cell expresses both antigens 1 and 2 at its cell surface, simultaneous binding of polypeptide P1 and polypeptide P2 to the surface of this cell brings P1 and P2 in close proximity, causes association of fragments F1 and F2 and restoration of the biological function of domain F by complementation. No restoration of biological function occurs if only antigen A1 (Figure 1C) or antigen A2 (Figure 1D) is present on the cell surface.

Figure 2 shows an exemplary embodiment of the invention in an allogeneic transplantation setting for haematopoietic neoplasias with mismatched HLA antigens. In this situation, the dual information of recipient HLA haplotype ($HLA_{patient}$) and haematopoietic lineage origin (CD45) is displayed exclusively on leukemic blasts and other haematopoietic cells of the patient. The first polypeptide P1 comprises a single-chain variable fragment antibody construct directed against the HLA of the patient (targeting moiety T1) fused to the V_L fragment of anti CD3 (fragment F1). The second polypeptide P2 comprises a single-chain variable fragment construct specific for the haematopoietic lineage marker CD45 (targeting moiety T2), fused to the V_H split-fragment of anti CD3 Fv (fragment F2).
CD45: antigen specific for haematopoietic cells. $HLA_{patient}$: HLA-antigen specific for patient cells, i.e. an allelic variant of the human MHC that is present on the surface of patient cells (= cells of the recipient of cell transplantation), but absent from the surface of donor cells. αCD45 scFv: scFv with binding specificity for CD45. $\alpha HLA_{patient}$ scFv: scFV with binding specificity for $HLA_{patient}$. CD3(V_H): variable region of an immunoglobulin heavy chain of an antibody with binding specificity for CD3. CD3(V_L): variable region of an immunoglobulin light chain of an antibody with binding specificity for CD3.
Upon binding of the two constructs through their αCD45 scFv and $\alpha HLA_{patient}$ scFv, respectively, to a cell carrying both the CD45 and the $HLA_{patient}$ antigen, assembly of CD3(V_H) with CD3(V_L) leads to functional complementation of the antibody with binding specificity for CD3, thus allowing for specific recruitment and activation of T cells through the CD3 molecules at their cell surface.

Figure 3 shows the constructs used in the experiments depicted in Figures 4-9. (Construct 85 differs from construct 71 by the fact that construct 85 has a Flag tag while construct 71 has a myc tag. Construct 75 differs from construct 82 by the fact that construct 75 has a Flag tag while construct 82 has a myc tag.) V_HCD3: variable region of the heavy chain of an anti-CD3 antibody; V_LCD3: variable region of the light chain of an anti-CD3 antibody; V_HA2: variable region of the heavy chain of an anti-HLA-A2 antibody; V_LA2: variable region of the light chain of an anti-HLA-A2 antibody; V_L45: variable region of the heavy chain of an anti-CD45 antibody; V_H45: variable region of the light chain of an anti-CD45 antibody; L18, L7, L15, L6, L19: linker of 18, 7, 15, 6, 19 amino acids, respectively.

Figure 4 shows conventional tandem bispecific single chain scFv constructs used to control the assay system. Briefly, bispecific antibody constructs with specificity for CD3 and HLA

A2 were titrated as indicated to a co-culture of U266, a HLA A2 positive, CD45 positive myeloma cell line, and HLA A2 negative T cells (monocyte depleted peripheral blood mononuclear cells), and production of interleukin 2 by T cells was determined. Substantial T cell stimulatory capacity was detected for the two FvCD3-HLA-A2 constructs 85 and 71, which differ by their respective Flag or Myc-Tags (For domain structure of constructs see Figure 3.). Bispecific tandem Fv constructs in HLA-A2-CD3 configuration were less efficient and single chain constructs addressing either HLA-A2 or CD3 did not stimulate T cells at all. Positive control is conducted using unspecific PHA-L (phytohemagglutinin) stimulation.

Figure 5 shows exquisite and highly specific T cell stimulatory capacity if a pair of complementing constructs according to the invention is used, but not if only one of the two constructs of a pair is used individually. Briefly, V_LCD3-scFvHLA-A2 (construct 42), V_HCD3-scFvCD45(V_L-V_H) (construct 45) and V_HCD3-scFvCD45(V_H-V_L) (construct 55) were titrated separately or in the combinations of constructs 42 and 45, or 42 and 55 to co-cultures of U266 and T cells as described. High T cell stimulatory capacity was demonstrated for the combinations of 42/45 or 42/55 with minute activity, if only one of these constructs was given separately. These results show that the V_L and V_H domains of FvCD3 have to cooperate in order to reconstitute or complement T cell engaging function. Importantly, the scFvCD45 targeting moiety could be switched from (V_L-V_H) to the (V_H-V_L) configuration, clearly indicating that the modular character of the constructs allows replacement of a targeting moiety by another targeting moiety with desired specificity. The assay system was controlled by the use of single chain constructs CD45(V_L-V_H) and CD45(V_H-V_L) which did not stimulate T cells to produce IL2.

Figure 6 shows a first of three competitive blocking experiments. The bispecific tandem construct FvCD3-HLA-A2 (construct 71) was given to co-cultures of U266 and T cells as described and stimulatory function was determined through induced IL2 production by T lymphocytes. The T cell stimulating function was blocked by single chain constructs that occupy the targeted epitope on the HLA A2 molecule (construct 4, concentration *100). Intrinsic stimulation of T cells by the HLA A2 or CD3 specific single chain constructs (construct 4 (concentration *100) or construct 36 (concentration *9)) was ruled out. PHA-L was used as positive control.

Figure 7 shows that "tridomain constructs" (i.e. constructs according to the invention) first

have to bind on the surface of a single cell to dimerize and complement T cell engaging functions the competitive epitope blocking experiments. Briefly, constructs 42 and 45 were given to co-cultures of U266 cells and HLA-A2 negative T lymphocytes and stimulatory capacity was determined by IL2 production of T cells. In experimental situations where the epitopes on HLA A2 or CD45 molecules were competitively blocked by constructs 4 or 46 (both concentrations *100), T cell stimulatory function was abrogated. These results clearly indicate that the two respective "tridomain constructs" have to bind simultaneously onto the surface of a cell in order to restore or to complement T cell engaging function. Intrinsic stimulatory activity of either construct (42, 45, 4, 46 and 36) was ruled out using different concentrations.

Figure 8 shows the analogous experiment to Figure 7 for the combination of constructs 42 and 55. Again, T cell stimulatory capacity of the combination of the two "tridomain constructs" was abrogated by competitive blocking of antigenic epitopes on the HLA A2 or the CD45 molecule. Importantly, these results again show that the targeting module can be easily replaced by another module with appropriate specificity. More importantly, the V_L-V_H-V_L configuration of construct 42 and the V_H-V_H-V_L configuration of construct 55 impede homo- or hetero-dimerization or self-assembling of the constructs without prior binding to a substrate expressing both, HLA A2 and CD45 antigens.

Figure 9 shows lysis of U266 cells by HLA A2 negative T cells in a sample comprising both V_LCD3-scFvHLA-A2 and V_HCD3-scFvCD45(V_H-V_L) constructs ("both constructs"). No significant lysis was observed in control samples comprising only one of the two constructs.

Figure 10 shows the On-target restoration of the polypeptides. Binding of two separate polypeptides (P1 and P2) to their respective antigens on a target cell, each consisting of a specific single-chain variable antibody fragment (scFv, V_H-V_L) fused to the variable light (V_L) or variable heavy chain domain (V_H) of a CD3-specific antibody (Fragment F1 and F2), enables V_H/V_L heterodimerization and the formation of a functional CD3 binding site to engage T cells.

Figure 11 shows that CD3 V_H/V_L dimerization engages T cells and is dual-antigen-restricted. U266 myeloma, primary T cell pro-lymphocytic leukemia (T-PLL), and THP-1 acute myeloid leukemia cells, all HLA-A2-positive and CD45-positive, were probed with HLA-A2–negative donor peripheral blood mononuclear cells (PBMC) and the polypeptides as

indicated. T-cell engagement was assessed by reactive interleukin-2 (IL-2) production (A) and target cell lysis (B). The bispecific tandem scFv (CD3(V_H-V_L) - HLA-A2(V_H-V_L) antibody was used as a positive control. (C), Binding of the polypeptides on THP-1 cells is competitively blocked by an excess of scFvCD45 (left) and scFvHLA-A2 (right) inhibitors (blocking the individual antigen epitopes on the target cell), as indicated, and reactive IL2 production by donor PBMCs was investigated. (D), The single or double antigen negative cell lines RAJI and KMS-12-BM were probed with the polypeptides. PHA-L was used as a nonspecific stimulus control for PBMCs.

Figure 12 shows targeted therapy by conditional CD3V_H/V_L complementation *in vivo*. (A), Survival of mice (n = 6 per group) after intraperitoneal injection of 5×10^6 THP-1 acute leukemic cells together with 1.25×10^5 CMV-specific, HLA-A2–negative donor T cells and the polypeptides (0.5 μg) as indicated (tumor cells: T-cell ratio = 40/1). (B), Caspase 3 activation was assessed *in vitro* by flow cytometry in HLA-A2/CD45 double-positive THP-1 and CD45-positive but HLA-A2–negative bystander cells after co-culture with donor T cells and the polypeptides (3 nM) as indicated. The bispecific tandem scFv (CD3(V_H-V_L) - HLA-A2(V_H-V_L)) antibody was used as a positive control.

Figure 13 shows that EGFR- and EpCAM-directed polypeptides engage T cells for carcinoma cell destruction. EGFR and EpCAM double-positive human colon cancer cell line COLO-206F and melanoma cell line FM-55 (EGFR-positive but EpCAM-negative) were probed with PBMCs in the presence of polypeptides specific for EGFR (CD3(V_H)-EGFR(V_H-V_L)) and EpCAM (CD3(V_L)-EpCAM(V_H-V_L)) as indicated. T cell engagement was assessed by reactive interferon-γ (IFNγ) production (A) and activation of caspase 3 in target cells (B).

Figure 14 shows that HLA-A2 and CEA directed polypeptides redirect T cells for tumor cell destruction. Human colon cancer cell line COLO-206F, melanoma cell line FM-55 and ovarian cancer cell line OVCAR were probed with PBMCs in the presence of polypeptides specific for HLA-A2 (CD3(V_L)-HLA-A2(V_H-V_L)) and CEA (CD3(V_H)-CEA(V_H-V_L)) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 15 shows that HLA-A2 and EGFR directed polypeptides redirect T cells for tumor cell destruction. Human cell lines COLO-206F, FM-55 and OVCAR were probed with PBMCs in the presence of polypeptides specific for HLA-A2 ($CD3(V_L)$-$HLA\text{-}A2(V_H\text{-}V_L)$) and EGFR ($CD3(V_H)$-$EGFR(V_H\text{-}V_L)$) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 16 shows that HLA-A2 and Her2 directed polypeptides redirect T cells for tumor cell destruction. Human cell lines COLO-206F, FM-55 and OVCAR were probed with PBMCs in the presence of polypeptides specific for HLA-A2 ($CD3(V_L)$-$HLA\text{-}A2(V_H\text{-}V_L)$) and Her2 ($CD3(V_H)$-$Her2(V_H\text{-}V_L)$) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 17 shows that CD45 and HLA-A2 directed polypeptides redirect T cells for tumor cell destruction. In this experiment the split antiCD3 fragments ($CD3(V_H)$ and $CD3(V_L)$) for the anti-CD45 and anti-HLA-A2 targeting moieties were exchanged, compared to the CD45 and HLA-A2 polypeptides used in Fig. 5,7-9, 11,12, 14-16. Human myeloma cell line U266 was probed with PBMCs in the presence of polypeptides specific for CD45 ($CD3(V_L)$-$CD45(V_H\text{-}V_L)$) and HLA-A2 ($CD3(V_H)$-$HLA\text{-}A2(V_H\text{-}V_L)$) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 18 shows that EGFR and EpCAM directed polypeptides redirect T cells for tumor cell destruction. Human colon cancer cell lines COLO-206F and CX-1 and ovarian cancer cell line OVCAR were probed with PBMCs in the presence of polypeptides specific for EpCAM ($CD3(V_L)$-$EpCAM(V_H\text{-}V_L)$) and EGFR ($CD3(V_H)$-$EGFR(V_H\text{-}V_L)$) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 19 shows that Her2 and EpCAM directed polypeptides redirect T cells for tumor cell destruction. Human ovarian cancer cell line OVCAR were probed with PBMCs in the presence of polypeptides specific for EpCAM ($CD3(V_L)$-$EpCAM(V_H\text{-}V_L)$) and Her2 ($CD3(V_H)$-$Her2(V_H\text{-}V_L)$) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 20 shows that CD45 and CD138 directed polypeptides redirect T cells for tumor cell destruction. Human myeloma cell line AMO-1 was probed with PBMCs in the presence of polypeptides specific for CD45 ($CD3(V_L)$-$CD45(V_H\text{-}V_L)$ upper panel, $CD3(V_H)$-$CD45(V_H\text{-}$

V_L) lower panel) and CD138 (CD3(V_H)-CD138(V_H-V_L) upper panel, CD3(V_L)-CD138(V_H-V_L) lower panel) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 21 shows that targeting a single antigen (CD138) with CD138 directed polypeptides redirect T cells for tumor cell destruction. Human myeloma cell line AMO-1 was probed with PBMCs in the presence of polypeptides specific for CD138 (CD3(V_L)-CD138(V_H-V_L) and (CD3(V_H)-CD138(V_H-V_L)) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 22 shows that targeting a single antigen (CD45) with CD45 directed polypeptides redirect T cells for tumor cell destruction. Human myeloma cell lines AMO-1 and U266 were probed with PBMCs in the presence of polypeptides specific for CD45 (CD3(V_L)-CD45(V_H-V_L) and (CD3(V_H)-CD45(V_H-V_L)) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 23 shows the On-target restoration of two polypeptides directed against a single antigen on the cell surface, targeting two different epitopes (upper part) or the same epitope (lower part) on the antigen. Binding of two separate polypeptides (P1 and P2) to their respective epitope, on the same antigen, on a target cell. For targeting two different epitopes, the targeting moiety of each polypeptide consists of a specific single-chain variable antibody fragment (scFv). For targeting the same epitope, the targeting moiety of each polypeptide consists of the same single-chain variable antibody fragment (scFv). The targeting moieties are fused via peptide linkers to the variable light (V_L) or variable heavy chain domain (V_H) of a CD3-specific antibody (Fragment F1 and F2), enables V_H/V_L heterodimerization and the formation of a functional CD3 binding site (functional domain) to engage T cells.

Figure 24 shows the possibility to use different effector ways to kill a target cell with a kit of polypeptide parts. To this end, the anti-CD3 module (F1 and F2) is replaced by an anti-HIS (hexa-histidine) module which, after simultaneous binding of polypeptide 1 and 2, complements a hexa-histidine binding site and thus binds histidine labeled payloads (eg. a HIS-tagged toxin). The targeting moiety T1 (V_H-V_L) of polypeptide P1 specifically binds to HLA-A2, the targeting moiety T2 (V_H-V_L) of polypeptide P2 specifically binds to CD45. The fragment F1 of polypeptide P1 comprises of a V_H domain of an antibody against a hexahistidine-tag and fragment F2 of polypeptide P2 comprises a V_L domain of the same

antibody. Human myeloid leukemia cell line THP-1 was probed with a histidine (His) tagged Clostridium perfringens Iota toxin component Ia at 0.01µg/ml in combination with indicated polypeptides. After 48 hours in culture the cell viability was measured using the alamarBlue® assay. The results show a reduction of viability against the background of the assay for cells probed with the combination, but not with individual polypeptides. Control THP-1 cells were grown simultaneously in culture without toxin. Samples were run and analyzed as duplicates.

Figure 25 shows that HLA-A2 and CD45 directed polypeptides, comprising of a split antibody against a His-tag, kill tumor cells using a histidine (His) tagged Shiga toxin subunit A at a concentration of 0.01µg/ml. The same experimental setup was used as in figure F24.

Figure 26 shows that HLA-A2 and CD45 directed polypeptides, comprising of a split antibody against a His-tag, kill tumor cells using a histidine (His) tagged Shiga toxin subunit A at a concentration of 0.1µg/ml. The same experimental setup was used as in figure F24/25.

Figure 27 shows that EGFR and EpCAM directed polypeptides, comprising of a functional domain F with F1 and F2 are V_H and H_L of a antibody specific for digoxigenin (aDig), mark tumor cells using a digoxigenin labeled horse radish peroxidase (HRP) molecule. The targeting moiety T1 (V_H-V_L) of polypeptide P1 specifically binds to EGFR, the targeting moiety T2 (V_H-V_L) of polypeptide P2 specifically binds to EpCAM. The fragment F1 of polypeptide P1 comprises of a V_H domain of an antibody against digoxigenin and fragment F2 of polypeptide P2 comprises a V_L domain of the same antibody. Human colon cancer cell line Colo-206F was first probed with indicated polypeptides followed by probing with digoxigenin labeled HRP. The samples were analyzed using the (Invitrogen™, ELISA Kit) and the absorbance was read with a BioRAD-micro plate reader. For analysis the chromogen blank sample (no Digoxigenin-HRP) was set to 0. Samples were run and analyzed as duplicates.

Figure 28 shows that CD45 and HLA-CW6 directed polypeptides redirect T cells for patient cell destruction. Primary patient cells with known HLA-haplotypes were used. A51 = cells of a patient with MDS (myelodysplastic syndrom), homozygous for the HLA-Cw6 haplotype. A49 = cells of a patient after allogeneic bone marrow transplantation, heterozygous for the HLA-Cw6 haplotype. Patient cells were incubated with healthy PBMCs for 30 hours, in the presence of polypeptides specific for CD45 (CD3(V_L)-CD45(V_H-V_L) and

HLA-Cw6 (CD3(V_H)-HLA-CW6(V_H-V_L)) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 29 shows that EGFR and EpCAM directed polypeptides redirect T cells for primary cancer patient cell destruction. A44 tumor cells were collected from the malignant ascites of a 48 years old male patient with metastatic pancreatic cancer. Patient tumor cells were incubated with patients own PBMCs (collected by phlebotomy) for 30 hours, in the presence of polypeptides specific for EpCAM (CD3(V_L)-EpCAM(V_H-V_L) and EGFR (CD3(V_H)-EGFR(V_H-V_L)) as indicated. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 30 shows that CD45 and HLA-A2 directed polypeptides redirect CMV restricted CD8+ T cells for tumor cell destruction. Human tumor cells THP-1 and U266 were incubated with CMV restricted T-cells from a HLA-A2 negative healthy donor for 30 hours, in the presence of polypeptides specific for HLA-A2 (CD3(V_L)-HLA-A2(V_H-V_L) and CD45 (CD3(V_H)-CD45(V_H-V_L)) as indicated. The bispecific tandem scFv (CD3(V_H-V_L) x HLA-A2(V_H-V_L))-antibody was used as a positive control. T cell engagement was assessed by reactive IFNγ production. Samples were run and analyzed as duplicates.

Figure 31 shows the principle idea to eliminate autoimmune or hypersensitivity disorder causing B-cell clones with a kit of polypeptide parts, consisting of an allergen specific polypeptide and a cell type specific polypeptide. The first polypeptide P1 has at its targeting moiety an allergen (eg. Betv-1A, Der-f2, Conglutin-7, Can-f1, Feld-d1). The second polypeptide P2 has at its targeting moiety a specific single-chain variable antibody fragment (scFv, V_H-V_L) targeting a cell surface protein (eg. CD19, CD138, CD38). Both targeting moieties are fused to either the variable light (V_L) or variable heavy chain domain (V_H) of a CD3-specific antibody (Fragment F1 and F2).

In the following, reference is made to certain (human) genes or proteins also referred to in the specification, the appended examples and figures as well as (partially) in the claims. Herein below, corresponding (exemplary) gene accession numbers are provided. Further accession numbers are also provided in the specification elsewhere herein as well as the appended examples.

CD45: Gene ID: 5788, updated on 13-Jan-2013, 3. Protein = P08575-1 = Isoform 1, Last modified July 19, 2003. Version 2

CD34: Protein: P28906-1/2 Last modified July 15, 1998. Version 2.

CD33: Gene ID: 945, updated on 30-Dec-2012: Protein: P20138 [UniParc]. Last modified October 17, 2006. Version 2. Checksum: 1C73E588240FBAD8

CD138: Gene ID: 6382, updated on 6-Jan-2013, 4. Protein = P18827 [UniParc]. Last modified May 5, 2009. Version 3.

CD15: Gene ID: 2526, updated on 5-Jan-2013

CD1a: Gene ID: 909, updated on 30-Dec-2012, P06126 [UniParc]. Last modified February 9, 2010. Version 4. Checksum: C575C3C538F0AA29

CD2: Gene ID: 914, updated on 5-Jan-2013; P06729 [UniParc]. Last modified October 23, 2007. Version 2. Checksum: A03D853C3B618917

CD3e: Gene ID: 916, updated on 5-Jan-2013, P07766 [UniParc]. Last modified February 1, 1996. Version 2. Checksum: A1603D01CE9957D7

CD4: Gene ID: 920, updated on 13-Jan-2013; P01730 [UniParc]. Last modified November 1, 1988. Version 1. Checksum: 20ED893F9E56D236

CD5: Gene ID: 921, updated on 30-Dec-2012; P06127 [UniParc]. Last modified November 30, 2010. Version 2. Checksum: 9131AEC9683EE1D3

CD8a: Gene ID: 925, updated on 30-Dec-2012; Isoform 1/2 (membrane) P01732-1/2 (mCD8alpha) [UniParc]. Last modified July 21, 1986. Version 1. Checksum: FCCA29BAA73726BB

CD20: Gene ID: 931, updated on 6-Jan-2013; P11836 [UniParc]. Last modified October 1, 1989. Version 1. Checksum: AC5420F8B626BDD1

CD23: Gene ID: 2208, updated on 4-Jan-2013; P06734 [UniParc]. Last modified January 1, 1988. Version 1. Checksum: F86708C0E6515B87

CD31: Gene ID: 5175, updated on 13-Jan-2013; Isoform Long [UniParc]. Last modified April 1, 1990. Version 1. Checksum: C57BBFA200A407A6, P16284-1/2/3/4/5/6 = Isoforms 1-6

CD43: Gene ID: 6693, updated on 30-Dec-2012; P16150 [UniParc]. Last modified April 1, 1990. Version 1. Checksum: C9C9AB8435D5E1FE

CD56: Gene ID: 4684, updated on 30-Dec-2012; Isoform 1 [UniParc]. Last modified July 22, 2008. Version 3. Checksum: FD3B9DE80D802554, P13591-2/1/3/4/4/6, Isoforms 1-6

CD57: Gene ID: 27087, updated on 5-Jan-2013

CD68: Gene ID: 968, updated on 6-Jan-2013; Isoform Long (CD68.1) [UniParc]. Last modified May 15, 2007. Version 2. Checksum: 69E68D69EDE8EFB0, P34810-1/2, Isoform 1/2

CD79a: Gene ID: 973, updated on 5-Jan-2013; Isoform 1 (Long) [UniParc]. Last modified June 1, 1994. Version 2. , Checksum: 6E5B837409969292, P11912-1/2, Isoform 1/2

CD146: Gene ID: 4162, updated on 30-Dec-2012; Isoform 1 [UniParc]. Last modified January 10, 2006. Version 2. Checksum: E46CB8AC7BA0738E, P43121-1/2, Isoform 1/2.

surfactant proteins (A and B):

Gene ID: 6440, updated on 30-Dec-2012 and Gene ID: 6439, updated on 30-Dec-2012, P07988 [UniParc]. Last modified May 1, 1992. Version 3. Checksum: 9FD7F66678A35153, and Isoform 1 [UniParc]. Last modified April 1, 1990. Version 2. Checksum: C26A21E33C60AA78, P11686-1/2, Isoform 1/2

synaptophysin:

Gene ID: 6855, updated on 30-Dec-2012, P08247 [UniParc]. Last modified August 1, 1991. Version 3. Checksum: 592289C43B12EFA7

nicotinic acetylcholine receptors:

Gene ID: 1138, updated on 30-Dec-2012, Gene ID: 1136, updated on 6-Jan-2013, Gene ID: 1139, updated on 13-Jan-2013, Gene ID: 1137, updated on 30-Dec-2012, Gene ID: 1141, updated on 5-Jan-2013

muscle-specific kinase MUSK:

Gene ID: 4593, updated on 8-Jan-2013, Isoform 1 [UniParc]. Last modified January 1, 1998. Version 1. Checksum: 3DDC20E179FA010C, O15146-1/2, Isoform 1/2

voltage-gated calcium channel (P/Q-type):

Gene ID: 773, updated on 5-Jan-2013; Isoform 1 (1A-1) (BI-1-GGCAG) [UniParc]. Last modified July 15, 1999. Version 2. Checksum: 2F2F378ACE02FD56, O00555-1/2/3/4/5/6/7, Isoforms 1-7, Gene ID: 25398, updated on 11-Jan-2013, J3KP41 [UniParc]. Last modified October 3, 2012. Version 1. Checksum: AEDF4D2A5E49263F

voltage-gated potassium channel (VGKC):

Gene ID: 3737, updated on 30-Dec-2012, Gene ID: 3736, updated on 8-Jan-2013, Gene ID: 3742, updated on 8-Jan-2013

N-methyl-D-aspartate receptor (NMDA):

Gene ID: 2904, updated on 5-Jan-2013, Q13224 [UniParc]. Last modified June 20, 2001. Version 3. Checksum: 40AEB12BE6E50CEF; Gene ID: 2902, updated on 30-Dec-2012, Isoform 3 (Long) (NR1-3) [UniParc]. Last modified June 1, 1994. Version 1. Checksum: CDF5402769E530AB, Q05586-1/2/3/4/5, Isoforms 1-5

TSHR: Gene ID: 7253, updated on 4-Jan-2013, Isoform Long [UniParc]. Last modified March 29, 2005. Version 2. Checksum: D2EE9CEBFD64A65F, P16473-1/2/3, Isoforms 1-3

Amphiphysin:

Gene ID: 273, updated on 8-Jan-2013, Isoform 1 (128 kDa) [UniParc]. Last modified February 1, 1996. Version 1., Checksum: 78B4F75AB75BA357, P49418-1/2, Isoform 1-2

ganglioside GQ1B: Gene ID: 29906, updated on 30-Dec-2012

GD3: Gene ID: 117189, updated on 22-Jun-2012

Ca-125: Gene ID: 94025, updated on 30-Dec-2012, Q8WXI7 [UniParc]. Last modified March 1, 2003. Version 2. Checksum: B3E7BDF19997A440

Her-2/neu: Gene ID: 2064, updated on 13-Jan-2013, 4. Protein = P04626-1/2/3/4 = Isoform 1-4 , Last modified August 13, 1987. Version 1.
gross cystic disease fluid protein 15; Gene ID: 5304, updated on 30-Dec-2012

CD117: Gene ID: 3815, updated on 6-Jan-2013

CD30: Gene ID: 943, updated on 6-Jan-2013; Isoform Long [UniParc]. Last modified December 1, 1992. Version 1. Checksum: 7A407CC78A6E0BC8, P28908-1/2, Isoform 1/2

Platelet derived growth factor receptor PDGFR alpha:

Gene ID: 5159, updated on 13-Jan-2013, Gene ID: 5156, updated on 13-Jan-2013, Isoform 1 [UniParc]. Last modified April 1, 1990. Version 1. Checksum: 5E3FB9940ACD1BE8, P16234-1/2/3, Isoforms 1-3; P09619 [UniParc]. Last modified July 1, 1989. Version 1. Checksum: 038C15E531D6E89D

Melanoma associated marker/Mart 1:

Gene ID: 2315, updated on 30-Dec-2012; Q16655 [UniParc]. Last modified November 1, 1996. Version 1. Checksum: B755BFF39CFCB16E

CD133: Gene ID: 8842, updated on 13-Jan-2013; Isoform 1 (AC133-1) (S2) [UniParc].
Last modified June 1, 1998. Version 1. Checksum: D21CBC05ADB2DEDF, O43490-1/2/3/4/5/6/7, Isoforms 1-7

In the following, reference is made to the examples which are given to illustrate, not to limit the present invention.

Examples

Example 1

Cloning of recombinant antibody constructs

DNA sequences derived from hybridoma cells and coding for the variable domains of anti-CD3, anti-CD45 and anti-HLA A2 antibodies, respectively, were used to generate the antibody constructs depicted in Figure 3 by standard methods of molecular biology (see, e.g. Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York (2001)). The constructs were designed to carry different affinity tags to facilitate identification and purification upon expression of recombinant proteins (Myc-, Flag, His-Tag). For details on domain arrangement, affinity tags and linkers of the constructs, see Figure 3.

pelB Leader codes for an amino acid sequence that directs a protein expressed in bacteria to the bacterial periplasm. The leader sequence is cleaved by bacterial enzymes and the protein can be isolated.

Example 2

Expression and Purification of Recombinant Antibodies

Periplasmic Protein Expression:

Recombinant antibody constructs were expressed in the periplasm of *E. coli* strain TG1

using an appropriate prokaryotic expression vector. Two litres of 2 × TY medium including 0.1 % glucose and 100 µg/ml ampicillin were inoculated with 20 ml of an overnight culture of transformed TG1 and grown to exponential phase (OD600 0.8 – 0.9) at 37°C. Since the antibody fragments are under control of the lactose promotor, protein expression was induced by addition of 1 mM IPTG followed by incubation at RT (room temperature) with shaking for additional 3 h. Cells were harvested by centrifugation for 10 min at 2,750 × g and 4°C and were resuspended in 100 ml or an appropriate buffer. Cell lysis was performed by adding 50 µg/ml freshly dissolved lysozyme [Roche Diagnostics] and incubating for 25 min on ice. Following, 10 mM $MgSO_4$ were added to stabilise spheroblasts, and cells were centrifuged for 10 min at 6,200 × g and 4°C. Finally, the supernatant obtained, containing the periplasmic protein, was dialysed against PBS overnight at 4°C and was centrifuged again for 15 min as stated above. Afterwards, recombinant proteins were purified by Ni-NTA-IMAC (Nickel Nitrilo-triacetic acid Immobilised Metal Affinity Chromatography).

Immobilised-Metal Affinity Chromatography (IMAC):

For purification of recombinant proteins with a His_6 tag, an IMAC was performed by means of immobilised nickel-nitrilotriacetic acid (NTA) agarose beads [Qiagen]. First, a column of 1 ml Ni-NTA agarose needed to be equilibrated with approximately 10 ml of sterile PBS or a sodium phosphate buffered solution with 20 mM imidazole. Then, crude protein, either precipitated from cytoplasmic expression or dialysed from periplasmic expression, was gradually applied to the column. After washing with about 20 ml of an appropriate IMAC wash buffer (sodium phosphate buffered solution containing 20 – 35 mM imidazole) until no more protein was detectable in the flow, bound protein was eluted from the column in 500 µl fractions with a sodium phosphate-buffered solution including 250 mM imidazole.

All collected wash and elution fractions were tested for presence of protein by a qualitative Bradford assay by adding 10 µl of each sample to 90 µl of 1 × Bradford solution. Verification of the purification process was performed by an SDS-PAGE analysis. For this purpose, eluted fractions were run in parallel with crude protein, flow, and wash fraction under reducing conditions. Finally, positive fractions determined by the colorimetric reaction were pooled into peak and minor fractions and dialysed against PBS overnight at 4°C. For usage in stimulation assays, purified proteins needed to be sterile filtrated, and their concentration has been determined. In addition, after protein quantification, 2 µg of further used fractions were also analysed by SDS-PAGE and Western blotting under reducing and

non-reducing conditions.

In an alternative of Example 2, DNA coding for (V_H)CD3-EGFR(V_H-V_L), (V_H)CD3-CEA(V_H-V_L), (V_H)CD3-Her2(V_H-V_L), (V_H)CD3-HLA-A2(V_H-V_L), (V_H)CD3-HLA-CW6(V_H-V_L) (V_H)CD3-CD138(V_H-V_L), (V_H)antiDig-EGFR(V_H-V_L), (V_H)antiHis-HLA-A2(V_H-V_L), (V_L)CD3-CEA(V_H-V_L), (V_L)CD3-EpCAM(V_H-V_L), (V_L)antiDig-EpCAM(V_H-V_L), (V_L)antiHis-CD45(V_H-V_L), (V_L)CD3-CD45(V_H-V_L) were synthesised and proteins were produced and isolated by GenScript (Piscataway, NJ, USA). The DNA was codon optimized for E.coli expression (vector E3), expression optimized, grown in 2 litres standard LB-medium, protein was obtained from inclusion bodies or periplasm (pelB leader) in one step by Ni-HiTrap column. Bacterial endotoxins were removed by dialysis against 5 litres 1x phosphate buffered saline (PBS). The concentration was measured by Bradford protein assay with bovine serum albumin (BSA) as standard. The purity was estimated by densitometric analysis of a Coomassie Blue-stained SDS-PAGE gel. Aliquots were stored at -80°C or +4°C. Storage buffer was used 1xPBS, 5% Glycerol, 0.5% sodium lauroyl sarcosine, pH 7.4.

Example 3

Cell Culture Techniques

Cell Cultivation:

Mammalian cells were cultivated in T75 tissue culture flasks in 20 ml of the appropriate culture medium at 37°C with 5 % CO_2. Cells were split every 2 – 3 days. Adherent cells first needed to be detached with 1 × trypsin-EDTA. Cells were counted using a vital stain, eosin or trypan blue. For storage, cells of 60 – 80 % confluence were harvested by centrifugation for 5 min at 450 × g, resuspended in FCS with 10 % DMSO, aliquoted in cryovials, and gradually frozen to a temperature of –80°C. Cells were thawed quickly at 37°C in a water bath and cautiously added to 5 ml medium. In order to remove DMSO, cells were centrifuged again, resuspended in fresh medium and transferred into a tissue culture flask.

Preparation of Peripheral Blood Mononuclear Cells (PBMC):

PBMC, comprising lymphocytes and monocytes, were previously isolated from the buffy coat of a healthy human donor by density centrifugation using the Ficoll based lymphocyte

separation solution LSM 1077 (PAA Laboratories, Pasching, Austria). Since, during usage, these PBMC nevertheless appeared as an inhomogeneous cell population, the separation from remaining erythrocytes, granulocytes, and thrombocytes was repeated as follows. Thawed PBMC, resuspended in 30 ml RPMI 1640 medium containing 10 % FCS and Pen-Strep, were cautiously layered onto 10 ml of LSM 1077 and centrifuged for 5 min at 800 × g without braking. After discarding the upper phase, PBMC concentrated in the interphase were transferred into a fresh tube, resuspended in 30 ml of medium, and centrifuged for 5 min at 450 × g. Monocytes were removed by cultivating PBMC in a Ø 10 cm tissue culture plate overnight, allowing adherence of monocytes to the plate. Finally, PBMC, remaining in solution, were harvested.

In an alternative of Example 3, Primary human cancer cells from a patient with metastatic pancreatic cancer were extracted from the ascites bags of the patient (Figure 29). 4 litres with fresh collected malignant ascites were stored in 2 litres glass bottles at 4°C over night. The next day the cell pellet from the glass bottom was washed in 1xPBS and resuspended in culture medium (DMED supplemented with 200 µM l-glutamine, 10% heat inactivated FBS, penicillin (200 U/mL), streptomycin (200 µg/mL) and sodium pyruvate (1mM) (Gibco®)). Adherend cells were cultured in incubator 36°C, 5%CO_2, 90% humidity. The same day the ascites was collected from the patient, 20ml peripheral blood for PBMC extraction was collected. Primary leukemic cells were obtained from a 71 year old male patient with T-cell-prolymphocytic leukemia (T-PLL) (Figure 11A) relapsing 32 days after matched allogeneic stem cell transplantation. The leukemic T-PLL cells were extracted as PBMCs from the peripheral blood of the patients. At the time the sample was drawn the patient had >90% leukemic blast in his blood count in routine clinic diagnostic. From all patients an informed consent, approved by the University hospital of Würzburg ethical committee, was signed.

In an alternative of Example 3, generation of cytomegalievirus (CMV)-specific human T-cells: Briefly, dendritic cells (DC) were generated from plastic adherent monocytes from PBMC of HLA-A0201 negative, B0702+ donor. After 72h of culture in GM-CSF/IL4-containing DC medium (Cellgenix), DC were matured in medium containing IL4(100ng/ml), GM-CSF(800IU/ml), LPS (10ng/ml) and IFNγ (100U/ml) plus 2.5ug/ml CMV pp65 derived peptide TPRVTGGG. After 16h, DC were irradiated (30Gy) and co-incubated with $CD45RO^-$, $CD57^-$ naïve $CD8^+$ T-cells at a 1:4 ratio in medium containing 5% AB serum and IL21 (10ng/ml). Fresh medium, IL7 and IL15 was added on days 3, 5 and 7 of culture,

before evaluation on day 10-12. Cells were cultured in Cellgenix DC medium. Human AB serum was used from PAA. One single batch was used throughout all experiments. IL4, IL7, IL15, IL21 were either purchased from Peprotech or Cellgenix (with identical results). GM-CSF was purchased from Gentaur. LPS (E.coli O:15) was purchased from Sigma. The HLA-B0702-restricted CMV-specific peptide TPRVTGGG was purchased from jpt. For *in vivo* experiments, CMV-specific T-cells were further purified using APC-labelled MHC-multimers (Immudex). MHC multimer staining was performed at room temperature, followed by isolation of MHC-multimer+ T-cells with anti-APC-beads (Miltenyi).

Example 4

Functional Assays

Flow Cytometry:

Binding of antibody fusion proteins to antigen-presenting tumour cells and/or T lymphocytes was tested by flow cytometry. For this purpose, 2.5 – 5 × 10^5 cells were incubated with 10 µg/ml of scFv or 0.004 – 4 µg/ml of titrated fusion proteins in 100 µl of a suitable buffer solution (such as PBS + bovine serum albumin, or other acceptable buffer solution) per well on a 96-well V-shaped plate at 4°C for 2 h. After washing three times with 150 µl of a suitable buffer solution, cells were incubated with FITC-conjugated anti-His_6 tag or anti-Flag Tag or anti-myc Tag antibody at RT for 30 min and washed again two times. For gating and testing for background staining, additionally two samples of each cell type were prepared, one of unstained cells and one stained with FITC-conjugated anti-His_6 tag antibody without any protein. Finally, cells were resuspended in 500 µl of a suitable buffer solution, transferred into FACS tubes, and analysed by flow cytometry.

PBMC Stimulation Assay:

Stimulatory properties of recombinant proteins were tested in a cell-based stimulation assay. Thereby, T-cell activation mediated by bispecific antibodies and "tridomain constructs" was determined by measuring PBMC stimulation in terms of the IL-2 release induced.

Measurement of stimulatory Activity of Constructs:

CD45 pos/HLA A2 myeloma cell line U266 were seeded in a flat-bottomed 96-well cell culture plate at a density of 105 cells per well in 100 µl of culture medium. Titrated stimulatory proteins were added as indicated in 100 µl medium per well and were preincubated for 1 h at 37°C and 5 % CO2 to ensure sufficient binding. Unstimulated PBMC, thawed and isolated the day before, were then added at indicated density and incubated for 24 h at 37°C and 5 % CO_2. Finally, plates were centrifuged for 5 min at 450 × g to harvest cell-free supernatants for IL-2 quantification in ELISA.

IL-2 Sandwich ELISA:

As an indicator for the stimulatory activity, T-cell activation induced by bispecific antibodies was measured in terms of the IL-2 release. Upon PBMC stimulation, concentration of secreted IL-2 in the supernatant was determined by an IL-2 sandwich ELISA.

First, a 96-well ELISA plate was coated with 400 ng/100 µl per well of mouse anti-human IL-2 antibody overnight at 4°C, followed by saturation of nonspecific binding sites with a suitable blocking buffer for 2 h at RT. In the meantime, serial 1 : 2 dilutions of an IL-2 standard were prepared in duplicate in reagent diluent starting with a maximum IL-2 concentration of 1,000 pg/ml. Then, supernatants containing IL-2 were 1 : 3 diluted in RPMI 1640 medium containing 10 % FCS and Pen-Strep (Penicillin-Streptomycine). Both diluted supernatants and standards were transferred into the ELISA plate and incubated for 2 h at RT. Following, IL-2 was detected by incubation with 17.5 ng/100 µl per well of biotinylated goat anti-human IL-2 antibody for 2 h at RT. Finally, 100 µl of HRP-conjugated streptavidin, 1 : 200 diluted in reagent diluent, was added per well and incubated for 20 min at RT. Each plate was developed using a TMB substrate solution. In order to achieve a background signal, at least 2 wells on each plate were incubated with reagent diluent or medium only and the detecting antibody plus TMB. Between each incubation step, the plate was washed three times with PBS containing 0.05 % Tween-20 and once with PBS only.

A seven point standard curve was created by plotting the absorbance signals of each standard sample against the IL-2 concentration. Thus, the amount of IL-2 of each supernatant could be determined by interpolation of the standard curve fitted with the nonlinear regression

equation for one phase exponential association using GraphPad Prism®.

IFN-γ ELISA (alternative of Example 4):

In 100µl cell culture supernatant the IFN-γ concentration was measured using the human IFN-γ ELISA Kit (Invitrogen™) after manufacturer's protocol. Briefly 50 µL of Incubation Buffer was added to each well of a precoated 96-well plat. 50 µL of the Standard Diluent Buffer to zero wells. 50 µL of standards and samples to each well. 50 µL of biotinylated Hu IFN-γ Biotin Conjugate solution into each well. Taped gently on the side of the plate to mix. Covered plate with plate cover and incubate for 1 hour and 30 minutes at room temperature. Thoroughly aspirated solution from wells and discarded the liquid. Washed wells 4 times. Added 100 µL Streptavidin-HRP Working Solution to each well. Covered plate with the plate cover and incubated for 45 minutes at room temperature. Thoroughly aspirated solution from wells and discarded the liquid. Added 100 µL of Stabilized Chromogen to each well. The liquid in wells turned blue. We incubated for 15-30 minutes at room temperature and in the dark. Added 100 µL of Stop Solution to each well. Taped side of plate gently to mix. The solution in the wells changed from blue to yellow. The absorbance of each well was read with a BioRad plate reader at 450 nm.

Cytotoxicity Assay:

The HLA-A2/CD45 positive cell line U266 or myeloma cell line U266 was labelled with 10 µM CFSE (Invitrogen Vybrant CFDA SE Cell Tracer Kit) in 350 µl PBS for 10 min at room temperature (RT) in the dark. The labelling reaction was stopped by the addition of 5 ml fetal calf serum (FCS), followed by a 1-minute incubation at RT. After 2 washes, the CFSE-labelled target cells were resuspended in assay medium and co-incubated with Peripheral Blood Mononuclear Cells (PBMC) from a HLA-A2 negative healthy donor at a ration of 1:10 ($5*10^5$ U266 and $5*10^6$ PBMCs in 2 ml) and 27 nM of antibody constructs as indicated. A sample treated with Triton was used as positive control (100% lysis) and a sample without antibody construct as negative control (0% lysis). After 24h, apoptotic cells were visualized by 7AAD stain (Biozol, 10 min at RT) and % specific Lysis of CFSE labelled U266 cells was calculated employing flow cytometry techniques.

Caspase-3 Assay (alternative of Example 4):

Staining was performed after co-incubating of the target cells with T-cells (tumor cells: T-cells ratio 2:1) with or without the specific polypeptides for 4h. Surface staining for HLA-A2 and CD45 was performed first, followed by fixation and permeabilization (Fix+Perm, BD Biosciences). Activated Caspase-3 antibody was then added for 30 min. (BD Biosciences). Cells were washed with 1xPBS +5% human serum (HS, PAA Laboratories) and analyzed on a BD-FACS Canto-II. % specific apoptosis was calculated as (% experimental value - % spontaneous release)/(100% - % spontaneous release)*100.

Alamar blue assay (alternative of Example 4):

The alamarBlue® assay (Abd Serotec) was used to measure proliferation and viability of cells after exposure to toxins. Briefly, cells were grown in 100µl cell culture medium per well (96 well plate). For analysis 10µl alamarBlue was added per well and incubated in the incubator for 30-120 minutes. The absorbance was read with a BioRad plate reader at 570nM and 600nM. For blank media only was used. The percent difference in reduction of cell proliferation between the different polypeptide groups was calculated as indicated by the manufacturer, using cells growing in culture without toxin as control.

Digoxigenin Assay (alternative of Example 4):

First peroxidise from horseradish (HRP, Sigma-Aldrich Chemie gmbH) was labelled with digoxigenin NHS-ester (Sigma-Aldrich Chemie gmbH) in a 1/3 molar ratio. Dig-HRP was cleaned up with micro Bio-Spin™ chromatography columns (BioRad and and stored at 4°C in the dark. Colo-206F cells were first incubated with indicated polypeptides at various concentrations for 90 minutes. Cells were washed with PBS and resuspended in cell culture medium with Dig-HRP and incubated for 30 minutes. Afterward cells were washed twice with PBS and resuspended in 50µl PBS. 50µL of Stabilized Chromogen (Invitrogen™) was added for 15-30 minutes at room temperature in the dark. 50 µL of Stop Solution was added and the absorbance was read with a BioRad plate reader at 450 nm.

Mice (alternative of Example 4):

The HLA.A2 transgenic, immunodeficient mice (NodScid IL-2rg -/- HLA.A2/B2m tg; Stock number 14570, The Jackson Laboratory, Bar Harbor, Maine, USA) for the in vivo experiment (Figure 12A) were maintained in our certified animal facility (ZEMM, Center for experimental molecular medicine, University hospital Würzburg) in accordance with European guidelines. Female Mice, 6-10 weeks old, were divided into five groups, six mice

per group (n=30). $5x10^6$ THP-1 cells, $1,25x10^5$CMV specific CD8+ T-cells (tumour cell: T-cell ratio 40/1) and the 0.5µg of the polypeptides were injected intraperitoneally (i.p.) as indicated. After injection, mice were monitored by daily inspection. A second injection of $1.16x10^5$ CMV-specific CD8+ T-cells/mouse was given at day 13 and injections of the polypeptides were repeated every three days a week. The animals were sacrificed when the increase in body weight was greater 80% or if they appeared moribund according to institutional guidelines.

Domain structure, affinity tags and linkers of the constructs or poypeptides used in Examples 5-9 or Figures 4-11 are shown in Figure 3. These constructs and all constructs or poypeptides used in Figures 4-30 were prepared as described in Examples 1 and 2. Cell culture and functional assays in Examples 5-9 and culture, functional assays and in vivo work as to Figures 4-30 were carried out as described in Examples 3 and 4.

Example 5

The CD45 and HLA A2 positive myeloma target cell line U266 was co-incubated with HLA A2 negative T cells (monocyte depleted PBMCs (peripheral blood mononuclear cells) from a healthy donor and varying amounts of HLA A2 and CD3 bispecific antibody constructs as indicated (Numbers 85, 82, 75 and 71). PHA-L (phytohemagglutinin, a lectin that causes unspecific stimulation of T cells; 1 µg/ml final concentration) was used as positive control and single chain scFv constructs with specificity for HLA A2 (Number 4) or CD3 (Number 36) were investigated. IL2 (Interleukin-2) production by T cells was measured by ELISA techniques. No IL2 production was found in experimental situations without any constructs. Data obtained is depicted in Figure 4.

Example 6

The CD45 and HLA A2 positive myeloma target cell line U266 was co-incubated with HLA A2 negative T cells (monocyte depleted PBMCs) from a healthy donor and varying amounts of "tridomain constructs" added either separately (Numbers 42, 45, 55; numbers referring to constructs as depicted in Figure 3) or in combinations (42 + 45 or 42 +55). PHA-L and single chain scFv constructs with specificity for CD45 (Numbers 46 and 17) were given as controls. IL2 production by T cells was measured by ELISA techniques. No IL production

was found in experimental situations without any constructs. Data obtained is depicted in Figure 5.

Example 7

The CD45 and HLA A2 positive myeloma target cell line U266 was co-incubated with HLA A2 negative T cells (monocyte depleted PBMCs) from a healthy donor and the HLA A2 and CD3 bispecific antibody construct alone (number 71, 27 nM) or in combination with single chain scFv constructs that block the antigenic epitopes on HLA A2 (Number 4, hundredfold excess compared to the concentration of construct 71, i.e. 2700 nM) or CD3 (Number 36, ninefold excess compared to the concentration of construct 71, i.e. 243 nM). IL2 production by T cells was measured by ELISA techniques and PHA-L is given as control. Data obtained is depicted in Figure 6.

Example 8

The CD45 and HLA A2 positive myeloma target cell line U266 was co-incubated with HLA A2 negative T cells (monocyte depleted PBMCs) from a healthy donor and the combination of constructs 42 and 45. T cell stimulatory function was blocked by single chain constructs specific for HLA A2 (number 4) or CD45 (number 46). Complementation of T cell stimulatory function was tested by assaying constructs 42 and 45 separately or the single chain scFv construct directed against CD3 (number 36). IL2 production by T cells was measured by ELISA techniques and PHA-L is given as control. Concentration of constructs was 27 nM, unless indicated otherwise. ("9x" indicates a concentration of 243 nM, "100x" a concentration of 2700 nM.) Data obtained is depicted in Figure 7.

Example 9

The CD45 and HLA A2 positive myeloma target cell line U266 was co-incubated with HLA A2 negative T cells (monocyte depleted PBMCs) from a healthy donor and the combination of constructs 42 and 55. T cell stimulatory function was blocked by single chain constructs specific for HLA A2 (number 4) or CD45 (number 46). Complementation of T cell stimulatory function was tested by assaying constructs 42 and 55 separately or the single chain scFv construct directed against CD3 (number 36). IL2 production by T cells was measured by ELISA techniques and PHA-L is given as control. Concentration of constructs

was 27 nM, unless indicated otherwise. ("9x" indicates a concentration of 243 nM, "100x" a concentration of 2700 nM.) Data obtained is depicted in Figure 8.

The results of the preceding Examples clearly demonstrate that two constructs (42+45) or (42+55) first have to bind their ligands on the surface of a single cell in order to subsequently complement T cell engaging function.

Example 10

Lysis of the CD45 and HLA A2 positive myeloma target cell line U266 by HLA A2 negative T cells (monocyte depleted PBMCs) in the presence of V_LCD3-scFvHLA A2 (27 nMol) or V_H-scFvCD45 (27 nMol) or the combination of both of these constructs (27 nMol each) was determined using flow cytometry based techniques. Percent lysis was calculated by apoptotic U266 cells divided through total U266 cells and background apoptosis was subtracted. Data obtained is depicted in Figure 9.

Example 11

As parts of the final bipartite construct, two polypeptides were designed, each composed of an antigen-binding single-chain variable fragment (scFv) and either the variable light (V_L) or variable heavy chain (V_H) domain of a T cell-activating anti-CD3 antibody (Figure 10). When these two polypeptides bind their respective antigens on the surface of a single cell, the V_L and V_H domains interact with each other to reconstitute the original anti-CD3 binding site. The thus on-target formed trispecific heterodimer engages and stimulates T cells for tumor cell destruction.

This scenario is fully validated *in vitro* when T lymphocytes are confronted with target cells that have been incubated with the two different polypeptides. As proof of principle, major histocompatibility antigen HLA-A2 and the hematopoetic lineage marker CD45 were targeted as first and second antigens, which both are expressed on U266 myeloma cells, primary cells from a patient with pro-lymphocytic leukemia of the T cell lineage (T-PLL), and THP-1 acute myeloid leukemic blasts (Figure 11). Due to the described V_L/V_H interaction, the now trispecific heterodimer potently stimulates T cells to secrete interleukin-2 (IL-2) (Figure 11a) and to lyse the labeled tumor cells at nanomolar concentration (Figure 11b), the cytotoxic efficacy being quite similar to that of a bispecific T cell-activating antibody, which was employed as a positive control (Figure 11A, left panel), Mack, 1995,

Proc Natl Acad Sci 92, 7021-7025. When the polypeptides were added separately from each other, they did not induce T lymphocytes to lyse target cells. These results are in line with structural data indicating that both, V_H and V_L domains are required to confer sufficient affinity to the target antigen (Figure 11A, B), Colman, 1987, *Nature* 326, 358-363; Amit, 1986, *Science* 233, 747-753. Moreover, the results reveal that possible homodimerization of either V_H or V_L arms results in a negligible measurable biological effect.

To demonstrate that the two molecules must first bind their antigens on the surface of the target cell for V_H/V_L heterodimerization to occur, single-chain variable fragments specific for HLA-A2 and CD45 were used to block the respective epitopes on the target. As shown in Figure 11c, when present in great excess, these inhibitors prevented the two polypeptides from triggering T cells in a dose-dependent manner. Furthermore, T cells were not stimulated when the target cells were omitted (data not shown) or when target cells were probed that express CD45 only (RAJI cells, Fig. 11D) or neither target molecule (KMS-12-BM, Fig. 11D).

Example 12

For *in vivo* proof of concept, a model of allogeneic mismatch stem cell transplantation was resorted in which a patient's residual leukemic and hematopoietic cells, all HLA-A2 and CD45-positive, must be eliminated to give the allogeneic donor stem cells (HLA-A2–negative, CD45-positive) a chance to engraft and to reconstitute hematopoesis (see Figure 2). To put the specificity of the bipartite construct to the test, immunodeficient mice expressing the human HLA-A2 transgene on virtually all nucleated cells were used, the question being whether HLA-A2–positive but CD45-negative murine tissues would suffer collateral damage. THP-1 cells were injected intraperitoneally with or without CD8 T lymphocytes from an HLA-A2–negative donor, which had been selected for specificity to cytomegalovirus (CMV) to avoid human anti-murine immune reactivity. Intraperitoneal tumors developed rapidly in mice that did not receive the polypeptides, and in mice treated either with single molecule types or with the combination of both polypeptides but without T cells. In all instances, fatal disseminated disease developed within 3 to 4 weeks (Fig. 12A). In stark contrast, all tumor-bearing mice treated with T cells and repeated injections of both polypeptides survived the end of the experiment on day 31, albeit with palpable tumors at the injection site. These results clearly show that the bipartite construct truly redirects T cells irrespective of their specificity at tumor cells that simultaneously express both target

molecules (HLA-A2 and CD45) in vivo. As an aside, a T cell recruiting bispecific antibodies against HLA-A2 would wreak havoc by redirecting T cells against all HLA-A2 positive murine tissues. Likewise, a CD45-binding bispecific antibody would have mediated lysis of all hematopoietic cells, including THP-1 leukemic blasts and T cells from the donor. In our set-up, however, injection of HLA-A2–specific polypeptide into the HLA-A2 transgenic animals caused no apparent toxicity.

To further examine possible toxicity to bystanders, we employed a highly sensitive apoptosis assay on THP-1 cells and HLA-A2–negative but CD45-positive monocytes, the latter representing the healthy bystander compartment. As depicted in Figure 12B, we observed caspase-3 activation in THP-1 cells but not in monocytes treated in the same well with the combination of the polypeptides or the bispecific positive control and donor T cells. THP-1 cells cultured with T cells and individual polypeptides were unaffected. These observations again clearly show initiation of apoptosis exclusively in the double antigen positive target population, while the HLA-A2–negative bystander cells are spared. These experiments model quite accurately the dire clinical situation of leukemia patients with a HLA-mismatched stem cell transplant. The combinatorial approach of using a distinctive HLA molecule and CD45 aims at enhancing the desired graft versus leukemia effects by retargeting the donor's T cells against leukemic blasts of both, myeloid and lymphoid origin.

Example 13

To venture into solid tumors, we targeted the combinatorial approach to epithelial cell adhesion molecule (EpCAM) and epidermal growth factor receptor (EGFR) antigens. Both antigens are over-expressed in various carcinomas and have been extensively studied in clinical phase II and III trials. The expression of EGFR is closely associated with cell proliferation, while EpCAM is present at the basolateral surface of virtually all simple epithelia and was recently found to act like a signaling protein in the *Wnt* pathway, Maetzel, 2009, *Nat Cell Biol* **11**, 162-171. As Figure 13a illustrates, the two polypeptides trigger the release of interferon-γ (IFNγ) from co-incubated donor lymphocytes and mediate apoptosis of the double-positive cancer cell line COLO-206F at nanomolar concentrations (Fig. 13a, b), but only when given in combination and not with either part alone. As a descendant of neuroepithelial tissue, the melanoma cell line FM-55 lacks EpCAM, and therefore was completely resistant to the polypeptides (Fig. 13a, b). Though the expression of EGFR and EpCAM overlaps broadly on proliferating carcinoma cells, non-proliferating epithelial cells,

e.g., of liver and pancreas solely expressing EGFR or EpCAM antigens, respectively, should be less susceptible to or protected from the two-pronged attack. Notably, hepatic and pancreatic toxicities have been dose-limiting for high-affinity monoclonal EpCAM antibodies in clinical trials (for review see, Munz, 2010, *Cancer Cell Int* **10**:44).

Example 14

The further validation of the bipartite functional complementation strategy was performed by extensive *in vitro* experiments, using a combination of different polypeptides, targeting various cell surface antigens on different human cell lines.

The HLA A2 positive human tumor cell lines FM-55 (myeloma), Colo-206F (colon cancer) and OVCAR (ovarian cancer) were co-incubated with HLA-A2 negative PBMCs from a healthy donor, polypeptide against HLA-A2 (CD3(V_L) - HLA-A2(V_H-V_L)) and with a second polypeptide targeting either CEA (CD3(V_H) - CEA(V_H-V_L)), EGFR (CD3(VH) - EGFR(VH-VL)) or Her2 (CD3(V_H) - Her2(V_H-V_L)). IL2 or IFN-γ production by lymphocytes was measured by ELISA techniques. These data demonstrate that (i) a specific combination of antigens, an antigen signature, can be expressed on carcinomas of various origin (skin, neuroepithelial, gut and ovary tissue), (ii) the antigen signature is approachable with our bipartite functional complementation strategy using a set of polypeptides specific for the antigen signature . Data obtained are depicted in Figures 14, 15 and 16.

Example 15

To demonstrate the exchangeability of the functional domain, the fragments F1 and F2 of a set of polypeptides were exchanged with each other, retaining their specific complementation ability for on target restoration of their original antibody domain to engage T cells. Therefore the set of polypeptides against the CD45 and HLA-A2 target antigen was used. The polypeptide against CD45 had CD3(V_L) as fragment F1 and the polypeptide against HLA-A2 had CD3(V_H) as fragment F2. The CD45 and HLA-A2 positive myeloma cell line U266 was co-incubated with HLA-A2 negative T cells from a healthy donor and polypeptides against CD45 (CD3(V_L) - CD45(V_H-V_L)) and HLA-A2 (CD3(V_H) – HLA-A2(V_H-V_L)) in varying amounts. T cell engagement was assessed by reactive IFNγ production, measured by ELISA techniques. No IFNγ production was found in experimental situations without any polypeptides. Data obtained is depicted in Figure 17.

Example 16

The bipartite functional complementation strategy was further tested by targeting a set of antigens, already used as targets for antibody therapy of cancer (EGFR, EpCAM and Her2) (Her2 is a target for Trastuzumab in breast cancer, EGFR is a target for Cetuximab in colorectal cancer and EpCAM is a target for Catumazumab for the treatment of neoplastic ascites). The EGFR, EpCAM and Her2 positive cells (Colo-206F, CX-1 and OVCAR) were co-incubated with PBMCs from a healthy donor and the combination of polypeptides against EGFR (CD3(V_H) - EGFR(V_H+V_L)), EpCAM (CD3(V_L) - EpCAM(V_H+V_L)) and Her2 (CD3(V_H) - Her2(V_H+V_L)). Complementation of lymphocyte stimulatory function was assessed by reactive IFNγ production, measured by ELISA techniques. No IFNγ production was found in experimental situations without any polypeptides. Data obtained is depicted in Figures 18 and 19.

Example 17

To test an antigen combination with close clinical correlation, the combination CD45 and CD138 was used to target human multiple myeloma (MM) cells. The majority of human MM cells are positive for CD45 and CD138. A T cell recruiting bispecific antibodies against CD45 would kill all hematopoetic cells of a patient and against CD138 would cause severe side effects because of its expression on various normal tissues (epithelial cells, endothelia, trophoblastic cells and glandular cells of the GI tract, The Human Protein Atlas, Version: 10.0, Atlas updated: 2012-09-12). In contrast the combination of CD45 and CD138 is found exclusively on plasma cells and MM cells and is therefore a good antigen signature for the targeted therapy approach. The CD45 and CD138 positive human multiple myeloma cell line AMO-1 was co-incubated with PBMCs from a healthy donor and the combination of polypeptides against CD45 (CD3(V_L) - CD45(V_H+V_L)) and CD138 (CD3(V_H) - CD138(V_H+V_L)). Complementation of lymphocyte stimulatory function was assessed by reactive IFNγ production, measured by ELISA techniques. No IFNγ production was found in experimental situations with single polypeptides or without any polypeptides. Data obtained is depicted in Figure 20.

Example 18

A further application of the bipartite functional complementation strategy is to target single antigens on the cell surface and to kill single antigen positive tumor cells. One major

drawback for T cell recruiting bispecific antibodies with functional antiCD3 binding sides are severe side effects caused by unspecific T-cell activation and cytokine release (Linke, R. et al. Catumaxomab: clinical development and future directions. MAbs 2, 129-136 (2010)). The advantage of this bipartite functional complementation strategy is the fact, antibodies that the T-cell activating antiCD3 functional domain is exclusively restored on the target cell. Without the target cell, no T-cell activating domain is present. The CD45 and CD138 positive human multiple myeloma cells AMO-1 and U266 were co-incubated with PBMCs from a healthy donor and the combination of polypeptides against a single target antigen, either CD138 ($CD3(V_H)$ - $CD138(V_H+V_L)$ + $CD3(V_L)$ - $CD138(V_H+V_L)$) or CD45 ($CD3(V_H)$ – $CD45(V_H+V_L)$ + $CD3(V_L)$ – $CD45(V_H+V_L)$). Complementation of lymphocyte stimulatory function was assessed by reactive IFNγ production, measured by ELISA techniques. No IFNγ production was found in experimental situations with single polypeptides or without any polypeptides. Data obtained are depicted in Figure 21 and 22. In Figure 23 the single antigen approach is illustrated, by using a set of polypeptides targeting two different epitopes (upper part) or the same epitope (lower part) on the target antigen A1.

Example 19

This is an example to demonstrate that the functional complementation strategy can be further elaborated for targeted payload delivery and that different effector ways are possible to kill a target cell. By complementing the F1 and F2 fragments of a set of bound polypeptides on target, the newly formed antibody binding site can bind any molecule it is specific for. In order to direct a HIS-tagged payload precisely to a target cell, the V_H and V_L fragments of an anti-HIS(hexa-histidine)-antibody were used. After simultaneous binding of polypeptide 1 ($antiHis(V_L)$-$CD45(V_H-V_L)$ and polypeptide 2 ($antiHis(V_H)$-$HLA\text{-}A2(V_H-V_L)$ to their specific target antigens CD45 and HLA-A2, a hexa-histidine binding site is complemented on target that binds histidine labeled payloads with high high affinity. The payload be a HIS-tagged toxin as given in this example here. The CD45 and HLA-A2 positive cells THP-1 were co-incubated with a histidine(His)-tagged Clostridium perfringens Iota toxin component Ia (Figure 24) or a histidine(His)-tagged Shiga toxin subunit A (Figures 25, 26) in combination with polypeptides against CD45 ($antiHis(V_L)$-$CD45(V_H-V_L)$) and HLA-A2 ($antiHis(V_H)$-$HLA\text{-}A2(V_H-V_L)$). Complementation of his-tagged toxin binding and subsequent target cell killing was assessed by measuring cell viability using an

alamarBlue® assay. At the highest concentration of polypeptides used (80nM), a clear difference in target cell killing, measured as reduction in cell viability, was found in experimental situations with a combination of both polypeptides compared to single polypeptides.

Example 20

To further demonstrate the versatility, flexibility and the exchangeability of the bipartite functional complementation strategy, the V_H and V_L fragments of an anti-Digoxigenin antibody were used to identify and mark double antigen positive cells with Digoxigenin-labeled HRP (horse raddish peroxidase). EGFR and EpCAM positive Colo-206F cells were co-incubated with polypeptides against EGFR (antiDig(V_H) - EGFR(V_H+V_L)) and EpCAM (antiDig(V_L) - EpCAM(V_H+V_L)). On target complementation of the functional domain anti-Digoxigenin , indicated by Digoxigenin-HRP labelling of Colo-206F cells, was assessed by measuring the peroxidase activity, using a standard ELISA Kit (Invitrogen™). A clear difference in Dig-HRP labeled target cells was found in experimental situation with a combination of both polypeptides compared to single polypeptides. Data obtained are depicted in Figure 27.

Example 21

Using the human leucocytic antigens (HLA) as one arm for dual antigen restricted bipartite functional complementation, this haplotype strategy was further validated by exchanging the functional domains of the polypeptides with V_H and V_L fragments of an anti-HLA-Cw6 antibody. HLA-Cw6 positive primary patient PBMCs were co-incubated with HLA-Cw6 negative PBMCs from a healthy donor, polypeptide against CD45 (CD3(V_L) – CD45(V_H-V_L)) and HLA-Cw6 (CD3(V_H) – HLA-Cw6(V_H-V_L)). IFNγ production by lymphocytes was measured by ELISA techniques. These data demonstrate that hematopoietic cells of patients with other haplotypes than HLA-A2 can be targeted simply by exchanging one targeting domain (anti HLA-A2, Figure 5, 7-9, 11-12) by another (anti HLA-Cw6). Data obtained are depicted in Figures 28.

Example 22

The dual antigen-induced bipartite functional complementation strategy was further validated in an *in vitro* patient assay, using freshly isolated primary patient cancer cells and antigen targets already used for cancer therapy in clinic or clinical trials (EGFR, EpCAM,

CEA and Her2). Malignant cells of a 48 years old male patient with metastatic pancreatic cancer were co-incubated with the patients own peripheral blood lymphocytes and the combination of polypeptides against EGFR (CD3(V_H) - EGFR(V_H+V_L)), EpCAM (CD3(V_L) - EpCAM(V_H+V_L)), Her2 (CD3(V_H) - Her2(V_H+V_L)), CEA (CD3(V_H) - CEA(V_H-V_L)) and HLA-A2 (CD3(V_L) - HLA-A2(V_H-V_L)). Complementation of lymphocyte stimulatory function was assessed by reactive IFNγ production, measured by ELISA techniques. No IFNγ production was found in experimental situations without any polypeptides. These data demonstrate the potential of this strategy to use patients own immune cells to target and kill his malignant transformed cells. Data obtained are depicted in Figures 29.

Example 23

A highly enriched CD3/CD8 positive CMV restricted T-cell population was used to show that any T cell, irrespective of its specificity, can serve as effector cell an kill double antigen positive tumor cells by this complementation strategy. The CD45 and HLA-A2 positive U266 and THP-1 cells were co-incubated with cytomegalievirus (CMV) specific T-cells from a HLA-A2 negative healthy donor and polypeptides against CD45 (CD3(V_H) - CD45(V_H-V_L)) and HLA-A2 (CD3(V_L) – HLA-A2(V_H-V_L)) in varying amounts. The bispecific tandem scFv (CD3(V_H-V_L) x HLA-A2(V_H-V_L))-antibody was used as a positive control. T cell engagement was assessed by reactive IFNγ production, measured by ELISA techniques. No IFNγ production was found in experimental situations with single polypeptides or without any polypeptides. Data obtained are depicted in Figure 30. Cells from the same frozen aliquot batch, CMV specific T-cells and THP-1 cells, were used for the *in vivo* murine model (Figure 12A).

Example 24

This illustration depicts the potential to target allergen/ autoimmune specific B-cell clones with the bipartite functional complementation strategy. By using a synthetic allergen as targeting moiety , the allergen linked polypeptide will bind specifically to its clonotypic B-cell receptor expressed on the surface of the allergen specific B-cell clone. The second arm of the bipartite strategy will use a B-cell specific polypeptide (CD19, CD20, CD38, CD138), restricting the followed complementation of the effector domain with subsequent target cell killing to the allergen specific B-cell clone. The ultimate goal of this strategy is to eliminate the B cell clone that causes and allergic or autoimmune disease (upper part of Figure 31)

whilst sparing B cells with other specificities or cells other than B cells (eg. mast cells or basophilic cells) which bind the antibody responsible for the disease via Fc-receptors (lower part of Figure 31).

The features of the present invention disclosed in the specification, the claims, and/or in the accompanying drawings may, both separately and in any combination thereof, be material for realizing the invention in various forms thereof.

Claims

1. A set of polypeptides comprising:

a first polypeptide P1 comprising

(i) a targeting moiety T1,

wherein said targeting moiety T1 specifically binds to an antigen A1, and

(ii) a fragment F1 of a functional domain F,

wherein neither said fragment F1 by itself nor said polypeptide P1 by itself is functional with respect to the function of said domain F,

and

a second polypeptide P2 comprising

(i) a targeting moiety T2,

wherein said targeting moiety T2 specifically binds to an antigen A2, and

(ii) a fragment F2 of said functional domain F,

wherein neither said fragment F2 by itself nor said polypeptide P2 by itself is functional with respect to the function of said domain F,

wherein said antigen A1 is different from said antigen A2,

wherein said polypeptide P1 and said polypeptide P2 are not associated with each other in the absence of a substrate that has both antigens A1 and A2 at its surface, and

wherein, upon dimerization of said fragment F1 of said polypeptide P1 with said fragment F2 of said polypeptide P2, the resulting dimer is functional with respect to the function of said domain F.

2. The set of polypeptides according to claim 1, wherein said polypeptide P1 and said polypeptide P2 are not associated with each other in the absence of a cell that carries both antigens A1 and A2 at its cell surface.

3. The set of polypeptides according to claim 1 or 2, wherein a cell carrying both antigens A1 and A2 at its cell surface induces dimerization of the fragment F1 of said polypeptide P1 with the fragment F2 of said polypeptide P2, whereas a cell which does not carry both antigens A1 and A2 at its cell surface does not induce dimerization of the fragment F1 of said polypeptide P1 with the fragment F2 of said polypeptide P2.

4. The set of polypeptides according to any one of claims 1 to 3, wherein said polypeptides P1 and P2 have, in the absence of said substrate or cell, with each other a

dissociation constant K_D in the range of 10^{-8} M to 10^{-2} M, in the range of 10^{-7} M to 10^{-3} M or in the range of 10^{-6} M to 10^{-3} M; and /or said polypeptides P1 and P2 have, in the presence of said substrate or cell, with each other a dissociation constant K_D below 10^{-6} M, below 10^{-7} M below 10^{-8} M or below 10^{-9} M.

5. The set of polypeptides according to any one of claims 1 to 4, wherein said antigen A1 and/or said antigen A2 is an antigen expressed on the surface of cells of a tumour or on the surface of progenitor/precursor cells of a tumor.

6. The set of polypeptides according to any one of claims 1 to 5, wherein the combination of antigen A1 and antigen A2 is only found on cancerous cells, and not on cells that are not cancerous.

7. The set of polypeptides according to claim 6, wherein the combination of antigen A1 and antigen A2 is specific for cancerous cells of a certain type of cancer.

8. The set of polypeptides according to any one of claims 1 to 7, wherein said antigen A1 is an MHC antigen being an allelic variant selected from the group consisting of:
HLA-A2, HLA-Cw6, HLA-A1, HLA-A3, HLA-A25, HLA-B7, HLA-B8, HLA-B35, HLA-B44, HLA-Cw3, HLA-Cw4, and HLA-Cw7; and/or

said antigen A2 is an antigen that is specific for a certain cell type or cell lineage selected from the group consisting of:
CD45; CD34; CD33; CD138; CD15; CD1a; CD2; CD3; CD4; CD5; CD8; CD20; CD23; CD31; CD43; CD56; CD57; CD68; CD79a; CD146; surfactant proteins;. synaptophysin; CD56; CD57; nicotinic acetylcholine receptor; muscle-specific kinase MUSK; voltage-gated calcium channel (P/Q-type); voltage-gated potassium channel (VGKC); N-methyl-D-aspartate receptor (NMDA); TSH; amphiphysin; HepPar-1; ganglioside GQ1B, GD3 or GM1; and glycophorin-A.

9. The set of polypeptides according to any one of claims 1 to 8, wherein any of said antigens A1 and A2 is selected from the group consisting of:
HLA-A2; HLA-Cw6; EpCAM; CD20; CD33; CD38; CD45; Her2; EGFR; CD138; CEA; CD19; PSMA; E-cadherin; Ca-125; Her-2/neu; gross cystic disease fluid protein; BCA-225; CA 19-9; CD117; CD30; Epithelial antigen BER-EP4, Epithelial membrane antigen and Epithelial Related Antigen MOC-31; Epidermal growth factor

receptor HER1; Platelet derived growth factor receptor PDGFR alpha; Melanoma associated marker/Mart 1/Melan-A; CD133; TAG 72; aquaporin-2 and a clonotypic antibody on the surface of a B cell.

10. The set of polypeptides according to any one of claims 1 to 9, wherein

(i) one of said antigens A1 and A2 is EpCAM and the other one is EGFR, HER2/neu, CD10, VEGF-R or MDR;

(ii) one of said antigens A1 and A2 is MCSP and the other one is melanoferrin or EpCAM;

(iii) one of said antigens A1 and A2 is CA125 and the other one CD227

(iv) one of said antigens A1 and A2 is CD56 and the other one is CD140b or GD3 ganglioside;

(v) one of said antigens A1 and A2 is EGFR and the other one is HER2;

(vi) one of said antigens A1 and A2 is PSMA and the other one is HER2;

(vii) one of said antigens A1 and A2 is Sialyl Lewis and the other one is EGFR;

(viii) one of said antigens A1 and A2 is CD44 and the other one is ESA, CD24, CD133, MDR or CD117;

(ix) one of said antigens A1 and A2 is CD34 and the other one is CD19, CD79a, CD2, CD7, HLA-DR, CD13, CD117, CD33 or CD15;

(x) one of said antigens A1 and A2 is CD33 and the other one is CD19, CD79a, CD2, CD7, HLA-DR, CD13, CD117 or CD15;

(xi) one of said antigens A1 and A2 is MUC1 and the other one is CD10, CEA or CD57;

(xii) one of said antigens A1 and A2 is CD38 and the other one is CD138;

(xiii) one of said antigens A1 and A2 is CD 24 and the other one is CD29 or CD49f;

(xiv) one of said antigens A1 and A2 is carbonic anhydrase IX and the other one is aquaporin-2;

(xv) one of said antigens A1 and A2 is HLA-A2 and the other one is EpCAM;

(xvi) one of said antigens A1 and A2 is HLA-A2 and the other one is CD45;

(xvii) one of said antigens A1 and A2 is HLA-A2 and the other one is EGFR;

(xviii) one of said antigens A1 and A2 is HLA-A2 and the other one is Her2;

(xix) one of said antigens A1 and A2 is HLA-A2 and the other one is CEA;

(xx) one of said antigens A1 and A2 is EpCAM and the other one is CEA;

(xxi) one of said antigens A1 and A2 is CD45 or CD38 and the other one is CD138;

(xxii) one of said antigens A1 and A2 is EGFR and the other one is CEA;

(xxiii) one of said antigens A1 and A2 is Her2 and the other one is CEA; or

(xxiv) one of said antigens A1 and A2 is CD19 and the other one is a clonotypic antibody on the surface of a B cell.

11. The set of polypeptides according to any one of claims 1 to 10, wherein said targeting moiety T1 and/or T2 comprises an immunoglobulin module; or
wherein said targeting moiety T1 and/or T2 comprises an aptamer or a natural ligand of said antigen A1 or antigen A2, respectively.

12. The set of polypeptides according to claim 11, wherein said targeting moiety T1 comprises an immunoglobulin module I1 comprising a V_L domain linked to a V_H domain or comprising a variable domain V_HH of a llama antibody, camel antibody or shark antibody; and/or
said targeting moiety T2 comprises an immunoglobulin module I2 comprising a V_L domain linked to a V_H domain or comprising a variable domain V_HH of a llama antibody, camel antibody or shark antibody.

13. The set of polypeptides according to claim 12, wherein said immunoglobulin module I1 comprises a scFv (single-chain variant fragment), a Fab or a $F(ab')_2$ of an antibody or a complete antibody; and/or
said immunoglobulin module I2 comprises a scFv (single-chain variant fragment), a Fab or a $F(ab')_2$ of an antibody or a complete antibody.

14. The set of polypeptides according to any one of claims 1 to 4 and 7 to 13, wherein any one of said targeting moiety T1 and T2 comprises an allergen or substrate which binds to a clonotypic antibody on the surface of a B cell.

15. The set of polypeptides according to any one of claims 1 to 14, wherein said functional domain F is or comprises an immunoglobulin module, or a fluorescent molecule, or a molecule capable of mediating bioluminescence.

16. The set of polypeptides according to claim 15, wherein said functional domain F is a Fv (variant fragment) or a scFv (single-chain variant fragment) of an antibody.

17. The set of polypeptides according to any one of claims 1 to 16, wherein said fragment F1 comprises a V_L domain of an antibody and said fragment F2 comprises a V_H domain of the same antibody; or wherein said fragment F1 comprises a V_H domain of an antibody and said fragment F2 comprises a V_L domain of the same antibody.

18. The set of polypeptides according to any one of claims 1 to 17, wherein said fragment F1 comprises a V_L domain of an anti-CD3, anti-His or anti-DIG antibody and said fragment F2 comprises a V_H domain of the same antibody, or wherein said fragment F1 comprises a V_H domain of an anti-CD3 anti-His or anti-DIG antibody and said fragment F2 comprises a V_L domain of the same antibody.

19. The set of polypeptides according to any one of claims 15 to 18, wherein said immunoglobulin module comprises a V domain selected from the group consisting of:

(i) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NO: 2 and/or a V_H domain comprising SEQ ID NO: 1;

(ii) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NO: 4 and/or a V_H domain comprising SEQ ID NO: 3;

(iii) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NO: 6 and/or a V_H domain comprising SEQ ID NO: 5;

(iv) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NO: 8 and/or a V_H domain comprising SEQ ID NO: 7;

(v) a V domain of an anti-CD3 antibody comprising a V_L domain comprising SEQ ID NO: 10 and/or a V_H domain comprising SEQ ID NO: 9; and

(vi) a V domain of an anti-His antibody comprising a V_L domain comprising SEQ ID NO: 12 and/or a V_H domain comprising SEQ ID NO: 11;

(vii) a V domain of an anti-DIG antibody comprising a V_L domain comprising SEQ ID NO: 14 and/or a V_H domain comprising SEQ ID NO: 30.

20. The set of polypeptides according to any one of claims 1 to 19, wherein any of the polypeptides P1 and P2 is or comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 114-129 and 197.

21. The set of polypeptides according to any one of claims 1 to 20 for use in the treatment of a patient who is suffering from cancer and/or a tumour or for use in diagnosis in a patient who is suffering from cancer and/or a tumour.

22. A nucleic acid molecule or a set of nucleic acid molecules encoding the set of polypeptides or one of the polypeptides of the set of polypeptides according to any one of claims 1 to 20.

23. The nucleic acid molecule or set of nucleic acid molecules according to claim 22 comprising a nucleotide sequence as depicted in any one of SEQ ID NOS: 135-150 and 196.

24. A pharmaceutical composition comprising either the set of polypeptides according to any of claims 1 to 20 or the nucleic acid molecule/set of nucleic acid molecules according to claim 22 or 23, said pharmaceutical composition further comprises a pharmaceutically acceptable carrier.

25. A kit comprising the set of polypeptides according to any of claims 1-20 or the nucleic acid molecule or the set of nucleic acid molecules according to claim 22 or 23.