CONSTRAINED CONDITIONALLY ACTIVATED BINDING PROTEINS

I. CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority under 35 U.S.C. §119(e) to U.S. Provisional Patent Application 62/555,943 filed September 8, 2017, U.S. Provisional Patent Application 62/586,627 filed November 15, 2017, and U.S. Provisional Patent Application 62/587,318 filed November 16, 2017, all of which are expressly incorporated herein by reference in their entirety.

II. REFERENCE TO A "SEQUENCE LISTING," A TABLE, OR A COMPUTER PROGRAM LISTING APPENDIX SUBMITTED ON A COMPACT DISK.

[0002] The sequence listing contained in the file named "118459-5005_ST25.txt"and having a size of 984 kilobytes, has been submitted electronically herewith via EFS-Web, and the contents of the txt file are hereby incorporated by reference in their entirety.

III. BACKGROUND OF THE INVENTION

[0003] The selective destruction of an individual cell or a specific cell type is often desirable in a variety of clinical settings. For example, it is a primary goal of cancer therapy to specifically destroy tumor cells, while leaving healthy cells and tissues as intact and undamaged as possible. One such method is by inducing an immune response against the tumor, to make immune effector cells such as natural killer (NK) cells or cytotoxic T lymphocytes (CTLs) attack and destroy tumor cells.

[0004] The use of intact monoclonal antibodies (mAb), which provide superior binding specificity and affinity for a tumor-associated antigen, have been successfully applied in the area of cancer treatment and diagnosis. However, the large size of intact mAbs, their poor bio-distribution, low potency and long persistence in the blood pool have limited their clinical applications. For example, intact antibodies can exhibit specific accumulation within the tumor area. In biodistribution studies, an inhomogeneous antibody distribution with

primary accumulation in the peripheral regions is noted when precisely investigating the tumor. Due to tumor necrosis, inhomogeneous antigen distribution and increased interstitial tissue pressure, it is not possible to reach central portions of the tumor with intact antibody constructs. In contrast, smaller antibody fragments show rapid tumor localization, penetrate deeper into the tumor, and also, are removed relatively rapidly from the bloodstream.

However, many antibodies, including scFvs and other constructs, show "on target/off tumor" effects, wherein the molecule is active on non-tumor cells, causing side effects, some of which can be toxic. The present invention is related to novel constructs that are selectively activated in the presence of tumor proteases.

IV. SUMMARY OF THE INVENTION

[0005] The present invention provides a number of different protein compositions for the treatment of cancer. Accordingly, in one aspect, the invention provides "Format 2" proteins comprising, from N- to C-terminal: a first single domain antigen binding domain (sdABD) that binds to a human tumor target antigen (TTA) (sdABD-TTA); b) a first domain linker; c) a constrained Fv domain comprising: i) a first variable heavy domain comprising a vhCDR1, vhCDR2 and vhCDR3; ii) a constrained non-cleavable linker (CNCL); and iii) a first variable light domain comprising vlCDR1, vlCDR2 and vlCDR3; d) a second domain linker; e) a second sdABD-TTA; f) a cleavable linker (CL); g) a constrained pseudo Fv domain comprising: i) a first pseudo light variable domain; ii) a non-cleavable linker (NCL); and iii) a first pseudo heavy variable domain; h) a third domain linker; and i) a third sdABD that binds to human serum albumin; wherein said first variable heavy domain and said first variable light domain are capable of binding human CD3 but said constrained Fv domain does not bind CD3; said first variable heavy domain and said first pseudo variable light domain intramolecularly associate to form an inactive Fv; and said first variable light domain and said first pseudo variable heavy domain intramolecularly associate to form an inactive Fv.

[0006] In a further aspect, the invention provides "Format 1" proteins comprising, from N- to C-terminal: a) a first sdABD-TTA; b) a first domain linker; c) a constrained Fv domain comprising: i) a first variable heavy domain comprising a vhCDR1, vhCDR2 and vhCDR3;

ii) a constrained cleavable linker (CCL); and iii) a first variable light domain comprising vlCDR1, vlCDR2 and vlCDR3; d) a second domain linker; e) a second sdABD-TTA; f) a cleavable linker (CL); g) a constrained pseudo Fv domain comprising: i) a first pseudo light variable domain; ii) a non-cleavable linker (NCL); and iii) a first pseudo heavy variable domain; h) a third domain linker; and i) a third sdABD that binds to human serum albumin; wherein said first variable heavy domain and said first variable light domain are capable of binding human CD3 but said constrained Fv domain does not bind CD3; wherein said first variable heavy domain and said first pseudo variable light domain intramolecularly associate to form an inactive Fv; and wherein said first variable light domain and said first pseudo variable heavy domain intramolecularly associate to form an inactive Fv.

In an additional aspect, the invention provides "Format 4" proteins comprising, from N- to C-terminal: a) a single domain antigen binding domain (sdABD) that binds to a human tumor target antigen (TTA) (sdABD-TTA); b) a first domain linker; c) a constrained Fv domain comprising: i) a first variable heavy domain comprising a vhCDR1, vhCDR2 and vhCDR3; ii) a constrained non-cleavable linker (CNCL); and iii) a first variable light domain comprising vlCDR1, vlCDR2 and vlCDR3; d) a cleavable linker (CL); e) a second sdABD that binds to human serum albumin; f) a domain linker; g) a constrained pseudo Fv domain comprising: i) a first pseudo light variable domain; ii) a non-cleavable linker (NCL); and iii) a first pseudo heavy variable domain; wherein said first variable heavy domain and said first variable light domain are capable of binding human CD3 but said constrained Fv domain does not bind CD3; wherein said first variable heavy domain and said first pseudo variable light domain intramolecularly associate to form an inactive Fv; and wherein said first variable light domain and said first pseudo variable heavy domain intramolecularly associate to form an inactive Fv.

[0007] In a further aspect to the Format 1, Format 2 and Format 4 proteins listed above, said first variable heavy domain is N-terminal to said first variable light domain and said pseudo light variable domain is N-terminal to said pseudo variable heavy domain.

[0008] In a further aspect to the Format 1, Format 2 and Format 4 proteins listed above, said first variable heavy domain is N-terminal to said first variable light domain and said pseudo variable heavy domain is N-terminal to said pseudo variable light domain.

[0009] In a further aspect to the Format 1, Format 2 and Format 4 proteins listed above, said first variable light domain is N-terminal to said first variable heavy domain and said pseudo light variable domain is N-terminal to said pseudo variable heavy domain.

[0010] In a further aspect to the Format 1, Format 2 and Format 4 proteins listed above, said first variable light domain is N-terminal to said first variable heavy domain and said pseudo variable heavy domain is N-terminal to said pseudo variable light domain.

[0011] In an additional aspect, the invention provides Format 1 and 2 proteins wherein said first and second TTA are the same.

[0012] In a further aspect, the invention provides Format 1 and 2 proteins wherein said first and second TTA are different.

[0013] In an additional aspect, the invention provides Format 1, 2 and 4 proteins wherein said first and second TTA are selected from EGFR, EpCAM, FOLR1 and B7H3. These sequences can be selected from the group consisting of SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29; SEQ ID NO:33; SEQ ID NO:37 and SEQ ID NO:41.

[0014] In a further aspect, the invention provides Format 1, 2 and 4 proteins wherein said half-life extension domain has SEQ ID NO:45.

[0015] In an additional aspect, the invention provides Format 1, 2 and 4 proteins wherein said cleavable linker is cleaved by a human protease selected from the group consisting of MMP2, MMP9, Meprin A, Meprin B, Cathepsin S, Cathepsin K, Cathespin L, GranzymeB, uPA, Kallekriein7, matriptase and thrombin.

[0016] In a further aspect, the invention provides a protein selected from the group consisting of Pro186, Pro225, Pro226, Pro233, Pro311, Pro312, Pro313, Pro495, Pro246, Pro254, Pro255, Pro256, Pro420, Pro421, Pro432, Pro479, Pro480, Pro187, Pro221, Pro222, Pro223, Pro224, Pro393, Pro394, Pro395, Pro396, Pro429, Pro430 and Pro431.

[0017] In an additional aspect, the invention provides nucleic acids encoding a Format 1, Format 2 or Format 4 protein as described herein, as well as expression vectors and host cells comprising the nucleic acids encoding the protein.

[0018] In a further aspect, the invention provides methods of making the proteins of the invention and methods of treating patients in need thereof.

[0019] In an additional aspect, the invention provides compositions comprising "Format 3A" pairs of pro-drug proteins, comprising: a) a first protein comprising, from N- to C-terminal: i) a first sdABD-TTA; ii) a first domain linker; iii) a pseudo Fv domain comprising, from N- to C-terminal: 1) a variable heavy chain comprising a vhCDR1, vhCDR2 and vhCDR3; 2) a cleavable linker; and 3) a first pseudo variable light domain comprising iVLCDR1, iVLCDR2 and iVLCDR3; iv) a second domain linker; v) a sdABD-HSA; a) a first second protein comprising, from N- to C-terminal: i) a third sdABD that binds to a human tumor target antigen; ii) a third domain linker; iii) a pseudo Fv domain comprising, from N- to C-terminal: 1) a variable light chain comprising a VLCDR1, VLCDR2 and VLCDR3; 2) a cleavable linker; and 3) a first pseudo variable heavy domain comprising iVHCDR1, iVHCDR2 and iVHCDR3; iv) a fourth domain linker; v) a sdABD-HSA;; wherein said first variable heavy domain and said first variable light domain are capable of binding human CD3 when associated; wherein said first variable heavy domain and said first pseudo variable light domain intermolecularly associate to form an inactive Fv; wherein said first variable light domain and said first pseudo variable heavy domain intermolecularly associate to form an inactive Fv; and wherein said first and third sdABD are selected from the group consisting of SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29; SEQ ID NO:33; SEQ ID NO:37 and SEQ ID NO:41.

[0020] In a further aspect, the invention provides compositions comprising "Format 3B" pairs of pro-drug proteins, comprising a) a first protein comprising, from N- to C-terminal: i) a first sdABD-TTA; ii) a first domain linker; iii) a second sdABD-TTA; iv) a second domain linker; iii) a pseudo Fv domain comprising, from N- to C-terminal: 1) a variable heavy chain comprising a vhCDR1, vhCDR2 and vhCDR3; 2) a cleavable linker; and 3) a first pseudo variable light domain comprising iVLCDR1, iVLCDR2 and iVLCDR3; iv) a third domain linker; and v) a sdABD-HSA; a) a first second protein comprising, from N- to C-terminal: i) a third sdABD-TTA; ii) a fourth domain linker; iii) a fourth sdABD-TTA; iv) a fifth domain linker; iii) a pseudo Fv domain comprising, from N- to C-terminal: 1) a variable light chain comprising a VLCDR1, VLCDR2 and VLCDR3; 2) a cleavable linker; and 3) a first pseudo

variable heavy domain comprising iVHCDR1, iVHCDR2 and iVHCDR3; iv) a sixth domain linker; v) a sdABD-HSA; wherein said first variable heavy domain and said first variable light domain are capable of binding human CD3 when associated; wherein said first variable heavy domain and said first pseudo variable light domain intermolecularly associate to form an inactive Fv; and wherein said first variable light domain and said first pseudo variable heavy domain intermolecularly associate to form an inactive Fv.

[0021] In an additional aspect, Format 3A and Format 3B proteins have sdABD-HSA that have SEQ ID NO:45.

[0022] In a further aspect, Format 3A and Format 3B proteins have sdABD-TTA that binds to a TTA selected from EGFR, EpCAM, FOLR1 and B7H3. The sdABD-TTAs can be selected from the group consisting of SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29; SEQ ID NO:33; SEQ ID NO:37 and SEQ ID NO:41.

[0023] In a further aspect, the invention provides nucleic acid compositions comprising first nucleic acids that encode the first protein members of the prodrug pair and second nucleic acids that encode the second protein members of the pairs, and expression vectors and host cells containing the nucleic acids.

V. BRIEF DESCRIPTION OF THE DRAWINGS

[0024] Figure 1 depicts the "format 1" type of protease activation of the present invention, referred to herein as "constrained, cleavable constructs" or "cc constructs". In this embodiment, a representative construct is Pro140: there are ABDs for two TTA (as depicted in Figure 1, these are both the same, although as described herein they can be different). Upon cleavage, the prodrug construct splits into three components, one containing an α-TTA domain linked via a domain linker to an active VH of αCD3, the second containing an α-TTA domain linked via a domain linker to an active VL of αCD3, and a "leftover" piece comprising the half life extension domain linked to the inactive VH and VL. The two active variable domains then are free to associate to form a functional anti-CD3 binding domain. It should be noted that in "format 1" embodiments, the resulting active component is trivalent: there is monovalent binding to CD3 and bivalent binding to the TTA, rendering a bispecific binding protein, although in some cases this trivalency could be trispecifics, with

monovalent binding to CD3, monovalent binding to a first TTA and monovalent binding to a second TTA. Figure 1 also shows an anti-human serum albumin (HSA) domain as a half-life extension domain, in many embodiments an sdABD as defined herein, although as discussed herein, this is optional and/or can be replaced by other half-life extension domains; additionally, the half-life extension domain can also be N-terminal to the construct or internal as well. Figure 1 also has the VH and VL of the Fv and iVH and iVL of the pseudo Fv in a specific order, e.g. from N- to C-terminal, VH-linker-VL (and iVL-linker-iVH) although as will be appreciated by those in the art, these can be reversed (VL-linker-VH and iVH-linker-iVL). Alternatively, one of these Fvs can be in one orientation and the other in the other orientation, although the expression of protein in the orientation as shown here was surprisingly higher than the other orientations.

[0025] Figure 2 depicts the "format 2" type of protease activation of the present invention, referred to herein as "constrained, non-cleavable constructs", or "CNCL constructs", also sometimes referred to herein as "dimerization constructs" as discussed herein. These constructs do not isomerize as discussed herein. Upon cleavage, two prodrug construct splits into four components, two half-life extension domains (in this case, sdABDs to HSA) linked to two pseudo domains (which may or may not be able to self-associate, depending on the length of the linkers and the inactivating mutations), and two active moieties that self-assemble into a dimeric active moiety that contains four anti-TTA domains (which can be all the same or two are the same and the other two are different). It should be noted that in "format 2" embodiments, the resulting active component is hexavalent: there is bivalent binding to CD3 and quadrivalent binding to the TTA, rendering a bispecific binding protein, although in some cases this hexavalency could be trispecifics, with bivalent binding to CD3, bivalent binding to a first TTA and bivalent binding to a second TTA. Figure 2 also shows an anti-human serum albumin (HSA) domain as a half-life extension domain, in many embodiments an sdABD as defined herein, although as discussed herein, this is optional and/or can be replaced by other half-life extension domains; additionally, the half-life extension domain can also be N-terminal to the construct or internal as well. Figure 2 also has the VH and VL of the Fv and iVH and iVL of the pseudo Fv in a specific order, e.g. from N- to C-terminal, VH-linker-VL (and iVL-linker-iVH) although as will be appreciated by those in the art, these can be reversed (VL-linker-VH and iVH-linker-iVL). Alternatively,

one of these Fvs can be in one orientation and the other in the other orientation, although the expression of protein in the orientation as shown here was surprisingly higher than the other orientations.

[0026] Figure 3A - Figure 3B depict "format 3" type of constructs, also sometimes referred to as "hemi-constructs" or "hemi-COBRA™" as outlined herein, as these are two different polypeptide chains that together make up an MCE therapeutic as is further discussed herein. In this embodiment, the constructs are delivered in pairs, with the pre-cleavage intramolecular self-assembly resulting in inactive anti-CD3 Fv domains. Upon cleavage, the inert variable domains are released, and the two active variable domains then intermolecularly assemble, to form an active anti-CD3 binding domain. The two sdABD-TTAs bind to the corresponding receptor on the tumor cell surface, and the cleavage is done by a protease. This allows the intermolecular assembly, since the molecules are physically held in place, favoring the assembly of the active anti-CD3 domain. As above for formats 1 and 2, in this embodiment, the N- to C-terminal order of the variable domains can be reversed, or mixed as well. Furthermore, the sdABD(HSA) can be either at the N- or C-terminus of each hemi-construct. Pro16 has the sdABD(HSA) at the C terminus and Pro17 has it at the N-terminus (see Pro19, SEQ ID NO:XX, has the sdABD(HSA) at the C-terminus). Figure 3A shows Format 3 constructs with a single sdABD-TTA domain per hemi-construct, and Figure 3B shows Format 3 constructs with two sdABD-TTAs per hemi-construct, in a "dual targeting" or "hetero-targeting" format. Note that Figure 3B uses FOLR1 and EGFR as the two TTAs, but other combinations as outlined herein can also be used.

[0027] Figure 4 depicts "format 4" type of constructs that are similar to "format 2" constructs but have only a single sdABD-TTA. The figure shows the sdABD-TTA to EGFR, but as will be appreciated by those in the art, other TTA can be used as well. Upon cleavage, the prodrug construct splits into two components, a half-life extension domain (in this case, sdABDs to HSA) linked to a pseudo Fv and an active moiety, that in the presence of a second active moiety from a different cleaved molecule, self-assembles into a dimeric active moiety that contains two anti-TTA domains. It should be noted that in "format 4" embodiments, the resulting active component is quadrivalent: there is bivalent binding to CD3 and bivalent binding to the TTA, rendering a bispecific binding protein. Figure 4 also shows an anti-human serum albumin (HSA) domain as a half-life extension domain, in

many embodiments an sdABD(½) as defined herein, although as discussed herein, this is optional and/or can be replaced by other half-life extension domains; additionally, the half-life extension domain can also be N-terminal to the construct or internal as well. Figure 4 also has the VH and VL of the Fv and iVH and iVL of the pseudo Fv in a specific order, e.g. from N- to C-terminal, VH-linker-VL (and iVL-linker-iVH) although as will be appreciated by those in the art, these can be reversed (VL-linker-VH and iVH-linker-iVL). Alternatively, one of these Fvs can be in one orientation and the other in the other orientation, although the expression of protein in the orientation as shown here was surprisingly higher than the other orientations.

[0028] Figure 5A – Figure 5G depict a number of sequences of the invention. For antigen binding domains, the CDRs are underlined. As is more fully outlined herein, these domains can be assembled in a wide variety of configurations in the present invention, including "format 1", "format 2", "format 3" and "format 4" orientations. Of note is that SEQ ID NO:90 is cleaved by MMP9 slightly faster than SEQ ID NO:s 75 and 76, and SEQ ID NO:91 is cleaved slower than SEQ ID NO:s 75 and 76.

[0029] Figure 6A – Figure 6B depict a number of suitable protease cleavage sites. As will be appreciated by those in the art, these cleavage sites can be used as cleavable linkers. In some embodiments, for example when more flexible cleavable linkers are required, there can be additional amino acids (generally glycines and serines) that are either or both N- and C-terminal to these cleavage sites.

[0030] Figure 7A – Figure 7D depict some data associated with the "Format 3" or "hemi-COBRA™" structures. This shows that Format 3 constructs bind co-operatively to CD3 after cleavage by protease (in this case EK protease, although any of the protease cleavage sites outlined herein and depicted in Figure 5 and Figure 6 can be used) and create a CD3 binding site, as shown by a sandwich FACS analysis.

[0031] Figure 8A – Figure 8D shows that the protease cleavage co-operatively activates T-cell killing of EGFR+ target cells with complimentary hemi-COBRA™ pairs. Figure A and Figure B show that the constructs in isolation, but cleaved with different concentrations of protease, do not affect target cell viability. However, Figure C shows that in combination, in

the presence of protease, target cell viability is significantly diminished. Figure D shows the general mechanism.

[0032] Figure 8 shows some non-target controls for use in the assays to test efficacy of the Format 1 constructs.

[0033] Figure 9A – Figure 10F shows the generation of an active CD3 binding domain is dependent on target binding of both "arms", e.g. the sdABD-TTA domains, one of which is on each of the two constructs. The TDCC assay was done as described in the Examples.

[0034] Figure 10 shows the schematic of suitable hemi-COBRA™ pairs. "Mep" stands for a meprin protease cleavage site, "His-6" is a tag as more fully discussed herein, ST14 is a matriptase protease cleavage site and "Thb" is a thrombin protease cleavage site.

[0035] Figure 11A – Figure 12C shows the TDCC data associated with the constructs of Figure 10. Figure 11A shows that addition of pre-cleaved hemi-COBRA pairs results in efficacy on OvCAR8 cells, Figure 11B shows that addition of pre-cleaved hemi-COBRA pairs results in efficacy on HCT116 cells, and Figure 11C shows that addition of pre-cleaved hemi-COBRA pairs results in efficacy on LoVo cells, all of which are cancer cell lines.

[0036] Figure 12A – Figure 13B shows that the MMP9 linker is stable in vivo. NSG mice were administered a single intravenous bolus dose of either Pro40 (MMP9 cleavable), Pro74 (non-cleavable) via the tail vein at a dose level of 0.5 mg/kg. The dose solution for each compound was prepared in a vehicle of 25mM citric acid, 75-mM L-arginine, 75mM NaCl and 4% sucrose pH 7.0. Two blood samples were collected at preselected times from each animal, one towards the beginning of the study, collected by orbital bleed or submandibular bleed, and another at the terminal time point by cardiac puncture. The time points for blood collection were 0.083, 1, 6, 24, 72, and 168h. Plasma was prepared from each individual blood sample using K_2 EDTA tubes. Concentrations were determined using an MSD assay with a MAb specific to the anti-HSA sdABD and detected with the EGFR extracellular domain.

[0037] Figure 13 depicts the schematics of the Format 3A hemi-COBRA™ constructs used in the experiments depicted in Figure 14. Pro51 is the positive control, as it is "always on", since it forms an active anti-CD3 Fv. Pro98 is a negative control, since it's sdABD is directed against hen egg lysozyme, which isn't expressed by the tumor. Pro77 and Pro53 are the pro-

drug Format 3A pair, using sdABDs against EGFR and an MMP9 cleavage site. Pro74 and Pro72 is a negative control Format 3A pair, since they don't have cleavage sites.

[0038] Figure 14 shows that Format 1 constructs work to regress tumors in vivo, using two different tumor cell lines implanted into mice using the protocols in the Examples. Anti-tumor activity with the hemi-COBRA constructs (Pro77 and Pro53) was dependent on the inclusion of both the anti-EGFR sdABDs and the MMP9 cleavable linkers, along with the active anti-CD3 Fv.

[0039] Figure 15 shows the schematic of the next generation format, a full length construct that has two pseudo Fv domains with cleavable sites between them, as is generally described in US 2018/0134789, hereby incorporated by reference. However, as shown in the following figures, this first generation full length construct does not show very good conditionality, as it can isomerize to form both an active and inactive construct.

[0040] Figure 16 shows that the Format 3A construct pairs actually show better conditionality than the Pro100 first generation full length constructs.

[0041] Figure 17 depicts additional first generation full length constructs that were tested in Figure 18.

[0042] Figure 18 shows that the first generation constructs show high activity even in the uncleaved format, e.g. poor conditionality.

[0043] Figure 19 shows that the first generation full length constructs show two monomer peaks on analytical SEC.

[0044] Figure 20 shows the schematic of the reason for the noncleaved activity, which is that the full length first generation constructs isomerize to form two conformations, one which is inactive since there is no active anti-CD3 Fv formed (the "bivalent scFv"), and the other which is active in the absence of protease, a "single chain diabody" type of configuration. See PEDS 23(8):667-677 (2010).

[0045] Figure 21 shows the results of a TDCC assay, run at 37C for 2 days, with the first generation single chain constructs. The results show that the uncleaved constructs show strong killing. These results led to the generation of the Format 1 constructs.

[0046] Figure 22A - Figure 23G shows Format 1 constructs used in the invention. As will be appreciated by those in the art and described herein, these are depicted with a sdABD-EGFR targeting moiety, although sdABDs to other TTAs can be used.

[0047] Figure 23 shows that the Format 1 constructs (Pro140 in this case) form a single isomer that is stable at 37C.

[0048] Figure 24 depicts that Format 1 constructs have very low binding to human CD3 in the uncleaved format, as measured by an Octet assay. The top line is Pro120, the middle line is Pro51 (the positive control) and the bottom lines are Pro140 held at either 4C or 37C for 3 days.

[0049] Figure 25 similarly depicts that the Format 1 constructs have very low TDCC activity in the uncleaved form.

[0050] Figure 26 depicts a specific Format 1 construct, Pro140, used in *in vivo* testing, using sdABD-EGFR as the targeting moieties and an MMP9 cleavage site.

[0051] Figure 27A – Figure 28B shows tumor regression using a Format 1 construct.

[0052] Figure 28 depicts that due to the cleavage site in the constrained Fv, several different fragments can be generated: a partially cleaved fragment and the fully cleaved fragment. Surprisingly, the partially cleaved format is more active than the fully cleaved format, leading to the generation of Format 2.

[0053] Figure 29 shows a number of Format 2 schematics, all of which use sdABD-EGFR targeting domains, although as outlined herein and listed in the sequences, sdABDs to other TTAs can be used. Pro51 and Pro201 are positive controls (in an active "hemi" configuration), and Pro214 is a full length negative control, as there is no cleavage site.

[0054] Figure 30 shows the TDCC activity of Format 2 construct Pro187, which uses a meprin cleavage site. Pro187 in the TDCC assay was 1200-fold more active when added pre-cleaved than when added uncleaved. The pre-cleaved Pro187 demonstrated activity that fell between the positive controls Pro51 and Pro201. The uncleaved Pro187 demonstrated activity similar to Pro214, which does not contain a protease cleavable linker.

[0055] Figure 31 shows the TDCC activity of Format 2 construct Pro186, which uses n MMP9 cleavage site. Pro186 in the TDCC assay was 18-fold more active when added pre-

cleaved than when added uncleaved. The pre-cleaved Pro186 demonstrated activity that fell between the positive controls Pro51 and Pro201. The uncleaved Pro186 demonstrated more activity than Pro214, which does not contain a protease cleavable linker.

[0056] Figure 32 depicts that the Pro186 construct binds to cells that have different levels of EGFR receptors, with CHO cells not expressing EGFR on the cell surface. Pro186 saturates cells expressing differing levels of EGFR at similar COBRA concentrations.

[0057] Figure 33 shows the schematics of Format 2 constructs used in the *in vivo* studies of Figure 34, all of which use sdABD-EGFR targeting domains.

[0058] Figure 34 shows that the Format 2 construct Pro186 is highly efficacious at both concentrations, and better than the Format 1 construct Pro140 at the lower concentration.

[0059] Figure 35 depicts a number of Format 2 constructs based on Pro186 but with different protease cleavage sites. While all of these constructs utilize sdABD-EGFRs for both targeting domains, other sdABDs to different TTAs can be used, and can be the same or different. That is, both homo-targeting (both targeting sdABDs to the same TTA) or hetero-targeting (one sdABD to a first TTA and the other to a different TTA) can be done.

[0060] Figure 36 depicts the schematics for different Format 2 constructs that vary linker length between the Fv domains. These are shown using an MMP9 cleavage site, although others can be used as outlined herein. Similarly, while all of these constructs utilize sdABD-EGFRs for both targeting domains, other sdABDs to different TTAs can be used, and can be the same or different.

[0061] Figure 37 shows that the linker length for the pseudo Fv can be varied, e.g. that a Format 2 construct with a short linker between the active Fv ("short active") with a longer linker between the pseudo Fv ("long inactive") exhibits similar activity to a "short active" with a "short inactive". Thus conditionality of the COBRA construct is not dependent on both the active and inactive scFv linkers being constrained; as long as one of them is constrained, single chain diabody folding appears to be favored over bivalent scFv folding.

[0062] Figure 38 shows that the linker length for the active Fv can be varied, e.g. that Format 2 constructs with "long active" and "short inactive" behaves similarly to a "short active" and "short inactive" construct. Thus conditionality of the COBRA construct is not dependent on

both the active and inactive scFv linkers being constrained; as long as one of them is constrained, single chain diabody folding appears to be favored over bivalent scFv folding.

[0063] Figure 39A – Figure 40C shows the schematics for a number of different constructs. Pro188 is a Format 1 construct which is similar to Pro140 except with a long linker (16mer) in the pseudo Fv. Pro189 and Pro190 (Format 2 constructs) are similar to Pro186 and Pro187 except with a long linker (16mer) in the pseudo Fv domain. Pro191 and Pro192 (also Format 2 constructs) are similar to Pro189 and Pro190 except they have an additional cleavage site upstream of the sdABD(1/2). Pro193 (Format 4) has a single EGFR targeting domain, the iVH and iVL rearranged to be in reversed order, and an additional cleavage site upstream of the sdABD(1/2). Pro195 is a Format 2 construct similar to Pro186, with targeting domains that bind to the same TTA, EGFR, but to different epitopes. Pro196, Pro197 and Pro198 are Format 2 constructs with rearranged variable domains.

[0064] Figure 40 depicts the fact that different sdABD clones directed to human FOLR1 show differential killing. A Pro22 type construct (Pro51 with a FLAG sequence instead of a NCL) that binds to human FOLR1 was compared to a Pro22-EGFR construct against a number of cell line families.

[0065] Figure 41 depicts the schematics for four sdABD-FOLR1 constructs, including the use of the Pro201 positive control using sdABD-EGFR2 (with two molecules intermolecularly associating to form two active Fvs against CD3), and two Format 2 test articles, Pro311, using the h77.2 sdABD and Pro312 using the h59.3 sdABD, as well as two negative controls, Pro299, using the h77.2 sdABD and Pro303 using the h59.3 sdABD.

[0066] Figure 42 depicts the schematics of the Format 2 constructs for the FOLR/MMP9 in vivo design.

[0067] Figure 43 shows the efficacy of the Pro312 construct *in vivo*, and demonstrates the MMP9 cleavable linker is necessary for anti-tumor activity.

[0068] Figure 44 depicts the schematics of some formats using sdABDs to human B7H3 (sdABD-B7H3), including Pro244, the positive control (using sdABD-B7H3 (hF7) (with two molecules intermolecularly associating to form two active Fvs against CD3), and two Format 2 test articles, Pro225, a Format 2 construct, and Pro295, the negative control lacking a cleavage site.

[0069] Figure 45 shows that Pro225 has great conditionality as compared to the control, Pro295.

[0070] Figure 46 shows that a Format 2 construct of using a meprin linker, Pro373, shows great conditionality compared to Pro295.

[0071] Figure 47 depicts a number of sdABD-B7H3 (using the hF12 sequence) constructs, showing the Pro51 positive control using sdABD-EGFR, the Pro244 positive control using sdABD-hF12 B7H3, the test construct, Pro226, and the negative control Pro296 without a cleavage site.

[0072] Figure 48 shows the good conditionality of the Pro226 construct in a TDCC assay.

[0073] Figure 49 shows the humanization of sdABDs to human EpCAM.

[0074] Figure 50 shows the schematics of a number of Formats: Pro22hVIB13 and Pro205 are positive controls, Pro199 is a Format 2 construct and Pro175 is the negative control.

[0075] Figure 51 shows the TDCC activity of sdABD-EpCAM constructs, showing good conditionality.

[0076] Figure 52A – Figure 53B shows the TDCC activity of sdABD-EpCAM Pro199 construct, showing good conditionality in HT29 and LoVo cell models.

[0077] Figure 53A – Figure 54B shows the TDCC activity of sdABD-EpCAM Pro200 construct, showing good conditionality in HT29 and LoVo cell models.

[0078] Figure 54 shows a schematic of Pro255, which uses two different sdABD-TTA, one to EGFR (sdABD-EGFR) and the other to EpCAM (sdABD-EpCAM), as compared to Pro199, with dual EpCAM sdABDs. These are sometimes referred to herein as "hetero-targeting" constructs, in this case, a Format 2 construct.

[0079] Figure 55 shows that the Pro255 dual targeting molecule with an MMP9 cleavage site, shows good conditionality.

[0080] Figure 57A – Figure 57D shows the results of experiments on three different cell types. First, Raji transfectants were created with similar expression levels of EpCAM, EGFR and EpCAM + EGFR (data not shown). Then Pro255, which targets both EpCAM and EGFR, was tested in TDCC assays using each cell type. Figure A shows the parental Raji line, that

doesn't express either receptor. Figure B shows conditionality on the EpCAM line. Figure C shows conditionality on the EGRF line. Figure D shows conditionality on the EpCAM/EGFR line.

[0081] Figure 56 depicts the schematics of a Format 4 construct, Pro258.

[0082] Figure 57A – Figure 59B shows that Pro258 is conditional in both FBS and human serum. The conditionality of the MMP9 linker is underestimated due to the MMP9 activity in the culture. Interestingly, Pro51 TDCC activity is inhibited by HSA binding while Pro258 TDCC activity is similar to Pro51 in the presence of HSA. Finally, the Pro258 conditionality is somewhat enhanced in the presence of HSA by 6X.

[0083] Figure 58A – Figure 60C shows the cleavage of the MMP9 substrate by other MMPs.

[0084] Figure 59A – Figure 61B shows some of the exemplary constructs and their formats.

[0085] Figure 60A – Figure 62U shows a number of sequences of the invention, although many additional sequences are also found in the sequence listing. CDRs are underlined and bolded, linkers are double underlined (with cleavable linkers being italicized and double underlined) and domain separations are indicated by "/". All His6 tags are optional, as they can be used to reduce immunogenicity in humans as well as be purification tags.

VI. DETAILED DESCRIPTION OF THE INVENTION

A. Introduction

[0086] The present invention is directed to methods of reducing the toxicity and side effects of bispecific antibodies (including antibody-like functional proteins) that bind to important physiological targets such as CD3 and tumor antigens. Many antigen binding proteins, such as antibodies, can have significant off-target side effects, and thus there is a need to only activate the binding capabilities of a therapeutic molecule in the vicinity of the disease tissue, to avoid off-target interactions. Accordingly, the present invention is directed to multivalent conditionally effective ("MCE") proteins that have a number of functional protein domains. In general, one of these domains is an antigen binding domain (ABD) that will bind a target tumor antigen (TTA), and another is an ABD that will bind a T-cell antigen such as CD3 under certain conditions. Additionally, the MCE proteins also include one or more protease cleavage sites. That is, the therapeutic molecules are made in a "pro-drug"

like format, wherein the CD3 binding domain is inactive until exposed to a tumor environment. The tumor environment contains proteases, such that upon exposure to the protease, the prodrug is cleaved and becomes active.

[0087] This is generally accomplished herein by using proteins that include a "pseudo" variable heavy domain and a "pseudo" variable light domain directed to the T-cell antigen such as CD3, that restrain the CD3 Fvs of the MCE into an inactive format as is discussed herein. As the TTA targets the MCE into the proximity of the tumor, the MCE is thus exposed to the protease. Upon cleavage, the active variable heavy domain and active light domain are now able to pair to form one or more active ABDs to CD3 and thus recruit T cells to the tumor, resulting in treatment.

[0088] In general, the CD3 binding domain ("Fv") is in a constrained format, wherein the linker between the active variable heavy domain and the active variable light domain that traditionally form an Fv is too short to allow the two active variable domains to bind each other; this is referred to as "constrained linker"; these can be constrained and cleavable (CCL, as used in Format 1) or constrained and not cleavable (CNCL, as used in Format 2). Rather, in the prodrug (e.g. uncleaved) format, the prodrug polypeptide also comprises a "pseudo Fv domain". The pseudo Fv domain comprises a variable heavy and light domain, with standard framework regions, but "inert" or "inactive" CDRs. The pseudo Fv domain also has a constrained linker between the inactive variable heavy and inactive variable light domains. Since neither Fv nor pseudo Fv domains can self-assemble due to the steric constraints, there is an intramolecular assembly that pairs the aVL with the iVH and the aVH with the iVL, due to the affinity of the framework regions of each. However, due to the "inert" CDRs of the pseudo domain, the resulting ABDs will not bind CD3, thus preventing off target toxicities. However, in the presence of proteases that are in or near the tumor, the prodrug construct is cleaved such that the pseudo-Fv domain is released from the surface and thus allows the "real" variable heavy and variable light domains to associate intermolecularly (e.g. two cleaved constructs come together), thus triggering active CD3 binding and the resulting tumor efficacy. These constructs are generally referred to herein as **CO**nditional **B**ispecific **R**edirected **A**ctivation constructs, or "COBRAs™". The stability of the intramolecular assembly is shown by the conditionality experiments herein, whereby in

the absence of protease, the uncleaved constructs have no activity (e.g. no active CD3 binding domain is formed).

[0089] Interestingly, for ease of description, while these constructs are all referred to herein as "constrained", additional work shows that the intramolecular assembly is favored even if one of the Fv domains is not constrained, e.g. one of the domains can have a longer, flexible linker. That is, as shown in Figure 36, Figure 37 and Figure 38, intramolecular assembly still occurs (e.g. the uncleaved constructs are inactive in the absence of protease cleavage) if only one of the Fv domains, either the one with an active VL and VH, or the pseudo Fv domain, is constrained. However, in the current systems, when both linkers are constrained, the protein has better expression. However, as will be appreciated by those of skill in the art, any of the Format 1, Format 2 or Format 4 constructs herein can have one of these Fv domains with an "unconstrained" or "flexible" linker. For ease of reference, the constructs are shown with both Fv domains in a constrained format.

[0090] The constructs and formats of the invention are variations over inventions described in WO2017/156178, hereby expressly incorporated by reference in its entirety. As shown in Figure 20, previous constructs have the ability to isomerize due to the presence of two sets of VH and VL domains in a single polypeptide, forming both a bivalent scFv and a single chain diabody. Even after purification of each isoform, the bivalent construct can still reach equilibrium with the diabody isoform. As the single chain diabody has the ability to bind to CD3 in the absence of protease cleavage, the utility of the construct is diminished.

[0091] To solve this issue, the present invention provides for four separate types of constructs to accomplish this conditional activation. The prodrug activation can happen in one of four general ways, as is generally shown in the Figures. In Figure 1, a "format 1" mechanism is shown. In this embodiment, the prodrug construct has two cleavage sites: one between the VH and vl domains of the constrained Fv, thus freeing the two variable domains to associate, and a second at a site that releases the pseudo Fv domain from the prodrug construct, leaving two molecules that associate due to the innate self-assembly of the variable heavy and variable light domains, each having an antigen binding domain to a tumor antigen as well, thus allowing the recruitment of T cells to the tumor site.

[0092] In an alternate embodiment, the prodrug construct is shown in Figure 2, a "format 2" mechanism. In this embodiment, the domain linker between the active variable heavy and active light chains is a constrained but not cleavable linker ("CNCL"). In the prodrug format, the inactive VH and VL of the constrained pseudo Fv domain associate with the VH and VL of the constrained Fv domain, such that there is no CD3 binding. However, once cleavage in the tumor environment happens, two different activated proteins, each comprising an active variable heavy and light domain, associate to form two anti-CD3 binding domains.

[0093] In addition to the "single chain protein" COBRA formats discussed above, where all of the components are contained on a single amino acid sequence, there are also constructs that rely on two proteins "hemi-COBRAs", which act in pairs, as shown in Figure 3. In this embodiment, each protein has one active and one inert variable domain separated by a protease cleavage site. Each molecule contains a TTA binding domain, such that when the molecules are bound to the TTA and exposed to tumor protease, the inert domains are cleaved off and the two active variable domains self-assemble to form an anti-CD3 binding domain.

[0094] Furthermore, the invention provides "format 4" constructs as well, as depicted in Figure 4. These are similar to the "format 2" designs, except that a single ABD to a TTA is used, such that upon cleavage, two of the pro-drug molecules now form a tetravalent, bispecific construct containing two active anti-CD3 domains, as is further described below.

[0095] Accordingly, the formats and constructs of the invention find use in the treatment of disease.

B. Definitions

[0096] In order that the application may be more completely understood, several definitions are set forth below. Such definitions are meant to encompass grammatical equivalents.

[0097] By "amino acid" and "amino acid identity" as used herein is meant one of the 20 naturally occurring amino acids or any non-natural analogues that may be present at a specific, defined position. In many embodiments, "amino acid" means one of the 20 naturally occurring amino acids. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides.

[0098] By "amino acid modification" herein is meant an amino acid substitution, insertion, and/or deletion in a polypeptide sequence or an alteration to a moiety chemically linked to a protein. For example, a modification may be an altered carbohydrate or PEG structure attached to a protein. For clarity, unless otherwise noted, the amino acid modification is always to an amino acid coded for by DNA, e.g. the 20 amino acids that have codons in DNA and RNA. The preferred amino acid modification herein is a substitution.

[0099] By "amino acid substitution" or "substitution" herein is meant the replacement of an amino acid at a particular position in a parent polypeptide sequence with a different amino acid. In particular, in some embodiments, the substitution is to an amino acid that is not naturally occurring at the particular position, either not naturally occurring within the organism or in any organism. For clarity, a protein which has been engineered to change the nucleic acid coding sequence but not change the starting amino acid (for example exchanging CGG (encoding arginine) to CGA (still encoding arginine) to increase host organism expression levels) is not an "amino acid substitution"; that is, despite the creation of a new gene encoding the same protein, if the protein has the same amino acid at the particular position that it started with, it is not an amino acid substitution.

[00100] By "amino acid insertion" or "insertion" as used herein is meant the addition of an amino acid sequence at a particular position in a parent polypeptide sequence.

[00101] By "amino acid deletion" or "deletion" as used herein is meant the removal of an amino acid sequence at a particular position in a parent polypeptide sequence.

[00102] The polypeptides of the invention specifically bind to CD3 and target tumor antigens (TTAs) such as target cell receptors, as outlined herein. “Specific binding” or “specifically binds to” or is “specific for” a particular antigen or an epitope means binding that is measurably different from a non-specific interaction. Specific binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule, which generally is a molecule of similar structure that does not have binding activity. For example, specific binding can be determined by competition with a control molecule that is similar to the target.

[00103] Specific binding for a particular antigen or an epitope can be exhibited, for example, by an antibody having a KD for an antigen or epitope of at least about 10^{-4} M, at

least about 10^{-5} M, at least about 10^{-6} M, at least about 10^{-7} M, at least about 10^{-8} M, at least about 10^{-9} M, alternatively at least about 10^{-10} M, at least about 10^{-11} M, at least about 10^{-12} M, or greater, where KD refers to a dissociation rate of a particular antibody-antigen interaction. Typically, an antibody that specifically binds an antigen will have a KD that is 20-, 50-, 100-, 500-, 1000-, 5,000-, 10,000- or more times greater for a control molecule relative to the antigen or epitope.

[00104] Also, specific binding for a particular antigen or an epitope can be exhibited, for example, by an antibody having a KA or Ka for an antigen or epitope of at least 20-, 50-, 100-, 500-, 1000-, 5,000-, 10,000- or more times greater for the epitope relative to a control, where KA or Ka refers to an association rate of a particular antibody-antigen interaction. Binding affinity is generally measured using a Biacore assay or Octet as is known in the art.

[00105] By "parent polypeptide" or "precursor polypeptide" (including Fc parent or precursors) as used herein is meant a polypeptide that is subsequently modified to generate a variant. Said parent polypeptide may be a naturally occurring polypeptide, or a variant or engineered version of a naturally occurring polypeptide. Parent polypeptide may refer to the polypeptide itself, compositions that comprise the parent polypeptide, or the amino acid sequence that encodes it. Accordingly, by "parent Fc polypeptide" as used herein is meant an unmodified Fc polypeptide that is modified to generate a variant, and by "parent antibody" as used herein is meant an unmodified antibody that is modified to generate a variant antibody.

[00106] By "position" as used herein is meant a location in the sequence of a protein. Positions may be numbered sequentially, or according to an established format, for example the EU index for antibody numbering.

[00107] By "target antigen" as used herein is meant the molecule that is bound specifically by the variable region of a given antibody. A target antigen may be a protein, carbohydrate, lipid, or other chemical compound. A range of suitable exemplary target antigens are described herein.

[00108] By "target cell" as used herein is meant a cell that expresses a target antigen. Generally, for the purposes of the invention, target cells are either tumor cells that express TTAs or T cells that express the CD3 antigen.

[00109] By "Fv" or "Fv domain" or "Fv region" as used herein is meant a polypeptide that comprises the VL and VH domains of an antigen binding domain, generally from an antibody. Fv domains usually form an "antigen binding domain" or "ABD" as discussed herein, if they contain active VH and VL domains (although in some cases, an Fv containing a constrained linker is used, such that an active ABD isn't formed prior to cleavage). As discussed below, Fv domains can be organized in a number of ways in the present invention, and can be "active" or "inactive", such as in a scFv format, a constrained Fv format, a pseudo Fv format, etc. It should be understood that in the present invention, in some cases an Fv domain is made up of a VH and VL domain on a single polypeptide chain, such as shown in Figure 1 and Figure 2 but with a constrained linker such that an intramolecular ABD cannot be formed. In these embodiments, it is after cleavage that two active ABDs are formed. In some cases an Fv domain is made up of a VH and a VL domain, one of which is inert, such that only after cleavage is an intermolecular ABD formed. As discussed below, Fv domains can be organized in a number of ways in the present invention, and can be "active" or "inactive", such as in a scFv format, a constrained Fv format, a pseudo Fv format, etc. In addition, as discussed herein, Fv domains containing VH and VL can be/form ABDs, and other ABDs that do not contain VH and VL domains can be formed using sdABDs.

[00110] By "variable domain" herein is meant the region of an immunoglobulin that comprises one or more Ig domains substantially encoded by any of the Vκ, Vλ, and/or VH genes that make up the kappa, lambda, and heavy chain immunoglobulin genetic loci respectively. In some cases, a single variable domain, such as a sdFv (also referred to herein as sdABD) can be used.

[00111] In embodiments utilizing both variable heavy (VH) and variable light (VL) domains, each VH and VL is composed of three hypervariable regions ("complementary determining regions," "CDRs") and four "framework regions", or "FRs", arranged from amino-terminus to carboxy-terminus in the following order: FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4. Thus, the VH domain has the structure vhFR1-vhCDR1-vhFR2-vhCDR2-vhFR3-vhCDR3-vhFR4 and the VL domain has the structure vlFR1-vlCDR1-vlFR2-vlCDR2-vlFR3-vlCDR3-vlFR4. As is more fully described herein, the vhFR regions and the vlFR regions self assemble to form Fv domains. In general, in the prodrug formats of the invention, there

are "constrained Fv domains" wherein the VH and VL domains cannot self associate, and "pseudo Fv domains" for which the CDRs do not form antigen binding domains when self associated.

[00112] The hypervariable regions confer antigen binding specificity and generally encompasses amino acid residues from about amino acid residues 24-34 (LCDR1; "L" denotes light chain), 50-56 (LCDR2) and 89-97 (LCDR3) in the light chain variable region and around about 31-35B (HCDR1; "H" denotes heavy chain), 50-65 (HCDR2), and 95-102 (HCDR3) in the heavy chain variable region; Kabat et al., SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991) and/or those residues forming a hypervariable loop (e.g. residues 26-32 (LCDR1), 50-52 (LCDR2) and 91-96 (LCDR3) in the light chain variable region and 26-32 (HCDR1), 53-55 (HCDR2) and 96-101 (HCDR3) in the heavy chain variable region; Chothia and Lesk (1987) J. Mol. Biol. 196:901-917. Specific CDRs of the invention are described below.

[00113] As will be appreciated by those in the art, the exact numbering and placement of the CDRs can be different among different numbering systems. However, it should be understood that the disclosure of a variable heavy and/or variable light sequence includes the disclosure of the associated (inherent) CDRs. Accordingly, the disclosure of each variable heavy region is a disclosure of the vhCDRs (e.g. vhCDR1, vhCDR2 and vhCDR3) and the disclosure of each variable light region is a disclosure of the vlCDRs (e.g. vlCDR1, vlCDR2 and vlCDR3).

[00114] A useful comparison of CDR numbering is as below, see Lafranc et al., Dev. Comp. Immunol. 27(1):55-77 (2003):

TABLE 1

	Kabat+ Chothia	IMGT	Kabat	AbM	Chothia	Contact
vhCDR1	26-35	27-38	31-35	26-35	26-32	30-35
vhCDR2	50-65	56-65	50-65	50-58	52-56	47-58

vhCDR3	95-102	105-117	95-102	95-102	95-102	93-101
vlCDR1	24-34	27-38	24-34	24-34	24-34	30-36
vlCDR2	50-56	56-65	50-56	50-56	50-56	46-55
vlCDR3	89-97	105-117	89-97	89-97	89-97	89-96

[00115] Throughout the present specification, the Kabat numbering system is generally used when referring to a residue in the variable domain (approximately, residues 1-107 of the light chain variable region and residues 1-113 of the heavy chain variable region) and the EU numbering system for Fc regions (e.g, Kabat et al., supra (1991)).

[00116] The present invention provides a large number of different CDR sets. In this case, a "full CDR set" in the context of the anti-CD3 component comprises the three variable light and three variable heavy CDRs, e.g. a vlCDR1, vlCDR2, vlCDR3, vhCDR1, vhCDR2 and vhCDR3. As will be appreciated by those in the art, each set of CDRs, the VH and VL CDRs, can bind to antigens, both individually and as a set. For example, in constrained Fv domains, the vhCDRs can bind, for example to CD3 and the vlCDRs can bind to CD3, but in the constrained format they cannot bind to CD3.

[00117] In the context of a single domain ABD ("sdABD") such as are generally used herein to bind to target tumor antigens (TTA), a CDR set is only three CDRs; these are sometimes referred to in the art as "VHH" domains as well.

[00118] These CDRs can be part of a larger variable light or variable heavy domain, respectfully. In addition, as more fully outlined herein, the variable heavy and variable light domains can be on separate polypeptide chains or on a single polypeptide chain in the case of scFv sequences, depending on the format and configuration of the moieties herein.

[00119] The CDRs contribute to the formation of the antigen-binding, or more specifically, epitope binding sites. "Epitope" refers to a determinant that interacts with a specific antigen binding site in the variable regions known as a paratope. Epitopes are groupings of molecules such as amino acids or sugar side chains and usually have specific

structural characteristics, as well as specific charge characteristics. A single antigen may have more than one epitope.

[00120] The epitope may comprise amino acid residues directly involved in the binding (also called immunodominant component of the epitope) and other amino acid residues, which are not directly involved in the binding, such as amino acid residues which are effectively blocked by the specific antigen binding peptide; in other words, the amino acid residue is within the footprint of the specific antigen binding peptide.

[00121] Epitopes may be either conformational or linear. A conformational epitope is produced by spatially juxtaposed amino acids from different segments of the linear polypeptide chain. A linear epitope is one produced by adjacent amino acid residues in a polypeptide chain. Conformational and nonconformational epitopes may be distinguished in that the binding to the former but not the latter is lost in the presence of denaturing solvents.

[00122] An epitope typically includes at least 3, and more usually, at least 5 or 8-10 amino acids in a unique spatial conformation. Antibodies that recognize the same epitope can be verified in a simple immunoassay showing the ability of one antibody to block the binding of another antibody to a target antigen, for example “binning.” As outlined below, the invention not only includes the enumerated antigen binding domains and antibodies herein, but those that compete for binding with the epitopes bound by the enumerated antigen binding domains.

[00123] The variable heavy and variable light domains of the invention can be “active” or “inactive”.

[00124] As used herein, "inactive VH" (“iVH”) and "inactive VL" (“iVL”) refer to components of a pseudo Fv domain, which, when paired with their cognate VL or VH partners, respectively, form a resulting VH/VL pair that does not specifically bind to the antigen to which the "active" VH or "active" VL would bind were it bound to an analogous VL or VH, which was not "inactive". Exemplary "inactive VH" and "inactive VL" domains are formed by mutation of a wild type VH or VL sequence as more fully outlined below. Exemplary mutations are within CDR1, CDR2 or CDR3 of VH or VL. An exemplary mutation includes placing a domain linker within CDR2, thereby forming an "inactive VH"

or "inactive VL" domain. In contrast, an "active VH" or "active VL" is one that, upon pairing with its "active" cognate partner, i.e., VL or VH, respectively, is capable of specifically binding to its target antigen. Thus, it should be understood that a pseudo Fv can be a VH/iVL pair, a iVH/VL pair, or a iVH/iVL pair.

[00125] In contrast, as used herein, the term "active" refers to a CD-3 binding domain that is capable of specifically binding to CD-3. This term is used in two contexts: (a) when referring to a single member of an Fv binding pair (i.e., VH or VL), which is of a sequence capable of pairing with its cognate partner and specifically binding to CD-3; and (b) the pair of cognates (i.e., VH and VL) of a sequence capable of specifically binding to CD-3. An exemplary "active" VH, VL or VH/VL pair is a wild type or parent sequence.

[00126] "CD-x" refers to a cluster of differentiation (CD) protein. In exemplary embodiments, CD-x is selected from those CD proteins having a role in the recruitment or activation of T-cells in a subject to whom a polypeptide construct of the invention has been administered. In an exemplary embodiment, CD-x is CD3, the sequence of which is shown in Figure 5.

[00127] The term "binding domain" characterizes, in connection with the present invention, a domain which (specifically) binds to/interacts with/recognizes a given target epitope or a given target site on the target molecules (antigens), for example: EGFR and CD-3, respectively. The structure and function of the target antigen binding domain (recognizing EGFR), and preferably also the structure and/or function of the CD-3 binding domain (recognizing CD3), is/are based on the structure and/or function of an antibody, e.g. of a full-length or whole immunoglobulin molecule, including sdABDs. According to the invention, the target antigen binding domain is generally characterized by the presence of three CDRs that bind the target tumor antigen (generally referred to in the art as variable heavy domains, although no corresponding light chain CDRs are present). Alternatively, ABDs to TTAs can include three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region) and/or three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region). The CD-3 binding domain preferably also comprises at least the minimum structural requirements of an antibody which allow for the target binding. More preferably, the CD-3 binding domain comprises at least three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region)

and/or three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region). It is envisaged that in exemplary embodiments the target antigen and/or CD-3 binding domain is produced by or obtainable by phage-display or library screening methods.

[00128] By "domain" as used herein is meant a protein sequence with a function, as outlined herein. Domains of the invention include tumor target antigen binding domains (TTA domains), variable heavy domains, variable light domains, linker domains, and half life extension domains.

[00129] By "domain linker" herein is meant an amino acid sequence that joins two domains as outlined herein. Domain linkers can be cleavable linkers, constrained cleavable linkers, non-cleavable linkers, constrained non-cleavable linkers, scFv linkers, etc.

[00130] By "cleavable linker" ("CL") herein is meant an amino acid sequence that can be cleaved by a protease, preferably a human protease in a disease tissue as outlined herein. Cleavable linkers generally are at least 3 amino acids in length, with from 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more amino acids finding use in the invention, depending on the required flexibility. A number of cleavable linker sequences are found in Figure 6 and Figure 5.

[00131] By "non cleavable linker" ("NCL") herein is meant an amino acid sequence that cannot be cleaved by a human protease under normal physiological conditions.

[00132] By "constrained cleavable linker" ("CCL") herein is meant a short polypeptide that contains a protease cleavage site (as defined herein) that joins two domains as outlined herein in such a manner that the two domains cannot significantly interact with each other until after they reside on different polypeptide chains, e.g. after cleavage. When the CCL joins a VH and a VL domain as defined herein, the VH and VL cannot self-assemble to form a functional Fv prior to cleavage due to steric constraints in an intramolecular way (although they may assemble into pseudo Fv domains in an intermolecular way). Upon cleavage by the relevant protease, the VH and VL can assemble to form an active antigen binding domain in an intermolecular way. In general, CCLs are less than 10 amino acids in length, with 9, 8, 7, 6, 5 and 4 amino acids finding use in the invention. In general, protease cleavage sites generally are at least 4+ amino acids in length to confer sufficient specificity, as is shown in Figure 6.

[00133] By "constrained non-cleavable linker" ("CNCL") herein is meant a short polypeptide that that joins two domains as outlined herein in such a manner that the two domains cannot significantly interact with each other, and that is not significantly cleaved by human proteases under physiological conditions.

[00134] By "constrained Fv domain" herein is meant an Fv domain that comprises an active variable heavy domain and an active variable light domain, linked covalently with a constrained linker as outlined herein, in such a way that the active heavy and light variable domains cannot intramolecularly interact to form an active Fv that will bind an antigen such as CD3. Thus, a constrained Fv domain is one that is similar to an scFv but is not able to bind an antigen due to the presence of a constrained linker (although they may assemble intermolecularly with inert variable domains to form pseudo Fv domains).

[00135] By "pseudo Fv domain" herein is meant a domain that comprises a pseudo or inactive variable heavy domain or a pseudo or inactive variable light domain, or both, linked using a domain linker (which can be cleavable, constrained, non-cleavable, non-constrained, etc.). The iVH and iVL domains of a pseudo Fv domain do not bind to a human antigen when either associated with each other (iVH/iVL) or when associated with an active VH or VL; thus iVH/iVL, iVH/VL and iVL/VH Fv domains do not appreciably bind to a human protein, such that these domains are inert in the human body.

[00136] By "single chain Fv" or "scFv" herein is meant a variable heavy (VH) domain covalently attached to a variable light (VL) domain, generally using a domain linker as discussed herein, to form a scFv or scFv domain. A scFv domain can be in either orientation from N- to C-terminus (VH -linker- VL or VL-linker-VH).

[00137] By "single domain Fv", "sdFv" or "sdABD" herein is meant an antigen binding domain that only has three CDRs, generally based on camelid antibody technology. See: Protein Engineering 9(7):1129-35 (1994); Rev Mol Biotech 74:277-302 (2001); Ann Rev Biochem 82:775-97 (2013). As outlined herein, there are two general types of sdABDs used herein: sdABDs that bind to TTAs, and are annotated as such (sdABD-TTA for the generic term, or sdABD-EGFR for one that binds to EGFR, sdABD-FOLR1 for one that binds to FOLR1, etc.) and sdABDs that bind to HSA ("sdABD-HSA" or "sdABD(½)".

[00138] By "protease cleavage site" refers to the amino acid sequence recognized and cleaved by a protease. Suitable protease cleavage sites are outlined below and shown in Figure 5 and Figure 6.

[00139] As used herein, "protease cleavage domain" refers to the peptide sequence incorporating the "protease cleavage site" and any linkers between individual protease cleavage sites and between the protease cleavage site(s) and the other functional components of the constructs of the invention (e.g., V_H, V_L, iVH, iVL, target antigen binding domain(s), half-life extension domain, etc.). As outlined herein, a protease cleavage domain may also include additional amino acids if necessary, for example to confer flexibility.

[00140] The term "COBRA™" and "conditional bispecific redirected activation" refers to a bispecific conditionally effective protein that has a number of functional protein domains. In some embodiments, one of the functional domains is an antigen binding domain (ABD) that binds a target tumor antigen (TTA). In certain embodiments, another domain is an ABD that binds to a T cell antigen under certain conditions. The T cell antigen includes but is not limited to CD3. The term "hemi-COBRA™" refers to a conditionally effective protein that can bind a T cell antigen when a variable heavy chain of a hemi-COBRA can associate to a variable light chain of another hemi-COBRA™ (a complementary hemi-COBRA™) due to innate self-assembly when concentrated on the surface of a target expressing cell.

VII. Fusion Proteins of the Invention

[00141] The fusion proteins of the invention have a number of different components, generally referred to herein as domains, that are linked together in a variety of ways. Some of the domains are binding domains, that each bind to a target antigen (e.g. a TTA or CD3, for example). As they bind to more than one antigen, they are referred to herein as "multispecific"; for example, a prodrug construct of the invention may bind to a TTA and CD3, and thus are "bispecific". A protein can also have higher specificities; for example, if the first αTTA binds to EGFR, the second to EpCAM and there is an anti-CD3 binding domain, this would be a "trispecific" molecule. Similarly, the addition of an anti-HSA binding domain to this construct would be "tetraspecific", as shown in Figure 3B.

[00142] As will be appreciated by those in the art, the proteins of the invention can have different valencies as well as be multispecific. That is, proteins of the invention can bind a target with more than one binding site; for example, Pro140 is bivalent for EGFR.

[00143] The proteins of the invention can include CD3 antigen binding domains arranged in a variety of ways as outlined herein, tumor target antigen binding domains, half-life extension domains, linkers, etc.

A. CD3 Antigen Binding Domains

[00144] The specificity of the response of T cells is mediated by the recognition of antigen (displayed in context of a major histocompatibility complex, MHC) by the T cell receptor complex. As part of the T cell receptor complex, CD3 is a protein complex that includes a CD3γ (gamma) chain, a CD3δ (delta) chain, two CD3e (epsilon) chains and two CD3ζ (zeta) chains, which are present at the cell surface. CD3 molecules associate with the α (alpha) and β (beta) chains of the T cell receptor (TCR) to comprise the TCR complex. Clustering of CD3 on T cells, such as by Fv domains that bind to CD3 leads to T cell activation similar to the engagement of the T cell receptor but independent of its clonal-typical specificity.

[00145] However, as is known in the art, CD3 activation can cause a number of toxic side effects, and accordingly the present invention is directed to providing active CD3 binding of the polypeptides of the invention only in the presence of tumor cells, where specific proteases are found, that then cleave the prodrug polypeptides of the invention to provide an active CD3 binding domain. Thus, in the present invention, binding of an anti-CD-3 Fv domain to CD-3 is regulated by a protease cleavage domain which restricts binding of the CD-3 Fv domain to CD-3 only in the microenvironment of a diseased cell or tissue with elevated levels of proteases, for example in a tumor microenvironment as is described herein.

[00146] Accordingly, the present invention provides two sets of VH and VL domains, an active set (VH and VL) and an inactive set (iVH and iVL) with all four being present in the prodrug construct. The construct is formatted such that the VH and VL set cannot self-associate, but rather associates with an inactive partner, e.g. iVH and VL and iVL and VH as is shown herein.

1. Active anti-CD3 variable heavy and variable light domains

[00147] There are a number of suitable active CDR sets, and/or VH and VL domains, that are known in the art that find use in the present invention. For example, the CDRs and/or VH and VL domains are derived from known anti-CD-3 antibodies, such as, for example, muromonab-CD-3 (OKT3), otelixizumab (TRX4), teplizumab (MGA031), visilizumab (Nuvion), SP34 or I2C, TR-66 or X35-3, VIT3, BMA030 (BW264/56), CLB-T3/3, CRIS7, YTH12.5, F111-409, CLB-T3.4.2, TR-66, WT32, SPv-T3b, 11D8, XIII-141, XIII-46, XIII-87, 12F6, T3/RW2-8C8, T3/RW2-4B6, OKT3D, M-T301, SMC2, F101.01, UCHT-1 and WT-31.

[00148] In one embodiment, the VH and VL sequences that form an active Fv domain that binds to human CD3 are shown in Figure 5. As is shown herein, these active VH ("aVH") and active VL ("aVL") domains can be used in different configuations and Formats 1, 2, 3 and 4.

2. Inactive anti-CD3 variable heavy and variable light domains

[00149] The inactive iVH and iVL domains contain "regular" framework regions (FRs) that allow association, such that an inactive variable domain will associate with an active variable domain, rendering the pair inactive, e.g. unable to bind CD3.

[00150] As will be appreciated by those in the art, there are a number of "inactive" variable domains that find use in the invention. Basically, any variable domain with human framework regions that allows self-assembly with another variable domain, no matter what amino acids are in the CDR location in the variable region, can be used. For clarity, the inactive domains are said to include CDRs, although technically the inactive variable domains do not confer binding capabilities.

[00151] As will be appreciated in the art, it is generally straightforward to generate inactive VH or VL domains, and can be done in a variety of ways. In some embodiments, the generation of inactive variable domains is generally done by altering one or more of the CDRs of an active Fv, including making changes in one or more of the three CDRs of an active variable domain. This can be done by making one or more amino acid substitutions at functionally important residues in one or more CDRs, replacing some or all CDR residues with random sequences, replacing one or more CDRs with tag or flag sequences, and/or

swapping CDRs and/or variable regions with those from an irrelevant antibody (one directed to a different organism's protein for example.

[00152] In some cases, only one of the CDRs in a variable region can be altered to render it inactive, although other embodiments include alterations in one, two, three, four, five or six CDRs.

[00153] In some cases, the inactive domains can be engineered to promote selective binding in the prodrug format, to encourage formation of intramolecular iVH-VL and VH-iVL domains prior to cleavage (over, for example, intermolecular pair formation). See for example Igawa et al., Protein Eng. Des. Selection 23(8):667-677 (2010), hereby expressly incorporated by reference in its entirety and specifically for the interface residue amino acid substitutions.

[00154] In certain embodiments, the CD-3 binding domain of the polypeptide constructs described herein exhibit not only potent CD-3 binding affinities with human CD-3, but show also excellent cross reactivity with the respective cynomolgus monkey CD-3 proteins. In some instances, the CD-3 binding domain of the polypeptide constructs is cross-reactive with CD-3 from cynomolgus monkey. In certain instances, human:cynomolgous KD ratios for CD-3 are between 5 and 0.2.

[00155] In some embodiments, the CD-3 binding domain of the antigen binding protein can be any domain that binds to CD-3 including but not limited to domains from a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody. In some instances, it is beneficial for the CD-3 binding domain to be derived from the same species in which the antigen binding protein will ultimately be used in. For example, for use in humans, it may be beneficial for the CD-3 binding domain of the antigen binding protein to comprise human or humanized residues from the antigen binding domain of an antibody or antibody fragment.

[00156] Thus, in one aspect, the antigen-binding domain comprises a humanized or human binding domain. In one embodiment, the humanized or human anti-CD-3 binding domain comprises one or more (e.g., all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a humanized or human anti- CD-3

binding domain described herein, and/or one or more (e.g., all three) heavy chain complementary determining region 1 (HC CDR1), heavy chain complementary determining region 2 (HC CDR2), and heavy chain complementary determining region 3 (HC CDR3) of a humanized or human anti-CD-3 binding domain described herein, e.g., a humanized or human anti-CD-3 binding domain comprising one or more, e.g., all three, LC CDRs and one or more, e.g., all three, HC CDRs.

[00157] In some embodiments, the humanized or human anti-CD-3 binding domain comprises a humanized or human light chain variable region specific to CD-3 where the light chain variable region specific to CD-3 comprises human or non-human light chain CDRs in a human light chain framework region. In certain instances, the light chain framework region is a λ (lambda) light chain framework. In other instances, the light chain framework region is a κ (kappa) light chain framework.

[00158] In some embodiments, one or more CD-3 binding domains are humanized or fully human. In some embodiments, one or more activated CD-3 binding domains have a KD binding of 1000 nM or less to CD-3 on CD-3 expressing cells. In some embodiments, one or more activated CD-3 binding domains have a KD binding of 100 nM or less to CD-3 on CD-3 expressing cells. In some embodiments, one or more activated CD-3 binding domains have a KD binding of 10 nM or less to CD-3 on CD-3 expressing cells. In some embodiments, one or more CD-3 binding domains have crossreactivity with cynomolgus CD-3. In some embodiments, one or more CD-3 binding domains comprise an amino acid sequence provided herein.

[00159] In some embodiments, the humanized or human anti-CD-3 binding domain comprises a humanized or human heavy chain variable region specific to CD-3 where the heavy chain variable region specific to CD-3 comprises human or non-human heavy chain CDRs in a human heavy chain framework region.

[00160] In one embodiment, the anti-CD-3 binding domain is an Fv comprising a light chain and a heavy chain of an amino acid sequence provided herein. In an embodiment, the anti-CD-3 binding domain comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions) of an amino

acid sequence of a light chain variable region provided herein, or a sequence with 95-99% identity with an amino acid sequence provided herein; and/or a heavy chain variable region comprising an amino acid sequence having at least one, two or three modifications (e.g., substitutions) but not more than 30, 20 or 10 modifications (e.g., substitutions) of an amino acid sequence of a heavy chain variable region provided herein, or a sequence with 95-99% identity to an amino acid sequence provided herein. In one embodiment, the humanized or human anti-CD-3 binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, is attached to a heavy chain variable region comprising an amino acid sequence described herein, via a scFv linker. The light chain variable region and heavy chain variable region of a scFv can be, e.g., in any of the following orientations: light chain variable region- scFv linker-heavy chain variable region or heavy chain variable region- scFv linker-light chain variable region.

[00161] In some embodiments, CD-3 binding domain of an antigen binding protein has an affinity to CD-3 on CD-3 expressing cells with a KD of 1000 nM or less, 100 nM or less, 50 nM or less, 20 nM or less, 10 nM or less, 5 nM or less, 1 nM or less, or 0.5 nM or less. In some embodiments, the CD-3 binding domain of an antigen binding protein has an affinity to CD-3ε with a KD of 1000 nM or less, 100 nM or less, 50 nM or less, 20 nM or less, 10 nM or less, 5 nM or less, 1 nM or less, or 0.5 nM or less. In further embodiments, CD-3 binding domain of an antigen binding protein has low affinity to CD-3, i.e., about 100 nM or greater.

[00162] The affinity to bind to CD-3 can be determined, for example, by the ability of the antigen binding protein itself or its CD-3 binding domain to bind to CD-3 coated on an assay plate; displayed on a microbial cell surface; in solution; etc., as is known in the art, generally using Biacore or Octet assays. The binding activity of the antigen binding protein itself or its CD-3 binding domain of the present disclosure to CD-3 can be assayed by immobilizing the ligand (e.g., CD-3) or the antigen binding protein itself or its CD-3 binding domain, to a bead, substrate, cell, etc. Agents can be added in an appropriate buffer and the binding partners incubated for a period of time at a given temperature. After washes to remove unbound material, the bound protein can be released with, for example, SDS, buffers with a high pH, and the like and analyzed, for example, by Surface Plasmon Resonance (SPR).

[00163] In many embodiments, preferred active and inert binding domains are those shown in Figure 5.

B. Antigen Binding Domains to Tumor Target Antigens

[00164] In addition to the described CD3 and half-life extension domains, the polypeptide constructs described herein also comprise target domains that bind to one or more target antigens or one or more regions on a single target antigen. It is contemplated herein that a polypeptide construct of the invention is cleaved, for example, in a disease-specific microenvironment or in the blood of a subject at the protease cleavage domain and that each target antigen binding domain will bind to a target antigen on a target cell, thereby activating the CD3 binding domain to bind a T cell. In general, the TTA binding domains can bind to their targets before protease cleavage, so they can "wait" on the target cell to be activated as T-cell engagers. At least one target antigen is involved in and/or associated with a disease, disorder or condition. Exemplary target antigens include those associated with a proliferative disease, a tumorous disease, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, a viral disease, an allergic reaction, a parasitic reaction, a graft-versus-host disease or a host-versus-graft disease. In some embodiments, a target antigen is a tumor antigen expressed on a tumor cell. Alternatively in some embodiments, a target antigen is associated with a pathogen such as a virus or bacterium. At least one target antigen may also be directed against healthy tissue.

[00165] In some embodiments, a target antigen is a cell surface molecule such as a protein, lipid or polysaccharide. In some embodiments, a target antigen is a on a tumor cell, virally infected cell, bacterially infected cell, damaged red blood cell, arterial plaque cell, or fibrotic tissue cell.

[00166] Preferred embodiments of the invention utilize sdABDs as the targeting domains. These are preferred over scFv ABDs, since the addition of other VH and VL domains into a construct of the invention may complicate the formation of pseudo Fv domains.

[00167] In some embodiments, the pro-drug constructs of the invention utilize a single TTA binding domain, such as generally depicted in Figure 3A, as pairs of sdABD-

TTAs, and Figure 4, as a "format 4" configuration. Figure 4 shows the use of a single anti-EGFR ABD, although other TTA binding domains can be used.

[00168] In some embodiments, particularly in the Format 1 and Format 2 constructs, the pro-drug constructs of the invention utilize two TTA ABDs, again preferably in the sdABD-TTA format. When dual targeting domains are used, they can bind to the same epitope of the same TTA. For example, as discussed herein, many of the constructs herein utilize two identical targeting domains. In some embodiments, two targeting domains can be used that bind to different epitopes of the same TTA, for example as shown in Figure 5, the two EGFR sdABDs bind to different epitopes on human EGFR. In some embodiments, the two targeting domains bind to different TTAs, see for example Figure 54.

[00169] Polypeptide constructs contemplated herein include at least one antigen binding domain, wherein the antigen binding domain binds to at least one target antigen. In some embodiments, the target antigen binding domains specifically bind to a cell surface molecule. In some embodiments, the target antigen binding domains specifically bind to a tumor antigen. In some embodiments, the target antigen binding domains specifically and independently bind to a tumor target antigen ("TTA") selected from at least one of EpCAM, EGFR, HER-2, HER-3, cMet, LyPD3, B7H3, CEA, and FOLR1.

[00170] Of particular use in the present invention are sdABDs to human EGFR as shown in Figure 5.

[00171] Additional embodiments of use in the invention are sdABDs to human FOLR1 as shown in Figure 5.

[00172] Further embodiments of use in the invention are sdABDs to human B7H3 as shown in Figure 5.

[00173] Additional embodiments of use in the invention are sdABDs to human EpCAM as shown in Figure 5.

[00174] In some embodiments, the protein prior to cleavage of the protease cleavage domain is less than about 100 kDa. In some embodiments, the protein after cleavage of the protease cleavage domain is about 25 to about 75 kDa. In some embodiments, the protein prior to protease cleavage has a size that is above the renal threshold for first-pass clearance.

In some embodiments, the protein prior to protease cleavage has an elimination half-time of at least about 50 hours. In some embodiments, the protein prior to protease cleavage has an elimination half-time of at least about 100 hours. In some embodiments, the protein has increased tissue penetration as compared to an IgG to the same target antigen. In some embodiments, the protein has increased tissue distribution as compared to an IgG to the same target antigen.

C. Half Life Extension Domains

[00175] The MCE proteins of the invention (again, also referred to herein as "COBRA™" proteins or constructs) optionally include half-life extension domains. Such domains are contemplated to include but are not limited to HSA binding domains, Fc domains, small molecules, and other half-life extension domains known in the art.

[00176] Human serum albumin (HSA) (molecular mass ~67 kDa) is the most abundant protein in plasma, present at about 50 mg/ml (600 uM), and has a half-life of around 20 days in humans. HSA serves to maintain plasma pH, contributes to colloidal blood pressure, functions as carrier of many metabolites and fatty acids, and serves as a major drug transport protein in plasma.

[00177] Noncovalent association with albumin extends the elimination half-time of short lived proteins. For example, a recombinant fusion of an albumin binding domain to a Fab fragment resulted in a reduced in vivo clearance of 25- and 58-fold and a half-life extension of 26- and 37-fold when administered intravenously to mice and rabbits respectively as compared to the administration of the Fab fragment alone. In another example, when insulin is acylated with fatty acids to promote association with albumin, a protracted effect was observed when injected subcutaneously in rabbits or pigs. Together, these studies demonstrate a linkage between albumin binding and prolonged action.

[00178] In one aspect, the antigen-binding proteins described herein comprise a half-life extension domain, for example a domain which specifically binds to HSA. In other embodiments, the HSA binding domain is a peptide. In further embodiments, the HSA binding domain is a small molecule. It is contemplated that the HSA binding domain of an antigen binding protein is fairly small and no more than 25 kD, no more than 20 kD, no

more than 15 kD, or no more than 10 kD in some embodiments. In certain instances, the HSA binding domain is 5 kD or less if it is a peptide or small molecule.

[00179] In many embodiments, the half-life extension domain is a single domain antigen binding domain from a single domain antibody that binds to HSA. This domain is generally referred to herein as "sdABD" to human HSA (sdABD-HSA), or alternatively "sdABD(½)", to distinguish these binding domains from the sdABDs to TTAs. A particularly useful sdABD(½) is shown in Figure 5.

[00180] The half-life extension domain of an antigen binding protein provides for altered pharmacodynamics and pharmacokinetics of the antigen binding protein itself. As above, the half-life extension domain extends the elimination half-time. The half-life extension domain also alters pharmacodynamic properties including alteration of tissue distribution, penetration, and diffusion of the antigen-binding protein. In some embodiments, the half-life extension domain provides for improved tissue (including tumor) targeting, tissue penetration, tissue distribution, diffusion within the tissue, and enhanced efficacy as compared with a protein without a half-life extension binding domain. In one embodiment, therapeutic methods effectively and efficiently utilize a reduced amount of the antigen-binding protein, resulting in reduced side effects, such as reduced non-tumor cell cytotoxicity.

[00181] Further, characteristics of the half-life extension domain, for example a HSA binding domain, include the binding affinity of the HSA binding domain for HSA. Affinity of said HSA binding domain can be selected so as to target a specific elimination half-time in a particular polypeptide construct. Thus, in some embodiments, the HSA binding domain has a high binding affinity. In other embodiments, the HSA binding domain has a medium binding affinity. In yet other embodiments, the HSA binding domain has a low or marginal binding affinity. Exemplary binding affinities include KD concentrations at 10 nM or less (high), between 10 nM and 100 nM (medium), and greater than 100 nM (low). As above, binding affinities to HSA are determined by known methods such as Surface Plasmon Resonance (SPR).

D. Protease cleavage sites

[00182] The protein compositions of the invention, and particularly the prodrug constructs, include one or more protease cleavage sites, generally resident in cleavable linkers, as outlined herein.

[00183] As described herein, the prodrug constructs of the invention include at least one protease cleavage site comprising an amino acid sequence that is cleaved by at least one protease. In some cases, the MCE proteins described herein comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more protease cleavage sites that are cleaved by at least one protease. As is more fully discussed herein, when more than one protease cleavage site is used in a prodrug construction, they can be the same (e.g. multiple sites that are cleaved by a single protease) or different (two or more cleavage sites are cleaved by at least two different proteases). As will be appreciated by those in the art, constructs containing three or more protease cleavage sites can utilize one, two, three, etc.; e.g. some constructs can utilize three sites for two different proteases, etc.

[00184] The amino acid sequence of the protease cleavage site will depend on the protease that is targeted. As is known in the art, there are a number of human proteases that are found in the body and can be associated with disease states.

[00185] Proteases are known to be secreted by some diseased cells and tissues, for example tumor or cancer cells, creating a microenvironment that is rich in proteases or a protease-rich microenvironment. In some cases, the blood of a subject is rich in proteases. In some cases, cells surrounding the tumor secrete proteases into the tumor microenvironment. Cells surrounding the tumor secreting proteases include but are not limited to the tumor stromal cells, myofibroblasts, blood cells, mast cells, B cells, NK cells, regulatory T cells, macrophages, cytotoxic T lymphocytes, dendritic cells, mesenchymal stem cells, polymorphonuclear cells, and other cells. In some cases, proteases are present in the blood of a subject, for example proteases that target amino acid sequences found in microbial peptides. This feature allows for targeted therapeutics such as antigen-binding proteins to have additional specificity because T cells will not be bound by the antigen binding protein except in the protease rich microenvironment of the targeted cells or tissue.

[00186] Proteases are proteins that cleave proteins, in some cases, in a sequence-specific manner. Proteases include but are not limited to serine proteases, cysteine

proteases, aspartate proteases, threonine proteases, glutamic acid proteases, metalloproteases, asparagine peptide lyases, serum proteases, Cathepsins (e.g. Cathepsin B, Cathepsin C, Cathepsin D, Cathepsin E, Cathepsin K, Cathepsin L, CathepsinS), kallikreins, hK1, hK10, hK15, KLK7, GranzymeB, plasmin, collagenase, Type IV collagenase, stromelysin, factor XA, chymotrypsin-like protease, trypsin-like protease, elastase-like protease, subtilisin-like protease, actinidain, bromelain, calpain, Caspases (e.g. Caspase-3), Mir1-CP, papain, HIV-1 protease, HSV protease, CMV protease, chymosin, renin, pepsin, matriptase, legumain, plasmepsin, nepenthesin, metalloexopeptidases, metalloendopeptidases, matrix metalloproteases (MMP), MMP1, MMP2, MMP3, MMP8, MMP9, MMP13, MMP11, MMP14, meprin, urokinase plasminogen activator (uPA), enterokinase, prostate-specific antigen (PSA, hK3), interleukin-1β converting enzyme, thrombin, FAP (FAP-α), dipeptidyl peptidase, and dipeptidyl peptidase IV (DPPIV/CD26).

[00187] Some suitable proteases and protease cleavage sequences are shown in Figure 5 and Figure 6.

E. Linkers

[00188] As is discussed herein, the different domains of the invention are generally linked together using amino acid linkers, which can confer functionality as well, including flexibility or inflexibility (e.g. steric constraint) as well as the ability to be cleaved using an *in situ* protease. These linkers can be classified in a number of ways.

[00189] The invention provides "domain linkers", which are used to join two or more domains (e.g. a VH and a VL, a target tumor antigen binding domain (TTABD, sometimes also referred to herein as "αTTA" (for "anti-TTA") to a VH or VL, a half life extension domain to another component, etc. Domain linkers can be non-cleavable (NCL), cleavable ("CL"), constrained and cleavable (CCL) and constrained and non-cleavable (CNCL), for example.

1. Non-cleavable linkers

[00190] In some embodiments, the domain linker is non-cleavable. Generally, these can be one of two types: non-cleavable and flexible, allowing for the components "upstream" and "downstream" of the linker in the constructs to intramolecularly self-assemble in certain ways; or non-cleavable and constrained, where the two components

separated by the linker are not able to intramolecularly self-assemble. It should be noted, however, that in the latter case, while the two component domains that are separated by the non-cleavable constrained linker do not intramolecularly self-assemble, other intramolecular components will self-assemble to form the pseudo Fv domains.

(i) Non-cleavable but Flexible Linkers

[00191] In this embodiment, the linker is used to join domains to preserve the functionality of the domains, generally through longer, flexible domains that are not cleaved by in situ proteases in a patient. Examples of internal, non-cleavable linkers suitable for linking the domains in the polypeptides of the invention include but are not limited to (GS)n, (GGS)n, (GGGS)n, (GGSG)n, (GGSGG)n, or (GGGGS)n, wherein n is 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10. In some embodiments the length of the linker can be about 15 amino acids.

(ii) Non-Cleavable and Constrained Linkers

[00192] In some cases, the linkers do not contain a cleavage site and are also too short to allow the protein domains separated by the linker to intramolecularly self-assemble, and are "constrained non-cleavable linkers" or "CNCLs". For example, in Pro186, an active VH and an active VL are separated by 8 amino acids (an "8mer") that does not allow the VH and VL to self-assemble into an active antigen binding domain. In some embodiments, the linker is still flexible; for example, (GGGS)n where n = 2. In other embodiments, although generally less preferred, more rigid linkers can be used, such as those that include proline or bulky amino acids.

2. Cleavable linkers

[00193] All of the prodrug constructs herein include at least one cleavable linker. Thus, in one embodiment, the domain linker is cleavable (CL), sometimes referred to herein as a "protease cleavage domain" ("PCD"). In this embodiment, the CL contains a protease cleavage site, as outlined herein and as depicted in Figure 5 and Figure 6. In some cases, the CL contains just the protease cleavage site. Optionally, depending on the length of the cleavage recognition site, there can be an extra few linking amino acids at either or both of the N- or C-terminal end of the CL; for example, there may be from 1, 2, 3, 4 or 5 amino acids on either or both of the N- and C-termini of the cleavage site. Thus, cleavable linkers can also be constrained (e.g. 8mers) or flexible.

[00194] Of particular interest in the present invention are MMP9 cleavable linkers and Meprin cleavable linkers, particularly MMP9 constrained cleavable linkers and Meprin constrained cleavable linkers.

VIII. Domains of the Invention

[00195] The present invention provides a number of different formats for the prodrug polypeptides of the invention. The present invention provides constrained Fv domains and constrained pseudo Fv domains. Additionally, the present invention provides multivalent conditionally effective ("MCE") proteins which contain two Fv domains but are non-isomerizing constructs. As outlined herein, these can be non-isomerizing cleavable formats or non-isomerizing non-cleavable formats, although every construct contains at least one protease cleavage domain.

[00196] Importantly, while both of these domains (Fv domains and pseudo Fv domains) are referred to herein as "constrained", meaning that as discussed above and shown in Figure 36, Figure 37 and Figure 38, only one of these needs to be constrained, although generally, when both linkers are constrained, the protein has better expression.

[00197] Those of skill in the art will appreciate that for Formats 1, 2 and 4, there are four possibilities for the N- to C-terminal order of the constrained and pseudo Fv domains of the invention (not showing the linkers): aVH-aVL and iVL-iVH, aVH-aVL and iVH-iVL, aVL-aVH and iVL-iVH, aVL-aVH and iVH-iVL. All four have been tested and all four have activity, although the first order, aVH-aVL and iVL-iVH, shows better expression than the other three. Thus while the description herein is generally shown in this aVH-aVL and iVL-iVH format, all disclosure herein includes the other orders for these domains as well.

[00198] Note that generally, the N to C-terminal order for the full length constructs of the invention is based on the aVH-aVL and iVL-iVH orientation.

[00199] Additionally, it is known in the art that there can be immunogenicity in humans originating from the C-terminal sequences of certain ABDs. Accordingly, in general, particularly when the C-terminus of the constructs terminates in an sdABD (for example, the sdABD-HSA domains of many of the constructs, a histidine tag (either His6 or His10) can be used. Many or most of the sequences herein were generated using His6 C-terminal tags for purification reasons, but these sequences can also be used to reduce

immunogenicity in humans, as is shown by Holland et al., DOI 10.1007/s10875-013-9915-0 and WO2013/024059.

A. Constrained Fv domains

[00200] The present invention provides constrained Fv domains, that comprise an active VH and an active VL domain that are covalently attached using a constrained linker (which, as outlined herein, can be cleavable (Formats 1 and 3) or non-cleavable (Formats 2 and 4)). The constrained linker prevents intramolecular association between the aVH and aVL in the absence of cleavage. Thus, a constrained Fv domain general comprises a set of six CDRs contained within variable domains, wherein the vhCDR1, vhCDR2 and vhCDR3 of the VH bind human CD-3 and the vlCDR1, vCDR2 and vlCDR3 of the VL bind human CD-3, but in the prodrug format (e.g. uncleaved), the VH and VL are unable to sterically associate to form an active binding domain, preferring instead to pair intramolecularly with the pseudo Fv.

[00201] The constrained Fv domains can comprise active VH and active VL (aVH and aVL) or inactive VH and VL (iVH and iVL, in which case it is a constrained pseudo Fv domain) or combinations thereof as described herein.

[00202] As will be appreciated by those in the art, the order of the VH and VL in a constrained Fv domain can be either (N- to C-terminal) VH-linker-VL or VL-linker-VH.

[00203] As outlined herein, for Format 1 constructs, the constrained Fv domains can comprise a VH and a VL linked using a cleavable linker, in cases such as those shown in Figure 5 and Figure 6. In this embodiment, the constrained Fv domain has the structure (N- to C-terminus) vhFR1-vhCDR1-vhFR2-vhCDR2-vhFR3-vhCDR3-vhFR4-CCL-vlFR1-vlCDR1-vlFR2-vlCDR2-vlFR3-vlCDR3-vlFR4. In general, the constrained Fv domain contains active VH and VL domains (e.g. able to bind CD3 when associated) and thus has the structure (N- to C-terminus) vhFR1-avhCDR1-vhFR2-avhCDR2-vhFR3-avhCDR3-vhFR4-CCL-vlFR1-avlCDR1-vlFR2-avlCDR2-vlFR3-avlCDR3-vlFR4.

[00204] As outlined herein, for Format 2 constructs, the constrained Fv domains can comprise a VH and a VL linked using a non-cleavable linker. In this embodiment, the constrained Fv domain has the structure (N- to C-terminus) vhFR1-vhCDR1-vhFR2-vhCDR2-vhFR3-vhCDR3-vhFR4-CNCL-vlFR1-vlCDR1-vlFR2-vlCDR2-vlFR3-vlCDR3-vlFR4.

In general, the constrained Fv domain contains active VH and VL domains (e.g. able to bind CD3 when associated) and thus has the structure (N- to C-terminus) vhFR1-avhCDR1-vhFR2-avhCDR2-vhFR3-avhCDR3-vhFR4-CNCL-vlFR1-avlCDR1-vlFR2-avlCDR2-vlFR3-avlCDR3-vlFR4.

[00205] Of particular use in the present invention are constrained non-cleavable Fv domains having an aVH having SEQ ID NO:61, an aVL having SEQ ID NO:49, and a domain linker having SEQ ID NO:74.

B. Constrained pseudo Fv domains

[00206] The present invention provides constrained pseudo Fv domains, comprising inactive or pseudo iVH and iVL domains that are covalently attached using a constrained linker (which, as outlined herein, can be cleavable or non-cleavable). The constrained linker prevents intramolecular association between the iVH and iVL in the absence of cleavage. Thus, a constrained pseudo Fv domain general comprises an iVH and an iVL with framework regions that allow association (when in a non-constrained format) of the iVH and iVL, although the resulting pseudo Fv domain does not bind to a human protein. iVH domains can assemble with aVL domains, and iVL domains can assemble with aVH domains, although the resulting structures do not bind to CD3.

[00207] The constrained pseudo Fv domains comprise inactive VH and VL (iVH and iVL).

[00208] As will be appreciated by those in the art, the order of the VH and VL in a constrained pseudo Fv domain can be either (N- to C-terminal) VH-linker-VL or VL-linker-VH.

[00209] As outlined herein, the constrained pseudo Fv domains can comprise a iVH and an iVL linked using a non-cleavable linker, as shown in Formats 1, 2 and 4, or with cleavable linkers, as shown in Format 3.

[00210] In general, the constrained Fv domain contains inert VH and VL domains (e.g. able to bind CD3 when associated) and thus has the structure (N- to C-terminus) vhFR1-ivlCDR1-vhFR2-ivlCDR2-vhFR3-ivlCDR3-vhFR4-CNCL-vlFR1-ivhCDR1-vlFR2-ivhCDR2-vlFR3-ivhCDR3-vlFR4.

[00211] Of particular use in the present invention are constrained non-cleavable pseudo Fv domains having an iVH having SEQ ID NO:65 or SEQ ID NO:69, an iVL having SEQ ID NO:53 or SEQ ID NO:57, and a domain linker having SEQ ID NO:74.

IX. Formats of the Invention

As discussed herein, the pro-drug constructs of the invention can take on a number of different formats, including cleavable formats with dual TTA binding domains, non-cleavable formats with dual TTA binding domains (either of which can have the same TTA binding domains or different binding domains), and non-cleavable formats with a single targeting domain.

A. Cleavable formats with dual targeting

[00212] The invention provides non-isomerizing cleavable formats of the "format 1" type in Figure 1. In this embodiment, the constrained Fv domain comprise VH and VL domains that are linked using constrained cleavable linkers and the constrained pseudo Fv domain uses constrained non-cleavable linkers. For ease of discussion, both of these are referred to herein as "constrained", but as discussed above and shown in Figure 36, Figure 37 and Figure 38, only one of these needs to be constrained, although generally, when both linkers are constrained, the protein has better expression.

[00213] All constructs in Format 1 (as well as the other formats) also have a cleavable linker (CL) that is cleaved by a human tumor protease.

[00214] The invention provides prodrug proteins, comprising, from N- to C-terminal, (sdABD-TTA1)-domain linker-constrained Fv domain-domain linker-(sdABD-TTA2)-CL-constrained pseudo Fv domain-domain linker-sdABD-HSA.

[00215] As will be appreciated by those in the art, the order of the VH and VL in either a constrained Fv domain or a constrained pseudo Fv domain can be either (N- to C-terminal) VH-linker-VL or VL-linker-VH.

[00216] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA.

[00217] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CCL-aVL-domain linker-(sdABD-TTA2)-CL-iVH-CCL-iVL-domain linker-sdABD-HSA.

[00218] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVL-CCL-aVH-domain linker-(sdABD-TTA2)-CL-iVL-CCL-iVH-domain linker-sdABD-HSA.

[00219] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVL-CCL-aVH-domain linker-(sdABD-TTA2)-CL-iVH-CCL-iVL-domain linker-sdABD-HSA.

[00220] In some embodiments, the prodrug construct comprises sdABD(TTA1)-domain linker-aVH-CCL-aVL-domain linker-sdABD(TTA2)-CL-iVL-CNCL-iVH-NCL-sdABD(½). In this embodiment, the aVH, aVL, iVH and iVL have the sequences shown in Figure 5.

[00221] In some embodiments, the prodrug construct comprises sdABD(TTA1)-domain linker-aVH-CCL-aVL-domain linker-sdABD(TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD(½). In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to the same TTA, which can be EGFR, EpCAM, FOLR1 or B7H3, the sequences for which are depicted in Figure 5.

[00222] In some embodiments, the prodrug construct comprises sdABD(TTA1)-domain linker-aVH-CCL-aVL-domain linker-sdABD(TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD(½). In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to different TTAs.

[00223] In some embodiments, the prodrug construct comprises sdABD(TTA1)-domain linker-aVH-CCL-aVL-domain linker-sdABD(TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD(½). In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to EGFR and EpCAM, and the sdABD-TTAs have the sequences in Figure 5.

[00224] In some embodiments, the prodrug construct comprises sdABD(TTA1)-domain linker-aVH-CCL-aVL-domain linker-sdABD(TTA2)-CL-iVL-CNCL-iVH-domain

linker-sdABD(½). In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to EGFR and FOLR1, and the sdABD-TTAs have the sequences in Figure 5.

[00225] In some embodiments, the prodrug construct comprises sdABD(TTA1)-domain linker-aVH-CCL-aVL-domain linker-sdABD(TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD(½). In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to EGFR and B7H3, and the sdABD-TTAs have the sequences in Figure 5.

[00226] In some embodiments, the prodrug construct comprises sdABD(TTA1)-domain linker-aVH-CCL-aVL-domain linker-sdABD(TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD(½). In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to EpCAM and FOLR1, and the sdABD-TTAs have the sequences in Figure 5.

[00227] In some embodiments, the prodrug construct comprises sdABD(TTA1)-domain linker-aVH-CCL-aVL-domain linker-sdABD(TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD(½). In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to EpCAM and B7H3, and the sdABD-TTAs have the sequences in Figure 5.

[00228] In some embodiments, the prodrug construct comprises sdABD(TTA1)-domain linker-aVH-CCL-aVL-domain linker-sdABD(TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD(½). In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to B7H3 and FOLR1, and the sdABD-TTAs have the sequences in Figure 5.

[00229] In some embodiments, the prodrug construct comprises sdABD(TTA1)-domain linker-aVH-CCL-aVL-domain linker-sdABD(TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD(½). In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to the same TTA, which can be EGFR, FOLR1, B7H3 or EpCAM, the sequences for which are depicted in Figure 5, and the CCL and CL is selected from a linker that is cleaved by MMP9 or meprin, and the sdABD(½) has SEQ ID NO:45.

[00230] In Format 1, a preferred domain linker is SEQ ID NO:74 (which also serves as a preferred constrained non cleavable linker).

[00231] In Format 1, preferred constructs are Pro140 and Pro140b.

B. Non-cleavable formats

[00232] As shown in Figure 2, the invention provides non-isomerizing non-cleavable formats. In this embodiment, it is understood that the "non-cleavable" applies only to the linkage of the constrained Fv domain, as there is the activating cleavage site in the prodrug construct. In this embodiment, the constrained Fv domain comprise VH and VL domains that are linked using constrained non-cleavable linkers and the constrained pseudo Fv domain uses constrained non-cleavable linkers.

[00233] As will be appreciated by those in the art, the order of the VH and VL in either a constrained Fv domain or a constrained pseudo Fv domain can be either (N- to C-terminal) VH-linker-VL or VL-linker-VH.

[00234] The invention provides prodrug proteins, comprising, from N- to C-terminal, sdABD(TTA1)-domain linker-constrained Fv domain-domain linker-sdABD(TTA2)-cleavable linker-constrained pseudo Fv domain-domain linker-sdABD-HSA.

[00235] As will be appreciated by those in the art, the order of the VH and VL in either a constrained Fv domain or a constrained pseudo Fv domain can be either (N- to C-terminal) VH-linker-VL or VL-linker-VH.

[00236] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA.

[00237] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVH-CNCL-iVL-domain linker-sdABD-HSA.

[00238] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVL-CNCL-aVH-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA.

[00239] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVL-CNCL-aVH-domain linker-(sdABD-TTA2)-CL-iVH-CNCL-iVL-domain linker-sdABD-HSA.

[00240] In some embodiments, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA. In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to the same TTA, which can be EGFR, EpCAM, FOLR1 or B7H3, the sequences for which are depicted in Figure 5.

[00241] In some embodiments, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA. In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to different TTAs.

[00242] In some embodiments, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA. In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to EGFR and EpCAM, and the sdABD-TTAs have the sequences in Figure 5.

[00243] In some embodiments, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA. In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to EGFR and FOLR1, and the sdABD-TTAs have the sequences in Figure 5.

[00244] In some embodiments, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA. In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to EGFR and B7H3, and the sdABD-TTAs have the sequences in Figure 5.

[00245] In some embodiments, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA. In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to EpCAM and FOLR1, and the sdABD-TTAs have the sequences in Figure 5.

[00246] In some embodiments, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA. In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to EpCAM and B7H3, and the sdABD-TTAs have the sequences in Figure 5.

[00247] In some embodiments, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA. In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to FOLR1 and B7H3, and the sdABD-TTAs have the sequences in Figure 5.

[00248] In some embodiments, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA1)-domain linker-aVH-CNCL-aVL-domain linker-(sdABD-TTA2)-CL-iVL-CNCL-iVH-domain linker-sdABD-HSA. In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the two targeting domains bind to the same TTA, which can be EGFR, FOLR1, B7H3 or EpCAM, the sequences for which are depicted in Figure 5, and the CCL and CL is selected from a linker that is cleaved by MMP9 or meprin, and the sdABD(½) has SEQ ID NO:45.

[00249] In Format 2, a preferred domain linker is SEQ ID NO:74 (which also serves as a preferred constrained non cleavable linker).

[00250] In Format 2, embodiments of particular use include, but are not limited to, Pro186, Pro225, Pro226, Pro233, Pro311, Pro312, Pro313, Pro495, Pro246, Pro254, Pro255, Pro256, Pro420, Pro421, Pro432, Pro479, Pro480, Pro187, Pro221, Pro222, Pro223, Pro224, Pro393, Pro394, Pro395, Pro396, Pro429, Pro430 and Pro431.

C. Single TTA constructs

[00251] As is shown in Figure 4, "format 4" constructs are also included in the compositions of the invention, that are similar to Format 2 constructs but without a second TTA ABD. In this embodiment, it is understood that the "non-cleavable" applies only to the linkage of the constrained Fv domain, as there is the activating cleavage site in the prodrug construct. In this embodiment, the constrained Fv domain comprise VH and VL domains that are linked using constrained non-cleavable linkers and the constrained pseudo Fv domain uses constrained non-cleavable linkers.

[00252] As will be appreciated by those in the art, the order of the VH and VL in either a constrained Fv domain or a constrained pseudo Fv domain can be either (N- to C-terminal) VH-linker-VL or VL-linker-VH.

[00253] The invention provides prodrug proteins, comprising, from N- to C-terminal, sdABD(TTA)-domain linker-constrained Fv domain-cleavable linker- sdABD-HSA-constrained pseudo Fv domain. (Note that for all constructs for this format, the sdABD-HSA does not generally have a His6 tag, although it can be included).

[00254] As will be appreciated by those in the art, the order of the VH and VL in either a constrained Fv domain or a constrained pseudo Fv domain can be either (N- to C-terminal) VH-linker-VL or VL-linker-VH.

[00255] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA)-domain linker-aVH-CNCL-aVL-CL-(sdABD-HSA)-domain linker-iVL-CNCL-iVH.

[00256] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA)-domain linker-aVH-CNCL-aVL-CL-(sdABD-HSA)-domain linker-iVH-CNCL-iVL.

[00257] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA)-domain linker-aVL-CNCL-aVH-CL-(sdABD-HSA)-domain linker-iVH-CNCL-iVL.

[00258] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA)-domain linker-aVL-CNCL-aVH-CL-(sdABD-HSA)-domain linker-iVL-CNCL-iVH.

[00259] Thus, in one embodiment, the prodrug protein comprises, from N- to C-terminal: (sdABD-TTA)-domain linker-aVH-CNCL-aVL-CL-(sdABD-HSA)-domain linker-iVL-CNCL-iVH. In this embodiment, the aVH, aVL, iVH, iVL have the sequences shown in Figure 5. In this embodiment, the targeting domain binds to a TTA which can be EGFR, EpCAM, FOLR1 or B7H3, the sequences for which are depicted in Figure 5.

[00260] In Format 4, a preferred domain linker is SEQ ID NO:74 (which also serves as a preferred constrained non cleavable linker).

[00261] In Format 4, a preferred sdABD-HSA is that of SEQ ID NO:45.

D. Two Protein Compositions

[00262] In some embodiments, the compositions of the invention comprise two different molecules, sometimes referred to as "hemi-COBRAs™", or "hemi-constructs", that in the absence of cleavage, intramolecularly associate to form pseudo-Fvs. In the presence of the protease, the cleavage sites are cleaved, releasing the inert variable domains, and the protein pair then forms an active antigen binding domain to CD3, as generally depicted in Figure 3.

[00263] What is important in the design of the hemi-constructs is that the active variable domain and the sdABD-TTA remain together after cleavage, such that the two cleaved portions are held together by the tumor antigen receptor on the tumor surface and then can form an active anti-CD3 binding domain.

[00264] There are two different general Format 3 constructs, those wherein each member of the pair has a single sdABD-TTA (Figure 3A) and those with two different sdABD-TTAs, each to a different TTA (Figure 3B).

1. Hemi-COBRA™ Constructs with single TTA binding domains (Format 3A)

[00265] In some embodiments, the first hemi-COBRA™ has, from N- to C-terminal, sdABD(TTA1)-domain linker-aVH-CL-iVL-domain linker- sdABD(½) and the second has sdABD(½)-domain linker-iVH-CL-aVL-domain linker-sdABD(TTA2). In this embodiment, the aVH, aVL, iVH, iVL and sdABD(½) have the sequences shown in Figure 5, and the

sdABD-TTAa bind to human EGFR, EpCAM, FOLR1 and/or B7H3, and has a sequence depicted in Figure 5.

2. Hemi-COBRA™ Constructs with Dual TTA ABDs

[00266] In some embodiments, the paired pro-drug constructs can have two sdABD-TTA binding domains per construct, as is shown in Figure 3B. In this embodiments, the first member of the pair comprises, from N- to C-terminal, sdABD-TTA1-domain linker-sdABD-TTA2-domain linker-aVH-CL-iVL-domain linker-sdABD(HAS), and the second member comprises, from N- to C-terminal, sdABD-TTA1-domain linker-sdABD-TTA2-aVL-CL-iVH-domain linker-sdABD-HSA.

[00267] The two sdABD-TTAs on each member of the pair are different, but generally both members (hemi-COBRAs™) have the same two sdABD-TTAs, e.g. both have EGFR and FOLR1 or EGFR and B7H3, etc.

[00268] The two sdABD-TTAs are in some embodiments selected from the ones shown in Figure 5.

X. Methods of Making the Compositions of the Invention

[00269] The pro-drug compositions of the invention are made as will generally be appreciated by those in the art and outlined below.

[00270] The invention provides nucleic acid compositions that encode the pro-drug compositions of the invention. As will be appreciated by those in the art, the nucleic acid compositions will depend on the format of the pro-drug polypeptide(s). Thus, for example, when the format requires two amino acid sequences, such as the "format 3" constructs, two nucleic acid sequences can be incorporated into one or more expression vectors for expression. Similarly, prodrug constructs that are a single polypeptide (formats 1, 2 and 4), need a single nucleic acid in a single expression vector for production.

[00271] As is known in the art, the nucleic acids encoding the components of the invention can be incorporated into expression vectors as is known in the art, and depending on the host cells used to produce the prodrug compositions of the invention. Generally ,the nucleic acids are operably linked to any number of regulatory elements (promoters, origin of

replication, selectable markers, ribosomal binding sites, inducers, etc.). The expression vectors can be extra-chromosomal or integrating vectors.

[00272] The nucleic acids and/or expression vectors of the invention are then transformed into any number of different types of host cells as is well known in the art, including mammalian, bacterial, yeast, insect and/or fungal cells, with mammalian cells (e.g. CHO cells, 293 cells), finding use in many embodiments.

[00273] The prodrug compositions of the invention are made by culturing host cells comprising the expression vector(s) as is well known in the art. Once produced, traditional antibody purification steps are done, including an Protein A affinity chromatography step and/or an ion exchange chromatography step.

XI. Formulation and Administration of the Pro-drug compositions of the invention

[00274] Formulations of the pro-drug compositions used in accordance with the present invention are prepared for storage by mixing the pro-drugs (single proteins in the case of formats 1, 2 and 4 and two proteins in the case of format 3) having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (as generally outlined in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. [1980]), in the form of lyophilized formulations or aqueous solutions.

[00275] The pro-drug compositions of the invention are administered to a subject, in accord with known methods, such as intravenous administration as a bolus or by continuous infusion over a period of time.

[00276] The pro-drug compositions of the invention are useful in the treatment of cancer.

XII. Examples

A. Example 1: Pro Construct Construction and purification

[00277] Transfections

[00278] Each protein (e.g. single proteins for Formats 1, 2 and 4) or pairs of constructs (Format 3) were expressed from a separate expression vector (pcdna3.4 derivative). Equal amounts of plasmid DNA that encoded the pair of hemi-cobra or single chain constructs were mixed and transfected to Expi293 cells following the manufacture's transfection

protocol. Conditioned media was harvested 5 days post transfection by centrifugation (6000rpm x 25') and filtration (0.2uM filter). Protein expression was confirmed by SDS-PAGE. Constructs were purified and the final buffer composition was: 25 mM Citrate, 75 mM Arginine, 75 mM NaCl, 4% Sucrose, pH 7. The final preparations were stored at -80°C.

[00279] Activation of MMP9

[00280] Recombinant human (rh) MMP9 was activated according to the following protocol. Recombinant human MMP-9 (R&D # 911-MP-010) is at 0.44 mg/ml (4.7 uM). p-aminophenylmercuric acetate (APMA) (Sigma) is prepared at the stock concentration of 100 mM in DMSO. Assay buffer is 50 mM Tris pH 7.5, 10 mM CaCl2, 150 mM NaCl, 0.05% Brij-35.

[00281] - Dilute rhMMP9 with assay buffer to ~100 ug/ml (25 ul hMMP9 + 75 uL assay buffer)

[00282] - Add p-aminophenylmercuric acetate (APMA) from 100 mM stock in DMSO to a final concentration of 1 mM (1 uL to 100 uL)

[00283] - Incubate at 37'C for 24 hrs

[00284] - Dilute MMP9 to 10 ng/ul (add 900 ul of assay buffer to 100 ul of activated solution)

[00285] The concentration of the activated rhMMP9 is ~ 100 nM.

[00286] Cleavage of Constructs for TDCC Assays

[00287] To cleave the constructs, 100 ul of the protein sample at 1 mg/ml concentration (10.5 uM) in the formulation buffer (25 mM Citric acid, 75 mM L-arginine, 75 mM NaCl, 4% sucrose) was supplied with $CaCl_2$ up to 10 mM. Activated rhMMP9 was added to the concentration 20-35 nM. The sample was incubated at room temperature overnight (16-20 hrs). The completeness of cleavage was verified using SDS PAGE (10-20% TG, TG running buffer, 200v, 1hr). Samples were typically 98% cleaved.

B. Example 2: T cell Dependent Cellular Cytotoxicity (TDCC) assays

[00288] Firefly Luciferase transduced HT-29 cells were grown to approximately 80% confluency and detached with Versene (0.48 mM EDTA in PBS – Ca - Mg). Cells were centrifuged and resuspended in TDCC media (5% Heat Inactivated FBS in RPMI 1640 with HEPES, GlutaMax, Sodium Pyruvate, Non-essential amino acids, and β-mercaptoethanol). Purified human Pan-T cells were thawed, centrifuged and resuspended in TDCC media.

[00289] A coculture of HT-29_Luc cells and T cells was added to 384-well cell culture plates. Serially diluted COBRAs were then added to the coculture and incubated at 37◎C for 48 hours. Finally, an equal volume of SteadyGlo luciferase assay reagent was added to the plates and incubated for 20 minutes. The plates were read on the Perkin Elmer Envision with an exposure time of 0.1s/well. Total luminescence was recorded and data were analyzed on GraphPad Prism 7.

C. Example 3: General Protocol Design of the *In Vivo* Adoptive T Cell Transfer Efficacy Model

[00290] These protocols were used in many of the experiments of the figures. Tumor cells were implanted subcutaneous (SC) in the right flank of NSG (NOD.Cg-Prkdcscid Il2rgtm1Wjl/SzJ) mice (*The Jackson Laboratory*, Cat. No. 005557) and allowed to grow until an established tumor with a mean volume of around 200 mm^3 was reached. In parallel human T cells were cultured in T cell media (X-VIVO 15 [*Lonza,* Cat.No. 04-418Q], 5% Human Serum, 1% Penicillin/Streptomycin, 0.01mM 2-Mercaptoethanol) in a G-Rex100M gas permeable flask (*Wilson Wolf* Cat. No. 81100S) with MACSiBeads from the T Cell Activation/Expansion Kit (*Miltenyi* Cat. No. 130-091-441) for around 10 days and supplemented with recombinant human IL-2 protein. Tumor growth in mice and human T cell activation/expansion were coordinated so that on Day 0 of the study mice were randomized into groups (N=6) based on tumor size; each were then injected intravenous (IV) with $2.5x10^6$ cultured human T cells and administered the first dose of the COBRA or control molecules. Mice were dosed every 3 days for 7 doses (Days 0, 3, 6, 9, 12, 15 and 18) and then followed for an additional 2-3 weeks until tumors reached >2000mm^3 in volume or the study was terminated. Tumor volumes were measured every 3 days.

D. Example 4: *In Vivo* Activity with EGFR/MMP9 Hemi-COBRA Pair Pro77 and Pro53.

[00291] 5 x 10^6 LoVo cells or 5 x 10^6 HT29 cells were implanted subcutaneous in the right flank of NSG (NOD.Cg-Prkdcscid Il2rgtm1Wjl/SzJ) mice (*The Jackson Laboratory*, Cat. No. 005557) and allowed to grow until tumors were established. In parallel human T cells were cultured in T cell media (X-VIVO 15 [*Lonza,* Cat.No. 04-418Q], 5% Human Serum, 1% Penicillin/Streptomycin, 0.01mM 2-Mercaptoethanol) in a G-Rex100M gas permeable flask (*Wilson Wolf* Cat. No. 81100S) with MACSiBeads from the T Cell Activation/Expansion Kit (*Miltenyi* Cat. No. 130-091-441) for 10 days and supplemented with recombinant human IL-2 protein. Tumor growth in mice and human T cell activation/expansion were coordinated so that on Day 0 of the study mice were randomized into groups (N=6) based on tumor size; each were then injected intravenous (IV) with 2.5x10^6 cultured human T cells and administered the first dose of the COBRA or control molecules. Mice were dosed every 3 days for 7 doses (Days 0, 3, 6, 9, 12, 15 and 18) and then followed until tumors reach >2000mm^3 in volume or the study was terminated. Groups received 0.2 mg/kg (mpk) of the anti-EGFR x CD3 positive control Pro51 bispecific antibody (bsAb), 0.5 mpk of the negative control anti-hen egg lysozyme (HEL) x CD3 bsAb Pro98, 0.5 mpk each of the MMP9 cleavable linker containing anti-EGFR hemi-COBRA pair Pro77 and Pro53, or 0.5 mpk each of the non-cleavable(NCL) linker containing anti-EGFR hemi-COBRA pair Pro74 and Pro72. Tumor volumes were measured every 3 days.

E. Example 5: *In Vivo* Activity with EGFR/MMP9 COBRA Pro140.

[00292] 5 x 10^6 LoVo cells or 5 x 10^6 HT29 cells were implanted subcutaneous in the right flank of NSG (NOD.Cg-Prkdcscid Il2rgtm1Wjl/SzJ) mice (*The Jackson Laboratory*, Cat. No. 005557) and allowed to grow until tumors were established. In parallel human T cells are cultured in T cell media (X-VIVO 15 [*Lonza,* Cat.No. 04-418Q], 5% Human Serum, 1% Penicillin/Streptomycin, 0.01mM 2-Mercaptoethanol) in a G-Rex100M gas permeable flask (*Wilson Wolf* Cat. No. 81100S) with MACSiBeads from the T Cell Activation/Expansion Kit (*Miltenyi* Cat. No. 130-091-441) for 10 days and supplemented with recombinant human IL-2 protein. Tumor growth in mice and human T cell activation/expansion were coordinated so that on Day 0 of the study mice were randomized into groups (N=6) based on tumor size; each were then injected intravenous (IV) with 2.5x10^6 cultured human T cells and administered the first dose of the COBRA or control molecules. Mice were dosed every 3 days for 7 doses (Days 0, 3, 6, 9, 12, 15 and 18) and then followed until tumors reach

>2000mm^3 in volume or the study was terminated. Groups received 0.2 mpk of the anti-EGFR x CD3 positive control Pro51 bispecific antibody (bsAb), 0.5 mpk of the negative control anti-hen egg lysozyme (HEL) x CD3 bsAb Pro98, or 0.5 mpk of the MMP9 cleavable linker containing anti-EGFR COBRA Pro140. Tumor volumes were measured every 3 days.

F. Example 6: *In Vivo* Activity with EGFR/MMP9 COBRA Pro186.

[00293] 5 x 10^6 HT29 cells were implanted subcutaneous in the right flank of NSG (NOD.Cg-Prkdcscid Il2rgtm1Wjl/SzJ) mice (*The Jackson Laboratory*, Cat. No. 005557) and allowed to grow until tumors were established. In parallel human T cells are cultured in T cell media (X-VIVO 15 [*Lonza,* Cat.No. 04-418Q], 5% Human Serum, 1% Penicillin/Streptomycin, 0.01mM 2-Mercaptoethanol) in a G-Rex100M gas permeable flask (*Wilson Wolf* Cat. No. 81100S) with MACSiBeads from the T Cell Activation/Expansion Kit (*Miltenyi* Cat. No. 130-091-441) for 10 days and supplemented with recombinant human IL-2 protein. Tumor growth in mice and human T cell activation/expansion were coordinated so that on Day 0 of the study mice were randomized into groups (N=6) based on tumor size; each were then injected intravenous (IV) with 2.5x10^6 cultured human T cells and administered the first dose of the COBRA or control molecules. Mice were dosed every 3 days for 7 doses (Days 0, 3, 6, 9, 12, 15 and 18) and then followed until tumors reach >2000mm^3 in volume or the study was terminated. Groups received 0.1 mg/kg (mpk) of the anti-EGFR x CD3 positive control Pro51 bispecific antibody (bsAb), 0.3 mpk of the of the non-cleavable (NCL) control linker containing anti-EGFR COBRA Pro214, 0.1 or 0.3 mpk of the MMP9 cleavable linker containing anti-EGFR COBRA Pro140, or 0.1 or 0.3 mpk of the MMP9 cleavable linker containing anti-EGFR COBRA Pro186. Tumor volumes were measured every 3 days.

G. Example: Successful Humanization of anti-EGFR Sequences

[00294] The results are shown below.

Molecule	KD (M)	Kon (1/Ms)	Kdis(1/s)
Pro22 (parental EGFR)	2.58E-09M/2.6 nM	2.05E+05	5.27E-04

Pro90 (hEGFR1)	2.00E-09M/2.0 nM	2.21E+05	4.40E-04
Pro48 (EGFR2)	2.89E-09M/2.9 nM	6.09E+05	1.76E-03
Pro137 (hEGFR2)	4.36E-09M/4.4. nM	5.85E+05	2.55E-03
Pro51 (hEGFR2)	3.27E-09M/3.2 nM	6.45E+05	2.11E-03
Pro201 (hEGFR2 with 2 binding sites)	2.25E-12M/2.3 pM	1.55E+06	3.48E-06

[00295] These results show both that the humanization of the EGFR binding domains was successful, and that there is strong avidity to the target EGFR when two binding sites are on the molecule.

[00296] Example: Successful Humanization of EpCAM sdABDs

[00297] The results are shown below.

Clone	Human binding affinity (nM)	Cyno binding affinity (nM)	Cyno/Human cross reactivity
VIB-13	2.3	11.6	5
hVIB-13	2.8	12.7	4.5
VIB-23	4.2	46.7	11.1
hVIB-23	4.1	58.8	12.6

[00298] These results show both that the humanization of the EpCAM binding domains was successful.

XIII. CLAIMS

1. A protein comprising, from N- to C-terminal:

a) a first single domain antigen binding domain (sdABD) that binds to a human tumor target antigen (TTA) (sdABD-TTA);

b) a first domain linker;

c) a constrained Fv domain comprising:

i) a first variable heavy domain comprising a vhCDR1, vhCDR2 and vhCDR3;

ii) a constrained non-cleavable linker (CNCL); and

iii) a first variable light domain comprising vlCDR1, vlCDR2 and vlCDR3;

d) a second domain linker;

e) a second sdABD-TTA;

f) a cleavable linker (CL);

g) a constrained pseudo Fv domain comprising:

i) a first pseudo light variable domain;

ii) a non-cleavable linker (NCL); and

iii) a first pseudo heavy variable domain;

h) a third domain linker; and

i) a third sdABD that binds to human serum albumin;

wherein said first variable heavy domain and said first variable light domain are capable of binding human CD3 but said constrained Fv domain does not bind CD3; wherein said first variable heavy domain and said first pseudo variable light domain intramolecularly associate to form an inactive Fv; and wherein said first variable light domain and said first pseudo variable heavy domain intramolecularly associate to form an inactive Fv.

2. A protein comprising, from N- to C-terminal:

a) a first sdABD-TTA;

b) a first domain linker;

c) a constrained Fv domain comprising:

i) a first variable heavy domain comprising a vhCDR1, vhCDR2 and vhCDR3;

ii) a constrained cleavable linker (CCL); and

iii) a first variable light domain comprising vlCDR1, vlCDR2 and vlCDR3;

d) a second domain linker;

e) a second sdABD-TTA;

f) a cleavable linker (CL);

g) a constrained pseudo Fv domain comprising:

i) a first pseudo heavy variable domain;

ii) a non-cleavable linker (NCL); and

iii) a first pseudo light variable domain;

h) a third domain linker; and

i) a third sdABD that binds to human serum albumin;

wherein said first variable heavy domain and said first variable light domain are capable of binding human CD3 but said constrained Fv domain does not bind CD3; wherein said first variable heavy domain and said first pseudo variable light domain intramolecularly associate to form an inactive Fv; and wherein said first variable light domain and said first pseudo variable heavy domain intramolecularly associate to form an inactive Fv.

3. A protein according to any of claims 1 to 2 wherein said first variable heavy domain is N-terminal to said first variable light domain and said pseudo light variable domain is N-terminal to said pseudo variable heavy domain.

4. A protein according to any of claims 1 to 2 wherein said first variable heavy domain is N-terminal to said first variable light domain and said pseudo variable heavy domain is N-terminal to said pseudo variable light domain.

5. A protein according to any of claims 1 to 2 wherein said first variable light domain is N-terminal to said first variable heavy domain and said pseudo light variable domain is N-terminal to said pseudo variable heavy domain.

6. A protein according to any of claims 1 to 2 wherein said first variable light domain is N-terminal to said first variable heavy domain and said pseudo variable heavy domain is N-terminal to said pseudo variable light domain.

7. A protein according to any of claims 1-6 wherein said first and second TTA is the same.

8. A protein according to any of claims 1-6 wherein said first and second TTA are different.

9. A protein according to any of claims 1-8 wherein said first and second TTA are selected from EGFR, EpCAM, FOLR1 and B7H3.

10. A protein according to any of claims 1-9 wherein said first and second sdABD-TTAs are selected from the group consisting of SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID

NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29; SEQ ID NO:33; SEQ ID NO:37 and SEQ ID NO:41.

11. A protein according to claim 1 to 10 wherein said half-life extension domain has SEQ ID NO:45.

12. A protein according to claim 1 to 11 wherein said cleavable linker is cleaved by a human protease selected from the group consisting of MMP2, MMP9, Meprin A, Meprin B, Cathepsin S, Cathepsin K, Cathespin L, GranzymeB, uPA, Kallekriein7, matriptase and thrombin.

13. A protein according to claim 1 comprising a protein selected from the group consisting of Pro186, Pro225, Pro226, Pro233, Pro311, Pro312, Pro313, Pro495, Pro246, Pro254, Pro255, Pro256, Pro420, Pro421, Pro432, Pro479, Pro480, Pro187, Pro221, Pro222, Pro223, Pro224, Pro393, Pro394, Pro395, Pro396, Pro429, Pro430 and Pro431.

14. A nucleic acid encoding a protein according to any of claims 1 to 13.

15. An expression vector comprising the nucleic acid of claim 14.

16. A host cell comprising the expression vector of claim 15.

17. A method of making a protein comprising culturing the host cell of claim 16 under conditions wherein said protein is expressed and recovering said protein.

18. A method of treating cancer comprising administering the protein of any of claims 1 to 13 to a patient.

19. A composition comprising:

a) a first protein comprising, from N- to C-terminal:

i) a first sdABD-TTA;

ii) a first domain linker;

iii) a pseudo Fv domain comprising, from N- to C-terminal:

1) a variable heavy chain comprising a vhCDR1, vhCDR2 and vhCDR3;

2) a cleavable linker; and

3) a first pseudo variable light domain comprising iVLCDR1, iVLCDR2 and iVLCDR3;

iv) a second domain linker;

v) a first sdABD that binds to human serum albumin;

a) a second protein comprising, from N- to C-terminal:

i) a third sdABD that binds to a human tumor target antigen;

ii) a third domain linker;

iii) a pseudo Fv domain comprising, from N- to C-terminal:

1) a variable light chain comprising a VLCDR1, VLCDR2 and VLCDR3;

2) a cleavable linker; and

3) a first pseudo variable heavy domain comprising iVHCDR1, iVHCDR2 and iVHCDR3;

iv) a fourth domain linker;

v) a fourth sdABD that binds to human serum albumin;

wherein

said first variable heavy domain and said first variable light domain are capable of binding human CD3 when associated;

said first variable heavy domain and said first pseudo variable light domain intermolecularly associate to form an inactive Fv;

said first variable light domain and said first pseudo variable heavy domain intermolecularly associate to form an inactive Fv;

wherein said first and third sdABD are selected from the group consisting of SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29; SEQ ID NO:33; SEQ ID NO:37 and SEQ ID NO:41.

20. A protein according to claim 19 wherein said first and second TTA is the same.

21. A protein according to claim 19 wherein said first and second TTA are different.

22. A protein according to any of claims 19 to 21 wherein said third and fourth sdABDs have SEQ ID NO:45.

23. A nucleic acid composition comprising:

a) a first nucleic acid encoding a first protein according to any of claims 19 to 22; and

b) a second nucleic acid encoding a second protein according to any of claims 19 to 22.

24. An expression vector composition comprising:

a) a first expression vector comprising the first nucleic acid of claim 23; and

b) a second expression vector comprising the second nucleic acid of claim 23.

25. A host cell comprising the expression vector composition of claim 24.

26. A method of making a composition comprising culturing the host cell of claim 25 under conditions wherein said proteins are expressed and recovering said proteins.

27. A method of treating cancer comprising administering the protein of any of claims 19 to 22 to a patient.

28. A composition comprising:

a) a first protein comprising, from N- to C-terminal:

i) a first sdABD-TTA;

ii) a first domain linker;

iii) a second sdABD-TTA;

iv) a second domain linker;

iii) a pseudo Fv domain comprising, from N- to C-terminal:

1) a variable heavy chain comprising a vhCDR1, vhCDR2 and vhCDR3;

2) a cleavable linker; and

3) a first pseudo variable light domain comprising iVLCDR1, iVLCDR2 and iVLCDR3;

iv) a third domain linker; and

v) a sdABD-HSA;

a) a second protein comprising, from N- to C-terminal:

i) a third sdABD-TTA;

ii) a fourth domain linker;

iii) a fourth sdABD-TTA;

iv) a fifth domain linker;

iii) a pseudo Fv domain comprising, from N- to C-terminal:

1) a variable light chain comprising a VLCDR1, VLCDR2 and VLCDR3;

2) a cleavable linker; and

3) a first pseudo variable heavy domain comprising iVHCDR1, iVHCDR2 and iVHCDR3;

iv) a sixth domain linker;

v) a sdABD-HSA;

wherein

said first variable heavy domain and said first variable light domain are capable of binding human CD3 when associated;

said first variable heavy domain and said first pseudo variable light domain intermolecularly associate to form an inactive Fv;

said first variable light domain and said first pseudo variable heavy domain intermolecularly associate to form an inactive Fv.

29. A composition according to claim 28 wherein said sdABD-HSAs have SEQ ID NO:45.

30. A nucleic acid composition comprising:

a) a first nucleic acid encoding a first protein according to any of claims 28 to 29; and

b) a second nucleic acid encoding a second protein according to any of claims 28 to 29, respectively.

31. An expression vector composition comprising:

a) a first expression vector comprising the first nucleic acid of claim 30; and

b) a second expression vector comprising the second nucleic acid of claim 30.

32. A host cell comprising the expression vector composition of claim 31.

33. A method of making a composition comprising culturing the host cell of claim 32 under conditions wherein said proteins are expressed and recovering said proteins.

34. A method of treating cancer comprising administering the protein of any of claims 28 to 29 to a patient.

35. A protein comprising, from N- to C-terminal:

a) a single domain antigen binding domain (sdABD) that binds to a human tumor target antigen (TTA) (sdABD-TTA);

b) a first domain linker;

c) a constrained Fv domain comprising:

i) a first variable heavy domain comprising a vhCDR1, vhCDR2 and vhCDR3;

ii) a constrained non-cleavable linker (CNCL); and

iii) a first variable light domain comprising vlCDR1, vlCDR2 and vlCDR3;

d) a cleavable linker (CL);

e) a second sdABD that binds to human serum albumin;

f) a domain linker;

g) a constrained pseudo Fv domain comprising:

i) a first pseudo light variable domain;

ii) a non-cleavable linker (NCL); and

iii) a first pseudo heavy variable domain;

wherein said first variable heavy domain and said first variable light domain are capable of binding human CD3 but said constrained Fv domain does not bind CD3;

said first variable heavy domain and said first pseudo variable light domain intramolecularly associate to form an inactive Fv; and

said first variable light domain and said first pseudo variable heavy domain intramolecularly associate to form an inactive Fv.

36. A protein according to claim 35 wherein said first variable heavy domain is N-terminal to said first variable light domain and said pseudo light variable domain is N-terminal to said pseudo variable heavy domain.

37. A protein according to claim 35 wherein said first variable heavy domain is N-terminal to said first variable light domain and said pseudo variable heavy domain is N-terminal to said pseudo variable light domain.

38. A protein according to claim 35 wherein said first variable light domain is N-terminal to said first variable heavy domain and said pseudo light variable domain is N-terminal to said pseudo variable heavy domain.

39. A protein according to claim 35 wherein said first variable light domain is N-terminal to said first variable heavy domain and said pseudo variable heavy domain is N-terminal to said pseudo variable light domain.

40. A protein according to claim 35 to 39 wherein said TTA is selected from EGFR, EpCAM, FOLR1 and B7H3.

41. A protein according to any of claims 35 to 40 wherein said sdABD-TTA is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NO:25, SEQ ID NO:29; SEQ ID NO:33; SEQ ID NO:37 and SEQ ID NO:41.

42. A protein according to any of claims 35 to 41 wherein said half-life extension domain has SEQ ID NO:45.

43. A protein according to any of claims 35 to 42 wherein said cleavable linker is cleaved by a human protease selected from the group consisting of MMP2, MMP9, Meprin A, Meprin B, Cathepsin S, Cathepsin K, Cathespin L, GranzymeB, uPA, Kallekrien7, matriptase and thrombin.

44. A protein according to claim 35 comprising Pro258, Pro356, Pro359, Pro388 and Pro364.

45. A nucleic acid encoding a protein according to any of claims 35 to 44.

46. An expression vector comprising the nucleic acid of claim 45.

47. A host cell comprising the expression vector of claim 46.

48. A method of making a protein comprising culturing the host cell of claim 47 under conditions wherein said protein is expressed and recovering said protein.

49. A method of treating cancer comprising administering the protein of any of claims 35 to 44 to a patient.