BISPECIFIC ANTIBODIES THAT BIND TO CD38 AND CD3

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority under 35 U.S.C. §119 to U.S. Provisional Patent Applications No. 61/972,172, filed March 28, 2014, 62/025,974, filed July 7, 2014, and 62/025,931, filed July 17, 2014, the entire contents of which are incorporated herein for all purposes by this reference and specifically for the Figures, Legends and data outlined herein.

TECHNICAL FIELD

[0002] The present invention describes novel immunoglobulin compositions that simultaneously co-engage antigens, where both of the antigens are bound monovalently. The novel immunoglobulins described preferably utilize heterodimeric Fc regions. Methods of using the novel immunoglobulin compositions, particularly for therapeutic purposes, are also described herein.

BACKGROUND OF THE INVENTION

[0003] Antibody-based therapeutics have been used successfully to treat a variety of diseases, including cancer and autoimmune/inflammatory disorders. Yet improvements to this class of drugs are still needed, particularly with respect to enhancing their clinical efficacy. One avenue being explored is the engineering of additional and novel antigen binding sites into antibody-based drugs such that a single immunoglobulin molecule co-engages two different antigens. Such non-native or alternate antibody formats that engage two different antigens are often referred to as bispecifics. Because the considerable diversity of the antibody variable region (Fv) makes it possible to produce an Fv that recognizes virtually any molecule, the typical approach to bispecific generation is the introduction of new variable regions into the antibody.

[0004] A number of alternate antibody formats have been explored for bispecific targeting (Chames & Baty, 2009, mAbs 1[6]:1-9; Holliger & Hudson, 2005, Nature Biotechnology 23[9]:1126-1136; and Kontermann, 2012 MAbs 4(2):182, all of which are expressly incorporated herein by reference). Initially, bispecific antibodies were made by fusing two cell lines that each produced a single monoclonal antibody (Milstein et al., 1983, Nature 305:537-540). Although the resulting hybrid hybridoma or quadroma did produce bispecific antibodies, they were only a minor population, and extensive purification was required to

isolate the desired antibody. An engineering solution to this was the use of antibody fragments to make bispecifics. Because such fragments lack the complex quaternary structure of a full length antibody, variable light and heavy chains can be linked in single genetic constructs. Antibody fragments of many different forms have been generated, including diabodies, single chain diabodies, tandem scFv's, and Fab_2 bispecifics (Chames & Baty, 2009, mAbs 1[6]:1-9; Holliger & Hudson, 2005, Nature Biotechnology 23[9]:1126-1136; expressly incorporated herein by reference). While these formats can be expressed at high levels in bacteria and may have favorable penetration benefits due to their small size, they clear rapidly in vivo and can present manufacturing obstacles related to their production and stability. A principal cause of these drawbacks is that antibody fragments typically lack the constant region of the antibody with its associated functional properties, including larger size, high stability, and binding to various Fc receptors and ligands that maintain long half-life in serum (i.e., the neonatal Fc receptor FcRn) or serve as binding sites for purification (i.e., protein A and protein G).

[0005] More recent work has attempted to address the shortcomings of fragment-based bispecifics by engineering dual binding into full length antibody -like formats (Wu et al., 2007, Nature Biotechnology 25[11]:1290-1297; USSN12/477,711; Michaelson et al., 2009, mAbs 1[2]:128-141; PCT/US2008/074693; Zuo et al., 2000, Protein Engineering 13[5]:361-367; USSN09/865,198; Shen et al., 2006, J Biol Chem 281[16]:10706-10714; Lu et al., 2005, J Biol Chem 280[20]:19665-19672; PCT/US2005/025472; and Kontermann, 2012 MAbs 4(2):182, all of which are expressly incorporated herein by reference). These formats overcome some of the obstacles of the antibody fragment bispecifics, principally because they contain an Fc region. One significant drawback of these formats is that, because they build new antigen binding sites on top of the homodimeric constant chains, binding to the new antigen is always bivalent.

[0006] For many antigens that are attractive as co-targets in a therapeutic bispecific format, the desired binding is monovalent rather than bivalent. For many immune receptors, cellular activation is accomplished by cross-linking of a monovalent binding interaction. The mechanism of cross-linking is typically mediated by antibody/antigen immune complexes, or via effector cell to target cell engagement. For example, the low affinity Fc gamma receptors (FcγRs) such as FcγRIIa, FcγRIIb, and FcγRIIIa bind monovalently to the antibody Fc region. Monovalent binding does not activate cells expressing these FcγRs; however, upon immune complexation or cell-to-cell contact, receptors are cross-linked and clustered on the cell

surface, leading to activation. For receptors responsible for mediating cellular killing, for example FcγRIIIa on natural killer (NK) cells, receptor cross-linking and cellular activation occurs when the effector cell engages the target cell in a highly avid format (Bowles & Weiner, 2005, J Immunol Methods 304:88-99, expressly incorporated by reference). Similarly, on B cells the inhibitory receptor FcγRIIb downregulates B cell activation only when it engages into an immune complex with the cell surface B-cell receptor (BCR), a mechanism that is mediated by immune complexation of soluble IgG's with the same antigen that is recognized by the BCR (Heyman 2003, Immunol Lett 88[2]:157-161; Smith and Clatworthy, 2010, Nature Reviews Immunology 10:328-343; expressly incorporated by reference). As another example, CD3 activation of T-cells occurs only when its associated T-cell receptor (TCR) engages antigen-loaded MHC on antigen presenting cells in a highly avid cell-to-cell synapse (Kuhns et al., 2006, Immunity 24:133-139). Indeed nonspecific bivalent cross-linking of CD3 using an anti-CD3 antibody elicits a cytokine storm and toxicity (Perruche et al., 2009, J Immunol 183[2]:953-61; Chatenoud & Bluestone, 2007, Nature Reviews Immunology 7:622–632; expressly incorporated by reference). Thus for practical clinical use, the preferred mode of CD3 co-engagement for redirected killing of targets cells is monovalent binding that results in activation only upon engagement with the co-engaged target.

[0007] CD38, also known as cyclic ADP ribose hydrolase, is a type II transmembrane glycoprotein with a long C-terminal extracellular domain and a short N-terminal cytoplasmic domain. Among hematopoietic cells, an assortment of functional effects have been ascribed to CD38 mediated signaling, including lymphocyte proliferation, cytokine release, regulation of B and myeloid cell development and survival, and induction of dendritic cell maturation. CD38 is unregulated in many hematopoeitic malignancies and in cell lines derived from various hematopoietic malignancies including non-Hodgkin's lymphoma (NHL), Burkitt's lymphoma (BL), multiple myeloma (MM), B chronic lymphocytic leukemia (B-CLL), B and T acute lymphocytic leukemia (ALL), T cell lymphoma (TCL), acute myeloid leukemia (AML), hairy cell leukemia (HCL), Hodgkin's Lymphoma (HL), and chronic myeloid leukemia (CML). On the other hand, most primitive pluripotent stem cells of the hematopoietic system are CD38-. In spite of the recent progress in the discovery and development of anti-cancer agents, many forms of cancer involving CD38-expressing tumors still have a poor prognosis. Thus, there is a need for improved methods for treating such forms of cancer.

[0008] Thus while bispecifics generated from antibody fragments suffer biophysical and pharmacokinetic hurdles, a drawback of those built with full length antibody -like formats is that they engage co-target antigens multivalently in the absence of the primary target antigen, leading to nonspecific activation and potentially toxicity. The present invention solves this problem by introducing a novel bispecific format that enables the co-engagement of distinct target antigens.

SUMMARY

[0009] Accordingly, the present invention provides a heterodimeric antibody comprising: a) a first heavy chain comprising: i) a first Fc domain variant; ii) a single chain Fv region (scFv) that binds CD3; and b) a second heavy chain comprising: i) a second Fc domain variant; and ii) a first variable heavy domain; and c) a first light chain comprising a first variable light domain and a first constant light domain; wherein said first variable heavy domain and said first variable light domain bind to CD38, and wherein the second heavy chain comprises CDR sequences RSWMN, EINPDSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDTWVA, SASYRYS, and QQYDSYPLT; the second heavy chain comprises CDR sequences RSWMN, EINPDSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDTNVA, SASYRYS, and QQYDSYPLT; the second heavy chain comprises CDR sequences RSWMN, EINPDSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDYWVA, AASWRYS, and QQYDVYPLT; the second heavy chain comprises CDR sequences YSWMN, EINPQSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDYWVA, AASWRYS, and QQYDVYPLT; the second heavy chain comprises CDR sequences YSWMN, EINPQSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDYWVA, SASWRYS, and QQYDVYPLT; the second heavy chain comprises CDR sequences YSWMN, EINPQSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDYWVA, SASWRYS, and QQYDVYPLT; the second heavy chain comprises CDR sequences RSWMN, EINPQSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDYWVA, AASWRYS, and QQYDVYPLT; or the second heavy chain comprises CDR sequences YSWMN, EINPQSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR

sequences RASQNVDTWVA, SASYRYS, and QQYDSYPLT. The heterodimeric antibodies comprise a first heavy chain comprising a first variable Fc domain and a single chain Fv region (scFv) that binds CD3. The heterodimeric antibodies also comprise a second heavy chain comprising a second Fc variable Fc domain and a first variable heavy domain. The heterodimeric antibodies further comprise a first light chain comprising a first variable light domain and a first constant light domain, wherein said first variable heavy domain and said first variable light domain bind to CD38.

[0010] Also disclosed are heterodimeric antibodies selected from the group consisting of XENP13243; XENP13545; XENP13546; XENP13547; XENP13548; XENP13549; XENP13550; XENP13551; XENP13544; XENP13752; XENP13753; XENP13754; XENP13756; XENP13757 and XENP13694.

[0011] In an additional example, the scFv has a sequence comprising a vhCDR1 having the sequence T-Y-A-M-Xaa1, wherein Xaa1 is N, S or H (SEQ ID NO:435), a vhCDR2 having the sequence R-I-R-S-K-Xaa1-N-Xaa2-Y-A-T-Xaa3-Y-Y-A-Xaa4-S-V-K-G, wherein Xaa1 is Y or A, Xaa2 is N or S, Xaa3 is Y or A and Xaa4 is D or A (SEQ ID NO:436), a vhCDR3 having the sequence H-G-N-F-G-Xaa1-S-Y-V-S-W-F-Xaa2-Y, wherein Xaa1 is N, D or Q and Xaa2 is A or D (SEQ ID NO:437), a vlCDR1 having the sequence Xaa1-S-S-T-G-A-V-T-Xaa2-Xaa3-Xaa4-Y-A-N, wherein Xaa1 is G, R or K, Xaa2 is T or S, Xaa3 is S or G and Xaa4 is N or H, (SEQ ID NO:438), a vlCDR2 having the sequence Xaa1-T-N-Xaa2-R-A-Xaa3, wherein Xaa1 is G or D, Xaa2 is K or N, and Xaa3 is P or S (SEQ ID NO:439) and a vlCDR3 having the sequence Xaa1-L-W-Y-S-N-Xaa2-W-V, wherein Xaa1 is A or L and Xaa2 is L or H (SEQ ID NO:440).

[0012] In a further example, the scFv is selected from the group consisting of H1.30_L1.47, H1.33_L1.47 and H1.31_L1.47.

[0013] In an additional example, the anti-CD3 variable region has a sequence selected from the group consisting of:

[0014] a) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0015] b) a sequence comprising a vhCDR1 having SEQ ID NO:412, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0016] c) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:414, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0017] d) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:417, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0018] e) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:418, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0019] f) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:421, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0020] g) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:422, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0021] h) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:427 and a vlCDR3 having SEQ ID NO:430;

[0022] i) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:428 and a vlCDR3 having SEQ ID NO:430;

[0023] j) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:431;

[0024] k) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0025] l) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:423, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:432;

[0026] m) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:424, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:432;

[0027] n) a sequence comprising a vhCDR1 having SEQ ID NO:412, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:417, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0028] o) a sequence comprising a vhCDR1 having SEQ ID NO:412, a vhCDR2 having SEQ ID NO:414, a vhCDR3 having SEQ ID NO:419, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0029] p) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:415, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0030] q) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:415, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0031] r) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:417, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0032] s) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:419, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430;

[0033] t) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:417, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:433;

[0034] u) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:413, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:433 and

[0035] v) a sequence comprising a vhCDR1 having SEQ ID NO:411, a vhCDR2 having SEQ ID NO:434, a vhCDR3 having SEQ ID NO:416, a vlCDR1 having SEQ ID NO:420, a vlCDR2 having SEQ ID NO:425 and a vlCDR3 having SEQ ID NO:430.

[0036] In an additional example, the anti-CD3 variable region comprises a variable heavy region and a variable light region selected from the group consisting of:

[0037] SEQ ID NOs: 5 and 6; SEQ ID NOs: 9 and 10; SEQ ID NOs: 13 and 14; SEQ ID NOs: 17 and 18; SEQ ID NOs: 21 and 22; SEQ ID NOs: 25 and 26; SEQ ID NOs: 29 and 30; SEQ ID NOs: 33 and 34; SEQ ID NOs: 37 and 38; SEQ ID NOs: 41 and 42; SEQ ID NOs: 45 and 46; SEQ ID NOs: 49 and 50; SEQ ID NOs: 53 and 54; SEQ ID NOs: 57 and 58; SEQ ID NOs: 61 and 62; SEQ ID NOs: 65 and 66; SEQ ID NOs: 69 and 70; SEQ ID NOs: 73 and 74; SEQ ID NOs: 77 and 78; SEQ ID NOs: 81 and 82; SEQ ID NOs: 85 and 86; SEQ ID NOs: 89 and 90; SEQ ID NOs: 93 and 94; SEQ ID NOs: 97 and 98; SEQ ID NOs: 101 and 102; SEQ ID NOs: 105 and 106; SEQ ID NOs: 109 and 110; SEQ ID NOs: 113 and 114; SEQ ID NOs: 117 and 118; SEQ ID NOs: 121 and 122; SEQ ID NOs: 125 and 126; SEQ ID NOs: 129 and 130; SEQ ID NOs: 133 and 134; SEQ ID NOs: 137 and 138; SEQ ID NOs: 141 and 142; SEQ ID NOs: 145 and 146; SEQ ID NOs: 149 and 150; SEQ ID NOs: 153 and 154; SEQ ID NOs: 157 and 158; SEQ ID NOs: 161 and 162; SEQ ID NOs: 165 and 166; SEQ ID NOs: 169 and 170; SEQ ID NOs: 173 and 174; SEQ ID NOs: 177 and 178; SEQ ID NOs: 181 and 182; SEQ ID NOs: 185 and 186; SEQ ID NOs: 189 and 190; SEQ ID NOs: 193 and 194; SEQ ID NOs: 197 and 198; SEQ ID NOs: 201 and 202; SEQ ID NOs: 205 and 206; SEQ ID NOs: 209 and 210; SEQ ID NOs: 213 and 214; SEQ ID NOs: 217 and 218; SEQ ID NOs: 221 and 222; SEQ ID NOs: 225 and 226; SEQ ID NOs: 229 and 230; SEQ ID NOs: 233 and 234; SEQ ID NOs: 237 and 238; SEQ ID NOs: 241 and 242; SEQ ID NOs: 245 and 246; SEQ ID NOs: 249 and 250; SEQ ID NOs: 253 and 254; SEQ ID NOs: 257 and 258; SEQ ID NOs: 261 and 262; SEQ ID NOs: 265 and 266; SEQ ID NOs: 269 and 270; SEQ ID NOs: 273 and 274; SEQ ID NOs: 277 and 278; SEQ ID NOs: 281 and 282; SEQ ID

NOs: 285 and 286; SEQ ID NOs: 289 and 290; SEQ ID NOs: 293 and 294; SEQ ID NOs: 297 and 298; SEQ ID NOs: 301 and 302; SEQ ID NOs: 305 and 306; SEQ ID NOs: 309 and 310; SEQ ID NOs: 313 and 314; SEQ ID NOs: 317 and 318; SEQ ID NOs: 321 and 322; SEQ ID NOs: 325 and 326; SEQ ID NOs: 329 and 330; SEQ ID NOs: 333 and 334; SEQ ID NOs: 337 and 338; SEQ ID NOs: 341 and 342; SEQ ID NOs: 345 and 346; SEQ ID NOs: 349 and 350; SEQ ID NOs: 353 and 354; SEQ ID NOs: 357 and 358; SEQ ID NOs: 361 and 362; SEQ ID NOs: 365 and 366; SEQ ID NOs: 369 and 370; SEQ ID NOs: 373 and 374; SEQ ID NOs: 377 and 378; SEQ ID NOs: 381 and 382; SEQ ID NOs: 385 and 386; SEQ ID NOs: 389 and 390; SEQ ID NOs: 393 and 394; SEQ ID NOs: 397 and 398; SEQ ID NOs: 401 and 402; SEQ ID NOs: 405 and 406; SEQ ID NOs: 409 and 410.

[0038] In an additional example, the heterodimeric antibodies have the first variable heavy domain and the first variable light domain are selected from the pairs consisting of H1 and L1; H1 and L1.24; H1 and L1.96; H1.77 and L1.96; H1.77 and L1.97; H1.72 and L1.97; H1.71 and L1.96 and H1.77 and L1.24.

[0039] Also disclosed are heterodimeric antibodies as above, wherein the scFv has a charged scFv linker. The charged scFv linker can have a positive charge from 3 to 8 and is selected from the group consisting of SEQ ID NO:s 443 to 451.

[0040] In an additional example, the scFv has a sequence selected from the group consisting of: SEQ ID NO: 4; SEQ ID NO: 8; SEQ ID NO: 12; SEQ ID NO: 16; SEQ ID NO: 20; SEQ ID NO: 24; SEQ ID NO: 28; SEQ ID NO: 32; SEQ ID NO: 36; SEQ ID NO: 40; SEQ ID NO: 44; SEQ ID NO: 48; SEQ ID NO: 52; SEQ ID NO: 56; SEQ ID NO: 60; SEQ ID NO: 64; SEQ ID NO: 68; SEQ ID NO: 72; SEQ ID NO: 76; SEQ ID NO: 80; SEQ ID NO: 84; SEQ ID NO: 88; SEQ ID NO: 92; SEQ ID NO: 96; SEQ ID NO: 100; SEQ ID NO: 104; SEQ ID NO: 108; SEQ ID NO: 112; SEQ ID NO: 116; SEQ ID NO: 120; SEQ ID NO: 124; SEQ ID NO: 128; SEQ ID NO: 132; SEQ ID NO: 136; SEQ ID NO: 140; SEQ ID NO: 144; SEQ ID NO: 148; SEQ ID NO: 152; SEQ ID NO: 156; SEQ ID NO: 160; SEQ ID NO: 164; SEQ ID NO: 168; SEQ ID NO: 172; SEQ ID NO: 176; SEQ ID NO: 180; SEQ ID NO: 184; SEQ ID NO: 188; SEQ ID NO: 192; SEQ ID NO: 196; SEQ ID NO: 200; SEQ ID NO: 204; SEQ ID NO: 208; SEQ ID NO: 212; SEQ ID NO: 216; SEQ ID NO: 220; SEQ ID NO: 224; SEQ ID NO: 228; SEQ ID NO: 232; SEQ ID NO: 236; SEQ ID NO: 240; SEQ ID NO: 244; SEQ ID NO: 248; SEQ ID NO: 252; SEQ ID NO: 256; SEQ ID NO: 260; SEQ ID NO: 264; SEQ ID NO: 268; SEQ ID NO: 272; SEQ ID NO: 276; SEQ ID NO: 280; SEQ ID NO: 284; SEQ ID NO: 288; SEQ ID NO: 292; SEQ ID NO: 296; SEQ ID NO: 300; SEQ ID NO: 304; SEQ

ID NO: 308; SEQ ID NO: 312; SEQ ID NO: 316; SEQ ID NO: 320; SEQ ID NO: 324; SEQ ID NO: 328; SEQ ID NO: 332; SEQ ID NO: 336; SEQ ID NO: 340; SEQ ID NO: 344; SEQ ID NO: 348; SEQ ID NO: 352; SEQ ID NO: 356; SEQ ID NO: 360; SEQ ID NO: 364; SEQ ID NO: 368; SEQ ID NO: 372; SEQ ID NO: 376; SEQ ID NO: 380; SEQ ID NO: 384; SEQ ID NO: 388; SEQ ID NO: 392; SEQ ID NO: 396; SEQ ID NO: 400; SEQ ID NO: 404; SEQ ID NO: 408.

[0041] In a further example, the Fc region of the heavy chains further comprises an FcRn variant, including but not limited to 428L/434S.

[0042] In an additional aspect, the invention provides a nucleic acid composition comprising: a) a first nucleic acid encoding the first heavy chain as described herein; b) a second nucleic acid encoding the second heavy chain as described herein; and c) a third nucleic acid encoding said light chain as described herein. In additional aspect, the invention provides a nucleic acid composition comprising: a) a first expression vector comprising a first nucleic acid encoding the first heavy chain as described herein; b) a second expression vector comprising a second nucleic acid encoding the second heavy chain as described herein; and c) a third expression vector comprising a third nucleic acid encoding the light chain as described herein. Also disclosed are nucleic acid compositions comprising a first nucleic acid encoding a first heavy chain comprising an Fc region and a scFv that binds to CD3, a second nucleic acid encoding a second heavy chain that comprises a heavy constant chain and a heavy variable chain, and a third nucleic acid encoding a light chain, wherein the Fv regions of the second heavy chain and the light chain bind CD38. These nucleic acids can be in different expression vectors or the same. The invention provides host cells comprising the nucleic acid compositions.

[0043] In a further aspect, the present invention provides methods of producing heterodimeric antibodies of the invention comprising providing a first expression vector comprising a first nucleic acid encoding the second heavy chain comprising the second Fc domain variant; and the first variable heavy domain; and providing a second expression vector comprising a second nucleic acid encoding the first heavy chain comprising the first Fc domain variant and the single chain Fv region (scFv) that binds CD3; providing a third expression vector comprising a third nucleic acid encoding the first light chain; wherein said first variable heavy domain and the variable light domain of the first light chain bind CD38; wherein said first, second and third expression vectors are transfected into host cells at a ratio selected from the group consisting of 1:1.5:1.5, 1:2:1.5, 1:0.667:2, 1:1:2, 1:1.5:2, and 1:2:2; and expressing said first, second and third nucleic acids in said host cells to

produce a first, second and third amino acid sequence, respectively, such that said first, second and third amino acid sequences form said heterodimeric antibody.

[0043A] In an additional aspect, the present invention provides a pharmaceutical composition comprising the heterodimeric antibody as described herein. In another aspect, the present invention refers to a nucleic acid composition comprising an expression vector comprising a nucleic acid encoding the first heavy chain of the present invention and an expression vector comprising a second nucleic acid encoding the second heavy chain of the present invention and a third nucleic acid encoding the first light chain of the present invention.

[0043] In an additional aspect, the invention provides use of a heterodimeric antibody as described herein in the manufacture of a medicament for treating cancer in a patient in need thereof. Also disclosed is a methods of treating a patient in need thereof by administering a heterodimeric antibody as described herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0044] Figure 1A and 1B depict the sequence of human CD38. Figure 1A depicts the full length sequence and Figure 1B depicts the extracellular domain.

[0046] Figure 2 depicts the sequence of human CD3.

[0047] Figures 3A to3YY depict the amino acid sequences of stability-optimized, humanized anti-CD3 variant scFvs, variable heavy and variable light sequences. (Note also that the first sequence is the histidine tagged version for ease of purification). CDRs are underlined. It should be understood that the increased stability of the optimized variable and optimized light chains (as well as the scFv chains) can be attributed to framework regions as well as the CDRs. Thus, it should be understood that the disclosure of the entire variable region includes the disclosure of the framework regions, although they are not separately numbered. In addition, the scFv linkers are shown in grey. Each scFv linker can be replaced with a charged scFv linker as depicted in Figure 5. That is, any charged scFv linker, whether positive or negative, including those depicted in Figure 5 can be substituted for the highlighted region in Figures 3A to 3YY.

[0048] Figures 4A to 4I depict a collation of all the CD3 vhCDR1-3 and vlCDR1-3 sequences useful in the present invention and consensus CDRs.

[0049] Figure 5 depicts suitable positive and negatively charged scFv linkers. A single prior art scFv linker with a single charge is referenced as "Whitlow", from Whitlow et al., Protein Engineering 6(8):989-995 (1993). It should be noted that this linker was used for reducing aggregation and enhancing proteolytic stability in scFvs.

[0050] Figures 6A, 6B, 6C and 6D depict novel steric variants. As will be understood by those in the art, the first column of each table represents "corresponding" monomer pairs; that is, monomer 1 has 405A and the corresponding steric variant is 394F. It is important to note that in the context of the asymmetrical triple F format, either monomer can have either variant. That is, the scFv monomer can be monomer 1 or monomer 2. Again, these sets can be optionally and independently combined with other steric variants as well as other heterodimerization variants including charge pairs, isotypic variants, isosteric variants, pI variants, etc,, as long as some "strandedness" is maintained. In addition, the "monomer" refers to the Fc domains; that is, in the triple F format, one monomer is the scFv construct and the other monomer is the Fab construct, despite the fact that there are actually two amino acid sequences that comprise the Fab construct (the heavy and light chains). show a number of suitable steric or "skew" variants of use in the present invention. Figure a6 depicts a number of steric variants that can be used alone or in combination with pI variants (as is true of all the variants in Figure 6); however, as will be appreciated by those in the art, if there are pI

variants, the "strandedness" of the pI variants and steric variants should be maintained. That is, if for example the pI variants S364K/E357Q (monomer 1) and L368D/K370S (monomer 2) are to be combined with Figure 29C variants, the pI of the steric variants should be considered and assigned to the correct monomer. That is, steric variants that alter charge (T411E) for example, are added to the "negative" monomer.

[0051] Figure 7 depicts a list of engineered heterodimer-skewing (e.g. "steric heterodimerization") Fc variants with heterodimer yields (determined by HPLC-CIEX) and thermal stabilities (determined by DSC). Not determined thermal stability is denoted by "n.d.".

[0052] Figure 8A to 8C. Illustration of the "triple F" format for bispecific immunoglobulins. Figure 8A shows a scFv-Fc format. Figure 8C depicts a more standard bispecific format, also utilizing the pI variants of the invention (and optionally and independently the other heterodimerization variants). Figure 8B shows the "triple F" format (sometimes also referred to as the "bottle-opener" configuration; (and optionally and independently the other heterodimerization variants). Many of the embodiments listed herein have the anti-CD3 component of the bispecific antibody as the scFv, and the anti-CD38 component as the Fab fragment, although as will be appreciated by those in the art, these may be switched, with the anti-CD38 component being the scFv, optionally with a charged linker, and the Fv regions of the scFv of the anti-CD3 sequences herein being reengineered to be Fab fragments.

[0053] Figure 9 depicts a number of suitable "knock out" ("KO") variants to reduce binding to some or all of the FcγR receptors. As is true for many if not all variants herein, these KO variants can be independently and optionally combined, both within the set described in Figure 9 and with any heterodimerization variants outlined herein, including steric and pI variants. For example, E233P/L234V/L235A/G236del can be combined with any other single or double variant from the list. In addition, while it is preferred in some embodiments that both monomers contain the same KO variants, it is possible to combine different KO variants on different monomers, as well as have only one monomer comprise the KO variant(s). Reference is also made to the Figures and Legends of USSN 61/913,870, all of which is expressly incorporated by reference in its entirety as it relates to "knock out" or "ablation" variants.

[0054] Figure 10 shows a list of engineered heterodimer-skewing Fc variants with heterodimer yields (determined by HPLC-CIEX) and thermal stabilities (determined by DSC). Not determined thermal stability is denoted by "n.d.".

[0055] Figure 11. Schematic showing the structure of Anti-CD38 x Anti-CD3 bispecific molecule.

[0056] Figure 12. Surface plasmon resonance (SPR) data of affinity/stability engineered variant Anti-CD38 x Anti-CD3 bispecific molecules.

[0057] Figure 13. Fluorescent LDH re-directed T-cell cytotoxicity (RTCC) assay showing killing of RPMI8226 multiple myeloma cells by Anti-CD28 x Anti-CD3 bispecific molecules.

[0058] Figure 14. RTCC assay (Annexin V+) assay showing killing of RPMI8226 multiple myeloma cells by Anti-CD38 x Anti-CD3 bispecific molecules. The ratio of T-cell to RPMI8226 cells and the incubation time is varied.

[0059] Figure 15. Table listing properties of affinity/stability engineered variant Anti-CD38 x Anti-CD3 bispecific molecules. Numbering is according to Kabat.

[0060] Figure 16. Binding of Anti-CD38 x Anti-CD3 bispecific molecules to cynomolgus monkey (Macaca fascicularis) CD20+ cells.

[0061] Figure 17. Human plasma cell killing by Anti-CD38 x Anti-CD3 bispecifics in huPBMC-engrafted SCID mice. Significant reductions in human IgG2 and IgE isotypes are seen. Mean ± SEM for Day 22 are shown. BLQ for IgG2 is < 1 μg/mL and for IgE is < 16 ng/mL. Datapoints less than BLQ were assigned the BLQ value.

[0062] Figure 18. Human plasma cell killing by Anti-CD38 x Anti-CD3 bispecifics in huPBMC-engrafted SCID mice. Significant reduction in human IgM is seen. Mean ± SEM for Day 22 are shown. BLQ for IgM is < 0.03 μg/mL. Datapoints less than BLQ were assigned the BLQ value.

[0063] Figure 19. CD38+CD138+ cell depletion in MM PBMC by Anti-CD38 x Anti-CD3 bispecific antibodies.

[0064] Figure 20A-20Q shows the sequences of the CD38 X CD3 scFv bottle openers of the invention.

[0065] Figure 21 shows the variants of some useful Fc domains of the CD38 X CD3 bottle openers.

[0066] Figures 22A and 22B depict the amino acid sequences for anti-CD38 x anti-CD3 bispecifics XENP13243 and XENP13551, with the CDRs underlined and the charged linker (which may be uncharged or substituted with any other charged linker, either positive or negative, from Figure 7).

[0067] Figure 23A, 23B, 23C and 23D show DNA sequences encoding anti-CD38 x anti-CD3 bispecifics XENP13243 and XENP13551.

[0068] Figure 24 shows the DNA transfection ratio chart for stable pool generation for XENP13243 and XENP13551. Relative amounts of transfected DNA for HC-Fab, HC-scFv, and LC are listed.

[0069] Figure 25A, 25B, 25C and 25D depict cation exchange chromatograms of protein A purified material from stable pool supernatants collected after 7 days of batch culture for XENP13243 and XENP13551. DNA transfection ratios are as listed in Fig. 24. Integrated peak areas are noted.

[0070] Figure 26. Summary of different protein species generated by stable pools as identified by the cation exchange chromatograms shown in Fig. 25. DNA transfection ratios are as listed in Fig. 24.

[0071] Figure 27. Pharmacokinetics of anti-CD38 x anti-CD3 bispecifics XENP13243 and XENP13551 in C57BL/6 mice (n = 5 mice per group). Half-life values calculated by non-compartmental analysis are noted in the figure legend.

[0072] Figure 28. Redirected T cell cytotoxicity of CD38+ RPMI8226 cells. Assay consisted of a 24 h incubation at 37°C of 10,000 RPMI8226 cells with 400,000 purified human T cells. Readout of cytotoxicity was by lactate dehydrogenase (LDH).

[0073] Figure 29. Kinetics of human and cyno CD38 and CD3 binding to XENP13243 and XENP13551, as determined by surface plasmon resonance. Assay format is as specified.

[0074] Figure 30 Depletion of CD20-CD38+ cells in cynomolgus monkeys by XENP13243 (top panel) and XENP13551 (bottom panel).

[0075] Figure 31. Upregulation of CD69 in CD8+ T cells in cynomolgus monkeys by XENP13243 (top panel) and XENP13551 (bottom panel).

[0076] Figure 32 depicts a list of isosteric variant antibody constant regions and their respective substitutions. pI_(-) indicates lower pI variants, while pI_(+) indicates higher pI variants. These can be optionally and independently combined with other heterodimerization variants of the invention.

[0077] Figure 33 shows some charged linkers and data for particular anti-CD3 scFvs.

[0078] Figure 34 depicts a schematic associated with the use of separation variants, also referred to herein as "pI variants", and combined with the heterodimer assembly variants, also referred to herein as "skew variants". These variants can be used in a "plug and play" format, in that the effects of the variants transfer into different antibodies with different Fv regions easily and are very stable.

[0079] Figure 35 depicts the optimization of a common anti-CD3 scFv-Fc. The stability was increased in a variety of ways, including replacing rare amino acids, replacing amino acids with unusual contact residues, doing linker engineering (for stability and enhanced purification, e.g. charged scFv linkers) and conversion to the VL-VH orientation.

[0080] Figure 36 depicts the use of an Fc knock-out (or ablation variant) that retains wild type stability but removing all FcγR binding.

[0081] Figure 37 depicts the in vitro killing and stability data for an anti-CD3X anti-CD38 bottle opener format.

[0082] Figure 38 depicts the killing of a human myeloma cell line. XmAb13551 has high affinity for CD3, while XmAb13243 has lower affinity. Daratumumab is a anti-CD38 bivalent monospecific antibody.

[0083] Figure 39 shows the long half-life activity of the bottle opener bispecifics of the invention and the corresponding suppression of human Igs in mice.

[0084] Figure 40 shows the anti-CD38 X anti-CD3 functions of XmAb13551 and XmAb13243, including the depletion of monkey CD38+ cells in blood and bone marrow.

[0085] Figure 41 shows the CD38+ cell depletion correlates with T cell redistribution and activation.

[0086] Figure 42 shows the development of a stable cell line for production of XmAb13551 (high CD3 affinity) and their corresponding yields.

[0087] Figure 43 shows some cell culture optimization for improved yield, with titers of ≥3 g/L being obtained, with no significant difference in heterodimer/homodimer ratios being seen from scale up.

[0088] Figure 44 shows the analytical results from the three step process of manufacturing. The process produces high yields, over 55%, of very pure heterodimeric bispecific molecules, and effectively removes homodimeric, HMW and LMW contaminants as well as HCP.

[0089] Figure 45A-45U shows a variety of additional heterodimerization formats, any one of which can include the anti-CD3 and anti-CD38 sequences of the invention. Figures 45A to 45U depicts a wide variety of the multispecific (e.g. heterodimerization) formats and the combinations of different types of heterodimerization variants that can be used in the present invention (these are sometimes referred to herein as "heterodimeric scaffolds"). Note in addition that all of these formats can include addition variants in the Fc region, as more fully discussed below, including "ablation" or "knock out" variants (Figure 7), Fc variants to alter FcγR binding (FcγRIIb, FcγRIIIa, etc.), Fc variants to alter binding to FcRn receptor, etc. Figure 45A shows a dual scFv-Fc format, that, as for all heterodimerization formats herein can include heterodimerization variants such as pI variants, knobs in holes (KIH, also referred to herein as steric variants or "skew" variants), charge pairs (a subset of steric variants), isosteric variants, and SEED body ("strand-exchange engineered domain"; see Klein et al., mAbs 4:6 653-663 (2012) and Davis et al, Protein Eng Des Sel 2010 23:195-202) which rely on the fact that the CH3 domains of human IgG and IgA do not bind to each other. Figure 45B depicts a bispecific IgG, again with the option of a variety of heterodimerization variants. Figure 45C depicts the "one armed" version of DVD-Ig which utilizes two different variable heavy and variable light domains. Figure 45D is similar, except that rather than an "empty arm", the variable heavy and light chains are on opposite heavy chains. Figure 45E is generally referred to as "mAb-Fv". Figure 45F depicts a multi-scFv format; as will be appreciated by those in the art, similar to the "A, B, C, D" formats discussed herein, there may be any number of associated scFvs (or, for that matter, any other binding ligands or functionalities). Thus, Figure 45F could have 1, 2, 3 or 4 scFvs (e.g. for bispecifics, the scFv could be "cis" or "trans", or both on one "end" of the molecule). Figure 45G depicts a heterodimeric FabFc with the Fab being formed by two different heavy chains one containing heavy chain Fab sequences and the other containing light chain Fab sequences. Figure 45H depicts the "one armed Fab-Fc", where one heavy chain comprises the Fab. Figure 45I depicts a "one armed scFv-Fc", wherein one heavy chain Fc comprises an scFv and the other

heavy chain is "empty". Figure 45J shows a scFv-CH3, wherein only heavy chain CH3 regions are used, each with their own scFv. Figure 45K depicts a mAb-scFv, wherein one end of the molecule engages an antigen bivalently with a monovalent engagement using an scFv on one of the heavy chains. Figure 45L depicts the same structure except that both heavy chains comprise an additional scFv, which can either bind the same antigen or different antigens. Figure 45M shows the "CrossMab" structure, where the problem of multiplex formation due to two different light chains is addressed by switching sequences in the Fab portion. Figure 45N depicts an scFv, Figure 45O is a "BiTE" or scFv-scFv linked by a linker as outlined herein, Figure 45P depicts a DART, Figure 45Q depicts a TandAb, and Figure 45R shows a diabody. Figures 45S, 45T and 45U depict additional alternative scaffold formats that find use in the present invention.

[0090] Figures 46A, 46B and 46C depict staqbility-optimized, humanized anti-CD3 variant scFvs. Substitutions are given relative to the H1.1_L1.4 scFv sequence. Amino acid numbering is Kabat numbering.

[0091] Figures 47A and 47B. Variable heavy and variable light chains for anti-CD3 sequences of use in the present invention, include both "strong" and "lower" binding sequences. As will be appreciated by those in the art, these can be used in Fab or scFv constructs in combination with any target tumor antigen binding domains.

[0092] Figure 48 shows binding affinities in a Biacore assay.

[0093] Figure 49 shows the Heterodimer purity during stable pool generation using varied Light chain, Fab-Fc, and scFv-Fc ratios.

[0094] Figure 50 Human IgM and IgG2 depletion by anti-CD38 x anti-CD3 bispecifics in a huPBMC mouse model.

[0095] Figure 51A and 51B show the purification of XENP13243 & XENP13551 are designed with low & high affinity, respectively, for CD38.

[0096] Figure 52A, 52B and 52C show the binding to human and monkey CD38 and CD3, and the Kd.

[0097] Figure 53 shows the killing of myeloma cells.

[0086] Figure 54 shows the T cells are seial killers even when outnumbered by target cells.

[0087] Figure 55 shows the Fc domain prolongs the half-life.

[0088] Figure 56 shows the dosing for Figure 14 experiment.

[0089] Figure 57 shows greater hIg depletion versus daratumumab.

[0090] Figure 58 shows the dosing for Figure 16 experiment.

[0091] Figure 59A and 59B Bispecifics deplete CD38+ cells in blood & lymphoid organs in monkeys.

[0092] Figures 60A, 60B and 60C. Figure 60A (redistribution from blood), Figure 60B (CD69 induction) and Figure 60C (cytokine release) shows CD38+ cell depletion correlates with T cell redistribution & activation.

[0093] Figure 61 depicts several embodiments of particular use in the present invention.

DETAILED DESCRIPTION OF THE INVENTION

I. Overview

[0098] The present invention is directed to novel constructs to provide bispecific antibodies that bind to both CD3 and CD38 antigens. An ongoing problem in antibody technologies is the desire for "bispecific" (and/or multispecific) antibodies that bind to two (or more) different antigens simultaneously, in general thus allowing the different antigens to be brought into proximity and resulting in new functionalities and new therapies. In general, these antibodies are made by including genes for each heavy and light chain into the host cells. This generally results in the formation of the desired heterodimer (A-B), as well as the two homodimers (A-A and B-B). However, a major obstacle in the formation of multispecific antibodies is the difficulty in purifying the heterodimeric antibodies away from the homodimeric antibodies and/or biasing the formation of the heterodimer over the formation of the homodimers.

[0099] The present invention is generally directed to the creation of heterodimeric proteins such as antibodies that can co-engage antigens in several ways, relying on amino acid variants in the constant regions that are different on each chain to promote heterodimeric formation and/or allow for ease of purification of heterodimers over the homodimers.

[00100] Thus, the present invention is directed to novel immunoglobulin compositions that co-engage at least a first and a second antigen. First and second antigens of the invention are herein referred to as antigen-1 and antigen-2 respectively. One heavy chain of the antibody contains an single chain Fv ("scFv", as defined below) and the other heavy chain is a

"regular" FAb format, comprising a variable heavy chain and a light chain. This structure is sometimes referred to herein as "triple F" format (scFv-FAb-Fc) or the "bottle-opener" format, due to a rough visual similarity to a bottle-opener (see Figure). The two chains are brought together by the use of amino acid variants in the constant regions (e.g. the Fc domain and/or the hinge region) that promote the formation of heterodimeric antibodies as is described more fully below.

[00101] There are several distinct advantages to the present "triple F" format. As is known in the art, antibody analogs relying on two scFv constructs often have stability and aggregation problems, which can be alleviated in the present invention by the addition of a "regular" heavy and light chain pairing. In addition, as opposed to formats that rely on two heavy chains and two light chains, there is no issue with the incorrect pairing of heavy and light chains (e.g. heavy 1 pairing with light 2, etc.)

[00102] There are a number of mechanisms that can be used to generate the heterodimers of the present invention. In addition, as will be appreciated by those in the art and described more fully below, these mechanisms can be combined to ensure high heterodimerization.

[00103] One mechanism is generally referred to in the art as "knobs and holes" ("KIH"), or sometimes herein as "skew" variants, referring to amino acid engineering that creates steric influences to favor heterodimeric formation and disfavor homodimeric formation can also optionally be used; this is sometimes referred to as "knobs and holes", as described in USSN 61/596,846, Ridgway et al., Protein Engineering 9(7):617 (1996); Atwell et al., J. Mol. Biol. 1997 270:26; US Patent No. 8,216,805, all of which are hereby incorporated by reference in their entirety. The figures identify a number of "monomer A – monomer B" pairs that rely on "knobs and holes". In addition, as described in Merchant et al., Nature Biotech. 16:677 (1998), these "knobs and hole" mutations can be combined with disulfide bonds to skew formation to heterodimerization.

[0094] An additional mechanism that finds use in the generation of heterodimers is sometimes referred to as "electrostatic steering" as described in Gunasekaran et al., J. Biol. Chem. 285(25):19637 (2010), hereby incorporated by reference in its entirety. This is sometimes referred to herein as "charge pairs". In this embodiment, electrostatics are used to skew the formation towards heterodimerization. As those in the art will appreciate, these may also have have an effect on pI, and thus on purification, and thus could in some cases also be considered pI variants. However, as these were generated to force heterodimerization

and were not used as purification tools, they are classified as "steric variants". These include, but are not limited to, D221E/P228E/L368E paired with D221R/P228R/K409R (e.g. these are "monomer corresponding sets) and C220E/P228E/368E paired with C220R/E224R/P228R/K409R. (Note the 220 mutation is to remove a cysteine no longer needed for heavy and light chain disulfide formation, as more fully described below).

[0087] In the present invention, there are several basic mechanisms that can lead to ease of purifying heterodimeric proteins; one relies on the use of pI variants, such that each monomer has a different pI, thus allowing the isoelectric purification of A-A, A-B and B-B dimeric proteins. Alternatively, the "triple F" format also allows separation on the basis of size. As is further outlined below, it is also possible to "skew" the formation of heterodimers over homodimers, as is generally outlined below. Thus, a combination of steric heterodimerization variants and pI or charge pair variants find particular use in the invention. Additionally, as more fully outlined below, the scFv monomer of the Triple F format can include charged scFv linkers (either positive or negative), that give a further pI boost for purification purposes. As will be appreciated by those in the art, some Triple F formats are useful with just charged scFv linkers and no additional pI adjustments, although the invention does provide the use of skew variants with charged scFv linkers as well (and combinations of Fc, FcRn and KO variants).

[0088] In the present invention that utilizes pI as a separation mechanism to create the heterodimeric Triple F format, amino acid variants can be introduced into one or both of the monomer polypeptides; that is, the pI of one of the monomers (referred to herein for simplicity as "monomer A") can be engineered away from monomer B, or both monomer A and B change be changed, with the pI of monomer A increasing and the pI of monomer B decreasing. As is outlined more fully below, the pI changes of either or both monomers can be done by removing or adding a charged residue (e.g. a neutral amino acid is replaced by a positively or negatively charged amino acid residue, e.g. glycine to glutamic acid), changing a charged residue from positive or negative to the opposite charge (aspartic acid to lysine) or changing a charged residue to a neutral residue (e.g. loss of a charge; lysine to serine). A number of these variants are shown in the Figures.

[0089] Accordingly, in this embodiment of the present invention provides for creating a sufficient change in pI in at least one of the monomers such that heterodimers can be separated from homodimers. As will be appreciated by those in the art, and as discussed further below, this can be done by using a "wild type" heavy chain constant region and a

variant region that has been engineered to either increase or decrease it's pI (wt A-+B or wt A - -B), or by increasing one region and decreasing the other region (A+ -B- or A- B+). It should be noted that in this discussion it does not matter which monomer comprises the scFv and which the Fab.

[0090] Thus, in general, a component of the present invention are amino acid variants in the constant regions of antibodies that are directed to altering the isoelectric point (pI) of at least one, if not both, of the monomers of a dimeric protein to form "pI heterodimers" (when the protein is an antibody, these are referred to as "pI antibodies") by incorporating amino acid substitutions ("pI variants" or "pI substitutions") into one or both of the monomers. As shown herein, the separation of the heterodimers from the two homodimers can be accomplished if the pIs of the two monomers differ by as little as 0.1 pH unit, with 0.2, 0.3, 0.4 and 0.5 or greater all finding use in the present invention.

[0091] As will be appreciated by those in the art, the number of pI variants to be included on each or both monomer(s) to get good separation will depend in part on the starting pI of the scFv and Fab of interest. That is, to determine which monomer to engineer or in which "direction" (e.g. more positive or more negative), the Fv sequences of the two target antigens are calculated and a decision is made from there. As is known in the art, different Fvs will have different starting pIs which are exploited in the present invention. In general, as outlined herein, the pIs are engineered to result in a total pI difference of each monomer of at least about 0.1 logs, with 0.2 to 0.5 being preferred as outlined herein.

[0092] Furthermore, as will be appreciated by those in the art and outlined herein, heterodimers can be separated from homodimers on the basis of size. For example, as shown in Figure 8, heterodimers with two scFvs (Figure 8A) can be separated by those of the "triple F" format (figure 8B) and a bispecific mAb (Figure 8C). This can be further exploited in higher valency with additional antigen binding sites being utilized. For example, as additionally shown, one monomer will have two Fab fragments and the other will have one scFv, resulting in a differential in size and thus molecular weight.

[0093] In addition, as will be appreciated by those in the art and outlined herein, the format outlined herein can be expanded to provide trispecific and tetraspecific antibodies as well. In this embodiment, some variations of which are depicted in the Figures, it will be recognized that it is possible that some antigens are bound divalently (e.g. two antigen binding sites to a single antigen; for example, A and B could be part of a typical bivalent association and C and

D can be optionally present and optionally the same or different). As will be appreciated, any combination of Fab and scFvs can be utilized to achieve the desired result and combinations.

[0094] In the case where pI variants are used to achieve heterodimerization, by using the constant region(s) of the heavy chain(s), a more modular approach to designing and purifying multispecific proteins, including antibodies, is provided. Thus, in some embodiments, heterodimerization variants (including skew and purification heterodimerization variants) are not included in the variable regions, such that each individual antibody must be engineered. In addition, in some embodiments, the possibility of immunogenicity resulting from the pI variants is significantly reduced by importing pI variants from different IgG isotypes such that pI is changed without introducing significant immunogenicity. Thus, an additional problem to be solved is the elucidation of low pI constant domains with high human sequence content, e.g. the minimization or avoidance of non-human residues at any particular position.

[0095] In one embodiment, the heterodimeric antibody provides for monovalent engagement of one antigen using a scFv and monovalent engagement of the other antigen using a FAb. As outlined below, this format can also be varied; in some embodiments, there is monovalent engagement of three antigens, divalent engagement of one antigen and monovalent engagement of a second antigen (e.g. A and C are to the same antigen and B is to a different antigen), etc.

[0096] A side benefit that can occur with this pI engineering is also the extension of serum half-life and increased FcRn binding. That is, as described in USSN 13/194,904 (incorporated by reference in its entirety), lowering the pI of antibody constant domains (including those found in antibodies and Fc fusions) can lead to longer serum retention in vivo. These pI variants for increased serum half life also facilitate pI changes for purification.

[0097] Furthermore, as outlined herein, additional amino acid variants may be introduced into the bispecific antibodies of the invention, to add additional functionalities. For example, amino acid changes within the Fc region can be added (either to one monomer or both) to facilitiate increased ADCC or CDC (e.g. altered binding to Fcγ receptors); to allow or increase yield of the addition of toxins and drugs (e.g. for ADC), as well as to increase binding to FcRn and/or increase serum half-life of the resulting molecules. As is further described herein and as will be appreciated by those in the art, any and all of the variants outlined herein can be optionally and independently combined with other variants.

[0098] Similarly, another category of functional variants are "Fcγ ablation variants" or "Fc knock out (FcKO or KO) variants. In these embodiments, for some therapeutic applications, it is desirable to reduce or remove the normal binding of the Fc domain to one or more or all of the Fcγ receptors (e.g. FcγR1, FcγRIIa, FcγRIIb, FcγRIIIa, etc.) to avoid additional mechanisms of action. That is, for example, in many embodiments, it is generally desirable to ablate FcγRIIIa binding to eliminate or significantly reduce ADCC activity.

[0099] In addition, the invention provides novel humanized anti-CD3 sequences, including sets of CDRs, full variable light and heavy chains, as well as the associated scFvs, which can optionally include charged scFv linkers. These optimized sequences can be used in other antibody formats.

[00100] The invention further provides novel anti-CD38 sequences, including sets of CDRs, full variable light and heavy chains, as well as the associated scFvs, which can optionally include charged scFv linkers. These optimized sequences can be used in other antibody formats.

[00101] Accordingly, the present invention provides novel constructs to produce bispecific, bivalent antibodies that bind to both CD3 and CD38.

[00102] In addition, the present invention provides antigen binding domains of differing affinities. That is, in some indications, stronger affinities may be preferred, while in others, lesser affinities can find use, for both anti-CD3 and anti-CD38 sequences. Accordingly, in some embodiments the present invention provides antibody constructs comprising anti-CD3 antigen binding domains that are "strong" or "high affinity" binders to CD3 (e.g. one example are heavy and light variable domains depicted as H1.30_L1.47 (optionally including a charged linker as appropriate)). In other embodiments, the present invention provides antibody constructs comprising anti-CD3 antigen binding domains that are "lite" or "lower affinity" binders to CD3, as shown in Figure 47.

II. Definitions

[00103] In order that the application may be more completely understood, several definitions are set forth below. Such definitions are meant to encompass grammatical equivalents.

[00104] By "ablation" herein is meant a decrease or removal of activity. Thus for example, "ablating FcγR binding" means the Fc region amino acid variant has less than 50% starting binding as compared to an Fc region not containing the specific variant, with less than 70-80-

90-95-98% loss of activity being preferred, and in general, with the activity being below the level of detectable binding in a Biacore assay. Variants of particular use when ablation variants (also sometimes referred to herein as "FcγR ablation variants", "Fc ablation variants", "Fc knock outs" ("FcKO") or "knock out" ("KO") variants) are used are those depicted in Figure 35.

[00105] By "ADCC" or "antibody dependent cell-mediated cytotoxicity" as used herein is meant the cell-mediated reaction wherein nonspecific cytotoxic cells that express FcγRs recognize bound antibody on a target cell and subsequently cause lysis of the target cell. ADCC is correlated with binding to FcγRIIIa; increased binding to FcγRIIIa leads to an increase in ADCC activity.

[00106] By "ADCP" or antibody dependent cell-mediated phagocytosis as used herein is meant the cell-mediated reaction wherein nonspecific cytotoxic cells that express FcγRs recognize bound antibody on a target cell and subsequently cause phagocytosis of the target cell.

[00107] By "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. By "amino acid modification" herein is meant an amino acid substitution, insertion, and/or deletion in a polypeptide sequence. 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.

[00108] 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 example, the substitution E272Y refers to a variant polypeptide, in this case an Fc variant, in which the glutamic acid at position 272 is replaced with tyrosine. 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.

[00109] 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. For example, -233E or 233E designates an insertion of glutamic acid after position 233 and before position 234. Additionally, -233ADE or A233ADE designates an insertion of AlaAspGlu after position 233 and before position 234.

[00110] 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. For example, G236- or G236# or G236del designates a deletion of glycine at position 236. Additionally, EDA233- or EDA233# designates a deletion of the sequence GluAspAla that begins at position 233. Similarly, some of the heterodimerization variants include "K447del", meaning the lysine at position 447 has been deleted.

[00111] By "variant protein" or "protein variant", or "variant" as used herein is meant a protein that differs from that of a parent protein by virtue of at least one amino acid modification. Protein variant may refer to the protein itself, a composition comprising the protein, or the amino sequence that encodes it. Preferably, the protein variant has at least one amino acid modification compared to the parent protein, e.g. from about one to about seventy amino acid modifications, and preferably from about one to about five amino acid modifications compared to the parent. As described below, in some embodiments the parent polypeptide, for example an Fc parent polypeptide, is a human wild type sequence, such as the Fc region from IgG1, IgG2, IgG3 or IgG4, although human sequences with variants can also serve as "parent polypeptides". The protein variant sequence herein will preferably possess at least about 80% identity with a parent protein sequence, and most preferably at least about 90% identity, more preferably at least about 95-98-99% identity . Variant protein can refer to the variant protein itself, compositions comprising the protein variant, or the DNA sequence that encodes it. Accordingly, by "antibody variant" or "variant antibody" as used herein is meant an antibody that differs from a parent antibody by virtue of at least one amino acid modification, "IgG variant" or "variant IgG" as used herein is meant an antibody that differs from a parent IgG (again, in many cases, from a human IgG sequence) by virtue of at least one amino acid modification, and "immunoglobulin variant" or "variant immunoglobulin" as used herein is meant an immunoglobulin sequence that differs from that of a parent immunoglobulin sequence by virtue of at least one amino acid modification. "Fc

variant" or "variant Fc" as used herein is meant a protein comprising an amino acid modification in an Fc domain. The Fc variants of the present invention are defined according to the amino acid modifications that compose them. Thus, for example, N434S or 434S is an Fc variant with the substitution serine at position 434 relative to the parent Fc polypeptide, wherein the numbering is according to the EU index. Likewise, M428L/N434S defines an Fc variant with the substitutions M428L and N434S relative to the parent Fc polypeptide. The identity of the WT amino acid may be unspecified, in which case the aforementioned variant is referred to as 428L/434S. It is noted that the order in which substitutions are provided is arbitrary, that is to say that, for example, 428L/434S is the same Fc variant as M428L/N434S, and so on. For all positions discussed in the present invention that relate to antibodies, unless otherwise noted, amino acid position numbering is according to the EU index. The EU index or EU index as in Kabat or EU numbering scheme refers to the numbering of the EU antibody (Edelman et al., 1969, Proc Natl Acad Sci USA 63:78-85, hereby entirely incorporated by reference.) The modification can be an addition, deletion, or substitution. Substitutions can include naturally occurring amino acids and, in some cases, synthetic amino acids. Examples include U.S. Pat. No. 6,586,207; WO 98/48032; WO 03/073238; US2004-0214988A1; WO 05/35727A2; WO 05/74524A2; J. W. Chin et al., (2002), Journal of the American Chemical Society 124:9026-9027; J. W. Chin, & P. G. Schultz, (2002), ChemBioChem 11:1135-1137; J. W. Chin, et al., (2002), PICAS United States of America 99:11020-11024; and, L. Wang, & P. G. Schultz, (2002), Chem. 1-10, all entirely incorporated by reference.

[00112] As used herein, "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The peptidyl group may comprise naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures, i.e. "analogs", such as peptoids (see Simon et al., PNAS USA 89(20):9367 (1992), entirely incorporated by reference). The amino acids may either be naturally occurring or synthetic (e.g. not an amino acid that is coded for by DNA); as will be appreciated by those in the art. For example, homo-phenylalanine, citrulline, ornithine and noreleucine are considered synthetic amino acids for the purposes of the invention, and both D- and L-(R or S) configured amino acids may be utilized. The variants of the present invention may comprise modifications that include the use of synthetic amino acids incorporated using, for example, the technologies developed by Schultz and colleagues, including but not limited to methods described by Cropp & Shultz, 2004, Trends Genet.

20(12):625-30, Anderson et al., 2004, Proc Natl Acad Sci USA 101 (2):7566-71, Zhang et al., 2003, 303(5656):371-3, and Chin et al., 2003, Science 301(5635):964-7, all entirely incorporated by reference. In addition, polypeptides may include synthetic derivatization of one or more side chains or termini, glycosylation, PEGylation, circular permutation, cyclization, linkers to other molecules, fusion to proteins or protein domains, and addition of peptide tags or labels.

[00113] By "residue" as used herein is meant a position in a protein and its associated amino acid identity. For example, Asparagine 297 (also referred to as Asn297 or N297) is a residue at position 297 in the human antibody IgG1.

[00114] By "Fab" or "Fab region" as used herein is meant the polypeptide that comprises the VH, CH1, VL, and CL immunoglobulin domains. Fab may refer to this region in isolation, or this region in the context of a full length antibody, antibody fragment or Fab fusion protein. By "Fv" or "Fv fragment" or "Fv region" as used herein is meant a polypeptide that comprises the VL and VH domains of a single antibody.

[00115] By "IgG subclass modification" or "isotype modification" as used herein is meant an amino acid modification that converts one amino acid of one IgG isotype to the corresponding amino acid in a different, aligned IgG isotype. For example, because IgG1 comprises a tyrosine and IgG2 a phenylalanine at EU position 296, a F296Y substitution in IgG2 is considered an IgG subclass modification.

[00116] By "non-naturally occurring modification" as used herein is meant an amino acid modification that is not isotypic. For example, because none of the IgGs comprise a serine at position 434, the substitution 434S in IgG1, IgG2, IgG3, or IgG4 (or hybrids thereof) is considered a non-naturally occurring modification. "Isotypic" modifications refer to the importation of one isotype amino acid at a position into the backbone of a different isotype; for example, the importation of an IgG1 amino acid into an IgG2 backbone at the same position.

[00117] By "amino acid" and "amino acid identity" as used herein is meant one of the 20 naturally occurring amino acids that are coded for by DNA and RNA.

[00118] By "effector function" as used herein is meant a biochemical event that results from the interaction of an antibody Fc region with an Fc receptor or ligand. Effector functions include but are not limited to ADCC, ADCP, and CDC.

[00119] By "IgG Fc ligand" as used herein is meant a molecule, preferably a polypeptide, from any organism that binds to the Fc region of an IgG antibody to form an Fc/Fc ligand complex. Fc ligands include but are not limited to FcγRIs, FcγRIIs, FcγRIIIs, FcRn, C1q, C3, mannan binding lectin, mannose receptor, staphylococcal protein A, streptococcal protein G, and viral FcγR. Fc ligands also include Fc receptor homologs (FcRH), which are a family of Fc receptors that are homologous to the FcγRs (Davis et al., 2002, Immunological Reviews 190:123-136, entirely incorporated by reference). Fc ligands may include undiscovered molecules that bind Fc. Particular IgG Fc ligands are FcRn and Fc gamma receptors. By "Fc ligand" as used herein is meant a molecule, preferably a polypeptide, from any organism that binds to the Fc region of an antibody to form an Fc/Fc ligand complex.

[00120] By "Fc gamma receptor", "FcγR" or "FcqammaR" as used herein is meant any member of the family of proteins that bind the IgG antibody Fc region and is encoded by an FcγR gene. In humans this family includes but is not limited to FcγRI (CD64), including isoforms FcγRIa, FcγRIb, and FcγRIc; FcγRII (CD32), including isoforms FcγRIIa (including allotypes H131 and R131), FcγRIIb (including FcγRIIb-1 and FcγRIIb-2), and FcγRIIc; and FcγRIII (CD16), including isoforms FcγRIIIa (including allotypes V158 and F158) and FcγRIIIb (including allotypes FcγRIIb-NA1 and FcγRIIb-NA2) (Jefferis et al., 2002, Immunol Lett 82:57-65, entirely incorporated by reference), as well as any undiscovered human FcγRs or FcγR isoforms or allotypes. An FcγR may be from any organism, including but not limited to humans, mice, rats, rabbits, and monkeys. Mouse FcγRs include but are not limited to FcγRI (CD64), FcγRII (CD32), FcγRIII (CD16), and FcγRIII-2 (CD16-2), as well as any undiscovered mouse FcγRs or FcγR isoforms or allotypes.

[00121] By "FcRn" or "neonatal Fc Receptor" as used herein is meant a protein that binds the IgG antibody Fc region and is encoded at least in part by an FcRn gene. The FcRn may be from any organism, including but not limited to humans, mice, rats, rabbits, and monkeys. As is known in the art, the functional FcRn protein comprises two polypeptides, often referred to as the heavy chain and light chain. The light chain is beta-2-microglobulin and the heavy chain is encoded by the FcRn gene. Unless otherwise noted herein, FcRn or an FcRn protein refers to the complex of FcRn heavy chain with beta-2-microglobulin. A variety of FcRn variants used to increase binding to the FcRn receptor, and in some cases, to increase serum half-life. Fc variants conferring increased binding to the FcRn receptor and corresponding increases in serum half life include, but are not limited to, 434A, 434S, 428L, 308F, 259I,

428L/434S, 259I/308F, 436I/428L, 436I or V/434S, 436V/428L, 252Y, 252Y/254T/256E and 259I/308F/428L. That is, the Triple F format of Figure 8B can have any of these FcRn variants on either or both monomer sequences. For clarity, as each heavy chain is different, FcRn variants (as well as the Fc variants) can reside on one or both monomers.

[00122] By "parent polypeptide" as used herein is meant a starting polypeptide that is subsequently modified to generate a variant. The 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 immunoglobulin" as used herein is meant an unmodified immunoglobulin 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. It should be noted that "parent antibody" includes known commercial, recombinantly produced antibodies as outlined below.

[00123] By "Fc fusion protein" or "immunoadhesin" herein is meant a protein comprising an Fc region, generally linked (optionally through a linker moiety, as described herein) to a different protein, such as a binding moiety to a target protein, as described herein)..

[00124] 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.

[00125] By "strandedness" in the context of the monomers of the heterodimeric proteins of the invention herein is meant that, similar to the two strands of DNA that "match", heterodimerization variants are incorporated into each monomer so as to preserve the ability to "match" to form heterodimers. For example, if some pI variants are engineered into monomer A (e.g. making the pI higher) then steric variants that are "charge pairs" that can be utilized as well do not interfere with the pI variants, e.g. the charge variants that make a pI higher are put on the same "strand" or "monomer" to preserve both functionalities.

[00126] 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. Preferred target antigens of the present invention are CD3 and CD38.

[00127] By "target cell" as used herein is meant a cell that expresses a target antigen.

[00128] By "variable region" as used herein is meant the region of an immunoglobulin that comprises one or more Ig domains substantially encoded by any of the V.kappa., V.lamda., and/or VH genes that make up the kappa, lambda, and heavy chain immunoglobulin genetic loci respectively.

[00129] By "wild type or WT" herein is meant an amino acid sequence or a nucleotide sequence that is found in nature, including allelic variations. A WT protein has an amino acid sequence or a nucleotide sequence that has not been intentionally modified.

[00130] By "single chain variable fragment", "scFv" or "single chain Fv" as is well understood in the art, herein is meant a fusion protein of the variable heavy and light chains of an antibody, usually linked with a linker peptide. Typical scFv linkers are well known in the art, are generally 10 to 25 amino acids in length and include glycines and serines.

[00131] By "charged scFv linker" herein is meant a scFv linker that utilizes charged amino acids for use in the creation and purification of heterodimeric antibodies that include at least one scFv. Suitable charged scFv linkers are shown in Figure, although others can be used. In general, the charged scFv linkers for use in the present invention have a charge change from 3 to 8 (3, 4, 5, 6, 7 or 8 all being possible) as compared to the standard uncharged scFv linkers such as $(GGGGS)_{3-5}$ sequences traditionally used (either negative or positive). As will be appreciated by those in the art, heterodimeric antibodies that utilize two scFvs can have one charged and one neutral linker (e.g. either a positively or negatively charged scFv linker) or two oppositely charged scFv linkers (one positive and one negative).

Heterodimeric Proteins

[00132] The present invention is directed to the generation of multispecific, particularly bispecific binding proteins, and in particular, multispecific antibodies that have one monomer comprising an scFv and the other an Fv. As discussed herein, many of the disclosed embodiments use an scFv that binds CD3 and the Fv (or Fab) that binds CD38. Alternatively, the vh and vl anti-CD38 sequences herein can be used in scFv constructs, where the anti-CD3 monomer is a Fab.

Antibodies

[00133] The present invention relates to the generation of multispecific antibodies, generally therapeutic antibodies. As is discussed below, the term "antibody" is used generally. Antibodies that find use in the present invention can take on a number of formats

as described herein, including traditional antibodies as well as antibody derivatives, fragments and mimetics, described below. In general, the term "antibody" includes any polypeptide that includes at least one constant domain, including, but not limited to, CH1, CH2, CH3 and CL. Particularly preferred antibodies herein are the "triple F" format antibodies.

[00134] Traditional antibody structural units typically comprise a tetramer. Each tetramer is typically composed of two identical pairs of polypeptide chains, each pair having one "light" (typically having a molecular weight of about 25 kDa) and one "heavy" chain (typically having a molecular weight of about 50-70 kDa). Human light chains are classified as kappa and lambda light chains. The present invention is directed to the IgG class, which has several subclasses, including, but not limited to IgG1, IgG2, IgG3, and IgG4. Thus, "isotype" as used herein is meant any of the subclasses of immunoglobulins defined by the chemical and antigenic characteristics of their constant regions. It should be understood that therapeutic antibodies can also comprise hybrids of isotypes and/or subclasses. For example, as shown in US Publication 2009/0163699, incorporated by reference, the present invention covers pI engineering of IgG1/G2 hybrids.

[00135] The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition, generally referred to in the art and herein as the "Fv domain" or "Fv region". In the variable region, three loops are gathered for each of the V domains of the heavy chain and light chain to form an antigen-binding site. Each of the loops is referred to as a complementarity-determining region (hereinafter referred to as a "CDR"), in which the variation in the amino acid sequence is most significant. "Variable" refers to the fact that certain segments of the variable region differ extensively in sequence among antibodies. Variability within the variable region is not evenly distributed. Instead, the V regions consist of relatively invariant stretches called framework regions (FRs) of 15-30 amino acids separated by shorter regions of extreme variability called "hypervariable regions" that are each 9-15 amino acids long or longer.

[00136] Each VH and VL is composed of three hypervariable regions ("complementary determining regions," "CDRs") and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4.

[00137] The hypervariable region 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.

[00138] 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) (e.g, Kabat et al., supra (1991)).

[00139] The CDRs contribute to the formation of the antigen-binding, or more specifically, epitope binding site of antibodies. "Epitope" refers to a determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule 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.

[00140] 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 specifically antigen binding peptide; in other words, the amino acid residue is within the footprint of the specifically antigen binding peptide.

[00141] 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.

[00142] 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."

[00143] The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. Kabat et al. collected numerous primary sequences of the variable regions of heavy chains and light chains. Based on the degree of conservation of the sequences, they classified individual primary sequences into the CDR and the framework and made a list thereof (see SEQUENCES OF IMMUNOLOGICAL INTEREST, 5th edition, NIH publication, No. 91-3242, E.A. Kabat et al., entirely incorporated by reference).

[00144] In the IgG subclass of immunoglobulins, there are several immunoglobulin domains in the heavy chain. By "immunoglobulin (Ig) domain" herein is meant a region of an immunoglobulin having a distinct tertiary structure. Of interest in the present invention are the heavy chain domains, including, the constant heavy (CH) domains and the hinge domains. In the context of IgG antibodies, the IgG isotypes each have three CH regions. Accordingly, "CH" domains in the context of IgG are as follows: "CH1" refers to positions 118-220 according to the EU index as in Kabat. "CH2" refers to positions 237-340 according to the EU index as in Kabat, and "CH3" refers to positions 341-447 according to the EU index as in Kabat. As shown herein and described below, the pI variants can be in one or more of the CH regions, as well as the hinge region, discussed below.

[0143] It should be noted that the sequences depicted herein start at the CH1 region, position 118; the variable regions are not included except as noted. For example, the first amino acid of SEQ ID NO: 2, while designated as position"1" in the sequence listing, corresponds to position 118 of the CH1 region, according to EU numbering.

[0144] Another type of Ig domain of the heavy chain is the hinge region. By "hinge" or "hinge region" or "antibody hinge region" or "immunoglobulin hinge region" herein is meant the flexible polypeptide comprising the amino acids between the first and second constant domains of an antibody. Structurally, the IgG CH1 domain ends at EU position 220, and the IgG CH2 domain begins at residue EU position 237. Thus for IgG the antibody hinge is herein defined to include positions 221 (D221 in IgG1) to 236 (G236 in IgG1), wherein the numbering is according to the EU index as in Kabat. In some embodiments, for example in the context of an Fc region, the lower hinge is included, with the "lower hinge" generally referring to positions 226 or 230. As noted herein, pI variants can be made in the hinge region as well.

[0145] The light chain generally comprises two domains, the variable light domain (containing the light chain CDRs and together with the variable heavy domains forming the Fv region), and a constant light chain region (often referred to as CL or Cκ).

[0146] Another region of interest for additional substitutions, outlined below, is the Fc region. By "Fc" or "Fc region" or "Fc domain" as used herein is meant the polypeptide comprising the constant region of an antibody excluding the first constant region immunoglobulin domain and in some cases, part of the hinge. Thus Fc refers to the last two constant region immunoglobulin domains of IgA, IgD, and IgG, the last three constant region immunoglobulin domains of IgE and IgM, and the flexible hinge N-terminal to these domains. For IgA and IgM, Fc may include the J chain. For IgG, the Fc domain comprises immunoglobulin domains Cγ2 and Cγ3 (Cγ2 and Cγ3) and the lower hinge region between Cγ1 (Cγ1) and Cγ2 (Cγ2). Although the boundaries of the Fc region may vary, the human IgG heavy chain Fc region is usually defined to include residues C226 or P230 to its carboxyl-terminus, wherein the numbering is according to the EU index as in Kabat. In some embodiments, as is more fully described below, amino acid modifications are made to the Fc region, for example to alter binding to one or more FcγR receptors or to the FcRn receptor.

[0147] In some embodiments, the antibodies are full length. By "full length antibody" herein is meant the structure that constitutes the natural biological form of an antibody, including variable and constant regions, including one or more modifications as outlined herein.

[0148] Alternatively, the antibodies can include a variety of structures, including, but not limited to, antibody fragments, monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as "antibody mimetics"), chimeric antibodies, humanized antibodies, antibody fusions (sometimes referred to as "antibody conjugates"), and fragments of each, respectively.

[0149] In one embodiment, the antibody is an antibody fragment, as long as it contains at least one constant domain which can be engineered to produce heterodimers, such as pI engineering. Other antibody fragments that can be used include fragments that contain one or more of the CH1, CH2, CH3, hinge and CL domains of the invention that have been pI engineered. For example, Fc fusions are fusions of the Fc region (CH2 and CH3, optionally with the hinge region) fused to another protein. A number of Fc fusions are known the art and can be improved by the addition of the heterodimerization variants of the invention. In

the present case, antibody fusions can be made comprising CH1; CH1, CH2 and CH3; CH2; CH3; CH2 and CH3; CH1 and CH3, any or all of which can be made optionally with the hinge region, utilizing any combination of heterodimerization variants described herein.

[0150] In some embodiments of the present invention, one monomer comprises a heavy chain comprises a scFV linked to an Fc domain, and the other monomer comprises a heavy chain comprising a Fab linked to an Fc domain, e.g. a "typical" heavy chain, and a light chain. By "Fab" or "Fab region" as used herein is meant the polypeptide that comprises the VH, CH1, VL, and CL immunoglobulin domains. Fab may refer to this region in isolation, or this region in the context of a full length antibody, antibody fragment or Fab fusion protein. By "Fv" or "Fv fragment" or "Fv region" as used herein is meant a polypeptide that comprises the VL and VH domains of a single antibody.

Chimeric and Humanized Antibodies

[0151] In some embodiments, the antibody can be a mixture from different species, e.g. a chimeric antibody and/or a humanized antibody. In general, both "chimeric antibodies" and "humanized antibodies" refer to antibodies that combine regions from more than one species. For example, "chimeric antibodies" traditionally comprise variable region(s) from a mouse (or rat, in some cases) and the constant region(s) from a human. "Humanized antibodies" generally refer to non-human antibodies that have had the variable-domain framework regions swapped for sequences found in human antibodies. Generally, in a humanized antibody, the entire antibody, except the CDRs, is encoded by a polynucleotide of human origin or is identical to such an antibody except within its CDRs. The CDRs, some or all of which are encoded by nucleic acids originating in a non-human organism, are grafted into the beta-sheet framework of a human antibody variable region to create an antibody, the specificity of which is determined by the engrafted CDRs. The creation of such antibodies is described in, e.g., WO 92/11018, Jones, 1986, Nature 321:522-525, Verhoeyen et al., 1988, Science 239:1534-1536, all entirely incorporated by reference. "Backmutation" of selected acceptor framework residues to the corresponding donor residues is often required to regain affinity that is lost in the initial grafted construct (US 5530101; US 5585089; US 5693761; US 5693762; US 6180370; US 5859205; US 5821337; US 6054297; US 6407213, all entirely incorporated by reference). The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region, typically that of a human immunoglobulin, and thus will typically comprise a human Fc region. Humanized antibodies can also be generated using mice with a genetically engineered immune system. Roque et al., 2004,

Biotechnol. Prog. 20:639-654, entirely incorporated by reference. A variety of techniques and methods for humanizing and reshaping non-human antibodies are well known in the art (See Tsurushita & Vasquez, 2004, Humanization of Monoclonal Antibodies, Molecular Biology of B Cells, 533-545, Elsevier Science (USA), and references cited therein, all entirely incorporated by reference). Humanization methods include but are not limited to methods described in Jones et al., 1986, Nature 321:522-525; Riechmann et al.,1988; Nature 332:323-329; Verhoeyen et al., 1988, Science, 239:1534-1536; Queen et al., 1989, Proc Natl Acad Sci, USA 86:10029-33; He et al., 1998, J. Immunol. 160: 1029-1035; Carter et al., 1992, Proc Natl Acad Sci USA 89:4285-9, Presta et al., 1997, Cancer Res. 57(20):4593-9; Gorman et al., 1991, Proc. Natl. Acad. Sci. USA 88:4181-4185; O'Connor et al., 1998, Protein Eng 11:321-8, all entirely incorporated by reference. Humanization or other methods of reducing the immunogenicity of nonhuman antibody variable regions may include resurfacing methods, as described for example in Roguska et al., 1994, Proc. Natl. Acad. Sci. USA 91:969-973, entirely incorporated by reference. In one embodiment, the parent antibody has been affinity matured, as is known in the art. Structure-based methods may be employed for humanization and affinity maturation, for example as described in USSN 11/004,590. Selection based methods may be employed to humanize and/or affinity mature antibody variable regions, including but not limited to methods described in Wu et al., 1999, J. Mol. Biol. 294:151-162; Baca et al., 1997, J. Biol. Chem. 272(16):10678-10684; Rosok et al., 1996, J. Biol. Chem. 271(37): 22611-22618; Rader et al., 1998, Proc. Natl. Acad. Sci. USA 95: 8910-8915; Krauss et al., 2003, Protein Engineering 16(10):753-759, all entirely incorporated by reference. Other humanization methods may involve the grafting of only parts of the CDRs, including but not limited to methods described in USSN 09/810,510; Tan et al., 2002, J. Immunol. 169:1119-1125; De Pascalis et al., 2002, J. Immunol. 169:3076-3084, all entirely incorporated by reference.

Multispecific Antibody Constructs

[0152] As will be appreciated by those in the art and discussed more fully below, the heterodimeric fusion proteins of the present invention take on a number variety of configurations, with a preferred embodiment shown in Figure B as a "triple F" construct.

Heterodimeric Heavy Chain Constant Regions

[0153] Accordingly, the present invention provides heterodimeric proteins based on the use of monomers containing variant heavy chain constant regions as a first domain. By "monomer" herein is meant one half of the heterodimeric protein. It should be noted that

traditional antibodies are actually tetrameric (two heavy chains and two light chains). In the context of the present invention, one pair of heavy-light chains (if applicable, e.g. if the monomer comprises an Fab) is considered a "monomer". Similarly, a heavy chain region comprising the scFv is considered a monomer. Essentially, each monomer comprises sufficient heavy chain constant region to allow heterodimerization engineering, whether that be all the constant region, e.g. Ch1-hinge-CH2-CH3, the Fc region (CH2-CH3), or just the CH3 domain.

[0154] The variant heavy chain constant regions can comprise all or part of the heavy chain constant region, including the full length construct, CH1-hinge-CH2-CH3, or portions thereof, including for example CH2-CH3 or CH3 alone. In addition, the heavy chain region of each monomer can be the same backbone (CH1-hinge-CH2-CH3 or CH2-CH3) or different. N- and C-terminal truncations and additions are also included within the definition; for example, some pI variants include the addition of charged amino acids to the C-terminus of the heavy chain domain.

[0155] Thus, in general, one monomer of the present "triple F" construct is a scFv region-hinge-Fc domain) and the other is (VH-CH1-hinge- CH2-CH3 plus associated light chain), with heterodimerization variants, including steric and pI variants, Fc and FcRn variants, and additional antigen binding domains (with optional linkers) included in these regions.

[0156] In addition to the heterodimerization variants (e.g. steric and pI variants) outlined herein, the heavy chain regions may also contain additional amino acid substitutions, including changes for altering FcγR and FcRn binding as discussed below.

[0157] In addition, some monomers can utilize linkers for the scFv portion of the "bottle-opener". In the Triple F format, one charged scFv linker is used. As noted herein, depending on the inherent pI of the scFv for the target antigen and the inherent pI of the Fab of the other target antigen, the charged scFv linker can either be positive or negative. In dual scFv formats, either a single charged scFv linker is used on one monomer (again, either positive or negative) or both (one positive and one negative). In this embodiment, the charge of each of the two linkers need not be the same (e.g. +3 for one and -4 for the other, etc.).

[0158] In one embodiment, it is the anti-CD3 antigen binding site that is the scFv, and includes a positively charged scFv linker. Alternatively, it can be the anti-CD38 antigen binding site that is the scFv of the "bottle opener" construct.

[0159] The heterodimerization variants include a number of different types of variants, including, but not limited to, steric variants (including charge variants) and pI variants, that can be optionally and independently combined with any other variants. In these embodiments, it is important to match "monomer A" with "monomer B"; that is, if a heterodimeric protein relies on both steric variants and pI variants, these need to be correctly matched to each monomer: e.g. the set of steric variants that work (1 set on monomer A, 1 set on monomer B) is combined with pI variant sets (1 set on monomer A, 1 set on monomer B), such that the variants on each monomer are designed to achieve the desired function. In the case for example where steric variants may also change the charge, the correct sets have to be matched to the correct monomer.

[0160] It is important to note that the heterodimerization variants outlined herein (for example, including but not limited to those variants shown in the Figures), can be optionally and independently combined with any other variants, and on any other monomer. Thus, for example, pI variants for monomer 1 from one figure can be added to other heterodimerization variants for monomer 1 in a different figure or from monomer 2. That is, what is important for the heterodimerization is that there are "sets" of variants, one set for one monomer and one set for the other. Whether these are combined from the Figures 1 to 1 (e.g. monomer 1 listings can go together) or switched (monomer 1 pI variants with monomer 2 steric variants) is irrelevant. However, as noted herein, "strandedness" should be preserved when combinations are made as outlined above such that heterodimerization is favored; e.g. charge variants that increase pI should be used with increased pI variants and/or an scFv linker with increase pI, etc. Furthermore, for the additional Fc variants (such as for FcγR binding, FcRn binding, ablation variants etc.), either monomer, or both monomers, can include any of the listed variants, independently and optionally. In some cases, both monomers have the additional variants and in some only one monomer has the additional variants, or they can be combined.

Heterodimerization Variants

[0161] The present invention provides multispecific antibody formats, on a "triple F" or "bottle opener" scaffold as depicted in Figure 8B, for example.

Steric Variants

[0162] In some embodiments, the formation of heterodimers can be facilitated by the addition of steric variants. That is, by changing amino acids in each heavy chain, different heavy chains are more likely to associate to form the heterodimeric structure than to form

homodimers with the same Fc amino acid sequences. Suitable steric variants are shown in the Figures

[0163] One mechanism is generally referred to in the art as "knobs and holes", referring to amino acid engineering that creates steric influences to favor heterodimeric formation and disfavor homodimeric formation can also optionally be used; this is sometimes referred to as "knobs and holes", as described in USSN 61/596,846, Ridgway et al., Protein Engineering 9(7):617 (1996); Atwell et al., J. Mol. Biol. 1997 270:26; US Patent No. 8,216,805, all of which are hereby incorporated by reference in their entirety. Figures 4 and 5, further described below, identifies a number of "monomer A – monomer B" pairs that rely on "knobs and holes". In addition, as described in Merchant et al., Nature Biotech. 16:677 (1998), these "knobs and hole" mutations can be combined with disulfide bonds to skew formation to heterodimerization.

[0164] An additional mechanism that finds use in the generation of heterodimers is sometimes referred to as "electrostatic steering" as described in Gunasekaran et al., J. Biol. Chem. 285(25):19637 (2010), hereby incorporated by reference in its entirety. This is sometimes referred to herein as "charge pairs". In this embodiment, electrostatics are used to skew the formation towards heterodimerization. As those in the art will appreciate, these may also have have an effect on pI, and thus on purification, and thus could in some cases also be considered pI variants. However, as these were generated to force heterodimerization and were not used as purification tools, they are classified as "steric variants". These include, but are not limited to, variants resulting in greater than 75% heterodimerization in the Figures such as D221E/P228E/L368E paired with D221R/P228R/K409R (e.g. these are "monomer corresponding sets) and C220E/P228E/368E paired with C220R/E224R/P228R/K409R.

[0165] Additional monomer A and monomer B variants that can be combined with other variants, optionally and independently in any amount, such as pI variants outlined herein or other steric variants that are shown in Figure 37 of US 2012/0149876, the figure and legend of which are incorporated expressly by reference herein.

[0166] In some embodiments, the steric variants outlined herein can be optionally and independently incorporated with any heterodimerization variants including pI variants (or other variants such as Fc variants, FcRn variants, ablation variants, etc.) into one or both monomers.

pI (Isoelectric point) Variants for Heterodimers

[0167] In general, as will be appreciated by those in the art, there are two general categories of pI variants: those that increase the pI of the protein (basic changes) and those that decrease the pI of the protein (acidic changes). As described herein, all combinations of these variants can be done: one monomer may be wild type, or a variant that does not display a significantly different pI from wild-type, and the other can be either more basic or more acidic. Alternatively, each monomer is changed, one to more basic and one to more acidic.

[0168] Preferred combinations of pI variants are shown in the Figures.

Heavy Chain Acidic pI Changes

[0169] Accordingly, when one monomer comprising a variant heavy chain constant domain is to be made more positive (e.g. lower the pI), one or more of the following substitutions can be made: S119E, K133E, K133Q, T164E, K205E, K205Q, N208D, K210E, K210Q, K274E, K320E, K322E, K326E, K334E, R355E, K392E, a deletion of K447, adding peptide DEDE at the c-terminus, G137E, N203D, K274Q, R355Q, K392N and Q419E. As outlined herein and shown in the figures, these changes are shown relative to IgG1, but all isotypes can be altered this way, as well as isotype hybrids.

[0170] In the case where the heavy chain constant domain is from IgG2-4, R133E and R133Q can also be used.

Basic pI changes

[0171] Accordingly, when one monomer comprising a variant heavy chain constant domain is to be made more negative (e.g. increase the pI), one or more of the following substitutions can be made: Q196K, P217R, P228R, N276K and H435R. As outlined herein and shown in the figures, these changes are shown relative to IgG1, but all isotypes can be altered this way, as well as isotype hybrids.

Antibody Heterodimers Light chain variants

[0172] In the case of antibody based heterodimers, e.g. where at least one of the monomers comprises a light chain in addition to the heavy chain domain, pI variants can also be made in the light chain. Amino acid substitutions for lowering the pI of the light chain include, but are not limited to, K126E, K126Q, K145E, K145Q, N152D, S156E, K169E, S202E, K207E and adding peptide DEDE at the c-terminus of the light chain. Changes in this category based on the constant lambda light chain include one or more substitutions at R108Q, Q124E,

K126Q, N138D, K145T and Q199E. In addition, increasing the pI of the light chains can also be done.

Isotypic Variants

[0173] In addition, many embodiments of the invention rely on the "importation" of pI amino acids at particular positions from one IgG isotype into another, thus reducing or eliminating the possibility of unwanted immunogenicity being introduced into the variants. That is, IgG1 is a common isotype for therapeutic antibodies for a variety of reasons, including high effector function. However, the heavy constant region of IgG1 has a higher pI than that of IgG2 (8.10 versus 7.31). By introducing IgG2 residues at particular positions into the IgG1 backbone, the pI of the resulting monomer is lowered (or increased) and additionally exhibits longer serum half-life. For example, IgG1 has a glycine (pI 5.97) at position 137, and IgG2 has a glutamic acid (pI 3.22); importing the glutamic acid will affect the pI of the resulting protein. As is described below, a number of amino acid substitutions are generally required to significant affect the pI of the variant antibody. However, it should be noted as discussed below that even changes in IgG2 molecules allow for increased serum half-life.

[0174] In other embodiments, non-isotypic amino acid changes are made, either to reduce the overall charge state of the resulting protein (e.g. by changing a higher pI amino acid to a lower pI amino acid), or to allow accommodations in structure for stability, etc. as is more further described below.

[0175] In addition, by pI engineering both the heavy and light constant domains, significant changes in each monomer of the heterodimer can be seen. As discussed herein, having the pIs of the two monomers differ by at least 0.5 can allow separation by ion exchange chromatography or isoelectric focusing, or other methods sensitive to isoelectric point.

Isosteric Variants

[0176] In addition, as shown in Figure 47, pI variants that are isosteric, e.g. charge variants that are roughly the same size as the parent amino acid can be made.

Calculating pI

[0177] The pI of each monomer can depend on the pI of the variant heavy chain constant domain and the pI of the total monomer, including the variant heavy chain constant domain and the fusion partner. Thus, in some embodiments, the change in pI is calculated on the basis of the variant heavy chain constant domain, using the chart in the Figures.

Alternatively, the pI of each monomer can be compared. Similarly, the pIs of the "starting" variable regions (e.g. either scFv or Fab) are calculated to inform which monomer will be engineered in which direction.

pI Variants that also confer better FcRn in vivo binding

[0178] In the case where the pI variant decreases the pI of the monomer, they can have the added benefit of improving serum retention in vivo.

[0179] Although still under examination, Fc regions are believed to have longer half-lives *in vivo*, because binding to FcRn at pH 6 in an endosome sequesters the Fc (Ghetie and Ward, 1997 Immunol Today. 18(12): 592-598, entirely incorporated by reference). The endosomal compartment then recycles the Fc to the cell surface. Once the compartment opens to the extracellular space, the higher pH, ~7.4, induces the release of Fc back into the blood. In mice, Dall' Acqua et al. showed that Fc mutants with increased FcRn binding at pH 6 and pH 7.4 actually had reduced serum concentrations and the same half life as wild-type Fc (Dall' Acqua et al. 2002, J. Immunol. 169:5171-5180, entirely incorporated by reference). The increased affinity of Fc for FcRn at pH 7.4 is thought to forbid the release of the Fc back into the blood. Therefore, the Fc mutations that will increase Fc's half-life *in vivo* will ideally increase FcRn binding at the lower pH while still allowing release of Fc at higher pH. The amino acid histidine changes its charge state in the pH range of 6.0 to 7.4. Therefore, it is not surprising to find His residues at important positions in the Fc/FcRn complex.

[0180] Recently it has been suggested that antibodies with variable regions that have lower isoelectric points may also have longer serum half-lives (Igawa et al., 2010 PEDS. 23(5): 385-392, entirely incorporated by reference). However, the mechanism of this is still poorly understood. Moreover, variable regions differ from antibody to antibody. Constant region variants with reduced pI and extended half-life would provide a more modular approach to improving the pharmacokinetic properties of antibodies, as described herein.

[0181] pI variants that find use in this embodiment, as well as their use for purification optimization, are disclosed in the Figures.

Combination of Variants

[0182] As will be appreciated by those in the art, all of the recited heterodimerization variants can be optionally and independently combined in any way, as long as they retain their "strandedness" or "monomer partition". In addition, all of these variants can be combined into any of the heterodimerization formats.

[0183] In the case of pI variants, while embodiments finding particular use are shown in the Figures, other combinations can be generated, following the basic rule of altering the pI difference between two monomers to facilitate purification.

[0184] The antibodies of the present invention are generally isolated or recombinant. "Isolated," when used to describe the various polypeptides disclosed herein, means a polypeptide that has been identified and separated and/or recovered from a cell or cell culture from which it was expressed. Ordinarily, an isolated polypeptide will be prepared by at least one purification step. An "isolated antibody," refers to an antibody which is substantially free of other antibodies having different antigenic specificities.

[0185] "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.

[0186] 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.

[0187] 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.

Modified Antibodies

[0188] In addition to the modifications outlined above, other modifications can be made. For example, the molecules may be stabilized by the incorporation of disulphide bridges linking the VH and VL domains (Reiter et al., 1996, Nature Biotech. 14:1239-1245, entirely

incorporated by reference). In addition, there are a variety of covalent modifications of antibodies that can be made as outlined below.

[0189] Covalent modifications of antibodies are included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the antibody are introduced into the molecule by reacting specific amino acid residues of the antibody with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues.

[0190] Cysteinyl residues most commonly are reacted with α-haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues may also be derivatized by reaction with bromotrifluoroacetone, α-bromo-β-(5-imidozoyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole and the like.

[0191] In addition, modifications at cysteines are particularly useful in antibody-drug conjugate (ADC) applications, further described below. In some embodiments, the constant region of the antibodies can be engineered to contain one or more cysteines that are particularly "thiol reactive", so as to allow more specific and controlled placement of the drug moiety. See for example US Patent No. 7,521,541, incorporated by reference in its entirety herein.

[0192] Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1M sodium cacodylate at pH 6.0.

[0193] Lysinyl and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[0194] Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin.

Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[0195] The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl residues are iodinated using 125I or 131I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

[0196] Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides (R'—N=C=N--R'), where R and R' are optionally different alkyl groups, such as 1-cyclohexyl-3-(2-morpholinyl-4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

[0197] Derivatization with bifunctional agents is useful for crosslinking antibodies to a water-insoluble support matrix or surface for use in a variety of methods, in addition to methods described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis (succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cynomolgusogen bromide-activated carbohydrates and the reactive substrates described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440, all entirely incorporated by reference, are employed for protein immobilization.

[0198] Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[0199] Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine,

arginine, and histidine side chains (T. E. Creighton, Proteins: Structure and Molecular Properties, W. H. Freeman & Co., San Francisco, pp. 79-86 [1983], entirely incorporated by reference), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[0200] In addition, as will be appreciated by those in the art, labels (including fluorescent, enzymatic, magnetic, radioactive, etc. can all be added to the antibodies (as well as the other compositions of the invention).

Glycosylation

[0201] Another type of covalent modification is alterations in glycosylation. In another embodiment, the antibodies disclosed herein can be modified to include one or more engineered glycoforms. By "engineered glycoform" as used herein is meant a carbohydrate composition that is covalently attached to the antibody, wherein said carbohydrate composition differs chemically from that of a parent antibody. Engineered glycoforms may be useful for a variety of purposes, including but not limited to enhancing or reducing effector function. A preferred form of engineered glycoform is afucosylation, which has been shown to be correlated to an increase in ADCC function, presumably through tighter binding to the FcγRIIIa receptor. In this context, "afucosylation" means that the majority of the antibody produced in the host cells is substantially devoid of fucose, e.g. 90-95-98% of the generated antibodies do not have appreciable fucose as a component of the carbohydrate moiety of the antibody (generally attached at N297 in the Fc region). Defined functionally, afucosylated antibodies generally exhibit at least a 50% or higher affinity to the FcγRIIIa receptor.

[0202] Engineered glycoforms may be generated by a variety of methods known in the art (Umaña et al., 1999, Nat Biotechnol 17:176-180; Davies et al., 2001, Biotechnol Bioeng 74:288-294; Shields et al., 2002, J Biol Chem 277:26733-26740; Shinkawa et al., 2003, J Biol Chem 278:3466-3473; US 6,602,684; USSN 10/277,370; USSN 10/113,929; PCT WO 00/61739A1; PCT WO 01/29246A1; PCT WO 02/31140A1; PCT WO 02/30954A1, all entirely incorporated by reference; (Potelligent® technology [Biowa, Inc., Princeton, NJ]; GlycoMAb® glycosylation engineering technology [Glycart Biotechnology AG, Zürich, Switzerland]). Many of these techniques are based on controlling the level of fucosylated and/or bisecting oligosaccharides that are covalently attached to the Fc region, for example by expressing an IgG in various organisms or cell lines, engineered or otherwise (for example Lec-13 CHO cells or rat hybridoma YB2/0 cells, by regulating enzymes involved in the

glycosylation pathway (for example FUT8 [α1,6-fucosyltranserase] and/or β1-4- N-acetylglucosaminyltransferase III [GnTIII]), or by modifying carbohydrate(s) after the IgG has been expressed. For example, the "sugar engineered antibody" or "SEA technology" of Seattle Genetics functions by adding modified saccharides that inhibit fucosylation during production; see for example 20090317869, hereby incorporated by reference in its entirety. Engineered glycoform typically refers to the different carbohydrate or oligosaccharide; thus an antibody can include an engineered glycoform.

[0203] Alternatively, engineered glycoform may refer to the IgG variant that comprises the different carbohydrate or oligosaccharide. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (e.g., the presence or absence of particular glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Particular expression systems are discussed below.

[0204] Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[0205] Addition of glycosylation sites to the antibody is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the antibody amino acid sequence is preferably altered through changes at the DNA level, particularly by mutating the DNA encoding the target polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[0206] Another means of increasing the number of carbohydrate moieties on the antibody is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has

glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330 and in Aplin and Wriston, 1981, CRC Crit. Rev. Biochem., pp. 259-306, both entirely incorporated by reference.

[0207] Removal of carbohydrate moieties present on the starting antibody (e.g. post-translationally) may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin et al., 1987, Arch. Biochem. Biophys. 259:52 and by Edge et al., 1981, Anal. Biochem. 118:131, both entirely incorporated by reference. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., 1987, Meth. Enzymol. 138:350, entirely incorporated by reference. Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as described by Duskin et al., 1982, J. Biol. Chem. 257:3105, entirely incorporated by reference. Tunicamycin blocks the formation of protein-N-glycoside linkages.

[0208] Another type of covalent modification of the antibody comprises linking the antibody to various nonproteinaceous polymers, including, but not limited to, various polyols such as polyethylene glycol, polypropylene glycol or polyoxyalkylenes, in the manner set forth in, for example, 2005-2006 PEG Catalog from Nektar Therapeutics (available at the Nektar website) US Patents 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337, all entirely incorporated by reference. In addition, as is known in the art, amino acid substitutions may be made in various positions within the antibody to facilitate the addition of polymers such as PEG. See for example, U.S. Publication No. 2005/0114037A1, entirely incorporated by reference.

Additional Fc Variants for Additional Functionality

[0209] In addition to pI amino acid variants, there are a number of useful Fc amino acid modification that can be made for a variety of reasons, including, but not limited to, altering binding to one or more FcγR receptors, altered binding to FcRn receptors, etc.

[0210] Accordingly, the proteins of the invention can include amino acid modifications, including the heterodimerization variants outlined herein, which includes the pI variants

FcγR Variants

[0211] Accordingly, there are a number of useful Fc substitutions that can be made to alter binding to one or more of the FcγR receptors. Substitutions that result in increased binding as well as decreased binding can be useful. For example, it is known that increased binding to Fc RIIIa generally results in increased ADCC (antibody dependent cell-mediated cytotoxicity; the cell-mediated reaction wherein nonspecific cytotoxic cells that express FcγRs recognize bound antibody on a target cell and subsequently cause lysis of the target cell). Similarly, decreased binding to FcγRIIb (an inhibitory receptor) can be beneficial as well in some circumstances. Amino acid substitutions that find use in the present invention include those listed in USSNs 11/124,620 (particularly Figure 41), 11/174,287, 11/396,495, 11/538,406, all of which are expressly incorporated herein by reference in their entirety and specifically for the variants disclosed therein. Particular variants that find use include, but are not limited to, 236A, 239D, 239E, 332E, 332D, 239D/332E, 267D, 267E, 328F, 267E/328F, 236A/332E, 239D/332E/330Y, 239D, 332E/330L and 299T.

[0212] In addition, there are additional Fc substitutions that find use in increased binding to the FcRn receptor and increased serum half life, as specifically disclosed in USSN 12/341,769, hereby incorporated by reference in its entirety, including, but not limited to, 434S, 428L, 308F, 259I, 428L/434S, 259I/308F, 436I/428L, 436I or V/434S, 436V/428L and 259I/308F/428L.

Fc Ablation Variants

[0213] Additional variants which find use in the present invention are those that ablate (e.g. reduce or eliminate) binding to Fcγ receptors. This can be desirable to reduce the potential mechanisms of action (e.g. reduce ADCC activity) of the heterodimeric antibodies of the invention. A number of suitable Fc ablation variants are depicted in Figure 35, and can be optionally and independently included or excluded in combination with any other heterodimerization variants, including pI and steric variants.

[0214] Of particular use in some embodiments are a first monomer (the "negative side") that contains the pI variants N208D/Q295E/N384D/Q418E/N421D, skew variants 368D/370S, and ablation variants E233P/L234V/L235A/G236del/S267K, paired with a positive side comprising no pI variants, skew variants S364K/E357Q and and ablation

variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker (particularly when the scFv is anti-CD3). A second embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/Q419E/K447del, skew variants S364K/E357Q and and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side comprising pI variants Q196K/I199T/P271R/P228R/N276K, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker (particularly when the scFv is anti-CD3). A third embodiment utilizes utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447del, skew variants S364K/E357Q and and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side monomer with no pI variants, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker (particularly when the scFv is anti-CD3). A fourth embodiment a first monomer (the "negative side") that contains the pI variants N208D/Q295E/N384D/Q418E/N421D, skew variants 368D/370S, and ablation variants E233P/L234V/L235A/G236del/S239K, paired with a positive side comprising no pI variants, skew variants S364K/E357Q and and ablation variants E233P/L234V/L235A/G236del/S239K (optionally both monomers containing FcRn variants 428L/434S). A fifth embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/Q419E/K447del, skew variants S364K/E357Q and and ablation variants E233P/L234V/L235A/G236del/S239K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side comprising pI variants Q196K/I199T/P271R/P228R/N276K, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S239K (optionally both monomers containing FcRn variants 428L/434S). A sixth embodiment utilizes utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447del, skew variants S364K/E357Q and and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side monomer skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S239K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is

the scFv monomer and contains a charged scFv linker (particularly when the scFv is anti-CD3). A seventh embodiment utilizes a first monomer (the "negative side") that contains the pI variants N208D/Q295E/N384D/Q418E/N421D, skew variants 368D/370S, and ablation variants S239K/S267K, paired with a positive side comprising no pI variants, skew variants S364K/E357Q and and ablation variants S239K/S267K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker (particularly when the scFv is anti-CD3). An eighth embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/Q419E/K447del, skew variants S364K/E357Q and and ablation variants S239K/S267K, (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side comprising pI variants Q196K/I199T/P271R/P228R/N276K, skew variants S364K/E357Q and ablation variants S239K/S267K, (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker (particularly when the scFv is anti-CD3). A ninth embodiment utilizes utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447del, skew variants S364K/E357Q and and ablation variants S239K/S267K, (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side monomer with no pI variants, skew variants S364K/E357Q and ablation variants S239K/S267K, (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker (particularly when the scFv is anti-CD3). A tenth embodiment utilizes a first monomer (the "negative side") that contains the pI variants N208D/Q295E/N384D/Q418E/N421D, skew variants 368D/370S, and ablation variants S267K/P329K, paired with a positive side comprising no pI variants, skew variants S364K/E357Q and and ablation variants S267K/P329K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker (particularly when the scFv is anti-CD3). An eleventh embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/Q419E/K447del, skew variants S364K/E357Q and and ablation variants S267K/P329K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side comprising pI variants Q196K/I199T/P271R/P228R/N276K, skew variants S364K/E357Q and ablation variants S267K/P329K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker (particularly when the

scFv is anti-CD3). A 12th embodiment utilizes utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447del, skew variants S364K/E357Q and and ablation variants S267K/P329K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side monomer with no pI variants, skew variants S364K/E357Q and ablation variants S267K/P329K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker (particularly when the scFv is anti-CD3).

Linkers

[0215] The present invention optionally provides linkers as needed, for example in the addition of additional antigen binding sites, as depicted for example in Figures 11, 12 and 13, where "the other end" of the molecule contains additional antigen binding components. In addition, as outlined below, linkers are optionally also used in antibody drug conjugate (ADC) systems. When used to join the components of the central mAb-Fv constructs, the linker is generally a polypeptide comprising two or more amino acid residues joined by peptide bonds and are used to link one or more of the components of the present invention. Such linker polypeptides are well known in the art (see e.g., Holliger, P., et al. (1993) Proc. Natl. Acad. Sci. USA 90:6444-6448; Poljak, R. J., et al. (1994) Structure 2:1121-1123). A variety of linkers may find use in some embodiments described herein. As will be appreciated by those in the art, there are at least three different linker types used in the present invention.

[0216] "Linker" herein is also referred to as "linker sequence", "spacer", "tethering sequence" or grammatical equivalents thereof. Homo-or hetero-bifunctional linkers as are well known (see, 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated entirely by reference). (Note the distinction between generic "linkers" and "scFv linkers and "charged scFv linkers"). A number of strategies may be used to covalently link molecules together. These include, but are not limited to polypeptide linkages between N- and C-termini of proteins or protein domains, linkage via disulfide bonds, and linkage via chemical cross-linking reagents. In one aspect of this embodiment, the linker is a peptide bond, generated by recombinant techniques or peptide synthesis. The linker peptide may predominantly include the following amino acid residues: Gly, Ser, Ala, or Thr. The linker peptide should have a length that is adequate to link two molecules in such a way that they assume the correct conformation relative to one another so that they retain the desired activity. In one embodiment, the linker is from about 1 to 50 amino acids in length,

preferably about 1 to 30 amino acids in length. In one embodiment, linkers of 1 to 20 amino acids in length may be used. Useful linkers include glycine-serine polymers, including for example (GS)n, (GSGGS)n, (GGGGS)n, and (GGGS)n, where n is an integer of at least one, glycine-alanine polymers, alanine-serine polymers, and other flexible linkers. Alternatively, a variety of nonproteinaceous polymers, including but not limited to polyethylene glycol (PEG), polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol, may find use as linkers, that is may find use as linkers.

[0217] Other linker sequences may include any sequence of any length of CL/CH1 domain but not all residues of CL/CH1 domain; for example the first 5-12 amino acid residues of the CL/CH1 domains. Linkers can be derived from immunoglobulin light chain, for example Cκ or Cλ. Linkers can be derived from immunoglobulin heavy chains of any isotype, including for example Cγ1, Cγ2, Cγ3, Cγ4, Cα1, Cα2, Cδ, Cε, and Cμ. Linker sequences may also be derived from other proteins such as Ig-like proteins (e.g. TCR, FcR, KIR), hinge region-derived sequences, and other natural sequences from other proteins.

Antibody-Drug Conjugates

[0218] In some embodiments, the multispecific antibodies of the invention are conjugated with drugs to form antibody-drug conjugates (ADCs). In general, ADCs are used in oncology applications, where the use of antibody-drug conjugates for the local delivery of cytotoxic or cytostatic agents allows for the targeted delivery of the drug moiety to tumors, which can allow higher efficacy, lower toxicity, etc. An overview of this technology is provided in Ducry et al., Bioconjugate Chem., 21:5-13 (2010), Carter et al., Cancer J. 14(3):154 (2008) and Senter, Current Opin. Chem. Biol. 13:235-244 (2009), all of which are hereby incorporated by reference in their entirety.

[0219] Thus the invention provides multispecific antibodies conjugated to drugs. Generally, conjugation is done by covalent attachment to the antibody, as further described below, and generally relies on a linker, often a peptide linkage (which, as described below, may be designed to be sensitive to cleavage by proteases at the target site or not). In addition, as described above, linkage of the linker-drug unit (LU-D) can be done by attachment to cysteines within the antibody. As will be appreciated by those in the art, the number of drug moieties per antibody can change, depending on the conditions of the reaction, and can vary from 1:1 to 10:1 drug:antibody. As will be appreciated by those in the art, the actual number is an average.

[0220] Thus the invention provides multispecific antibodies conjugated to drugs. As described below, the drug of the ADC can be any number of agents, including but not limited to cytotoxic agents such as chemotherapeutic agents, growth inhibitory agents, toxins (for example, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (that is, a radioconjugate) are provided. In other embodiments, the invention further provides methods of using the ADCs.

[0221] Drugs for use in the present invention include cytotoxic drugs, particularly those which are used for cancer therapy. Such drugs include, in general, DNA damaging agents, anti-metabolites, natural products and their analogs. Exemplary classes of cytotoxic agents include the enzyme inhibitors such as dihydrofolate reductase inhibitors, and thymidylate synthase inhibitors, DNA intercalators, DNA cleavers, topoisomerase inhibitors, the anthracycline family of drugs, the vinca drugs, the mitomycins, the bleomycins, the cytotoxic nucleosides, the pteridine family of drugs, diynenes, the podophyllotoxins, dolastatins, maytansinoids, differentiation inducers, and taxols.

[0222] Members of these classes include, for example, methotrexate, methopterin, dichloromethotrexate, 5-fluorouracil, 6-mercaptopurine, cytosine arabinoside, melphalan, leurosine, leurosideine, actinomycin, daunorubicin, doxorubicin, mitomycin C, mitomycin A, caminomycin, aminopterin, tallysomycin, podophyllotoxin and podophyllotoxin derivatives such as etoposide or etoposide phosphate, vinblastine, vincristine, vindesine, taxanes including taxol, taxotere retinoic acid, butyric acid, N8-acetyl spermidine, camptothecin, calicheamicin, esperamicin, ene-diynes, duocarmycin A, duocarmycin SA, calicheamicin, camptothecin, maytansinoids (including DM1), monomethylauristatin E (MMAE), monomethylauristatin F (MMAF), and maytansinoids (DM4) and their analogues.

[0223] Toxins may be used as antibody-toxin conjugates and include bacterial toxins such as diphtheria toxin, plant toxins such as ricin, small molecule toxins such as geldanamycin (Mandler et al (2000) J. Nat. Cancer Inst. 92(19):1573-1581; Mandler et al (2000) Bioorganic & Med. Chem. Letters 10:1025-1028; Mandler et al (2002) Bioconjugate Chem. 13:786-791), maytansinoids (EP 1391213; Liu et al., (1996) Proc. Natl. Acad. Sci. USA 93:8618-8623), and calicheamicin (Lode et al (1998) Cancer Res. 58:2928; Hinman et al (1993) Cancer Res. 53:3336-3342). Toxins may exert their cytotoxic and cytostatic effects by mechanisms including tubulin binding, DNA binding, or topoisomerase inhibition.

[0224] Conjugates of a multispecific antibody and one or more small molecule toxins, such as a maytansinoids, dolastatins, auristatins, a trichothecene, calicheamicin, and CC1065, and the derivatives of these toxins that have toxin activity, are contemplated.

Maytansinoids

[0225] Maytansine compounds suitable for use as maytansinoid drug moieties are well known in the art, and can be isolated from natural sources according to known methods, produced using genetic engineering techniques (see Yu et al (2002) PNAS 99:7968-7973), or maytansinol and maytansinol analogues prepared synthetically according to known methods. As described below, drugs may be modified by the incorporation of a functionally active group such as a thiol or amine group for conjugation to the antibody.

[0226] Exemplary maytansinoid drug moieties include those having a modified aromatic ring, such as: C-19-dechloro (U.S. Pat. No. 4,256,746) (prepared by lithium aluminum hydride reduction of ansamytocin P2); C-20-hydroxy (or C-20-demethyl) +/-C-19-dechloro (U.S. Pat. Nos. 4,361,650 and 4,307,016) (prepared by demethylation using Streptomyces or Actinomyces or dechlorination using LAH); and C-20-demethoxy, C-20-acyloxy (--OCOR), +/-dechloro (U.S. Pat. No. 4,294,757) (prepared by acylation using acyl chlorides) and those having modifications at other positions

[0227] Exemplary maytansinoid drug moieties also include those having modifications such as: C-9-SH (U.S. Pat. No. 4,424,219) (prepared by the reaction of maytansinol with H2S or P2S5); C-14-alkoxymethyl(demethoxy/CH2OR) (U.S. Pat. No. 4,331,598); C-14-hydroxymethyl or acyloxymethyl (CH2OH or CH2OAc) (U.S. Pat. No. 4,450,254) (prepared from Nocardia); C-15-hydroxy/acyloxy (U.S. Pat. No. 4,364,866) (prepared by the conversion of maytansinol by Streptomyces); C-15-methoxy (U.S. Pat. Nos. 4,313,946 and 4,315,929) (isolated from Trewia nudlflora); C-18-N-demethyl (U.S. Pat. Nos. 4,362,663 and 4,322,348) (prepared by the demethylation of maytansinol by Streptomyces); and 4,5-deoxy (U.S. Pat. No. 4,371,533) (prepared by the titanium trichloride/LAH reduction of maytansinol).

[0228] Of particular use are DM1 (disclosed in US Patent No. 5,208,020, incorporated by reference) and DM4 (disclosed in US Patent No. 7,276,497, incorporated by reference). See also a number of additional maytansinoid derivatives and methods in 5,416,064, WO/01/24763, 7,303,749, 7,601,354, USSN 12/631,508, WO02/098883, 6,441,163,

7,368,565, WO02/16368 and WO04/1033272, all of which are expressly incorporated by reference in their entirety.

[0229] ADCs containing maytansinoids, methods of making same, and their therapeutic use are disclosed, for example, in U.S. Pat. Nos. 5,208,020; 5,416,064; 6,441,163 and European Patent EP 0 425 235 B1, the disclosures of which are hereby expressly incorporated by reference. Liu et al., Proc. Natl. Acad. Sci. USA 93:8618-8623 (1996) described ADCs comprising a maytansinoid designated DM1 linked to the monoclonal antibody C242 directed against human colorectal cancer. The conjugate was found to be highly cytotoxic towards cultured colon cancer cells, and showed antitumor activity in an in vivo tumor growth assay.

[0230] Chari et al., Cancer Research 52:127-131 (1992) describe ADCs in which a maytansinoid was conjugated via a disulfide linker to the murine antibody A7 binding to an antigen on human colon cancer cell lines, or to another murine monoclonal antibody TA.1 that binds the HER-2/neu oncogene. The cytotoxicity of the TA.1-maytansonoid conjugate was tested in vitro on the human breast cancer cell line SK-BR-3, which expresses 3x105 HER-2 surface antigens per cell. The drug conjugate achieved a degree of cytotoxicity similar to the free maytansinoid drug, which could be increased by increasing the number of maytansinoid molecules per antibody molecule. The A7-maytansinoid conjugate showed low systemic cytotoxicity in mice.

Auristatins and Dolastatins

[0231] In some embodiments, the ADC comprises a multispecific antibody conjugated to dolastatins or dolostatin peptidic analogs and derivatives, the auristatins (U.S. Pat. Nos. 5,635,483; 5,780,588). Dolastatins and auristatins have been shown to interfere with microtubule dynamics, GTP hydrolysis, and nuclear and cellular division (Woyke et al (2001) Antimicrob. Agents and Chemother. 45(12):3580-3584) and have anticancer (U.S. Pat. No. 5,663,149) and antifungal activity (Pettit et al (1998) Antimicrob. Agents Chemother. 42:2961-2965). The dolastatin or auristatin drug moiety may be attached to the antibody through the N (amino) terminus or the C (carboxyl) terminus of the peptidic drug moiety (WO 02/088172).

[0232] Exemplary auristatin embodiments include the N-terminus linked monomethylauristatin drug moieties DE and DF, disclosed in "Senter et al, Proceedings of the American Association for Cancer Research, Volume 45, Abstract Number 623, presented

Mar. 28, 2004 and described in United States Patent Publication No. 2005/0238648, the disclosure of which is expressly incorporated by reference in its entirety.

[0233] An exemplary auristatin embodiment is MMAE (see US Patent No. 6,884,869 expressly incorporated by reference in its entirety).

[0234] Another exemplary auristatin embodiment is MMAF (see US 2005/0238649, 5,767,237 and 6,124,431, expressly incorporated by reference in their entirety).

[0235] Additional exemplary embodiments comprising MMAE or MMAF and various linker components (described further herein) have the following structures and abbreviations (wherein Ab means antibody and p is 1 to about 8):

[0236] Typically, peptide-based drug moieties can be prepared by forming a peptide bond between two or more amino acids and/or peptide fragments. Such peptide bonds can be prepared, for example, according to the liquid phase synthesis method (see E. Schroder and K. Lubke, "The Peptides", volume 1, pp 76-136, 1965, Academic Press) that is well known in the field of peptide chemistry. The auristatin/dolastatin drug moieties may be prepared according to the methods of: U.S. Pat. No. 5,635,483; U.S. Pat. No. 5,780,588; Pettit et al (1989) J. Am. Chem. Soc. 111:5463-5465; Pettit et al (1998) Anti-Cancer Drug Design 13:243-277; Pettit, G. R., et al. Synthesis, 1996, 719-725; Pettit et al (1996) J. Chem. Soc. Perkin Trans. 1 5:859-863; and Doronina (2003) Nat Biotechnol 21(7):778-784.

Calicheamicin

[0237] In other embodiments, the ADC comprises an antibody of the invention conjugated to one or more calicheamicin molecules. For example, Mylotarg is the first commercial ADC drug and utilizes calicheamicin γ1 as the payload (see US Patent No. 4,970,198, incorporated by reference in its entirety). Additional calicheamicin derivatives are described in US Patent Nos. 5,264,586, 5,384,412, 5,550,246, 5,739,116, 5,773,001, 5,767,285 and 5,877,296, all expressly incorporated by reference. The calicheamicin family of antibiotics are capable of producing double-stranded DNA breaks at sub-picomolar concentrations. For the preparation of conjugates of the calicheamicin family, see U.S. Pat. Nos. 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, 5,877,296 (all to American Cyanamid Company). Structural analogues of calicheamicin which may be used include, but are not limited to, γ1I, α2I, α2I, N-acetyl- γ1I, PSAG and θI1 (Hinman et al., Cancer Research 53:3336-3342 (1993), Lode et al., Cancer Research 58:2925-2928 (1998) and the aforementioned U.S. patents to American Cyanamid). Another anti-tumor drug that the

antibody can be conjugated is QFA which is an antifolate. Both calicheamicin and QFA have intracellular sites of action and do not readily cross the plasma membrane. Therefore, cellular uptake of these agents through antibody mediated internalization greatly enhances their cytotoxic effects.

Duocarmycins

[0238] CC-1065 (see 4,169,888, incorporated by reference) and duocarmycins are members of a family of antitumor antibiotics utilized in ADCs. These antibiotics appear to work through sequence-selectively alkylating DNA at the N3 of adenine in the minor groove, which initiates a cascade of events that result in apoptosis.

[0239] Important members of the duocarmycins include duocarmycin A (US Patent No. 4,923,990, incorporated by reference) and duocarmycin SA (U.S. Pat. No. 5,101,038, incorporated by reference), and a large number of analogues as described in US Patent Nos. 7,517,903, 7,691,962, 5,101,038; 5,641,780; 5,187,186; 5,070,092; 5,070,092; 5,641,780; 5,101,038; 5,084,468, 5,475,092, 5,585,499, 5,846,545, WO2007/089149, WO2009/017394A1, 5,703,080, 6,989,452, 7,087,600, 7,129,261, 7,498,302, and 7,507,420, all of which are expressly incorporated by reference.

Other Cytotoxic Agents

[0240] Other antitumor agents that can be conjugated to the antibodies of the invention include BCNU, streptozoicin, vincristine and 5-fluorouracil, the family of agents known collectively LL-E33288 complex described in U.S. Pat. Nos. 5,053,394, 5,770,710, as well as esperamicins (U.S. Pat. No. 5,877,296).

[0241] Enzymatically active toxins and fragments thereof which can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin and the tricothecenes. See, for example, WO 93/21232 published Oct. 28, 1993.

[0242] The present invention further contemplates an ADC formed between an antibody and a compound with nucleolytic activity (e.g., a ribonuclease or a DNA endonuclease such as a deoxyribonuclease; DNase).

[0243] For selective destruction of the tumor, the antibody may comprise a highly radioactive atom. A variety of radioactive isotopes are available for the production of radioconjugated antibodies. Examples include At211, I131, I125, Y90, Re186, Re188, Sm153, Bi212, P32, Pb212 and radioactive isotopes of Lu.

[0244] The radio- or other labels may be incorporated in the conjugate in known ways. For example, the peptide may be biosynthesized or may be synthesized by chemical amino acid synthesis using suitable amino acid precursors involving, for example, fluorine-19 in place of hydrogen. Labels such as Tc99m or I123, Re186, Re188 and In111 can be attached via a cysteine residue in the peptide. Yttrium-90 can be attached via a lysine residue. The IODOGEN method (Fraker et al (1978) Biochem. Biophys. Res. Commun. 80: 49-57 can be used to incorporate Iodine-123. "Monoclonal Antibodies in Immunoscintigraphy" (Chatal, CRC Press 1989) describes other methods in detail.

[0245] For compositions comprising a plurality of antibodies, the drug loading is represented by p, the average number of drug molecules per Antibody. Drug loading may range from 1 to 20 drugs (D) per Antibody. The average number of drugs per antibody in preparation of conjugation reactions may be characterized by conventional means such as mass spectroscopy, ELISA assay, and HPLC. The quantitative distribution of Antibody-Drug-Conjugates in terms of p may also be determined.

[0246] In some instances, separation, purification, and characterization of homogeneous Antibody-Drug-conjugates where p is a certain value from Antibody-Drug-Conjugates with other drug loadings may be achieved by means such as reverse phase HPLC or electrophoresis. In exemplary embodiments, p is 2, 3, 4, 5, 6, 7, or 8 or a fraction thereof.

[0247] The generation of Antibody-drug conjugate compounds can be accomplished by any technique known to the skilled artisan. Briefly, the Antibody-drug conjugate compounds can include a multispecific antibody as the Antibody unit, a drug, and optionally a linker that joins the drug and the binding agent.

[0248] A number of different reactions are available for covalent attachment of drugs and/or linkers to binding agents. This is can be accomplished by reaction of the amino acid residues of the binding agent, for example, antibody molecule, including the amine groups of lysine, the free carboxylic acid groups of glutamic and aspartic acid, the sulfhydryl groups of cysteine and the various moieties of the aromatic amino acids. A commonly used non-specific methods of covalent attachment is the carbodiimide reaction to link a carboxy (or

amino) group of a compound to amino (or carboxy) groups of the antibody. Additionally, bifunctional agents such as dialdehydes or imidoesters have been used to link the amino group of a compound to amino groups of an antibody molecule.

[0249] Also available for attachment of drugs to binding agents is the Schiff base reaction. This method involves the periodate oxidation of a drug that contains glycol or hydroxy groups, thus forming an aldehyde which is then reacted with the binding agent. Attachment occurs via formation of a Schiff base with amino groups of the binding agent. Isothiocyanates can also be used as coupling agents for covalently attaching drugs to binding agents. Other techniques are known to the skilled artisan and within the scope of the present invention.

[0250] In some embodiments, an intermediate, which is the precursor of the linker, is reacted with the drug under appropriate conditions. In other embodiments, reactive groups are used on the drug and/or the intermediate. The product of the reaction between the drug and the intermediate, or the derivatized drug, is subsequently reacted with an multispecific antibody of the invention under appropriate conditions.

[0251] It will be understood that chemical modifications may also be made to the desired compound in order to make reactions of that compound more convenient for purposes of preparing conjugates of the invention. For example a functional group e.g. amine, hydroxyl, or sulfhydryl, may be appended to the drug at a position which has minimal or an acceptable effect on the activity or other properties of the drug

Linker Units

[0252] Typically, the antibody-drug conjugate compounds comprise a Linker unit between the drug unit and the antibody unit. In some embodiments, the linker is cleavable under intracellular or extracellular conditions, such that cleavage of the linker releases the drug unit from the antibody in the appropriate environment. For example, solid tumors that secrete certain proteases may serve as the target of the cleavable linker; in other embodiments, it is the intracellular proteases that are utilized. In yet other embodiments, the linker unit is not cleavable and the drug is released, for example, by antibody degradation in lysosomes.

[0253] In some embodiments, the linker is cleavable by a cleaving agent that is present in the intracellular environment (for example, within a lysosome or endosome or caveolea). The linker can be, for example, a peptidyl linker that is cleaved by an intracellular peptidase or protease enzyme, including, but not limited to, a lysosomal or endosomal protease. In some

embodiments, the peptidyl linker is at least two amino acids long or at least three amino acids long or more.

[0254] Cleaving agents can include,without limitation, cathepsins B and D and plasmin, all of which are known to hydrolyze dipeptide drug derivatives resulting in the release of active drug inside target cells (see, e.g., Dubowchik and Walker, 1999, Pharm. Therapeutics 83:67-123). Peptidyl linkers that are cleavable by enzymes that are present in CD38-expressing cells. For example, a peptidyl linker that is cleavable by the thiol-dependent protease cathepsin-B, which is highly expressed in cancerous tissue, can be used (e.g., a Phe-Leu or a Gly-Phe-Leu-Gly linker (SEQ ID NO: X)). Other examples of such linkers are described, e.g., in U.S. Pat. No. 6,214,345, incorporated herein by reference in its entirety and for all purposes.

[0255] In some embodiments, the peptidyl linker cleavable by an intracellular protease is a Val-Cit linker or a Phe-Lys linker (see, e.g., U.S. Pat. No. 6,214,345, which describes the synthesis of doxorubicin with the val-cit linker).

[0256] In other embodiments, the cleavable linker is pH-sensitive, that is, sensitive to hydrolysis at certain pH values. Typically, the pH-sensitive linker hydrolyzable under acidic conditions. For example, an acid-labile linker that is hydrolyzable in the lysosome (for example, a hydrazone, semicarbazone, thiosemicarbazone, cis-aconitic amide, orthoester, acetal, ketal, or the like) may be used. (See, e.g., U.S. Pat. Nos. 5,122,368; 5,824,805; 5,622,929; Dubowchik and Walker, 1999, Pharm. Therapeutics 83:67-123; Neville et al., 1989, Biol. Chem. 264:14653-14661.) Such linkers are relatively stable under neutral pH conditions, such as those in the blood, but are unstable at below pH 5.5 or 5.0, the approximate pH of the lysosome. In certain embodiments, the hydrolyzable linker is a thioether linker (such as, e.g., a thioether attached to the therapeutic agent via an acylhydrazone bond (see, e.g., U.S. Pat. No. 5,622,929).

[0257] In yet other embodiments, the linker is cleavable under reducing conditions (for example, a disulfide linker). A variety of disulfide linkers are known in the art, including, for example, those that can be formed using SATA (N-succinimidyl-5-acetylthioacetate), SPDP (N-succinimidyl-3-(2-pyridyldithio)propionate), SPDB (N-succinimidyl-3-(2-pyridyldithio)butyrate) and SMPT (N-succinimidyl-oxycarbonyl-alpha-methyl-alpha-(2-pyridyl-dithio)toluene)- , SPDB and SMPT. (See, e.g., Thorpe et al., 1987, Cancer Res. 47:5924-5931; Wawrzynczak et al., In Immunoconjugates: Antibody Conjugates in

Radioimagery and Therapy of Cancer (C. W. Vogel ed., Oxford U. Press, 1987. See also U.S. Pat. No. 4,880,935.)

[0258] In other embodiments, the linker is a malonate linker (Johnson et al., 1995, Anticancer Res. 15:1387-93), a maleimidobenzoyl linker (Lau et al., 1995, Bioorg-Med-Chem. 3(10):1299-1304), or a 3'-N-amide analog (Lau et al., 1995, Bioorg-Med-Chem. 3(10):1305-12).

[0259] In yet other embodiments, the linker unit is not cleavable and the drug is released by antibody degradation. (See U.S. Publication No. 2005/0238649 incorporated by reference herein in its entirety and for all purposes).

[0260] In many embodiments, the linker is self-immolative. As used herein, the term "self-immolative Spacer" refers to a bifunctional chemical moiety that is capable of covalently linking together two spaced chemical moieties into a stable tripartite molecule. It will spontaneously separate from the second chemical moiety if its bond to the first moiety is cleaved. See for example, WO 2007059404A2, WO06110476A2, WO05112919A2, WO2010/062171, WO09/017394, WO07/089149, WO 07/018431, WO04/043493 and WO02/083180, which are directed to drug-cleavable substrate conjugates where the drug and cleavable substrate are optionally linked through a self-immolative linker and which are all expressly incorporated by reference.

[0261] Often the linker is not substantially sensitive to the extracellular environment. As used herein, "not substantially sensitive to the extracellular environment," in the context of a linker, means that no more than about 20%, 15%, 10%, 5%, 3%, or no more than about 1% of the linkers, in a sample of antibody-drug conjugate compound, are cleaved when the antibody-drug conjugate compound presents in an extracellular environment (for example, in plasma).

[0262] Whether a linker is not substantially sensitive to the extracellular environment can be determined, for example, by incubating with plasma the antibody-drug conjugate compound for a predetermined time period (for example, 2, 4, 8, 16, or 24 hours) and then quantitating the amount of free drug present in the plasma.

[0263] In other, non-mutually exclusive embodiments, the linker promotes cellular internalization. In certain embodiments, the linker promotes cellular internalization when conjugated to the therapeutic agent (that is, in the milieu of the linker-therapeutic agent moiety of the antibody-drug conjugate compound as described herein). In yet other

embodiments, the linker promotes cellular internalization when conjugated to both the auristatin compound and the multispecific antibodies of the invention.

[0264] A variety of exemplary linkers that can be used with the present compositions and methods are described in WO 2004-010957, U.S. Publication No. 2006/0074008, U.S. Publication No. 20050238649, and U.S. Publication No. 2006/0024317 (each of which is incorporated by reference herein in its entirety and for all purposes).

Drug Loading

[0265] Drug loading is represented by p and is the average number of Drug moieties per antibody in a molecule. Drug loading ("p") may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more moieties (D) per antibody, although frequently the average number is a fraction or a decimal. Generally, drug loading of from 1 to 4 is frequently useful, and from 1 to 2 is also useful. ADCs of the invention include collections of antibodies conjugated with a range of drug moieties, from 1 to 20. The average number of drug moieties per antibody in preparations of ADC from conjugation reactions may be characterized by conventional means such as mass spectroscopy and, ELISA assay.

[0266] The quantitative distribution of ADC in terms of p may also be determined. In some instances, separation, purification, and characterization of homogeneous ADC where p is a certain value from ADC with other drug loadings may be achieved by means such as electrophoresis.

[0267] For some antibody-drug conjugates, p may be limited by the number of attachment sites on the antibody. For example, where the attachment is a cysteine thiol, as in the exemplary embodiments above, an antibody may have only one or several cysteine thiol groups, or may have only one or several sufficiently reactive thiol groups through which a linker may be attached. In certain embodiments, higher drug loading, e.g. $p>5$, may cause aggregation, insolubility, toxicity, or loss of cellular permeability of certain antibody-drug conjugates. In certain embodiments, the drug loading for an ADC of the invention ranges from 1 to about 8; from about 2 to about 6; from about 3 to about 5; from about 3 to about 4; from about 3.1 to about 3.9; from about 3.2 to about 3.8; from about 3.2 to about 3.7; from about 3.2 to about 3.6; from about 3.3 to about 3.8; or from about 3.3 to about 3.7. Indeed, it has been shown that for certain ADCs, the optimal ratio of drug moieties per antibody may be less than 8, and may be about 2 to about 5. See US 2005-0238649 A1 (herein incorporated by reference in its entirety).

[0268] In certain embodiments, fewer than the theoretical maximum of drug moieties are conjugated to an antibody during a conjugation reaction. An antibody may contain, for example, lysine residues that do not react with the drug-linker intermediate or linker reagent, as discussed below. Generally, antibodies do not contain many free and reactive cysteine thiol groups which may be linked to a drug moiety; indeed most cysteine thiol residues in antibodies exist as disulfide bridges. In certain embodiments, an antibody may be reduced with a reducing agent such as dithiothreitol (DTT) or tricarbonylethylphosphine (TCEP), under partial or total reducing conditions, to generate reactive cysteine thiol groups. In certain embodiments, an antibody is subjected to denaturing conditions to reveal reactive nucleophilic groups such as lysine or cysteine.

[0269] The loading (drug/antibody ratio) of an ADC may be controlled in different ways, e.g., by: (i) limiting the molar excess of drug-linker intermediate or linker reagent relative to antibody, (ii) limiting the conjugation reaction time or temperature, (iii) partial or limiting reductive conditions for cysteine thiol modification, (iv) engineering by recombinant techniques the amino acid sequence of the antibody such that the number and position of cysteine residues is modified for control of the number and/or position of linker-drug attachements (such as thioMab or thioFab prepared as disclosed herein and in WO2006/034488 (herein incorporated by reference in its entirety)).

[0270] It is to be understood that where more than one nucleophilic group reacts with a drug-linker intermediate or linker reagent followed by drug moiety reagent, then the resulting product is a mixture of ADC compounds with a distribution of one or more drug moieties attached to an antibody. The average number of drugs per antibody may be calculated from the mixture by a dual ELISA antibody assay, which is specific for antibody and specific for the drug. Individual ADC molecules may be identified in the mixture by mass spectroscopy and separated by HPLC, e.g. hydrophobic interaction chromatography.

[0271] In some embodiments, a homogeneous ADC with a single loading value may be isolated from the conjugation mixture by electrophoresis or chromatography.

Methods of Determining Cytotoxic Effect of ADCs

[0272] Methods of determining whether a Drug or Antibody-Drug conjugate exerts a cytostatic and/or cytotoxic effect on a cell are known. Generally, the cytotoxic or cytostatic activity of an Antibody Drug conjugate can be measured by: exposing mammalian cells expressing a target protein of the Antibody Drug conjugate in a cell culture medium;

culturing the cells for a period from about 6 hours to about 5 days; and measuring cell viability. Cell-based in vitro assays can be used to measure viability (proliferation), cytotoxicity, and induction of apoptosis (caspase activation) of the Antibody Drug conjugate.

[0273] For determining whether an Antibody Drug conjugate exerts a cytostatic effect, a thymidine incorporation assay may be used. For example, cancer cells expressing a target antigen at a density of 5,000 cells/well of a 96-well plated can be cultured for a 72-hour period and exposed to 0.5 μCi of 3H-thymidine during the final 8 hours of the 72-hour period. The incorporation of 3H-thymidine into cells of the culture is measured in the presence and absence of the Antibody Drug conjugate.

[0274] For determining cytotoxicity, necrosis or apoptosis (programmed cell death) can be measured. Necrosis is typically accompanied by increased permeability of the plasma membrane; swelling of the cell, and rupture of the plasma membrane. Apoptosis is typically characterized by membrane blebbing, condensation of cytoplasm, and the activation of endogenous endonucleases. Determination of any of these effects on cancer cells indicates that an Antibody Drug conjugate is useful in the treatment of cancers.

[0275] Cell viability can be measured by determining in a cell the uptake of a dye such as neutral red, trypan blue, or ALAMAR™ blue (see, e.g., Page et al., 1993, Intl. J. Oncology 3:473-476). In such an assay, the cells are incubated in media containing the dye, the cells are washed, and the remaining dye, reflecting cellular uptake of the dye, is measured spectrophotometrically. The protein-binding dye sulforhodamine B (SRB) can also be used to measure cytoxicity (Skehan et al., 1990, J. Natl. Cancer Inst. 82:1107-12).

[0276] Alternatively, a tetrazolium salt, such as MTT, is used in a quantitative colorimetric assay for mammalian cell survival and proliferation by detecting living, but not dead, cells (see, e.g., Mosmann, 1983, J. Immunol. Methods 65:55-63).

[0277] Apoptosis can be quantitated by measuring, for example, DNA fragmentation. Commercial photometric methods for the quantitative in vitro determination of DNA fragmentation are available. Examples of such assays, including TUNEL (which detects incorporation of labeled nucleotides in fragmented DNA) and ELISA-based assays, are described in Biochemica, 1999, no. 2, pp. 34-37 (Roche Molecular Biochemicals).

[0278] Apoptosis can also be determined by measuring morphological changes in a cell. For example, as with necrosis, loss of plasma membrane integrity can be determined by measuring uptake of certain dyes (e.g., a fluorescent dye such as, for example, acridine

orange or ethidium bromide). A method for measuring apoptotic cell number has been described by Duke and Cohen, Current Protocols in Immunology (Coligan et al. eds., 1992, pp. 3.17.1-3.17.16). Cells also can be labeled with a DNA dye (e.g., acridine orange, ethidium bromide, or propidium iodide) and the cells observed for chromatin condensation and margination along the inner nuclear membrane. Other morphological changes that can be measured to determine apoptosis include, e.g., cytoplasmic condensation, increased membrane blebbing, and cellular shrinkage.

[0279] The presence of apoptotic cells can be measured in both the attached and "floating" compartments of the cultures. For example, both compartments can be collected by removing the supernatant, trypsinizing the attached cells, combining the preparations following a centrifugation wash step (e.g., 10 minutes at 2000 rpm), and detecting apoptosis (e.g., by measuring DNA fragmentation). (See, e.g., Piazza et al., 1995, Cancer Research 55:3110-16).

[0280] In vivo, the effect of a therapeutic composition of the multispecific antibody of the invention can be evaluated in a suitable animal model. For example, xenogenic cancer models can be used, wherein cancer explants or passaged xenograft tissues are introduced into immune compromised animals, such as nude or SCID mice (Klein et al., 1997, Nature Medicine 3: 402-408). Efficacy can be measured using assays that measure inhibition of tumor formation, tumor regression or metastasis, and the like.

[0281] The therapeutic compositions used in the practice of the foregoing methods can be formulated into pharmaceutical compositions comprising a carrier suitable for the desired delivery method. Suitable carriers include any material that when combined with the therapeutic composition retains the anti-tumor function of the therapeutic composition and is generally non-reactive with the patient's immune system. Examples include, but are not limited to, any of a number of standard pharmaceutical carriers such as sterile phosphate buffered saline solutions, bacteriostatic water, and the like (see, generally, Remington's Pharmaceutical Sciences 16th Edition, A. Osal., Ed., 1980).

Antibody Compositions for In Vivo Administration

[0282] Formulations of the antibodies used in accordance with the present invention are prepared for storage by mixing an antibody having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. [1980]), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at

the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g. Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

[0283] The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. For example, it may be desirable to provide antibodies with other specifcities. Alternatively, or in addition, the composition may comprise a cytotoxic agent, cytokine, growth inhibitory agent and/or small molecule antagonist. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[0284] The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980).

[0285] The formulations to be used for in vivo administration should be sterile, or nearly so. This is readily accomplished by filtration through sterile filtration membranes.

[0286] Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g. films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for

example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and .gamma. ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods.

[0287] When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37oC, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S--S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

Administrative modalities

[0288] The antibodies and chemotherapeutic agents 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, by intramuscular, intraperitoneal, intracerobrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation routes. Intravenous or subcutaneous administration of the antibody is preferred.

Treatment modalities

[0289] In the methods of the invention, therapy is used to provide a positive therapeutic response with respect to a disease or condition. By "positive therapeutic response" is intended an improvement in the disease or condition, and/or an improvement in the symptoms associated with the disease or condition. For example, a positive therapeutic response would refer to one or more of the following improvements in the disease: (1) a reduction in the number of neoplastic cells; (2) an increase in neoplastic cell death; (3) inhibition of neoplastic cell survival; (5) inhibition (i.e., slowing to some extent, preferably halting) of tumor growth; (6) an increased patient survival rate; and (7) some relief from one or more symptoms associated with the disease or condition.

[0290] Positive therapeutic responses in any given disease or condition can be determined by standardized response criteria specific to that disease or condition. Tumor response can be assessed for changes in tumor morphology (i.e., overall tumor burden, tumor size, and the like) using screening techniques such as magnetic resonance imaging (MRI) scan, x-radiographic imaging, computed tomographic (CT) scan, bone scan imaging, endoscopy, and tumor biopsy sampling including bone marrow aspiration (BMA) and counting of tumor cells in the circulation.

[0291] In addition to these positive therapeutic responses, the subject undergoing therapy may experience the beneficial effect of an improvement in the symptoms associated with the disease.

[0292] Thus for B cell tumors, the subject may experience a decrease in the so-called B symptoms, i.e., night sweats, fever, weight loss, and/or urticaria. For pre-malignant conditions, therapy with an multispecific therapeutic agent may block and/or prolong the time before development of a related malignant condition, for example, development of multiple myeloma in subjects suffering from monoclonal gammopathy of undetermined significance (MGUS).

[0293] An improvement in the disease may be characterized as a complete response. By "complete response" is intended an absence of clinically detectable disease with normalization of any previously abnormal radiographic studies, bone marrow, and cerebrospinal fluid (CSF) or abnormal monoclonal protein in the case of myeloma.

[0294] Such a response may persist for at least 4 to 8 weeks, or sometimes 6 to 8 weeks, following treatment according to the methods of the invention. Alternatively, an improvement in the disease may be categorized as being a partial response. By "partial response" is intended at least about a 50% decrease in all measurable tumor burden (i.e., the number of malignant cells present in the subject, or the measured bulk of tumor masses or the quantity of abnormal monoclonal protein) in the absence of new lesions, which may persist for 4 to 8 weeks, or 6 to 8 weeks.

[0295] Treatment according to the present invention includes a "therapeutically effective amount" of the medicaments used. A "therapeutically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve a desired therapeutic result.

[0296] A therapeutically effective amount may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the medicaments to

elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects of the antibody or antibody portion are outweighed by the therapeutically beneficial effects.

[0297] A "therapeutically effective amount" for tumor therapy may also be measured by its ability to stabilize the progression of disease. The ability of a compound to inhibit cancer may be evaluated in an animal model system predictive of efficacy in human tumors.

[0298] Alternatively, this property of a composition may be evaluated by examining the ability of the compound to inhibit cell growth or to induce apoptosis by in vitro assays known to the skilled practitioner. A therapeutically effective amount of a therapeutic compound may decrease tumor size, or otherwise ameliorate symptoms in a subject. One of ordinary skill in the art would be able to determine such amounts based on such factors as the subject's size, the severity of the subject's symptoms, and the particular composition or route of administration selected.

[0299] Dosage regimens are adjusted to provide the optimum desired response (e.g., a therapeutic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. Parenteral compositions may be formulated in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier.

[0300] The specification for the dosage unit forms of the present invention are dictated by and directly dependent on (a) the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

[0301] The efficient dosages and the dosage regimens for the multispecific antibodies used in the present invention depend on the disease or condition to be treated and may be determined by the persons skilled in the art.

[0302] An exemplary, non-limiting range for a therapeutically effective amount of an multispecific antibody used in the present invention is about 0.1-100 mg/kg, such as about 0.1-50 mg/kg, for example about 0.1-20 mg/kg, such as about 0.1-10 mg/kg, for instance

about 0.5, about such as 0.3, about 1, or about 3 mg/kg. In another embodiment, he antibody is administered in a dose of 1 mg/kg or more, such as a dose of from 1 to 20 mg/kg, e.g. a dose of from 5 to 20 mg/kg, e.g. a dose of 8 mg/kg.

[0303] A medical professional having ordinary skill in the art may readily determine and prescribe the effective amount of the pharmaceutical composition required. For example, a physician or a veterinarian could start doses of the medicament employed in the pharmaceutical composition at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved.

[0304] In one embodiment, the multispecific antibody is administered by infusion in a weekly dosage of from 10 to 500 mg/kg such as of from 200 to 400 mg/kg Such administration may be repeated, e.g., 1 to 8 times, such as 3 to 5 times. The administration may be performed by continuous infusion over a period of from 2 to 24 hours, such as of from 2 to 12 hours.

[0305] In one embodiment, the multispecific antibody is administered by slow continuous infusion over a long period, such as more than 24 hours, if required to reduce side effects including toxicity.

[0306] In one embodiment the multispecific antibody is administered in a weekly dosage of from 250 mg to 2000 mg, such as for example 300 mg, 500 mg, 700 mg, 1000 mg, 1500 mg or 2000 mg, for up to 8 times, such as from 4 to 6 times. The administration may be performed by continuous infusion over a period of from 2 to 24 hours, such as of from 2 to 12 hours. Such regimen may be repeated one or more times as necessary, for example, after 6 months or 12 months. The dosage may be determined or adjusted by measuring the amount of compound of the present invention in the blood upon administration by for instance taking out a biological sample and using anti-idiotypic antibodies which target the antigen binding region of the multispecific antibody.

[0307] In a further embodiment, the multispecific antibody is administered once weekly for 2 to 12 weeks, such as for 3 to 10 weeks, such as for 4 to 8 weeks.

[0308] In one embodiment, the multispecific antibody is administered by maintenance therapy, such as, e.g., once a week for a period of 6 months or more.

[0309] In one embodiment, the multispecific antibody is administered by a regimen including one infusion of an multispecific antibody followed by an infusion of an

multispecific antibody conjugated to a radioisotope. The regimen may be repeated, e.g., 7 to 9 days later.

[0310] As non-limiting examples, treatment according to the present invention may be provided as a daily dosage of an antibody in an amount of about 0.1-100 mg/kg, such as 0.5, 0.9, 1.0, 1.1, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 40, 45, 50, 60, 70, 80, 90 or 100 mg/kg, per day, on at least one of day 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40, or alternatively, at least one of week 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 after initiation of treatment, or any combination thereof, using single or divided doses of every 24, 12, 8, 6, 4, or 2 hours, or any combination thereof.

[0311] In some embodiments the multispecific antibody molecule thereof is used in combination with one or more additional therapeutic agents, e.g. a chemotherapeutic agent. Non-limiting examples of DNA damaging chemotherapeutic agents include topoisomerase I inhibitors (e.g., irinotecan, topotecan, camptothecin and analogs or metabolites thereof, and doxorubicin); topoisomerase II inhibitors (e.g., etoposide, teniposide, and daunorubicin); alkylating agents (e.g., melphalan, chlorambucil, busulfan, thiotepa, ifosfamide, carmustine, lomustine, semustine, streptozocin, decarbazine, methotrexate, mitomycin C, and cyclophosphamide); DNA intercalators (e.g., cisplatin, oxaliplatin, and carboplatin); DNA intercalators and free radical generators such as bleomycin; and nucleoside mimetics (e.g., 5-fluorouracil, capecitibine, gemcitabine, fludarabine, cytarabine, mercaptopurine, thioguanine, pentostatin, and hydroxyurea).

[0312] Chemotherapeutic agents that disrupt cell replication include: paclitaxel, docetaxel, and related analogs; vincristine, vinblastin, and related analogs; thalidomide, lenalidomide, and related analogs (e.g., CC-5013 and CC-4047); protein tyrosine kinase inhibitors (e.g., imatinib mesylate and gefitinib); proteasome inhibitors (e.g., bortezomib); NF-κB inhibitors, including inhibitors of IκB kinase; antibodies which bind to proteins overexpressed in cancers and thereby downregulate cell replication (e.g., trastuzumab, rituximab, cetuximab, and bevacizumab); and other inhibitors of proteins or enzymes known to be upregulated, over-expressed or activated in cancers, the inhibition of which downregulates cell replication.

[0313] In some embodiments, the antibodies of the invention can be used prior to, concurrent with, or after treatment with Velcade® (bortezomib).

[0314] All cited references are herein expressly incorporated by reference in their entirety.

[0315] Whereas particular embodiments of the invention have been described above for purposes of illustration, it will be appreciated by those skilled in the art that numerous variations of the details may be made without departing from the invention as described in the appended claims.

Examples

[0316] Examples are provided below to illustrate the present invention. These examples are not meant to constrain the present invention to any particular application or theory of operation. For all constant region positions discussed in the present invention, numbering is according to the EU index as in Kabat (Kabat et al., 1991, Sequences of Proteins of Immunological Interest, 5th Ed., United States Public Health Service, National Institutes of Health, Bethesda, entirely incorporated by reference). Those skilled in the art of antibodies will appreciate that this convention consists of nonsequential numbering in specific regions of an immunoglobulin sequence, enabling a normalized reference to conserved positions in immunoglobulin families. Accordingly, the positions of any given immunoglobulin as defined by the EU index will not necessarily correspond to its sequential sequence.

EXAMPLE 1. Prototype "triple F" bispecific antibody.

[0317] The present invention describes novel immunoglobulin compositions that co-engage a first and second antigen. One heavy chain of the antibody contains a single chain Fv ("scFv", as defined herein) and the other heavy chain is a "regular" Fab format, comprising a variable heavy chain and a light chain (see Fig. 1). This structure is sometimes referred to herein as "triple F" format (scFv-Fab-Fc). The two chains are brought together by the dimeric Fc region (see Fig. 2). The Fc region can be modified by amino acid substitution to allow for efficient purification of the "triple F" heterodimer. Further, the Fc region can be modified by amino acid substitution to promote the formation of the "triple F" heterodimer. Examples of Fc substitutions are described more fully below.

[0318] Fc substitutions can be included in the "triple F" format to allow for efficient purification of the desired "triple F" heterodimer over the undesired dual scFv-Fc and mAb homodimers. An example of this is in the inclusion of Fc substitutions that alter the isoelectric point (pI) of each monomer so that such that each monomer has a different pI. In this case the desired "triple F" heterodimer will have a different pI than that of the undesired dual scFv-Fc and mAb homodimers, thus facilitating isoelectric purification of the "triple F"

heterodimer (e.g., anionic exchange columns, cationic exchange columns). These substitutions also aid in the determination and monitoring of any contaminating dual scFv-Fc and mAb homodimers post-purification (e.g., IEF gels, cIEF, and analytical IEX columns). See Fig. 3 for a list of substitutions that can be made in Fc monomer 1 and Fc monomer 2 to allow for efficient purification of the desired "triple F" heterodimer.

[0319] Fc substitutions can be included in the "triple F" format to "skew" the formation toward the desired "triple F" heterodimer over the undesired dual scFv-Fc and mAb homodimers. For example, see Fig. 4 for a list of substitutions that can be made in Fc monomer 1 and Fc monomer 2 to "skew" production toward the "triple F" heterodimer. Amino acid subsitutions listed in Fig. 3 and Fig. 4 can be combined, leading to an increased yield of "triple F" heterodimer that can be easily purified away from any contaminating dual scFv-Fc and mAb homodimers.

[0320] After optimization of an scFv domain for inclusion in the "triple F" format, an optimized scFv domain can be coupled with a variety of standard antibody heavy chains in a convenient fashion. For example, an anti-CD3 scFv for recruiting T cell cytotoxicity can be coupled with a variety of anti-tumor antigen antibody heavy chains (e.g., those binding CD5, CD20, CD30, CD40, CD33, CD38, EGFR, EpCAM, Her2, HM1.24, or other tumor antigen). Further examples of optimized scFv domains that can be conveniently coupled with standard antibody heavy chains include anti-CD16 scFv for natural killer cell cytotoxicity; anti-CD32b scFv for inhibitory activity (here the coupled antibody heavy chain would bind, e.g., CD19, CD40, CD79a, CD79b, or other immune receptors); and anti-transferrin receptor scFv, anti-insulin receptor, or anti-LRP1 for transport across the blood-brain barrier.

EXAMPLE 2. Multi-specific antibodies derived from the "triple F" format.

[0321] Multi-specific antibodies can be constructed by attaching additional scFv or Fab domains that bind a third antigen to the C-terminus of one of the "triple F" heavy chains. See Fig. 5 for examples. Alternatively, the C-terminal scFv or Fab may bind the first or second antigen, thus conferring bivalency and an increase in overall binding affinity for that antigen.

[0322] Multi-specific antibodies can also be constructed by coupling the scFv-Fc heavy chain of the "triple F" format may with rearranged antibody heavy chains as depicted in Fig. 6. Such rearranged heavy chains may include an additional Fv region that binds a third antigen or an additional Fv region that binds the first antigen or second antigen, thus conferring bivalency and an increase in overall binding affinity for that antigen.

EXAMPLE 3. Anti-CD19 Fab x anti-CD3 scFv "triple F" bispecific.

[0323] Amino acid sequences for anti-CD19 Fab x anti-CD3 scFv "triple F" bispecifics are listed in the figures. Amino acid substitutions made to allow for efficient purification of the desired "triple F" heterodimer over the undesired dual scFv-Fc and mAb homodimers are underlined. Amino acid sequences for preferred humanized anti-CD3 variable regions are listed in Figures 2 and 6 (with CDRs underlined). Some examples of expression and purification of the desired "triple F" species and its bioactivity are given below.

[0324] The production of XENP11874, a "triple F" bispecific with an anti-CD19 Fab and anti-CD3 scFv, is outlined in Fig. 9. In Fig. 9A, the ion exchange purification of the desired "triple F" heterodimer from the undesired dual scFv-Fc and mAb homodimers is shown. The purity of the "triple F" fraction was checked by IEF gel, (data shown in Figure 9B of USSN 61/818,410, all figures and legends of which are expressly incorporated by reference). Finally, SEC was used to confirm the homogenous size of the "triple F" product (data shown in Figure 9C of USSN 61/818,410, expressly incorporated by reference).

[0325] XENP11874, anti-CD19 Fab x anti-CD3 scFv "triple F" bispecific, was shown to have potent bioactivity. The ability of XENP11874 to potently recruit T cells for B cell depletion is shown in Fig. 10 of of USSN 61/818,410, expressly incorporated by reference).

[0326] The production of XENP11924, a "triple F" bispecific with an anti-CD19 Fab and anti-CD3 scFv, is outlined in Fig. 11 of of USSN 61/818,410, expressly incorporated by reference. In Fig. 11A of USSN 61/818,410, the ion exchange purification of the desired "triple F" heterodimer from the undesired dual scFv-Fc and mAb homodimers is shown. The purity of the "triple F" fraction was checked by IEF gel, shown in Fig. 11B (of USSN 61/818,410). Finally, SEC was used to confirm the homogenous size of the "triple F" product (see Fig. 11C of USSN 61/818,410).

[0327] XENP11924, anti-CD19 Fab x anti-CD3 scFv "triple F" bispecific, was shown to have potent bioactivity. The ability of XENP11924 to potently recruit T cells for the killing of the Raji tumor cell line is shown in Fig. 12 of USSN 61/818,410.

EXAMPLE 4. Anti-CD38 Fab x anti-CD3 scFv "triple F" bispecific.

[0328] Amino acid sequences for anti-CD38 Fab x anti-CD3 scFv "triple F" bispecifics are listed in Fig. 13 of USSN 61/818,410. Amino acid substitutions made to allow for efficient purification of the desired "triple F" heterodimer over the undesired dual scFv-Fc and mAb

homodimers are underlined. Some examples of expression and purification of the desired "triple F" species and its bioactivity are given below.

[0329] The production of XENP11925, a "triple F" bispecific with an anti-CD38 Fab and anti-CD3 scFv, is outlined in Fig. 14 of USSN 61/818,410. In Fig. 14A of USSN 61/818,410, the ion exchange purification of the desired "triple F" heterodimer from the undesired dual scFv-Fc and mAb homodimers is shown. The purity of the "triple F" fraction was checked by IEF gel, shown in Fig. 14B of USSN 61/818,410. Finally, SEC was used to confirm the homogenous size of the "triple F" product (see Fig. 14C of USSN 61/818,410).

[0330] XENP11925, anti-CD38 Fab x anti-CD3 scFv "triple F" bispecific, was shown to have potent bioactivity. The ability of XENP11925 to potently recruit T cells for the killing of the RPMI8226 tumor cell line is shown in Fig. 15 of USSN 61/818,410.

[0331] EXAMPLE 5. Identification and repair of destabilizing pI-altering isotypic constant region variants.

[0332] As described above, efforts can be made to minimize the risk that substitutions that increase or decrease pI will elicit immunogenicity by utilizing the isotypic differences between the IgG subclasses (IgG1, IgG2, IgG3, and IgG4). A new set of novel isotypes was designed based on this principle. These new variants are called ISO(-), ISO(+), and ISO(+RR). The thermal stability of these novel isotypes were determined in a Hinge-CH2-CH3 (H-CH2-CH3) system (Fc region only). Proteins were expressed and purified as described above. Sequences for this proof-of-concept system are listed in figure 16.

[0333] Thermal stability measurements (Fig. 17) determined by differential scanning calorimetry (DSC) revealed that the ISO(-)/ISO(+RR) heterodimer (XENP12488, see Fig. 16 for sequence) was less stable than wild-type IgG1 (XENP8156, see Fig. 16 for sequence). Subsequent engineering efforts identified substitutions N384S/K392N/M397V in the ISO(-) heavy chain as the source of the destabilization. As a result, the variant designated ISO(-NKV) was designed and tested (see Fig. 16). In this variant, positions 384, 392, and 397 were reverted to wild-type IgG1 (S384N/N392K/M397V). The thermal stability of the ISO(-NKV)/ISO(+RR) heterodimer (XENP12757, see Fig. 16 for sequence) was measured by DSC and found to be equivalent to that of wild-type IgG1 (Fig. 17). This result underscores the importance of choosing or not choosing particular pI-altering isotypic substitutions to avoid those that are destabilizing.

[0334] EXAMPLE 6. Additional heterodimer-skewing Fc variants.

[0335] As described above, heterodimer-skewing Fc variants can be made to bias toward the formation of the desired heterodimer versus the undesired homodimers. Additional heterodimer-skewing Fc variants L368D/K370S-S364K/E357Q (XENP12760, see Fig. 18 for sequence) were designed and tested in a Hinge-CH2-CH3 system (Fc region only). Protein was expressed and purified as described above.

[0336] The proteins present after only a single standard protein A purification step were examined by high-performance liquid chromatography (HPLC) using a cation exchange (CIEX) column (see Fig. 19). This allowed the determination of the yield of desired heterodimer versus undesired homodimers. The presence of the L368D/K370S-S364K/E357Q variant (XENP12760, Fig. 19, bottom panel) introduced an extreme bias toward the desired formation of heterodimer compared against the absence of this variant (XENP12757, Fig. 19, top panel). Note that heterodimer yield is 95.8% with the L368D/K370S-S364K/E357Q variant versus only 52.7% without.

[0337] Additional heterodimer-skewing Fc variants were also designed and tested. Fig. 36 provides a list of engineered heterodimer-skewing Fc variants with heterodimer yields (determined by HPLC-CIEX) and thermal stabilities (determined by DSC). The L368D/K370S-S364K/E357Q variant with high heterodimer yield and high thermal stability is especially preferred.

[0338] EXAMPLE 7. Additional heterodimer-skewing Fc variants in the Fab-scFv-Fc context.

[0339] Heterodimer-skewing Fc variants L368D/K370S-S364K/E357Q were engineered into an anti-CD19 x anti-CD3 Fab-scFv-Fc (see Fig. 15 for amino acid sequences). Control Fab-scFv-Fc XENP13228 lacked these heterodimer-skewing Fc variants. The proteins present after only a single standard protein A purification step were examined by an isoelectric focusing (IEF) gel. This allowed the determination of the yield of desired heterodimer versus undesired homodimers. The presence of the L368D/K370S-S364K/E357Q variant (XENP13122, Fig. 22, right lane) introduced an extreme bias toward the desired formation of heterodimer (center band) compared against the absence of this variant (XENP13228, Fig. 22, left lane).

[0340] Example 7. Constructing Anti-CD38 x Anti-CD3 bispecific antibodies

[0341] The anti-CD38 antibody OKT10 was humanized by optimization of human string content (Lazar et al., Mol. Immunol., (2007), 44: 1986-1998), and a bispecific molecule

containing the humanized anti-CD38 Fv and an anti-CD3 domain was created (Figure 37). Desired gene segments were synthesized by Blue Heron Biotechnologies (Bothell, WA) from synthetic oligonucleotides and PCR products by automated gene synthesis. Antibody constructs in the pTT5 vector were expressed in 293E cells and purified by standard Protein A, followed by IEX chromatography using a GE HiTrap SP cation exchange column in order to isolate the desired heterodimeric bispecific. Antibody Fc domains contained an engineered heterodimeric Fc region to facilitate efficient purification of bispecific molecules. Affinity of the bispecifics for CD38 was improved by screening a library of Fv region variants on SPR using a Biacore 3000 (Figure 38).

[0342] Example 8. In vitro properties of Anti-CD38 x Anti-CD3 bispecific antibodies

[0343] Optimized bispecific molecules were screened for their ability to kill RPMI8226 multiple myeloma (MM) cells in a LDH re-directed T-cell cytotoxicity (RTCC) assay (Figure 39) and in an Annexin V+ RTCC assay utilizing different T-cell:RPMI8226 ratios (Figure 40). Optimized molecules were also assessed for cross reactivity to cynomolgus anti-CD38 using a direct binding assay (Figure 41). A table summarizing various properties of the optimized Anti-CD38 x Anti-CD3 bispecific molecules is shown in Figure 42.

[0344] Example 8. Human plasma cell killing by Anti-CD38 x Anti-CD3 bispecifics in huPBMC-engrafted SCID mice

[0345] Optimized bispecific molecules were screened for their ability to kill human plasma cells in a huPBMC-engrafted SCID mouse model. Groups of 10 mice each were treated with α-ASGM1 to deplete SCID NK cells on Day 0, followed by engraftment of 3 x 107 human PBMCs on Day 1. Groups were randomized based on total IgG levels on Day 4. Anti-CD38 x Anti-CD3 bispecific molecules or controls were dosed on Day 7 and 15 after PBMC engraftment. IgG2, IgE, and IgM titers were determined at Day 14 and 21. Daratumumab (an anti-CD38 IgG1 antibody) was included as a control at a dose of 5 mg/kg. Significant reductions in human Ig isotypes were seen with Anti-CD38 x Anti-CD3 bispecific molecules compared to daratumumab. (Figures 43 and 44).

[0346] Example 4. CD38+CD138+ cell depletion in multiple myeloma patient PBMC by Anti-CD38 x Anti-CD3 bispecific antibodies

[0347] PBMC from two MM donors were incubated with 1 μg/mL Anti-CD38 x Anti-CD3 bispecific molecules for 24 hours and cells counted. CD38+CD138+ cells from pre-gated live cells (sorted by FSC vs SSC) were counted and events were normalized against the PBS

treated control. Results are shown in Figure 45. Bispecifics were able to potently deplete MM cells at this concentration.

[0348] EXAMPLE 5. Amino acid and DNA sequences for anti-CD38 x anti-CD3 bispecifics.

[0349] Amino acid and DNA sequences for anti-CD38 x anti-CD3 bispecifics XENP13243 and XENP13551 are listed in Fig. 50 and 51, respectively.

[0350] EXAMPLE 6. Stable pool generation in Chinese Hamster Ovary (CHO) cells for anti-CD38 x anti-CD3 bispecifics.

[0351] Chinese Hamster Ovary (CHO) cells were transfected with DNA encoding XENP13243 and XENP13551 to generate parallel stable pools according to the ratios listed in Fig. 3 using Selexis's proprietary SURE Technology Platform™. Transfected DNA consisted of monocistronic vectors containing the DNA listed in Fig. 52. Stable pool cells were cultured for 7 days in 10 mL spin tubes, and on the 7th day, 5 mL of the culture supernatant was extracted, purified by protein A affinity chromatography, and analyzed by cation exchange chromatography. As the possible proteins that could be generated were designed to have different isoelectric points, cation exchange chromatography allowed for the analysis of which protein species were secreted by the CHO cells as a function of the different DNA ratios. Fig. 4 catalogues the cation exchange chromatograms for each of the specified DNA ratios listed in Fig. 3 for both XENP13243 and XENP13551. Under the conditions used for the cation exchange chromatographic analysis, HC-Fab homodimers elute at ~15 min; desired heterodimeric bispecifics elute at ~22 min; HC-scFv monomers elute at ~26 min; and HC-scFv homodimers elute at ~29 min. A summary of the amounts of the different protein species is listed in Fig. 54.

[0352] Surprisingly, heterodimer formation can be driven by transfection ratios of the three nucleic acids in a host cell (the HC-scFv, the HC and the LC). Several DNA transfection ratios provided for formation of the preferred bispecific heterodimer in amounts greater than 80% of the total protein A purified material. Preferred ratios for formation of greater than 80% heterodimer are 1:1.5:1.5, 1:2:1.5, 1:0.667:2, 1:1:2, 1:1.5:2, and 1:2:2 (all listed as HC-Fab:HC-scFv:LC). Some DNA ratios provided for formation of the preferred bispecific heterodimer in amounts greater than 90%. Preferred ratios for formation of greater than 90% heterodimer are 1:1.5:1.5, 1:2:1.5, 1:1:2, and 1:2:2 (all listed as HC-Fab:HC-scFv:LC). One DNA ratio provided for formation of the preferred bispecific heterodimer in an amount

greater than 95%. An especially preferred ratio for formation of greater than 95% heterodimer is 1:2:2 (listed as HC-Fab:HC-scFv:LC).

[0353] EXAMPLE 7. Pharmacokinetics of anti-CD38 x anti-CD3 bispecifics in C57BL/6 mice.

[0354] C57BL/6 mice (n = 5 per group) were given single 2 mg/kg intravenous doses of anti-CD38 x anti-CD3 bispecifics XENP13243 and XENP13551. Mice were bled via orbital sinus puncture (OSP) at 1 hr and at 1, 3, 6, 10, 14, 17 and 21 days post-test article administration, and blood was processed to serum for determination of test article levels. Serum concentrations were determined by immunoassay and are plotted in Fig. 6. Test article half-lifes were determined using the non-compartmental analysis module of Phoenix WinNonlin 6.3. Half-lifes are listed in Fig. 55. Note that inclusion of an Fc region in the design of the bispecifics resulted in half-lifes comparable to typical monoclonal antibodies. Typical non-Fc-containing bispecifics, such as BiTE or DART formats, have much shorter half-lifes on the order of hours.

[0355] EXAMPLE 8. Redirected T cell cytotoxicity of CD38+ RPMI8226 cells mediated by anti-CD38 x anti-CD3 bispecifics.

[0356] Anti-CD38 x anti-CD3 bispecifics XENP13243 and XENP13551 were used to mediate redirected T cell cytotoxicity of CD38+ RPMI 8226 cells. The assay consisted of a 24 h incubation at 37°C of 10,000 RPMI 8226 cells with 400,000 purified human T cells. Readout of cytotoxicity was by lactate dehydrogenase (LDH). Results are shown in the figures. .

[0357] EXAMPLE 9. Binding affinities of anti-CD38 x anti-CD3 bispecifics.

[0358] Surface plasmon resonance measurements via Biacore 3000 were made of the affinities of XENP13243 and XENP13551 for human and cyno CD38 and CD3. Standard methods were used, and the kinetic parameters were determined using BIAevaluation software. Results are listed in the figures.

[0359] EXAMPLE 10. Depletion of CD38+ cells in cynomolgus monkeys by anti-CD38 x anti-CD3 bispecifics.

[0360] Six groups of cynomolgus monkeys (n = 2 per group) where administered via intravenous infusion either XENP13243 or XENP13551. Two doses were administered per monkey, separated by 3 weeks. Initial doses were 5, 50, and 500 ng/kg, and secondary doses

were 2, 5, and 20 μg/kg. Depletion of CD20-CD38+ cells was observed in a dose dependent manner (see Fig.). Evidence of the recruitment of T cells was seen in the upregulation of CD69 on CD8+ T cells (see Fig.).

CLAIMS

1. A heterodimeric antibody comprising:

a) a first heavy chain comprising:

i) a first Fc domain variant;

ii) a single chain Fv region (scFv) that binds CD3; and

b) a second heavy chain comprising:

i) a second Fc domain variant; and

ii) a first variable heavy domain; and

c) a first light chain comprising a first variable light domain and a first constant light domain; wherein said first variable heavy domain and said first variable light domain bind to CD38, and wherein

the second heavy chain comprises CDR sequences RSWMN, EINPDSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDTWVA, SASYRYS, and QQYDSYPLT;

the second heavy chain comprises CDR sequences RSWMN, EINPDSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDTNVA, SASYRYS, and QQYDSYPLT;

the second heavy chain comprises CDR sequences RSWMN, EINPDSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDYWVA, AASWRYS, and QQYDVYPLT;

the second heavy chain comprises CDR sequences YSWMN, EINPQSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDYWVA, AASWRYS, and QQYDVYPLT;

the second heavy chain comprises CDR sequences YSWMN, EINPQSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDYWVA, SASWRYS, and QQYDVYPLT;

the second heavy chain comprises CDR sequences YSWMN, EINPQSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDYWVA, SASWRYS, and QQYDVYPLT;

the second heavy chain comprises CDR sequences RSWMN, EINPQSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDYWVA, AASWRYS, and QQYDVYPLT; or

the second heavy chain comprises CDR sequences YSWMN, EINPQSSTINYATSVKG, and YGNWFPY and the first light chain comprises CDR sequences RASQNVDTWVA, SASYRYS, and QQYDSYPLT.

2. A heterodimeric antibody according to claim 1, wherein said second heavy chain and said first light chain are selected from the pairs consisting of

(i) H1 of Figure 20D (EVQLVESGGG LVQPGGSLRLSCAASG FDFSRSWM NWVRQAPG KG LEWVSEIN PDSSTINYATSVKGRFTISRDNSKNTLYLQM NSLRAE DTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVV VDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEA LHNHYTQKSLSLSPGK)
and L1.24 of Figure 20D (DIVMTQSPSSLSASVGDRVTITCRASQNVDTWVAWYQQKPGQSPKALIYSASYRYS GVPDRFTGSGSGTDFTLTISSLQPEDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC);

(ii) H1 of Figure 20E (EVQLVESGGG LVQPGGSLRLSCAASG FD FS RSWM NWVRQAPGKGLEWVSEINPDSSTINYATSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD VKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI AVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALH NHYTQKSLSLSPG) and L1.96 of Figure 20E (DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYAASWRY SGVPDRFTGSGSGTDFTLTISSLQPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYE KH KVYACEVTHQG LSSPVTKSFN RG EC);

(iii) H1.77 of Figure 20F (EVQLVESGGG LVQPGGSLRLSCAASGFTFSYSWM NWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD VKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI AVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALH NHYTQKSLSLSPG) and L1.96 of Figure 20F (DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYAASWRY SGVPDRFTGSGSGTDFTLTISSLQPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYEKH KVYACEVTHQG LSSPVTKSFN RG ECSEQ);

(iv) H1.77 of Figure 20G (EVQLVESGGG LVQPGGSLRLSCAASGFTFSYSWM NWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD VKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI AVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALH NHYTQKSLSLSPGKSEQ) and L1.97 of Figure 20G (DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYSASWRYS GVPDRFTGSGSGTDFTLTISSLQPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKH KVYACEVTHQG LSSPVTKSFN RG ECSEQ);

(v) H1.72 of Figure 20H (EVQLVESGGG LVQPGGSLRLSCAASG FDFSYSWM NWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNTLYLQMNSLRAEDT AVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD VKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI AVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALH

NHYTQKSLSLSPGKSEQ) and L1.97 of Figure 20H (DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYSASWRYS GVPDRFTGSGSGTDFTLTISSLQPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFN RG ECSEQ);

(vi) H1.71 of Figure 20I (EVQLVESGGG LVQPG GSLRLSCAASG FTFSRSW M NWVRQAPG KG LEWVSEI NPQSSTINYATSVKG RFTISRDNSKNTLYLQM NS LRAE DTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV VVDVKH E DP EVKFNWYVDGVEVH NAKTKPREEEYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGF YPSDIAVEWES DGQPENNYKTTPPVLDS DGSFFLYSKLTVDKSRWEQGDVFSCSVM HEALHNHYTQKSLSLSPGK) and L1.96 of Figure 20I (DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYAASWRY SGVPDRFTGSGSGTDFTLTISSLQPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD STYSLSSTLTLSKADYE KH KVYACEVTHQG LSSPVTKSFN RG EC), and

(vii) H1.77 of Figure 20J (EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSWMNWVRQAPGKGLEWVSEINPQS STINYATSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTL VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPP CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKH EDP EVKFNWYVDGVEVH NAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWEQGDVFSCSVMH EALHNHYTQKSLSLSPGK) and L1.24 of Figure 20J (DIVMTQSPSSLSASVGDRVTITCRASQNVDTWVAWYQQKPGQSPKALIYSASYRYS GVPDRFTGSGSGTDFTLTISSLQPEDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKH KVYACEVTHQGLSSPVTKSFNRGEC).

3. A heterodimeric antibody according to claim 1 wherein said second heavy chain and said first light chain are H1 (EVQLVESGGG LVQPGGSLRLSCAASG FDFSRSWM NWVRQAPG KG LEWVSEIN PDSSTINYATSVKGRFTISRDNSKNTLYLQM NSLRAE DTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVV VDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEA LHNHYTQKSLSLSPGK) and L1.24 (DIVMTQSPSSLSASVGDRVTITCRASQNVDTWVAWYQQKPGQSPKALIYSASYRYS GVPDRFTGSGSGTDFTLTISSLQPEDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC).

4. A heterodimeric antibody according to any one of claims 1 to 3 wherein said scFv has a charged scFv linker.

5. A heterodimeric antibody according to claim 4 wherein charged scFv linker has a positive charge from 3 to 8 and is selected from the group consisting of SEQ ID NOs: 443 to 451.

6. A nucleic acid composition comprising:

a) a first nucleic acid encoding the first heavy chain of any one of claims 1 to 5;

b) a second nucleic acid encoding the second heavy chain of any one of claims 1 to 5; and

c) a third nucleic acid encoding said light chain of any one of claims 1 to 5.

7. A nucleic acid composition comprising:

a) a first expression vector comprising a first nucleic acid encoding the first heavy chain of any one of claims 1 to 5;

b) a second expression vector comprising a second nucleic acid encoding the second heavy chain of any one of claims 1 to 5; and

c) a third expression vector comprising a third nucleic acid encoding the light chain of any one of claims 1 to 5.

8. A host cell comprising the nucleic acid composition of claim 6.

9. A host cell comprising the nucleic acid composition of claim 7.

10. A method of producing a heterodimeric antibody according to any of claims 1 to 5 comprising:

a) providing a first expression vector comprising a first nucleic acid encoding the second heavy chain comprising:

i) the second Fc domain variant; and

ii) the first variable heavy domain; and

b) providing a second expression vector comprising a second nucleic acid encoding the first heavy chain comprising:

i) the first Fc domain variant; and

ii) the single chain Fv region (scFv) that binds CD3;

c) providing a third expression vector comprising a third nucleic acid encoding the first light chain; wherein said first variable heavy domain and the variable light domain of the first light chain bind CD38;

d) wherein said first, second and third expression vectors are transfected into host cells at a ratio selected from the group consisting of 1:1.5:1.5, 1:2:1.5, 1:0.667:2, 1:1:2, 1:1.5:2, and 1:2:2; and

e) expressing said first, second and third nucleic acids in said host cells to produce a first, second and third amino acid sequence, respectively, such that said first, second and third amino acid sequences form said heterodimeric antibody.

11. The method of claim 10, further comprising (f) formulating the heterodimeric antibody into a pharmaceutical composition.

12. A pharmaceutical composition comprising the heterodimeric antibody of any one of claims 1-5.

13. Use of a heterodimeric antibody according to any of claims 1 to 5 in the manufacture of a medicament for treating cancer in a patient in need thereof.

14. A nucleic acid composition comprising an expression vector comprising a nucleic acid encoding the first heavy chain of claim 1 and an expression vector comprising a second nucleic acid encoding the second heavy chain of claim 1 and a third nucleic acid encoding the first light chain of claim 1.