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Inventor(s)	GANESAN; Rajkumar et al.

ANTI-Vbeta17/ANTI-CD123 BISPECIFIC ANTIBODIES

Abstract

Anti-Vβ17/anti-CD123 bispecific antibodies or antigen-binding fragments thereof are described. Also described are nucleic acids encoding the antibodies, compositions comprising the antibodies, methods of producing the antibodies, and methods of using the antibodies.

Inventors: **GANESAN; Rajkumar (Blue Bell, PA), GREWAL; Iqbal S. (Newtown, PA), SEPULVEDA; Manuel Alejandro (West Windsor, NJ)**

Applicant: **Janssen Biotech, Inc.** (Horsham, PA)

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Background/Summary

CROSS REFERENCE TO RELATED APPLICATIONS [0001] This application is a continuation of U.S. patent application Ser. No. 17/437,771, filed on Sep. 9, 2021, which is the U.S. National Stage Application under 35 U.S.C. § 371 of International Patent Application No. PCT/IB2020/000342, filed on Mar. 11, 2020, which claims the benefit of U.S. Provisional Application No. 62/816,464, filed on Mar. 11, 2019, the disclosure of each of which is incorporated by reference herein in its entirety.

FIELD OF THE INVENTION

[0002] This invention relates to monoclonal anti-Vβ17/anti-CD123 bispecific antibodies, nucleic acids and expression vectors encoding the antibodies, recombinant cells containing the vectors, and compositions comprising the antibodies. Methods of making the antibodies, and methods of using the antibodies to kill cancer cells, are also provided.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

[0003] This application contains a sequence listing, which is submitted electronically. The contents of the electronic sequence listing (065768.133US3.xml; size 72,235 bytes; and creation date Feb. 24, 2025) is herein incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

[0004] Cytotoxic T cells (e.g., CD8+ T cells) can be utilized to directly kill cancer cells. Finding a way to direct cytotoxic T cells to a cancer cell could lead to the killing of such cells and an inhibition of cancer cell propagation. It has been demonstrated that cytotoxic T cells can be activated against cancer cells expressing cancer-associated antigens, by bring said cytotoxic T cells into close proximity to the cancer cells for an extended period of time using a bispecific antibody that binds both the cytotoxic T cell and the cancer cell. A variety of potential complications to this approach of killing cancer cells exist, such as selecting T cell and cancer cell antigens that mediate T cell activation, selecting parental antibodies that will have adequate affinity to mediate binding in the context of a bispecific antibody, and choosing a cancer cell antigen that will activate T cells to act specifically against cancer cells, rather than elicit nonspecific T cell activation. These complications are only compounded in the context of attempting to activate T cells to destroy cancer cells in an animal subject.

BRIEF SUMMARY OF THE INVENTION

[0005] Provided herein are bispecific antibodies capable of binding Vβ17, an antigen associated with T cells, and CD123, an antigen associated with cancer cells. Cytotoxic T cells express T cell receptors that consist of α- and β-chains, such as Vβ17. It is hypothesized that a bispecific antibody binding to Vβ17 and a cancer-associated antigen, such as CD123, may direct a cytotoxic T cell to an antigen-expressing cancer cell. Utilizing a bispecific antibody of this sort to recruit, or redirect, the cytotoxic T cell to an antigen-expressing cancer cell and could allow the T cell to kill the cancer cell.

[0006] In one general aspect, the present disclosure relates to isolated bispecific antibodies or antigen-binding fragments thereof that bind to Vβ17 and CD123.

[0007] Provided herein are isolated Vβ17 bispecific antibodies or antigen-binding fragments thereof. The isolated Vβ17 bispecific antibody or antigen-binding fragment thereof comprises:

[0008] a. a first heavy chain (HC1); [0009] b. a second heavy chain (HC2); [0010] c. a first light chain (LC1); and [0011] d. a second light chain (LC2),

wherein HC1 is associated with LC1 and HC2 is associated with LC2, and wherein HC1 comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3, respectively, and LC1 comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and

LCDR3 comprising the amino acid sequences of SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6, respectively, to form a binding site for a first antigen, and wherein HC2 and LC2 form a binding site for a second antigen. In certain embodiments, the binding site for the first antigen binds to a Vβ17 on the surface of a CD8+ or CD4+ T cell. In certain embodiments, the binding site for the second antigen binds to a tumor antigen present on the surface of a cancer cell.
[0012] In certain embodiments, the binding of the bispecific antibody to Vβ17 present on the surface of the CD8+ or CD4+ T cell and the binding of the tumor antigen present on the surface of the cancer cells results in the killing of the cancer cell.
[0013] In certain embodiments, HC2 and LC2 bind to CD123.
[0014] In certain embodiments, the bispecific antibody or antigen-binding fragment thereof is an IgG isotype, such as IgG4.
[0015] In certain embodiments, the bispecific antibody or antigen-binding fragment thereof induces CD8+ or CD4+ T-cell dependent cytotoxicity of a cancer cell in vitro with an EC.sub.50 of less than about 0.2 pM.
[0016] Also provided are isolated anti-Vβ17/anti-CD123 bispecific antibodies or antigen-binding fragments thereof. The anti-Vβ17/anti-CD123 bispecific antibodies or antigen-binding fragments thereof comprise: [0017] a. a first heavy chain (HC1); [0018] b. a second heavy chain (HC2) [0019] c. a first light chain (LC1); and [0020] d. a second light chain (LC2),
wherein HC1 is associated with LC1 and HC2 is associated with LC2, and wherein HC1 comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NO: 1, SEQ ID NO:2, and SEQ ID NO:3, respectively, and LC1 comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6, respectively, to form a binding site for a first antigen that specifically binds Vβ17, and wherein HC2 comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NO:34, SEQ ID NO:35, and SEQ ID NO: 36, respectively, and LC2 comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NO:37, SEQ ID NO: 38, and SEQ ID NO:39, respectively, to form a biding site for a second antigen that specifically binds CD123. In certain embodiments, the HC1 comprises the amino acid sequence of SEQ ID NO: 13 and LC1 comprises the amino acid sequence of SEQ ID NO: 14, and the HC2 comprises the amino acid sequence of SEQ ID NO:15 and LC2 comprises the amino acid sequence of SEQ ID NO: 16. In certain embodiments, the Vβ17 is on the surface of a CD8+ or CD4+ T cell. In certain embodiments, the CD123 is on the surface of a cancer cell. In certain embodiments, the bispecific antibody or antigen-binding fragment thereof induces CD8+ or CD4+ T-cell dependent cytotoxicity of a cancer cell in vitro with an EC50 of less than about 0.2 pM.
[0021] In certain embodiments, the anti-Vβ17/anti-CD123 bispecific antibodies or antigen-binding fragments thereof are chimeric, partially humanized, or fully humanized.
[0022] Also provided are isolated humanized Vβ17 monoclonal antibodies or antigen-binding fragments thereof. The isolated humanized Vβ17 monoclonal antibody or antigen-binding fragment thereof can comprise an amino acid sequence with at least 95% identity to the amino acid sequence of SEQ ID NO:28. In certain embodiments, the isolated humanized Vβ17 monoclonal antibody or antigen-binding fragment thereof comprises an amino acid sequence of SEQ ID NO:28.
[0023] Also provided are isolated nucleic acids encoding the monoclonal antibodies or antigen-binding fragments thereof and the bispecific antibodies or antigen-binding fragments thereof disclosed herein.
[0024] Also provided are vectors comprising the isolated nucleic acids encoding the monoclonal antibodies or antigen-binding fragments thereof and the bispecific antibodies or antigen-binding fragments thereof disclosed herein.
[0025] Also provided are host cells comprising the vectors comprising the isolated nucleic acids

disclosed herein.
[0026] Also provided are methods of directing a Vβ17-expressing CD8+ or CD4+ T cell to a cancer cell. The methods comprise contacting a Vβ17-expressing CD8+ or CD4+ T cell with a anti-Vβ17/anti-CD123 bispecific antibodies or antigen-binding fragments thereof disclosed herein. Contacting the Vβ17-expressing CD8+ or CD4+ T cell with the anti-Vβ17/anti-CD123 bispecific antibodies or antigen-binding fragments thereof can direct the Vβ17-expressing CD8+ or CD4+ T cell to a cancer cell.
[0027] Also provided are methods for inhibiting growth or proliferation of cancer cells. The methods comprise contacting the cancer cells with the bispecific antibodies disclosed herein. Contacting the cancer cells with the described antibodies can, for example, inhibit the growth or proliferation of the cancer cells, or promote T cell mediated killing of the cancer cells.
[0028] Also provided are methods of producing the bispecific antibodies or antigen-binding fragments thereof disclosed herein. The methods comprise culturing a cell comprising a nucleic acid encoding one heavy and light chain pair of the bispecific antibody under conditions to produce the heavy and light chains or an antigen-binding fragment thereof, and recovering the heavy and light chains of the bispecific antibody or an antigen-binding fragment thereof from the cell or culture. Following collection of heavy and light chains for both arms of the bispecific antibody, the heavy and light chain pairs are mixed in conditions suitable to allow for self-assembly, after which the self-assembled bispecific antibodies are collected.
[0029] Also provided are methods of producing compositions comprising the bispecific antibodies or antigen-binding fragments disclosed herein, such as buffered compositions or purified compositions and the like. For example, the methods may comprise combining the bispecific antibody or antigen-binding fragment thereof with a buffer acceptable that is acceptable for storage and use of the bispecific antibody.
[0030] Also provided are kits comprising bispecific antibodies or antigen-binding fragments thereof disclosed herein and packaging for the same.

Description

BRIEF DESCRIPTION OF THE DRAWINGS
[0031] The foregoing summary, as well as the following detailed description of preferred embodiments of the present application, will be better understood when read in conjunction with the appended drawings. It should be understood, however, that the application is not limited to the precise embodiments shown in the drawings.
[0032] FIG. **1** shows a schematic demonstrating the binding of an anti-Vβ17/anti-tumor antigen bispecific antibody to recruit T-cells to a cancer cell and to induce cancer cell death.
[0033] FIGS. **2**A-**2**B shows that Vβ17+CD8+ T cells exist in healthy subjects and upon culture with M1 peptide these cells can be expanded in vitro. FIG. **2**A shows FACS histograms of gated peripheral blood mononuclear cells (PBMCs) for CD8+ T cells expressing Vβ17 (Vβ17+) on the cells surface from healthy subjects. FIG. **2**B shows HLA sub-type of various donors and presence of percent Vβ17+CD8+ T cells identified as day 0, and after in vitro expansion with M1 peptide for 14 days (Day 14).
[0034] FIG. **3** shows Vβ17+CD8+ T cells have hallmarks of killer cytotoxic cells. Bar graph indicates expression of CD107a, CD69, Granzyme B (Gzb) and Interferon-γ (IFNγ) on gated PBMCs for CD8+ T cells expressing Vβ17 (Vβ17+) on the cell surface at day 0 (no M1) and at day 14 after stimulation with M1 peptide (+M1).
[0035] FIG. **4** shows binding of Vβ11 [anti-Vβ17/anti-CD123] bispecific as well as Vβ13 [Vβ17 null control bispecific] antibodies to CD8+ T cells. Data presented from CD8+ T cells isolated from PBMCs from 3 different donors (D203517, HPU09381 and HPU08694). The table below each

graph presents EC.sub.50 values for binding in nM.
[0036] FIG. **5** shows binding of Vβ17 and CD123 bispecific (Vβ11) as well as Vβ17 null control bispecific (Vβ13) antibodies to AML cancer cell line. Data presented shows binding of bispecific antibodies to Kasumi3 AML cell line. The table below the graph presents EC.sub.50 values for binding in nM.
[0037] FIG. **6** shows redirection of Vβ17+ T cells by bispecific antibodies that induce efficient killing of AML cancer cells. Data in the left graph shows killing of Kasumi3 cancer cells at an effector to target (E:T) ratio 0.5:1 and dose titration of bispecific antibodies. Data in the middle graph shows killing of Kasumi3 cancer cells at an E:T ratio 1:1 and dose titration of bispecific antibodies. Data in the right graph shows killing of Kasumi3 cancer cells at an ET ratio 5:1 and dose titration of bispecific antibodies. The table below the graphs shows EC.sub.50 values calculated from the above graphs given in pM.
[0038] FIGS. **7**A-**7**B show specific binding of an anti-Vβ17/anti-CD123 bispecific antibody (Vβ11) and a Vβ17 null bispecific antibody (Vβ13) to CD8+ T cells isolated from PBMCs. FIG. **7**A shows FACS histograms of gated PBMCs for CD8+ T cells expressing Vβ17 (Vβ17+) on the cell surface from healthy subjects (left graph, Vβ17 non-depleted) and from PBMCs that were depleted of Vβ17+ T cells using negative selection (right graph, Vβ17 depleted). FIG. **7**B shows specific binding of an anti-Vβ17/anti-CD123 bispecific antibody (Vβ11) and a Vβ17 null bispecific antibody (Vβ13) to CD8+ T cells from FIG. **7**A. A dose response of bispecific antibodies is shown in the figure. The table below the graph shows EC.sub.50 values for binding calculated from the above graph given in nM.
[0039] FIG. **8** shows specific recruitment of Vβ17 T cells by a Vβ17-bispecific antibody for killing of Kasumi3 cancer cells. Left figure shows killing of Kasumi3 AML cell line when effectors cells were isolated from PBMCs containing CD8+ T cells expressing Vβ17 (Vβ17+) on the cell surface (untouched CD8 T cells). Insert shows presence of 10.1% Vβ17+CD8 T cells in the effector cell population. Right figure shows killing of Kasumi3 AML cell line when effector CD8+ T cells were isolated from PBMCs, but Vβ17+ T cells were depleted by negative selection. Insert shows presence of a minor population (0.086%) Vβ17+CD8+ T cells in the effector cell population.
[0040] FIGS. **9**A-**9**B show that there is no pan activation of T cells when using Vβ17 bispecific antibodies. FIG. **9**A shows FACS plots of Vβ17+ and Vβ17-gated CD8+ T cells. When T cells were activated with Vβ17 bispecific antibody there was high level of upregulation of CD69 (62.5%) on Vβ17+ as compared to Vβ17-CD8+ T cells (1.80%). FIG. **9**B shows a bar graph for upregulation of CD69 on Vβ17+ and Vβ17-gated CD8+ T cells when activated using Vβ17 bispecific antibody.
[0041] FIG. **10** shows that Vβ17+ T cells from HLA A2 negative donor are also effector killer cells and no pre-stimulation of Vβ17+ cell required. Efficient cytotoxicity mediated by Vβ17 bispecific antibody of Kasumi3 cancer cells is shown from PBMCs containing Vβ17+ T cells from HLA A2 negative donor (HPU 09381).

DETAILED DESCRIPTION OF THE INVENTION

[0042] Discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is for the purpose of providing context for the invention. Such discussion is not an admission that any or all of these matters form part of the prior art with respect to any inventions disclosed or claimed.
[0043] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention pertains. Otherwise, certain terms used herein have the meanings as set forth in the specification.
[0044] Unless otherwise stated, any numerical values, such as a concentration or a concentration range described herein, are to be understood as being modified in all instances by the term “about.” Thus, a numerical value typically includes ±10% of the recited value. For example, a concentration of 1 mg/mL includes 0.9 mg/mL to 1.1 mg/mL. Likewise, a concentration range of 1% to 10% (w/v) includes 0.9% (w/v) to 11% (w/v). As used herein, the use of a numerical range expressly

includes all possible subranges, all individual numerical values within that range, including integers within such ranges and fractions of the values unless the context clearly indicates otherwise.

[0045] Unless otherwise indicated, the term “at least” preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the invention.

[0046] It must be noted that as used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural reference unless the context clearly dictates otherwise.

[0047] As used herein, the terms “comprises,” “comprising,” “includes,” “including,” “has,” “having,” “contains” or “containing,” or any other variation thereof, will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers and are intended to be non-exclusive or open-ended. For example, a composition, a mixture, a process, a method, an article, or an apparatus that comprises a list of elements is not necessarily limited to only those elements but can include other elements not expressly listed or inherent to such composition, mixture, process, method, article, or apparatus. Further, unless expressly stated to the contrary, “or” refers to an inclusive or and not to an exclusive or. For example, a condition A or B is satisfied by any one of the following: A is true (or present) and B is false (or not present), A is false (or not present) and B is true (or present), and both A and B are true (or present).

[0048] As used herein, the conjunctive term “and/or” between multiple recited elements is understood as encompassing both individual and combined options. For instance, where two elements are conjoined by “and/or,” a first option refers to the applicability of the first element without the second. A second option refers to the applicability of the second element without the first. A third option refers to the applicability of the first and second elements together. Any one of these options is understood to fall within the meaning, and therefore satisfy the requirement of the term “and/or” as used herein. Concurrent applicability of more than one of the options is also understood to fall within the meaning, and therefore satisfy the requirement of the term “and/or.”

[0049] It should also be understood that the terms “about,” “approximately,” “generally,” “substantially,” and like terms, used herein when referring to a dimension or characteristic of a component of the preferred invention, indicate that the described dimension/characteristic is not a strict boundary or parameter and does not exclude minor variations therefrom that are functionally the same or similar, as would be understood by one having ordinary skill in the art. At a minimum, such references that include a numerical parameter would include variations that, using mathematical and industrial principles accepted in the art (e.g., rounding, measurement or other systematic errors, manufacturing tolerances, etc.), would not vary the least significant digit.

[0050] The terms “identical” or percent “identity,” in the context of two or more nucleic acids or polypeptide sequences (e.g., anti-Vβ17/anti-CD123 bispecific antibodies and polynucleotides that encode them, Vβ17 polypeptides and Vβ17 polynucleotides that encode them, CD123 polypeptides and CD123 polynucleotides that encode them), refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection.

[0051] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

[0052] Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (see generally, *Current Protocols in Molecular Biology*, F. M. Ausubel et al., eds., *Current Protocols, a joint venture between* Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (1995 Supplement) (Ausubel)).

[0053] Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1990) *J. Mol. Biol.* 215:403-410 and Altschul et al. (1997) *Nucleic Acids Res.* 25:3389-3402, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased.

[0054] Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=−4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

[0055] In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

[0056] A further indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions.

Antibodies

[0057] Described herein are isolated anti-Vβ17 bispecific antibodies or antigen-binding fragments thereof, nucleic acids and expression vectors encoding the antibodies, recombinant cells containing the vectors, and compositions comprising the antibodies. The invention additionally relates to

isolated anti-Vβ17/anti-CD123 bispecific antibodies or antigen-binding fragments thereof, nucleic acids and expression vectors encoding the antibodies, recombinant cells containing the vectors, and compositions comprising the bispecific antibodies. Methods of making the antibodies, and methods of using the antibodies to treat diseases, including cancer, are also provided. The antibodies disclosed herein possess one or more desirable functional properties, including but not limited to high-affinity binding to Vβ17 and/or CD123, high specificity to Vβ17 and/or CD123, and the ability to treat or prevent cancer when administered alone or in combination with other anti-cancer therapies.

[0058] As used herein, the term “antibody” is used in a broad sense and includes immunoglobulin or antibody molecules including human, humanized, composite and chimeric antibodies and antibody fragments that are monoclonal or polyclonal. In general, antibodies are proteins or peptide chains that exhibit binding specificity to a specific antigen. Antibody structures are well known. Immunoglobulins can be assigned to five major classes (i.e., IgA, IgD, IgE, IgG and IgM), depending on the heavy chain constant domain amino acid sequence. IgA and IgG are further sub-classified as the isotypes IgA1, IgA2, IgG1, IgG2, IgG3 and IgG4. Antibody light chains of vertebrate species can be assigned to one of two clearly distinct types, namely kappa and lambda, based on the amino acid sequences of their constant domains. Accordingly, the antibodies of the invention can contain a kappa or lambda light chain constant domain. According to particular embodiments, the antibodies disclosed herein include heavy and/or light chain constant regions from mouse or human antibodies. In addition to the heavy and light constant domains, antibodies contain an antigen-binding region that is made up of a light chain variable region and a heavy chain variable region, each of which contains three domains (i.e., complementarity determining regions 1-3; CDR1, CDR2, and CDR3). The light chain variable region domains are alternatively referred to as LCDR1, LCDR2, and LCDR3, and the heavy chain variable region domains are alternatively referred to as HCDR1, HCDR2, and HCDR3.

[0059] As used herein, the term an “isolated antibody” refers to an antibody which is substantially free of other antibodies having different antigenic specificities (e.g., an isolated antibody that specifically binds to Vβ17 is substantially free of antibodies that do not bind to Vβ17; an isolated antibody that specifically binds to CD123 is substantially free of antibodies that do not bind to CD123). In addition, an isolated antibody is substantially free of other cellular material and/or chemicals.

[0060] As used herein, the term “monoclonal antibody” refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that can be present in minor amounts. The monoclonal antibodies disclosed herein can be made by the hybridoma method, phage display technology, single lymphocyte gene cloning technology, or by recombinant DNA methods. For example, the monoclonal antibodies can be produced by a hybridoma which includes a B cell obtained from a transgenic nonhuman animal, such as a transgenic mouse or rat, having a genome comprising a human heavy chain transgene and a light chain transgene.

[0061] As used herein, the term “antigen-binding fragment” refers to an antibody fragment such as, for example, a diabody, a Fab, a Fab′, a F(ab′)2, an Fv fragment, a disulfide stabilized Fv fragment (dsFv), a (dsFv).sub.2, a bispecific dsFv (dsFv-dsFv′), a disulfide stabilized diabody (ds diabody), a single-chain antibody molecule (scFv), a single domain antibody (sdab) an scFv dimer (bivalent diabody), a multispecific antibody formed from a portion of an antibody comprising one or more CDRs, a camelized single domain antibody, a nanobody, a domain antibody, a bivalent domain antibody, or any other antibody fragment that binds to an antigen but does not comprise a complete antibody structure. An antigen-binding fragment is capable of binding to the same antigen to which the parent antibody or a parent antibody fragment binds. According to particular embodiments, the antigen-binding fragment comprises a light chain variable region, a light chain constant region, and an Fd segment of the heavy chain. According to other particular embodiments, the antigen-binding

fragment comprises Fab and F(ab′).
[0062] As used herein, the term “humanized antibody” refers to a non-human antibody that is modified to increase the sequence homology to that of a human antibody, such that the antigen-binding properties of the antibody are retained, but its antigenicity in the human body is reduced.
[0063] As used herein, the term “multispecific antibody” refers to an antibody that comprises a plurality of immunoglobulin variable domain sequences, wherein a first immunoglobulin variable domain sequence of the plurality has binding specificity for a first epitope and a second immunoglobulin variable domain sequence of the plurality has binding specificity for a second epitope. In an embodiment, the first and second epitopes do not overlap or do not substantially overlap. In an embodiment, the first and second epitopes are on different antigens, e.g., the different proteins (or different subunits of a multimeric protein). In an embodiment, a multispecific antibody comprises a third, fourth, or fifth immunoglobulin variable domain. In an embodiment, a multispecific antibody is a bispecific antibody molecule, a trispecific antibody molecule, or a tetraspecific antibody molecule.
[0064] As used herein, the term “bispecifc antibody” refers to a multispecific antibody that binds no more than two epitopes or two antigens. A bispecific antibody is characterized by a first immunoglobulin heavy and light chain pair which has binding specificity for a first epitope (e.g., an epitope on a Vβ17 antigen) and a second immunoglobulin heavy and light chain pair that has binding specificity for a second epitope (e.g., an epitope on a CD123 antigen). In an embodiment, the first and second epitopes are on different antigens, e.g., the different proteins (or different subunits of a multimeric protein). In an embodiment, a bispecific antibody comprises a heavy chain variable domain sequence and a light chain variable domain sequence which have binding specificity for a first epitope and a heavy chain variable domain sequence and a light chain variable domain sequence which have binding specificity for a second epitope. In an embodiment, a bispecific antibody comprises a half antibody, or fragment thereof, having binding specificity for a first epitope and a half antibody, or fragment thereof, having binding specificity for a second epitope. In an embodiment, a bispecific antibody comprises a scFv, or fragment thereof, having binding specificity for a first epitope, and a scFv, or fragment thereof, having binding specificity for a second epitope. In an embodiment, the first epitope is located on Vβ17 and the second epitope is located on CD123. In an embodiment, the first epitope is located on Vβ17 and the second epitope is located on PD-1, PD-L1, CTLA-4, EGFR, HER-2, CD19, CD20, CD3 and/or other tumor associated immune suppressors or surface antigens.
[0065] The term “half antibody” as used herein refers to one immunoglobulin heavy chain associated with one immunoglobulin light chain. An exemplary half-antibody is depicted in SEQ ID NO: 28. One skilled in the art will readily appreciate that a half-antibody can encompass a fragment thereof and can also have an antigen binding domain consisting of a single variable domain, e.g., originating from a camelidae.
[0066] As used herein, the term “Vβ17” refers to a T cell receptor, which is expressed in response to an immune response on a cytotoxic T cell. Vβ17-expressing CD8+ T cells are commonly produced in response to influenza A virus exposure in a subject. Vβ17-expressing CD8+ T cells provide great recall in response to influenza exposure in the subject. The term “Vβ17” includes any Vβ17 variant, isoform, and species homolog, which is naturally expressed by cells (including T cells) or can be expressed on cells transfected with genes or cDNA encoding the polypeptide. Unless noted, preferably the Vβ17 is a human Vβ17. A human Vβ17 amino acid sequence is provided by GenBank Accession Number AAB49730.1.
[0067] The term “CD123” refers to a molecule that is found on cells which helps transmit the signal of interleukin-3, a soluble cytokine that is important in the immune system. CD123 can also be referred to as the “interleukin-3 receptor.” The receptor belongs to the type I cytokine receptor family and is a heterodimer with a unique alpha chain paired with the common beta subunit (beta c or CD131). The CD123 receptor can be found on pluripotent progenitor cells and can induce

tyrosine phosphorylation within the cell and promote proliferation and differentiation within hematopoietic cell lines. CD123 can also be expressed in acute myeloid leukemia (AML) subtypes. The term “CD123” includes any CD123 variant, isoform, and species homolog, which is naturally expressed by cells (including T cells) or can be expressed on cells transfected with genes or cDNA encoding those polypeptides, unless noted, preferably the “CD123” is a human CD123. A human CD123 amino acid sequence is provided by GenBank Accession Number AY789109.1.

[0068] As used herein, an antibody that “specifically binds to Vβ17” refers to an antibody that binds to a Vβ17, preferably a human Vβ17, with a KD of 1×10.sup.−7 M or less, preferably 1×10.sup.−8 M or less, more preferably 5×10.sup.−9 M or less, 1×10.sup.−9 M or less, 5×10.sup.−10 M or less, or 1×10.sup.−10 M or less. The term “KD” refers to the dissociation constant, which is obtained from the ratio of Kd to Ka (i.e., Kd/Ka) and is expressed as a molar concentration (M). KD values for antibodies can be determined using methods in the art in view of the present disclosure. For example, the KD of an antibody can be determined by using surface plasmon resonance, such as by using a biosensor system, e.g., a Biacore® system, or by using bio-layer interferometry technology, such as an Octet® RED96 system.

[0069] As used herein, an antibody that “specifically binds to CD123” refers to an antibody that binds to a CD123, preferably a human CD123, with a KD of 1×10.sup.−7 M or less, preferably 1×10.sup.−8 M or less, more preferably 5×10.sup.−9 M or less, 1×10.sup.−9 M or less, 5×10.sup.−10 M or less, or 1×10.sup.−10 M or less. The term “KD” refers to the dissociation constant, which is obtained from the ratio of Kd to Ka (i.e., Kd/Ka) and is expressed as a molar concentration (M). KD values for antibodies can be determined using methods in the art in view of the present disclosure. For example, the KD of an antibody can be determined by using surface plasmon resonance, such as by using a biosensor system, e.g., a Biacore® system, or by using bio-layer interferometry technology, such as an Octet® RED96 system.

[0070] The smaller the value of the KD of an antibody, the higher affinity that the antibody binds to a target antigen.

[0071] According to a particular aspect, the invention relates to an isolated Vβ17 bispecific antibody or antigen-binding fragment thereof comprising (a) a first heavy chain (HC1); (b) a second heavy chain (HC2); (c) a first light chain (LC1); and (d) a second light chain (LC2). The HC1 can be associated with the LC1 and the HC2 can be associated with LC2. The HC1 can comprise a heavy chain complementarity determining region 1 (HCDR1), HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NO: 1, SEQ ID NO:2, and SEQ ID NO:3, respectively, and LC1 can comprise a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6, respectively.

[0072] The HC1 and LC1 form a binding site for a first antigen, and the HC2 and LC2 form a binding site for a second antigen. By way of an example, the binding site for the first antigen can bind to a Vβ17 on a CD8+ or CD4+ T cell, and the binding site for the second antigen can, for example, bind a tumor antigen present on the surface of a cancer cell. The binding of the Vβ17 bispecific antibody to Vβ17 present on the surface of the CD8+ or CD4+ T cell, and the binding of the tumor antigen present on the surface of the cancer cells can, for example, result in the killing of the cancer cell.

[0073] Also provided herein are anti-Vβ17/anti-CD123 bispecific antibodies or antigen-binding fragments thereof comprising an anti-Vβ17 antibody or an antigen-binding fragment thereof and an anti-CD123 antibody or antigen-binding fragment thereof. In certain embodiments the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof comprises (a) a first heavy chain (HC1); (b) a second heavy chain (HC2); (c) a first light chain (LC1); and a second light chain (LC2). The HC1 is associated with the LC1 and the HC2 is associated with the LC2. In certain embodiments, the HC1 comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NO:1, SEQ ID

NO: 2, and SEQ ID NO:3, respectively, and LC1 comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NO: 4, SEQ ID NO:5, and SEQ ID NO:6, respectively. In certain embodiments, the HC2 comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NO:34, SEQ ID NO:35, and SEQ ID NO:36, respectively, and LC2 comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NO:37, SEQ ID NO:38, and SEQ ID NO:39, respectively

[0074] In certain embodiments, the HC1 can, for example, comprise an amino acid sequence of SEQ ID NO:13 and the LC1 can, for example, comprise an amino acid sequence of SEQ ID NO:14 to form a binding site for a first antigen that specifically binds Vβ17. The HC2 can, for example, comprise an amino acid sequence of SEQ ID NO:15 and the LC2 can, for example, comprise an amino acid sequence of SEQ ID NO:16 to form a binding site for a second antigen that specifically binds CD123.

[0075] In certain embodiments, the Vβ17 is on the surface of a CD8+ or CD4+ T cell. In certain embodiments, the CD123 is on the surface of a cancer cell (e.g., a leukemia cell).

[0076] In some embodiments, the bispecific antibodies disclosed herein can take the form of a diabody, a cross-body, or a bispecific antibody obtained via a controlled Fab arm exchange as described herein.

[0077] In some embodiments, the bispecific antibodies include IgG-like molecules with complementary CH3 domains that promote heterodimerization; recombinant IgG-like dual targeting molecules, wherein the two sides of the molecule each contain the Fab fragment or part of the Fab fragment of at least two different antibodies; IgG fusion molecules, wherein full length IgG antibodies are fused to an extra Fab fragment or parts of Fab fragment; Fc fusion molecules, wherein single chain Fv molecules or stabilized diabodies are fused to heavy-chain constant-domains, Fc-regions or parts thereof; Fab fusion molecules, wherein different Fab-fragments are fused together; ScFv- and diabody-based and heavy chain antibodies (e.g., domain antibodies, nanobodies) wherein different single chain Fv molecules or different diabodies or different heavy-chain antibodies (e.g. domain antibodies, nanobodies) are fused to each other or to another protein or carrier molecule.

[0078] In some embodiments, IgG-like molecules with complementary CH3 domains molecules include the Triomab®/Quadroma (Trion Pharma/Fresenius Biotech), the Knobs-into-Holes (Genentech), CrossMAbs® (Roche) and the electrostatically-matched (Amgen), the LUZ-Y (Genentech), the Strand Exchange Engineered Domain body (SEEDbody) (EMD Serono), the Biclonic® (Merus) and the DuoBody® (Genmab A/S).

[0079] In some embodiments, recombinant IgG-like dual targeting molecules include Dual Targeting (DT)-Ig (GSK/Domantis), Two-in-one Antibody (Genentech), Cross-linked Mabs (Karmanos Cancer Center), mAb2 (F-Star) and CovX®-body (CovX/Pfizer).

[0080] In some embodiments, IgG fusion molecules include Dual Variable Domain (DVD)-Ig (Abbott), IgG-like Bispecific (InnClone/Eli Lilly), Ts2Ab (MedImmunc/AZ) and BsAb (Zymogenetics), HERCULES (Biogen Idec) and TvAb (Roche).

[0081] In some embodiments, Fc fusion molecules can include ScFv/Fc Fusions (Academic Institution), SCORPION® (Emergent BioSolutions/Trubion, Zymogenetics/BMS), Dual Affinity Retargeting Technology (Fc-DART®) (MacroGenics) and Dual (ScFv).sub.2-Fab (National Research Center for Antibody Medicine—China).

[0082] In some embodiments, Fab fusion bispecific antibodies include F (ab) 2 (Medarex/AMGEN), Dual-Action or Bis-Fab (Genentech), Dock-and-Lock (DNL®) (ImmunoMedics), Bivalent Bispecific (Biotecnoland Fab-Fv (UCB-Celltech). ScFv-, diabody-based, and domain antibodies, include but are not limited to, Bispecific T Cell Engager (BiTE®) (Micromet), Tandem Diabody (Tandab®) (Affimed), Dual Affinity Retargeting Technology

(DART®) (MacroGenics), Single-chain Diabody (Academic), TCR-like Antibodies (AIT, ReceptorLogics), Human Serum Albumin ScFv Fusion (Merrimack) and COMBODY (Epigen Biotech), dual targeting Nanobodies® (Ablynx), dual targeting heavy chain only domain antibodies.

[0083] Full length bispecific antibodies disclosed herein can be generated for example using Fab arm exchange (or half molecule exchange) between two mono specific bivalent antibodies by introducing substitutions at the heavy chain CH3 interface in each half molecule to favor heterodimer formation of two antibody half molecules having distinct specificity either in vitro in cell-free environment or using co-expression. The Fab arm exchange reaction is the result of a disulfide-bond isomerization reaction and dissociation-association of CH3 domains. The heavy-chain disulfide bonds in the hinge regions of the parent mono specific antibodies are reduced. The resulting free cysteines of one of the parent monospecific antibodies form an inter heavy-chain disulfide bond with cysteine residues of a second parent mono specific antibody molecule and simultaneously CH3 domains of the parent antibodies release and reform by dissociation-association. The CH3 domains of the Fab arms can be engineered to favor heterodimerization over homodimerization. The resulting product is a bispecific antibody having two Fab arms or half molecules, each binding a distinct epitope, i.e. an epitope on Vβ17 and an epitope on a tumor antigen.

[0084] “Homodimerization” as used herein refers to an interaction of two heavy chains having identical CH3 amino acid sequences. “Homodimer” as used herein refers to an antibody having two heavy chains with identical CH3 amino acid sequences.

[0085] “Heterodimerization” as used herein refers to an interaction of two heavy chains having non-identical CH3 amino acid sequences. “Heterodimer” as used herein refers to an antibody having two heavy chains with non-identical CH3 amino acid sequences.

[0086] The “knob-in-hole” strategy (see, e.g., PCT Inti. Publ. No. WO 2006/028936) can be used to generate full length bispecific antibodies. Briefly, selected amino acids forming the interface of the CH3 domains in human IgG can be mutated at positions affecting CH3 domain interactions to promote heterodimer formation. An amino acid with a small side chain (hole) is introduced into a heavy chain of an antibody specifically binding a first antigen and an amino acid with a large side chain (knob) is introduced into a heavy chain of an antibody specifically binding a second antigen. After co-expression of the two antibodies, a heterodimer is formed as a result of the preferential interaction of the heavy chain with a “hole” with the heavy chain with a “knob”. Exemplary CH3 substitution pairs forming a knob and a hole are (expressed as modified position in the first CH3 domain of the first heavy chain/modified position in the second CH3 domain of the second heavy chain): T366Y/F405A, T366W/F405W, F405W/Y407A, T394W/Y407T, T394S/Y407A, T366W/T394S, F405W/T394S and T366W/T366S_L368A_Y407V.

[0087] Other strategies such as promoting heavy chain heterodimerization using electrostatic interactions by substituting positively charged residues at one CH3 surface and negatively charged residues at a second CH3 surface can be used, as described in US Pat. Publ. No. US2010/0015133; US Pat. Publ. No. US2009/0182127; US Pat. Publ. No. US2010/028637; or US Pat. Publ. No. US2011/0123532. In other strategies, heterodimerization can be promoted by the following substitutions (expressed as modified position in the first CH3 domain of the first heavy chain/modified position in the second CH3 domain of the second heavy chain): L351Y_F405AY407V/T394W, T366I_K392M_T394W/F405A_Y407V, T366L_K392M_T394W/F405A_Y407V, L351Y_Y407A/T366A_K409F, L351Y_Y407A/T366V K409F Y407A/T366A_K409F, or T350V_L351Y_F405A_Y407V/T350V_T366L_K392L_T394W as described in U.S. Pat. Publ. No. US2012/0149876 or U.S. Pat. Publ. No. US2013/0195849.

[0088] In addition to methods described above, bispecific antibodies disclosed herein can be generated in vitro in a cell-free environment by introducing asymmetrical mutations in the CH3 regions of two mono specific homodimeric antibodies and forming the bispecific heterodimeric

antibody from two parent monospecific homodimeric antibodies in reducing conditions to allow disulfide bond isomerization according to methods described in International Pat. Publ. No. WO2011/131746. In the methods, the first monospecific bivalent antibody (e.g., anti-CD33 antibody) and the second monospecific bivalent antibody (e.g., anti-CD3 antibody) are engineered to have certain substitutions at the CH3 domain that promotes heterodimer stability; the antibodies are incubated together under reducing conditions sufficient to allow the cysteines in the hinge region to undergo disulfide bond isomerization; thereby generating the bispecific antibody by Fab arm exchange. The incubation conditions can optionally be restored to non-reducing conditions. Exemplary reducing agents that may be used are 2-mercaptoethylamine (2-MEA), dithiothreitol (DTT), dithioerythritol (DTE), glutathione, tris(2-carboxyethyl) phosphine (TCEP), L-cysteine and beta-mercaptoethanol, preferably a reducing agent selected from the group consisting of: 2-mercaptocthylamine, dithiothreitol and tris(2-carboxyethyl) phosphine. For example, incubation for at least 90 min at a temperature of at least 20° C. in the presence of at least 25 mM 2-MEA or in the presence of at least 0.5 mM dithiothreitol at a pH from 5-8, for example at pH of 7.0 or at pH of 7.4 may be used.

[0089] In certain embodiments, the anti-Vβ17 antibody or antigen-binding fragment thereof comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequence of: [0090] a. SEQ ID NOs: 1, 2, 3, 4, 5, and 6, respectively;
and the anti-CD123 antibody or antigen-binding fragment thereof comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, HCDR3, a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3, having the polypeptide sequence of: [0091] 1. SEQ ID NOs: 34, 35, 36, 37, 38, and 39, respectively.

[0092] According to another particular aspect, the invention relates to an isolated anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof that induces antibody-dependent cell-mediated cytotoxicity (ADCC). The bispecific antibody or antigen-binding fragment thereof can, for example, induce ADCC in vitro. The bispecific antibody or antigen-binding fragment thereof can induce ADCC with an EC.sub.50 of less than about 1 pM. In certain embodiments, the EC.sub.50 is less than about 1 pM, less than about 0.9 pM, less than about 0.8 pM, less than about 0.7 pM, less than about 0.6 pM, less than about 0.5 pM, less than about 0.4 pM, less than about 0.300 PM, less than about 0.2 pM, less than about 0.19 pM, less than about 0.18 pM, less than about 0.17 pM, less than about 0.16 pM, less than about 0.15 pM, less than about 0.14 pM, less than about 0.13 pM, less than about 0.12 pM, less than about 0.11 pM, less than about 0.1 pM, less than about 0.09 pM, less than about 0.08 pM, less than about 0.07 pM, less than about 0.06 pM, less than about 0.05 pM, less than about 0.04 pM, less than about 0.03 pM, less than about 0.02 pM, or less than about 0.01 pM. In certain embodiments, the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof comprises an IgG1, IgG2, IgG3, or IgG4 backbone. In one such embodiment, the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof has an antibody backbone of the IgG4 isotype.

[0093] In some embodiments described herein, immune effector properties of the anti-Vβ17/anti-CD123 bispecific antibodies can be enhanced or silenced through Fc modifications by techniques known to those skilled in the art. For example, Fc effector functions such as Clq binding, complement dependent cytotoxicity (CDC), antibody-dependent cell-mediated cytotoxicity (ADCC), antibody-dependent cell-mediated phagocytosis (ADCP), down regulation of cell surface receptors (e.g., B cell receptor; BCR), etc. may be provided and/or controlled by modifying residues in the Fc responsible for these activities.

[0094] “Antibody-dependent cell-mediated cytotoxicity” or “ADCC” refers to a cell-mediated reaction in which non-specific cytotoxic cells that express Fc receptors (FcRs) (e.g. Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and subsequently cause lysis of the target cell.

[0095] The ability of antibodies to induce ADCC can be enhanced by engineering their oligosaccharide component. Human IgG1 or IgG3 are N-glycosylated at Asn297 with the majority of the glycans in the well-known biantennary G0, G0F, G1, G1F, G2 or G2F forms. Antibodies produced by non-engineered CHO cells typically have a glycan fucose content of about at least 85%. The removal of the core fucose from the biantennary complex-type oligosaccharides attached to the Fc regions enhances the ADCC of antibodies via improved FcγRIIIa binding without altering antigen-binding or CDC activity. Such Abs can be achieved using different methods reported to lead to the successful expression of relatively high defucosylated antibodies bearing the biantennary complex-type of Fc oligosaccharides such as control of culture osmolality (Konno et al., Cytotechnology 64:249-65, 2012), application of a variant CHO line Lec13 as the host cell line (Shields et al., J Biol Chem 277:26733-26740, 2002), application of a variant CHO line EB66 as the host cell line (Olivier et al., MAbs; 2 (4), 2010; Epub ahead of print; PMID:20562582), application of a rat hybridoma cell line YB2/0 as the host cell line (Shinkawa et al., J Biol Chem 278:3466-3473, 2003), introduction of small interfering RNA specifically against the α-1,6-fucosyltrasferase (FUT8) gene (Mori et al., Biotechnol Bioeng 88:901-908, 2004), or coexpression of β-1,4-N-acetylglucosaminyltransferase III and golgi α-mannosidase II or a potent alpha-mannosidase I inhibitor, kifunensine (Ferrara et al., J Biol Chem 281:5032-5036, 2006, Ferrara et al., Biotechnol Bioeng 93:851-861, 2006; Xhou et al., Biotechnol Bioeng 99:652-65, 2008).
[0096] In some embodiments described herein, ADCC elicited by the anti-Vβ17/anti-CD123 bispecific antibodies can also be enhanced by certain substitutions in the antibody Fc. Exemplary substitutions include, for example, substitutions at amino acid positions 256, 290, 298, 312, 356, 330, 333, 334, 360, 378 or 430 (residue numbering according to the EU index) as described in U.S. Pat. No. 6,737,056.
[0097] According to another particular aspect, the invention relates to an isolated anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof capable of inducing T-cell dependent cytotoxicity in Vβ17-expressing cells and/or CD123-expressing cells. The bispecific antibody or antigen-binding fragment thereof can, for example, induce T-cell dependent cytotoxicity in Vβ17-expressing cells and/or CD123-expressing cells in vitro with an EC.sub.50 value of less than about 2 nM. In certain embodiments, the EC.sub.50 is less than about 2.0 nM, less than about 1.9 nM, less than about 1.8 nM, less than about 1.7 nM, less than about 1.6 nM, less than about 1.5 nM, less than about 1.4 nM, less than about 1.3 nM, less than about 1.2 nM, less than about 1.1 nM, less than about 1.0 nM, less than about 0.9 nM, less than about 0.8 nM, less than about 0.7 nM, less than about 0.6 nM, less than about 0.5 nM, less than about 0.4 nM, less than about 0.3 nM, less than about 0.2 nM, and less than about 0.1 nM.
[0098] According to another particular aspect, the invention relates to an isolated anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof, wherein the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof is chimeric.
[0099] According to another particular aspect, the invention relates to an isolated anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof, wherein the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof is human or humanized.
[0100] In another general aspect, the invention relates to an isolated humanized Vβ17 monoclonal antibody or antigen-binding fragment thereof. The isolated humanized Vβ17 monoclonal antibody or antigen-binding fragment thereof comprises an amino acid sequence with at least 85%, preferably 90%, more preferably 95% or more, such as 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO:28. In certain embodiments, the humanized Vβ17 monoclonal antibody or antigen-binding fragment thereof comprises the amino acid sequence of SEQ ID NO:28.
[0101] In another general aspect, the invention relates to isolated nucleic acids encoding the monoclonal antibodies or antigen-binding fragments thereof disclosed herein. In another general aspect, the invention relates to isolated nucleic acids encoding the bispecific antibodies or antigen-

binding fragments thereof disclosed herein. It will be appreciated by those skilled in the art that the coding sequence of a protein can be changed (e.g., replaced, deleted, inserted, etc.) without changing the amino acid sequence of the protein. Accordingly, it will be understood by those skilled in the art that nucleic acid sequences encoding monoclonal antibodies and/or bispecific antibodies disclosed herein can be altered without changing the amino acid sequences of the proteins.

[0102] In another general aspect, the invention relates to vectors comprising the isolated nucleic acids disclosed herein. Any vector known to those skilled in the art in view of the present disclosure can be used, such as a plasmid, a cosmid, a phage vector or a viral vector. In some embodiments, the vector is a recombinant expression vector such as a plasmid. The vector can include any element to establish a conventional function of an expression vector, for example, a promoter, ribosome binding element, terminator, enhancer, selection marker, and origin of replication. The promoter can be a constitutive, inducible or repressible promoter. A number of expression vectors capable of delivering nucleic acids to a cell are known in the art and can be used herein for production of an antibody or antigen-binding fragment thereof in the cell. Conventional cloning techniques or artificial gene synthesis can be used to generate a recombinant expression vector according to embodiments disclosed herein. Such techniques are well known to those skilled in the art in view of the present disclosure.

[0103] In another general aspect, the invention relates to host cells comprising the isolated nucleic acids encoding the monoclonal antibodies and/or bispecific antibodies or antigen-binding fragments thereof disclosed herein. Any host cell known to those skilled in the art in view of the present disclosure can be used for recombinant expression of antibodies or antigen-binding fragments thereof disclosed herein. In some embodiments, the host cells are *E. coli* TG1 or BL21 cells (for expression of, e.g., an scFv or Fab antibody), CHO-DG44 or CHO-K1 cells or HEK293 cells (for expression of, e.g., a full-length IgG antibody). According to particular embodiments, the recombinant expression vector is transformed into host cells by conventional methods such as chemical transfection, heat shock, or electroporation, where it is stably integrated into the host cell genome such that the recombinant nucleic acid is effectively expressed.

[0104] In another general aspect, the invention relates to a method of producing a bispecific antibody or antigen-binding fragment thereof disclosed herein. The methods comprise culturing a cell comprising a nucleic acid encoding the bispecific antibody or antigen-binding fragment thereof under conditions to produce a bispecific antibody or antigen-binding fragment thereof disclosed herein, and recovering the antibody or antigen-binding fragment thereof from the cell or cell culture (e.g., from the supernatant). Expressed antibodies or antigen-binding fragments thereof can be harvested from the cells and purified according to conventional techniques known in the art and as described herein.

Methods of Use

[0105] In another general aspect, the invention relates to a method of targeting CD123 on the surface of a cancer cell, the method comprising exposing the cancer cell to an anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof.

[0106] The functional activity of bispecific antibodies and antigen-binding fragments thereof that bind Vβ17 and/or CD123 can be characterized by methods known in the art and as described herein. Methods for characterizing antibodies and antigen-binding fragments thereof that bind Vβ17 and/or CD123 include, but are not limited to, affinity and specificity assays including Biacore®, ELISA, and OctetRed® analysis; binding assays to detect the binding of antibodies to CD123 on cancer cells by FACS; binding assays to detect the binding of antibodies to Vβ17 on CD8+ or CD4+ T cells. According to particular embodiments, the methods for characterizing antibodies and antigen-binding fragments thereof that bind Vβ17 and/or CD123 include those described below.

[0107] In another general aspect, the invention relates to a method of directing Vβ17-expressing

CD8+ or CD4+ T cells to a cancer cell. The methods comprise contacting the Vβ17-expressing CD8+ or CD4+ T cell with a anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof, wherein the antibody or antibody fragment directs the Vβ17-expressing CD8+ or CD4+ T cell to a cancer cell having CD123 on its surface.

[0108] In another general aspect, the invention relates to a method for inhibiting growth or proliferation of cancer cells. The methods comprise contacting the Vβ17-expressing CD8+ T cells with a anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof, wherein contacting the cancer cells with the antibody or antibody fragment inhibits the growth or proliferation of the cancer cells.

[0109] According to embodiments of the invention, the described anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof can be provided in a buffered composition for storage or use. Suitable buffers for the storage of the described anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof would serve to maintain the stability of the antibody or antibody fragment by minimizing deterioration while stored, not promoting aggregation of the antibody or antibody fragment, or minimizing adhesion to the storage vessel.

EMBODIMENTS

[0110] This invention provides the following non-limiting embodiments.

[0111] Embodiment 1 is an isolated Vβ17 bispecific antibody or antigen-binding fragment thereof, the isolated Vβ17 bispecific antibody or antigen-binding fragment thereof comprising: [0112] a. a first heavy chain (HC1); [0113] b. a second heavy chain (HC2); [0114] c. a first light chain (LC1); and [0115] d. a second light chain (LC2),

wherein HC1 is associated with LC1 and HC2 is associated with LC2, and wherein HC1 comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3, respectively, and LC1 comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6, respectively, to form a binding site for a first antigen, and wherein HC2 and LC2 form a binding site for a second antigen.

[0116] Embodiment 2 is the Vβ17 bispecific antibody or antigen-binding fragment thereof of embodiment 1, wherein the binding site for the first antigen binds to Vβ17 on a CD8+ or CD4+ T cell.

[0117] Embodiment 3 is the Vβ17 bispecific antibody or antigen-binding fragment thereof of embodiment 1 or 2, wherein the binding site for the second antigen binds to a tumor antigen present on the surface of a cancer cell.

[0118] Embodiment 4 is the Vβ17 bispecific antibody or antigen-binding fragment of any one of embodiments 1 to 3, wherein HC1 and LC1 are humanized.

[0119] Embodiment 5 is the Vβ17 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1 to 4, wherein HC2 and LC2 bind to CD123.

[0120] Embodiment 6 is the Vβ17 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1 to 5, wherein the bispecific antibody or antigen-binding fragment thereof is a IgG isotype.

[0121] Embodiment 7 is the Vβ17 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1 to 6, wherein the bispecific antibody or antigen-binding fragment thereof is a IgG4 isotype.

[0122] Embodiment 8 is the Vβ17 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1 to 7, wherein the bispecific antibody or antigen-binding fragment thereof induces CD8+ or CD4+ T-cell dependent cytotoxicity of a cancer cell in vitro with an EC.sub.50 of less than about 0.2 pM.

[0123] Embodiment 9 is an isolated nucleic acid encoding HC1 and LC1 of the Vβ17 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1 to 8.

[0124] Embodiment 10 is an isolated nucleic acid encoding HC2 and LC2 of the Vβ17 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1 to 8.
[0125] Embodiment 11 is a vector comprising the isolated nucleic acid of embodiment 9 or embodiment 10.
[0126] Embodiment 12 is a host cell comprising the vector of embodiment 11.
[0127] Embodiment 13 is a buffered composition comprising the isolated Vβ17 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1 to 8 and a buffered solution.
[0128] Embodiment 14 is an isolated anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof comprising: [0129] a. a first heavy chain (HC1); [0130] b. a second heavy chain (HC2) [0131] c. a first light chain (LC1); and [0132] d. a second light chain (LC2),
wherein HC1 is associated with LC1 and HC2 is associated with LC2, and wherein HC1 comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3, respectively, and LC1 comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6, respectively, to form a binding site for a first antigen that specifically binds Vβ17, and wherein HC2 comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NO:34, SEQ ID NO:35, and SEQ ID NO: 36, respectively, and LC2 comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NO:37, SEQ ID NO: 38, and SEQ ID NO:39, respectively, to form a binding site for a second antigen that specifically binds CD123.
[0133] Embodiment 15 is the isolated anti-Vb17/anti-CD123 bispecific antibody or antigen-binding fragment of embodiment 14, wherein HC1 comprises the amino acid sequence of SEQ ID NO: 13 and LC1 comprises the amino acid sequence of SEQ ID NO: 14, and wherein HC2 comprises the amino acid sequence of SEQ ID NO: 15 and LC2 comprises the amino acid sequence of SEQ ID NO:16.
[0134] Embodiment 16 is the isolated anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof of embodiment 14 or embodiment 15, wherein the Vβ17 is on the surface of a CD8+ or CD4+ T cell.
[0135] Embodiment 17 is the isolated anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 14 to 16, wherein the CD123 is on the surface of a cancer cell.
[0136] Embodiment 18 is the isolated anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 14 to 17, wherein bispecific antibody or antigen-binding fragment thereof induces CD8+ or CD4+ T-cell dependent cytotoxicity of a cancer cell in vitro with an EC.sub.50 of less than about 0.2 pM.
[0137] Embodiment 19 is an isolated nucleic acid encoding the HC1 and LC1 of the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 14 to 18.
[0138] Embodiment 20 is an isolated nucleic acid encoding the HC2 and LC2 of the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 14 to 18.
[0139] Embodiment 21 is a vector comprising the isolated nucleic acid of embodiment 19 or embodiment 20.
[0140] Embodiment 22 is a host cell comprising the vector of embodiment 21.
[0141] Embodiment 23 is a buffered composition comprising the isolated anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 14 to 18 and a buffered solution.
[0142] Embodiment 24 is a method of directing a Vβ17-expressing CD8+ or CD4+ T cell to a

cancer cell, the method comprising contacting a Vβ17-expressing CD8+ or CD4+ T cell with the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1 to 8 or 14 to 18, wherein contacting the Vβ17-expressing CD8+ or CD4+ T cell with the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof directs the Vβ17-expressing CD8+ or CD4+ T cell to a cancer cell having CD123 on its surface.

[0143] Embodiment 24(a) is the method of embodiment 24, wherein the Vβ17-expressing CD8+ or CD4+ T cell is contacted with an anti-Vβ17/anti-CD123 bispecific antibody of any one of embodiments 1 to 8 or 14 to 18.

[0144] Embodiment 24(b) is the method of embodiment 24, wherein the Vβ17-expressing CD8+ or CD4+ T cell is contacted with an anti-Vβ17/anti-CD123 bispecific antibody fragment of any one of embodiments 1 to 8 or 14 to 18.

[0145] Embodiment 25 is a method for inhibiting growth or proliferation of cancer cells expressing CD123 on its surface, the method comprising contacting the cancer cells with the anti-Vβ17/anti-CD123 bispecific antibody or fragment thereof with any one of embodiments 1 to 8 or 14 to 18, wherein contacting the cancer cells with said antibody or antibody fragment inhibits the growth or proliferation of the cancer cells.

[0146] Embodiment 25 (a) is the method of embodiments 25, wherein the CD123-expressing cancer cell is in the presence of a Vβ17-expressing CD8+ T cell while in contact with an anti-Vβ17/anti-CD123 bispecific antibody or fragment thereof.

[0147] Embodiment 25 (b) is the method of embodiment 25 or 25 (a), wherein the CD123-expressing cancer cell is contacted with an anti-Vβ17/anti-CD123 bispecific antibody of any one of embodiments 1 to 8 or 14 to 18.

[0148] Embodiment 25 (c) is the method of embodiment 25 or 25 (a), wherein the CD123-expressing cancer cell is contacted with an anti-Vβ17/anti-CD123 bispecific antibody fragment of any one of embodiments 1 to 8 or 14 to 18.

[0149] Embodiment 26 is a kit comprising a Vβ17 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 1 to 8 and packaging for the same.

[0150] Embodiment 27 is a kit comprising an anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 14 to 18 and packaging for the same.

[0151] Embodiment 28 is a method of producing a Vβ17 bispecific antibody or antigen-binding fragment thereof, comprising culturing the host cell of embodiment 12 under conditions to produce the Vβ17 bispecific antibody or antigen-binding fragment thereof, and recovering the Vβ17 bispecific antibody or antigen-binding fragment thereof from the cell or culture.

[0152] Embodiment 29 is a method of producing an anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof of any one of embodiments 14 to 18, comprising culturing the host cell of embodiment 22 under conditions to produce the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof, and recovering the anti-Vβ17/anti-CD123 bispecific antibody or antigen-binding fragment thereof from the cell or culture.

[0153] Embodiment 30 is an isolated humanized Vβ17 monoclonal antibody or antigen-binding fragment thereof, the Vβ17 monoclonal antibody or antigen-binding fragment thereof comprising an amino acid sequence with at least 95% identity to the amino acid sequence of SEQ ID NO:28.

[0154] Embodiment 31 is isolated humanized Vβ17 monoclonal antibody or antigen-binding fragment thereof of embodiment 30, wherein the Vβ17 monoclonal antibody or antigen-binding fragment thereof comprises the amino acid sequence of SEQ ID NO:28.

[0155] Embodiment 32 is an isolated nucleic acid encoding the humanized Vβ17 monoclonal antibody or antigen-binding fragment thereof of embodiment 30 or embodiment 31.

[0156] Embodiment 33 is a vector comprising the isolated nucleic acid of embodiment 32.

[0157] Embodiment 34 is a host cell comprising the vector of embodiment 33.

[0158] Embodiment 35 is a buffered composition comprising the isolated humanized Vβ17 monoclonal antibody or antigen-binding fragment thereof of embodiment 30 or embodiment 31.

EXAMPLES

[0159] The following examples are based on the premise that influenza virus derived peptide M1 is capable of expanding a select set of T cells. These cells express TCR-haplotype-Vβ17 and majority of these cells exhibit efficient cytotoxicity of tumor target cells. This ability is then harnessed using bispecific antibodies constructed such that one arm binds to the Vβ17 structure and the other arm binds to an antigen expressed by the cancer cells. Thus, the bispecific antibody bridges the effector and target cells together-resulting in cancer cell killing. This mechanism of action is described in the schematic outlined in FIG. **1**.

[0160] The subsequent examples can be divided into the following categories: (1) Generation of bispecific antibodies capable of binding to the Vβ17 arm of T-cell receptors (TCR) on CTL (Examples 1 and 2); and (2) Evidence for bispecific antibody-enabled target cell killing by CTL expanded in vitro (Example 3).

Example 1: Human Framework Adaptation of Anti-Vβ17 mAb E17.5F

[0161] The mouse IgG1 anti-human T cell receptor Vβ17 clone E17.5F was obtained from BeckmanCoulter, Inc. (Brea, CA). Sample preparation and LC/MSMS analysis were performed at Protea Bioscience Inc. (Morgantown, WV). The sample was reduced and alkylated, divided into seven aliquots, and proteolytically digested with Trypsin/LysC, Chymotrypsin, LysC, Pepsin, and AspN, Elastase, and Proteinase K enzymes. Resulting peptides were desalted using a ZipTip C18 Pipette Tips and separated on-line using reverse phase chromatography. Mass spectrometry was performed on Thermo Q-Exactive spectrometer using HCD fragmentation. MS data sets were analyzed using PEAKS software by matching de novo sequence tags to an IMGT-based antibody sequences database. Gaps in the sequence were assigned using Contig sequence assembly of de novo identified peptides. All CDRs and hyper-mutations were confirmed by inspecting the MS/MS spectra

[0162] The sequences obtained are shown in Tables 1 and 2.

TABLE-US-00001 TABLE 1 CDR Sequences of TCR Vβ17 clone E17.5F. Antibody HCDR1 SEQ ID NO: HCDR2 SEQ ID NO: HCDR3 SEQ ID NO: E17.5F GYSITSGYFWN 1 YISYDGSNN 2 PSPGTGYAVDY 3 Antibody LCDR1 SEQ ID NO: LCDR2 SEQ ID NO: LCDR3 SEQ ID NO: E17.5F RSSQSLVHSNGNTYLH 4 KVSNRFS 5 SQSTHVPFT 6

TABLE-US-00002 TABLE 2 Heavy chain and light chain sequences of TCR Vb17 clone E17.5F. mAb ID Heavy Chain Amino Acid Sequence SEQ ID NO: B171B01 NVQLQESGPGLVKPSQSLSLTCSVAGYSITSGYFWNWIRQFPGNKLEWMGYIS 7
YDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCASPSPGTGYA
VDYWGQGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTV
TWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSQTVTCNVAHPASSTK
VDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISK
DDPEVQFSWFVDDVEVHTAQTKPREEQINSTFRSVSELPIMHQDWLNGKEFKC
RVNSAAFPAPIEKTISKTYGRPKAPQVYTIPPPKEQMAKDKVSLTCMITNFFP
EDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSV
LHEGLHNHHTEKSLSHSPGK Light Chain Amino Acid Sequence SEQ ID NO: B17B01 NVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKFLI 8
YKVSNRFSGVPDRFSGGGSGTEFTLKISRVEAEDLGVYFCSQSTHVPFTFGSG
TKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE
RQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SFNRNEC

[0163] Changes were made in the sequences for the preparation of bispecific antibodies (Table 3). The changes include the following: (1) a framework mutation Asn1 of the heavy chain was not conserved, so the sequence has been modified to have the DVQLW sequence; (2) another mutation identified in the Fc, K337Y, was deemed uncharacteristic, and, thus, a construct without this mutation was synthesized; and (3) a potential secondary glycosylation site on the heavy chain was

observed, and, thus, two versions of this mAb with and without the N-linked site (N82a, based on Chothia numbering) were synthesized.

TABLE-US-00003 TABLE 3 Heavy and Light Chain sequences for Vβ17 clone E17.5F antibody variants SEQ mAb ID ID Heavy Chain Amino Acid Sequence NO:
B17B1 NVQLQESGPGLVKPSQSLSLTCSVAGYSITSGYFWNWIRQFPGNKLEWMGYIS 9
YDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCASPSPGTGYAV
DYWGQGTSVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTK
VDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQEGNVFSC
SVMHEALHNHYTQKSLSLSLGK B17B2
DVQLKESGPGLVKPSQSLSVTCSVTGYSITSGYYWNWYRQFPGNKLEWMGYI 11
SYDGSNNYNPSLKNRISITRDTSKNQILLKLTYVTTEDTATYYCTRPSPGTGYA
VDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTK
VDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLLYSKLTVDKSRWQEGNVFSC
SVMHEALHNHYTQKSLSLSLGK SEQ ID Light Chain Amino Acid Sequence NO:
B17B1 NVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKFLIY 10
KVSNRFSGVPDRFSGGGSGTEFTLKISRVEAEDLGVYFCSQSTHVPFTFGSGTK
LEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQN
GVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNEC
B17B2 DIVMTQSPDSLAVSLGERATINCRSSQSLVHSNGNTYLHWYQQKPGQPPKLLI 12
YKVSNRFSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQSTHVPFTFGQGT
KVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ
NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC

[0164] The two antibodies (B17B1 and B17B2) were expressed in HEK293Expi cells. The supernatants were tested for Vβ17 binding (B17B1 and B17B2) and only B17B1 demonstrated binding. Thus, B17B1 was expressed having an IgG4 constant region with Fc substitutions.

[0165] The anti-human TCR Vβ17 mouse mAb B17B1 was humanized using the Human Framework Adaptation (HFA) method (Fransson J, et al. *J. Mol. Biol.* 2010; 398:214-231). To find the best combination of humanized heavy and light chains, several human V-region sequences were selected for testing (Table 4). Selection of human germlines was based solely on the overall sequence similarity to the mouse antibody in the framework (FR) region. Neither the CDR sequences, nor their length or canonical structures, were considered in this selection.

[0166] The CDR definition used in HFA is described in (Fransson J, et al. *J. Mol. Biol.* 2010; 398:214-231) and corresponds to the Martin's definition (Abhinandan K R and Martin A C. *Mol. Immunol.* 2008; 45:3832-3839). The CDRs (Table 1) were defined as described below (using the Chothia numbering scheme [Chothia C, and Lesk A. *J. Mol. Biol.* 1987; 196:901-917]):

TABLE-US-00004 HCDR1 (SEQ ID NO: 1) 26-35 HCDR2 (SEQ ID NO: 2) 50-58 HCDR3 (SEQ ID NO: 3) 95-102 LCDR1 (SEQ ID NO: 4) 24-34 LCDR2 (SEQ ID NO: 5) 50-56 LCDR3 (SEQ ID NO: 6) 89-97

[0167] The selected human germlines are provided in Table 4 (in the IMGT notation).

TABLE-US-00005 TABLE 4 VH and VL variants Ab VH Sequence SEQ ID NO:
B17H1 NVQLQESGPGLVKPSQSLSLTCVSVAGYSITSYGFWNWIRQFPGNKLEWMG 25
YSIYDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCASPSP

GTGYAVDYWGQGTSVTVSS B17H3
EVQLLESGGGLVQPGGSLRLSCAASGYSITSGYFWNWVRQAPGKGLEWVSY 19
ISYDGSNNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPSPG
TGYAVDYWGQGTLVTVSS B17H4
EVQLLESGGGLVQPGGSLRLSCAASGYSITSGYFWNWVRQAPGKGLEWVSY 20
ISYDGSNNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASPSPG
TGYAVDYWGQGTLVTVSS B17H5
QVQLVQESGPGLVKPSETLSLTCTVSGYSITSGYFWNWIRQPPGKGLEWIG 21
YISYDGSNNYNPSLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCASPSP
GTGYAVDYWGQGTLVTVSS Ab VL Sequence SEQ ID NO: B17L1
NVVMTQTPLSLPVSLGDQASISVRSSQSLVHSNGNTYLHWYLQKPGQSPKF 26
LIYKVSNRFSGVPDRFSGGGSGTEFTLKISRVEAEDLGVYFCSQSTHVPFT FGSGTKLEIK
B17L3 DIQMTQSPSSLSASVGDRVTITCRSSQLSVHSNGNTYLHWYQQKPGKAPKL 22
LIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTHVPFT FGQGTKLEIK
B17L4 DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKF 23
LIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTHVPFT FGQGTKLEIK
B17L5 DVVMTQSPLSLPVTLGQPASISCRSSQSLVHSNGNTYLHWFQQRPGQSPRF 24
LIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPFT FGQGTKLEIK
CRSs1-3 are underlined

[0168] “Back mutations” in several variants were introduced at FR positions that are known to be important for VL/VH pairing and CDR conformation. The selected human germlines are provided in Table 5 (in the IMGT notation), with the back mutations noted.

TABLE-US-00006 TABLE 5 The selected J-regions J-region Sequence SEQ ID NO: IGHJ1*01 HC WGQGTLVTVSS 42 IGKJ2*01 LC FGQGTKLEIK 43

[0169] Amino acid sequences of all nine pairwise combinations of three heavy chains and three light chains were back-translated to DNA, and cDNA was prepared using gene synthesis techniques (U.S. Pat. Nos. 6,670,127; 6,521,427). Heavy chain (HC) variable regions were subcloned onto human IgG4 constant region using an in-house expression vector with the CMV promoter using standard molecular biology techniques. Light chain (LC) variable regions were subcloned onto a human Lambda (2) constant regions using an in-house expression vector with the CMV promoter using standard molecular biology techniques. Resulting plasmids were transfected into HEK EXPI cells (LifeTechnologies; Carlsbad, CA) and mAbs were expressed. Purification was by standard methods using a Protein A column (hiTrap MAbSelect SuRe column). After elution, the pools were dialyzed into D-PBS, pH 7.2.

TABLE-US-00007 TABLE 6 Heavy and Light chains of nine humanized Vβ17 antibodies Concentration mAb Hc SEQ ID NO: Lc SEQ ID NO: (μg/mL) B17B14 B17H3 19 B17L3 22 686.3 B17B15 B17H3 19 B17L4 23 13.8 B17B16 B17H3 19 B17L5 24 14.6 B17B17 B17H4 20 B17L3 22 335.1 B17B18 B17H4 20 B17L4 23 45.2 B17B19 B17H4 20 B17L5 24 27.5 B17B20 B17H5 21 B17L3 22 602.1 B17B21 B17H5 21 B17L4 23 570.9 B17B22 B17H5 21 B17L5 24 320.5

[0170] The humanized antibodies were screened for binding to a TCRVβ17 (SEQ ID NO: 27)/Va10.2-Fc (SEQ ID NO:44) fusion protein by ELISA. Biotinylated TCRVβ17/Va10.2-Fc fusion protein was added to a streptavidin-coated ELISA plate. Unbound protein was washed away and mAb was added at a range of concentrations (0.01-10 μg/mL). Plates were washed and anti-kappa: HRP detection antibody was added. Plates were washed, chemiluminescent detection reagent was added, and the plates were read on a Perkin Elmer EnVision plate reader for luminescence. B17B20 and B17B21 showed positive binding to the TCR-Vβ17 protein. B17B22 showed weak binding to this protein. These antibodies were then purified as described above for further studies. B17B21 demonstrated the best binding to recombinant TCR-Vβ17 protein and to M1-stimulated T-cells and was thus chosen as the molecule for further functional studies, specifically T-cell re-directed cancer

cell killing as a bispecific antibody.

[0171] Thus, the variable region sequence of B17B21 (anti-Vβ17) and I3RB217 (anti-CD123 antibody) was used to generate a bispecific antibody to be tested for T-cell re-directed killing of acute myeloid leukemia (AML) cells.

Example 2. Preparation of Anti-Vβ17/Anti-CD123 Bispecific Antibodies

[0172] VB11 (anti-Vβ17/anti-CD123) and VB13 (Vβ17×Null) bispecific antibodies were produced as full-length antibodies in the knob-into-hole format as human IgG4, as previously described (Atwell et al. J. Mol. Biol. 270:26-35, 1997). Nucleic acid sequences encoding variable regions were subcloned into a custom mammalian expression vectors containing constant region of IgG4 expression cassettes using standard PCR restriction enzyme based cloning techniques. The bispecific antibodies were expressed by transient transfection in Chinese hamster ovary cell line. The antibodies were initially purified by Mab Select SuRe Protein A column (GE healthcare, Piscataway, New Jersey) (Brown, Bottomley et al. 1998). The column was equilibrated with Phosphate Buffer Saline (PBS), pH 7.2 and loaded with fermentation supernatant at a flow rate of 2 mL/min. After loading, the column was washed with PBS (4 CV) followed by elution in 30 mM sodium acetate, pH 3.5. Fractions containing protein peaks as monitored by Absorbance at 280 nm in Akta Explorer (GE healthcare) were pooled together and were neutralized to pH 5.0 by adding 1% of 3M sodium acetate, pH 9.0. As a polishing step, the antibodies were purified on a preparative size exclusion chromatography (SEC) using a Superdex 200 column (GE healthcare). The integrity of the sample was assessed by endotoxin measurement and SDS polyacrylamide gel electrophoresis under reducing and non-reducing conditions. The final protein concentrations were 0.48 mg/ml for anti-Vβ17/anti-CD123 and 0.24 mg/mL for Vβ17×Null. The final EU levels of anti-Vβ17/anti-CD123 and Vβ17×Null based on these protein concentrations were 2.053 EU/mg and 4.219 EU/mg, respectively.

TABLE-US-00008 TABLE 7 Sequences of half antibodies expressed in CHO cells

mAb ID	SEQ ID NO:	‘Knob’ arm and ‘hole’ arm amino acid sequence
B17B21 (Vβ17 half Ab)	28	MAWVWTLLFLMAAAQSIQADIQMTQSPSSLSASVGDRVTITCRSSQSLVHS NGNTYLHWYQQKPGKAPKFLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCSQSTHVPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGSEGKSSGSGSESKST EGKSSGSGSESKSTGGSQVQLQESGPGLVKPSETLSLTCTVSGYSITSGYF WNWIRQPPGKGLEWIGYISYDGSNNYNPSLKSRVTISRDTSKNQFSLKLSS VTAADTAVYYCASPSPGTGYAVDYWGQGTLVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK GQPREPQVYTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLVSRLTVDKSRWQEGNVFSCSVMHEALHNRFTQKSLS LSLGK
I3RB217 (CD123 half Ab)	30	MAWVWTLLFLMAAAQSIQAEIVLTQSPGTLSLSPGERATLSCRASQSVSSS YLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQDYGFPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGECGGSEGKSSGSGSESKSTEGKS SGSGSESKSTGGSEVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWISWVR QMPGKGLEWMGIIDPSDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKAS DTAMYYCARGDGSTDLDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFP

PKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ
FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREP
QVYTLPPSQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK B23B49
MAWVWTLLFLMAAAQSIQAEIVLTQSPGTLSLSPGERATLSCRASQSVSSS (Null
YLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED half Ab)
FAVYYCQQDYGFPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV
CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGECGGSEGKSSGSGSESKSTEGKS
SGSGSESKSTGGSEVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWISWVR
QMPGKGLEWMGIIDPSDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKAS
DTAMYYCARGDGSTDLDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSEST
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
SSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ
FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREP
QVYTLPPSQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK Half
Antibody DNA sequence B17B21
ATGGCCTGGGTGTGGACCCTGCTGTTCCTGATGGCCGCCGCCCAGAGCATC 29 (Vβ17
CAGGCCGACATCCAGATGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTG half Ab)
GGCGACCGCGTGACCATCACCTGCCGCAGCAGCCAGAGCCTGGTGCACAGC
AACGGCAACACCTACCTGCACTGGTACCAGCAGAAGCCAGGCAAGGCCCCA
AAGTTCCTGATCTACAAGGTGAGCAACCGCTTCAGCGGCGTGCCAAGCCGC
TTCAGCGGCAGCGGCAGCGGCACCGACTTCACCCTGACCATCAGCAGCCTG
CAGCCAGAGGACTTCGCCACCTACTACTGCAGCCAGAGCACCCACGTGCCA
TTCACCTTCGGCCAGGGCACCAAGCTGGAGATCAAGCGCACCGTGGCCGCC
CCAAGCGTGTTCATCTTCCCACCAAGCGACGAGCAGCTGAAGAGCGGCACC
GCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCACGCGAGGCCAAGGTG
CAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTG
ACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCACCCTGACC
CTGAGCAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACC
CACCAGGGCCTGAGCAGCCCAGTGACCAAGAGCTTCAACCGCGGCGAGTGC
GGCGGCAGCGAGGGCAAGAGCAGCGGCAGCGGCAGCGAGAGCAAGAGCACC
GAGGGCAAGAGCAGCGGCAGCGGCAGCGAGAGCAAGAGCACCGGCGGCAGC
CAGGTGCAGCTGCAGGAGAGCGGCCCAGGCCTGGTGAAGCCAAGCGAGACC
CTGAGCCTGACCTGCACCGTGAGCGGCTACAGCATCACCAGCGGCTACTTC
TGGAACTGGATCCGCCAGCCACCAGGCAAGGGCCTGGAGTGGATCGGCTAC
ATCAGCTACGACGGCAGCAACAACTACAACCCAAGCCTGAAGAGCCGCGTG
ACCATCAGCCGCGACACCAGCAAGAACCAGTTCAGCCTGAAGCTGAGCAGC
GTGACCGCCGCCGACACCGCCGTGTACTACTGCGCCAGCCCAAGCCCAGGC
ACCGGCTACGCCGTGGACTACTGGGGCCAGGGCACCCTGGTGACCGTGAGC
AGCGCCAGCACCAAGGGCCCAAGCGTGTTCCCACTGGCCCCATGCAGCCGC
AGCACCAGCGAGAGCACCGCCGCCCTGGGCTGCCTGGTGAAGGACTACTTC
CCAGAGCCAGTGACCGTGAGCTGGAACAGCGGCGCCCTGACCAGCGGCGTG
CACACCTTCCCAGCCGTGCTGCAGAGCAGCGGCCTGTACAGCCTGAGCAGC
GTGGTGACCGTGCCAAGCAGCAGCCTGGGCACCAAGACCTACACCTGCAAC
GTGGACCACAAGCCAAGCAACACCAAGGTGGACAAGCGCGTGGAGAGCAAG
TACGGCCCACCATGCCCACCATGCCCAGCCCCAGAGGCCGCCGGCGGCCCA
AGCGTGTTCCTGTTCCCACCAAAGCCAAAGGACACCCTGATGATCAGCCGC

ACCCCAGAGGTGACCTGCGTGGTGGTGGACGTGAGCCAGGAGGACCCAGAG
GTGCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACC
AAGCCACGCGAGGAGCAGTTCAACAGCACCTACCGCGTGGTGAGCGTGCTG
ACCGTGCTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTG
AGCAACAAGGGCCTGCCAAGCAGCATCGAGAAGACCATCAGCAAGGCCAAG
GGCCAGCCACGCGAGCCACAGGTGTACACCCTGCCACCAAGCCAGGAGGAG
ATGACCAAGAACCAGGTGAGCCTGAGCTGCGCCGTGAAGGGCTTCTACCCA
AGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCAGAGAACAACTAC
AAGACCACCCCACCAGTGCTGGACAGCGACGGCAGCTTCTTCCTGGTGAGC
CGCCTGACCGTGGACAAGAGCCGCTGGCAGGAGGGCAACGTGTTCAGCTGC
AGCGTGATGCACGAGGCCCTGCACAACCGCTTCACCCAGAAGAGCCTGAGC
CTGAGCCTGGGCAAGATGGCCTGGGTGTGGACCCTGCTGTTCCTGATGGCC
GCCGCCCAGAGCATCCAGGCCGACATCCAGATGACCCAGAGCCCAAGCAGC
CTGAGCGCCAGCGTGGGCGACCGCGTGACCATCACCTGCCGCAGCAGCCAG
AGCCTGGTGCACAGCAACGGCAACACCTACCTGCACTGGTACCAGCAGAAG
CCAGGCAAGGCCCCAAAGTTCCTGATCTACAAGGTGAGCAACCGCTTCAGC
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CGCACCGTGGCCGCCCCAAGCGTGTTCATCTTCCCACCAAGCGACGAGCAG
CTGAAGAGCGGCACCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCA
CGCGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAAC
AGCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTG
AGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGTAC
GCCTGCGAGGTGACCCACCAGGGCCTGAGCAGCCCAGTGACCAAGAGCTTC
AACCGCGGCGAGTGCGGCGGCAGCGAGGGCAAGAGCAGCGGCAGCGGCAGC
GAGAGCAAGAGCACCGAGGGCAAGAGCAGCGGCAGCGGCAGCGAGAGCAAG
AGCACCGGCGGCAGCCAGGTGCAGCTGCAGGAGAGCGGCCCAGGCCTGGTG
AAGCCAAGCGAGACCCTGAGCCTGACCTGCACCGTGAGCGGCTACAGCATC
ACCAGCGGCTACTTCTGGAACTGGATCCGCCAGCCACCAGGCAAGGGCCTG
GAGTGGATCGGCTACATCAGCTACGACGGCAGCAACAACTACAACCCAAGC
CTGAAGAGCCGCGTGACCATCAGCCGCGACACCAGCAAGAACCAGTTCAGC
CTGAAGCTGAGCAGCGTGACCGCCGCCGACACCGCCGTGTACTACTGCGCC
AGCCCAAGCCCAGGCACCGGCTACGCCGTGGACTACTGGGGCCAGGGCACC
CTGGTGACCGTGAGCAGCGCCAGCACCAAGGGCCCAAGCGTGTTCCCACTG
GCCCCATGCAGCCGCAGCACCAGCGAGAGCACCGCCGCCCTGGGCTGCCTG
GTGAAGGACTACTTCCCAGAGCCAGTGACCGTGAGCTGGAACAGCGGCGCC
CTGACCAGCGGCGTGCACACCTTCCCAGCCGTGCTGCAGAGCAGCGGCCTG
TACAGCCTGAGCAGCGTGGTGACCGTGCCAAGCAGCAGCCTGGGCACCAAG
ACCTACACCTGCAACGTGGACCACAAGCCAAGCAACACCAAGGTGGACAAG
CGCGTGGAGAGCAAGTACGGCCCACCATGCCCACCATGCCCAGCCCCAGAG
GCCGCCGGCGGCCCAAGCGTGTTCCTGTTCCCACCAAAGCCAAAGGACACC
CTGATGATCAGCCGCACCCCAGAGGTGACCTGCGTGGTGGTGGACGTGAGC
CAGGAGGACCCAGAGGTGCAGTTCAACTGGTACGTGGACGGCGTGGAGGTG
CACAACGCCAAGACCAAGCCACGCGAGGAGCAGTTCAACAGCACCTACCGC
GTGGTGAGCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAGGAG
TACAAGTGCAAGGTGAGCAACAAGGGCCTGCCAAGCAGCATCGAGAAGACC
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CCAAGCCAGGAGGAGATGACCAAGAACCAGGTGAGCCTGAGCTGCGCCGTG
AAGGGCTTCTACCCAAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAG

CCAGAGAACAACTACAAGACCACCCCACCAGTGCTGGACAGCGACGGCAGC
TTCTTCCTGGTGAGCCGCCTGACCGTGGACAAGAGCCGCTGGCAGGAGGGC
AACGTGTTCAGCTGCAGCGTGATGCACGAGGCCCTGCACAACCGCTTCACC
CAGAAGAGCCTGAGCCTGAGCCTGGGCAAGTGATAG I3RB217
ATGGCCTGGGTGTGGACCCTGCTGTTCCTGATGGCCGCCGCCCAGAGCATC 31 (CD123
CAGGCCGAGATCGTGCTGACCCAGAGCCCAGGCACCCTGAGCCTGAGCCCA half Ab)
GGCGAGCGCGCCACCCTGAGCTGCCGCGCCAGCCAGAGCGTGAGCAGCAGC
TACCTGGCCTGGTACCAGCAGAAGCCAGGCCAGGCCCCACGCCTGCTGATC
TACGGCGCCAGCAGCCGCGCCACCGGCATCCCAGACCGCTTCAGCGGCAGC
GGCAGCGGCACCGACTTCACCCTGACCATCAGCCGCCTGGAGCCAGAGGAC
TTCGCCGTGTACTACTGCCAGCAGGACTACGGCTTCCCATGGACCTTCGGC
CAGGGCACCAAGGTGGAGATCAAGCGCACCGTGGCCGCCCCAAGCGTGTTC
ATCTTCCCACCAAGCGACGAGCAGCTGAAGAGCGGCACCGCCAGCGTGGTG
TGCCTGCTGAACAACTTCTACCCACGCGAGGCCAAGGTGCAGTGGAAGGTG
GACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTGACCGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCC
GACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTG
AGCAGCCCAGTGACCAAGAGCTTCAACCGCGGCGAGTGCggcggcagcgag
ggcaagagcagcggcagcggcagcgagagcaagagcaccgagggcaagagc
agcggcagcggcagcgagagcaagagcaccggcggcagcGAGGTGCAGCTG
GTGCAGAGCGGCGCCGAGGTGAAGAAGCCAGGCGAGAGCCTGAAGATCAGC
TGCAAGGGCAGCGGCTACAGCTTCACCAGCTACTGGATCAGCTGGGTGCGC
CAGATGCCAGGCAAGGGCCTGGAGTGGATGGGCATCATCGACCCAAGCGAC
AGCGACACCCGCTACAGCCCAAGCTTCCAGGGCCAGGTGACCATCAGCGCC
GACAAGAGCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCAGC
GACACCGCCATGTACTACTGCGCCCGCGGCGACGGCAGCACCGACCTGGAC
TACTGGGGCCAGGGCACCCTGGTGACCGTGAGCAGCGCCAGCACCAAGGGC
CCAAGCGTGTTCCCACTGGCCCCATGCAGCCGCAGCACCAGCGAGAGCACC
GCCGCCCTGGGCTGCCTGGTGAAGGACTACTTCCCAGAGCCAGTGACCGTG
AGCTGGAACAGCGGCGCCCTGACCAGCGGCGTGCACACCTTCCCAGCCGTG
CTGCAGAGCAGCGGCCTGTACAGCCTGAGCAGCGTGGTGACCGTGCCAAGC
AGCAGCCTGGGCACCAAGACCTACACCTGCAACGTGGACCACAAGCCAAGC
AACACCAAGGTGGACAAGCGCGTGGAGAGCAAGTACGGCCCACCATGCCCA
CCATGCCCAGCCCCAGAGGCCGCCGGCGGCCCAAGCGTGTTCCTGTTCCCA
CCAAAGCCAAAGGACACCCTGATGATCAGCCGCACCCCAGAGGTGACCTGC
GTGGTGGTGGACGTGAGCCAGGAGGACCCAGAGGTGCAGTTCAACTGGTAC
GTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCACGCGAGGAGCAG
TTCAACAGCACCTACCGCGTGGTGAGCGTGCTGACCGTGCTGCACCAGGAC
TGGCTGAACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGGCCTGCCA
AGCAGCATCGAGAAGACCATCAGCAAGGCCAAGGGCCAGCCACGCGAGCCA
CAGGTGTACACCCTGCCACCAAGCCAGGAGGAGATGACCAAGAACCAGGTG
AGCCTGTGGTGCCTGGTGAAGGGCTTCTACCCAAGCGACATCGCCGTGGAG
TGGGAGAGCAACGGCCAGCCAGAGAACAACTACAAGACCACCCCACCAGTG
CTGGACAGCGACGGCAGCTTCTTCCTGTACAGCCGCCTGACCGTGGACAAG
AGCCGCTGGCAGGAGGGCAACGTGTTCAGCTGCAGCGTGATGCACGAGGCC
CTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGAGCCTGGGCAAG B23B49
ATGGCCTGGGTGTGGACCCTGCTGTTCCTGATGGCCGCCGCCCAGAGCATC (Null
CAGGCCGACATCGTGATGACCCAGAGCCCAGACAGCCTGGCCGTGAGCCTG half Ab)
GGCGAGCGCGCCACCATCAACTGCCGCGCCAGCCAGAGCGTGGACTACAAC
GGCATCAGCTACATGCACTGGTACCAGCAGAAGCCAGGCCAGCCACCAAAG

CTGCTGATCTACGCCGCCAGCAACCCAGAGAGCGGCGTGCCAGACCGCTTC
AGCGGCAGCGGCAGCGGCACCGACTTCACCCTGACCATCAGCAGCCTGCAG
GCCGAGGACGTGGCCGTGTACTACTGCCAGCAGATCATCGAGGACCCATGG
ACCTTCGGCCAGGGCACCAAGGTGGAGATCAAGCGCACCGTGGCCGCCCCA
AGCGTGTTCATCTTCCCACCAAGCGACGAGCAGCTGAAGAGCGGCACCGCC
AGCGTGGTGTGCCTGCTGAACAACTTCTACCCACGCGAGGCCAAGGTGCAG
TGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAGAGCGTGACC
GAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCACCCTGACCCTG
AGCAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCAC
CAGGGCCTGAGCAGCCCAGTGACCAAGAGCTTCAACCGCGGCGAGTGCGGC
GGCAGCGAGGGCAAGAGCAGCGGCAGCGGCAGCGAGAGCAAGAGCACCGAG
GGCAAGAGCAGCGGCAGCGGCAGCGAGAGCAAGAGCACCGGCGGCAGCCAG
ATCACCCTGAAGGAGAGCGGCCCAACCCTGGTGAAGCCAACCCAGACCCTG
ACCCTGACCTGCACCTTCAGCGGCTTCAGCCTGAGCACCAGCGGCATGGGC
GTGAGCTGGATCCGCCAGCCACCAGGCAAGGCCCTGGAGTGGCTGGCCCAC
ATCTACTGGGACGACGACAAGCGCTACAACCCAAGCCTGAAGAGCCGCCTG
ACCATCACCAAGGACACCAGCAAGAACCAGGTGGTGCTGACCATGACCAAC
ATGGACCCAGTGGACACCGCCACCTACTACTGCGCCCGCCTGTACGGCTTC
ACCTACGGCTTCGCCTACTGGGGCCAGGGCACCCTGGTGACCGTGAGCAGC
GCCAGCACCAAGGGCCCAAGCGTGTTCCCACTGGCCCCATGCAGCCGCAGC
ACCAGCGAGAGCACCGCCGCCCTGGGCTGCCTGGTGAAGGACTACTTCCCA
GAGCCAGTGACCGTGAGCTGGAACAGCGGCGCCCTGACCAGCGGCGTGCAC
ACCTTCCCAGCCGTGCTGCAGAGCAGCGGCCTGTACAGCCTGAGCAGCGTG
GTGACCGTGCCAAGCAGCAGCCTGGGCACCAAGACCTACACCTGCAACGTG
GACCACAAGCCAAGCAACACCAAGGTGGACAAGCGCGTGGAGAGCAAGTAC
GGCCCACCATGCCCACCATGCCCAGCCCCAGAGGCCGCCGGCGGCCCAAGC
GTGTTCCTGTTCCCACCAAAGCCAAAGGACACCCTGATGATCAGCCGCACC
CCAGAGGTGACCTGCGTGGTGGTGGACGTGAGCCAGGAGGACCCAGAGGTG
CAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAG
CCACGCGAGGAGCAGTTCAACAGCACCTACCGCGTGGTGAGCGTGCTGACC
GTGCTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTGAGC
AACAAGGGCCTGCCAAGCAGCATCGAGAAGACCATCAGCAAGGCCAAGGGC
CAGCCACGCGAGCCACAGGTGTACACCCTGCCACCAAGCCAGGAGGAGATG
ACCAAGAACCAGGTGAGCCTGTGGTGCCTGGTGAAGGGCTTCTACCCAAGC
GACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCAGAGAACAACTACAAG
ACCACCCCACCAGTGCTGGACAGCGACGGCAGCTTCTTCCTGTACAGCCGC
CTGACCGTGGACAAGAGCCGCTGGCAGGAGGGCAACGTGTTCAGCTGCAGC
GTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTG
AGCCTGGGCAAG

TABLE-US-00009 TABLE 8 Heavy and Light Chain Sequences for Vβ17 bispecific antibodies Bispecific Antibody Amino Acid Sequence Anti-Vβ17/ Heavy chain 1 QVQLQESGPGLVKPSETLSLTCTVSGYSITSGYFWNWIRQPP anti-CD123 B17B21 GKGLEWIGYISYDGSNNYNPSLKSRVTISRDTSKNQFSLKLS (SEQ ID NO: 13) SVTAADTAVYYCASPSPGTGYAVDYWGQGTLVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQVSLSCAVKGFYPSDIA

VEWESNGQPENNYKTTPPVLDSDGSFFLVSRLTVDKSRWQEG
NVFSCSVMHEALHNRFTQKSLSLSLGK Light Chain 1
DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQ B17B21
QKPGKAPKFLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQ (SEQ ID NO: 14)
PEDFATYYCSQSTHVPFTFGQGTKLEIKRTVAAPSVFIFPPS
DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPV TKSFNRGEC Heavy
chain 2 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWISWVRQMPG I3RB217
KGLEWMGIIDPSDSDTRYSPSFQGQVTISADKSISTAYLQWS (SEQ ID NO: 15)
SLKASDTAMYYCARGDGSTDLDYWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT
KVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK
AKGQPREPQVYTLPPSQEEMTKNQVSLWCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNV
FSCSVMHEALHNHYTQKSLSLSLGK Light Chain 2
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPG I3RB217
QAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDF (SEQ ID NO: 16)
AVYYCQQDYGFPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQL
KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC Vβ17 x Null
Heavy chain 1 QVQLQESGPGLVKPSETLSLTCTVSGYSITSGYFWNWIRQPP B17B21
GKGLEWIGYISYDGSNNYNPSLKSRVTISRDTSKNQFSLKLS (SEQ ID NO: 13)
SVTAADTAVYYCASPSPGTGYAVDYWGQGTLVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS
NTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLM
ISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI
SKAKGQPREPQVYTLPPSQEEMTKNQVSLSCAVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLVSRLTVDKSRWQEG
NVFSCSVMHEALHNRFTQKSLSLSLGK Light Chain 1
DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQ B17B21
QKPGKAPKFLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQ (SEQ ID NO: 14)
PEDFATYYCSQSTHVPFTFGQGTKLEIKRTVAAPSVFIFPPS
DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPV TKSFNRGEC Heavy
chain 2 QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQP Null
PGKALEWLAHIYWDDDKRYNPSLKSRLTITKDTSKNQVVLTM (SEQ ID NO: 17)
TNMDPVDTATYYCARLYGFTYGFAYWGQGTLVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS
NTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLM
ISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI
SKAKGQPREPQVYTLPPSQEEMTKNQVSLWCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG
NVFSCSVMHEALHNHYTQKSLSLSLGK Light Chain 2

DIVMTQSPDSLAVSLGERATINCRASQSVDYNGISYMHWYQQ Null
KPGQPPKLLIYAASNPESGVPDRFSGSGSGTDFTLTISSLQA (SEQ ID NO: 18)
EDVAVYYCQQIIEDPWTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT KSFNRGEC

Example 3. Evaluation of Binding and Cytotoxic Properties of Anti-Vβ17/Anti-CD123 Bispecific Antibody Using Kasumi-3 Cells and Human CD8+ T Cells

Stimulation and Expansion of Vβ17+CD8+ T Cells from Total PBMCs

[0173] To expand Vβ17.sup.+CD8.sup.+ T cells, whole PBMCs from HLA-A2 donor (HPU-08694) were stimulated with 1 μg/mL FLU MP 58 peptide (in DMSO). Frequency of Vβ17.sup.+ cells among total CD8.sup.+ T cells was determined on day 8 and 14 of the culture period. To enumerate the frequency of Vβ17.sup.+ cells among total CD8.sup.+ T cells, total live PBMCs were initially gated, doublets were excluded, total CD8.sup.+ T cells were gated and then Vβ17.sup.+ cells were gated (FIG. **3**A). Compared to the frequency of Vβ17.sup.+ cells among total CD8.sup.+ T cells on day 0, a substantial expansion of these cells were observed at day 8 of the culture period (FIG. **3**B). A larger fraction of CD8+ T cells on day 8 were Vβ17.sup.+ cells (FIG. **3**B) in this donor.

Anti-Vβ17/Anti-CD123 Bispecific Antibody Binding Assay

On Kasumi-3 Cells

[0174] To understand the binding kinetics of the anti-Vβ17/anti-CD123 bispecific antibody, Kasumi-3 cells were incubated with the anti-Vβ17/anti-CD123 bispecific antibody and Vβ17×NULL arm control at various concentrations (concentration range from 5 μg/mL to 0 μg/mL). Cell bound bispecific antibody was detected with mouse anti-human IgG4 Fc-PE secondary antibody. Table 9 shows the frequency of Kasumi-3 cells positive for PE (secondary antibody) when treated with different concentration of bispecific antibodies. The EC.sub.50 for anti-Vβ17/anti-CD123 and NULL×CD123 was determined as 6 and 42.7 nM respectively (Table 9).

TABLE-US-00010 TABLE 9 Binding affinity of Kasumi-3 cells for bispecific antibodies. anti-Vβ17/ Conc.(ug/mL) anti-CD123 Vβ17XNULL NULLXCD123 5 87.37 −0.02 47.47 1.667 74.37 0.09 16.37 0.556 24.07 0.15 1.2 0.185 1.65 0.35 0.31 0.062 0.32 0.12 0.04 0.021 0.16 0.14 0.05 0.007 0.23 0.19 −0.06 0.002 0.04 −0.09 −0.04 0.001 0.09 0 −0.18 EC.sub.50 (μg/mL) 0.9 ND 6.4 EC.sub.50 (nM) 6 ND 42.7

[0175] Bispecific antibody binding affinities to Kasumi-3 cells were determined by flow cytometry. Half maximal effective concentration (EC.sub.50) values were calculated as the bispecific concentration that generates 50% of maximal Binding (PE positive cells). ND: Not determined.

On Enriched CD8+ T Cells

[0176] Enriched FLU MP 58 peptide stimulated CD8+ T (from day 14 culture) cells were incubated with various concentrations of anti-Vβ17/anti-CD123 bispecific and Vβ17×NULL arm control antibodies. Mouse anti-human IgG4 Fc-PE secondary antibody was used to detect the bispecific antibody. Table 10 shows the frequency of CD8+ T cells positive for PE (secondary antibody) when treated with different concentration of bispecific antibodies. The EC.sub.50 for anti-Vβ17/anti-CD123, Vβ17×NULL, was determined as 9.0 nm, 18.7 nm respectively (Table 10).

TABLE-US-00011 TABLE 10 Binding activity of CD8.sup.+ T cell for bispecific antibodies. anti-Vβ17/ Conc.(μg/mL) anti-CD123 Vβ17XNULL NULLXCD123 20 74.7 76.2 0.1 10 72.4 75.4 0.4 5 70.8 64.6 0.3 2.5 64.8 42.5 0.5 1.25 38.0 32.4 0.4 0.625 41.4 21.7 −0.1 0.3125 26.5 11.8 0.8 0.15625 19.9 3.4 0.6 0.078125 10.8 1.8 0.7 EC.sub.50 (μg/mL) 1.35 2.80 ND EC.sub.50 (nM) 9 18.7 ND

[0177] Bispecific antibody binding affinities to CD8+ T cell were determined by flow cytometry. Half maximal effective concentration (EC.sub.50) values were calculated as the antibody concentration that generates 50% of the maximal binding (PE positive cells). ND: Not Determined

Bispecific Mediated Cytotoxicity Assay

[0178] In order to analyze the potency of the anti-Vβ17/anti-CD123 bispecific antibody mediated cytotoxicity, CFSE labelled target (Kasumi-3) cells were co-cultured with stimulated CD8+ T cells (effectors) from day 14 of culture at an effector to target (ET) ratio 0.5:1, 1:1, 5:1 for 14 and 24 hours with various concentrations of anti-Vβ17/anti-CD123 bispecific and Vβ17×NULL arm control antibody. CD123 expression on target Kasumi-3 cells were checked by using a commercially available anti-CD123 antibody. Target cells (Kasumi-3) were labelled with CFSE to identify them as CFSE.sup.+ during flow cytometry analysis. Post co-culture period, 7-AAD was added to analyze the percentage of 7-AAD.sup.+CFSE.sup.+ cells as a measure of cytotoxicity. Basal cytotoxicity observed in the absence of bispecific antibody was subtracted to obtain specific cytotoxicity in response to bispecific antibody. The assay was performed once with a single donor (HPU-08694). The EC.sub.50 for the anti-Vβ17/anti-CD123 bispecific antibody at 0.5:1, 1:1 and 5:1 ET ratios for 14-hour time point were 3.7, 0.1 and 0.133 pM respectively (Table 11).

TABLE-US-00012 TABLE 11 Summary of EC.sub.50 values for various bispecific antibodies upon co-culturing FLU MP 58 peptide stimulated CD8.sup.+ T cell with Kasumi-3 cells at ET ratios 0.5:1, 1:1 and 5:1 for 14 hours.

EC.sub.50 (ng/mL)	E:T Ratio	E:T Ratio	E:T Ratio
Bispecific Ab	(0.5:1)	(1:1)	(5:1)
NULLXCD123	UD	UD	UD
Vβ17XNULL	UD	UD	UD
Anti-Vβ17/anti-CD123	0.55	0.015	0.02

EC.sub.50 (pM)	E:T Ratio	E:T Ratio	E:T Ratio
Bispecific Ab	(0.5:1)	(1:1)	(5:1)
NULLXCD123	UD	UD	UD
Vβ17XNULL	UD	UD	UD
anti-Vβ17/anti-CD123	3.7	0.1	0.133

UD: Undetectable, as the activity was too low for proper curve fitting.

[0179] The EC.sub.50 for the anti-Vβ17/anti-CD123 bispecific at 0.5:1, 1:1 and 5:1 ET ratio for 24-hour time point were 0.4, 0.2 and 1.0 pM respectively (Table 12).

TABLE-US-00013 TABLE 12 Summary of EC.sub.50 values for various bispecific antibodies upon co-culturing FLU MP 58 peptide stimulated CD8.sup.+ T cells with Kasumi-3 cells at ET ratios 0.5:1, 1:1 and 5:1 for 24 hours.

EC.sub.50 (ng/mL)	E:T Ratio	E:T Ratio	E:T Ratio
Bispecific Ab	(0.5:1)	(1:1)	(5:1)
NULLXCD123	UD	UD	UD
Vβ17XNULL	UD	UD	UD
anti-Vβ17/anti-CD123	0.06	0.03	0.15

EC.sub.50 (pM)	E:T Ratio	E:T Ratio	E:T Ratio
Bispecific Ab	(0.5:1)	(1:1)	(5:1)
NULLXCD123	UD	UD	UD
Vβ17XNULL	UD	UD	UD
anti-Vβ17/anti-CD123	0.4	0.2	1.0

UD: Undetectable

[0180] Similarly, anti-Vβ17/anti-CD123 bispecific mediated unstimulated CD8+ T cell cytotoxicity was tested at ET ratio 0.5:1, 1:1, 5:1 for 14 (Table 13) and 24 (Table 14) hours. At 5 ng/ml anti-Vβ17/anti-CD123 bispecific concentration and 14-hour time point, unstimulated CD8+ T cells at 0.5:1 and 1:1 ET ratio showed 2.8% and 9.8% target cell cytotoxicity respectively (Table 13), compared to 77% and 73% cytotoxicity by stimulated CD8+ T cells. At 5:1 ET ratio, unstimulated CD8+ T cells exhibited 31.65% target cytotoxicity, compared to 70.9% by stimulated CD8+ T cells. Similar results were obtained from 24-hour time point (Table 12, 15, 16, and 17). At highest concentration (5 ng/ml) of anti-Vβ17/anti-CD123 bispecific tested, unstimulated CD8+ T cells exhibited higher cytotoxicity towards target cells at a higher ET ratio.

TABLE-US-00014 TABLE 13 Cytotoxicity assay with unstimulated CD8.sup.+ T cells at various ET ratios for 14 hours. Frequency of CFSE and 7-AAD positive cells when treated with different concentrations of bispecific antibodies.

Conc	E:T Ratio	E:T Ratio	E:T Ratio
Bispecific Ab	(ng/mL)	(0.5:1)	(1:1)	(5:1)
NULLXCD123	5	1.3	−0.6	−0.45
	0.005	1.3	−0.5	0.45
Vβ17XNULL	5	−0.6	−0.8	3.25
	0.005	−0.3	1	−1.35
anti-Vβ17/anti-	5	2.8	9.8	31.65
CD123	0.005	0.1	3.2	12.25

TABLE-US-00015 TABLE 14 Cytotoxicity assay with unstimulated CD8.sup.+ T cells at various ET ratios for 24 hours. Frequency of CFSE and 7-AAD positive cells when treated with different concentrations of bispecific antibodies.

Unstimulated CD8+ T cells	Conc	E:T Ratio	E:T Ratio	E:T Ratio
	(ng/mL)	(0.5:1)	(1:1)

(5:1) NULLXCD123 5 −1.3 −0.55 −4.85 0.005 −2 −0.85 −2.95 Vβ17XNULL 5 −0.8 −1.35 10.85 0.005 −1 −1.05 −1.95 anti-Vβ17/anti-CD123 5 4.8 11.55 30.65 0.005 1.5 1.75 10.95

TABLE-US-00016 TABLE 15 Cytotoxicity assay at 0.5:1 ET ratio (stimulated CD8.sup.+ T cell: Kasumi-3 cells) upon incubation for 14 hrs. Frequency of CFSE and 7-AAD positive cells when treated with different concentrations of bispecific antibodies at 0.5:1 ET ratio for 14 hrs. anti-Vβ17/ Conc.(ng/mL) NULLXCD123 Vβ17XNULL anti-CD123 50 3.47 2.57 77.07 5 2.67 2.17 77.47 0.5 −0.73 1.87 46.77 0.05 0.77 1.67 3.77 0.005 −0.03 1.47 1.97 0.0005 0.67 1.07 2.17 0.00005 1.67 0.17 0.17 0.000005 −0.43 3.27 0.87 EC.sub.50 (ng/mL) ND ND 0.55 EC.sub.50 (pM) ND ND 3.7

[0181] Half maximal effective concentration (EC.sub.50) values were calculated as the antibody concentration that generates 50% of maximal cytotoxicity (CFSE.sup.+7AAD.sup.+) cells. ND: Not Determined.

TABLE-US-00017 TABLE 16 Cytotoxicity assay at 1:1 ET ratio (stimulated CD8.sup.+ T cell: Kasumi-3 cells) upon incubation for 14 hrs. Frequency of CFSE and 7-AAD positive cells when treated with different concentrations of bispecific antibodies at 11 ET ratio for 14 hrs. anti-Vβ17/ Conc.(ng/mL) NULLXCD123 Vβ17XNULL anti-CD123 50 0.6 −0.5 76.0 5 0.1 0.9 73.0 0.5 1.0 0.9 77.9 0.05 0.4 1.8 59.4 0.005 1.8 0.9 36.8 0.0005 0.9 1.1 18.0 0.00005 0.7 0.9 6.1 0.000005 1.6 0.8 1.9 EC.sub.50 (ng/mL) ND ND 0.015 EC.sub.50 (pM) ND ND 0.1

[0182] Half maximal effective concentration (EC.sub.50) values were calculated as the antibody concentration that generates 50% of maximal cytotoxicity (CFSE.sup.+7AAD.sup.+) cells. ND: Not Determined

TABLE-US-00018 TABLE 17 Cytotoxicity assay at 5:1 E:T ratio (stimulated CD8.sup.+ T cell: Kasumi-3 cells) upon incubation for 14 hrs. Frequency of CFSE and 7-AAD positive cells when treated with different concentrations of bispecific antibodies at 5:1 ET ratio for 14 hrs. anti-Vβ17/ Conc.(ng/mL) NULLXCD123 Vβ17XNULL anti-CD123 50 2.3 0.0 70.2 5 3.1 2.7 70.9 0.5 1.8 4.4 74.5 0.05 3.0 1.5 73.2 0.005 2.1 1.6 2.5 0.0005 2.9 3.5 1.4 0.00005 3.2 5.5 2.5 0.000005 4.1 4.4 4.8 EC.sub.50 (ng/mL) UD UD 0.02 EC.sub.50 (pM) UD UD 0.13

[0183] Half maximal effective concentration (EC.sub.50) values were calculated as the antibody concentration that generates 50% of maximal cytotoxicity (CFSE.sup.+7AAD.sup.+) cells. UD: Undetectable.

[0184] It will be appreciated by those skilled in the art that changes could be made to the embodiments described above without departing from the broad inventive concept thereof. It is understood, therefore, that this invention is not limited to the particular embodiments disclosed, but it is intended to cover modifications within the spirit and scope of the present invention as defined by the present description.

TABLE-US-00019 SEQ ID NO: Type Species Description Sequence 1 PRT mouse B17B01-HCDR1 GYSITSGYFWN 2 PRT mouse B12B01-HCDR2 YISYDGSNN 3 PRT mouse B12B01-HCDR2 PSPGTGYAVDY 4 PRT mouse B17B01-LCDR1 RSSQSLVHSNGNTYLH 5 PRT mouse B12B01-LCDR2 KVSNRFS 6 PRT mouse B12B01-LCDR2 SQSTHVPFT 7 PRT mouse B17B01-HC

NVQLQESGPGLVKPSQSLSLTCSVAGYSITSGYFWNWIRQFPGNKLEWMGY
ISYDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCASPSPG
TGYAVDYWGQGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYF
PEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSQTVTCNV
AHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPK
VTCVVVDISKDDPEVQFSWFVDDVEVHTAQTKPREEQINSTFRSVSELPIM
HQDWLNGKEFKCRVNSAAFPAPIEKTISKTYGRPKAPQVYTIPPPKEQMAK
DKVSLTCMITNFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLN

VQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 8 PRT mouse B17B01-LC
NVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKF
LIYKVSNRFSGVPDRFSGGGSGTEFTLKISRVEAEDLGVYFCSQSTHVPFT
FGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKW
KIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHK
TSTSPIVKSFNRNEC 9 PRT mouse B17B1-HC
NVQLQESGPGLVKPSQSLSLTCSVAGYSITSGYFWNWIRQFPGNKLEWMGY
ISYDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCASPSPG
TGYAVDYWGQGTSVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCN
VDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLLYS
KLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 10 PRT mouse B17B1-LC
NVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKF
LIYKVSNRFSGVPDRFSGGGSGTEFTLKISRVEAEDLGVYFCSQSTHVPFT
FGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKW
KIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHK
TSTSPIVKSFNRNEC 11 PRT mouse B17B2-HC
DVQLKESGPGLVKPSQSLSVTCSVTGYSITSGYYWNWYRQFPGNKLEWMGY
ISYDGSNNYNPSLKNRISITRDTSKNQILLKLTYVTTEDTATYYCTRPSPG
TGYAVDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCN
VDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLLYS
KLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 12 PRT mouse B17B2-LC
DIVMTQSPDSLAVSLGERATINCRSSQSLVHSNGNTYLHWYQQKPGQPPKL
LIYKVSNRFSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQSTHVPFT
FGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKW
KIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHK
TSTSPIVKSFNRNEC 13 PRT artificial B17B21-HC
QVQLQESGPGLVKPSETLSLTCTVSGYSITSGYFWNWIRQPPGKGLEWIGY
ISYDGSNNYNPSLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCASPSPG
TGYAVDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCN
VDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE
MTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVS
RLTVDKSRWQEGNVFSCSVMHEALHNRFTQKSLSLSLGK 14 PRT artificial B17B21-LC
DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKF
LIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTHVPFT
FGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQ
GLSSPVTKSFNRGEC 15 PRT human I3RB217-HC
EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWISWVRQMPGKGLEWMGII
DPSDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARGDGS

TDLDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPE
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EVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMT
KNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRL
TVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 16 PRT human I3RB217-LC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYG
ASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQDYGFPWTFGQG
TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC 17 PRT human Null-HC
QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKALEWLA
HIYWDDDKRYNPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCARLYG
FTYGFAYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCN
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TPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVL
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MTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
RLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 18 PRT human Null-LC
DIVMTQSPDSLAVSLGERATINCRASQSVDYNGISYMHWYQQKPGQPPKLL
IYAASNPESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQIIEDPWTF
GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG
LSSPVTKSFNRGEC 19 PRT artificial B17H3
EVQLLESGGGLVQPGGSLRLSCAASGYSITSGYFWNWVRQAPGKGLEWVS
YISYDGSNNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPS
PGTGYAVDYWGQGTLVTVS 20 PRT artificial B17H4
EVQLLESGGGLVQPGGSLRLSCAASGYSITSGYFWNWVRQAPGKGLEWVSY
ISYDGSNNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASPSPG
TGYAVDYWGQGTLVTVSS 21 PRT artificial B17H5
QVQLQESGPGLVKPSETLSLTCTVSGYSITSGYFWNWIRQPPGKGLEWIGY
ISYDGSNNYNPSLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCASPSPG
TGYAVDYWGQGTLVTVSS 22 PRT artificial B17L3
DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKL
LIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTHVPFT FGQGTKLEIK 23
PRT artificial B17L4
DIQMTQSPSSLSASVGDRVTITCRSSQSLVHSNGNTYLHWYQQKPGKAPKF
LIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTHVPFT FGQGTKLEIK 24
PRT artificial B17L5
DVVMTQSPLSLPVTLGQPASISCRSSQSLVHSNGNTYLHWFQQRPGQSPRF
LIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPFT FGQGTKLEIK
25 PRT artificial B17H1
NVQLQESGPGLVKPSQSLSLTCSVAGYSITSGYFWNWIRQFPGNKLEWMGY
ISYDGSNNYNPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCASPSPG
TGYAVDYWGQGTSVTVSS 26 PRT artificial B17L1
NVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKF
LIYKVSNRFSGVPDRFSGGGSGTEFTLKISRVEAEDLGVYFCSQSTHVPFT FGSGTKLEIK
27 PRT human TCR-Vβ17

MAWVWTLLFLMAAAQSIQAVDGGITQSPKYLFRKEGQNVTLSCEQNLNHDA
MYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQ
KNPTAFYLCASSSRSSYEQYFGPGTRLTVTEDLKNVFPPEVAVFEPSEAEI
SHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDS
RYSLSSRLRVSATFWQNPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSA
EAWGRADepkscdkthtcppcpapeLLggpsvflfppkpkdtlmisrtpev
tcvvvDvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlh
qdwlngkeykckvsnkalpapiektiskakgqprepqvyVlppsreemtkn
qvslLclvkgfypsdiavewesngqpennyLtWppvldsdgsfflyskltv dksnvqqgnvfscsvmhealhnhytqkslslspg
28 PRT artificial B17B21
MAWVWTLLFLMAAAQSIQADIQMTQSPSSLSASVGDRVTITCRSSQSLVHS half antibody
NGNTYLHWYQQKPGKAPKFLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSL
QPEDFATYYCSQSTHVPFTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT
LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGSEGKSSGSGSESKST
EGKSSGSGSESKSTGGSQVQLQESGPGLVKPSETLSLTCTVSGYSITSGYF
WNWIRQPPGKGLEWIGYISYDGSNNYNPSLKSRVTISRDTSKNQFSLKLSS
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STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS
VVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT
KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK
GQPREPQVYTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNY
KTTPPVLDSDGSFFLVSRLTVDKSRWQEGNVFSCSVMHEALHNRFTQKSLS LSLGK 29
DNA artificial B17B21
ATGGCCTGGGTGTGGACCCTGCTGTTCCTGATGGCCGCCGCCCAGAGCATC half
antibody CAGGCCGACATCCAGATGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTG
GGCGACCGCGTGACCATCACCTGCCGCAGCAGCCAGAGCCTGGTGCACAGC
AACGGCAACACCTACCTGCACTGGTACCAGCAGAAGCCAGGCAAGGCCCCA
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CCAGAGCCAGTGACCGTGAGCTGGAACAGCGGCGCCCTGACCAGCGGCGTG
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GTGGTGACCGTGCCAAGCAGCAGCCTGGGCACCAAGACCTACACCTGCAAC
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AAGACCACCCCACCAGTGCTGGACAGCGACGGCAGCTTCTTCCTGGTGAGC
CGCCTGACCGTGGACAAGAGCCGCTGGCAGGAGGGCAACGTGTTCAGCTGC
AGCGTGATGCACGAGGCCCTGCACAACCGCTTCACCCAGAAGAGCCTGAGC
CTGAGCCTGGGCAAGATGGCCTGGGTGTGGACCCTGCTGTTCCTGATGGCC
GCCGCCCAGAGCATCCAGGCCGACATCCAGATGACCCAGAGCCCAAGCAGC
CTGAGCGCCAGCGTGGGCGACCGCGTGACCATCACCTGCCGCAGCAGCCAG
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CCAGGCAAGGCCCCAAAGTTCCTGATCTACAAGGTGAGCAACCGCTTCAGC
GGCGTGCCAAGCCGCTTCAGCGGCAGCGGCAGCGGCACCGACTTCACCCTG
ACCATCAGCAGCCTGCAGCCAGAGGACTTCGCCACCTACTACTGCAGCCAG
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CGCACCGTGGCCGCCCCAAGCGTGTTCATCTTCCCACCAAGCGACGAGCAG
CTGAAGAGCGGCACCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCA
CGCGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAAC
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GCCTGCGAGGTGACCCACCAGGGCCTGAGCAGCCCAGTGACCAAGAGCTTC
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AGCACCGGCGGCAGCCAGGTGCAGCTGCAGGAGAGCGGCCCAGGCCTGGTG
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ACCAGCGGCTACTTCTGGAACTGGATCCGCCAGCCACCAGGCAAGGGCCTG
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CTGAAGAGCCGCGTGACCATCAGCCGCGACACCAGCAAGAACCAGTTCAGC
CTGAAGCTGAGCAGCGTGACCGCCGCCGACACCGCCGTGTACTACTGCGCC
AGCCCAAGCCCAGGCACCGGCTACGCCGTGGACTACTGGGGCCAGGGCACC
CTGGTGACCGTGAGCAGCGCCAGCACCAAGGGCCCAAGCGTGTTCCCACTG
GCCCCATGCAGCCGCAGCACCAGCGAGAGCACCGCCGCCCTGGGCTGCCTG
GTGAAGGACTACTTCCCAGAGCCAGTGACCGTGAGCTGGAACAGCGGCGCC
CTGACCAGCGGCGTGCACACCTTCCCAGCCGTGCTGCAGAGCAGCGGCCTG
TACAGCCTGAGCAGCGTGGTGACCGTGCCAAGCAGCAGCCTGGGCACCAAG
ACCTACACCTGCAACGTGGACCACAAGCCAAGCAACACCAAGGTGGACAAG
CGCGTGGAGAGCAAGTACGGCCCACCATGCCCACCATGCCCAGCCCCAGAG
GCCGCCGGCGGCCCAAGCGTGTTCCTGTTCCCACCAAAGCCAAAGGACACC
CTGATGATCAGCCGCACCCCAGAGGTGACCTGCGTGGTGGTGGACGTGAGC
CAGGAGGACCCAGAGGTGCAGTTCAACTGGTACGTGGACGGCGTGGAGGTG

CACAACGCCAAGACCAAGCCACGCGAGGAGCAGTTCAACAGCACCTACCGC
GTGGTGAGCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAGGAG
TACAAGTGCAAGGTGAGCAACAAGGGCCTGCCAAGCAGCATCGAGAAGACC
ATCAGCAAGGCCAAGGGCCAGCCACGCGAGCCACAGGTGTACACCCTGCCA
CCAAGCCAGGAGGAGATGACCAAGAACCAGGTGAGCCTGAGCTGCGCCGTG
AAGGGCTTCTACCCAAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAG
CCAGAGAACAACTACAAGACCACCCCACCAGTGCTGGACAGCGACGGCAGC
TTCTTCCTGGTGAGCCGCCTGACCGTGGACAAGAGCCGCTGGCAGGAGGGC
AACGTGTTCAGCTGCAGCGTGATGCACGAGGCCCTGCACAACCGCTTCACC
CAGAAGAGCCTGAGCCTGAGCCTGGGCAAGTGATAG 30 PRT artificial I3RB217
MAWVWTLLFLMAAAQSIQAEIVLTQSPGTLSLSPGERATLSCRASQSVSSS half antibody
YLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED
FAVYYCQQDYGFPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV
CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGECGGSEGKSSGSGSESKSTEGKS
SGSGSESKSTGGSEVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWISWVR
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QVYTLPPSQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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artificial I3RB217
ATGGCCTGGGTGTGGACCCTGCTGTTCCTGATGGCCGCCGCCCAGAGCATC half
antibody CAGGCCGAGATCGTGCTGACCCAGAGCCCAGGCACCCTGAGCCTGAGCCCA
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AGCCGCTGGCAGGAGGGCAACGTGTTCAGCTGCAGCGTGATGCACGAGGCC
CTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGAGCCTGGGCAAG 32 PRT
artificial B23B49
MAWVWTLLFLMAAAQSIQAEIVLTQSPGTLSLSPGERATLSCRASQSVSSS half antibody
YLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED
FAVYYCQQDYGFPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV
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artificial B23B49
ATGGCCTGGGTGTGGACCCTGCTGTTCCTGATGGCCGCCGCCCAGAGCATC half
antibody CAGGCCGACATCGTGATGACCCAGAGCCCAGACAGCCTGGCCGTGAGCCTG
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CTGACCGTGGACAAGAGCCGCTGGCAGGAGGGCAACGTGTTCAGCTGCAGC
GTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTG
AGCCTGGGCAAG 34 PRT Artificial HCDR1 SYWIS 35 PRT Artificial HCDR2
IIDPSDSDTRYSPSFQG 36 PRT Artificial HCDR3 GDGSTDLDY 37 PRT Artificial LCDR1
RASQSVSSSYL 38 PRT Artificial LCDR2 GASSRAT 39 PRT Artificial LCDR3 QQDYGFPWT
40 PRT Artificial HC
EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWISWVRQMPGKGLEWMGII
DPSDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARGDGS
TDLDYWGQGTLVTVSS 41 PRT Artificial LC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYG
ASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQDYGFPWTFGQG TKVEIK 42 PRT
Artificial IGHJ1*01 WGQGTLVTVSS HC 43 PRT Artificial IGKJ2*01 FGQGTKLEIK LC 44
PRT Artificial Val0.2_Fc
MAWVWTLLFLMAAAQSIQAQLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQ
WYRQEPGEGPVLLVTVVTGGEVKKLKRLTFQFGDARKDSSLHITAAQPGDT
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syltvlhqdwingkeykckvsnkalpapiektiskakgqprepqvyVYpps
reemtknqvsltclvkgfypsdiavewesngqpennykttppvldsdgsfA
lVskltvdksrwqqgnvfscsvmhealhnhytqkslslspg

Claims

1.-**34**. (canceled)

35. A Vb17 bispecific antibody or antigen-binding fragment thereof comprising: (a) a first heavy

chain (HC1), (b) a second heavy chain (HC2), (c) a first light chain (LC1), and (d) a second light chain (LC2); wherein HC1 is associated with LC1 and HC2 is associated with LC2; and wherein HC1 comprises a heavy chain variable region comprising the amino acid sequences of SEQ ID NO: 25, SEQ ID NO: 19, SEQ ID NO: 20, or SEQ ID NO: 21, and LC1 comprises a light chain variable region comprising the amino acid sequences of SEQ ID NO: 26, SEQ ID NO: 22, SEQ ID NO: 23, or SEQ ID NO: 24.

36. The bispecific antibody of claim 35, wherein HC1 comprises a heavy chain variable region comprising the amino acid sequences of SEQ ID NO: 25 and LC1 comprises a light chain variable region comprising the amino acid sequences of SEQ ID NO: 26.

37. The bispecific antibody of claim 35, wherein the bispecific antibody or antigen-binding fragment thereof is an IgG isotype.

38. The bispecific antibody of claim 35, wherein HC1 and LC1 are humanized.

39. The bispecific antibody of claim 35, wherein HC2 and LC2 bind to CD123.

40. The bispecific antibody of claim 39, wherein HC2 comprises a heavy chain complementarity determining region 1 (HCDR1), HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NO:34, SEQ ID NO:35, and SEQ ID NO:36, respectively, and LC2 comprises a light chain complementarity determining region 1 (LCDR1), LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NO:37, SEQ ID NO:38, and SEQ ID NO:39, respectively.

41. The bispecific antibody of claim 35, HC1 comprises the amino acid sequence of SEQ ID NO:13 and LC1 comprises the amino acid sequence of SEQ ID NO:14, and wherein HC2 comprises the amino acid sequence of SEQ ID NO: 15 and LC2 comprises the amino acid sequence of SEQ ID NO:16.

42. A nucleic acid encoding the HC1, LC1, HC2, and LC2 of the Vb17 bispecific antibody or antigen-binding fragment thereof of claim 35.

43. A vector comprising the isolated nucleic acid of claim 42.

44. A host cell comprising the vector of claim 43.

45. A buffered composition comprising the isolated anti-Vb17/anti-CD123 bispecific antibody or antigen-binding fragment thereof of claim 35.

46. A method of directing a Vb17-expressing CD8+ or CD4+ T cell to a cancer cell, the method comprising contacting a Vb17-expressing CD8+ or CD4+ T cell with the bispecific antibody or antigen-binding fragment thereof of claim 35, wherein the contacting directs the Vb17-expressing CD8+ or CD4+ T cell to a cancer cell.

47. The method of claim 46, wherein the cancer cell is a CD123-expressing cancer cell.

48. A method for inhibiting growth or proliferation of cancer cells, the method comprising contacting the cancer cells with the bispecific antibody or antigen-binding fragment thereof of claim 35, wherein the contacting inhibits the growth or proliferation of the cancer cells.

49. The method of claim 48, wherein the cancer cell is a CD123-expressing cancer cell.

50. A kit comprising a bispecific antibody or antigen-binding fragment thereof of claim 35 and packaging for the same.

51. A method of producing a bispecific antibody or antigen-binding fragment thereof comprising culturing the host cell of claim 44 to produce the bispecific antibody or antigen-binding fragment thereof, and recovering the bispecific antibody or antigen-binding fragment thereof from the cell or culture.