

COMPOSITIONS AND METHODS COMPRISING ANTIBODIES THAT BIND TO COVALENT PEPTIDE CONJUGATES

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. provisional patent application no. 63/154,627,
5 filed February 26, 2021, and U.S. provisional patent application no. 63/253,499, filed
October 7, 2021, the entire disclosures of each of which are incorporated herein by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with government support under grant nos. CA194864,
CA267362 and CA049152 awarded by the National Institutes of Health. The government has
10 certain rights in the invention.

SEQUENCE LISTING

The instant application contains a Sequence Listing, which has been submitted
electronically in ASCII format and is hereby incorporated by reference in its entirety. Said
ASCII copy, created on February 24, 2022, is named 58636_00482_SL.txt, and is 212,998
15 bytes in size.

BACKGROUND

There is an ongoing and unmet need for agents that can bind to targets that include
drugs that are covalently bound to proteins or peptides. In particular, there is a need to
improve the efficacy of targeted therapy and also to increase tumor immunogenicity and the
20 efficacy of immune therapy against cancer driven by intracellular oncogenes. The disclosure
is pertinent to these needs.

BRIEF SUMMARY

The present disclosure provides compositions and methods that include binding
partners that bind with specificity to target sites on proteins or peptides that comprise a
25 covalently attached molecule. It is believed that this is the first disclosure of binding partners
with this binding function. The disclosure illustrates this approach using binding partners in
the form of numerous antibodies and antibody derivatives that specifically bind to proteins
and peptides that have been covalently modified by attachment of a molecule, wherein the
molecules are illustrated by a variety of drugs. Further, the disclosure demonstrates binding
30 partners that bind with specificity to peptides that have been covalently modified by
attachment of a small molecule drug are specific for the described covalently modified
peptides when presented in the context of a human leukocyte antigen (HLA), wherein HLA is a

representative example of a major histocompatibility complex (MHC). Thus, binding partners that are specific for peptide-drug conjugates in an HLA complex are demonstrated. The disclosure includes polynucleotides encoding the described binding partners and cells that are modified to express the binding partners. The disclosure includes diagnostic, prophylactic and therapeutic approaches using the binding partners.

In one aspect, the present disclosure relates to a composition comprising a binding partner or a polynucleotide encoding the binding partner, wherein the binding partner binds to a peptide conjugate in complex with a major histocompatibility complex (MHC), wherein the peptide conjugate comprises a peptide covalently linked to a small molecule, and wherein a dissociation constant (Kd) of the binding partner to the peptide conjugate in complex with the MHC is lower than a Kd of the binding partner to the peptide conjugate not in complex with the MHC.

In another aspect, the present disclosure relates to the composition as disclosed herein for use in therapy. In another aspect, the present disclosure relates to use of the composition as disclosed herein in the manufacture of a medicament for the treatment of cancer in a subject in need thereof.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. Graphs depicting results of phage enzyme-linked immunosorbent assay (ELISA) of phage-displayed antibody clones. Binding to KRAS^{G12C}-GDP and KRAS^{G12C}-GDP-ARS-1620 conjugate was determined. For each clone, the bars in the graph are, from left to right, Buffer, G12C-GDP-ARS, and G12C-GDP.

Figure 2. Graph showing 12C-ARS Fab59 binding to KRAS^{G12C} in GTPγS- or GDP-bound nucleotide state with or without ARS-1620 was characterized using the bead binding assay.

Figure 3. Graphs showing that 12C-ARS-Fab59 specifically binds KRAS^{G12C}-GDP conjugated to ARS-1620.

Figure 4. Shown in (A) is data obtained using 12C-ARS-Fab59 to measure ARS-1620/KRAS^{G12C} adducts by pull-down assays from lysates prepared from cell lines. Shown in (B) are immunoblots of whole cell lysates and 12C-ARS Fab-pull-downs (PD) from RAS-less MEFs reconstituted with the indicated *KRAS* mutants (4A) and KCP (*Kras*^{G12C}; *Tp53*^{R172H}; Pdx-Cre) mouse pancreas cancer cells (4B), treated in the presence or absence of ARS-1620. Shown in (C) are whole cell lysates and 12C-ARS Fab pull-downs (PD) from H358 and MIAPaCa-2 cells, treated as indicated. Shown in (D) is ARS-adduct formation in samples from C, quantified by LC/MS-MS assay. ARS-1620 and SHP099 concentrations were 10 μM in all panels.

Figure 5. Data showing that 12C-ARS-Fab59 can be used to measure the engagement of ARS-1620 to mutant KRAS by pull-down assay with lysates prepared from animal tissues. A, B, anti-pan RAS and anti-ERK2 (loading control) immunoblots of lysates and 12C-ARS Fab pull-downs (PD) from *LSL-KRAS*^{G12C}-*Tp53*^{R270H} (A) and *LSL-KRAS*^{G12C} (B) tumors after 3 days of oral gavage with ARS-1620 (200 mg/kg/d) alone or with the SHP2 inhibitor SHP099 (75 mg/kg/d) are shown.

Figure 6. Binding of antibody clones to AMG510 conjugated to the KRAS(G12C) peptide and the poly-Ser peptide. For each antibody clone, the bars are from left to right are

What is claimed is:

1. A composition comprising a binding partner or a polynucleotide encoding the binding partner, that wherein the binding partner binds to with specificity to a site on a protein or peptide that comprises a covalently linked molecule (a peptide conjugate).

2. ~~—The binding partner of claim 1, wherein the binding partner does not bind, or binds with a lower affinity, to a control protein or control peptide that does not comprise the covalently linked molecule.~~

3. ~~—The binding partner of claim 1, wherein the binding partner binds with specificity to the peptide conjugate, said peptide conjugate being in a in complex with a major histocompatibility complex (MHC), wherein the peptide conjugate comprises a peptide covalently linked to a small molecule, and wherein a dissociation constant (Kd) of the binding partner to the peptide conjugate in complex with the MHC is lower than a Kd of the binding partner to the peptide conjugate not in complex with the MHC.~~

2. The composition of claim 1, wherein the Kd of the binding partner to the peptide conjugate in complex with the MHC is at most 20 nM.

4. ~~—The binding partner of claim 3, wherein the MHC is a human leukocyte antigen (HLA).~~

3. The binding partner composition of claim 1 or 2, wherein the site on the peptide conjugate comprises a nucleophilic or an electrophilic residue, said residue optionally being one of Cys, Lys, Tyr, or His residue that is covalently linked to the small molecule.

4. The composition of any one of claims 1-3, wherein the peptide comprises a mutation.

5. The composition of any one of claims 1-4, wherein the small molecule is selected from the group consisting of AMG510, 2E07, 6H05, SML-8-73-1, MRTX849, JNJ74699157, LY3499446, ARS-853, ARS-1620, MRTX1275, and derivatives thereof.

6. ~~—The binding partner of claim 5, wherein the site comprises the Cys.~~

7. ~~The binding partner of claim 6, wherein the molecule is covalently linked to the Cys.~~

8. ~~The binding partner of claim 1, wherein the site is present as a peptide conjugate in an intact protein, and wherein optionally the intact protein is in its native confirmation.~~

9. ~~The binding partner of any one of claims 1-8, wherein the binding partner is comprised by an intact antibody, an antigen-binding (Fab) fragment, an Fab' fragment, an (Fab')₂ fragment, an Fd, an Fv, a dAb, a single domain fragment or single monomeric variable-antibody domain, a single-chain Diabody (scDb), a single-chain variable fragment (scFv), a Bi-specific T-cell engager (BiTE), bispecific killer cell engager (BiKE), CrossMab, a tri-specific binding partner, a or chimeric antigen receptor (CAR).~~

10. ~~The binding partner of claim 9, wherein the binding partner is conjugated to a detectable label, or a chemotherapeutic agent, a radioisotope, or a toxin.~~

11. ~~The binding partner of claim 9, wherein the binding partner is a component of a fusion protein.~~

12. ~~The binding partner of claim 9, wherein the peptide conjugate is comprised by a segment of a protein that is associated with a cancer.~~

13. ~~The binding partner of claim 9, wherein the peptide conjugate is comprised by a protein that has enzymatic activity, and wherein the covalently linked molecule is an inhibitor of said protein that has the enzymatic activity.~~

14. ~~The binding partner of claim 13, wherein the protein that has the enzymatic activity is a kinase or a GTPase.~~

156. The ~~binding partner of claim 9~~composition of any one of claims 1-5, wherein ~~the peptide conjugate comprises a mutation, and wherein peptide component of the peptide conjugate is or is derived~~is from a RAS protein that is selected from the group consisting of KRAS, HRAS and NRAS; Bruton's tyrosine kinase (BTK); any epidermal growth factor receptor (EGFR) family member that is selected from EGFR (ERBB1), HER2/NEU

(ERBB2), HER3 (ERBB3), and HER4 (ERBB4); MET (HGFR); any fibroblast growth factor receptor (FGFR); ~~any~~ cyclin-dependent kinase (CDK); Acetylcholine Esterase (ACHE); p90 ribosomal S6 kinase (RSK); TP53, IDH1, GNAS, FBXW7, CTNNB1, DNMT3A, a cathepsin that is selected from the group consisting of cathepsin B, C, F, H, K, L, O, S, V, W and X; ~~any~~ caspase; ~~and a protein involved in obesity that is optionally P~~pancreatic lipase; or METAP2.

~~167.~~ The ~~binding partner of claim 9~~composition of claim 6, wherein the peptide ~~conjugate is from KRAS and wherein the peptide~~ comprises a KRAS^{G12C} mutation.

~~8.~~ The composition of any one of claims 1-7, wherein the peptide comprises the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2.

~~179.~~ The ~~binding partner of claim 9~~composition of any one of claims 1-8, wherein the peptide conjugate comprises ~~the a peptide from KRAS having a~~ KRAS^{G12C}-G12C mutation covalently linked to AMG510~~mutation, and the drug comprises a G12C inhibitor.~~

~~18.~~ ~~The binding partner of claim 9, wherein the peptide conjugate comprises a fragment of EGFR and the drug comprises an inhibitor of an EGFR family kinase.~~

~~19.~~ ~~The binding partner of claim 9, wherein the molecule is one of: AMG510, Osimertinib, ARS 1620, MRTX849, JNJ74699157, LY3499446, MRTX 1275, or a G12C degrader.~~

~~2010.~~ The ~~binding partner of claim 9~~composition of any one of claims 1-9, wherein the ~~binding partner specifically binds to a KRAS(G12C) AMG510 peptide conjugate or said peptide conjugate presented~~ MHC is on HLA-A*03:01 ~~and/or~~ HLA-A*11:01.

~~21.~~ ~~The binding partner of claim 9, wherein the binding agent specifically binds to a peptide conjugate that is BTK Ibrutinib that is optionally presented on HLA A*01:01.~~

~~2211.~~ The ~~binding partner of claim 9~~composition of claim 6, wherein the ~~binding agent specifically binds to a peptide~~ is from EGFR or BTK, wherein the small molecule is osimertinib or ibrutinib, conjugate that is an epidermal growth factor receptor (EGFR)-

~~Osimertinib conjugate that is optionally presented on~~ and wherein the peptide conjugate is in complex with HLA-A*02:01 or HLA-A*01:01.

12. The composition of any one of claims 1-11, wherein the binding partner is an intact antibody, an antigen-binding (Fab) fragment, an Fab' fragment, an (Fab')₂ fragment, an Fd, an Fv, a dAb, a single domain fragment or single monomeric variable antibody domain, a single-chain Diabody (scDb), a single-chain variable fragment (scFv), a bi-specific T-cell engager (BiTE), bispecific killer cell engager (BiKE), CrossMab, a tri-specific binding partner, or a chimeric antigen receptor (CAR).

13. The composition of claim 12, wherein the binding partner is a bi-specific T-cell engager comprising a first antigen-binding domain that binds to the peptide conjugate in complex with the MHC and a second antigen-binding domain that binds to CD3ε of a T cell.

14. The composition of claim 12 or 13, wherein the binding partner comprises (i) a heavy chain having a heavy chain (HC) complementarity determining region (CDR) 1 of an amino acid sequence of DYSIH, a HC CDR2 of an amino acid sequence of SSSSSGSTSYADSVKG, and a HC CDR3 of an amino acid sequence of X1X2X3X4X5X6MDY, where X1 is G, X2 is selected from the group consisting of A, C, E, G, H, K, L, M, N, P, Q, R, S, T, W and Y, X3 is selected from the group consisting of G, P, R, T and W, X4 is selected from the group consisting of A, D, E, F, G, H, I, K, M, N, Q, R, S, T, W and Y, X5 is selected from the group consisting of A, P and V, X6 is selected from the group consisting of A, C, G, K, L, M, Q, R, S, T and Y, wherein one, two, or three of X1X2X3X4X5X6 are mutated relative to a parental sequence of SEQ ID NO:155; (ii) a light chain having a light chain (LC) CDR1 of an amino acid sequence of RASQSVSSAVA, a LC CDR2 of an amino acid sequence of SASSLYS, and a LC CDR3 of an amino acid sequence of QQX1X2X3X4X5X6X7X8T, where X1 is selected from the group consisting of A, I, L, P, S, T and V, X2 is selected from the group consisting of K, R, S and T, X3 is F or Y, X4 is selected from the group consisting of I, R, T and V, X5 is selected from the group consisting of A, E, H, K, L, M, N, Q, R, S, T and Y, X6 is K or R, X7 is selected from the group consisting of A, C, D, E, G, H, K, L, M, N, P, Q, R, S, T, V and W, and X8 is selected from the group consisting of I, L and V, wherein one, two, or three of X1X2X3X4X5X6X7X8 are mutated relative to a parental sequence of SEQ ID NO:153.

15. The composition of claim 14, wherein the binding partner comprises a heavy chain having at least 80% sequence identity to SEQ ID NO: 4, and a light chain having at least 80% sequence identity to SEQ ID NO: 3.

5 16. The composition of any one of claims 12-15, wherein the binding partner comprises
(i) a heavy chain having a heavy chain (HC) complementarity determining region (CDR) 1 of
an amino acid sequence of DYSIH, a HC CDR2 of an amino acid sequence of
SISSSSGSTSYADSVKG, and a HC CDR3 of an amino acid sequence of GGWYPAMDY;
(ii) a light chain having a light chain (LC) CDR1 of an amino acid sequence of
10 RASQSVSSAVA, a LC CDR2 of an amino acid sequence of SASSLYS, and a LC CDR3 of
an amino acid sequence of QQISYVKKLIT.

17. The composition of claim 16, wherein the binding partner comprises a heavy chain
having at least 80% sequence identity to SEQ ID NO: 4, and a light chain having at least 80%
15 sequence identity to SEQ ID NO: 3.

18. The composition of any one of claims 1-17, wherein the binding partner does not
bind, or binds with a lower affinity, to the peptide that is not covalently linked to a small
20 molecule.

19. The composition of any one of claims 1-18 for use in therapy.

20. Use of the composition of any one of claims 1-18 in the manufacture of a medicament
for the treatment of cancer in a subject in need thereof.

25 21. The use of claim 20, wherein the cancer is renal cell carcinoma, breast cancer,
prostate cancer, pancreatic cancer, lung cancer, liver cancer, ovarian cancer, cervical cancer,
colon cancer, esophageal cancer, glioma, glioblastoma or another brain cancer, stomach
cancer, bladder cancer, testicular cancer, head and neck cancer, melanoma or another skin
30 cancer, a sarcoma, or a blood cancer.

22. The use of claim 20 or 21, wherein the subject has been administered the small
molecule.

23. —The binding partner of claim 9, wherein the binding partner comprises at least one heavy chain (V_H), or at least one pair of a light chain (V_L) and a heavy chain that are each at least 90% identical to heavy and light chain pairs that comprise the sequences of:

AMRA3-7D:

V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQISYVKKLITFGQGTKVEIKRTV
(SEQ ID NO: 3)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYSIHWRQAPGKGLEWVASISSSS
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGGWYPAMDYWG
QGTLVTVSS (SEQ ID NO: 4);

OEA2-5:

V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQYSYWPITFGQGTKVEIKRTV (SEQ
ID NO: 5)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISSSYIHWRQAPGKGLEWVAYISPSY
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCAREYVTMALDYWGQ
GTLVTVSS (SEQ ID NO: 6)

P2AMR-1

V_L:QSVLIQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYDVSK
RPSGVPDRFSGSKSGNTASLTVSGLQAEDEADYYCGSYADTDITVFGTGTKLTVL
(SEQ ID NO: 24)

V_H:QVQLVQSEPEVKKPGSSVKLSCKASGGTFSTDAITWVRQAPGQGLEYMGGIPLL
DSVDYAQRFFQGRVTVSADKSTGTAYMEVRSLGSEDTAKYYCAKWSSVDTGLDYW
GQGTLVTVSS (SEQ ID NO: 25)

P2AMR-12

V_H:QVQLQESGPGLVKPSSETLSLTCTVSGDSIINDPHYWGWIRQSPGKGLEWIGSTSHS
GHTYFNPSLKSRSVMSIDVAKNQFSLNVRSVTAADTAVYYCARMRYYYSGTYPVYY
FDYWGQGTLVTVSS (SEQ ID NO: 26)

P2AMR-13

V_L:SYVLTQPPSASGTPGQRVTISCSGSSSNIGSNFVSWYQQLPGTAPKLLISSNNQRPS
GVDPDRFSGSKSDTSASLAISGLQSEDEADYYCAAWDDSLNGPVFGGGTQLTVL (SEQ
ID NO: 27)

V_H:QVQLVQSEAEVKKPGSSVKVSCASGGTFSTRYGVSWVRQAPGQGLEWMGGIIP
MFGTANYAQKFQGRVTITADESTSTAYMELRSLRSEDVAVYYCARGDNSAYSDAFN
IWGQGTMTVTVSS (SEQ ID NO: 28)

AMRA3-2

V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQSGWSYPITFGQGTKVEIKRTV (SEQ
ID NO: 32)

5 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFYSSYIHWVRQAPGKGLEWVASISPY
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSSYYALDYWGQGT
LVTVSS (SEQ ID NO: 33)

AMRA3-7

10 V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQISYVYSLITFGQGTKVEIKRTV (SEQ
ID NO: 34)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSIHWVRQAPGKGLEWVASIYSS
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGGWYPAMDYWG
QGTLVTVSS (SEQ ID NO: 35)

AMRA3-7KK

20 V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQISYVKKLITFGQGTKVEIKRTV
(SEQ ID NO: 36)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSIHWVRQAPGKGLEWVASIYSS
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGGWYPAMDYWG
QGTLVTVSS (SEQ ID NO: 37)

AMRA3-8

30 V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDLATYYCQQYQYGYNLITFGQGTKVEIKRTV
(SEQ ID NO: 38)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISYSSSIHWVRQAPGKGLEWVASIYSYS
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYSYGWVGPWGWR
IDYWGQGTLVTVSS (SEQ ID NO: 39)

AMRA3-11

40 V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQSSSVYKLLITFGQGTKVEIKRTV
(SEQ ID NO: 40)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVYYSSSIHWVRQAPGKGLEWVASISSY
SYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTALYYCARGGPGWYRAMDYW
GQGTLVTVSS (SEQ ID NO: 41)

AMRA3-15

45 V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 42)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSSIHWRQAPGKGLEWVASISSSSG
STSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGYFYYGWWAMAFD
YWGQGTLLTVSS (SEQ ID NO: 43)

5 AMRA3-17

V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQSQWYEPLITFGQGGTKVEIKRTV
(SEQ ID NO: 44)

10 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTIYSSYIHWRQAPGKGLEWVASISSSS
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSYSYMSQWGWYQ
YSGMDYWGQGTLLTVSS (SEQ ID NO: 45)

AMRA3-18

15 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQGSYTYRLITFGQGGTKVEIKRTV
(SEQ ID NO: 46)

20 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVSYSSIHWRQAPGKGLEWVASISSSS
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYAWWAHGLDYW
GQGTLLTVSS (SEQ ID NO: 47)

AMRA3-21

25 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQASYWYNLFTFGQGGTKVEIKRTV
(SEQ ID NO: 48)

30 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISSYSIHWVRQAPGKGLEWVASIYSSY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARQYSMHFPWGYGM
DYWGQGTLLTVSS (SEQ ID NO: 49)

AMRA3-22

35 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQSDMPPIFGQGGTKVEIKRTV (SEQ
ID NO: 50)

40 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFYSSSIHWVRQAPGKGLEWVAIYSSS
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARPVNYYYQGALDY
WGQGTLLTVSS (SEQ ID NO: 51)

AMRA3-23

45 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISLQPEDFATYYCQQYYVPITFGQGGTKVEIKRTV (SEQ
ID NO: 52)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVYSSSIHWVRQAPGKGLEWVASISPSS
GYTYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYHYMFYDKGES
KWGYYGFDYWGQGTLLTVSS (SEQ ID NO: 53)

50 AMRA11-1

V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQSQYFPITFGQGTKVEIKRTV (SEQ
ID NO: 54)

5 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISYSSIHWVRQAPGKGLEWVASIYSYY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARNWSWSYSGVGMD
YWGQGTLVTVSS (SEQ ID NO: 55)

AMRA11-2

10 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 56)

15 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISSSSIHWVRQAPGKGLEWVASISSYSS
STYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYPYGWGWGSGGLD
YWGQGTLVTVSS (SEQ ID NO: 57)

AMRA11-15

20 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQQDFQYLITFGQGTKVEIKRTV (SEQ
ID NO: 58)

25 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVYYSSIHWVRQAPGKGLEWVASIYSY
YGSTYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGEK WALDYWGQ
GTLVTVSS (SEQ ID NO: 59)

AMRA11-16

30 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQYMYQPLITFGQGTKVEIKRTV
(SEQ ID NO: 60)

35 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVYYSSIHWVRQAPGKGLEWVASISSSS
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCAREPYNYNWYGM DY
WGQGTLVTVSS (SEQ ID NO: 61)

AMRA311-2

40 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQSLWWPITFGQGTKVEIKRTV (SEQ
ID NO: 62)

45 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVSSSSIHWVRQAPGKGLEWVASIYSYS
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARHGSYGSWWALDY
WGQGTLVTVSS (SEQ ID NO: 63)

AMRA311-10

V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQYFYFPITFGQGTKVEIKRTV (SEQ
ID NO: 64)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFYSSSIHWVRQAPGKGLEWVASISSYY
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARASYYSYGSSYPY
YMGLDYWGQGTLVTVSS (SEQ ID NO: 65)

5 AMRA311-14

V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQGSYRNPLLTFGQGTKVEIKRTV
(SEQ ID NO: 66)

10 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSIHWVRQAPGKGLEWVASISSSS
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARMNWSHYAMDYW
GQGTLVTVSS (SEQ ID NO: 67)

AMRA311-16

15 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQSSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 68)

20 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISSSSIHWVRQAPGKGLEWVAYISSYS
GYTTYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYWYGHYHSYFGL
DYWGQGTLVTVSS (SEQ ID NO: 69)

AMRA311-17

25 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQSSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 70)

30 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISSSSIHWVRQAPGKGLEWVASISSYSG
STYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYPYGSHVYTGLDY
WGQGTLVTVSS (SEQ ID NO: 71)

AMRA311-18

35 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQWNWADYLVTFGQGTKVEIKRTV
(SEQ ID NO: 72)

40 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISSSSIHWVRQAPGKGLEWVASIYSSSG
STSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARVYSSRYWGWGVAF
DYWGQGTLVTVSS (SEQ ID NO: 73)

AMRA311-19

45 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQYYWYSLITFGQGTKVEIKRTV (SEQ
ID NO: 74)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVYSSSIHWVRQAPGKGLEWVAYIYSSS
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRSFPQWYNGSYTP
WPAMDYWGQGTLVTVSS (SEQ ID NO: 75)

50 AMRA311-20

V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQQYMWWPVTFGQGTKVEIKRTV
(SEQ ID NO: 76)

5 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVSSSSIHWVRQAPGKGLEWVASIYSYS
SYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARPFYWGERYALDY
WGQGTLLVTVSS (SEQ ID NO: 77)

AMRA3-5

10 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQQSYSTLVTFGQGTKVEIKRTV (SEQ
ID NO: 78)

15 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFYSSSIHWVRQAPGKGLEWVASIYSSY
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARIYGWSYQGWAGM
DYWGQGTLLVTVSS (SEQ ID NO: 79)

AMRA3-6

20 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQQSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 80)

25 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISYSSSIHWVRQAPGKGLEWVASIYPYY
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGGDYYWGWWV
AMDYWGQGTLLVTVSS (SEQ ID NO: 81)

AMRA3-9

30 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTIXSLQPEDFATYYCQKSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 82)

35 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSYIHWVRQAPGKGLEWVASISSY
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARMYYYTYPGMDYW
GQGTLLVTVSS (SEQ ID NO: 83)

AMRA3-10

40 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQKGSSYLLTFGQGTKVEIKRTV (SEQ
ID NO: 84)

45 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTIYSYSIHWVRQAPGKGLEWVASISPSS
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYHYGGWSHYMSG
MDYWGQGTLLVTVSS (SEQ ID NO: 85)

AMRA3-13

V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQQNYYYHKLITFGQGTKVEIKRTV
(SEQ ID NO: 86)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSSIHWVRQAPGKGLEWVASISSSY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGRYGGMDYWGQ
GTLVTVSS (SEQ ID NO: 87)

5 AMRA3-19
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQLSYVYKLITFGQGGTKVEIKRTV
(SEQ ID NO: 88)

10 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFYSSSIHWVRQAPGKGLEWVASISSSY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGWYKAMDYWGQ
GTLVTVSS (SEQ ID NO: 89)

15 AMRA3-24
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQSSSLITFGQGGTKVEIKRTV (SEQ ID
NO: 90)

20 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSSIHWVRQAPGKGLEWVASISSSY
GSTYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARMYYYYYPGIDYW
GQGTLVTVSS (SEQ ID NO: 91)

25 AMRA11-3
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDLATYYCQQYYYFPITFGQGGTKVEIKRTV (SEQ
ID NO: 92)

30 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSIHWVRQAPGKGLEWVASISPPY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSPYYWYQYFYGW
GLDYWGQGTLVTVSS (SEQ ID NO: 93)

35 AMRA11-4
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQSSSLITFGQGGTKVEIKRTV (SEQ ID
NO: 94)

40 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSSIHWVRQAPGKGLEWVASISSSS
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSPYWWNYMSAMD
YWGQGTLVTVSS (SEQ ID NO: 95)

45 AMRA11-7
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQGWWPFTFGQGGTKVEIKRTV (SEQ
ID NO: 96)

50 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVSSYSIHWVRQAPGKGLEWVASISPPY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWSWQYYSGHSSW
GLDYWGQGTLVTVSS (SEQ ID NO: 97)

50 AMRA11-8

V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQQSWYFPLTFGQGTKVEIKRTV (SEQ
ID NO: 98)

5 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVSSSSSIHWVRQAPGKGLEWVASIYSYY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWYNEYHYYW
DAMDYWGQGTLLTVSS (SEQ ID NO: 99)

AMRA11-9

10 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQQSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 100)

15 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTLYYSSSIHWVRQAPGKGLEWVASISSSS
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWMYWWSFALDY
WGQGTLLTVSS (SEQ ID NO: 101)

AMRA11-10

20 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQQSYLWPITFGQGTKVEIKRTV (SEQ
ID NO: 102)

25 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVSSSSSIHWVRQAPGKGLEWVASIYSYY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWQYHYNWYGM
DYWGQGTLLTVSS (SEQ ID NO: 103)

AMRA11-11

30 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQQYPMSLITFGQGTKVEIKRTV (SEQ
ID NO: 104)

35 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVSYSSSIHWVRQAPGKGLEWVASISPY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGYDYAGLDYWG
QGTLLTVSS (SEQ ID NO: 105)

AMRA11-12

40 V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQQYYYFPITFGQGTKVEIKRTV (SEQ
ID NO: 106)

45 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSSSIHWVRQAPGKGLEWVASISPY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWESEYSGTYEDY
WAGMDYWGQGTLLTVSS (SEQ ID NO: 107)

AMRA11-13

V_L:DIQMTQSPSSLSASVGDRVTTTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISSLQPEDFATYYCQQYMWWPITFGQGTKVEIKRTV (SEQ
ID NO: 108)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISYSSSIHWVRQAPGKGLEWVASISSSYS
YTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARTGYWQGYLALDYW
GQGTLVTVSS (SEQ ID NO: 109)

5 AMRA11-14
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 110)

10 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISYSSSIHWVRQAPGKGLEWVASISSSSG
STSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARTYYYYWNSTPAMD
YWGQGTLLVTVSS (SEQ ID NO: 111)

15 AMRA11-18
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQSYGYPVTFGQGTKVEIKRTV (SEQ
ID NO: 112)

20 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSIHWVRQAPGKGLEWVASISSSY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWYNSSWYYSNW
WYKGFMDYWGQGTLLVTVSS (SEQ ID NO: 113)

25 AMRA11-20
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQYYSSLTFGQGTKVEIKRTV (SEQ
ID NO: 114)

30 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFYSSSIHWVRQAPGKGLEWVASISSSY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARTSYTYPVYTYYG
FDYWGQGTLLVTVSS (SEQ ID NO: 115)

35 AMRA11-22
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQSWYYPLTFGQGTKVEIKRTV (SEQ
ID NO: 116)

40 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTLYSSSIHWVRQAPGKGLEWVASISSSY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYRYSSWNRGAIDY
WGQGTLLVTVSS (SEQ ID NO: 117)

45 AMRA11-24
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSGRSGTDFTLTISLQPEDFATYYCQQSYWWPLTFGQGTKVEIKRTV (SEQ
ID NO: 118)

50 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVSSSIHWVRQAPGKGLEWVASIYSYY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWSKSPWYYQGID
YWGQGTLLVTVSS (SEQ ID NO: 119)

50 IBA1-4

V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQYHYWASLITFGQGTKVEIKRTV
(SEQ ID NO: 120)

5 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTVSSSSIHWVRQAPGKGLEWVASIYSYS
GSTYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARQYSSSYVWPGM
DYWGQGTLLVTVSS (SEQ ID NO: 121)

IBA1-7

10 V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQSYWWKSLVTFGQGTKVEIKRTV
(SEQ ID NO: 122)

15 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTLSSSSIHWVRQAPGKGLEWVASISSYY
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARMHYSWQEYYSYD
WGMDYWGQGTLLVTVSS (SEQ ID NO: 123)

IBA1-8

20 V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQPYPLITFGQGTKVEIKRTV (SEQ
ID NO: 124)

25 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISYSSIHWVRQAPGKGLEWVASIYPSY
GSTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWQGYYPALDYW
GQGTLLVTVSS (SEQ ID NO: 125)

IBA1-12

30 V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQSSKYYYYPITFGQGTKVEIKRTV
(SEQ ID NO: 126)

35 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISSSSIHWVRQAPGKGLEWVASISPY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGYGWYWGGLD
YWGQGTLLVTVSS (SEQ ID NO: 127)

IBA1-13

40 V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQGHDMNPVTFGQGTKVEIKRTV
(SEQ ID NO: 128)

45 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTLSSSSIHWVRQAPGKGLEWVASIYSSY
GYTTYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYYYYWYGGMDY
WGQGTLLVTVSS (SEQ ID NO: 129)

IBA1-19

V_L:DIQMTQSPSSLSASVGDRVITTCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQSWMSDSLITFGQGTKVEIKRTV
(SEQ ID NO: 130)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSSIHWRQAPGKGLEWVASIYPSS
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARGWWYWMAWDY
AMDYWGQGTLVTVSS (SEQ ID NO: 131)

5 IBA1-21
V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSRSGTDFTLTISLQPEDFATYYCQQMQYSGWLITFGQGTKVEIKRTV
(SEQ ID NO: 132)

10 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTISSSSIHWRQAPGKGLEWVASISSYY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYYSYSSGYGYDY
FDWGAMDYWGQGTLVTVSS (SEQ ID NO: 133)

OEA2-1
15 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSRSGTDFTLTISLQPEDFATYYCQQSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 134)

20 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSSIHWRQAPGKGLEWVASISSSSG
STSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYYGYVWGGYWG
WYSKALDYWGQGTLVTVSS (SEQ ID NO: 135)

OEA2-12
25 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSRSGTDFTLTISLQPEDFATYYCQQYDWNYYLVTFGQGTKVEIKRTV
(SEQ ID NO: 136)

30 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTIYSSSIHWVRQAPGKGLEWVASISSYY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYQYYGSLYYSQQ
WAMDYWGQGTLVTVSS (SEQ ID NO: 137)

OEA2-16
35 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSRSGTDFTLTISLQPEDFATYYCQQSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 138)

40 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSSIHWRQAPGKGLEWVASISSSSG
STSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSPSSPYFMSWGWYW
QYGIDYWGQGTLVTVSS (SEQ ID NO: 139)

OEA2-21
45 V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFGSRSGTDFTLTISLQPEDFATYYCQQSSWGGLVTFGQGTKVEIKRTV
(SEQ ID NO: 140)

V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSYIHWVRQAPGKGLEWVASISPSY
GYTSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARDMYEWWHWAID
YWGQGTLVTVSS (SEQ ID NO: 141)

50 OEA2-24

V_L:DIQMTQSPSSLSASVGDRVTITCRASQSVSSAVAWYQQKPGKAPKLLIYSASSLYS
GVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQSSSSLITFGQGTKVEIKRTV (SEQ ID
NO: 142)

5 V_H:EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSSIHWVRQAPGKGLEWVASISSSSG
STSYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARYGHYLYYWGWGW
YWSAALDYWGQGTLLTVSS (SEQ ID NO: 143)

10 24. — The binding partner of claim 9, wherein the binding partner comprises a light chain
that comprises a complementary determining region 3 (CDR3) that comprises the sequence
SEQ ID NO:154 and a heavy chain that comprises a CDR3 that comprises the sequence of
SEQ ID NO:156, or wherein the binding partner comprises a light chain that comprises a
CDR3 that comprises the sequence of SEQ ID NO:158 and a heavy chain that comprises a
CDR3 that comprises the sequence of SEQ ID NO:160.

15 25. — The binding partner of claim 9, wherein the binding partner is a single chain Diabody
(scDb) and comprises a sequence that is at least 95% identical to SEQ ID NO: 165, SEQ ID
NO: 161, SEQ ID NO:162, SEQ ID NO: 163, or SEQ ID NO: 164.

20 26. — The binding partner of claim 9, wherein the binding partner is in a CrossMab format
and comprises the sequence of SEQ ID NO:149.

25 27. — The binding partner of claim 24, wherein the binding partner is comprised by a
chimeric antigen receptor.

28. — The binding partner of claim 27, wherein the binding partner is expressed by a T cell
or a natural killer cell.

30 29. — A complex comprising a binding agent of claim 9 and the peptide conjugate.

30. — A binding partner of claim 9, wherein the binding partner comprises an Fc segment.

35 31. — A polynucleotide encoding a binding partner of claim 9, wherein the polynucleotide
comprises DNA or mRNA, and wherein if the polynucleotide comprises DNA, the DNA is
optionally a component of an expression vector.

~~32. — A eukaryotic cell comprising a polynucleotide encoding a binding partner of claim 9, wherein the cell is optionally a totipotent, multipotent, or pluripotent stem cell, wherein optionally the stem cell has an induced stem cell phenotype, or wherein the cell is optionally a leukocyte, and wherein the leukocyte is optionally a T cell or a natural killer cell.~~

5

~~33. — A method comprising administering to an individual in need thereof a composition comprising a binding partner of claim 9, or a polynucleotide encoding said binding partner.~~

10

~~34. — The method of claim 33, wherein the binding partner is conjugated to a chemotherapeutic agent, a radioisotope, or a toxin.~~

~~35. — A method comprising administering to an individual in need thereof a cell of claim 32.~~

15

~~36. — A method comprising detecting a peptide conjugate, the method comprising forming a complex comprising the peptide conjugate and binding partner as in claim 9, wherein the binding partner is detectably labeled, and detecting the presence of the detectably labeled binding partner to determine the presence of the peptide conjugate.~~

20

~~37. — The method of claim 36, wherein detecting the binding partner comprises a diagnostic indication, and wherein the binding partner optionally comprises a radioconjugate.~~

25

~~38. — The method of claim 36, wherein the binding partner binds a peptide conjugate, and wherein said peptide conjugate is present on the surface of a cancer cell, wherein optionally the cancer cell is present in a tumor.~~

~~39. — The method of claim 36, comprising screening a plurality of molecules for binding to a protein or peptide comprising a covalently attached molecule using a binding partner of claim 9~~