ANTIBODY MOLECULES THAT BIND TO NKP30 AND USES THEREOF

CROSS REFERENCE

[0001] This application claims the benefit of U.S. provisional Application No. 63/589,149, filed on October 10, 2023, which is incorporated herein by reference in its entirety.

BACKGROUND

[0002] Natural Killer (NK) cells recognize and destroy tumors and virus-infected cells in an antibody-independent manner. The regulation of NK cells is mediated by activating and inhibiting receptors on the NK cell surface. One family of activating receptors is the natural cytotoxicity receptors (NCRs) which include NKp30, NKp44 and NKp46.

[0003] Given the importance of immune checkpoint pathways in regulating an immune response, the need exists for developing novel agents that modulate the activity of immunoinhibitory proteins, such as PD-1, thus leading to activation of immune system. Such agents can be used, *e.g.*, for cancer immunotherapy and treatment of other conditions, such as chronic infection.

SUMMARY

[0003a] In an aspect, there is provided a composition comprising an agent that comprises an antigen binding domain that binds to NKp30, wherein the antigen binding domain comprises:

(a) a heavy chain variable region (VH) comprising a heavy chain complementarity determining region 1 (VHCDR1) comprising the sequence of GFSIIRVGYHWN (SEQ ID NO: 502), a heavy chain complementarity determining region 2 (VHCDR2) comprising the sequence of YIHRSGSTSYNPSLKS (SEQ ID NO: 503), and a heavy chain complementarity determining region 3 (VHCDR3) comprising the sequence of GDWHYFDY (SEQ ID NO: 504), and

(b) a light chain variable region (VL) comprising a light chain complementarity determining region 1 (VLCDR1) comprising the sequence of SGEKLSDKYVH (SEQ ID NO: 26), a light chain complementarity determining region 2 (VLCDR2) comprising the sequence of ENDRRPS (SEQ ID NO: 28), and a light chain complementarity determining region 3 (VLCDR3) comprising the sequence of QFWDSTNSAV (SEQ ID NO: 86).

[0004] In an example, provided herein is, inter alia, a composition comprising an agent that comprises an antigen binding domain that binds to NKp30, wherein the antigen binding domain comprises a heavy chain variable region (VH) comprising:

(i) a heavy chain complementarity determining region 3 (VHCDR3) comprising the sequence of GDWHYFDY (SEQ ID NO: 504); and

(ii) a heavy chain complementarity determining region 1 (VHCDR1) comprising the sequence of GFSIIRVGYHWN (SEQ ID NO: 502), a heavy chain complementarity determining region 2 (VHCDR2) comprising the sequence of YIHRSGSTSYNPSLKS (SEQ ID NO: 503), or a combination thereof.

[0005] In some examples, the antigen binding domain comprises a VH comprising the VHCDR1 comprising the sequence of GFSIIRVGYHWN (SEQ ID NO: 502), the VHCDR2 comprising

the sequence of YIHRSGSTSYNPSLKS (SEQ ID NO: 503), and the VHCDR3 comprising the sequence of GDWHYFDY (SEQ ID NO: 504).

[0006] In some examples, the antigen binding domain comprises a light chain variable region (VL) comprising a light chain complementarity determining region 1 (VLCDR1) comprising the sequence of SGEKLSDKYVH (SEQ ID NO: 26), a light chain complementarity determining region 2 (VLCDR2) comprising the sequence of ENDRRPS (SEQ ID NO: 28), a light chain complementarity determining region 3 (VLCDR3) comprising the sequences of QFWDSTNSAV (SEQ ID NO: 86), or any combination thereof.

[0007] In some examples, the antigen binding domain comprises a VL comprising a VLCDR1 comprising the sequence of SGEKLSDKYVH (SEQ ID NO: 26), a VLCDR2 comprising the sequence of ENDRRPS (SEQ ID NO: 28), and a VLCDR3 comprising the sequences of QFWDSTNSAV (SEQ ID NO: 86).

[0008] In some examples, the antigen binding domain comprises a VH comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 505.

[0009] In some examples, the antigen binding domain comprises a VH comprising the sequence of SEQ ID NO: 505.

[0010] In some examples, the antigen binding domain comprises a VL comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 13.

[0011] In some examples, the antigen binding domain comprises a VL comprising the sequence of SEQ ID NO: 13.

[0012] In some examples, the antigen binding domain comprises a VH comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 505 and a VL comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 13.

[0013] In some examples, the antigen binding domain comprises a VH comprising the sequence of SEQ ID NO: 505 and a VL comprising the sequence of SEQ ID NO: 13.

[0014] In some examples, the antigen binding domain is a full antibody or antigen-binding fragment thereof, a bivalent antibody, bispecific antibody, or a biparatopic antibody.

[0015] In some examples, the antigen binding domain is a Fab, F(ab')2, Fv, an single chain Fv (scFv), a diabody, a single domain antibody, or a camelid antibody.

[0016] In some examples, the antigen binding domain is a Fab or an scFv.

[0017] In some examples, the antigen binding domain comprises one or more heavy chain constant regions selected from the group consisting of IgG1 heavy chain constant region or functional fragment thereof, IgG2 heavy chain constant region or functional fragment thereof, IgG3 heavy chain constant region or functional fragment thereof, IgGA1 heavy chain constant region or functional fragment thereof, IgGA2 heavy chain constant region or functional fragment thereof, IgG4 heavy chain constant region or functional fragment thereof, IgJ heavy chain constant region or functional fragment thereof, IgM heavy chain constant region or functional fragment thereof, IgD heavy chain constant region or functional fragment thereof, and IgE heavy chain constant region or functional fragment thereof.

[0018] In some examples, the one or more heavy chain constant regions comprises a sequence having at least 75% sequence identity to any one heavy chain constant region sequences listed in Tables 3, 7, 8, 16, 17, 39, 40, 42C, 43A, 43B, and 46-51.

[0019] In some examples, the one or more heavy chain constant regions comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO: 41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 3451, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ ID NO: 514, the sequence of SEQ ID NO:

515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, or the sequence of SEQ ID NO: 511.

[0020] In some examples, the antigen binding domain comprises a kappa light chain constant region or functional fragment thereof, a lambda light chain constant region or functional fragment thereof, or a combination thereof.

[0021] In some examples, the kappa light chain constant region comprises a sequence having at least 75% sequence identity to any one light chain constant region sequences listed in Tables 3, 7, 8, 16, 17, 39, 40, 42C, 43A, 43B, and 46-51.

[0022] In some examples, the kappa light chain constant region comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 39 or the sequence of SEQ ID NO: 3644.

[0023] In some examples, the agent is a polypeptide molecule.

[0024] In some examples, the agent is a multifunctional molecule.

[0025] In some examples, the agent is a multispecific molecule.

[0026] In some examples, the agent comprises at least one cytokine molecule or a functional fragment or variant thereof or a functional fragment or variant thereof, an antigen binding domain that binds to T cell receptor beta chain constant domain (TRBC), a second antigen binding domain that binds to NKp30, an immune cell engager, a tumor-targeting moiety, or any combination thereof.

[0027] In some examples, the agent comprises at least two non-contiguous polypeptide chains comprising a first polypeptide chain and a second polypeptide chain;
wherein the first polypeptide chain comprises, from N-terminus to C-terminus, the following configuration:
A-[a first member of a dimerization module]-C,
And the second polypeptide chain comprises, from N-terminus to C-terminus, the following configuration:
B-[a second member of a dimerization module]-D;
wherein the first member of the dimerization module comprises a first immunoglobulin constant domain; and the second member of the dimerization module comprises a second immunoglobulin constant domain;
wherein at least one of A, B, C, and D is the antigen binding domain; and
wherein the first polypeptide chain and the second polypeptide chain dimerize via interaction between the first member of the dimerization module and the second member of the dimerization module.

[0028] In some examples, (i) A is the antigen binding domain, and B, C, and D are independently (a) absent, (b) at least one cytokine molecule or a functional fragment or variant thereof, (c) an antigen binding domain that binds to T cell receptor beta chain constant domain (TRBC), (d) a second antigen binding domain that binds to NKp30, (e) an immune cell engager, or (f) a tumor-targeting moiety;
(ii) B is the antigen binding domain, and A, C, and D are independently (a) absent, (b) at least one cytokine molecule or a functional fragment or variant thereof, (c) an antigen binding domain that binds to

T cell receptor beta chain constant domain (TRBC), (d) a second antigen binding domain that binds to NKp30, (e) an immune cell engager, or (f) a tumor-targeting moiety;
(iii) C is the antigen binding domain, and A, B, and D are independently (a) absent, (b) at least one cytokine molecule or a functional fragment or variant thereof, (c) an antigen binding domain that binds to T cell receptor beta chain constant domain (TRBC), (d) a second antigen binding domain that binds to NKp30, (e) an immune cell engager, or (f) a tumor-targeting moiety;
(iv) D is the antigen binding domain, and A, B, and C are independently (a) absent, (b) at least one cytokine molecule or a functional fragment or variant thereof, (c) an antigen binding domain that binds to T cell receptor beta chain constant domain (TRBC), (d) a second antigen binding domain that binds to NKp30, (e) an immune cell engager, or (f) a tumor-targeting moiety.

[0029] In some examples, the agent comprises at least one cytokine molecule or a functional fragment or variant thereof.

[0030] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-2 or a functional fragment or variant thereof, IL-7 or a functional fragment or variant thereof, IL-12 or a functional fragment or variant thereof, IL-15 or a functional fragment or variant thereof, IL-18 or a functional fragment or variant thereof, IL-21 or a functional fragment or variant thereof, interferon gamma or a functional fragment or variant thereof, or any combination thereof.

[0031] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the cytokine sequences listed in Tables 40, 42C, 43A, 43B, and 46-51.

[0032] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises any one sequence selected from the group consisting of the cytokine sequences listed in Tables 40, 42C, 43A, 43B, and 46-51.

[0033] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-2 or a functional fragment or variant thereof.

[0034] In some examples, the IL-2 or a functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 2191, the sequence of SEQ ID NO: 2270, or the sequence of SEQ ID NO: 2280.

[0035] In some examples, the IL-2 or a functional fragment or variant thereof comprises a sequence the sequence of SEQ ID NO: 2191, the sequence of SEQ ID NO: 2270, or the sequence of SEQ ID NO: 2280.

[0036] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof IL-15 or a functional fragment or variant thereof.

[0037] In some examples, the IL-15 or a functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 2170, SEQ ID NO: 3670, or SEQ ID NO: 3673.

[0038] In some examples, the IL-15 or a functional fragment or variant thereof comprises the sequence of SEQ ID NO: 2170, the sequence of SEQ ID NO: 3670, or the sequence of SEQ ID NO: 3673.

[0039] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof further comprises an IL15Ralpha dimerizing domain covalently linked the IL-15 or a functional fragment or variant thereof.

[0040] In some examples, the IL15Ralpha dimerizing domain comprises an IL-15 receptor alpha sushi domain or a functional fragment or variant thereof.

[0041] In some examples, the IL15Ralpha dimerizing domain comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3472.

[0042] In some examples, the IL15Ralpha dimerizing domain comprises the sequence of SEQ ID NO: 3472.

[0043] In some examples, the IL-15 or a functional fragment or variant thereof is covalently linked to the IL15Ralpha dimerizing domain via a linker.

[0044] In some examples, the IL-15 or a functional fragment or variant thereof is covalently linked to the IL15Ralpha dimerizing domain via a linker comprising the sequence of SEQ ID NO: 3473.

[0045] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3474, SEQ ID NO: 3671, or SEQ ID NO: 8689.

[0046] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3474, the sequence of SEQ ID NO: 3671, or the sequence of SEQ ID NO: 8689.

[0047] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-7 or a functional fragment or variant thereof.

[0048] In some examples, the IL-7 or the functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3540.

[0049] In some examples, the IL-7 or the functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3540.

[0050] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-12 or a functional fragment or variant or variant thereof.

[0051] In some examples, the IL-12 or the functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3542, the sequence of SEQ ID NO: 3543, or the sequence of SEQ ID NO: 3545.

[0052] In some examples, the IL-12 or the functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3542, the sequence of SEQ ID NO: 3543, or the sequence of SEQ ID NO: 3545.

[0053] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-18 of a functional fragment or variant thereof.

[0054] In some examples, the IL-18 or the functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 2192.

[0055] In some examples, the IL-18 or the functional fragment or variant thereof comprises the sequence of SEQ ID NO: 2192.

[0056] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-21 or a functional fragment or variant thereof.

[0057] In some examples, the IL-21 or the functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3540.

[0058] In some examples, the IL-21 or the functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3540.

[0059] In some examples, the agent comprises an antigen binding domain that binds to TRBC.

[0060] In some examples, the antigen binding domain that binds to TRBC binds to TRBC1 or TRBC2.

[0061] In some examples, the antigen binding domain that binds to TRBC binds to TRBC1, and wherein the antigen binding domain that binds to TRBC comprises a VH comprising:

(i) a VHCDR1 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VHCDR1 sequences listed in Tables 2A, 2B, 3A, 3B, 5A, 5B, 7, 8, 16, 39, and 40;

(ii) a VHCDR2 comprising a sequence having at least 75% sequence identity any one sequence selected from the group consisting of the VHCDR2 sequences listed in Tables 2A, 2B, 3A, 3B, 5A, 5B, 7, 8, 16, 39, and 40;

(iii) a VHCDR3 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VHCDR3 sequences listed in Tables 2A, 2B, 3A, 3B, 5A, 5B, 7, 8, 16, 39, and 40; or

(iv) any combination thereof.

[0062] In some examples, the antigen binding domain that binds to TRBC binds to TRBC1, and wherein the antigen binding domain that binds to TRBC comprises a VH comprising:

(i) a VHCDR1 comprising to any one sequence selected from the group consisting of the VHCDR1 sequences listed in Tables 2A, 2B, 3A, 3B, 5A, 5B, 7, 8, 16, 39, and 40;

(ii) a VHCDR2 comprising any one sequence selected from the group consisting of the VHCDR2 sequences listed in Tables 2A, 2B, 3A, 3B, 5A, 5B, 7, 8, 16, 39, and 40;

(iii) a VHCDR3 comprising any one sequence selected from the group consisting of the VHCDR3 sequences listed in Tables 2A, 2B, 3A, 3B, 5A, 5B, 7, 8, 16, 39, and 40; or

(iv) any combination thereof.

[0063] In some examples, the antigen binding domain that binds to TRBC binds to TRBC1, and wherein the antigen binding domain that binds to TRBC comprises a VH comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VH sequences listed in Tables 7, 8, 16, 39, and 40.

[0064] In some examples, the antigen binding domain that binds to TRBC binds to TRBC1, and wherein the antigen binding domain that binds to TRBC comprises a VH comprising any one sequence selected from the group consisting of the VH sequences listed in Tables 7, 8, 16, 39, and 40.

[0065] In some examples, the antigen binding domain that binds to TRBC binds to TRBC1, and wherein the antigen binding domain that binds to TRBC comprises a VL comprising:

(i) a VLCDR1 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VLCDR1 sequences listed in Tables 4, 6, 7, 8, 16, 39, and 40;

(ii) a VLCDR2 comprising a sequence having at least 75% sequence identity any one sequence selected from the group consisting of the VLCDR2 sequences listed in Tables 4, 6, 7, 8, 16, 39, and 40;

(iii) a VLCDR3 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VLCDR3 sequences listed in Tables 4, 6, 7, 8, 16, 39, and 40; or

(iv) any combination thereof.

[0066] In some examples, the antigen binding domain that binds to TRBC binds to TRBC1, and wherein the antigen binding domain that binds to TRBC comprises a VL comprising:

(i) a VLCDR1 comprising any one sequence selected from the group consisting of the VLCDR1 sequences listed in Tables 4, 6, 7, 8, 16, 39, and 40;

(ii) a VLCDR2 comprising any one sequence selected from the group consisting of the VLCDR2 sequences listed in Tables 4, 6, 7, 8, 16, 39, and 40;

(iii) a VLCDR3 comprising any one sequence selected from the group consisting of the VLCDR3 sequences listed in Tables 4, 6, 7, 8, 16, 39, and 40; or

(iv) any combination thereof.

[0067] In some examples, the antigen binding domain that binds to TRBC binds to TRBC1, and wherein the antigen binding domain that binds to TRBC comprises a VL comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VL sequences listed in Tables 7, 8, 16, 39, and 40.

[0068] In some examples, the antigen binding domain that binds to TRBC binds to TRBC1, and wherein the antigen binding domain that binds to TRBC comprises a VL comprising any one sequence selected from the group consisting of the VL sequences listed in Tables 7, 8, 16, 39, and 40.

[0069] In some examples, the antigen binding domain that binds to TRBC binds to TRBC2, and wherein the antigen binding domain that binds to TRBC comprises a VH comprising:

(i) a VHCDR1 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VHCDR1 sequences listed in Tables 9A, 9B, 11, 12, 13, 14, 15, 17, 39, and 40;

(ii) a VHCDR2 comprising a sequence having at least 75% sequence identity any one sequence selected from the group consisting of the VHCDR2 sequences listed in Tables 9A, 9B, 12, 13, 14, 15, 17, 39, and 40;

(iii) a VHCDR3 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VHCDR3 sequences listed in Tables 9A, 9B, 12, 13, 14, 15, 17, 39, and 40; or

(iv) any combination thereof.

[0070] In some examples, the antigen binding domain that binds to TRBC binds to TRBC2, and wherein the antigen binding domain that binds to TRBC comprises a VH comprising:

(i) a VHCDR1 comprising to any one sequence selected from the group consisting of the VHCDR1 sequences listed in Tables 9A, 9B, 12, 13, 14, 15, 17, 39, and 40;

(ii) a VHCDR2 comprising any one sequence selected from the group consisting of the VHCDR2 sequences listed in Tables 9A, 9B, 12, 13, 14, 15, 17, 39, and 40;

(iii) a VHCDR3 comprising any one sequence selected from the group consisting of the VHCDR3 sequences listed in Tables 9A, 9B, 12, 13, 14, 15, 17, 39, and 40; or

(iv) any combination thereof.

[0071] In some examples, the antigen binding domain that binds to TRBC binds to TRBC2, and wherein the antigen binding domain that binds to TRBC comprises a VH comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VH sequences listed in Tables 11, 15, 17, 39, and 40.

[0072] In some examples, the antigen binding domain that binds to TRBC binds to TRBC2, and wherein the antigen binding domain that binds to TRBC comprises a VH comprising any one sequence selected from the group consisting of the VH sequences listed in Tables 11, 15, 17, 39, and 40.

[0073] In some examples, the antigen binding domain that binds to TRBC binds to TRBC2, and wherein the antigen binding domain that binds to TRBC comprises a VL comprising:

(i) a VLCDR1 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VLCDR1 sequences listed in Tables 10, 12, 13, 14, 15, 17, 39, and 40;

(ii) a VLCDR2 comprising a sequence having at least 75% sequence identity any one sequence selected from the group consisting of the VLCDR2 sequences listed in Tables 10, 12, 13, 14, 15, 17, 39, and 40;

(iii) a VLCDR3 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VLCDR3 sequences listed in Tables 10, 12, 13, 14, 15, 17, 39, and 40; or

(iv) any combination thereof.

[0074] In some examples, the antigen binding domain that binds to TRBC binds to TRBC2, and wherein the antigen binding domain that binds to TRBC comprises a VL comprising:

(i) a VLCDR1 comprising any one sequence selected from the group consisting of the VLCDR1 sequences listed in Tables 10, 12, 13, 14, 15, 17, 39, and 40;

(ii) a VLCDR2 comprising any one sequence selected from the group consisting of the VLCDR2 sequences listed in Tables 10, 12, 13, 14, 15, 17, 39, and 40;

(iii) a VLCDR3 comprising any one sequence selected from the group consisting of the VLCDR3 sequences listed in Tables 10, 12, 13, 14, 15, 17, 39, and 40; or

(iv) any combination thereof.

[0075] In some examples, the antigen binding domain that binds to TRBC binds to TRBC2, and wherein the antigen binding domain that binds to TRBC comprises a VL comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VL sequences listed in Tables 11, 15, 17, 39, and 40.

[0076] In some examples, the antigen binding domain that binds to TRBC binds to TRBC2, and wherein the antigen binding domain that binds to TRBC comprises a VL comprising any one sequence selected from the group consisting of the VL sequences listed in Tables 11, 15, 17, 39, and 40.

[0077] In some examples, the antigen binding domain that binds to TRBC binds to TRBC2, and wherein the antigen binding domain that binds to TRBC comprises a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the scFv sequences listed in Tables 12, 15, 17, 39, and 40.

[0078] In some examples, the antigen binding domain that binds to TRBC binds to TRBC2, and wherein the antigen binding domain that binds to TRBC comprises a VL comprising any one sequence selected from the group consisting of the scFv sequences listed in Tables 12, 15, 17, 39, and 40.

[0079] In some examples, the agent comprises a second antigen binding domain that binds to NKp30.

[0080] In some examples, the antigen binding domain and the second antigen binding domain that binds to NKp30 are same.

[0081] In some examples, the antigen binding domain and the second antigen binding domain that binds to NKp30 are different.

[0082] In some examples, the second antigen binding domain that binds to NKp30 comprises a heavy chain variable region (VH) comprising:

(i) a heavy chain complementarity determining region 3 (VHCDR3) comprising the sequence of GDWHYFDY (SEQ ID NO: 504); and

(ii) a heavy chain complementarity determining region 1 (VHCDR1) comprising the sequence of GFSIIRVGYHWN (SEQ ID NO: 502), a heavy chain complementarity determining region 2 (VHCDR2) comprising the sequence of YIHRSGSTSYNPSLKS (SEQ ID NO: 503), or a combination thereof.

[0083] In some examples, the second antigen binding domain that binds to NKp30 comprises a VH comprising the VHCDR1 comprising the sequence of GFSIIRVGYHWN (SEQ ID NO: 502), the VHCDR2 comprising the sequence of YIHRSGSTSYNPSLKS (SEQ ID NO: 503), and the VHCDR3 comprising the sequence of GDWHYFDY (SEQ ID NO: 504).

[0084] In some examples, the second antigen binding domain that binds to NKp30 comprises a light chain variable region (VL) comprising a light chain complementarity determining region 1 (VLCDR1) comprising the sequence of SGEKLSDKYVH (SEQ ID NO: 26), a light chain complementarity determining region 2 (VLCDR2) comprising the sequence of ENDRRPS (SEQ ID NO: 28), a light chain complementarity determining region 3 (VLCDR3) comprising the sequences of QFWDSTNSAV (SEQ ID NO: 86), or any combination thereof.

[0085] In some examples, the second antigen binding domain that binds to NKp30 comprises a VL comprising a VLCDR1 comprising the sequence of SGEKLSDKYVH (SEQ ID NO: 26), a VLCDR2 comprising the sequence of ENDRRPS (SEQ ID NO: 28), and a VLCDR3 comprising the sequences of QFWDSTNSAV (SEQ ID NO: 86).

[0086] In some examples, the second antigen binding domain that binds to NKp30 comprises a VH comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 505.

[0087] In some examples, the second antigen binding domain that binds to NKp30 comprises a VH comprising the sequence of SEQ ID NO: 505.

[0088] In some examples, the second antigen binding domain that binds to NKp30 comprises a VL comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 13.

[0089] In some examples, the second antigen binding domain that binds to NKp30 comprises a VL comprising the sequence of SEQ ID NO: 13.

[0090] In some examples, the second antigen binding domain that binds to NKp30 comprises a VH comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 505 and a VL comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 13.

[0091] In some examples, the second antigen binding domain that binds to NKp30 comprises a VH comprising the sequence of SEQ ID NO: 505 and a VL comprising the sequence of SEQ ID NO: 13.

[0092] In some examples, the second antigen binding domain that binds to NKp30 comprises a heavy chain variable region (VH) comprising:

(i) a VHCDR1 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VHCDR1 sequences listed in Tables 20A, 20B, 21A, 21B, 23A, 23B, 25, 26, 16, and 17;

(ii) a VHCDR2 comprising a sequence having at least 75% sequence identity any one sequence selected from the group consisting of the VHCDR2 sequences listed in Tables 20A, 20B, 21A, 21B, 23A, 23B, 25, 26, 16, and 17;

(iii) a VHCDR3 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VHCDR3 sequences listed in Tables 20A, 20B, 21A, 21B, 23A, 23B, 25, 26, 16, and 17; or

(iv) any combination thereof.

[0093] In some examples, the second antigen binding domain that binds to NKp30 comprises a VH comprising:

(i) a VHCDR1 comprising to any one sequence selected from the group consisting of the VHCDR1 sequences listed in Tables 20A, 20B, 21A, 21B, 23A, 23B, 25, 26, 16, and 17;

(ii) a VHCDR2 comprising any one sequence selected from the group consisting of the VHCDR2 sequences listed in Tables 20A, 20B, 21A, 21B, 23A, 23B, 25, 26, 16, and 17;

(iii) a VHCDR3 comprising any one sequence selected from the group consisting of the VHCDR3 sequences listed in Tables 20A, 20B, 21A, 21B, 23A, 23B, 25, 26, 16, and 17; or

(iv) any combination thereof.

[0094] In some examples, the second antigen binding domain that binds to NKp30 comprises a VH comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VH sequences listed in Tables 25, 26, 16, and 17.

[0095] In some examples, the second antigen binding domain that binds to NKp30 comprises a VH comprising any one sequence selected from the group consisting of the VH sequences listed in Tables 25, 26, 16, and 17.

[0096] In some examples, the second antigen binding domain that binds to NKp30 comprises a VL comprising:

(i) a VLCDR1 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VLCDR1 sequences listed in Tables 22, 24, 25, 26, 16, and 17;

(ii) a VLCDR2 comprising a sequence having at least 75% sequence identity any one sequence selected from the group consisting of the VLCDR2 sequences listed in Tables 22, 24, 25, 26, 16, and 17;

(iii) a VLCDR3 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VLCDR3 sequences listed in Tables 22, 24, 25, 26, 16, and 17; or

(iv) any combination thereof.

[0097] In some examples, the second antigen binding domain that binds to NKp30 comprises a VL comprising:

(i) a VLCDR1 comprising any one sequence selected from the group consisting of the VLCDR1 sequences listed in Tables 22, 24, 25, 26, 16, and 17;

(ii) a VLCDR2 comprising any one sequence selected from the group consisting of the VLCDR2 sequences listed in Tables 22, 24, 25, 26, 16, and 17;

(iii) a VLCDR3 comprising any one sequence selected from the group consisting of the VLCDR3 sequences listed in Tables 22, 24, 25, 26, 16, and 17; or

(iv) any combination thereof.

[0098] In some examples, the second antigen binding domain that binds to NKp30 comprises a VL comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VL sequences listed in Tables 25, 26, 16, and 17.

[0099] In some examples, the second antigen binding domain that binds to NKp30 comprises a VL comprising any one sequence selected from the group consisting of the VL sequences listed in Tables 25, 26, 16, and 17.

[0100] In some examples, the agent comprises an immune cell engager.

[0101] In some examples, the immune cell engager is selected from the group consisting of a T cell engager, an NK cell engager, a B cell engager, a dendritic cell engager, and the macrophage cell engager.

[0102] In some examples, the agent comprises a T cell engager.

[0103] In some examples, the T cell engager comprises an antigen binding domain that binds to a T cell receptor beta chain region (TCRβV).

[0104] In some examples, the antigen binding domain that binds to a T cell receptor beta chain region (TCRβV) binds to a TCRβV of any one T cell receptor beta chain (TCRβ) subfamily member selected from the group consisting of TCRβ subfamily members listed in Tables 29 and 42A.

[0105] In some examples, the antigen binding domain that binds to a TCRβV comprises a heavy chain variable region (VH) comprising:

(i) a VHCDR1 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VHCDR1 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51;

(ii) a VHCDR2 comprising a sequence having at least 75% sequence identity any one sequence selected from the group consisting of the VHCDR2 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51;

(iii) a VHCDR3 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VHCDR3 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51; or

(iv) any combination thereof.

[0106] In some examples, the antigen binding domain that binds to a TCRβV comprises a VH comprising:

(i) a VHCDR1 comprising to any one sequence selected from the group consisting of the VHCDR1 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51;

(ii) a VHCDR2 comprising any one sequence selected from the group consisting of the VHCDR2 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51;

(iii) a VHCDR3 comprising any one sequence selected from the group consisting of the VHCDR3 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51; or

(iv) any combination thereof.

[0107] In some examples, the antigen binding domain that binds to a TCRβV comprises a VH comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VH sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51.

[0108] In some examples, the antigen binding domain that binds to a TCRβV comprises a VH comprising any one sequence selected from the group consisting of the VH sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51.

[0109] In some examples, the antigen binding domain that binds to a TCRβV comprises a VL comprising:

(i) a VLCDR1 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VLCDR1 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51;

(ii) a VLCDR2 comprising a sequence having at least 75% sequence identity any one sequence selected from the group consisting of the VLCDR2 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51;

(iii) a VLCDR3 comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VLCDR3 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51; or
(iv) any combination thereof.

[0110] In some examples, the antigen binding domain that binds to a TCRβV comprises a VL comprising:
(i) a VLCDR1 comprising any one sequence selected from the group consisting of the VLCDR1 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51;
(ii) a VLCDR2 comprising any one sequence selected from the group consisting of the VLCDR2 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51;
(iii) a VLCDR3 comprising any one sequence selected from the group consisting of the VLCDR3 sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51; or
(iv) any combination thereof.

[0111] In some examples, the antigen binding domain that binds to a TCRβV comprises a VL comprising a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the VL sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51.

[0112] In some examples, the antigen binding domain that binds to a TCRβV comprises a VL comprising any one sequence selected from the group consisting of the VL sequences listed in Tables 30, 32, 42B, 42C, 43A, 43B, and 43-51.

[0113] In some examples, the agent comprises a NK cell engager.

[0114] In some examples, the NK cell engager does not bind to NKp30.

[0115] In some examples, the NK cell engager comprise a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the sequences listed in Table 27.

[0116] In some examples, the NK cell engager comprise any one sequence selected from the group consisting of the sequences listed in Table 27.

[0117] In some examples, the agent comprises a tumor-targeting moiety.

[0118] In some examples, the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, the tumor-targeting moiety, or any combination thereof is a full antibody or antigen-binding fragment thereof, a bivalent antibody, bispecific antibody, or a biparatopic antibody.

[0119] In some examples, the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, the tumor-targeting moiety, or any combination thereof is a Fab, F(ab')2, Fv, an single chain Fv (scFv), a diabody, a single domain antibody, or a camelid antibody.

[0120] In some examples, the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, the tumor-targeting moiety, or any combination thereof is a Fab or an scFv.

[0121] In some examples, the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, the tumor-targeting moiety, or any combination thereof comprises one or more heavy chain constant regions selected from the group consisting of IgG1 heavy chain constant region or functional fragment thereof, IgG2 heavy chain constant region or functional fragment thereof, IgG3 heavy chain constant region or functional fragment thereof, IgGA1 heavy chain constant region or functional fragment thereof, IgGA2 heavy chain constant region or functional fragment thereof, IgG4 heavy chain constant region or functional fragment thereof, IgJ heavy chain constant region or functional fragment thereof, IgM heavy chain constant region or functional fragment thereof, IgD heavy chain constant region or functional fragment thereof, and IgE heavy chain constant region or functional fragment thereof.

[0122] In some examples, the one or more heavy chain constant regions comprises a sequence having at least 75% sequence identity to any one heavy chain constant region sequences listed in Tables 3, 7, 8, 16, 17, 39, 40, 42C, 43A, 43B, and 46-51.

[0123] In some examples, the one or more heavy chain constant regions comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO: 41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 3451, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ ID NO: 514, the sequence of SEQ ID NO: 515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, or the sequence of SEQ ID NO: 511.

[0124] In some examples, the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, the tumor-targeting moiety, or any combination thereof comprises a kappa light chain constant region or functional fragment thereof, a lambda light chain constant region or functional fragment thereof, or a combination thereof.

[0125] In some examples, the kappa light chain constant region comprises a sequence having at least 75% sequence identity to any one light chain constant region sequences listed in Tables 3, 7, 8, 16, 17, 39, 40, 42C, 43A, 43B, and 46-51.

[0126] In some examples, the kappa light chain constant region comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 39 or the sequence of SEQ ID NO: 3644.

[0127] In some examples, the first member of the dimerization module comprises a first Fc region and the second member of the dimerization module comprises a second Fc region.

[0128] In some examples, the first Fc region is selected from the group consisting of an IgG1 Fc region or a functional fragment thereof, an IgG2 Fc region or a functional fragment thereof, an IgG3 Fc region or a functional fragment thereof, an IgGA1 Fc region or a functional fragment thereof, an IgGA2 Fc region or a functional fragment thereof, an IgG4 Fc region or a functional fragment thereof, an IgJ Fc

region or a functional fragment thereof, an IgM Fc region or a functional fragment thereof, an IgD Fc region or a functional fragment thereof, and an IgE Fc region or a functional fragment thereof.

[0129] In some examples, the second Fc region is selected from the group consisting of an IgG1 Fc region or a functional fragment thereof, an IgG2 Fc region or a functional fragment thereof, an IgG3 Fc region or a functional fragment thereof, an IgGA1 Fc region or a functional fragment thereof, an IgGA2 Fc region or a functional fragment thereof, an IgG4 Fc region or a functional fragment thereof, an IgJ Fc region or a functional fragment thereof, an IgM Fc region or a functional fragment thereof, an IgD Fc region or a functional fragment thereof, and an IgE Fc region or a functional fragment thereof.

[0130] In some examples, the first Fc region, the second Fc region, or a combination thereof comprises an Fc interface with one or more of: a paired cavity-protuberance, an electrostatic interaction, or a strand-exchange, wherein the dimerization of the first Fc region and the second Fc region is enhanced as indicated by a greater ratio of heteromultimer:homomultimer forms relative to a dimerization of Fc regions with a non-engineered interface.

[0131] In some examples,

(i) the first Fc region comprises:

(a) an Ala at position 297 in a heavy chain constant region according to EU Numbering

(b) a Cys at position 349 in a heavy chain constant region according to EU Numbering),

(c) a Ser at position 366 in a heavy chain constant region according to EU Numbering),

(d) an Ala at position 368 in a heavy chain constant region according to EU Numbering); and

(e) a Val at position 407 in a heavy chain constant region according to EU Numbering); and

(ii) the second Fc region comprises:

(a) an Ala at position 297 in a heavy chain constant region according to EU Numbering),

(b) a Cys at position 354 in a heavy chain constant region according to EU Numbering), and

(c) a Trp at position 366 in a heavy chain constant region according to EU Numbering).

[0132] In some examples,

(i) the first Fc region comprises:

(a) an Ala at position 297 in a heavy chain constant region according to EU Numbering),

(b) a Cys at position 354 in a heavy chain constant region according to EU Numbering), and

(c) a Trp at position 366 in a heavy chain constant region according to EU Numbering); and

(ii) the second Fc region comprises:

(a) an Ala at position 297 in a heavy chain constant region according to EU Numbering

(b) a Cys at position 349 in a heavy chain constant region according to EU Numbering),

(c) a Ser at position 366 in a heavy chain constant region according to EU Numbering),

(d) an Ala at position 368 in a heavy chain constant region according to EU Numbering); and

(e) a Val at position 407 in a heavy chain constant region according to EU Numbering).

[0133] In some examples, the first Fc region comprises a mutation that decreases Fc receptor binding to the agent relative to an agent without the mutation.

[0134] In some examples, the first Fc region comprises an Asn297Ala (N297A) mutation or a Leu234Ala/Leu235Ala (LALA) mutation, or a combination thereof according to EU Numbering.
[0135] In some examples, the second Fc region comprises a mutation that decreases Fc receptor binding to the agent relative to an agent without the mutation.
[0136] In some examples, the second Fc region comprises an Asn297Ala (N297A) mutation or a Leu234Ala/Leu235Ala (LALA) mutation, or a combination thereof according to EU Numbering.
[0137] In some examples, the first Fc region comprises a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO: 41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 8687, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ ID NO: 514, the sequence of SEQ ID NO: 515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, and the sequence of SEQ ID NO: 511.
[0138] In some examples, the second Fc region comprises a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO: 41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 8687, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ ID NO: 514, the sequence of SEQ ID NO: 515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, and the sequence of SEQ ID NO: 511.
[0139] In some examples, the first Fc region comprises any one sequence selected from the group consisting of the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO: 41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 8687, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ ID NO: 514, the sequence of SEQ ID NO: 515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, and the sequence of SEQ ID NO: 511.
[0140] In some examples, the second Fc region comprises any one sequence selected from the group consisting of the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO:

41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 8687, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ ID NO: 514, the sequence of SEQ ID NO: 515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, and the sequence of SEQ ID NO: 511.

[0141] In some examples, the first Fc region comprises a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3477, the sequence of SEQ ID NO: 511, the sequence of SEQ ID NO: 515, and the sequence of SEQ ID NO: 516.

[0142] In some examples, the second Fc region comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3477, the sequence of SEQ ID NO: 511, the sequence of SEQ ID NO: 515, or the sequence of SEQ ID NO: 516.

[0143] In some examples, the first Fc region comprises any one sequence selected from the group consisting of the sequence of SEQ ID NO: 3648, SEQ ID NO: 508 or 8686, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 3477, SEQ ID NO: 511, SEQ ID NO: 515, or SEQ ID NO: 516.

[0144] In some examples, the second Fc region comprises any one sequence selected from the group consisting of the sequence of SEQ ID NO: 3648, SEQ ID NO: 508 or 8686, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 3477, SEQ ID NO: 511, SEQ ID NO: 515, or SEQ ID NO: 516.

[0145] In some examples,

(i) the first Fc region comprises the sequence of SEQ ID NO: 506 or the sequence of SEQ ID NO: 507, and the second Fc region comprises the sequence of SEQ ID NO: 3648 or the sequence of SEQ ID NO: 508 or 8686; or

(ii) the first Fc region comprises the sequence of SEQ ID NO: 3447 or the sequence of SEQ ID NO: 511, and the second Fc region comprises the sequence of SEQ ID NO: 515 or the sequence of SEQ ID NO: 516.

[0146] In some examples,

(i) the first Fc region comprises the sequence of SEQ ID NO: 3648 or the sequence of SEQ ID NO: 508 or 8686, and the second Fc region comprises the sequence of SEQ ID NO: 506 or the sequence of SEQ ID NO: 507; or

(ii) the first Fc region comprises the sequence of SEQ ID NO: 515 or the sequence of SEQ ID NO: 516, and the second Fc region comprises the sequence of SEQ ID NO: 3447 or the sequence of SEQ ID NO: 511.

[0147] In some examples, the agent comprises a first polypeptide, a second polypeptide, and at least one cytokine molecule or a functional fragment or variant thereof, wherein the first polypeptide and the second polypeptide are non-contiguous;

wherein:
(i) the first polypeptide comprises a first member of the dimerization module linked to:
(a) the antigen binding domain comprising a VH and a VL, or
(b) a first portion of the antigen binding domain comprising the VH, wherein the agent further comprises a third polypeptide comprising a second portion of the antigen binding domain comprising a VL, wherein the third polypeptide is non-contiguous with the first polypeptide and the second polypeptide; and
(ii) the second polypeptide comprises a second member of the dimerization module, and
wherein the at least one cytokine molecule or a functional fragment or variant thereof is covalently linked to the second polypeptide or the first polypeptide.

[0148] In some examples, the agent comprises a first polypeptide, a second polypeptide, and at least one cytokine molecule or a functional fragment or variant thereof, wherein the first polypeptide and the second polypeptide are non-contiguous;
wherein:
(i) the first polypeptide comprises a first member of a dimerization module linked to a first portion of the antigen binding domain comprising the VH, wherein the agent further comprises a third polypeptide comprising a second portion of the antigen binding domain comprising the VL, wherein the third polypeptide is non-contiguous with the first polypeptide and the second polypeptide; and
(ii) the second polypeptide comprises a second member of the dimerization module, and
wherein the at least one cytokine molecule or a functional fragment or variant thereof is covalently linked to the second polypeptide.

[0149] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof is covalently linked to the N-terminus of the second polypeptide, the C-terminus of the second polypeptide, or a combination thereof.

[0150] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof is within a single contiguous polypeptide chain of the second polypeptide.

[0151] In some examples, the first polypeptide comprises:
(i) the antigen binding domain comprising the VH and the VL, wherein the antigen binding domain further comprises a heavy chain constant domain 1 (CH1) linked to the VH; or
(ii) the first portion of the first antigen binding domain comprising the VH, wherein the first portion of the antigen binding domain further comprises a CH1 linked to the VH.

[0152] In some examples, the CH1 is linked to the C-terminus of the VH.

[0153] In some examples, the agent comprises:
(i) the first polypeptide comprising the antigen binding domain that comprises the VH and the VL, wherein the antigen binding domain further comprises a light chain constant domain (CL) linked to the VL; or
(ii) the first polypeptide comprising the first portion of the antigen binding domain and the third polypeptide comprising the second portion of the antigen binding domain, wherein the second portion of the antigen binding domain further comprises a CL linked to the VL.

[0154] In some examples, the CL is linked to the C-terminus of the VL.

[0155] In some examples, the first member of the dimerization module is linked to the C-terminus of the antigen binding domain comprising the VH and the VL, or the C-terminus of the first portion of the first antigen binding domain comprising the VH.

[0156] In some examples, the second polypeptide comprises:

(i) an antigen binding domain that binds TRBC, an second antigen binding domain that binds to NKp30, an immune cell engager, or an tumor-targeting moiety comprising a VH and a VL, wherein the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety further comprises a heavy chain constant domain 1 (CH1) linked to the VH; or

(ii) the first portion of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety comprising the VH, wherein the first portion of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety further comprises a CH1 linked to the VH.

[0157] In some examples, the CH1 is linked to the C-terminus of the VH.

[0158] In some examples, the agent comprises:

(i) the second polypeptide comprising an antigen binding domain that binds TRBC, an second antigen binding domain that binds to NKp30, an immune cell engager, or an tumor-targeting moiety that comprises a VH and a VL, wherein the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety further comprises a light chain constant domain (CL) linked to the VL; or

(ii) the second polypeptide comprising the first portion of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety,

wherein the agent further comprises a fourth polypeptide comprising the second portion of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety, wherein the fourth polypeptide is non-contiguous with the first polypeptide, the second polypeptide, and third polypeptide, and

wherein the second portion of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety further comprises a CL linked to the VL.

[0159] In some examples, the CL is linked to the C-terminus of the VL.

[0160] In some examples, the second member of the dimerization module is linked to the C-terminus of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety comprising the VH and the VL, or the C-terminus of the first portion of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety comprising the VH.

[0161] In some examples, the agent further comprises:
(i) a linker between the first member of the dimerization module and the antigen binding domain comprising a VH and a VL, or the first portion of the antigen binding domain comprising a VH;
(ii) a linker between the second member of the dimerization module and an antigen binding domain that binds TRBC, an second antigen binding domain that binds to NKp30, an immune cell engager, or an tumor-targeting moiety comprising a VH and a VL, or the first portion of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety comprising a VH;
(iii) a linker between the VH and the VL of the antigen binding domain;
(iv) a linker between the CH1 and the VH of the antigen binding domain;
(v) a linker between the CL and the VL of the antigen binding domain;
(vi) a linker between the VH and the VL of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety;
(vii) a linker between the CH1 and the VH of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety;
(viii) a linker between the CL and the VL of the antigen binding domain that binds TRBC, the second antigen binding domain that binds to NKp30, the immune cell engager, or the tumor-targeting moiety;
(ix) a linker between the at least one cytokine molecule or a functional fragment or variant thereof and the first polypeptide, a linker between the at least one cytokine molecule or a functional fragment or variant thereof and the second polypeptide, or any combination thereof; or
(x) any combination thereof.
[0162] In some examples, the linker is selected from the group consisting of a cleavable linker, a non-cleavable linker, a peptide linker, a flexible linker, a rigid linker, a helical linker, and a non-helical linker.
[0163] In some examples, the linker is the peptide linker comprises the sequence of SEQ ID NO: 3473, SEQ ID NO: 3308, or SEQ ID NO: 8291.
[0164] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof is linked to the N-terminus of the first polypeptide, the C-terminus of the first polypeptide, the N-terminus of the second polypeptide, the C-terminus of the second polypeptide, the N-terminus of the third polypeptide, the C-terminus of the third polypeptide, or any combination thereof.
[0165] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof is within a single contiguous polypeptide chain of the first polypeptide, the second polypeptide, or the third cytokine polypeptide to which the at least one cytokine molecule or a functional fragment or variant thereof is linked.
[0166] In some examples, the agent comprises:
(i) the first polypeptide comprising the first portion of the dimerization module linked to the C-terminus of the first portion of the antigen binding domain;
(ii) the second polypeptide comprising the second portion of the dimerization module;

(iii) the third polypeptide comprising the second portion of the antigen binding domain; and
(iv) the at least one cytokine molecule or a functional fragment or variant thereof covalently linked to the N-terminus of the second polypeptide.

[0167] In some examples, the agent comprises:
(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 505, and the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3472, the sequence of SEQ ID NO: 2170, and the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[0168] In some examples, the agent comprises:
(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3472 operatively linked to the sequence of SEQ ID NO: 2170 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 13 operatively linked to the sequence of SEQ ID NO: 3644.

[0169] In some examples, the second polypeptide chain comprises, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3472 operatively linked to the sequence of SEQ ID NO: 3473 operatively linked to the sequence of SEQ ID NO: 2170 operatively linked to the sequence of SEQ ID NO: 3308 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686.

[0170] In some examples, the agent comprises:
(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 505, and the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3474, and the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[0171] In some examples, the agent comprises:
(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3474 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 13 operatively linked to the sequence of SEQ ID NO: 3644.

[0172] In some examples, the second polypeptide comprises, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3474 operatively linked to the sequence of SEQ ID NO: 3308 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686.

[0173] In some examples, the agent comprises:

(i) a first polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 500;

(ii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3420; and

(iii) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 501.

[0174] In some examples, the agent comprises:

(i) a first polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 4702;

(ii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 4703; and

(iii) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 501.

[0175] In some examples, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 500;

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3420; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 501.

[0176] In some examples, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 4702;

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3420; and

[0177] (iii) a third polypeptide comprising the sequence of SEQ ID NO: 4703.In some examples, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 505, and the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3472, the sequence of SEQ ID NO: 3670, and the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[0178] In some examples, the agent comprises:

(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;

(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3472 operatively linked to the sequence of SEQ ID NO: 3670 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and

(iii) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 13 operatively linked to the sequence of SEQ ID NO: 3644.

[0179] In some examples, the second polypeptide comprises, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3472 operatively linked to the sequence of SEQ ID NO: 3473 operatively linked to the sequence of SEQ ID NO: 3670 operatively linked to the sequence of SEQ ID NO: 3308 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686.

[0180] In some examples, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 505, and the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3671, and the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[0181] In some examples, the agent comprises:

(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;

(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3671 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686;

(iii) a third polypeptide comprising, from the N-terminus to the C-terminus, comprising the sequence of SEQ ID NO: 13, and the sequence of SEQ ID NO: 3644.

[0182] In some examples, the second polypeptide comprises, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3671 operatively linked to the sequence of SEQ ID NO: 3308 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686.

[0183] In some examples, the wherein the agent comprises:

(i) a first polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 500;

(ii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3669; and

(iii) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 501.

[0184] In some examples, the wherein the agent comprises:

(i) a first polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 4702;

(ii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 4708; and

(iii) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 501.

[0185] In some examples, the wherein the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 500;

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3669; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 501.

[0186] In some examples, the wherein the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 4702;

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 4708; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 501.

[0187] In some examples, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 505, and the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;

(ii) a second polypeptide chain comprising the sequence of 2270, and the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[0188] In some examples, the agent comprises:

(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;

(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of 2270 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[0189] In some examples, the second polypeptide comprises from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 2270 operatively linked to the sequence of SEQ ID NO: 3308 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686.

[0190] In some examples, the agent comprises:

(i) a first polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 500;

(ii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3340; and

(iii) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 501.

[0191] In some examples, the agent comprises:

(i) a first polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 4702;

(ii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 4706; and

(iii) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 501.

[0192] In some examples, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 500;

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3340; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 501.

[0193] In some examples, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 4702;

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 4706; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 501.

[0194] In some examples, the agent comprises a first polypeptide and a second polypeptide, wherein the first polypeptide and the second polypeptide are non-contiguous, and wherein:

(i) the first polypeptide comprises a first member of the dimerization module linked to:

(a) the antigen binding domain comprising a VH of the antigen binding domain and a VL of the antigen binding domain, or

(b) a first portion of the antigen binding domain comprising the VH of the antigen binding domain, wherein the agent further comprises a third polypeptide comprising a second portion of the antigen binding domain comprising a VL of the antigen binding domain, wherein the third polypeptide is non-contiguous with the first polypeptide and the second polypeptide; and

(ii) the second polypeptide comprises a second member of the dimerization module linked to:

(a) an antigen binding domain that binds to T cell receptor beta chain constant domain (TRBC) comprising a VH and a VL, or

(b) a first portion of the antigen binding domain that binds to TRBC comprising the VH of the antigen binding domain that binds to TRBC, wherein the agent further comprises a fourth polypeptide comprising a second portion of the antigen binding domain that binds to TRBC comprising a VL of the antigen binding domain that binds to TRBC, wherein the fourth polypeptide is non-contiguous with the first polypeptide, the second polypeptide, and the third polypeptide.

[0195] In some examples, the agent comprises a first polypeptide and a second polypeptide, wherein the first polypeptide and the second polypeptide are non-contiguous, wherein:

(i) the first polypeptide comprises a first member of the dimerization module linked to a first portion of the antigen binding domain comprising the VH of the antigen binding domain, wherein the agent further comprises a third polypeptide comprising a second portion of the antigen binding domain comprising a VL of the antigen binding domain, wherein the third polypeptide is non-contiguous with the first polypeptide and the second polypeptide; and

(ii) the second polypeptide comprises a second member of the dimerization module linked to an antigen binding domain that binds to TRBC.

[0196] In some examples, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 505, the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3447 or SEQ ID NO: 511;

(ii) a third polypeptide comprising the sequence of SEQ ID NO: 8308 and the sequence of SEQ ID NO: 3644; and

(iii) a second polypeptide chain comprising the sequence of SEQ ID NO: 517 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514; or a second polypeptide chain comprising the sequence of SEQ ID NO: 512 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514.

[0197] In some examples, the agent comprises:

(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 13 operatively linked to the sequence of SEQ ID NO: 3447 or SEQ ID NO: 511;

(ii) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 8308 operatively linked to the sequence of SEQ ID NO: 3644; and

(iii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 517 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514; or a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 512 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514.

[0198] In some examples, the first polypeptide comprises, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 8291 operatively linked to the sequence of SEQ ID NO: 13.

[0199] In some examples, the agent comprises:

(i) a first polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 509 or the sequence of SEQ ID NO: 4704;

(ii) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 7380; and

(iii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 7382, the sequence of SEQ ID NO: 4677, the sequence of SEQ ID NO: 7379, or the sequence of 4675.

[0200] In some examples, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 509 or the sequence of SEQ ID NO: 4704;

(ii) a third polypeptide comprising the sequence of SEQ ID NO: 7380; and

(iii) a second polypeptide chain comprising the sequence of SEQ ID NO: 7382, the sequence of SEQ ID NO: 4677, the sequence of SEQ ID NO: 7379, or the sequence of SEQ ID NO: 4675.

[0201] In some examples, the agent comprises a first polypeptide chain comprising the sequence of SEQ ID NO: 505, the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3447 or SEQ ID NO: 511.

[0202] In some examples, the agent comprises a first polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 13 operatively linked to sequence of SEQ ID NO: 3447 or SEQ ID NO: 511.

[0203] In some examples, the first polypeptide comprises, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 8291 operatively linked to the sequence of SEQ ID NO: 13.

[0204] In some examples, the agent comprises a first polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 509.

[0205] In some examples, the agent comprises a first polypeptide chain comprising the sequence of SEQ ID NO: 509.

[0206] In some examples, the agent comprises:

(i) a third polypeptide comprising the sequence of SEQ ID NO: 7419 and the sequence of SEQ ID NO: 3644; and

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 7420 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514 or a second polypeptide chain comprising the sequence of SEQ ID NO: 7423 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514.

[0207] In some examples, the agent comprises:

(i) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 7419 operatively linked to the sequence of SEQ ID NO: 3644; and

(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 7420 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514 or a second polypeptide chain comprising the sequence of SEQ ID NO: 7423 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514.

[0208] In some examples, the agent comprises:

(i) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 7439; and

(ii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 4680, the sequence of SEQ ID NO: 7438, the sequence of SEQ ID NO: 4681, or the sequence of SEQ ID NO: 7440.

[0209] In some examples, the agent comprises:

(i) a third polypeptide comprising the sequence of SEQ ID NO: 7439; and

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 4680, the sequence of SEQ ID NO: 7438, the sequence of SEQ ID NO: 4681, or the sequence of SEQ ID NO: 7440.

[0210] In some examples, the agent comprises:

(i) a third polypeptide comprising the sequence of SEQ ID NO: 8012 and the sequence of SEQ ID NO: 3644; and

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 8011 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514.

[0211] In some examples, the agent comprises:

(i) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 8012 operatively linked to the sequence of SEQ ID NO: 3644; and

(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 8011 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514.

[0212] In some examples, the agent comprises:

(i) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 8002; and

(ii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 8001 or 8697.

[0213] In some examples, the agent comprises:

(i) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 8002; and

(ii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 4682.

[0214] In some examples, the agent comprises:

(i) a third polypeptide comprising the sequence of SEQ ID NO: 8002; and

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 8001 or 8697.

[0215] In some examples, the agent comprises:

(i) a third polypeptide comprising the sequence of SEQ ID NO: 8002; and

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 4682.

[0216] In some examples, the agent comprises:

(i) a third polypeptide comprising the sequence of SEQ ID NO: 8014 and the sequence of SEQ ID NO: 3644; and

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 8013 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514, a second polypeptide chain comprising the sequence of SEQ ID NO: 8299 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514, or a second polypeptide chain comprising the sequence of SEQ ID NO: 8303 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514.

[0217] In some examples, the agent comprises:

(i) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 8014 operatively linked to the sequence of SEQ ID NO: 3644; and

(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 8013 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514, a second polypeptide chain comprising the sequence of SEQ ID NO: 8299 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514, or a second polypeptide chain comprising the sequence of SEQ ID NO: 8303 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514.

[0218] In some examples, the agent comprises:
(i) a third polypeptide comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 8005; and
(ii) a second polypeptide chain comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 8004, the sequence of SEQ ID NO: 4685, the sequence of SEQ ID NO: 8007, the sequence of SEQ ID NO: 4686, the sequence of SEQ ID NO: 4687, or the sequence of SEQ ID NO: 8009.
[0219] In some examples, the agent comprises:
(i) a third polypeptide comprising the sequence of SEQ ID NO: 8005; and
(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 8004, the sequence of SEQ ID NO: 4685, the sequence of SEQ ID NO: 8007, the sequence of SEQ ID NO: 4686, the sequence of SEQ ID NO: 4687, or the sequence of SEQ ID NO: 8009.
[0220] In some examples, the agent further comprises at least one cytokine molecule or a functional fragment or variant thereof, wherein the at least one cytokine molecule or a functional fragment or variant thereof is linked to the first member of the dimerization module, the second member of the dimerization module, the antigen binding domain, the antigen binding domain that binds to TRBC, or any combination thereof.
[0221] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-2 or a functional fragment or variant thereof, IL-7 or a functional fragment or variant thereof, IL-12 or a functional fragment or variant thereof, IL-15 or a functional fragment or variant thereof, IL-18 or a functional fragment or variant thereof, IL-21 or a functional fragment or variant thereof, interferon gamma or a functional fragment or variant thereof, or any combination thereof.
[0222] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to any one sequence selected from the group consisting of the cytokine sequences listed in Tables 40, 42C, 43A, 43B, and 46-51.
[0223] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises any one sequence selected from the group consisting of the cytokine sequences listed in Tables 40, 42C, 43A, 43B, and 46-51.
[0224] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-2 or a functional fragment or variant thereof.
[0225] In some examples, the IL-2 or a functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 2191, the sequence of SEQ ID NO: 2270, or the sequence of SEQ ID NO: 2280.
[0226] In some examples, the IL-2 or a functional fragment or variant thereof comprises a sequence the sequence of SEQ ID NO: 2191, the sequence of SEQ ID NO: 2270, or the sequence of SEQ ID NO: 2280.
[0227] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof IL-15 or a functional fragment or variant thereof.

[0228] In some examples, the IL-15 or a functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 2170, SEQ ID NO: 3670, or SEQ ID NO: 3673.

[0229] In some examples, the IL-15 or a functional fragment or variant thereof comprises the sequence of SEQ ID NO: 2170, the sequence of SEQ ID NO: 3670, or the sequence of SEQ ID NO: 3673.

[0230] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof further comprises an IL15Ralpha dimerizing domain covalently linked the IL-15 or a functional fragment or variant thereof.

[0231] In some examples, the IL15Ralpha dimerizing domain comprises an IL-15 receptor alpha sushi domain or a functional fragment or variant thereof.

[0232] In some examples, the IL15Ralpha dimerizing domain comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3472.

[0233] In some examples, the IL15Ralpha dimerizing domain comprises the sequence of SEQ ID NO: 3472.

[0234] In some examples, the IL-15 or a functional fragment or variant thereof is covalently linked to the IL15Ralpha dimerizing domain via a linker.

[0235] In some examples, the IL-15 or a functional fragment or variant thereof is covalently linked to the IL15Ralpha dimerizing domain via a linker comprising the sequence of SEQ ID NO: 3473.

[0236] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3474, SEQ ID NO: 3671, or SEQ ID NO: 8689.

[0237] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3474, the sequence of SEQ ID NO: 3671, or the sequence of SEQ ID NO: 8689.

[0238] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-7 or a functional fragment or variant thereof.

[0239] In some examples, the IL-7 or the functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3540.

[0240] In some examples, the IL-7 or the functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3540.

[0241] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-12 or a functional fragment or variant or variant thereof.

[0242] In some examples, the IL-12 or the functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3542, the sequence of SEQ ID NO: 3543, or the sequence of SEQ ID NO: 3545.

[0243] In some examples, the IL-12 or the functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3542, the sequence of SEQ ID NO: 3543, or the sequence of SEQ ID NO: 3545.

[0244] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-18 of a functional fragment or variant thereof.

[0245] In some examples, the IL-18 or the functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 2192.

[0246] In some examples, the IL-18 or the functional fragment or variant thereof comprises the sequence of SEQ ID NO: 2192.

[0247] In some examples, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-21 or a functional fragment or variant thereof.

[0248] In some examples, the IL-21 or the functional fragment or variant thereof comprises a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 3540.

[0249] In some examples, the IL-21 or the functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3540.

[0250] In another example, provided herein is a recombinant polynucleotide molecule comprising a polynucleotide sequence encoding the agent of the composition as provided herein.

[0251] In some examples, the recombinant polynucleotide molecule is an isolated recombinant polynucleotide molecule.

[0252] In another example, provided herein is a vector comprising the recombinant polynucleotide molecule as provided herein.

[0253] In another example, provided herein is a cell comprising the recombinant polynucleotide molecule as provided herein, or the vector as provided herein.

[0254] In another example, provided herein is a method of making the agent of the composition of any one as provided herein, comprising culturing the cell as provided herein under conditions suitable for expression of the agent.

[0255] In another example, provided herein is a pharmaceutical composition comprising the composition as provided herein, the recombinant polynucleotide molecule as provided herein, the vector as provided herein, or the cell as provided herein, and a pharmaceutically acceptable carrier, excipient, or diluent.

[0256] In another example, provided herein is a method of treating a condition or disease in a subject in need thereof comprising administering to the subject a therapeutically effective amount of the composition as provided herein, the recombinant polynucleotide molecule as provided herein, the vector as provided herein, the cell as provided herein, the pharmaceutical composition as provided herein, or any combination thereof, thereby treating the condition or disease in the subject.

[0256a] Thus, in an aspect, there is provided the composition as described herein for use in the treatment of a disease or condition in a subject in need thereof.

[0257] In some examples, the condition or disease is cancer.

[0258] In some examples, the cancer is leukemia or lymphoma.

[0259] In some examples, the cancer is selected from the group consisting of acquired immune deficiency syndrome (AIDS)-associated lymphoma, Angioimmunoblastic T-cell lymphoma, Adult T-cell

leukemia/lymphoma, Burkitt lymphoma, Central nervous system (CNS) lymphoma, Diffuse large B-cell lymphoma (DLBCL), Lymphoblastic lymphoma, Mantle cell lymphoma (MCL), Peripheral T-cell lymphoma (PTCL), Transformed follicular and transformed mucosa-associated lymphoid tissue (MALT) lymphomas, Cutaneous T-cell lymphoma (mycosis fungoides and Sézary syndrome), Follicular lymphoma, Lymphoplasmacytic lymphoma/Waldenström macroglobulinemia, Marginal zone B-cell lymphoma, Gastric mucosa-associated lymphoid tissue (MALT) lymphoma, Chronic lymphocytic leukemia/small-cell lymphocytic lymphoma (CLL/SLL), Extranodal T-/NK-cell lymphoma, and Anaplastic large-cell lymphoma.

[0260] In some examples, peripheral T-cell lymphoma (PTCL) is Hepatosplenic T-cell lymphoma (HSGDTCL), Subcutaneous paniculitis-like T-cell lymphoma, or Enteropathy-associated T-cell lymphoma.

[0261] In some examples, the cutaneous T-cell lymphoma is mycosis fungoides and Sézary syndrome.

[0262] In some examples, the extranodal T-/NK-cell lymphoma is a nasal type.

[0263] In some examples, the anaplastic large-cell lymphoma is primary cutaneous anaplastic large-cell lymphoma or systemic anaplastic large-cell lymphoma.

[0264] In some examples, the cancer is a solid tumor.

[0265] In some examples, the solid tumor is selected from the group consisting of pancreatic cancer, breast cancer, colon cancer, colorectal cancer, lung cancer, skin cancer, ovarian cancer, liver cancer, esophageal cancer, endometrial cancer, gastric cancer, head and neck cancer, kidney cancer, and prostate cancer.

[0266] In some examples, the pancreatic cancer is pancreatic adenocarcinoma or pancreatic ductal adenocarcinoma.

[0267] In some examples, the lung cancer is small cell lung cancer (SCLC) or non-small cell lung cancer (NSCLC).

[0268] In another example, provided herein is a method of expanding and/or activating NK cells in a NK cell population comprising contacting the NK cell population with an effective amount of the composition as provided herein, the recombinant polynucleotide molecule as provided herein, the vector as provided herein, the cell as provided herein, the pharmaceutical composition as provided herein, or any combination thereof, thereby, expanding and/or activating the NK cells in the NK cell population.

[0269] In some examples, the expanding and/or activating NK cells is in vivo or ex vivo expansion and/or activation.

BRIEF DESCRIPTION OF THE DRAWINGS

[0270] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0456] In some embodiments, the antigen binding domain that binds to TRBC1 comprises a VH comprising a heavy chain complementarity determining region 1 (VHCDR1), a VHCDR2, and a VHCDR3, and a VL comprising a light chain complementarity determining region 1 (VLCDR1), a VLCDR2, and a VLCDR3.

[0457] In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 7355, and 202, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 201, and 202, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7354, 201, and 202, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7354, 7355, and 202, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0458] In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 223, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7367, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 223, 7368, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 223, 224, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7367, 7368, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0459] In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 7355, 202, 223, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 201, 202, 223, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of: **SEQ ID NOs:** 8643, 7355, 202, 7367, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 7355, 202, 223, 7368, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 7355, 202, 223, 224, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 7355, 202, 7367, 7368, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 202, 7367, 224, and 225 or 8680, respectively (or a sequence

having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 202, 223, 7368, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 202, 223, 224, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 202, 7367, 7368, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 201, 202, 223, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 201, 202, 7367, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 201, 202, 223, 7368, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 201, 202, 223, 224, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 201, 202, 7367, 7368, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 7355, 202, 223, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 7355, 202, 7367, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 7355, 202, 223, 7368, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 7355, 202, 223, 224, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or **SEQ ID NOs:** 7354, 7355, 202, 7367, 7368, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0460] In some embodiments, the VH comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 7351, 253, 250-252, 254, 7343, 7344, 7350, and 7352 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 258, 255-257, 259, 260, and 7357-7360 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7351 and 258, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 253 and 258, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0461] In some embodiments, the antigen binding domain (e.g., first antigen binding domain) that binds to a tumor antigen on a lymphoma cell (e.g., a T cell), e.g., a T cell receptor comprising TRBC1, TRBC1, a T cell receptor comprising TRBC2, or TRBC2 comprises any CDR amino acid sequence, framework region (FWR) amino acid sequence, or variable region amino acid sequence Table 1, Table 2A or Table 2B,Table 3A or Table 3B, Table 4, Table 7, and Table 8. In some embodiments, the antigen binding domain (e.g., first antigen binding domain) that binds to a tumor antigen on a lymphoma cell (e.g., a T cell), e.g., a T cell receptor comprising TRBC1, TRBC1, a T cell receptor comprising TRBC2, or TRBC2 comprises heavy and/or light chain amino acid sequences of Table 8. In some embodiments, the antigen binding domain (e.g., first antigen binding domain) that selectively targets lymphocytes expressing a T cell receptor comprising TRBC1, TRBC1, a T cell receptor comprising TRBC2, or TRBC2 comprises any CDR amino acid sequence, framework region (FWR) amino acid sequence, or variable region amino

acid sequence disclosed in Table 1, Table 2A or Table 2B,Table 3A or Table 3B, Table 4, Table 7, and Table 8. In some embodiments, the antigen binding domain (e.g., first antigen binding domain) that selectively targets lymphocytes expressing a T cell receptor comprising TRBC1, TRBC1, a T cell receptor comprising TRBC2, or TRBC2 comprises heavy and/or light chain amino acid sequences of Table 8. An antigen binding domain that binds to a tumor antigen comprising TRBC1 or selectively targets lymphocytes expressing TRBC1 may be said to target TRBC1 (i.e., a TRBC1-targeting antigen binding domain). An antigen binding domain that binds to a tumor antigen comprising TRBC2 or selectively targets lymphocytes expressing TRBC2 may be said to target TRBC2 (i.e., a TRBC2-targeting antigen binding domain).

[0462] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a heavy chain complementarity determining region 1 (VHCDR1) amino acid sequence of **SEQ ID NO: 8643** (or a sequence with no more than 1, 2, 3, or 4 mutations, e.g., substitutions, additions, or deletions), a VHCDR2 amino acid sequence of **SEQ ID NO:** 201 (or a sequence with no more than 1, 2, 3, or 4 mutations, e.g., substitutions, additions, or deletions), and/or a VHCDR3 amino acid sequence of **SEQ ID NO:** 202 (or a sequence with no more than 1, 2, 3, or 4 mutations, e.g., substitutions, additions, or deletions). In some embodiments, the TRBC1 antigen binding domain comprises a VH comprising a VHCDR1 amino acid sequence of **SEQ ID NO: 8643**, a VHCDR2 amino acid sequence of **SEQ ID NO:** 201, and/or a VHCDR3 amino acid sequence of **SEQ ID NO:** 202.

[0463] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VL comprising a light chain complementarity determining region 1 (VLCDR1) amino acid sequence of **SEQ ID NO:** 223 (or a sequence with no more than 1, 2, 3, or 4 mutations, e.g., substitutions, additions, or deletions), a VLCDR2 amino acid sequence of **SEQ ID NO:** 224 (or a sequence with no more than 1, 2, 3, or 4 mutations, e.g., substitutions, additions, or deletions), and/or a VLCDR3 amino acid sequence of **SEQ ID NO:** 225 or 8680 (or a sequence with no more than 1, 2, 3, or 4 mutations, e.g., substitutions, additions, or deletions). In some embodiments, the antigen binding domain that targets TRBC1 comprises a VL comprising a VLCDR1 amino acid sequence of **SEQ ID NO:** 223, a VLCDR2 amino acid sequence of **SEQ ID NO:** 224, and a VLCDR3 amino acid sequence of **SEQ ID NO:** 225 or 8680.

[0464] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a heavy chain framework region 1 (VHFWR1) amino acid sequence of **SEQ ID NO:** 203, a VHFWR2 amino acid sequence of **SEQ ID NO:** 204, a VHFWR3 amino acid sequence of **SEQ ID NO:** 8679, and/or a VHFWR4 amino acid sequence of **SEQ ID NO:** 206.

[0465] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VL comprising a light chain framework region 1 (VLFWR1) amino acid sequence of **SEQ ID NO:** 226, a VLFWR2 amino acid sequence of **SEQ ID NO:** 227, a VLFWR3 amino acid sequence of **SEQ ID NO:** 228, and/or a VLFWR4 amino acid sequence of **SEQ ID NO:** 229.

[0466] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a VHFWR1 amino acid sequence of **SEQ ID NO:** 203 (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR2 amino acid

sequence of **SEQ ID NO:** 204 (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR3 amino acid sequence of **SEQ ID NO:** 8679 (or a sequence with no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 mutations, e.g., substitutions, additions, or deletions), and/or a VHFWR4 amino acid sequence of **SEQ ID NO:** 206.

[0467] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VL comprising a VLFWR1 amino acid sequence of **SEQ ID NO:** 226 (or a sequence with no more than 1, 2, or 3 mutations, e.g., substitutions, additions, or deletions), a VLFWR2 amino acid sequence of **SEQ ID NO:** 227 (or a sequence with no more than 1 mutation, e.g., substitution, addition, or deletion), a VLFWR3 amino acid sequence of **SEQ ID NO:** 228 (or a sequence with no more than 1 mutation, e.g., substitution, addition, or deletion), and/or a VLFWR4 amino acid sequence of **SEQ ID NO:** 229.

[0468] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a heavy chain framework region 1 (VHFWR1) amino acid sequence of **SEQ ID NO:** 207, a VHFWR2 amino acid sequence of **SEQ ID NO:** 208, a VHFWR3 amino acid sequence of **SEQ ID NO:** 209, and/or a VHFWR4 amino acid sequence of **SEQ ID NO:** 210.

[0469] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a VHFWR1 amino acid sequence of **SEQ ID NO:** 207 (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR2 amino acid sequence of **SEQ ID NO:** 208 (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR3 amino acid sequence of **SEQ ID NO:** 209 (or a sequence with no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 mutations, e.g., substitutions, additions, or deletions), and/or a VHFWR4 amino acid sequence of **SEQ ID NO:** 210.

[0470] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a heavy chain framework region 1 (VHFWR1) amino acid sequence of **SEQ ID NO: 207**, a VHFWR2 amino acid sequence of **SEQ ID NO: 208**, a VHFWR3 amino acid sequence of **SEQ ID NO:** 213, and/or a VHFWR4 amino acid sequence of **SEQ ID NO: 210**.

[0471] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a VHFWR1 amino acid sequence of **SEQ ID NO: 207** (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR2 amino acid sequence of **SEQ ID NO: 208** (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR3 amino acid sequence of **SEQ ID NO:** 213 (or a sequence with no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 mutations, e.g., substitutions, additions, or deletions), and/or a VHFWR4 amino acid sequence of **SEQ ID NO: 210**.

[0472] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a heavy chain framework region 1 (VHFWR1) amino acid sequence of **SEQ ID NO: 7345**, a VHFWR2 amino acid sequence of **SEQ ID NO: 208**, a VHFWR3 amino acid sequence of **SEQ ID NO:** 217, and/or a VHFWR4 amino acid sequence of **SEQ ID NO: 210**.

[0473] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a VHFWR1 amino acid sequence of **SEQ ID NO: 7345** (or a sequence with no more than 1,

2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR2 amino acid sequence of **SEQ ID NO: 208** (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR3 amino acid sequence of **SEQ ID NO:** 217 (or a sequence with no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 mutations, e.g., substitutions, additions, or deletions), and/or a VHFWR4 amino acid sequence of **SEQ ID NO: 210**.

[0474] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a heavy chain framework region 1 (VHFWR1) amino acid sequence of **SEQ ID NO: 207**, a VHFWR2 amino acid sequence of **SEQ ID NO: 212**, a VHFWR3 amino acid sequence of **SEQ ID NO:** 221, and/or a VHFWR4 amino acid sequence of **SEQ ID NO: 210**.

[0475] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VH comprising a VHFWR1 amino acid sequence of **SEQ ID NO: 207** (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR2 amino acid sequence of **SEQ ID NO: 212** (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR3 amino acid sequence of **SEQ ID NO:** 221 (or a sequence with no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 mutations, e.g., substitutions, additions, or deletions), and/or a VHFWR4 amino acid sequence of **SEQ ID NO: 210**.

[0476] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VL comprising a light chain framework region 1 (VLFWR1) amino acid sequence of **SEQ ID NO:** 230, a VLFWR2 amino acid sequence of **SEQ ID NO:** 231, a VLFWR3 amino acid sequence of **SEQ ID NO:** 232, and/or a VLFWR4 amino acid sequence of **SEQ ID NO:** 8685.

[0477] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VL comprising a VLFWR1 amino acid sequence of **SEQ ID NO:** 230 (or a sequence with no more than 1, 2, or 3 mutations, e.g., substitutions, additions, or deletions), a VLFWR2 amino acid sequence of **SEQ ID NO:** 231 (or a sequence with no more than 1 mutation, e.g., substitution, addition, or deletion), a VLFWR3 amino acid sequence of **SEQ ID NO:** 232 (or a sequence with no more than 1 mutation, e.g., substitution, addition, or deletion), and/or a VLFWR4 amino acid sequence of **SEQ ID NO:** 8685.

[0478] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VL comprising a light chain framework region 1 (VLFWR1) amino acid sequence of **SEQ ID NO:** 234, a VLFWR2 amino acid sequence of **SEQ ID NO:** 235, a VLFWR3 amino acid sequence of **SEQ ID NO:** 236, and/or a VLFWR4 amino acid sequence of **SEQ ID NO:** 237.

[0479] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VL comprising a VLFWR1 amino acid sequence of **SEQ ID NO:** 234 (or a sequence with no more than 1, 2, or 3 mutations, e.g., substitutions, additions, or deletions), a VLFWR2 amino acid sequence of **SEQ ID NO:** 235 (or a sequence with no more than 1 mutation, e.g., substitution, addition, or deletion), a VLFWR3 amino acid sequence of **SEQ ID NO:** 236 (or a sequence with no more than 1 mutation, e.g., substitution, addition, or deletion), and/or a VLFWR4 amino acid sequence of **SEQ ID NO:** 237.

[0480] In some embodiments, the antigen binding domain that targets TRBC1 comprises a VL comprising a light chain framework region 1 (VLFWR1) amino acid sequence of **SEQ ID NO:** 238, a

[0509] In some embodiments, the antigen binding domain that targets TRBC1 comprises a heavy chain comprising the amino acid sequence of **SEQ ID NO:** 6167 (or an amino acid sequence having at least about 93%, 95%, or 99% sequence identity to **SEQ ID NO:** 6167) and a light chain comprising the amino acid sequence of **SEQ ID NO:** 6169 (or an amino acid sequence having at least about 93%, 95%, or 99% sequence identity to **SEQ ID NO:** 6169). In some embodiments, the antigen binding domain that targets TRBC1 comprises a heavy chain comprising the amino acid sequence of **SEQ ID NO:** 6167 and a light chain comprising the amino acid sequence of **SEQ ID NO:** 6169.

[0510] In some embodiments, the antigen binding domain that targets TRBC1 comprises a heavy chain comprising the amino acid sequence of **SEQ ID NO:** 6168 (or an amino acid sequence having at least about 93%, 95%, or 99% sequence identity to **SEQ ID NO:** 6168) and a light chain comprising the amino acid sequence of **SEQ ID NO:** 6169 (or an amino acid sequence having at least about 93%, 95%, or 99% sequence identity to **SEQ ID NO:** 6169). In some embodiments, the antigen binding domain that targets TRBC1 comprises a heavy chain comprising the amino acid sequence of **SEQ ID NO:** 6168 and a light chain comprising the amino acid sequence of **SEQ ID NO:** 6169.

TRBC2 Antigen Binding Domains

[0511] In some embodiments, the antigen binding domain that binds to TRBC2 comprises one or more CDRs (e.g., VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and/or VLCDR3) disclosed in Table 9A, Table 9B, or Table 10, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antigen binding domain that binds to TRBC2 comprises one or more framework regions (e.g., VHFWR1, VHFWR2, VHFWR3, VHFWR4, VLFWR1, VLFWR2, VLFWR3, and/or VLFWR4) disclosed in Table 9A, Table 9B, or Table 10, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antigen binding domain that binds to TRBC2 comprises a VH and/or a VL disclosed in Table 11, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antigen binding domain that binds to TRBC2 comprises an amino acid sequence disclosed in Table 12, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[0512] In some embodiments, the antigen binding domain that binds to TRBC2 comprises a VH comprising a heavy chain complementarity determining region 1 (VHCDR1), a VHCDR2, and a VHCDR3, and a VL comprising a light chain complementarity determining region 1 (VLCDR1), a VLCDR2, and a VLCDR3.

[0513] In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of GX1X2MH, wherein X1 is Y or F, and X2 is P, H, V, Y, K, or A and **SEQ ID NOs:** 201, and 7442, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7422, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7401, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1,

VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7394, 201, and 307, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 201, and 8695, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 201, and 7400, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7405, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7407, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7427, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7430, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0514] In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7443, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0515] In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of GX1X2MH, wherein X1 is Y or F, and X2 is P, H, V, Y, K, or A and **SEQ ID NOs:** 201, 7442, 7443, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7422, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7401, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of: **SEQ ID NOs:** 7394, 201, 307, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 8695, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 7400, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7405, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:**

7407, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7427, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7430, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7422, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7401, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7394, 201, 307, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 8695, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 7400, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7405, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7407, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7427, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or **SEQ ID NOs:** 7430, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0516] In some embodiments, the VH comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 7420, 7423, 7411, 7412, 7413, 7414, 7415, 7416, 7417, 7425, 7428, and 7431 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 7419 and 7418 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7420 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7423 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7411 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7412 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7413 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7414 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7415 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7416 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7417 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some

[0531] In some embodiments, the TRBC2 antigen binding domain may comprise a mutation in the light chain variable domain, the mutation may be at position N35, or at R55 with respect to the VL domain of an antibody as described in **SEQ ID NO: 8025**. In some embodiments, the VL domain of the TRBC2 antigen binding domain may comprise a N35M, N35F, N35Y, N35K or N35R mutation at position 35 with respect to the VL domain of an antibody as described in **SEQ ID NO:** 8025.

[0532] SEQ ID NO: 8024 – Reference antibody VH domain: QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYVMHWVRQAPGQGLEWMGFINPYNDDIQSNERFRGRVTMTRDT SISTAYMELSRLRSDDTAVYYCARGAGYNFDGAYRFFDFWGQGTMVTVSS **(SEQ ID NO: 8024**).

[0533] SEQ ID NO: 8025 – Reference antibody VL domain: DIVMTQSPLSLPVTPGEPASISCRSSQRLVHSNGNTYLHWYLQKPGQSPRLLIYRVSNRFPGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC*SQSTHVPYT*FGQGTKLEIK **(SEQ ID NO: 8025**).

[0534] In some embodiments, the bispecific antibody comprises a second antigen binding domain that binds to NKp30. In some embodiments, an exemplary NKp30 binding domain comprises a heavy chain and a light chain of NKp30 binder 1. In some embodiments, an exemplary NKp30 binding domain comprises a heavy chain having an amino acid sequence of **SEQ ID NO: 8006 or 8698**. In some embodiments, an exemplary NKp30 binding domain comprises a heavy chain having an amino acid sequence that is at least 90% identical to a sequence of **SEQ ID NO: 8006 or 8698**. In some embodiments, an exemplary NKp30 binding domain comprises a heavy chain having an amino acid sequence that is at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a sequence of **SEQ ID NO: 8006 or 8698**.

[0535] In some embodiments, an exemplary NKp30 binding domain comprises a heavy chain and a light chain of NKp30 binder 1. In some embodiments, an exemplary NKp30 binding domain comprises a heavy chain having an amino acid sequence of **SEQ ID NO: 4684 or 8690**. In some embodiments, an exemplary NKp30 binding domain comprises a heavy chain having an amino acid sequence that is at least 90% identical to a sequence of **SEQ ID NO: 4684 or 8690**. In some embodiments, an exemplary NKp30 binding domain comprises a heavy chain having an amino acid sequence that is at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a sequence of **SEQ ID NO: 4684 or 8690**.

[0536] In some embodiments, an exemplary NKp30 binding domain comprises a light chain of **SEQ ID NO: 8003.** In some embodiments, an exemplary NKp30 binding domain comprises a light chain of SEQ ID NO: 4683**.** In some embodiments, an exemplary NKp30 binding domain comprises a light chain having an amino acid sequence that is at least 90% identical to a sequence of **SEQ ID NO: 8003**. In some embodiments, an exemplary NKp30 binding domain comprises a light chain having an amino acid sequence that is at least 90% identical to a sequence of **SEQ ID NO: 4683**. In some embodiments, an exemplary NKp30 binding domain comprises a light chain having an amino acid sequence that is at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a sequence of **SEQ ID NO: 8003**. In some embodiments, an exemplary NKp30

[0543] In some embodiments, the bi-specific antibody comprising : (i) a first antigen binding domain comprising a TRBC2 binding domain that comprises a single chain variable fragment (scFv); wherein the scFv comprises a heavy chain and a light chain that are linked by a short linker, and (ii) a second antigen binding domain comprising a NKp30 binding domain that comprises a single chain variable fragment (scFv); wherein scFv comprises a heavy chain and a light chain that are linked by a short linker.

[0544] In some embodiments, the heavy chain of a TRBC2 binding domain comprises a HC CDR1, a CDR2 and a CDR3. In some embodiments, the light chain of a TRBC2 binding domain comprises a LC CDR1, a CDR2 and a CDR3. In one embodiment, the heavy chain of a TRBC2 binding domain comprises a HC CDR1 having an amino acid sequence comprising PRGFYGYHMH (SEQ ID NO: 8272) {or PRGFYGY (**SEQ ID NO: 8041** according to Chothia numbering system)}, or PRGFYGYAMH (**SEQ ID NO: 8701**). In one embodiment, the heavy chain of a TRBC2 binding domain comprises a HC CDR1 having an amino acid sequence RSGFHGYAMH (**SEQ ID NO: 8207**) or PRGFHGYHMH (**SEQ ID NO: 8211**). In some embodiments, the heavy chain TRBC2 binding domain comprises a HC CDR1 comprising an amino acid sequence SRSGFHGYAMH (**SEQ ID NO: 8215**). In some embodiments, the heavy chain TRBC2 binding domain comprises a HC CDR1 comprising an amino acid sequence PRGFYGYHMH (**SEQ ID NO: 8272**). In some embodiments, the heavy chain TRBC2 binding domain comprises a HC CDR1 comprising an amino acid sequence RSSQNLVHSNGRTYLH (**SEQ ID NO: 8226**). In one embodiment, the heavy chain of a TRBC2 binding domain comprises a HC CDR2 having an amino acid sequence MGFINPYTNDIQYNERFRG (**SEQ ID NO: 8042**). In one embodiment, the heavy chain of a TRBC2 binding domain comprises a HC CDR3 having an amino acid sequence GNGKWGDGAYRFFDL (**SEQ ID NO: 8043**). In one embodiment, the heavy chain of a TRBC2 binding domain comprises a HC CDR2 comprising an amino acid sequence FINPYNNHIQYNERFRG (**SEQ ID NO: 8044**) or FINPYNDDIQYNQKFQG (**SEQ ID NO: 8208**) or *YINPYNRDIKYNQKFQG* (**SEQ ID NO: 8212**). In some embodiments, the HC CDR2 has an amino acid sequence FINPYNHAIKYNQKFQG (**SEQ ID NO: 8213**). In some embodiments, the HC CDR2 has an amino acid sequence YINPYTGDIKYNERFRG (**SEQ ID NO: 8217**). In some embodiments, the HC CDR2 has an amino acid sequence FINPYNDDIQYNERFRG (**SEQ ID NO. 8221**). In some embodiments, the HC CDR2 has an amino acid sequence TINPYNAEIKYNQKFQG (**SEQ ID NO: 8222**). In some embodiments, the HC CDR2 has an amino acid sequence TINPYNRDIQYNQKFQG (**SEQ ID NO: 8225**). In some embodiments, the HC CDR2 has an amino acid sequence FINPYNRDIKYNERFRG (**SEQ ID NO: 8228**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYTNDIKYNERFRG (**SEQ ID NO: 8229**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYTNHIQYNERFRG (**SEQ ID NO: 8230**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYTRAIKYNERFRG (**SEQ ID NO: 8231**). In some embodiments, the HC CDR2 has an amino acid sequence TINPYNGDIQYNERFRG (**SEQ ID NO: 8232**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYNTDIKYNERFRG (**SEQ ID NO: 8233**). In some embodiments, the HC CDR2 has an amino acid sequence YINPYNGAIKYNQKFQG (**SEQ ID NO: 8234**). In some embodiments, the HC CDR2 has an amino acid sequence

AINPYNDDIQSNERFRG (**SEQ ID NO: 8235**). In some embodiments, the HC CDR2 has an amino acid sequence FINPYNRAIQYNQKFQG (**SEQ ID NO: 8236**). In some embodiments, the HC CDR2 has an amino acid sequence FINPYTNEIQYNERFRG (**SEQ ID NO: 8237**). In some embodiments, the HC CDR2 has an amino acid sequence YINPYNHDIQYNQKFQG (**SEQ ID NO: 8700**). In some embodiments, the HC CDR2 has an amino acid sequence SINPYTHDIQYNERFRG (**SEQ ID NO: 8238**). In some embodiments, the HC CDR2 has an amino acid sequence YINPYKNAIQYNQKFQG (**SEQ ID NO: 8239**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYNTDIQYNERFRG (**SEQ ID NO: 8240**). In some embodiments, the HC CDR2 has an amino acid sequence SINPYNGDIQYNERFRG (**SEQ ID NO: 8241**). In some embodiments, the HC CDR2 has an amino acid sequence TINPYNHDAQYNERFRG (**SEQ ID NO: 8242**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYNDDIKYNERFRG (**SEQ ID NO: 8243**). In some embodiments, the HC CDR2 has an amino acid sequence YINPYTHEIKYNERFRG (**SEQ ID NO: 8245**). In some embodiments, the HC CDR2 has an amino acid sequence FINPYKDDIKYNERFRG **(SEQ ID NO: 8246**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYNDDIKYNQKFQG (**SEQ ID NO: 8247**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYNRDIKYNERFRG (**SEQ ID NO: 8248).** In some embodiments, the HC CDR2 has an amino acid sequence AINPYNGDIKYNERFRG (**SEQ ID NO: 8249).** In some embodiments, the HC CDR2 has an amino acid sequence YINPYTRDIKYNERFRG (**SEQ ID NO: 8250**). In some embodiments, the HC CDR2 has an amino acid sequence TINPYNTDIKYNERFRG (**SEQ ID NO: 8251**). In some embodiments, the HC CDR2 has an amino acid sequence TINPYNNDIQYNERFRG (**SEQ ID NO: 8252**). In some embodiments, the HC CDR2 has an amino acid sequence YINPYNGNIQYNERFRG (**SEQ ID NO: 8253**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYTNEIQYNERFRG (**SEQ ID NO: 8254**). In some embodiments, the HC CDR2 has an amino acid sequence SINPYNHDIKYNERFRG (**SEQ ID NO: 8255**). In some embodiments, the HC CDR2 has an amino acid sequence FINPYKNEIKYNERFRG (**SEQ ID NO: 8256**). In some embodiments, the HC CDR2 has an amino acid sequence YINPYNNEIQYNERFRGR (**SEQ ID NO: 8257**) or a sequence SINPYNRHIQYNERFRG (**SEQ ID NO: 8258**) or a sequence SINPYTREIQYNERFRG (**SEQ ID NO: 8259**). In some embodiments, the HC CDR2 has an amino acid sequence FINPYTNDIQYNERFRG (**SEQ ID NO: 8260**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYTNEIKYNERFRG (**SEQ ID NO: 8261**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYNDDIQYNERFRG (**SEQ ID NO: 8263**). In some embodiments, the HC CDR2 has an amino acid sequence YINPYNNDIKYNQKFQG (**SEQ ID NO: 8264**) or an amino acid sequence TINPYTREIQYNQKFQG (**SEQ ID NO: 8266**) or YINPYNNEIQYNQKFQG (**SEQ ID NO: 8267**). In some embodiments, the HC CDR2 has an amino acid sequence AINPYNHEIQYNQKFQG (**SEQ ID NO: 8268**). In some embodiments, the HC CDR2 has an amino acid sequence TINPYKHHIKYNERFRG (**SEQ ID NO: 8269**). In some embodiments, the HC CDR2 has an amino acid sequence FINPYTRAIKYNERFRG (**SEQ ID NO: 8270**). In some

- T28K, Y32F, A100N, A107S in the VH domain,
- T28K, Y32F, A100N, N103E in the VH domain and N35M in the VL domain,
- T28K, Y32F, A100N, V2K in the VH domain,
- T28K, Y32F, A100N, N103E in the VH domain,
- T28K, Y32F, A100N, Y102F, N103M in the VH domain and N35K in the VL domain,
- T28K, Y32F, A100N, Y102F, N103M in the VH domain and N35F in the VL domain,
- T28K, Y32F, A100N, Y102F, N103M in the VH domain and N35R in the VL domain,
- T28K, Y32F, A100N, Y102F in the VH domain and N35R in the VL domain,
- T28K, Y32F, A100N, N103M in the VH domain and N35M in the VL domain,
- T28K, Y32F, A100N, N103M in the VH domain and N35Y in the VL domain,
- T28K, Y32F, A100N, N103M in the VH domain and N35R in the VL domain,
- T28K, Y32F, A100N, N103F in the VH domain and N35K in the VL domain,
- T28K, Y32F, A100N, Y102L, N103W in the VH domain and N35R in the VL domain,
- T28K, Y32F, A100N, Y102L, N103W in the VH domain and N35K in the VL domain,
- T28K, Y32F, A100N, Y102F in the VH domain, and
- T28K, Y32F, A100N, Y102L, N103M in the VH domain and N35R in the VL domain.

[0554] The residues describing the mutations as list above are considered with respect to a TCRBC1 or a TRBC2 wild type sequence. In some embodiments, the TCRBC1 or a TRBC2 wild type sequences or reference sequences. In some embodiments, the reference VH and VL sequences as depicted in **SEQ ID NO:** 8024 and **SEQ ID NO:**8025 respectively.

[0555] In some embodiments, the bispecific antibody comprises: (i) a first antigen binding domain comprising an scFv that binds to TRBC2 domain, and may comprise a heavy chain amino acid sequence that is at least 85%, 90%, 95%, 96%, 97%, 98%, 99% identical to the amino acid sequence:

[0556] QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYVMHWVRQAPGQGLEWMGFINPYTNDI QYNERFRGRVTITSDKSTTTAYMELSSLRSEDTAVYYCAR***GNGKWGDGAYRFFDL***WGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK (**SEQ ID NO: 8697**).

[0557] In some embodiments, the bispecific antibody comprises: (i) a first antigen binding domain comprising an scFv that binds to TRBC2 domain, and may comprise a light chain amino acid sequence that is at least 85%, 90%, 95%, 96%, 97%, 98%, 99% identical to the amino acid sequence: DVVMTQSPLSLPVTLGQPASISCRSSENLVHSNGRTYLQWYQQRPGQSPRLLIY*RVSNRFP*GVPD RFSGSGSGTDFTLKISRVEAEDVGVYFCSQSSLEPYTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKS GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC (**SEQ ID NO: 8002**).

thereto), an anti-NKp30 VH of **SEQ ID NO:** 8030 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), and an anti-NKp30 VL of **SEQ ID NO:** 7305 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the anti-TRBC1/NKp30 antibody molecule comprises an anti-TRBC1 VH of **SEQ ID NO:** 7351 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), an anti-TRBC1 VL of **SEQ ID NO:** 258 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), and an anti-NKp30 scFv of **SEQ ID NO:** 7310 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the anti-TRBC1/NKp30 antibody molecule comprises **SEQ ID NOs:** 7382, 4677, 7380, 4679, and 7384 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0566] In some embodiments, the multifunctional antibody molecule comprises an anti-TRBC1 VH of **SEQ ID NO:** 253 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), an anti-TRBC1 VL of **SEQ ID NO:** 258 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), an anti-NKp30 VH of **SEQ ID NO:** 8030 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), and an anti-NKp30 VL of **SEQ ID NO:** 7305 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the anti-TRBC1/NKp30 antibody molecule comprises an anti-TRBC1 VH of **SEQ ID NO:** 253 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), an anti-TRBC1 VL of **SEQ ID NO:** 258 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), and an anti-NKp30 scFv of **SEQ ID NO:** 7310 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the anti-TRBC1/NKp30 antibody molecule comprises **SEQ ID NOs:** 7379, 4675, 7380, 4679, and 7384 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0567] In some embodiments provided herein is an antibody or a fragment thereof that binds to a TRBC1 molecule, wherein the antibody or fragment thereof that binds to the TRBC1 comprises a heavy chain comprising an HC-CDR1, having a sequence GYVMH (SEQ ID NO 8643); an HC-CDR2, having a sequence of FINPYNDDIQSNERFRG (SEQ ID NO: 201); and an HC-CDR3, having a sequence of GAGYNFDGAYRFFDF (SEQ ID NO: 202); and a light chain comprising an LC-CDR1 of RSSQRLVHSNGNTYLH (SEQ ID NO: 8646), an LC-CDR2 of RVSNRFP (SEQ ID NO: 224), an LC-CDR3 of SQSTHVPYT (SEQ ID NO: 225).

[0568] In some embodiments provided herein is an antibody or a fragment thereof that binds to a TRBC1 molecule, wherein the antibody or fragment thereof that binds to the TRBC1 comprises a heavy chain comprising an HC-CDR1, having a sequence GYVMH (SEQ ID NO 8643); an HC-CDR2, having a sequence FIIPIFGTANYAQKFQG (SEQ ID NO: 7355) and an HC-CDR3, having a sequence GAGYNFDGAYRFFDF (SEQ ID NO: 202); and a light chain comprising an LC-CDR1 having a sequence, RSSQRLVHSNGNTYLH (SEQ ID NO: 8651), an LC-CDR2 having sequence RVSNRFP (SEQ ID NO: 224), and an LC-CDR3 having a sequence SQSTHVPYT (SEQ ID NO: 225).

[0569] In some embodiments, provided herein is an antibody or a fragment thereof that binds to a TRBC1 molecule, wherein the antibody or fragment thereof that binds to the TRBC1 comprises a heavy chain comprising an HC-CDR1, having a sequence GYVMH (SEQ ID NO 8643); an HC-CDR2, having

[0596] In some embodiments, the antibody molecule, or fragment thereof, that binds to TRBC1 comprises a VH comprising a heavy chain complementarity determining region 1 (VHCDR1), a VHCDR2, and a VHCDR3, and a VL comprising a light chain complementarity determining region 1 (VLCDR1), a VLCDR2, and a VLCDR3.

[0597] In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 7355, and 202, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 201, and 202, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7354, 201, and 202, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7354, 7355, and 202, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0598] In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 223, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7367, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 223, 7368, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 223, 224, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7367, 7368, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0599] In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 7355, 202, 223, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 201, 202, 223, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of: **SEQ ID NOs:** 8643, 7355, 202, 7367, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 7355, 202, 223, 7368, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 7355, 202, 223, 224, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 7355, 202, 7367, 7368, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 202, 7367, 224, and 225 or 8680, respectively (or a sequence

having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 202, 223, 7368, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 202, 223, 224, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 202, 7367, 7368, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 201, 202, 223, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 201, 202, 7367, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 201, 202, 223, 7368, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 201, 202, 223, 224, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 201, 202, 7367, 7368, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 7355, 202, 223, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 7355, 202, 7367, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 7355, 202, 223, 7368, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7354, 7355, 202, 223, 224, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or **SEQ ID NOs:** 7354, 7355, 202, 7367, 7368, and 7369, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0600] In some embodiments, the VH comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 7351, 253, 250-252, 254, 7343, 7344, 7350, and 7352 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 258, 255-257, 259, 260, and 7357-7360 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7351 and 258, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 253 and 258, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0601] In some embodiments, the antibody molecule or fragment thereof comprises:

[0602] a heavy chain variable region (VH) comprising a heavy chain framework region 1 (VHFWR1) amino acid sequence of **SEQ ID NO: 7345** (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR2 amino acid sequence of **SEQ ID NO: 208** (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VHFWR3 amino acid sequence of **SEQ ID NO:** 217 (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), and/or a VHFWR4 amino acid sequence of **SEQ ID NO: 210** (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), and

[0603] a light chain variable region (VL) comprising a light chain framework region 1 (VLFWR1) amino acid sequence of **SEQ ID NO:** 238 (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g.,

substitutions, additions, or deletions, therefrom), a VLFWR2 amino acid sequence of **SEQ ID NO:** 239 (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), a VLFWR3 amino acid sequence of **SEQ ID NO:** 240 (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom), and/or a VLFWR4 amino acid sequence of **SEQ ID NO:** 241 (or a sequence with no more than 1, 2, 3, 4, 5, or 6 mutations, e.g., substitutions, additions, or deletions, therefrom).

[0604] In some embodiments, the antibody molecule or fragment thereof comprises a VH comprising a VHCDR1 amino acid sequence of **SEQ ID NO: 8643**, a VHCDR2 amino acid sequence of **SEQ ID NO:** 201, and/or a VHCDR3 amino acid sequence of **SEQ ID NO:** 202.

[0605] In some embodiments, the antibody molecule or fragment thereof comprises a VL comprising a VLCDR1 amino acid sequence of **SEQ ID NO:** 223, a VLCDR2 amino acid sequence of **SEQ ID NO:** 224, and a VLCDR3 amino acid sequence of **SEQ ID NO:** 225 or 8680.

[0606] In some embodiments, the antibody molecule or fragment thereof comprises a VH comprising the amino acid sequence of **SEQ ID NO:** 253 (or an amino acid sequence having at least about 75%, 80%, 85%, 90%, 95%, or 99% sequence identity thereto), and/or a VL comprising the amino acid sequence of **SEQ ID NO:** 258 (or an amino acid sequence having at least about 93%, 95%, or 99% sequence identity thereto). In some embodiments, the antibody molecule or fragment thereof comprises a VH and/or VL substantially homologous to **SEQ ID NOs:** 253 and/or 258.

Antibody Molecules Targeting TRBC2

[0607] In another aspect, the present disclosure features an antibody molecule, e.g., a monoclonal antibody molecule, or fragment thereof that binds TRBC2.

[0608] In some embodiments, the antibody molecule, or fragment thereof, that binds to TRBC2 comprises one or more CDRs (e.g., VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and/or VLCDR3) disclosed in Table 9A, Table 9B or Table 10, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antibody molecule, or fragment thereof, that binds to TRBC2 comprises one or more framework regions (e.g., VHFWR1, VHFWR2, VHFWR3, VHFWR4, VLFWR1, VLFWR2, VLFWR3, and/or VLFWR4) disclosed in Table 9A, Table 9B or Table 10, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antibody molecule, or fragment thereof, that binds to TRBC2 comprises a VH and/or a VL disclosed in Table 11, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antibody molecule, or fragment thereof, that binds to TRBC2 comprises an amino acid sequence disclosed in Table 12, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[0609] In some embodiments, the antibody molecule, or fragment thereof, that binds to TRBC2 comprises a VH comprising a heavy chain complementarity determining region 1 (VHCDR1), a VHCDR2, and a VHCDR3, and a VL comprising a light chain complementarity determining region 1 (VLCDR1), a VLCDR2, and a VLCDR3.

[0610] In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of GX1X2MH, wherein X1 is Y or F, and X2 is P, H, V, Y, K, or A and **SEQ ID NOs:** 201, and 7442, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7422, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7401, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7394, 201, and 307, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 201, and 8695, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 8643, 201, and 7400, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7405, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7407, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7427, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7430, 201, and 7403, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0611] In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7443, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0612] In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of GX1X2MH, wherein X1 is Y or F, and X2 is P, H, V, Y, K, or A and **SEQ ID NOs:** 201, 7442, 7443, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7422, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7401, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity

thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of: **SEQ ID NOs:** 7394, 201, 307, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 8695, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 7400, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7405, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7407, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7427, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7430, 201, 7403, 7410, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7422, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7401, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7394, 201, 307, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 8695, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 8643, 201, 7400, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7405, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7407, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); **SEQ ID NOs:** 7427, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or **SEQ ID NOs:** 7430, 201, 7403, 7409, 224, and 225 or 8680, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0613] In some embodiments, the VH comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 7420, 7423, 7411, 7412, 7413, 7414, 7415, 7416, 7417, 7425, 7428, and 7431 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 7419 and 7418 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7420 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7423 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7411 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7412 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7413 and 7419, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:**

(or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 6070, 6064, and 7321, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto).

[0660] In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7313, 6001, 7315, 26, 28, and 86, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7313, 6001, 6002, 6063, 6064, and 7293, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7313, 6008, 6009, 6070, 6071, and 6072, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7313, 7385, 7315, 6070, 6064, and 7321, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7313, 7318, 6009, 6070, 6064, and 7321, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 19, 21, 23, 26, 28, and 30, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto)In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 33, 35, 37, 40, 42, and 44, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto)In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 47, 49, 51, 54, 56, and 8678, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto)In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 61, 63, 65, 26, 28, and 72, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto)In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 7397, 313, 79, 26, 28, and 86, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto)In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 89, 91, 93, 26, 28, and 86, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto)In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 103, 313, 107, 26, 28, and 113, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto)In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 116, 118, 120, 26, 28, and 127, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto).

[0661] In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 26, 28, and 30, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 26, 42, and 7395, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 26, 28, and 8678, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 26, 28, and 72, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 26, 28, and 86, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** C096, C098, and C100, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 26, 28, and 113, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of **SEQ ID NOs:** 123, 28, and 127, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto).

[0662] In some embodiments, the VH comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 505, 7298 or 7300-7304 (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto) and/or the VL comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 13, 7299 or 7305-7308 (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 8030 and 7305, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 8030 and 13, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 505 and 13, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto).

[0663] In some embodiments, the VH comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 6121 or 6123-6128 (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto) and/or the VL comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 7294 or 6137-6141 (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 6122 or 6129-6134 (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto) and/or the VL comprises an amino acid sequence selected from the group consisting of **SEQ ID NOs:** 6136 or 6142-6147 (or a sequence having at least 75%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of **SEQ ID NOs:** 7295 and 7296, respectively (or a sequence having at least 75%, 85%, 90%, 95%, or 99%

sequence in Table 1, Table 16, Table 23A, or Table 23B, or a sequence substantially identical (*e.g.*, at least 80%, 85%, 90%, 92%, 95%, 97%, 98%, 99% or higher identical) to any of the aforesaid sequences.

[0820] In some embodiments, the anti-TCRβV antibody molecule, *e.g.*, anti-TCRβ V6 (*e.g.*, anti-TCRβ V6-5*01) antibody molecule, comprises at least one or two heavy chain variable regions from an antibody described herein, *e.g.*, an antibody chosen from any one of A-H.1 to A-H.85, e.g., A-H.1, A-H.2 or A-H.68, or an antibody molecule described in Table 30, Table 43A, or Table 43B, or encoded by a nucleotide sequence in Table 30, Table 16, Table 23A, or Table 23B, or a sequence substantially identical (*e.g.*, at least 80%, 85%, 90%, 92%, 95%, 97%, 98%, 99% or higher identical) to any of the aforesaid sequences.

[0821] In some embodiments, the anti-TCRβV antibody molecule comprises a heavy chain variable region (VH) having a consensus sequence of SEQ ID NO: 8682 or 3290.

[0822] SEQ ID NO: 8682 – Consensus VH
QVQLVQSGAEVKKPGSSVKVSCKASGH/T/G/YD/T/SFH/R/D/K/TL/D/K/T/NW/F/T/I/Y/GYIHWV
RQAPGQGLEWMGR/WV/I/FF/S/YA/PGSGN/ST/V/Y/IK/RYNEKFKGRVTITADTSTSTAYMELSS
LRSEDTAVYYCAG/VSY/IYSY/AD/GVLDYWGQGTTVTVSS

[0823] SEQ ID NO: 3290 – Consensus VH
QVQLVQSGAEVKKPGSSVKVSCKASG$X_1X_2FX_3X_4X_5$YIHWVRQAPGQGLEWMG$X_6X_7X_8X_9$GSG$X_{10}X_{11}X_{12}$YNEKFKGRVTITADTSTSTAYMELSSLRSEDTAVYYCA$X_{13}SX_{14}YSX_{15}X_{16}$VLDYWGQGT
TVTVSS, where-in: X1 is H or T or G or Y; X2 is D or T or S; X3 is H or R or D or K or T; X4 is L or D or K or T or N; X5 is W or F or T or I or Y or G; X6 is R or W; X7 is V or I or F; X8 is F or S or Y; X9 is A or P; X10 is N or S; X11 is T or V or Y or I; X12 is K or R; X13 is G or V; X14 is Y or I; X15 is Y or A; and X16 is D or G.

[0824] In some embodiments, the anti-TCRβV antibody molecule, *e.g.*, anti-TCRβ V6 (*e.g.*, anti-TCRβ V6-5*01) antibody molecule, comprises at least one or two light chain variable regions from an antibody described herein, *e.g.*, an antibody chosen from any one of A-H.1 to A-H.85, e.g., A-H.1, A-H.2 or A-H.68, or an antibody described in Table 30, Table 43A, or Table 43B, or encoded by a nucleotide sequence in Table 30, Table 43A, or Table 43B, or a sequence substantially identical (*e.g.*, at least 80%, 85%, 90%, 92%, 95%, 97%, 98%, 99% or higher identical) to any of the aforesaid sequences.

[0825] In some embodiments, the anti-TCRβV antibody molecule comprises a light chain variable region (VL) having a consensus sequence of SEQ ID NO: 8681 or 3289.

[0826] SEQ ID NO: 8681 – Consensus VL
DIQMTQSPSFLSASVGDRVTITCKASQNVG/E/A/DN/DR/KVAWY/HQQKPGKAPKALIYSSSHRY
K/SGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCQQFKSYPLTFGQGTKLEIK

[0827] SEQ ID NO: 3289 – Consensus VL
DIQMTQSPSFLSASVGDRVTITCKASQNV$X_1X_2X_3$VAWX_4QQKPGKAPKALIYSSSHRYX_5GVPSRF
SGSGSGTEFTLTISSLQPEDFATYFCQQFKSYPLTFGQGTKLEIK, wherein X1 is G, E, A or D; X2 is N or D; X3 is R or K; X4 is Y or H; and X5 is K or S

43A, or Table 43B, or a sequence with at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more identity thereto.

[0861] In some embodiments, the anti-TCRβV antibody molecule, *e.g.*, anti-TCRβ V6 (*e.g.*, anti-TCRβ V6-5*01) antibody molecule comprises a VH and a VL of an antibody described in Table 30, Table 43A, or Table 43B, or a sequence with at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more identity thereto.

[0862] In some embodiments, an anti-TCRVb antibody as described herein has an antigen binding domain having a VL having a consensus sequence of SEQ ID NO: 8681, wherein position 30 is G, E, A or D; position 31 is N or D; position 32 is R or K; position 36 is Y or H; and/or position 56 is K or S.

[0863] In some embodiments, an anti-TCRVb antibody as described herein has an antigen binding domain having a VH having a consensus sequence of SEQ ID NO: 8682, wherein: position 27 is H or T or G or Y; position 28 is D or T or S; position 30 is H or R or D or K or T; position 31 is L or D or K or T or N; position 32 is W or F or T or I or Y or G; position 49 is R or W; position 50 is V or I or F; position 51 is F or S or Y; position 52 is A or P; position 56 is N or S; position 57 is T or V or Y or I; position 58 is K or R; position 97 is G or V; position 99 is Y or I; position 102 is Y or A; and/or position 103 is D or G.

Additional anti-TCRVβ antibodies

[0864] Additional exemplary anti-TCRβV antibodies are provided in Table 32, Table 42B, Table 42C, Table 43, Table 44, Table 45, Table 46, Table 47, Table 48, Table 49, Table 50, and Table 51. In some embodiments, the anti-TCRβV antibody is a humanized antibody, e.g., as provided in Table 32, Table 42B, Table 42C, Table 43, Table 44, Table 45, Table 46, Table 47, Table 48, Table 49, Table 50, and Table 51. In some embodiments, the anti-TCRβV antibody comprises one or more (e.g., all three) of a LC CDR1, LC CDR2, and LC CDR3 provided in Table 2, Table 42B, Table 42C, Table 43, Table 44, Table 45, Table 46, Table 47, Table 48, Table 49, Table 50, and Table 51; and/or one or more (e.g., all three) of a HC CDR1, HC CDR2, and HC CDR3 provided in Table 2, Table 42B, Table 42C, Table 43, Table 44, Table 45, Table 46, Table 47, Table 48, Table 49, Table 50, and Table 51, or a sequence with at least 95% sequence identity thereto. In some embodiments, the anti-TCRβV antibody comprises a variable heavy chain (VH) and/or a variable light chain (VL) provided in Table 45, or a sequence with at least 95% sequence identity thereto.

B Cell, Macrophage & Dendritic Cell Engagers

[0865] Broadly, B cells, also known as B lymphocytes, are a type of white blood cell of the lymphocyte subtype. They function in the humoral immunity component of the adaptive immune system by secreting antibodies. Additionally, B cells present antigen (they are also classified as professional antigen-presenting cells (APCs)) and secrete cytokines. Macrophages are a type of white blood cell that engulfs and digests cellular debris, foreign substances, microbes, cancer cells via phagocytosis. Besides phagocytosis, they play important roles in nonspecific defense (innate immunity) and also help initiate specific defense mechanisms (adaptive immunity) by recruiting other immune cells such as lymphocytes.

Linkers

[0913] The multispecific or multifunctional molecule disclosed herein can further include a linker, e.g., a linker between one or more of: the antigen binding domain and the cytokine molecule, the antigen binding domain and the immune cell engager, the antigen binding domain and the stromal modifying moiety, the cytokine molecule and the immune cell engager, the cytokine molecule and the stromal modifying moiety, the immune cell engager and the stromal modifying moiety, the antigen binding domain and the immunoglobulin chain constant region, the cytokine molecule and the immunoglobulin chain constant region, the immune cell engager and the immunoglobulin chain constant region, or the stromal modifying moiety and the immunoglobulin chain constant region. In embodiments, the linker is chosen from: a cleavable linker, a non-cleavable linker, a peptide linker, a flexible linker, a rigid linker, a helical linker, or a non-helical linker, or any combination thereof.

[0914] In one embodiment, the multispecific molecule can include one, two, three or four linkers, e.g., a peptide linker. In one embodiment, the peptide linker includes Gly and Ser. In some embodiments, the peptide linker is selected from GGGGS (**SEQ ID NO:** 7249); GGGGSGGGGS (**SEQ ID NO:** 7250); GGGGSGGGGSGGGGS (**SEQ ID NO:** 7251); and DVPSGPGGGGGSGGGGS (**SEQ ID NO:** 7252). In some embodiments, the peptide linker is a A(EAAAK)nA (**SEQ ID NO:** 7255) family of linkers (e.g., as described in Protein Eng. (2001) 14 (8): 529-532). These are stiff helical linkers with n ranging from 2 – 5. In some embodiments, the peptide linker is selected from AEAAAKEAAAKAAA (**SEQ ID NO:** 302); AEAAAKEAAAKEAAAKAAA (**SEQ ID NO:** 303); AEAAAKEAAAKEAAAKEAAAKAAA (**SEQ ID NO:** 8683); and AEAAAKEAAAKEAAAKEAAAKEAAAKAAA(**SEQ ID NO:** 8684).

Nucleic Acids

[0915] Nucleic acids encoding the aforementioned multispecific or multifunctional molecules are also disclosed.

[0916] In certain embodiments, the invention features nucleic acids comprising nucleotide sequences that encode heavy and light chain variable regions and CDRs or hypervariable loops of the antibody molecules, as described herein. For example, the invention features a first and second nucleic acid encoding heavy and light chain variable regions, respectively, of an antibody molecule chosen from one or more of the antibody molecules disclosed herein. The nucleic acid can comprise a nucleotide sequence as set forth in the tables herein, or a sequence substantially identical thereto (*e.g.*, a sequence at least about 85%, 90%, 95%, 99% or more identical thereto, or which differs by no more than 3, 6, 15, 30, or 45 nucleotides from the sequences shown in the tables herein.

[0917] In certain embodiments, the nucleic acid can comprise a nucleotide sequence encoding at least one, two, or three CDRs or hypervariable loops from a heavy chain variable region having an amino acid sequence as set forth in the tables herein, or a sequence substantially homologous thereto (*e.g.*, a sequence at least about 85%, 90%, 95%, 99% or more identical thereto, and/or having one or more substitutions, *e.g.*, conserved substitutions). In other embodiments, the nucleic acid can comprise a nucleotide sequence encoding at least one, two, or three CDRs or hypervariable loops from a light chain

[0981] In some embodiments, the antigen binding domain comprises a VH comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 505 and a VL comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 13.

[0982] In some embodiments, the antigen binding domain comprises a VH comprising the sequence of SEQ ID NO: 505 and a VL comprising the sequence of SEQ ID NO: 13.

[0983] In some embodiments, the antigen binding domain is a full antibody or antigen-binding fragment thereof, a bivalent antibody, bispecific antibody, or a biparatopic antibody.

[0984] In some embodiments, the antigen binding domain is a Fab, F(ab')2, Fv, an single chain Fv (scFv), a diabody, a single domain antibody, or a camelid antibody.

[0985] In some embodiments, the antigen binding domain is a Fab or an scFv.

[0986] In some embodiments, the antigen binding domain comprises one or more heavy chain constant regions selected from the group consisting of IgG1 heavy chain constant region or functional fragment thereof, IgG2 heavy chain constant region or functional fragment thereof, IgG3 heavy chain constant region or functional fragment thereof, IgGA1 heavy chain constant region or functional fragment thereof, IgGA2 heavy chain constant region or functional fragment thereof, IgG4 heavy chain constant region or functional fragment thereof, IgJ heavy chain constant region or functional fragment thereof, IgM heavy chain constant region or functional fragment thereof, IgD heavy chain constant region or functional fragment thereof, and IgE heavy chain constant region or functional fragment thereof.

[0987] In some embodiments, the one or more heavy chain constant regions comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to any one heavy chain constant region sequences listed in Tables 3, 7, 8, 16, 17, 39, 40, 42C, 43A, 43B, and 46-51.

[0988] In some embodiments, the one or more heavy chain constant regions comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO: 41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 3451, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ ID NO: 514, the sequence of SEQ ID NO: 515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, or the sequence of SEQ ID NO: 511.

97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 2170, SEQ ID NO: 3670, or SEQ ID NO: 3673.

[1007] In some embodiments, the IL-15 or a functional fragment or variant thereof comprises the sequence of SEQ ID NO: 2170, the sequence of SEQ ID NO: 3670, or the sequence of SEQ ID NO: 3673.

[1008] In some embodiments, the at least one cytokine molecule or a functional fragment or variant thereof further comprises an IL15Ralpha dimerizing domain covalently linked the IL-15 or a functional fragment or variant thereof.

[1009] In some embodiments, the IL15Ralpha dimerizing domain comprises an IL-15 receptor alpha sushi domain or a functional fragment or variant thereof.

[1010] In some embodiments, the IL15Ralpha dimerizing domain comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 3472.

[1011] In some embodiments, the IL15Ralpha dimerizing domain comprises the sequence of SEQ ID NO: 3472.

[1012] In some embodiments, the IL-15 or a functional fragment or variant thereof is covalently linked to the IL15Ralpha dimerizing domain via a linker.

[1013] In some embodiments, the IL-15 or a functional fragment or variant thereof is covalently linked to the IL15Ralpha dimerizing domain via a linker comprising the sequence of SEQ ID NO: 3473.

[1014] In some embodiments, the at least one cytokine molecule or a functional fragment or variant thereof comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 3474, SEQ ID NO: 3671, or SEQ ID NO: 8689.

[1015] In some embodiments, the at least one cytokine molecule or a functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3474, the sequence of SEQ ID NO: 3671, or the sequence of SEQ ID NO: 8689.

[1016] In some embodiments, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-7 or a functional fragment or variant thereof.

[1017] In some embodiments, the IL-7 or the functional fragment or variant thereof comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 3540.

[1018] In some embodiments, the IL-7 or the functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3540.

[1019] In some embodiments, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-12 or a functional fragment or variant or variant thereof.

[1020] In some embodiments, the IL-12 or the functional fragment or variant thereof comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%,

(a) an Ala at position 297 in a heavy chain constant region according to EU Numbering
(b) a Cys at position 349 in a heavy chain constant region according to EU Numbering),
(c) a Ser at position 366 in a heavy chain constant region according to EU Numbering),
(d) an Ala at position 368 in a heavy chain constant region according to EU Numbering); and
(e) a Val at position 407 in a heavy chain constant region according to EU Numbering); and
(ii) the second Fc region comprises:
(a) an Ala at position 297 in a heavy chain constant region according to EU Numbering),
(b) a Cys at position 354 in a heavy chain constant region according to EU Numbering), and
(c) a Trp at position 366 in a heavy chain constant region according to EU Numbering).

[1103] In some embodiments,
(i) the first Fc region comprises:
(a) an Ala at position 297 in a heavy chain constant region according to EU Numbering),
(b) a Cys at position 354 in a heavy chain constant region according to EU Numbering), and
(c) a Trp at position 366 in a heavy chain constant region according to EU Numbering); and
(ii) the second Fc region comprises:
(a) an Ala at position 297 in a heavy chain constant region according to EU Numbering
(b) a Cys at position 349 in a heavy chain constant region according to EU Numbering),
(c) a Ser at position 366 in a heavy chain constant region according to EU Numbering),
(d) an Ala at position 368 in a heavy chain constant region according to EU Numbering); and
(e) a Val at position 407 in a heavy chain constant region according to EU Numbering).

[1104] In some embodiments, the first Fc region comprises a mutation that decreases Fc receptor binding to the agent relative to an agent without the mutation.

[1105] In some embodiments, the first Fc region comprises an Asn297Ala (N297A) mutation or a Leu234Ala/Leu235Ala (LALA) mutation, or a combination thereof according to EU Numbering.

[1106] In some embodiments, the second Fc region comprises a mutation that decreases Fc receptor binding to the agent relative to an agent without the mutation.

[1107] In some embodiments, the second Fc region comprises an Asn297Ala (N297A) mutation or a Leu234Ala/Leu235Ala (LALA) mutation, or a combination thereof according to EU Numbering.

[1108] In some embodiments, the first Fc region comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to any one sequence selected from the group consisting of the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO: 41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 8687, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ

ID NO: 514, the sequence of SEQ ID NO: 515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, and the sequence of SEQ ID NO: 511.

[1109] In some embodiments, the second Fc region comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to any one sequence selected from the group consisting of the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO: 41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 8687, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ ID NO: 514, the sequence of SEQ ID NO: 515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, and the sequence of SEQ ID NO: 511.

[1110] In some embodiments, the first Fc region comprises any one sequence selected from the group consisting of the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO: 41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 8687, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ ID NO: 514, the sequence of SEQ ID NO: 515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, and the sequence of SEQ ID NO: 511.

[1111] In some embodiments, the second Fc region comprises any one sequence selected from the group consisting of the sequence of SEQ ID NO: 73, the sequence of SEQ ID NO: 76, the sequence of SEQ ID NO: 74, the sequence of SEQ ID NO: 75, the sequence of SEQ ID NO: 40, the sequence of SEQ ID NO: 41, the sequence of SEQ ID NO: 42, the sequence of SEQ ID NO: 3645, the sequence of SEQ ID NO: 3646, the sequence of SEQ ID NO: 3649, the sequence of SEQ ID NO: 8687, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3647, the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 513, the sequence of SEQ ID NO: 514, the sequence of SEQ ID NO: 515, the sequence of SEQ ID NO: 516, the sequence of SEQ ID NO: 3447, and the sequence of SEQ ID NO: 511.

[1112] In some embodiments, the first Fc region comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to any one sequence selected from the group consisting of the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3477, the sequence of SEQ ID NO: 511, the sequence of SEQ ID NO: 515, and the sequence of SEQ ID NO: 516.

[1113] In some embodiments, the second Fc region comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 3648, the sequence of SEQ ID NO: 508 or 8686, the sequence of SEQ ID NO: 506, the sequence of SEQ ID NO: 507, the sequence of SEQ ID NO: 3477, the sequence of SEQ ID NO: 511, the sequence of SEQ ID NO: 515, or the sequence of SEQ ID NO: 516.

[1114] In some embodiments, the first Fc region comprises any one sequence selected from the group consisting of the sequence of SEQ ID NO: 3648, SEQ ID NO: 508 or 8686, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 3477, SEQ ID NO: 511, SEQ ID NO: 515, or SEQ ID NO: 516.

[1115] In some embodiments, the second Fc region comprises any one sequence selected from the group consisting of the sequence of SEQ ID NO: 3648, SEQ ID NO: 508 or 8686, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 3477, SEQ ID NO: 511, SEQ ID NO: 515, or SEQ ID NO: 516.

[1116] In some embodiments,

(i) the first Fc region comprises the sequence of SEQ ID NO: 506 or the sequence of SEQ ID NO: 507, and the second Fc region comprises the sequence of SEQ ID NO: 3648 or the sequence of SEQ ID NO: 508 or 8686; or

(ii) the first Fc region comprises the sequence of SEQ ID NO: 3447 or the sequence of SEQ ID NO: 511, and the second Fc region comprises the sequence of SEQ ID NO: 515 or the sequence of SEQ ID NO: 516.

[1117] In some embodiments,

(i) the first Fc region comprises the sequence of SEQ ID NO: 3648 or the sequence of SEQ ID NO: 508 or 8686, and the second Fc region comprises the sequence of SEQ ID NO: 506 or the sequence of SEQ ID NO: 507; or

(ii) the first Fc region comprises the sequence of SEQ ID NO: 515 or the sequence of SEQ ID NO: 516, and the second Fc region comprises the sequence of SEQ ID NO: 3447 or the sequence of SEQ ID NO: 511.

[1118] In some embodiments, the first Fc region, the second Fc region, or a combination thereof comprises one or more mutations and/or one or more modifications listed in Table 1 and Table 18.

[1119] In some embodiments, the agent comprises a first polypeptide, a second polypeptide, and at least one cytokine molecule or a functional fragment or variant thereof, wherein the first polypeptide and the second polypeptide are non-contiguous;

wherein:

(i) the first polypeptide comprises a first member of the dimerization module linked to:

(a) the antigen binding domain comprising a VH and a VL, or

(b) a first portion of the antigen binding domain comprising the VH, wherein the agent further comprises a third polypeptide comprising a second portion of the antigen binding domain comprising a VL, wherein the third polypeptide is non-contiguous with the first polypeptide and the second polypeptide; and

(ii) the second polypeptide comprises a second member of the dimerization module, and

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3472, the sequence of SEQ ID NO: 2170, and the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[1140] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3472 operatively linked to the sequence of SEQ ID NO: 2170 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 13 operatively linked to the sequence of SEQ ID NO: 3644.

[1141] In some embodiments, the second polypeptide chain comprises, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3472 operatively linked to the sequence of SEQ ID NO: 3473 operatively linked to the sequence of SEQ ID NO: 2170 operatively linked to the sequence of SEQ ID NO: 3308 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686.

[1142] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 505, and the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3474, and the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[1143] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3474 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 13 operatively linked to the sequence of SEQ ID NO: 3644.

[1144] In some embodiments, the second polypeptide comprises, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3474 operatively linked to the sequence of SEQ ID NO: 3308 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686.

[1145] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 500;

(ii) a second polypeptide chain comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 3420; and
(iii) a third polypeptide comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 501.

[1146] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 500;
(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3420; and
(iii) a third polypeptide comprising the sequence of SEQ ID NO: 501.

[1147] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 505, and the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3472, the sequence of SEQ ID NO: 3670, and the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[1148] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3472 operatively linked to the sequence of SEQ ID NO: 3670 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 13 operatively linked to the sequence of SEQ ID NO: 3644.

[1149] In some embodiments, the second polypeptide comprises, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3472 operatively linked to the sequence of SEQ ID NO: 3473 operatively linked to the sequence of SEQ ID NO: 3670 operatively linked to the sequence of SEQ ID NO: 3308 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686.

[1150] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 505, and the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3671, and the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[1151] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3671 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686;
(iii) a third polypeptide comprising, from the N-terminus to the C-terminus, comprising the sequence of SEQ ID NO: 13, and the sequence of SEQ ID NO: 3644.
[1152] In some embodiments, the second polypeptide comprises, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 3671 operatively linked to the sequence of SEQ ID NO: 3308 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686.
[1153] In some embodiments, the wherein the agent comprises:
(i) a first polypeptide chain comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 500;
(ii) a second polypeptide chain comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 3669; and
(iii) a third polypeptide comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 501.
[1154] In some embodiments, the wherein the agent comprises:
(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 500;
(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3669; and
(iii) a third polypeptide comprising the sequence of SEQ ID NO: 501.
[1155] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 505, and the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising the sequence of 2270, and the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.
[1156] In some embodiments, the agent comprises:
(i) a first polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 505 operatively linked to the sequence of SEQ ID NO: 3649 or SEQ ID NO: 3451;
(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of 2270 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686; and
(iii) a third polypeptide comprising the sequence of SEQ ID NO: 13 and the sequence of SEQ ID NO: 3644.

[1157] In some embodiments, the second polypeptide comprises from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 2270 operatively linked to the sequence of SEQ ID NO: 3308 operatively linked to the sequence of SEQ ID NO: 3648 or SEQ ID NO: 508 or 8686.

[1158] In some embodiments, the agent comprises:

(i) a first polypeptide chain comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 500;

(ii) a second polypeptide chain comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 3340; and

(iii) a third polypeptide comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 501.

[1159] In some embodiments, the agent comprises:

(i) a first polypeptide chain comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 4702;

(ii) a second polypeptide chain comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 4706; and

(iii) a third polypeptide comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 501.

[1160] In some embodiments, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 500;

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3340; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 501.

[1161] In some embodiments, the agent comprises:

(i) a first polypeptide chain comprising the sequence of SEQ ID NO: 4702;

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 3340; and

(iii) a third polypeptide comprising the sequence of SEQ ID NO: 4706.

[1162] In some embodiments, the agent comprises a first polypeptide and a second polypeptide, wherein the first polypeptide and the second polypeptide are non-contiguous, and wherein:

(i) the first polypeptide comprises a first member of the dimerization module linked to:

(a) the antigen binding domain comprising a VH of the antigen binding domain and a VL of the antigen binding domain, or

(b) a first portion of the antigen binding domain comprising the VH of the antigen binding domain, wherein the agent further comprises a third polypeptide comprising a second portion of the antigen

binding domain comprising a VL of the antigen binding domain, wherein the third polypeptide is non-contiguous with the first polypeptide and the second polypeptide; and

(ii) the second polypeptide comprises a second member of the dimerization module linked to:

(a) an antigen binding domain that binds to T cell receptor beta chain constant domain (TRBC) comprising a VH and a VL, or

(b) a first portion of the antigen binding domain that binds to TRBC comprising the VH of the antigen binding domain that binds to TRBC, wherein the agent further comprises a fourth polypeptide comprising a second portion of the antigen binding domain that binds to TRBC comprising a VL of the antigen binding domain that binds to TRBC, wherein the fourth polypeptide is non-contiguous with the first polypeptide, the second polypeptide, and the third polypeptide.

[1163] In some embodiments, the agent comprises a first polypeptide and a second polypeptide, wherein the first polypeptide and the second polypeptide are non-contiguous, wherein:

(i) the first polypeptide comprises a first member of the dimerization module linked to a first portion of the antigen binding domain comprising the VH of the antigen binding domain, wherein the agent further comprises a third polypeptide comprising a second portion of the antigen binding domain comprising a VL of the antigen binding domain, wherein the third polypeptide is non-contiguous with the first polypeptide and the second polypeptide; and

(ii) the second polypeptide comprises a second member of the dimerization module linked to an antigen binding domain that binds to TRBC.

[1164] In some embodiments, the second antigen domain that binds to TRBC1 comprises a VH comprising:

(a) a VHCDR1 comprising the sequence of SEQ ID NO: 8643;

(b) a VHCDR2 comprising the sequence of SEQ ID NO: 7355 or SEQ ID NO: 201; and

(c) a VHCDR3 comprising the sequence of SEQ ID NO: 202.

[1165] In some embodiments, the second antigen domain that binds to TRBC2 comprises a VH comprising:

(a) a VHCDR1 comprising the sequence of SEQ ID NO: 8543, SEQ ID NO: 7401, or SEQ ID NO: 8272;

(b) a VHCDR2 comprising the sequence of SEQ ID NO: 201, SEQ ID NO: 8260, or SEQ ID NO: 8044; and

(c) a VHCDR3 comprising the sequence of SEQ ID NO: 7403, SEQ ID NO: 8227, SEQ ID NO: 8046, or SEQ ID NO: 8047.

[1166] In some embodiments, the second antigen binding domain that binds to TRBC1 comprises a VL comprising:

(a) a VLCDR1 comprising the sequence of SEQ ID NO: 223;

(b) a VLCDR2 comprising the sequence of SEQ ID NO: 224; and

(c) a VLCDR3 comprising the sequence of SEQ ID NO: 225 or 8680.

[1167] In some embodiments, the second antigen domain that binds to TRBC2 comprises a VL comprising:

(a) a VLCDR1 comprising the sequence of SEQ ID NO: 7410, SEQ ID NO: 8048, SEQ ID NO: 8051;

(b) a VLCDR2 comprising the sequence of SEQ ID NO: 224; and

(c) a VLCDR3 comprising the sequence of SEQ ID NO: 225 or 8680 or SEQ ID NO: 8052.

[1168] In some embodiments, the second antigen binding domain that binds to TRBC1 comprises:

(a) a VH comprising VHCDR1-3 that comprise the sequences of:

SEQ ID NOs: 8643, 7355, 202, respectively; or

SEQ ID NOs: 8643, 201, 202, respectively;

(b) a VL comprising VLCDR1-3 that comprise the sequences of:

SEQ ID NOs: 223, 224, 225 or 8680, respectively; or

(c) any combination thereof.

[1169] In some embodiments, the second antigen domain that binds to TRBC2 comprises:

(a) a VH comprising VHCDR1-3 that comprise the sequences of:

SEQ ID NOs: 8543, 201, 7403, respectively;

SEQ ID NOs: 7401, 201, 7403, respectively;

SEQ ID NOs: 8272, 8260, 8227, respectively;

SEQ ID NOs: 8272, 8044, 7403, respectively;

SEQ ID NOs: 8272, 8044, 8046, respectively; or

SEQ ID NOs: 8272, 8044, 8047, respectively;

(b) a VL comprising VLCDR1-3 that comprise the sequences of:

SEQ ID NOs: 7410, 224, 225 or 8680, respectively;

SEQ ID NOs: 8048, 224, 8050, respectively; or

SEQ ID NOs: 8051, 224, 8052, respectively; or

(c) any combination thereof.

[1170] In some embodiments, the second antigen domain that binds to TRBC1 comprises a VH comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 517 or SEQ ID NO: 512.

[1171] In some embodiments, the second antigen domain that binds to TRBC2 comprises a VH comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 7420, SEQ ID NO: 7423, SEQ ID NO: 8011, SEQ ID NO: 8013, SEQ ID NO: 8299, or SEQ ID NO: 8023.

[1172] In some embodiments, the second antigen domain that binds to TRBC1 comprises a VH comprising the sequence of SEQ ID NO: 517 or SEQ ID NO: 512.

[1173] In some embodiments, the second antigen domain that binds to TRBC2 comprises a VH comprising the sequence of SEQ ID NO: 7420, SEQ ID NO: 7423, SEQ ID NO: 8011, SEQ ID NO: 8013, SEQ ID NO: 8299, or SEQ ID NO: 8023.

[1174] In some embodiments, the second antigen domain that binds to TRBC1 comprises a VL comprising a sequence having at least 75% sequence identity to the sequence of SEQ ID NO: 8308.

[1200] In some embodiments, the agent comprises:

(i) a third polypeptide comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 8002; and

(ii) a second polypeptide chain comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 8001 or 8697.

[1201] In some embodiments, the agent comprises:

(i) a third polypeptide comprising the sequence of SEQ ID NO: 8002; and

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 8001 or 8697.

[1202] In some embodiments, the agent comprises:

(i) a third polypeptide comprising the sequence of SEQ ID NO: 8014 and the sequence of SEQ ID NO: 3644; and

(ii) a second polypeptide chain comprising the sequence of SEQ ID NO: 8013 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514, a second polypeptide chain comprising the sequence of SEQ ID NO: 8299 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514, or a second polypeptide chain comprising the sequence of SEQ ID NO: 8303 and the sequence of SEQ ID NO: 513 or SEQ ID NO: 514.

[1203] In some embodiments, the agent comprises:

(i) a third polypeptide comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 8014 operatively linked to the sequence of SEQ ID NO: 3644; and

(ii) a second polypeptide chain comprising, from the N-terminus to the C-terminus, the sequence of SEQ ID NO: 8013 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514, a second polypeptide chain comprising the sequence of SEQ ID NO: 8299 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514, or a second polypeptide chain comprising the sequence of SEQ ID NO: 8303 operatively linked to the sequence of SEQ ID NO: 513 or SEQ ID NO: 514.

[1204] In some embodiments, the agent comprises:

(i) a third polypeptide comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 8005; and

(ii) a second polypeptide chain comprising a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 8004, the sequence of SEQ ID NO: 4685, the sequence of SEQ ID NO: 8007, the sequence of SEQ ID NO: 4686, the sequence of SEQ ID NO: 4687, or the sequence of SEQ ID NO: 8009.

[1205] In some embodiments, the agent comprises:

(i) a third polypeptide comprising the sequence of SEQ ID NO: 8005; and

[1215] In some embodiments, the IL-15 or a functional fragment or variant thereof comprises the sequence of SEQ ID NO: 2170, the sequence of SEQ ID NO: 3670, or the sequence of SEQ ID NO: 3673.

[1216] In some embodiments, the at least one cytokine molecule or a functional fragment or variant thereof further comprises an IL15Ralpha dimerizing domain covalently linked the IL-15 or a functional fragment or variant thereof.

[1217] In some embodiments, the IL15Ralpha dimerizing domain comprises an IL-15 receptor alpha sushi domain or a functional fragment or variant thereof.

[1218] In some embodiments, the IL15Ralpha dimerizing domain comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 3472.

[1219] In some embodiments, the IL15Ralpha dimerizing domain comprises the sequence of SEQ ID NO: 3472.

[1220] In some embodiments, the IL-15 or a functional fragment or variant thereof is covalently linked to the IL15Ralpha dimerizing domain via a linker.

[1221] In some embodiments, the IL-15 or a functional fragment or variant thereof is covalently linked to the IL15Ralpha dimerizing domain via a linker comprising the sequence of SEQ ID NO: 3473.

[1222] In some embodiments, the at least one cytokine molecule or a functional fragment or variant thereof comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 3474, SEQ ID NO: 3671, or SEQ ID NO: 8689.

[1223] In some embodiments, the at least one cytokine molecule or a functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3474, the sequence of SEQ ID NO: 3671, or the sequence of SEQ ID NO: 8689.

[1224] In some embodiments, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-7 or a functional fragment or variant thereof.

[1225] In some embodiments, the IL-7 or the functional fragment or variant thereof comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the sequence of SEQ ID NO: 3540.

[1226] In some embodiments, the IL-7 or the functional fragment or variant thereof comprises the sequence of SEQ ID NO: 3540.

[1227] In some embodiments, the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-12 or a functional fragment or variant or variant thereof.

[1228] In some embodiments, the IL-12 or the functional fragment or variant thereof comprises a sequence having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100% sequence identity to the

Table 1. Exemplary Fc KiH mutations and optional Cysteine mutations

Position	**Knob Mutation**	**Hole Mutation**
T366	T366W	T366S
L368	-	L368A
Y407	-	Y407V
Additional Cysteine Mutations to form a stabilizing disulfide bridge		
Position	**Knob CH3**	**Hole CH3**
S354	S354C	-
Y349	-	Y349C

Table 2A. Exemplary heavy chain CDRs and FWRs of TRBC1-targeting antigen binding domains derived from JOVI.1 (according to Kabat numbering convention)

AB ID	**VHFWR1**	**VHCDR1**	**VHFWR2**	**VHCDR2**	**VHFWR3**	**VHCDR3**	**VHFWR4**
mJOVI.1-H	EVRLQQSGPDLIKPGASVKMSCKASGYTFT (**SEQ ID NO:** 203)	GYVMH (**SEQ ID NO:** 8643)	WVKQRPGQGLEWIG (**SEQ ID NO:** 204)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	KATLTSDKSSTTAYMELSSLTSEDSAVYYCAR (**SEQ ID NO:** 8679)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTTLTVSS (**SEQ ID NO:** 206)
h1JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKASGYTFT (**SEQ ID NO:** 207)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)
h2JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKASGYTFT (**SEQ ID NO: 207**)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO: 208**)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	WVTMTSDKSITTAYMELSRLRSDDTAVYYCAR (**SEQ ID NO:** 213)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)
h3JOVI.1-H	QVQLVQSGAEVKKPGSSVKVSCKASGYTFT (**SEQ ID NO: 7345**)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO: 208**)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)
h4JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKASGYTFT (**SEQ ID NO: 207**)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQRLEWMG (**SEQ ID NO: 212**)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTITSDKSATTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 221)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)

Table 2B. Exemplary heavy chain CDRs and FWRs of TRBC1-targeting antigen binding domains derived from JOVI.1 shown in Table 2A (according to ABM numbering convention)

AB ID	VHFWR1	VHCDR1	VHFWR2	VHCDR2	VHFWR3	VHCDR3	VHFWR4
mJOVI.1-H	EVRLQQSGPDLIKPGASVKMSCKAS (**SEQ ID NO:** 8400)	GYTFTGYVMH (**SEQ ID NO:** 8401)	WVKQRPGQGLEWIG (**SEQ ID NO:** 204)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	KATLTSDKSSTTAYMELSSLTSEDSAVYYCAR (**SEQ ID NO:** 8679)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTTLTVSS (**SEQ ID NO:** 206)
h1JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8402)	GYTFTGYVMH (**SEQ ID NO:** 8401)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)
h2JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8403)	GYTFTGYVMH (**SEQ ID NO:** 8401)	WVRQAPGQGLEWMG (**SEQ ID NO: 208**)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	WVTMTSDKSITTAYMELSRLRSDDTAVYYCAR (**SEQ ID NO:** 213)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)
h3JOVI.1-H	QVQLVQSGAEVKKPGSSVKVSCKAS (**SEQ ID NO:** 8404)	GYTFTGYVMH (**SEQ ID NO:** 8401)	WVRQAPGQGLEWMG (**SEQ ID NO: 208**)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)
h4JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8405)	GYTFTGYVMH (**SEQ ID NO:** 8401)	WVRQAPGQRLEWMG (**SEQ ID NO: 212**)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTITSDKSATTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 221)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)

Table 3. Constant region amino acid sequences of human IgG heavy chains and human kappa light chain.

Human kappa constant region SEQ ID NO: 39	LC	RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC
Human Immunoglobulin kappa constant C region SEQ ID NO: 3644	LC	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C
IgG4 (S228P) mutant constant region (EU Numbering) SEQ ID NO: 40	HC	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPP CPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQ KSLSLSLG
IgG1 wild type SEQ ID NO: 41	HC	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHT

		VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
Human IgG1 hole cys N297A SEQ ID NO: 3649	HC	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK

Table 3A. Exemplary heavy chain CDRs and FWRs of TRBC1-targeting antigen binding domains derived from JOVI.1 (according to the Kabat numbering scheme)

Ab ID	VHFWR1	VHCDR1	VHFWR2	VHCDR2	VHFWR3	VHCDR3	VHFWR4
mJOVI.1-H	EVRLQQSGPDLIKPGASVKMSCKASGYTFT (**SEQ ID NO:** 7370)	GYVMH (**SEQ ID NO:** 8643)	WVKQRPGQGLEWIG (**SEQ ID NO:** 204)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	KATLTSDKSSTTAYMELSSLTSEDSAVYYCAR (**SEQ ID NO:** 8679)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTTLTVSS (**SEQ ID NO:** 206)
h1JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKASGYTFT (**SEQ ID NO: 207**)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)
h2JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKASGYTFT (**SEQ ID NO: 207**)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO: 208**)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	WVTMTSDKSITTAYMELSRLRSDDTAVYYCAR (**SEQ ID NO:** 213)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)
h3JOVI.1-H	QVQLVQSGAEVKKPGSSVKVSCKASGYTFT (**SEQ ID NO:** 7345)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO: 208**)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)
h4JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKASGYTFT (**SEQ ID NO: 207**)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQRLEWMG (**SEQ ID NO: 212**)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTITSDKSATTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 221)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)
h5JOVI.1-H	QVQLVQSGAEVKKPGSSVKVSCKASGYTFT (**SEQ ID NO:** 7345)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTTVTVSS (**SEQ ID NO:** 7347)
h6JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKASGYTFT	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO:** 201)	RVTMTSDKSITTAYMELSRLRSDDTAVYYCAR (**SEQ**	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTTVTVSS (**SEQ ID NO:** 7347)

	(**SEQ ID NO: 207**)				**ID NO:** 7349)		
H1 germlined-VH	QVQLVQSGAEVKKPGSSVKVSCKASGYTFS (**SEQ ID NO:** 7353)	GYAIS (**SEQ ID NO:** 7354)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)
H2 germlined-VH	QVQLVQSGAEVKKPGSSVKVSCKASGYTFT (**SEQ ID NO:** 7345)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FIIPIFGTANYAQKFQG (**SEQ ID NO:** 7355)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)
H1/H2 germlined-VH	QVQLVQSGAEVKKPGSSVKVSCKASGYTFS (**SEQ ID NO:** 7353)	GYAIS (**SEQ ID NO:** 7354)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FIIPIFGTANYAQKFQG (**SEQ ID NO:** 7355)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)

Table 3B. Exemplary heavy chain CDRs and FWRs of TRBC1-targeting antigen binding domains derived from JOVI.1 of Table 3A (according to the ABM numbering scheme)

Ab ID	VHFWR1	VHCDR1	VHFWR2	VHCDR2	VHFWR3	VHCDR3	VHFWR4
mJOVI.1-H	EVRLQQSGPDLIKPGASVKMSCKAS (**SEQ ID NO:** 8506)	GYTFTGYVMH (**SEQ ID NO:** 8507)	WVKQRPGQGLEWIG (**SEQ ID NO:** 204)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	KATLTSDKSSTTAYMELSSLTSEDSAVYYCAR (**SEQ ID NO:** 8679)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTTLTVSS (**SEQ ID NO:** 206)
h1JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8508)	GYTFTGYVMH (**SEQ ID NO:** 8507)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)
h2JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8508)	GYTFTGYVMH (**SEQ ID NO:** 8507)	WVRQAPGQGLEWMG (**SEQ ID NO: 208**)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	WVTMTSDKSITTAYMELSRLRSDDTAVYYCAR (**SEQ ID NO:** 213)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)
h3JOVI.1-H	QVQLVQSGAEVKKPGSSVKVSCKAS (**SEQ ID NO:** 8509)	GYTFTGYVMH (**SEQ ID NO:** 8507)	WVRQAPGQGLEWMG (**SEQ ID NO: 208**)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)
h4JOVI.1-H	QVQLVQSGAEVKKPGASVKVSCKAS	GYTFTGYVMH (**SEQ ID NO:** 8507)	WVRQAPGQRLEWMG (**SEQ ID NO: 212**)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTITSDKSATTAYMELSSLRSEDTAVYYCAR (**SEQ**	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO: 210**)

	(**SEQ ID NO:** 8508)				**ID NO:** 221)		
h5JOVI .1-H	QVQLVQ SGAEVK KPGSSVK VSCKAS (**SEQ ID NO:** 8510)	GYTFTG YVMH (**SEQ ID NO:** 8507)	WVRQA PGQGLE WMG (**SEQ ID NO:** 208)	FINPYND DIQSNER FRG (**SEQ ID NO: 201**)	RVTITSDK STTTAYM ELSSLRSE DTAVYYC AR (**SEQ ID NO:** 217)	GAGYNF DGAYRFF DF (**SEQ ID NO:** 202)	WGQGTT VTVSS (**SEQ ID NO:** 7347)
h6JOVI .1-H	QVQLVQ SGAEVK KPGASVK VSCKAS (**SEQ ID NO:** 8511)	GYTFTG YVMH (**SEQ ID NO:** 8507)	WVRQA PGQGLE WMG (**SEQ ID NO:** 208)	FINPYND DIQSNER FRG (**SEQ ID NO: 201**)	RVTMTSD KSITTAYM ELSRLRSD DTAVYYC AR (**SEQ ID NO:** 7349)	GAGYNF DGAYRFF DF (**SEQ ID NO:** 202)	WGQGTT VTVSS (**SEQ ID NO:** 7347)
H1 germlin ed-VH	QVQLVQ SGAEVK KPGSSVK VSCKAS (**SEQ ID NO:** 8512)	GYTFSG YAIS (**SEQ ID NO:** 8513)	WVRQA PGQGLE WMG (**SEQ ID NO:** 208)	FINPYND DIQSNER FRG (**SEQ ID NO: 201**)	RVTITSDK STTTAYM ELSSLRSE DTAVYYC AR (**SEQ ID NO:** 217)	GAGYNF DGAYRFF DF (**SEQ ID NO:** 202)	WGQGTL VTVSS (**SEQ ID NO:** 210)
H2 germlin ed-VH	QVQLVQ SGAEVK KPGSSVK VSCKAS (**SEQ ID NO:** 8514)	GYTFTG YVMH (**SEQ ID NO:** 8507)	WVRQA PGQGLE WMG (**SEQ ID NO:** 208)	FIIPIFGTA NYAQKF QG (**SEQ ID NO:** 7355)	RVTITSDK STTTAYM ELSSLRSE DTAVYYC AR (**SEQ ID NO:** 217)	GAGYNF DGAYRFF DF (**SEQ ID NO:** 202)	WGQGTL VTVSS (**SEQ ID NO:** 210)
H1/H2 germlin ed-VH	QVQLVQ SGAEVK KPGSSVK VSCKAS (**SEQ ID NO:** 8515)	GYTFSG YAIS (**SEQ ID NO:** 8513)	WVRQA PGQGLE WMG (**SEQ ID NO:** 208)	FIIPIFGTA NYAQKF QG (**SEQ ID NO:** 7355)	RVTITSDK STTTAYM ELSSLRSE DTAVYYC AR (**SEQ ID NO:** 217)	GAGYNF DGAYRFF DF (**SEQ ID NO:** 202)	WGQGTL VTVSS (**SEQ ID NO:** 210)

Table 4. Exemplary light chain CDRs and FWRs of TRBC1-targeting antigen binding domains derived from JOVI.1 (According to Kabat numbering scheme)

Ab ID	VLFWR1	VLCDR1	VLFWR2	VLCDR2	VLFWR3	VLCDR3	VLFWR4
mJOVI. 1-L	DVVMTQ SPLSLPVS LGDQASI SC (**SEQ ID NO:** 226)	RSSQRL VHSNGN TYLH (**SEQ ID NO:** 223)	WYLQKP GQSPKL LIY (**SEQ ID NO:** 227)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFS GSGSGTDF TLKISRVE AEDLGIYF C (**SEQ ID NO:** 228)	SQSTHVP YT (**SEQ ID NO:** 225)	FGGGTKL EIK (**SEQ ID NO:** 229)
h1JOVI .1-L	DVVMTQ SPLSLPV TPGEPASI SC (**SEQ ID NO:** 230)	RSSQRL VHSNGN TYLH (**SEQ ID NO:** 223)	WYLQKP GQSPQL LIY (**SEQ ID NO:** 231)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFS GSGSGTDF TLKISRVE AEDVGVY FC (**SEQ ID NO: 240**)	SQSTHVP YT (**SEQ ID NO:** 225)	FGGGTK VEIK (**SEQ ID NO:** 8685)
h2JOVI .1-L	EVVMTQ SPGTLSL SPGERAT LSC (**SEQ ID NO:** 234)	RSSQRL VHSNGN TYLH (**SEQ ID NO:** 223)	WYQQK PGQAPR LLIY (**SEQ ID NO:** 235)	*RVSNRFP* (**SEQ ID NO:** 224)	GIPDRFSG SGSGTDFT LTISRLEPE DFAVYFC (**SEQ ID NO:** 236)	SQSTHVP YT (**SEQ ID NO:** 225)	FGGGTK VEIK (**SEQ ID NO:** 237)

h3JOVI.1-L	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQRLVHSNGNTYLH (**SEQ ID NO:** 223)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO:** 240)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 241)
h4JOVI.1-L	DVVMTQTPLSLPVTPGEPASISC (**SEQ ID NO:** 242)	RSSQRLVHSNGNTYLH (**SEQ ID NO:** 223)	WYLQKPGQSPQLLIY (**SEQ ID NO:** 243)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO: 240**)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 245)
h5JOVI.1-L	DVVMTQTPLSLSVTPGQPASISC (**SEQ ID NO:** 246)	RSSQRLVHSNGNTYLH (**SEQ ID NO:** 223)	WYLQKPGQSPQLLIY (**SEQ ID NO:** 247)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO: 240**)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 249)
L1 germlined-VL	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQSLVYSDGNTYH (**SEQ ID NO:** 7367)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO: 240**)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 8685)
L2 germlined-VL	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQRLVHSNGNTYLH (**SEQ ID NO:** 223)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	KVSNRDS (**SEQ ID NO:** 7368)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO: 240**)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 8685)
L3 germlined-VL	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQRLVHSNGNTYLH (**SEQ ID NO:** 223)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO: 240**)	MQSTHWPYT (**SEQ ID NO:** 7369)	FGGGTKVEIK (**SEQ ID NO:** 8685)
L1/L2/L3 germlined-VL	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQSLVYSDGNTYH (**SEQ ID NO:** 7367)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	KVSNRDS (**SEQ ID NO:** 7368)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO: 240**)	MQSTHWPYT (**SEQ ID NO:** 7369)	FGGGTKVEIK (**SEQ ID NO:** 8685)

Table 5A. Exemplary heavy chain CDRs and FWRs of TRBC1-targeting antigen binding domains (According to Kabat numbering scheme)

Ab ID	VHFWR1	VHCDR1	VHFWR2	VHCDR2	VHFWR3	VHCDR3	VHFWR4
BKM0191	QVQLVQSGAEVKKPGSSVKVSCKASGYTFT (**SEQ ID NO:** 7345)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FIIPIFGTANYAQKFQG (**SEQ ID NO:** 7355)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)
BKM0192	QVQLVQSGAEVKKPGSSVKVSCKASGYTFT (**SEQ ID NO:** 7345)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FIIPIFGTANYAQKFQG (**SEQ ID NO:** 7355)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)

BKM0195	QVQLVQSGAEVKKPGSSVKVSCKAS (**SEQ ID NO:** 8524)	GYTFTGYVMH (**SEQ ID NO:** 8525)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FIIPIFGTANYAQKFQG (**SEQ ID NO:** 7355)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)
BKM0196	QVQLVQSGAEVKKPGSSVKVSCKAS (**SEQ ID NO:** 8526)	GYTFTGYVMH (**SEQ ID NO:** 8527)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FIIPIFGTANYAQKFQG (**SEQ ID NO:** 7355)	RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 217)	GAGYNFDGAYRFFDF (**SEQ ID NO:** 202)	WGQGTLVTVSS (**SEQ ID NO:** 210)

Table 6. Exemplary light chain CDRs and FWRs of TRBC1-targeting antigen binding domains (According to Kabat numbering scheme)

Ab ID	VLFWR1	VLCDR1	VLFWR2	VLCDR2	VLFWR3	VLCDR3	VLFWR4
BKM0191	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQRLVHSNANTYLH (**SEQ ID NO:** 367)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO:** 240)	SQSTHVPYTF (**SEQ ID NO:** 8680)	GGGTKVEIK (**SEQ ID NO:** 373)
BKM0192	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQRLVHSNGNAYLH (**SEQ ID NO:** 368)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO:** 240)	SQSTHVPYTF (**SEQ ID NO:** 8680)	GGGTKVEIK (**SEQ ID NO:** 373)
BKM0193	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQRLVHSNANAYLH (**SEQ ID NO:** 369)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO:** 240)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 8685)
BKM0194	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQRLVHSGGNTYLH (**SEQ ID NO:** 370)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO:** 240)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 8685)
BKM0195	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQRLVHSNGSTYLH (**SEQ ID NO:** 371)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO:** 240)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 8685)
BKM0196	DVVMTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 238)	RSSQRLVHSGGSTYLH (**SEQ ID NO:** 372)	WYQQRPGQSPRLLIY (**SEQ ID NO:** 239)	*RVSNRFP* (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO:** 240)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 8685)

SEQ ID NO: 4674	a_hTRBC1_Jovi1_Hum5_VH-hCHIg-Blank	Anti-TRBC1 heavy chain	METDTLLLWVLLLWVPGSTGQVQLVQSGAEVKKPGSSVKV SCKASGYTFTGYVMHWVRQAPGQGLEWMGFINPYNDDIQS NERFRGRVTITSDKSTTTAYMELSSLRSEDTAVYYCARGAG YNFDGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 6169	a_hTRBC1_Jovi1_Hum3_VL-hCLIg_vk-Blank	Anti-TRBC1 light chain	METDTLLLWVLLLWVPGSTGDVVMTQSPLSLPVTLGQPASI SCRSSQRLVHSNGNTYLHWYQQRPGQSPRLLIY*RV*SNRFPG VPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTHVPYTFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Table 9A. Exemplary heavy chain CDRs and FWRs of TRBC2-targeting antigen binding domains (According to Kabat numbering scheme)

Ab ID	VHFWR1	VHCDR1	VHFWR2	VHCDR2	VHFWR3	VHCDR3	VHFWR4
JVD3-VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFP (**SEQ ID NO:** 7393)	GFVMH (**SEQ ID NO:** 7394)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGMWFDGAYRFFDF (**SEQ ID NO:** 307)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD4-VH	QVQLVQSGAEVKKPGASVKVSCKASGYPFH (**SEQ ID NO:** 7397)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKNFDGAYRFFDF (**SEQ ID NO:** 8695)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD5-VH	QVQLVQSGAEVKKPGASVKVSCKASGYTYP (**SEQ ID NO:** 7399)	GYVMH (**SEQ ID NO:** 8643)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWFDGAYRFFDF (**SEQ ID NO:** 7400)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD6-VH	QVQLVQSGAEVKKPGASVKVSCKASNQNFH (**SEQ ID NO:** 8696)	GYHMH (**SEQ ID NO:** 7401)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD7-VH	QVQLVQSGAEVKKPGASVKVSCKASSQNFH (**SEQ ID NO:** 7404)	GFYMH (**SEQ ID NO:** 7405)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD8-VH	QVQLVQSGAEVKKP	GYKMH (**SEQ ID**	WVRQAPGQGLEW	FINPYNDDIQSNER	RVTMTSDKSTTTA	GNGKWGDGAYRFF	WGQGTLVTVSS

	GASVKVS CKASYQD FH (**SEQ ID NO:** 7406)	**NO:** 7407)	MG (**SEQ ID NO:** 208)	FRG (**SEQ ID NO: 201**)	YMELSSL RSEDTAV YYCAR (**SEQ ID NO:** 209)	DF (**SEQ ID NO:** 7403)	(**SEQ ID NO:** 210)
JVD9-VH	QVQLVQS GAEVKKP GASVKVS CKASGYN FH (**SEQ ID NO:** 7408)	GFYMH (**SEQ ID NO:** 7405)	WVRQAP GQGLEW MG (**SEQ ID NO:** 208)	FINPYND DIQSNER FRG (**SEQ ID NO: 201**)	RVTMTS DKSTTTA YMELSSL RSEDTAV YYCAR (**SEQ ID NO:** 209)	GNGKWG DGAYRFF DF (**SEQ ID NO:** 7403)	WGQGT LVTVSS (**SEQ ID NO:** 210)
BKM00 97 anti-TRBC2 VH; BJM11 84 VH	QVQLVQS GAEVKKP GASVKVS CKASTSGF H (**SEQ ID NO:** 7421)	GYPMH (**SEQ ID NO:** 7422)	WVRQAP GQGLEW MG (**SEQ ID NO:** 208)	FINPYND DIQSNER FRG (**SEQ ID NO: 201**)	RVTMTS DKSTTTA YMELSSL RSEDTAV YYCAR (**SEQ ID NO:** 209)	GNGKWG DGAYRFF DF (**SEQ ID NO:** 7403)	WGQGT LVTVSS (**SEQ ID NO:** 210)
BKM00 98 anti-TRBC2 VH; BJM11 85 VH	QVQLVQS GAEVKKP GASVKVS CKASPRGF H (**SEQ ID NO:** 7424)	GYHMH (**SEQ ID NO:** 7401)	WVRQAP GQGLEW MG (**SEQ ID NO:** 208)	FINPYND DIQSNER FRG (**SEQ ID NO: 201**)	RVTMTS DKSTTTA YMELSSL RSEDTAV YYCAR (**SEQ ID NO:** 209)	GNGKWG DGAYRFF DF (**SEQ ID NO:** 7403)	WGQGT LVTVSS (**SEQ ID NO:** 210)
BJM11 86 VH	QVQLVQS GAEVKKP GASVKVS CKASFQD FH (**SEQ ID NO:** 7426)	GYAMH (**SEQ ID NO:** 7427)	WVRQAP GQGLEW MG (**SEQ ID NO:** 208)	FINPYND DIQSNER FRG (**SEQ ID NO: 201**)	RVTMTS DKSTTTA YMELSSL RSEDTAV YYCAR (**SEQ ID NO:** 209)	GNGKWG DGAYRFF DF (**SEQ ID NO:** 7403)	WGQGT LVTVSS (**SEQ ID NO:** 210)
BJM11 87 VH	QVQLVQS GAEVKKP GASVKVS CKASSKD FH (**SEQ ID NO:** 7429)	GFAMH (**SEQ ID NO:** 7430)	WVRQAP GQGLEW MG (**SEQ ID NO:** 208)	FINPYND DIQSNER FRG (**SEQ ID NO: 201**)	RVTMTS DKSTTTA YMELSSL RSEDTAV YYCAR (**SEQ ID NO:** 209)	GNGKWG DGAYRFF DF (**SEQ ID NO:** 7403)	WGQGT LVTVSS (**SEQ ID NO:** 210)
BC2_Y R3_B11 -scFv VH	QVQLVQS GAEVKKP GASVKVS CKASPKG FH (**SEQ ID NO:** 7432)	GYHMH (**SEQ ID NO:** 7401)	WVRQAP GQGLEW MG (**SEQ ID NO:** 208)	FINPYND DIQSNER FRG (**SEQ ID NO: 201**)	RVTMTS DKSTTTA YMELSSL RSEDTAV YYCAR (**SEQ ID NO:** 209)	GNGKWG DGAYRFF DF (**SEQ ID NO:** 7403)	WGQGT LVTVSS (**SEQ ID NO:** 210)
Consens us VHCD R		GX1X2M H, wherein X1 is Y or F, and X2 is P, H, V, Y, K, or A		FINPYND DIQSNER FRG (**SEQ ID NO: 201**)		GNGX1X2 X3DGAY RFFDF,wh erein X1 is K or M, X2 is W or N, and X3 is G or F (**SEQ ID NO:** 7442)	

Table 9B. Exemplary heavy chain CDRs and FWRs of TRBC2-targeting antigen binding domains of Table 9A (According to ABM numbering scheme)

Ab ID	VHFWR1	VHCDR 1	VHFWR2	VHCDR2	VHFWR3	VHCDR3	VHFWR4
JVD3-VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8528)	GYTFPGFVMH (**SEQ ID NO:** 8529)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGMWFDGAYRFFDF (**SEQ ID NO:** 307)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD4-VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8530)	GYPFHGYVMH (**SEQ ID NO:** 8531)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKNFDGAYRFFDF (**SEQ ID NO:** 8695)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD5-VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8532)	GYTYPGYVMH (**SEQ ID NO:** 8533)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWFDGAYRFFDF (**SEQ ID NO:** 7400)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD6-VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8534)	NQNFHGYHMH (**SEQ ID NO:** 8535)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD7-VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8536)	SQNFHGFYMH (**SEQ ID NO:** 8537)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD8-VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8538)	YQDFHGYKMH (**SEQ ID NO:** 8539)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)
JVD9-VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8540)	GYNFHGFYMH (**SEQ ID NO:** 8541)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)
BKM0097 anti-TRBC2 VH; BJM1184 VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8542)	TSGFHGYPMH (**SEQ ID NO:** 8543)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)

BKM0098 anti-TRBC2 VH; BJM1185 VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8544)	PRGFHGYHMH (**SEQ ID NO:** 8545)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)
BJM1186 VH	QVQLVQSGAEVKKPGASVKVSCKASFQDFH (**SEQ ID NO:** 8546)	GYAMH (**SEQ ID NO:** 8547)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)
BJM1187 VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8548)	SKDFHGFAMH (**SEQ ID NO:** 8549)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)
BC2_YR3_B11-scFv VH	QVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO:** 8550)	PKGFHGYHMH (**SEQ ID NO:** 8551)	WVRQAPGQGLEWMG (**SEQ ID NO:** 208)	FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)	RVTMTSDKSTTTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO:** 209)	GNGKWGDGAYRFFDF (**SEQ ID NO:** 7403)	WGQGTLVTVSS (**SEQ ID NO:** 210)
Consensus VHCDR		GX1X2MH, wherein X1 is Y or F, and X2 is P, H, V, Y, K, or A		FINPYNDDIQSNERFRG (**SEQ ID NO: 201**)		GNGX1X2X3DGAYRFFDF,wherein X1 is K or M, X2 is W or N, and X3 is G or F (**SEQ ID NO:** 7442)	

Table 10. Exemplary light chain CDRs and FWRs of TRBC2-targeting antigen binding domains

Ab ID	VLFWR1	VLCDR1	VLFWR2	VLCDR2	VLFWR3	VLCDR3	VLFWR4
JVD2-VL	DVVMTQSPLSLPVTPGEPASISC (**SEQ ID NO:** 230)	RSSQNLVHSNGRTYLH (**SEQ ID NO:** 7409)	WYLQKPGQSPQLLIY (**SEQ ID NO:** 231)	RVSNRFP (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO: 240**)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 8685)
JVD34-VL	DVVMTQSPLSLPVTPGEPASISC (**SEQ ID NO:** 230)	RSSQNLVHSNGRTYLQ (**SEQ ID NO:** 7410)	WYLQKPGQSPQLLIY (**SEQ ID NO:** 231)	RVSNRFP (**SEQ ID NO:** 224)	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC (**SEQ ID NO: 240**)	SQSTHVPYT (**SEQ ID NO:** 225)	FGGGTKVEIK (**SEQ ID NO:** 8685)
Consensus LHCDR		RSSQNLVHSNGRTYLX, wherein X is Q or H (**SEQ ID NO:** 7443)		RVSNRFP (**SEQ ID NO:** 224)		SQSTHVPYT (**SEQ ID NO:** 225)	

L1L2P3-B11 VH	QVQLVQSGAEVKKPGSSVKVSCKAS**PRGFYGYHMH**WVRQAPGQGLEWMG*TINPY NRDIQYNQKFQG*RVTITADKSTSTAYMELSSLRSEDTAVYYCA***RGNGKWGDGAYRF FDL***WGQGTLVTVSS (**SEQ ID NO: 8077**)
L1L2P3-B11 VL	DVVMTQSPLSLPVTPGEPASISC**RSSQNLVHSNGRTYLQ**WYLQKPGQSPQLLIY*RVS NRFP*GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC***SQSTHVPYT***FGGGTKVEIK (**SEQ ID NO: 8078**)
L1L2P3-B12VH	QVQLVQSGAEVKKPGSSVKVSCKAS**PRGFYGYHMH**WVRQAPGQGLEWMG*TINPY NRDIQYNQKFQG*RVTITADKSTSTAYMELSSLRSEDTAVYYCA***RGNGKWGDGAYRF FDF***WGQGTLVTVSS (**SEQ ID NO: 8079**)
L1L2P3-B12 VL	DVVMTQSPLSLPVTPGEPASISC**RSSQNLVHSNGRTYLH**WYLQKPGQSPQLLIY*RVS NRFP*GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC***SQSTHVPYT***FGGGTKVEIK (**SEQ ID NO: 8080**)
L1L2P3-B2	QVQLVQSGAEVKKPGSSVKVSCKAS**PRGFYGYHMH**WVRQAPGQGLEWMGYINPY TNEIKYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCA***RGNGKWGDGAYRFF DL***WGQGTLVTVSS (**SEQ ID NO: 8081**)
VL	DVVMTQSPLSLPVTLGQPASISC**RSSKNLVHSNGRTYLQ**WYLQKPGQSPQLLIY*RVS NRFP*GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC***SQSTHVPYT***FGGGTKVEIK (**SEQ ID NO: 8699**)
L1L2P3-B3 VH	QVQLVQSGAEVKKPGSSVKVSCKAS**PRGFYGYHMH**WVRQAPGQGLEWMG*FINPY NDDIQYNQKFQG*RVTITADESTSTAYMELSSLRSEDTAVYYCAR***GNGKWGDGAYRF FDF***WGQGTLVTVSS (**SEQ ID NO: 8082**)
VL	DVVMTQSPLSLPVTPGEPASISC**RSSQNLVHSNGRTYLQ**WYLQKPGQSPQLLIY*RVS NRFP*GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC*SQSTHVPYT*FGGGTKVEIK (**SEQ ID NO: 8083**)
L1L2P3-B4 VH	QVQLVQSGAEVKKPGSSVKVSCKAS**PRGFYGYHMH**WVRQAPGQGLEWMG*TINPY NAEIKYNQKFQG*RVTITADKSTSTAYMELSSLRSEDTAVYYCAR***GNGKWGDGAYRFF DF***WGQGTLVTVSS (**SEQ ID NO: 8084**)
VL	DVVMTQSPLSLPVTPGEPASISC**RSSQNLVHSNGRTYLQ**WYLQKPGQSPQLLIY*RVS NRFP*GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC*SQSTYEPFT*FGGGTKVEIK (**SEQ ID NO: 8085**)
L1L2P3-B5VH	QVQLVQSGAEVKKPGSSVKVSCKAS**PRGFYGYHMH**WVRQAPGQGLEWMG*FINPY NRDIKYNERFRG*RVTITSDKSTTTAYMELSSLRSEDTAVYYCA***MGNGKWGDGAYRFF DL***WGQGTLVTVSS (**SEQ ID NO: 8086**)
VL	DVVMTQSPLSLPVTLGQPASISC**RSSKNLVHSNGRTYLQ**WYQQRPGQSPRLLIY*RVS NRFP*GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC***SQSSHIPYT***FGGGTKVEIK (**SEQ ID NO: 8087**)
L1L2P3-B7VH	QVQLVQSGAEVKKPGSSVKVSCKAS**PRGFYGYHMH**WVRQAPGQGLEWMG*AINPY TNDIKYNERFRG*RVTITSDKSTTTAYMELSSLRSEDTAVYYCAR***GNGKWGDGAYRFF DL***WGQGTLVTVSS (**SEQ ID NO: 8088**)
VL	DVVMTQSPLSLPVTPGEPASISC**RSSQNLVHSNGRTYLQ**WYLQKPGQSPQLLIY*RVS NRFP*GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC***SQSTHVPYT***FGGGTKVEIK (**SEQ ID NO: 8089**)
L1L2P3-B8VH	QVQLVHSGAEVKKPGSSVKVSCKAS**PRGFYGYHMH**WVRQAPGQGLEWMG*TINPY NRHIKYNQKFQG*RVTITADKSTTTAYMELSSLRSEDTAVYYCAR***GNGKWGDGAYRF FDF***WGQGTLVTVSS (**SEQ ID NO: 8090**)
VL	DVVMTQSPLSLPVTPGEPASISC**RSSQNLVHSNGRTYLQ**WYLQKPGQSPQLLIY*RVS NRFP*GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC***SQSTHVPYT***FGGGTKVEIK (**SEQ ID NO: 7419**)
L1L2P3-C1VH	QVQLVQSGAEVKKPGASVKVSCKAS**PRGFHGYHMH**WVRQAPGQGLEWMG*SINPY TDDIQYNERFRG*RVTITSDESTTTAYMELSSLRSEDTAVYYCAR***GNGKWGDGAYRFF DF***WGQGTLVTVSS (**SEQ ID NO: 8092**)
VL	DVVMTQSPLSLPVTLGQPASISCRSSENLVHSNGRTYLQWYQQRPGQSPRLLIY*RVSN RFP*GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC***SQSTHVPYT***FGGGTKVEIK (**SEQ ID NO: 8093**)
L1L2P3-C10VH	QVQLVQSGAEVKKPGSSVKVSCKAS**PRGFYGYHMH**WVRQAPGQGLEWMG*AINPY TNHIQYNERFRG*RVTITSDESTTTAYMELSSLRSEDTAVYYCAR***GNGKWGDGAYRFF DL***WGQGTLVTVSS (**SEQ ID NO: 8094**)
VL	DVVMTQSPLSLPVTLGQPASISC**RSSQNLVHSNGRTYLQ**WYQQRPGQSPRLLIY*RVS NRFP*GVPDRFSGSGSGTDFTLKISRVEAEDVGVYFC***SQSTHVPYT***FGGGTKVEIK (**SEQ ID NO: 8095**)
L1L2P3-C4 VH	QVQLVQSGAEVKKPGSSVKVSCKAS**PRGFYGYHMH**WVRQAPGQGLEWMG*FINPY NDDIQYNQKFQG*RVTITADKSTSTAYMELSSLRSEDTAVYYCA***RGNGKWGDGAYRF**

NO: 8002	2-BKM0238-LC	VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
SEQ ID NO: 8693/ **SEQ ID NO:** 8003	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4683	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
anti-TRBC2-NKp30 – BIS-2020-2		
SEQ ID NO: 8001	Anti-TRBC2-BKM0238-HC 1	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYTNDIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCAMGNGKWG DGAYRFFDLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4682	Anti-TRBC2-BKM0238-HC 1	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYTNDIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCAMGNGKWG DGAYRFFDLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 8002	Anti-TRBC2 -BKM0238-LC	DVVMTQSPLSLPVTLGQPASISCRSSENLVHSNGRTYLQWYQQRPGQSPRLLIY RVSNRFPGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSSLEPYTFGGGTK VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
SEQ ID NO: 7383/**SEQ ID NO:** 8006	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4684	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE

		EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
anti-TRBC2-NKp30 – BIS-2020-3		
SEQ ID NO: 8004	Anti-TRBC2 - BKM0240-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGNGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4685	Anti-TRBC2 - BKM0240-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGNGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 8005	Anti-TRBC2--BKM0240-LC	DVVMTQSPLSLPVTLGQPASISCRSSKNLVHSNGRTYLQWYQQRPGQSPRLLIY RVSNRFPGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTREPYTFGGGTK VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
SEQ ID NO: 8693/ **SEQ ID NO:** 8003	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4683	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
anti-TRBC2-NKp30 – BIS-2020-4		
SEQ ID NO: 8004	Anti-TRBC2--BKM0240-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGNGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4685	Anti-TRBC2--BKM0240-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGNGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ

		DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 8005	Anti-TRBC2-BKM0240-LC	DVVMTQSPLSLPVTLGQPASISCRSSKNLVHSNGRTYLQWYQQRPGQSPRLLIY RVSNRFPGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTREPYTFGGGTK VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
SEQ ID NO: 7383/**SEQ ID NO:** 8006	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4684	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
anti-TRBC2-NKp30 – BIS-2020-5		
SEQ ID NO: 8007	Anti-TRBC2-0311-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGEGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4686	Anti-TRBC2-0311-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGEGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 8005	Anti-TRBC2-0311-LC	DVVMTQSPLSLPVTLGQPASISCRSSKNLVHSNGRTYLQWYQQRPGQSPRLLIY RVSNRFPGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTREPYTFGGGTK VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
SEQ ID NO: 7384 **/SEQ ID NO:** 8698	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSSSETTQPPSVSVSPGQTASIT CSGEKLSDKYVHWYQQKPGQSPVMVIYENDRRPSGIPERFSGSNSGNTATLTIS GTQAMDEADYFCQFWDSTNSAVFGGGTQLTVLDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 8690	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSSSETTQPPSVSVSPGQTASIT CSGEKLSDKYVHWYQQKPGQSPVMVIYENDRRPSGIPERFSGSNSGNTATLTIS GTQAMDEADYFCQFWDSTNSAVFGGGTQLTVLDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
anti-TRBC2-NKp30 – BIS-2020-6		
SEQ ID NO: 8007	Anti-TRBC 2-0311-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGEGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4686	Anti-TRBC 2-0311-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGEGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 8005	Anti-TRBC 2-0311-LC	DVVMTQSPLSLPVTLGQPASISCRSSKNLVHSNGRTYLQWYQQRPGQSPRLLIY RVSNRFPGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTREPYTFGGGTK VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
SEQ ID NO: 7383/**SEQ ID NO:** 8006	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4684	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
anti-TRBC2-NKp30 – BIS-2020-7		
SEQ ID NO: 8009	Anti-TRBC 2-0314-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGAGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 4687	Anti-TRBC 2-0314-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGAGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 8005	Anti-TRBC 2-0314-LC	DVVMTQSPLSLPVTLGQPASISCRSSKNLVHSNGRTYLQWYQQRPGQSPRLLIY RVSNRFPGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTREPYTFGGGTK VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
SEQ ID NO: 7384 **/SEQ ID NO:** 8698	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSSSETTQPPSVSVSPGQTASIT CSGEKLSDKYVHWYQQKPGQSPVMVIYENDRRPSGIPERFSGSNSGNTATLTIS GTQAMDEADYFCQFWDSTNSAVFGGGTQLTVLDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 8690	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSSSETTQPPSVSVSPGQTASIT CSGEKLSDKYVHWYQQKPGQSPVMVIYENDRRPSGIPERFSGSNSGNTATLTIS GTQAMDEADYFCQFWDSTNSAVFGGGTQLTVLDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE QYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
anti-TRBC2-NKp30 – BIS-2020-8		
SEQ ID NO: 8009	Anti-TRBC 2-0314-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGAGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4687	Anti-TRBC 2-0314-HC	QVQLVQSGAEVKKPGSSVKVSCKASPRGFYGYHMHWVRQAPGQGLEWMGFI NPYNNHIQYNERFRGRVTITSDESTTTAYMELSSLRSEDTAVYYCALGAGKWG DGAYRFFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVS LWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 8005	Anti-TRBC 2-0314-LC	DVVMTQSPLSLPVTLGQPASISCRSSKNLVHSNGRTYLQWYQQRPGQSPRLLIY RVSNRFPGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTREPYTFGGGTK VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
SEQ ID NO: 7383/**SEQ ID**	Nk-p30 scFv	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYI YSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFD YWGQGTMVTVSSGGGGSGGGGSGGGGSGGGGSDSVTTQSPLSLPVTLGQPASI SCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLK ISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIKDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE

15E1_Humanized variant_VL3	QSVTTQPPSASGTPGQRVTISC (**SEQ ID NO:** 6081)	SGEKLSDKYVH (**SEQ ID NO:** 26)	WYQQLPGTAPKMLIY (**SEQ ID NO:** 6078)	ENDRRPS (**SEQ ID NO:** 28)	GVPDRFSGSNSGNSASLAISGLRSEDEADYFC (**SEQ ID NO:** 7338)	QFWDSTNSAV (**SEQ ID NO:** 86)	FGGGTQLTVL (**SEQ ID NO:** 6080)
15E1_Humanized variant_VL4	QSVTTQPPSVSGAPGQRVTISC (**SEQ ID NO:** 6077)	SGEKLSDKYVH (**SEQ ID NO:** 26)	WYQQLPGTAPKMLIY (**SEQ ID NO:** 6078)	ENDRRPS (**SEQ ID NO:** 28)	GVPDRFSGSNSGNSASLAITGLQAEDEADYFC (**SEQ ID NO:** 7339)	QFWDSTNSAV (**SEQ ID NO:** 86)	FGGGTQLTVL (**SEQ ID NO:** 6080)
15E1_Humanized variant_VL5	DSVTTQSPLSLPVTLGQPASISC (**SEQ ID NO:** 7340)	SGEKLSDKYVH (**SEQ ID NO:** 26)	WYQQRPGQSPRMLIY (**SEQ ID NO:** 7341)	ENDRRPS (**SEQ ID NO:** 28)	GVPDRFSGSNSGNDATLKISRVEAEDVGVYFC (**SEQ ID NO:** 7342)	QFWDSTNSAV (**SEQ ID NO:** 86)	FGGGTKVEIK (**SEQ ID NO:** 8685)

Table 23A. Exemplary heavy chain CDRs and FWRs of NKp30-targeting antigen binding domains

Ab ID	VHFWR1	VHCDR1	VHFWR2	VHCDR2	VHFWR3	VHCDR3	VHFWR4
BKM0138	EIQLLESGGGLVQPGGSLRLSCAVSGFS (SEQ ID NO: 301)	ITTTGYHWN (SEQ ID NO: 308)	WVRQAPGKGLEWVG (SEQ ID NO: 8667)	YIYSSGSTSYNPSLKS (SEQ ID NO: 6001)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 8668)	GDWHYFDY (SEQ ID NO: 504)	WGQGTMVTVSS (SEQ ID NO: 24)
BKM0139	EIQLLESGGGLVQPGGSLRLSCAVSGFS (SEQ ID NO: 301)	ITTTGYHWN (SEQ ID NO: 308)	WVRQAPGKGLEWVG (SEQ ID NO: 34)	YIYSSGSTSYNPSLKS (SEQ ID NO: 6001)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 36)	GDWHYFDY (SEQ ID NO: 504)	WGQGTMVTVSS (SEQ ID NO: 304)
BKM0140	EIQLLESGGGLVQPGGSLRLSCAVSGFS (SEQ ID NO: 301)	ITTTGYHWN (SEQ ID NO: 308)	WVRQAPGKGLEWVG (SEQ ID NO: 8676)	YIYSSGSTSYNPSLKS (SEQ ID NO: 6001)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 8677)	GDWHYFDY (SEQ ID NO: 504)	WGQGTMVTVSS (SEQ ID NO: 304)
BKM0141	EIQLLESGGGLVQPGGSLRLSCAVSGFS (SEQ ID NO: 301)	ITTTGYHWN (SEQ ID NO: 308)	WVRQAPGKGLEWVG (SEQ ID NO: 310)	YIYSSGSTSYNPSLKS (SEQ ID NO: 6001)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 316)	GDWHYFDY (SEQ ID NO: 504)	WGQGTMVTVSS (SEQ ID NO: 304)
BKM0142	EIQLLESGGGLVQPGGSLRLSCAVSGFS (SEQ ID NO: 301)	ITTTGYHWN (SEQ ID NO: 308)	WVRQAPGKGLEWVG (SEQ ID NO: 7398)	YIYSSGSTSYAPSLKS (SEQ ID NO: 313)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 316)	GDWHYFDY (SEQ ID NO: 504)	WGQGTMVTVSS (SEQ ID NO: 304)

BKM0143	EIQLLESGGGLVQPGGSLRLSCAVSGFS (SEQ ID NO: 301)	ITTTGYHWN (SEQ ID NO: 308)	WVRQAPGKGLEWVG (SEQ ID NO: 310)	YIYSSGSTSYAPSLKS (SEQ ID NO: 313)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 8702)	GDWHYFDY (SEQ ID NO: 504)	WGQGTMVTVSS (SEQ ID NO: 304)
BKM0144	EIQLLESGGGLVQPGGSLRLSCAVSGFS (SEQ ID NO: 301)	ITTTGYHWN (SEQ ID NO: 308)	WVRQAPGKGLEWVG (SEQ ID NO: 310)	YIYSSGSTSYAPSLKS (SEQ ID NO: 313)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 316)	GDWHYFDY (SEQ ID NO: 504)	WGQGTMVTVSS (SEQ ID NO: 304)
BKM0145	EIQLLESGGGLVQPGGSLRLSCAVSGFS (SEQ ID NO: 301)	ITTTGYHWN (SEQ ID NO: 308)	WVRQAPGKGLEWVG (SEQ ID NO: 310)	YIYSSGSTSYAPSLKS (SEQ ID NO: 313)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 316)	GDWHYFDY (SEQ ID NO: 504)	WGQGTMVTVSS (SEQ ID NO: 304)

Table 23B. Exemplary heavy chain CDRs and FWRs of NKp30-targeting antigen binding domains of Table 23A (According to the ABM numbering scheme)

Ab ID	VHFWR1	VHCDR1	VHFWR2	VHCDR2	VHFWR3	VHCDR3	VHFWR4
BKM0138	EIQLLESGGGLVQPGGSLRLSCAVS (**SEQ ID NO:** 8627)	GFSITTTGYHWN (**SEQ ID NO:** 8628)	WVRQAPGKGLEWVG (**SEQ ID NO: 310**)	YIYSSGSTSYNPSLKS (**SEQ ID NO:** 6001)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 316**)	GDWHYFDY (**SEQ ID NO:** 504)	WGQGTMVTVSS (**SEQ ID NO:** 304)
BKM0139	EIQLLESGGGLVQPGGSLRLSCAVS (**SEQ ID NO:** 8629)	GFSITTTGYHWN (**SEQ ID NO:** 8630)	WVRQAPGKGLEWVG (**SEQ ID NO: 310**)	YIYSSGSTSYNPSLKS (**SEQ ID NO:** 6001)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 316**)	GDWHYFDY (**SEQ ID NO:** 504)	WGQGTMVTVSS (**SEQ ID NO:** 304)
BKM0140	EIQLLESGGGLVQPGGSLRLSCAVS (**SEQ ID NO:** 8631)	GFSITTTGYHWN (**SEQ ID NO:** 8632)	WVRQAPGKGLEWVG (**SEQ ID NO: 310**)	YIYSSGSTSYNPSLKS (**SEQ ID NO:** 6001)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (**SEQ ID NO:** 316)	GDWHYFDY (**SEQ ID NO:** 504)	WGQGTMVTVSS (**SEQ ID NO:** 304)
BKM0141	EIQLLESGGGLVQPGGSLRLSCAVS (**SEQ ID NO:** 8633)	GFSITTTGYHWN (**SEQ ID NO:** 8634)	WVRQAPGKGLEWVG (**SEQ ID NO: 310**)	YIYSSGSTSYNPSLKS (**SEQ ID NO:** 6001)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 316**)	GDWHYFDY (**SEQ ID NO:** 504)	WGQGTMVTVSS (**SEQ ID NO:** 304)
BKM0142	EIQLLESGGGLVQPGGSLRLSCAVS (**SEQ ID NO:** 8635)	GFSITTTGYHWN (**SEQ ID NO:** 8636)	WVRQAPGKGLEWVG (**SEQ ID NO: 310**)	YIYSSGSTSYAPSLKS (**SEQ ID NO:** 313)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 316**)	GDWHYFDY (**SEQ ID NO:** 504)	WGQGTMVTVSS (**SEQ ID NO:** 304)

BKM0143	EIQLLESGGGLVQPGGSLRLSCAVS (**SEQ ID NO:** 8637)	GFSITTTGYHWN (**SEQ ID NO:** 8638)	WVRQAPGKGLEWVG (**SEQ ID NO: 310**)	YIYSSGSTSYAPSLKS (**SEQ ID NO:** 313)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 316**)	GDWHYFDY (**SEQ ID NO:** 504)	WGQGTMVTVSS (**SEQ ID NO:** 304)
BKM0144	EIQLLESGGGLVQPGGSLRLSCAVS (**SEQ ID NO:** 8639)	GFSITTTGYHWN (**SEQ ID NO:** 8640)	WVRQAPGKGLEWVG (**SEQ ID NO: 310**)	YIYSSGSTSYAPSLKS (**SEQ ID NO:** 313)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 316**)	GDWHYFDY (**SEQ ID NO:** 504)	WGQGTMVTVSS (**SEQ ID NO:** 304)
BKM0145	EIQLLESGGGLVQPGGSLRLSCAVS (**SEQ ID NO:** 8641)	GFSITTTGYHWN (**SEQ ID NO:** 8642)	WVRQAPGKGLEWVG (**SEQ ID NO: 310**)	YIYSSGSTSYAPSLKS (**SEQ ID NO:** 313)	RFTISRDTSKNTFYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 316**)	GDWHYFDY (**SEQ ID NO:** 504)	WGQGTMVTVSS (**SEQ ID NO:** 304)

Table 24. Exemplary light chain CDRs and FWRs of NKp30-targeting antigen binding domains

Ab ID	VLFWR1	VLCDR1	VLFWR2	VLCDR2	VLFWR3	VLCDR3	VLFWR4
BKM0138	DSVTTQSPLSLPVTLGQPASISC (SEQ ID NO: 7340)	SGEKLSDKYVH (SEQ ID NO: 26)	WYQQRPGQSPRMLIY (SEQ ID NO: 8670)	ENDRRPS (SEQ ID NO: 28)	GVPDRFSGSNSGNDATLKISRVEAEDVGVYFC (SEQ ID NO: 8672)	QFWDSTASAV (SEQ ID NO: 30)	FGGGTKVEIK (SEQ ID NO: 8685)
BKM0139	DSVTTQSPLSLPVTLGQPASISC (SEQ ID NO: 7340)	SGEKLSDKYVH (SEQ ID NO: 26)	WYQQRPGQSPRMLIY (SEQ ID NO: 300)	ENDRRPS (SEQ ID NO: 28)	GVPDRFSGSNSGNDATLKISRVEAEDVGVYFC (SEQ ID NO: 8694)	QFWASTNSAV (SEQ ID NO: 7395)	FGGGTKVEIK (SEQ ID NO: 8685)
BKM0140	SSETTQPPSVSVSPGQTASITC (SEQ ID NO: 7335)	SGEKLSDKYVH (SEQ ID NO: 26)	WYQQKPGQSPVMVIY (SEQ ID NO: 6106)	ENDRRPS (SEQ ID NO: 28)	GIPERFSGSNSGNTATLTISGTQAMDEADYFC (SEQ ID NO: 8692)	QFWASTNSAV (SEQ ID NO: 8678)	FGGGTQLTVL (SEQ ID NO: 6080)
BKM0141	SSETTQPPSVSVSPGQTASITC (SEQ ID NO: 7335)	SGEKLSDKYVH (SEQ ID NO: 26)	WYQQKPGQSPVMVIY (SEQ ID NO: 6106)	ENDRRPS (SEQ ID NO: 28)	GIPERFSGSNSGNTATLTISGTQAMDEADYFC (SEQ ID NO: 8692)	QFWDSTASAV (SEQ ID NO: 30)	FGGGTQLTVL (SEQ ID NO: 6080)
BKM0142	DSVTTQSPLSLPVTLGQPASISC (SEQ ID NO: 7340)	SGEKLSDKYVH (SEQ ID NO: 26)	WYQQRPGQSPRMLIY (SEQ ID NO: 300)	ENDRRPS (SEQ ID NO: 28)	GVPDRFSGSNSGNDATLKISRVEAEDVGVYFC (SEQ ID NO: 305)	QFWDSTNSAV (SEQ ID NO: 86)	FGGGTKVEIK (SEQ ID NO: 8685)

BKM0143	SSETTQPP SVSVSPG QTASITC (SEQ ID NO: 7335)	SGEKLSD KYVH (SEQ ID NO: 26)	WYQQKP GQSPVMV IY (SEQ ID NO: 6106)	ENDRRPS (SEQ ID NO: 28)	GIPERFSG SNSGNTA TLTISGTQ AMDEAD YFC (SEQ ID NO: 8692)	QFWDSTN SAV (SEQ ID NO: 86)	FGGGTQL TVL (SEQ ID NO: 6080)
BKM0144	DSVTTQS PLSLPVTL GQPASISC (SEQ ID NO: 7340)	SGEKLSD KYVH (SEQ ID NO: 26)	WYQQRP GQSPRML IY (SEQ ID NO: 300)	ENDRRPS (SEQ ID NO: 28)	GVPDRFS GSNSGND ATLKISRV EAEDVGV YFC (SEQ ID NO: 305)	QFWASTA SAV (SEQ ID NO: 330)	FGGGTKV EIK (SEQ ID NO: 8685)
BKM0145	SSETTQPP SVSVSPG QTASITC (SEQ ID NO: 7335)	SGEKLSD KYVH (SEQ ID NO: 26)	WYQQKP GQSPVMV IY (SEQ ID NO: 6106)	ENDRRPS (SEQ ID NO: 28)	GIPERFSG SNSGNTA TLTISGTQ AMDEAD YFC (SEQ ID NO: 8692)	QFWASTA SAV (SEQ ID NO: 330)	FGGGTQL TVL (SEQ ID NO: 6080)

Table 25. Exemplary variable regions of NKp30-targeting antigen binding domains

SEQ ID NO	Ab ID	Description	Sequence
SEQ ID NO: 6121	9G1-HC	9G1 heavy chain variable region	QIQLQESGPGLVKPSQSLSLTCSVTGFSINTGGYHWN WIRQFPGKKLEWMGYIYSSGSTSYNPSLKSRISITRD TSKNQFFLQLNSVTTEDTATYYCARGNWHYFDFWG QGTMVTVSS
SEQ ID NO: 6122	15H6-HC	15H6 heavy chain variable region	QIQLQESGPGLVKPSQSLSLTCSVTGFSINTGGYHWN WIRQFPGKKLEWMGYIYSSGTTRYNPSLKSRISITRD TSKNQFFLQLNSVTPEDTATYYCTRGNWHYFDYWG QGTLVAVSS
SEQ ID NO: 6123	9G1-HC_1	9G1 heavy chain variable region humanized variant 1	QIQLQESGPGLVKPSETLSLTCTVSGFSINTGGYHWN WIRQPAGKGLEWIGYIYSSGSTSYNPSLKSRVTMSRD TSKNQFSLKLSSVTAADTAVYYCARGNWHYFDFWG QGTMVTVSS
SEQ ID NO: 6124	9G1-HC_2	9G1 heavy chain variable region humanized variant 2	QIQLQESGPGLVKPSQTLSLTCTVSGFSINTGGYHWN WIRQHPGKGLEWIGYIYSSGSTSYNPSLKSLVTISRDT SKNQFSLKLSSVTAADTAVYYCARGNWHYFDFWG QGTMVTVSS
SEQ ID NO: 6125	9G1-HC_3	9G1 heavy chain variable region humanized variant 3	EIQLLESGGGLVQPGGSLRLSCAVSGFSINTGGYHW NWVRQAPGKGLEWVGYIYSSGSTSYNPSLKSRFTIS RDTSKNTFYLQMNSLRAEDTAVYYCARGNWHYFDF WGQGTMVTVSS
SEQ ID NO: 6126	9G1-HC_4	9G1 heavy chain variable region humanized variant 4	QIQLVQSGAEVKKPGSSVKVSCKVSGFSINTGGYHW NWVRQAPGQGLEWMGYIYSSGSTSYNPSLKSRVTIT RDTSTNTFYMELSSLRSEDTAVYYCARGNWHYFDF WGQGTMVTVSS
SEQ ID NO: 6127	9G1-HC_5	9G1 heavy chain variable region humanized variant 5	EIQLVESGGGLVQPGGSLRLSCAVSGFSINTGGYHW NWVRQAPGKGLEWVGYIYSSGSTSYNPSLKSRFTIS RDTAKNSFYLQMNSLRAEDTAVYYCARGNWHYFD FWGQGTMVTVSS
SEQ ID NO: 6128	9G1-HC_6	9G1 heavy chain variable region humanized variant 6	QIQLVQSGAEVKKPGASVKVSCKVSGFSINTGGYHW NWVRQAPGQGLEWMGYIYSSGSTSYNPSLKSRVTM TRDTSTNTFYMELSSLRSEDTAVYYCARGNWHYFD FWGQGTMVTVSS
SEQ ID NO: 6129	15H6-HC_1	15H6 heavy chain variable region humanized variant 1	QIQLQESGPGLVKPSQTLSLTCTVSGFSINTGGYHWN WIRQHPGKGLEWIGYIYSSGTTRYNPSLKSLVTISRD TSKNQFSLKLSSVTAADTAVYYCARGNWHYFDYW GQGTLVTVSS

SEQ ID NO: 7307	15E1_Humanized variant_VL3	15E1 light chain variable region humanized variant 3	QSVTTQPPSASGTPGQRVTISCSGEKLSDKYVHWYQQLPGTAPKMLIYENDRRPSGVPDRFSGSNSGNSASLAISGLRSEDEADYFCQFWDSTNSAVFGGGTQLTVL
SEQ ID NO: 7308	15E1_Humanized variant_VL4	15E1 light chain variable region humanized variant 4	QSVTTQPPSVSGAPGQRVTISCSGEKLSDKYVHWYQQLPGTAPKMLIYENDRRPSGVPDRFSGSNSGNSASLAITGLQAEDEADYFCQFWDSTNSAVFGGGTQLTVL
SEQ ID NO: 13	15E1_Humanized variant_VL5 (BJM0411 VL)	15E1 light chain variable region humanized variant 5	DSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLKISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIK
SEQ ID NO: 8030	BKM0138 VH	BKM0138 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYIYSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFDYWGQGTMVTVSS
SEQ ID NO: 8030	BKM0139 VH	BKM0139 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYIYSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFDYWGQGTMVTVSS
SEQ ID NO: 8030	BKM0140 VH	BKM0140 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYIYSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFDYWGQGTMVTVSS
SEQ ID NO: 8030	BKM0141 VH	BKM0141 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYIYSSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFDYWGQGTMVTVSS
SEQ ID NO: 7302	BKM0142 VH	BKM0142 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYIYSSGSTSYAPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFDYWGQGTMVTVSS
SEQ ID NO: 7302	BKM0143 VH	BKM0143 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYIYSSGSTSYAPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFDYWGQGTMVTVSS
SEQ ID NO: 7302	BKM0144 VH	BKM0144 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYIYSSGSTSYAPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFDYWGQGTMVTVSS
SEQ ID NO: 7302	BKM0145 VH	BKM0145 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHWNWVRQAPGKGLEWVGYIYSSGSTSYAPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFDYWGQGTMVTVSS
SEQ ID NO: 8691	BKM0138 VL	BKM0138 light chain variable region	DSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLKISRVEAEDVGVYFCQFWDSTASAVFGGGTKVEIK
SEQ ID NO: 380	BKM0139 VL	BKM0139 light chain variable region	DSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLKISRVEAEDVGVYFCQFWASTNSAVFGGGTKVEIK
SEQ ID NO: 381	BKM0140 VL	BKM0140 light chain variable region	SSETTQPPSVSVSPGQTASITCSGEKLSDKYVHWYQQKPGQSPVMVIYENDRRPSGIPERFSGSNSGNTATLTISGTQAMDEADYFCQFWASTNSAVFGGGTQLTVL
SEQ ID NO: 382	BKM0141 VL	BKM0141 light chain variable region	SSETTQPPSVSVSPGQTASITCSGEKLSDKYVHWYQQKPGQSPVMVIYENDRRPSGIPERFSGSNSGNTATLTISGTQAMDEADYFCQFWDSTASAVFGGGTQLTVL
SEQ ID NO: 13	BKM0142 VL	BKM0142 light chain variable region	DSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLKISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIK

SEQ ID NO: 89	VH+VL	QVQLVQSGAEVKKPGSSVKVSCKASGHDFKLTYIHWVRQAP GQGLEWMGRISAGSGNVKYNEKFKGRVTITADTSTSTAYME LSSLRSEDTAVYYCAGSYYSYDVLDYWGQGTTVTVSSGGGG SGGGGSGGGGSGGGGSDIQMTQSPSFLSASVGDRVTITCKAS QNVDNRVAWYQQKPGKAPKALIYSSSHRYKGVPSRFSGSGS GTEFTLTISSLQPEDFATYFCQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 90	VL	DIQMTQSPSFLSASVGDRVTITCKASQNVDNRVAWYQQKPG KAPKALIYSSSHRYKGVPSRFSGSGSGTEFTLTISSLQPEDFAT YFCQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 91	VH	QVQLVQSGAEVKKPGSSVKVSCKASGHDFKLTYIHWVRQAP GQGLEWMGRISAGSGNVKYNEKFKGRVTITADTSTSTAYME LSSLRSEDTAVYYCAGSYYSYDVLDYWGQGTTVTVSS
A-H.7		
SEQ ID NO: 92	VH+VL	QVQLVQSGAEVKKPGSSVKVSCKASGTDFKLTYIHWVRQAP GQGLEWMGRIFPGSGNVKYNEKFKGRVTITADTSTSTAYME LSSLRSEDTAVYYCAGSYYSYDVLDYWGQGTTVTVSSGGGG SGGGGSGGGGSGGGGSDIQMTQSPSFLSASVGDRVTITCKAS QNVENKVAWHQQKPGKAPKALIYSSSHRYKGVPSRFSGSGS GTEFTLTISSLQPEDFATYFCQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 93	VL	DIQMTQSPSFLSASVGDRVTITCKASQNVENKVAWHQQKPG KAPKALIYSSSHRYKGVPSRFSGSGSGTEFTLTISSLQPEDFAT YFCQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 94	VH	QVQLVQSGAEVKKPGSSVKVSCKASGTDFKLTYIHWVRQAP GQGLEWMGRIFPGSGNVKYNEKFKGRVTITADTSTSTAYME LSSLRSEDTAVYYCAGSYYSYDVLDYWGQGTTVTVSS
A-H.8		
SEQ ID NO: 95	VH+VL	QVQLVQSGAEVKKPGSSVKVSCKASGTDFDKIYIHWVRQAP GQGLEWMGRIFAGSGNTKYNEKFKGRVTITADTSTSTAYME LSSLRSEDTAVYYCAGSYYSYDVLDYWGQGTTVTVSSGGGG SGGGGSGGGGSGGGGSDIQMTQSPSFLSASVGDRVTITCKAS QNVDDRVAWYQQKPGKAPKALIYSSSHRYKGVPSRFSGSGS GTEFTLTISSLQPEDFATYFCQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 96	VL	DIQMTQSPSFLSASVGDRVTITCKASQNVDDRVAWYQQKPG KAPKALIYSSSHRYKGVPSRFSGSGSGTEFTLTISSLQPEDFAT YFCQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 97	VH	QVQLVQSGAEVKKPGSSVKVSCKASGTDFDKIYIHWVRQAP GQGLEWMGRIFAGSGNTKYNEKFKGRVTITADTSTSTAYME LSSLRSEDTAVYYCAGSYYSYDVLDYWGQGTTVTVSS
A-H.9		
SEQ ID NO: 98	VH+VL	QVQLVQSGAEVKKPGSSVKVSCKASGHDFDKFYIHWVRQAP GQGLEWMGRVSAGSGNVKYNEKFKGRVTITADTSTSTAYME LSSLRSEDTAVYYCAGSYYSYDVLDYWGQGTTVTVSSGGGG SGGGGSGGGGSGGGGSDIQMTQSPSFLSASVGDRVTITCKAS QNVGNRVAWYQQKPGKAPKALIYSSSHRYSGVPSRFSGSGS GTEFTLTISSLQPEDFATYFCQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 99	VL	DIQMTQSPSFLSASVGDRVTITCKASQNVGNRVAWYQQKPG KAPKALIYSSSHRYSGVPSRFSGSGSGTEFTLTISSLQPEDFAT YFCQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 100	VH	QVQLVQSGAEVKKPGSSVKVSCKASGHDFDKFYIHWVRQAP GQGLEWMGRVSAGSGNVKYNEKFKGRVTITADTSTSTAYME LSSLRSEDTAVYYCAGSYYSYDVLDYWGQGTTVTVSS
A-H.10		
SEQ ID NO: 101	VH+VL	QVQLVQSGAEVKKPGSSVKVSCKASGHDFDKFYIHWVRQAP GQGLEWMGRIFAGSGNVKYNEKFKGRVTITADTSTSTAYME LSSLRSEDTAVYYCAGSYYSYDVLDYWGQGTTVTVSSGGGG SGGGGSGGGGSGGGGSDIQMTQSPSFLSASVGDRVTITCKAS QNVGDRVAWYQQKPGKAPKALIYSSSHRYKGVPSRFSGSGS GTEFTLTISSLQPEDFATYFCQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 102	VL	DIQMTQSPSFLSASVGDRVTITCKASQNVGDRVAWYQQKPG KAPKALIYSSSHRYKGVPSRFSGSGSGTEFTLTISSLQPEDFAT YFCQQFKSYPLTFGQGTKLEIK

SEQ ID NO: 19	HC CDR3 (Combined)	RGEGAMDY
SEQ ID NO: 25	VH	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNFGMHWVRQA PGKGLEWVSYISSGSSTIYYADTLKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARRGEGAMDYWGQGTTVTVSS
SEQ ID NO: 32	DNA VH	GAGGTGCAGCTGGTTGAATCTGGCGGAGGATTGGTTCAG CCTGGCGGCTCTCTGAGACTGTCTTGTGCCGCTTCTGGCT TCACCTTCTCCAACTTCGGCATGCACTGGGTCCGACAGG CCCCTGGAAAAGGACTGGAATGGGTGTCCTACATCTCCT CCGGCTCCTCCACCATCTACTACGCTGACACCCTGAAGG GCAGATTCACCATCAGCCGGGACAACTCCAAGAACACCC TGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCG CCGTGTACTACTGTGCTAGAAGAGGCGAGGGCGCCATGG ATTATTGGGGCCAGGGAACCACAGTGACCGTGTCTAGC
Antibody B-H.1C HC-3		
SEQ ID NO: 17	HC CDR1 (Combined)	GFTFSNFGMH
SEQ ID NO: 18	HC CDR2 (Combined)	YISSGSSTIYYADTLKG
SEQ ID NO: 19	HC CDR3 (Combined)	RGEGAMDY
SEQ ID NO: 23	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGMHWVRQ APGKGLEWVAYISSGSSTIYYADTLKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARRGEGAMDYWGQGTTVTVSS
SEQ ID NO: 33	DNA VH	CAGGTGCAGCTGGTGGAATCTGGTGGCGGAGTTGTGCAG CCTGGCAGATCCCTGAGACTGTCTTGTGCCGCCTCTGGCT TCACCTTCTCCAACTTCGGCATGCACTGGGTCCGACAGG CCCCTGGAAAAGGATTGGAGTGGGTCGCCTACATCTCCT CCGGCTCCTCCACCATCTACTACGCTGACACCCTGAAGG GCAGATTCACCATCAGCCGGGACAACTCCAAGAACACCC TGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCG CCGTGTACTACTGTGCTAGAAGAGGCGAGGGCGCCATGG ATTATTGGGGCCAGGGAACCACAGTGACCGTGTCTAGC
Antibody B-H.1D LC-1		
SEQ ID NO: 20	LC CDR1 (Combined)	RASSSVNYIY
SEQ ID NO: 21	LC CDR2 (Combined)	YTSNLAP
SEQ ID NO: 22	LC CDR3(Combined)	QQFTSSPFT
SEQ ID NO: 8669	VL	DNQLTQSPSFLSASVGDRVTITCRASSSVNYIYWYQQKPGK APKLLIYYTSNLAPGVPSRFSGSGSGNEYTLTISSLQPEDFAT YYCQQFTSSPFTFGQGTKLEIK
SEQ ID NO: 8674	DNA VL	GATAACCAGCTGACCCAGTCTCCTAGCTTCCTGTCTGCCT CTGTGGGCGACAGAGTGACAATTACCTGCCGGGCCTCCT CCTCCGTGAACTACATCTACTGGTATCAGCAGAAGCCCG GCAAGGCCCCTAAGCTGCTGATCTACTACACCTCCAATC TGGCCCCTGGCGTGCCCTCTAGATTTTCCGGATCTGGCTC CGGCAACGAGTATACCCTGACAATCTCCAGCCTGCAGCC TGAGGACTTCGCCACCTACTACTGCCAGCAGTTCACCTC CTCTCCATTCACCTTTGGCCAGGGCACCAAGCTGGAAAT CAAA
Antibody B-H.1E LC-2		
SEQ ID NO: 20	LC CDR1 (Combined)	RASSSVNYIY
SEQ ID NO: 21	LC CDR2 (Combined)	YTSNLAP
SEQ ID NO: 22	LC CDR3(Combined)	QQFTSSPFT
SEQ ID NO: 27	VL	DNQLTQSPSSLSASVGDRVTITCRASSSVNYIYWYQQKPGK APKLLIYYTSNLAPGVPSRFSGSGSGNDYTLTISSLQPEDFA TYYCQQFTSSPFTFGQGTKLEIK
SEQ ID NO: 35	DNA VL	ATAACCAGCTGACCCAGTCTCCTTCCAGCCTGTCTGCTTC TGTGGGCGACAGAGTGACAATTACCTGCCGGGCCTCCTC CTCCGTGAACTACATCTACTGGTATCAGCAGAAGCCCGG CAAGGCCCCTAAGCTGCTGATCTACTACACCTCCAATCT GGCCCCTGGCGTGCCCTCTAGATTTTCCGGATCTGGCTCC GGCAACGACTATACCCTGACAATCTCCAGCCTGCAGCCT GAGGACTTCGCCACCTACTACTGCCAGCAGTTCACCTCC TCTCCATTCACCTTTGGCCAGGGCACCAAGCTGGAAATC AAA
Antibody B-H.1F LC-3		

SEQ ID NO: 20	LC CDR1 (Combined)	RASSSVNYIY
SEQ ID NO: 21	LC CDR2 (Combined)	YTSNLAP
SEQ ID NO: 22	LC CDR3(Combined)	QQFTSSPFT
SEQ ID NO: 8671	VL	ENVLTQSPATLSVSPGERATLSCRASSSVNYIYWYQQKPGQ APRLLIYYTSNLAPGIPARFSGSGSGNEYTLTISSLQSEDFAV YYCQQFTSSPFTFGQGTKLEIK
SEQ ID NO: 8675	DNA VL	GAGAATGTGCTGACCCAGTCTCCTGCCACACTGTCTGTT AGCCCTGGCGAGAGAGCTACCCTGAGCTGCAGAGCCTCT TCCTCCGTGAACTACATCTACTGGTATCAGCAGAAGCCC GGCCAGGCTCCTAGACTGCTGATCTACTACACCTCCAAT CTGGCCCCTGGCATCCCTGCCAGATTTTCCGGATCTGGCT CCGGCAACGAGTATACCCTGACCATCTCCAGCCTGCAGT CCGAGGACTTTGCTGTGTACTATTGCCAGCAGTTCACAA GCAGCCCTTTCACCTTTGGCCAGGGCACCAAGCTGGAAA TCAAA
Antibody B-H.1G LC-4		
SEQ ID NO: 20	LC CDR1 (Combined)	RASSSVNYIY
SEQ ID NO: 21	LC CDR2 (Combined)	YTSNLAP
SEQ ID NO: 22	LC CDR3(Combined)	QQFTSSPFT
SEQ ID NO: 29	VL	QNVLTQPPSASGTPGQRVTISCRASSSVNYIYWYQQLPGTA PKLLIYYTSNLAPGVPDRFSGSGSGNSYSLAISGLRSEDEAD YYCQQFTSSPFTFGTGTKVTVL
SEQ ID NO: 37	DNA VL	CAGAATGTGCTGACCCAACCTCCTTCCGCCTCTGGCACA CCTGGACAGAGAGTGACAATCTCCTGCCGGGCCTCCTCC TCCGTGAACTACATCTACTGGTATCAGCAGCTGCCCGGC ACCGCTCCTAAACTGCTGATCTACTACACCTCCAATCTG GCCCCTGGCGTGCCCGATAGATTTTCCGGATCTGGCTCC GGCAACTCCTACAGCCTGGCTATCTCTGGCCTGAGATCT GAGGACGAGGCCGACTACTACTGCCAGCAGTTCACCTCC TCTCCATTCACCTTTGGCACCGGCACCAAAGTGACAGTT CTT
Antibody B-H.1H LC-5		
SEQ ID NO: 20	LC CDR1 (Combined)	RASSSVNYIY
SEQ ID NO: 21	LC CDR2 (Combined)	YTSNLAP
SEQ ID NO: 22	LC CDR3(Combined)	QQFTSSPFT
SEQ ID NO: 8673	VL	SNELTQPPSVSVSPGQTARITCRASSSVNYIYWYQQKSGQA PVLVIYYTSNLAPGIPERFSGSGSGNMYTLTISGAQVEDEAD YYCQQFTSSPFTFGTGTKVTVL
SEQ ID NO: 38	DNA VL	TCTAATGAGCTGACCCAGCCTCCTTCCGTGTCCGTGTCTC CTGGACAGACCGCCAGAATTACCTGCCGGGCCTCCTCCT CCGTGAACTACATCTACTGGTATCAGCAGAAGTCCGGCC AGGCTCCTGTGCTCGTGATCTACTACACCTCCAATCTGGC CCCTGGCATCCCTGAGAGATTCTCCGGATCTGGCTCCGG CAACATGTACACCCTGACCATCTCTGGCGCCCAGGTGGA AGATGAGGCCGACTACTACTGCCAGCAGTTCACCTCCTC TCCATTCACCTTTGGCACCGGCACCAAAGTGACAGTTCT T
Antibody B-H.1		
SEQ ID NO: 3280	Chain 1: Fc only	METDTLLLWVLLLWVPGSTGDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTK NQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNRFTQKS LSLSPGK
SEQ ID NO: 4693	Chain 1: Fc only	METDTLLLWVLLLWVPGSTGDKTHTCPPCPAPELLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTK NQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNRFTQKS LSLSP

SEQ ID NO: 505	VH (BM130)	EIQLLESGGGLVQPGGSLRLSCAVSGFSIIRVGYHWNWVRQAPGKGLEWVGYIHRSGSTSYNPSLKSRFTISRDTSKNTFYLQMNSLRAEDTAVYYCARGDWHYFDYWGQGTMVTVSS
SEQ ID NO: 13	VL (BM130)	DSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVHWYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGNDATLKISRVEAEDVGVYFCQFWDSTNSAVFGGGTKVEIK
SEQ ID NO: 3649	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 3451	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 506	Heavy chain hinge - Fc region (CH2-CH3) Hole	EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 507	Heavy chain hinge - Fc region (CH2-CH3) Hole	EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 3644	Light chain constant region	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 3472	IL-15Rαsushi (AA 31-108 of IL-15Ralpha)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPS
SEQ ID NO: 3473	Linker	GGSGGGGSGGGSGGGGSGGG
SEQ ID NO: 3670	AA 49-162 of IL-15	NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVAMFINTS
SEQ ID NO: 3671	IL-15Rαsushi-IL-15 (AA 31-108 of IL-15Ralpha-Linker- AA 31-108 of IL-15Ralpha)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSGGSGGGGSGGGSGGGGSGGGNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVAMFINTS
SEQ ID NO: 3308	Linker	GGGGSGGGGS
SEQ ID NO: 3648	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 8686	Heavy chain hinge - Fc region (CH2-CH3) knob	KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP

SEQ ID NO: 3355	LC CDR2	SSSHRYK
SEQ ID NO: 3356	LC CDR3	QQFKSYPLT
SEQ ID NO: 1346	VH	QVQLVQSGAEVKKPGSSVKVSCKASGHDFRLTYIHWVRQAPG QGLEWMGRVSAGSGNVKYNEKFKGRVTITADTSTSTAYMELS SLRSEDTAVYYCAVSYYSYDVLDYWGQGTTVTVSS
SEQ ID NO: 1349	VL	DIQMTQSPSFLSASVGDRVTITCKASQNVADRVVWHQQKPGK APKALIYSSSHRYKGVPSRFSGSGSGTEFTLTISSLQPEDFATYF CQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 3649	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 3452	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 3447	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
SEQ ID NO: 511	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSP
SEQ ID NO: 3644	Light chain constant region	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 3472	IL-15Rαsushi (AA 31-108 of IL-15Ralpha)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTE CVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPS
SEQ ID NO: 3473	Linker	GGSGGGGSGGGSGGGGSGGG
SEQ ID NO: 3673	AA 49-162 of IL-15	NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELQVISLESGDASIHDTVEQLIILANNSLSSNGNVTESGCKEC EELEEKNIKEFLQSFVHIVQMFINTS
SEQ ID NO: 8689	IL-15Rαsushi-IL-15 (AA 31-108 of IL-15Ralpha-Linker- AA 31-108 of IL-15Ralpha)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTE CVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSGGSGGGGS GGGSGGGGSGGGNWVNVISDLKKIEDLIQSMHIDATLYTESDV HPSCKVTAMKCFLLELQVISLESGDASIHDTVEQLIILANNSLSS NGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS
SEQ ID NO: 3308	Linker	GGGGSGGGGS
SEQ ID NO: 3648	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
SEQ ID NO: 508	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN

SEQ ID NO: 1346	VH	QVQLVQSGAEVKKPGSSVKVSCKASGHDFRLTYIHWVRQAPG QGLEWMGRVSAGSGNVKYNEKFKGRVTITADTSTSTAYMELS SLRSEDTAVYYCAVSYYSYDVLDYWGQGTTVTVSS
SEQ ID NO: 3475	VL	DIQMTQSPSFLSASVGDRVTITCKASQNVADRVVWHQQKPGK APKALIYAASYLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYF CQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 3649	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 3452	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 3447	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
SEQ ID NO: 511	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSP
SEQ ID NO: 3644	Light chain constant region	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 3472	IL-15Rαsushi (AA 31-108 of IL-15Ralpha)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTE CVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPS
SEQ ID NO: 3473	Linker	GGSGGGGSGGGSGGGGSGGG
SEQ ID NO: 3673	AA 49-162 of IL-15	NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELQVISLESGDASIHDTVEQLIILANNSLSSNGNVTESGCKEC EELEEKNIKEFLQSFVHIVQMFINTS
SEQ ID NO: 8689	IL-15Rαsushi-IL-15 (AA 31-108 of IL-15Ralpha-Linker- AA 31-108 of IL-15Ralpha)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTE CVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSGGSGGGGS GGGSGGGGSGGGNWVNVISDLKKIEDLIQSMHIDATLYTESDV HPSCKVTAMKCFLLELQVISLESGDASIHDTVEQLIILANNSLSS NGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS
SEQ ID NO: 3308	Linker	GGGGSGGGGS
SEQ ID NO: 3648	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
SEQ ID NO: 508	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSP
BMM0357		

SEQ ID NO: 3476	VL	DIQMTQSPSFLSASVGDRVTITCKASQNVADRVVWHQQKPGK APKALIFAASYLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYF CQQFKSYPLTFGQGTKLEIK
SEQ ID NO: 3649	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 3452	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 3447	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
SEQ ID NO: 511	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSP
SEQ ID NO: 3644	Light chain constant region	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 3472	IL-15Rαsushi (AA 31-108 of IL-15Ralpha)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTE CVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPS
SEQ ID NO: 3473	Linker	GGSGGGGSGGGSGGGGSGGG
SEQ ID NO: 3673	AA 49-162 of IL-15	NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELQVISLESGDASIHDTVEQLIILANNSLSSNGNVTESGCKEC EELEEKNIKEFLQSFVHIVQMFINTS
SEQ ID NO: 8689	IL-15Rαsushi-IL-15 (AA 31-108 of IL-15Ralpha-Linker- AA 31-108 of IL-15Ralpha)	ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTE CVLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSGGSGGGGS GGGSGGGGSGGGNWVNVISDLKKIEDLIQSMHIDATLYTESDV HPSCKVTAMKCFLLELQVISLESGDASIHDTVEQLIILANNSLSS NGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS
SEQ ID NO: 3308	Linker	GGGGSGGGGS
SEQ ID NO: 3648	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
SEQ ID NO: 508	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSP

SEQ ID NO: 3448	VH	QVQLVQSGAEVKKPGASVKVSCKASGFNIKSAYMHWVRQAP GQEPGCMGRIDPATGKTKYAPKFQARVTMTADTSINTAYTEL SSLRSEDTATYYCARSLNWDYGLDYWGQGTLVTVSS
SEQ ID NO: 3449	VL	EIVLTQSPATLSLSPGERATLSCRASKSVSILGTHLIHWYQQKP GLAPRLLIYAASNLESGIPDRFSGSGSETDFTLTISRLEPEDFAV YFCQQSIEDPWTFGGGTKVEIK
SEQ ID NO: 3649	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 8687	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSP
SEQ ID NO: 3447	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
SEQ ID NO: 511	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSP
SEQ ID NO: 3644	Light chain constant region	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 2270	IL-2 C125A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFK FYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLI SNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIIST LT
SEQ ID NO: 3308	Linker	GGGGSGGGGS
SEQ ID NO: 3648	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
SEQ ID NO: 508	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSP
BLM0276, also referred to as BJ1324, BJ1330 Binds to human TCRVβ 20-1		
SEQ ID NO: 3328	Heavy chain (VH- CH)	QVQLVQSGAEVKKPGASVKVSCKASGFNIKSAYMHWVRQA PGQGLEWMGRIDPATGKTKYAPKFQARVTMTADTSTNTAY MELSSLRSEDTAVYYCARSLNWDYGLDYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP

		APIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4711	Heavy chain (VH- CH)	QVQLVQSGAEVKKPGASVKVSCKASGFNIKSAYMHWVRQA PGQGLEWMGRIDPATGKTKYAPKFQARVTMTADTSTNTAY MELSSLRSEDTAVYYCARSLNWDYGLDYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 3329	Light chain (VL-CL)	EIVLTQSPGTLSLSPGERATLSCRASKSVSILGTHLIHWYQQKP GQAPRLLIYAASNLESGIPDRFSGSGSETDFTLTISRLEPEDFA VYFCQQSIEDPWTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKS GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC
SEQ ID NO: 3340	IL-2 C125A - Heavy Chain Constant Domain (Fc Region)	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTF KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRD LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSII STLTGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4706	IL-2 C125A - Heavy Chain Constant Domain (Fc Region)	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTF KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRD LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSII STLTGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 3321	HC CDR1	GFNIKSAYMH
SEQ ID NO: 3322	HC CDR2	RIDPATGKTKYAPKFQA
SEQ ID NO: 3323	HC CDR3	SLNWDYGLDY
SEQ ID NO: 3324	LC CDR1	RASKSVSILGTHLIH
SEQ ID NO: 3325	LC CDR2	AASNLES
SEQ ID NO: 3326	LC CDR3	QQSIEDPWT
SEQ ID NO: 3450	VH	QVQLVQSGAEVKKPGASVKVSCKASGFNIKSAYMHWVRQAP GQGLEWMGRIDPATGKTKYAPKFQARVTMTADTSTNTAYME LSSLRSEDTAVYYCARSLNWDYGLDYWGQGTLVTVSS
SEQ ID NO: 8688	VL	EIVLTQSPGTLSLSPGERATLSCRASKSVSILGTHLIHWYQQKP GQAPRLLIYAASNLESGIPDRFSGSGSETDFTLTISRLEPEDFAV YFCQQSIEDPWTFGGGTKVEIK
SEQ ID NO: 3649	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 3451	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT

		KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 3447	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
SEQ ID NO: 511	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSP
SEQ ID NO: 3644	Light chain constant region	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 2270	IL-2 C125A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFK FYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLI SNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIIST LT
SEQ ID NO: 3308	Linker	GGGGSGGGGS
SEQ ID NO: 3648	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
SEQ ID NO: 508	Heavy chain hinge - Fc region (CH2-CH3) knob	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSP
BLM0000		
SEQ ID NO: 3328	Heavy chain (VH- CH)	QVQLVQSGAEVKKPGASVKVSCKASGFNIKSAYMHWVRQA PGQGLEWMGRIDPATGKTKYAPKFQARVTMTADTSTNTAY MELSSLRSEDTAVYYCARSLNWDYGLDYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 4711	Heavy chain (VH- CH)	QVQLVQSGAEVKKPGASVKVSCKASGFNIKSAYMHWVRQA PGQGLEWMGRIDPATGKTKYAPKFQARVTMTADTSTNTAY MELSSLRSEDTAVYYCARSLNWDYGLDYWGQGTLVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 3329	Light chain (VL-CL)	EIVLTQSPGTLSLSPGERATLSCRASKSVSILGTHLIHWYQQKP GQAPRLLIYAASNLESGIPDRFSGSGSETDFTLTISRLEPEDFA VYFCQQSIEDPWTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKS

		GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC
SEQ ID NO: 8703	IL-2 C125A - Heavy Chain Constant Domain (Fc Region)	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTF KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRD LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSII STLTGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 3350	IL-2 C125A - Heavy Chain Constant Domain (Fc Region)	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTF KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRD LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSII STLTGGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTISKAKGQPREPQVYTLPPCREEMTKNQVSLWCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 3321	HC CDR1	GFNIKSAYMH
SEQ ID NO: 3322	HC CDR2	RIDPATGKTKYAPKFQA
SEQ ID NO: 3323	HC CDR3	SLNWDYGLDY
SEQ ID NO: 3324	LC CDR1	RASKSVSILGTHLIH
SEQ ID NO: 3325	LC CDR2	AASNLES
SEQ ID NO: 3326	LC CDR3	QQSIEDPWT
SEQ ID NO: 3450	VH	QVQLVQSGAEVKKPGASVKVSCKASGFNIKSAYMHWVRQAP GQGLEWMGRIDPATGKTKYAPKFQARVTMTADTSTNTAYME LSSLRSEDTAVYYCARSLNWDYGLDYWGQGTLVTVSS
SEQ ID NO: 8688	VL	EIVLTQSPGTLSLSPGERATLSCRASKSVSILGTHLIHWYQQKP GQAPRLLIYAASNLESGIPDRFSGSGSETDFTLTISRLEPEDFAV YFCQQSIEDPWTFGGGTKVEIK
SEQ ID NO: 3649	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 3451	Heavy chain constant region (CH1-CH2-CH3) Hole	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVCTLPPSREEMTKNQVSLSCAVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP
SEQ ID NO: 3447	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
SEQ ID NO: 511	Heavy chain hinge - Fc region (CH2-CH3) Hole	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSP

CLAIMS

WHAT IS CLAIMED IS;

1. A composition comprising an agent that comprises an antigen binding domain that binds to NKp30, wherein the antigen binding domain comprises:
   (a) a heavy chain variable region (VH) comprising a heavy chain complementarity determining region 1 (VHCDR1) comprising the sequence of GFSIIRVGYHWN (SEQ ID NO: 502), a heavy chain complementarity determining region 2 (VHCDR2) comprising the sequence of YIHRSGSTSYNPSLKS (SEQ ID NO: 503), and a heavy chain complementarity determining region 3 (VHCDR3) comprising the sequence of GDWHYFDY (SEQ ID NO: 504), and
   (b) a light chain variable region (VL) comprising a light chain complementarity determining region 1 (VLCDR1) comprising the sequence of SGEKLSDKYVH (SEQ ID NO: 26), a light chain complementarity determining region 2 (VLCDR2) comprising the sequence of ENDRRPS (SEQ ID NO: 28), and a light chain complementarity determining region 3 (VLCDR3) comprising the sequence of QFWDSTNSAV (SEQ ID NO: 86).
2. The composition of claim 1, wherein the VH comprises the sequence of SEQ ID NO: 505.
3. The composition of claim 1 or 2, wherein the VL comprises the sequence of SEQ ID NO: 13.
4. The composition of any one of claims 1-3, wherein the agent further comprises at least one cytokine molecule or a functional fragment or variant thereof.
5. The composition of claim 4, wherein the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-2 or a functional fragment or variant thereof, IL-7 or a functional fragment or variant thereof, IL-12 or a functional fragment or variant thereof, IL-15 or a functional fragment or variant thereof, IL-18 or a functional fragment or variant thereof, IL-21 or a functional fragment or variant thereof, interferon gamma or a functional fragment or variant thereof, or any combination thereof.
6. The composition of claim 4 or 5, wherein the at least one cytokine molecule or a functional fragment or variant thereof comprises IL-15 or a functional fragment or variant thereof.
7. The composition of any one of claims 1-6, wherein the agent further comprises an antigen binding domain that binds to TRBC.
8. The composition of claim 7, wherein the antigen binding domain that binds to TRBC binds to TRBC1 or TRBC2.
9. The composition of any one of claims 1-8, wherein the agent further comprises an anti-T cell receptor beta chain variable region (TCRβV) antibody molecule.
10. The composition of claim 9, wherein the anti-TCRβV antibody molecule is an anti-TRBV9.

11. The composition of claim 9, wherein the anti-TCRβV antibody molecule is an anti-TRBV5.
12. The composition of claim 11, wherein the anti-TRBV5 comprises:
    (a) a heavy chain variable region (VH) comprising a heavy chain complementarity determining region 1 (VHCDR1) comprising the sequence of GYTFTDYNIH (SEQ ID NO: 3341), a heavy chain complementarity determining region 2 (VHCDR2) comprising the sequence of YINPYNGRTGYNQKFKA (SEQ ID NO: 3342), and a heavy chain complementarity determining region 3 (VHCDR3) comprising the sequence of WDGSSYFDY (SEQ ID NO: 3343), and
    (b) a light chain variable region (VL) comprising a light chain complementarity determining region 1 (VLCDR1) comprising the sequence of SASSSVSYMH (SEQ ID NO: 3344), a light chain complementarity determining region 2 (VLCDR2) comprising the sequence of EISKLAS (SEQ ID NO: 3345), a light chain complementarity determining region 3 (VLCDR3) comprising the sequence of QQWNYPLLT (SEQ ID NO: 3346).
13. The composition of claim 12, wherein the VH of the anti-TRBV5 comprises the sequence of SEQ ID NO: 3445.
14. The composition of claim 12, wherein the VL of the anti-TRBV5 comprises the sequence of SEQ ID NO: 3446.
15. The composition of any one of claims 1-14, wherein the agent further comprises an anti-T cell receptor alpha chain variable region (TCRαV) antibody molecule.
16. The composition of claim 15, wherein the anti-TCRαV antibody molecule is an anti-TRAV21.
17. The composition of any one of claims 1-16 for use in the treatment of a disease or condition in a subject in need thereof.