

METHODS OF DETECTING TRBC1 OR TRBC2

RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/070,793 filed on August 26, 2020, the entire contents of which are hereby incorporated by reference.

BACKGROUND

[0002] Lymphomas are cancers that arise from lymphocytes. T cell lymphoma (TCL) is a lymphoma that arises from T cells; these account for approximately 7% of all non-Hodgkin's lymphomas in the United States. Common subtypes of TCL include: Peripheral T Cell Lymphoma, Not Otherwise Specified (PTCLNOS), Anaplastic Large Cell Lymphoma (ALCL), Angioimmunoblastic T Cell Lymphoma (AITL), and Cutaneous T Cell Lymphoma (CTCL). Each type of TCL has its own pathology and symptoms. Given the ongoing need for improved treatment of lymphomas such as TCLs, new compositions and treatments targeting lymphomas, e.g., TCLs, are highly desirable.

SUMMARY OF THE INVENTION

[0003] Provided herein, inter alia, in an aspect, is a method of identifying a subject in need of treatment for cancer, e.g., a lymphoma or leukemia, e.g., a T cell lymphoma or leukemia, using a composition comprising a polypeptide molecule comprising: (i) a first antigen binding domain that binds to T cell receptor beta chain constant domain 1 (TRBC1) or T cell receptor beta chain constant domain 2 (TRBC2), and (ii) a second antigen binding domain that binds to NKp30, comprising determining (e.g., directly determining or indirectly determining, e.g., obtaining information regarding) whether a subject has cancer cells that express a T cell receptor comprising TRBC2, wherein: responsive to a determination that the subject has cancer cells that express a T cell receptor comprising TRBC2, identifying the subject as a candidate for treatment using a multifunctional molecule comprising an antigen binding domain that binds to TRBC2, and optionally not as a candidate for treatment using a multifunctional molecule comprising an antigen binding domain that binds to TRBC1.

[0003a] In another aspect, provided herein is a method of identifying a subject in need of treatment for cancer, the method comprising determining, based at least in part on an assay of a sample from a subject, whether the subject has cancer cells that express T cell receptor comprising T cell receptor beta chain constant domain 1 (TRBC1) or T cell receptor beta chain constant domain 2 (TRBC2); and identifying the subject as a candidate for the treatment based at least in part on the determination that the subject has cancer cells that express TRBC1 or identifying the subject as a candidate for the treatment based at least in part on the determination that the subject has cancer cells that TRBC2, wherein the treatment uses a composition comprising a polypeptide molecule that comprises a first antigen binding domain that binds to TRBC1 or TRBC2, and a second antigen binding domain that

binds to NKp30.

[0003b] In yet another aspect, provided herein is a use of a pharmaceutical composition comprising a polypeptide molecule in the manufacture of a medicament for treating cancer in a subject in need thereof, wherein the polypeptide molecule comprises a first antigen binding domain that binds to T cell receptor beta chain constant domain 1 (TRBC1) or T cell receptor beta chain constant domain 2 (TRBC2), and a second antigen binding domain that binds to NKp30; wherein the subject has been identified as a candidate for treatment using the polypeptide molecule, based at least in part on determination that the subject has cancer cells that express a T cell receptor comprising TRBC1 or TRBC2.

[0004] In some embodiments, the polypeptide molecule is a multifunctional polypeptide molecule.

[0005] In some embodiments, the polypeptide molecule is a multispecific polypeptide molecule.

[0006] In some embodiments, the first antigen binding domain binds to T cell receptor beta chain constant domain 2 (TRBC2), and the first antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 21-25, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto

[0007] In some embodiments, the first antigen binding domain binds to T cell receptor beta chain constant domain 2 (TRBC2), and the first antigen binding domain 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

[0020] In some embodiments, the first antigen binding domain binds to T cell receptor beta chain constant domain 1 (TRBC1), and wherein the first antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 3A-3B or 4 (e.g., any of SEQ ID NOs: ~~261-356~~~~B001-B095~~), or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[0021] In some embodiments, the first antigen binding domain binds to T cell receptor beta chain constant domain 1 (TRBC1), and wherein the second antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any one of Tables 8A-8B, 9, and 10 (e.g., any of SEQ ID NOs ~~C001-C128~~~~357-484~~): , or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[0022] In some embodiments, the second antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any one of Tables 7, 8, 8A, 8B, 9, 10, 18, and 25, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[0023] In some embodiments, the second antigen binding domain 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, wherein the VHCDR1, VHCDR2, and VHCDR3 of the second antigen binding domain comprise the amino acid sequences of: SEQ ID NOs: 7313, 6001, and 7315, respectively; SEQ ID NOs: 7313, 6001, and 6002, respectively; SEQ ID NOs: 7313, 6008, and 6009, respectively; SEQ ID NOs: 7313, 7385, and 7315, respectively; SEQ ID NOs: 7313, 7318, and 6009, respectively; SEQ ID NOs: ~~C019, C021, and C023~~~~375, 377, and 379~~, respectively; SEQ ID NOs: ~~C033, C035, and C037~~~~389, 391, and 393~~, respectively; SEQ ID NOs: ~~C047, C049, and C051~~~~403, 405, and 407~~, respectively; SEQ ID NOs: ~~C061, C063, and C065~~~~417, 419, and 421~~, respectively; SEQ ID NOs: ~~C075, C077, and C079~~~~431, 433, and 435~~, respectively; SEQ ID NOs: ~~C089, C091, and C093~~~~445, 447, and 449~~, respectively; SEQ ID NOs: ~~C103, C105, and C107~~~~459, 461, and 463~~, respectively; or SEQ ID NOs: ~~C116, C118, and C120~~~~472, 474, and 476~~, respectively.

[0024] In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 of the second antigen binding domain comprise the amino acid sequences of: SEQ ID NOs: 7326, 7327, and 7329, respectively; SEQ ID NOs: 6063, 6064, and 7293, respectively; SEQ ID NOs: 6070, 6071, and 6072, respectively; SEQ ID NOs: 6070, 6064, and 7321, respectively; SEQ ID NOs: ~~C026, C028, and C030~~~~382, 384, and 386~~, respectively; SEQ ID NOs: ~~C040, C042, and C044~~~~396, 398, and 400~~, respectively; SEQ ID NOs: ~~C054, C056, and C058~~~~410, 412, and 414~~, respectively; SEQ ID NOs: ~~C068, C070, and C072~~~~424, 426, and 428~~, respectively; SEQ ID NOs: ~~C082, C084, and C086~~~~438, 440, and 442~~, respectively; SEQ ID NOs: ~~C096, C098, and C100~~~~452, 454, and 456~~, respectively; SEQ ID NOs: ~~C110, C112, and C113~~~~466, 468, and 469~~, respectively; or SEQ ID NOs: ~~C123, C125, and C127~~~~479, 481, and 483~~, respectively.

[0025] In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 of the second antigen binding domain comprise the amino acid sequences of: SEQ ID NOs: 7313, 6001, 7315, 7326, 7327, and 7329, respectively; SEQ ID NOs: 7313, 6001, 6002, 6063, 6064, and 7293, respectively; SEQ ID NOs: 7313, 6008, 6009, 6070, 6071, and 6072, respectively; SEQ ID

NOs: 7313, 7385, 7315, 6070, 6064, and 7321, respectively; SEQ ID NOs: 7313, 7318, 6009, 6070, 6064, and 7321, respectively; SEQ ID NOs: ~~C019, C021, C023~~375, 377, 379, ~~C026, C028, and C030~~382, 384, and 386, respectively; SEQ ID NOs: ~~C033, C035, C037~~389, 391, 393, ~~C040, C042, and C044~~396, 398, and 400, respectively; SEQ ID NOs: ~~C047, C049, C051~~403, 405, 407, ~~C054, C056, and C058~~410, 412, and 414, respectively; SEQ ID NOs: ~~C061, C063, C065~~417, 419, 421, ~~C068, C070, and C072~~424, 426, and 428, respectively; SEQ ID NOs: ~~C075, C077, C079~~431, 433, 435, ~~C082, C084, and C086~~438, 440, and 442, respectively; SEQ ID NOs: ~~C089, C091, C093~~445, 447, 449, ~~C096, C098, and C100~~452, 454, and 456, respectively; SEQ ID NOs: ~~C103, C105, C107~~459, 461, 463, ~~C110, C112, and C113~~466, 468, and 469, respectively; or SEQ ID NOs: ~~C116, C118, C120~~472, 474, 476, ~~C123, C125, and C127~~479, 481, and 483, respectively.

[0026] In some embodiments, (i) the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7302, 7298, 7300, 7301, 7303, and 7304 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7309, 7305, 7299, and 7306-7308 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); (ii) the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6121 and 6123-6128 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7294 or 6137-6141 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or (iii) the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6122 and 6129-6134 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6136 or 6142-6147 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or (iv) the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: ~~C001-C008~~357-364 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: ~~C009-C016~~365-372 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0027] In some embodiments, the VH and VL of the second antigen binding domain comprise the amino acid sequences of: SEQ ID NOs: 7302 and 7309, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or SEQ ID NOs: 7302 and 7305, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[0028] In some embodiments, the second antigen binding domain comprise the amino acid sequences of: SEQ ID NO: 7311 or 7310 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); SEQ ID NO: 6187 or 6188 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); SEQ ID NO: 6189 or 6190 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or any of SEQ ID NOs: ~~C017-C024~~373 and 485-491.

Table 3A. Exemplary heavy chain CDRs and FWRs of TRBC1-targeting antigen binding domains

Ab ID	VHFWR1	VHCDR1	VHFWR2	VHCDR2	VHFWR3	VHCDR3	VHFWR4
BKM 0191	QVQLVQ SGAEVK KPGSSV KVSCKA SGYT (SEQ ID NO: B049280)	<u>FTGYVM</u> <u>H</u> (SEQ ID NO: B020281)	WVRQAP GQGLEW MG (SEQ ID NO: B024282)	<u>FIPIFGT</u> <u>ANYAQK</u> <u>FQG</u> (SEQ ID NO: B022283)	RVTITSD KSTTTA YMELSS LRSED AVYYCA R (SEQ ID NO: B023284)	<u>GAGYNF</u> <u>DGAYRF</u> <u>FDF</u> (SEQ ID NO: B024285)	WGQGT LTVSS (SEQ ID NO: B025286)
BKM 0192	QVQLVQ SGAEVK KPGSSV KVSCKA SGYT (SEQ ID NO: B033294)	<u>FTGYVM</u> <u>H</u> (SEQ ID NO: B034295)	WVRQAP GQGLEW MG (SEQ ID NO: B035296)	<u>FIPIFGT</u> <u>ANYAQK</u> <u>FQG</u> (SEQ ID NO: B036297)	RVTITSD KSTTTA YMELSS LRSED AVYYCA R (SEQ ID NO: B037298)	<u>GAGYNF</u> <u>DGAYRF</u> <u>FDF</u> (SEQ ID NO: B038299)	WGQGT LTVSS (SEQ ID NO: B039300)
BKM 0193	QVQLVQ SGAEVK KPGSSV KVSCKA SGYT (SEQ ID NO: B047308)	<u>FTGYVM</u> <u>H</u> (SEQ ID NO: B048309)	WVRQAP GQGLEW MG (SEQ ID NO: B049310)	<u>FIPIFGT</u> <u>ANYAQK</u> <u>FQG</u> (SEQ ID NO: B050311)	RVTITSD KSTTTA YMELSS LRSED AVYYCA R (SEQ ID NO: B051312)	<u>GAGYNF</u> <u>DGAYRF</u> <u>FDF</u> (SEQ ID NO: B052313)	WGQGT LTVSS (SEQ ID NO: B053314)
BKM 0194	QVQLVQ SGAEVK KPGSSV KVSCKA SGYT (SEQ ID NO: B064322)	<u>FTGYVM</u> <u>H</u> (SEQ ID NO: B062323)	WVRQAP GQGLEW MG (SEQ ID NO: B063324)	<u>FIPIFGT</u> <u>ANYAQK</u> <u>FQG</u> (SEQ ID NO: B064325)	RVTITSD KSTTTA YMELSS LRSED AVYYCA R (SEQ ID NO: B065326)	<u>GAGYNF</u> <u>DGAYRF</u> <u>FDF</u> (SEQ ID NO: B066327)	WGQGT LTVSS (SEQ ID NO: B067328)
BKM 0195	QVQLVQ SGAEVK KPGSSV KVSCKA SGYT (SEQ ID NO: B075336)	<u>FTGYVM</u> <u>H</u> (SEQ ID NO: B076337)	WVRQAP GQGLEW MG (SEQ ID NO: B077338)	<u>FIPIFGT</u> <u>ANYAQK</u> <u>FQG</u> (SEQ ID NO: B078339)	RVTITSD KSTTTA YMELSS LRSED AVYYCA R (SEQ ID NO: B079340)	<u>GAGYNF</u> <u>DGAYRF</u> <u>FDF</u> (SEQ ID NO: B080341)	WGQGT LTVSS (SEQ ID NO: B081342)
BKM 0196	QVQLVQ SGAEVK KPGSSV KVSCKA SGYT (SEQ ID NO: B089350)	<u>FTGYVM</u> <u>H</u> (SEQ ID NO: B090351)	WVRQAP GQGLEW MG (SEQ ID NO: B091352)	<u>FIPIFGT</u> <u>ANYAQK</u> <u>FQG</u> (SEQ ID NO: B092353)	RVTITSD KSTTTA YMELSS LRSED AVYYCA R (SEQ ID NO: B093354)	<u>GAGYNF</u> <u>DGAYRF</u> <u>FDF</u> (SEQ ID NO: B094355)	WGQGT LTVSS (SEQ ID NO: B095356)

Table 3B. Exemplary light chain CDRs and FWRs of TRBC1-targeting antigen binding domains

Ab ID	VLFWR1	VLCDR1	VLFWR2	VLCDR2	VLFWR3	VLCDR3	VLFWR4
BKM0 191	DVVMT QSPLSLP VTLGQP ASISC (SEQ ID NO: B013273)	<u>RSSQRL</u> <u>VHSNAN</u> <u>TYLH</u> (SEQ ID NO: B014274)	WYQQR PGQSPR LLIY (SEQ ID NO: B015275)	<u>RVSNRF</u> <u>P</u> (SEQ ID NO: B016276)	GVPDRF SGSGSG TDFTLKI SRVEAE DVG VYF C (SEQ ID NO: B016277)	<u>SQSTHV</u> <u>PYTF</u> (SEQ ID NO: B017278)	GGGTKV EIK (SEQ ID NO: B018279)
BKM0 192	DVVMT QSPLSLP VTLGQP ASISC (SEQ ID NO: B026287)	<u>RSSQRL</u> <u>VHSNGN</u> <u>AYLH</u> (SEQ ID NO: B027288)	WYQQR PGQSPR LLIY (SEQ ID NO: B028289)	<u>RVSNRF</u> <u>P</u> (SEQ ID NO: B029290)	GVPDRF SGSGSG TDFTLKI SRVEAE DVG VYF C (SEQ ID NO: B030291)	<u>SQSTHV</u> <u>PYTF</u> (SEQ ID NO: B031292)	GGGTKV EIK (SEQ ID NO: B032293)
BKM0 193	DVVMT QSPLSLP VTLGQP ASISC (SEQ ID NO: B040301)	<u>RSSQRL</u> <u>VHSNAN</u> <u>AYLH</u> (SEQ ID NO: B041302)	WYQQR PGQSPR LLIY (SEQ ID NO: B042303)	<u>RVSNRF</u> <u>P</u> (SEQ ID NO: B043304)	GVPDRF SGSGSG TDFTLKI SRVEAE DVG VYF C (SEQ ID NO: B044305)	<u>SQSTHV</u> <u>PYT</u> (SEQ ID NO: B045306)	FGGGTK VEIK (SEQ ID NO: B046307)
BKM0 194	DVVMT QSPLSLP VTLGQP ASISC (SEQ ID NO: B054315)	<u>RSSQRL</u> <u>VHSGGN</u> <u>TYLH</u> (SEQ ID NO: B055316)	WYQQR PGQSPR LLIY (SEQ ID NO: B056317)	<u>RVSNRF</u> <u>P</u> (SEQ ID NO: B057318)	GVPDRF SGSGSG TDFTLKI SRVEAE DVG VYF C (SEQ ID NO: B058319)	<u>SQSTHV</u> <u>PYT</u> (SEQ ID NO: B059320)	FGGGTK VEIK (SEQ ID NO: B060321)
BKM0 195	DVVMT QSPLSLP VTLGQP ASISC (SEQ ID NO: B068329)	<u>RSSQRL</u> <u>VHSNGS</u> <u>TYLH</u> (SEQ ID NO: B069330)	WYQQR PGQSPR LLIY (SEQ ID NO: B070331)	<u>RVSNRF</u> <u>P</u> (SEQ ID NO: B071332)	GVPDRF SGSGSG TDFTLKI SRVEAE DVG VYF C (SEQ ID NO: B072333)	<u>SQSTHV</u> <u>PYT</u> (SEQ ID NO: B073334)	FGGGTK VEIK (SEQ ID NO: B074335)
BKM0 196	DVVMT QSPLSLP VTLGQP ASISC (SEQ ID NO: B082343)	<u>RSSQRL</u> <u>VHSGGS</u> <u>TYLH</u> (SEQ ID NO: B083344)	WYQQR PGQSPR LLIY (SEQ ID NO: B084345)	<u>RVSNRF</u> <u>P</u> (SEQ ID NO: B085346)	GVPDRF SGSGSG TDFTLKI SRVEAE DVG VYF C (SEQ ID NO: B086347)	<u>SQSTHV</u> <u>PYT</u> (SEQ ID NO: B087348)	FGGGTK VEIK (SEQ ID NO: B088349)

Table 4. Exemplary variable regions of TRBC1-targeting antigen binding domains

SEQ ID NO	Ab ID	Description	Sequence
SEQ ID NO: 250	mJOVI.1-H	JOVI.1 heavy chain variable region	EVRLQQSGPDLIKPGASVKMSCKASGYTFTGYV MHWVKQRPGQGLEWIGFINPYNDIQSNERFRG KATLTSDKSSTTAYMELSSLTSEDSAVYYCARGA GYNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: 251	h1JOVI.1-H	JOVI.1 heavy chain variable region humanized variant 1	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYV MHWVRQAPGQGLEWMGFNIPYNDIQSNERFRG RVTMTSDKSTTTAYMELSSLRSEDTAVYYCARG AGYNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: 252	h2JOVI.1-H	JOVI.1 heavy chain variable region humanized variant 2	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYV MHWVRQAPGQGLEWMGFNIPYNDIQSNERFRG WVTMTSDKSITTA YMELSLRSDDTAVYYCARG AGYNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: 253	h3JOVI.1-H	JOVI.1 heavy chain variable region humanized variant 3	QVQLVQSGAEVKKPGSSVKVSKASGYTFTGYV MHWVRQAPGQGLEWMGFNIPYNDIQSNERFRG RVTITSDKSTTTAYMELSSLRSEDTAVYYCARGA GYNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: 254	h4JOVI.1-H	JOVI.1 heavy chain variable region humanized variant 4	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYV MHWVRQAPGQRLEWMGFNIPYNDIQSNERFRG RVTITSDKSATTAYMELSSLRSEDTAVYYCARGA GYNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: 7343	h5JOVI.1-H	JOVI.1 heavy chain variable region humanized variant 5	QVQLVQSGAEVKKPGSSVKVSKASGYTFTGYV MHWVRQAPGQGLEWMGFNIPYNDIQSNERFRG RVTITSDKSTTTAYMELSSLRSEDTAVYYCARGA GYNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: 7344	h6JOVI.1-H	JOVI.1 heavy chain variable region humanized variant 6	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYV MHWVRQAPGQGLEWMGFNIPYNDIQSNERFRG RVTMTSDKSITTA YMELSLRSDDTAVYYCARG AGYNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: 7350	H1 germlined-VH	JOVI.1 heavy chain variable region humanized H1	QVQLVQSGAEVKKPGSSVKVSKASGYTFSGYAI SWVRQAPGQGLEWMGFNIPYNDIQSNERFRGR VTITSDKSTTTAYMELSSLRSEDTAVYYCARGAG YNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: 7351	H2 germlined-VH	JOVI.1 heavy chain variable region humanized H2	QVQLVQSGAEVKKPGSSVKVSKASGYTFTGYV MHWVRQAPGQGLEWMGFIIPIFGTANYAQKFQ RVTITSDKSTTTAYMELSSLRSEDTAVYYCARGA GYNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: 7352	H1/H2 germlined-VH	JOVI.1 heavy chain variable region humanized H1/H2	QVQLVQSGAEVKKPGSSVKVSKASGYTFSGYAI SWVRQAPGQGLEWMGFIIPIFGTANYAQKFQGRV TITSDKSTTTAYMELSSLRSEDTAVYYCARGAGY NFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: <u>261</u> ~~B00~~ +	BKM0191 VH	BKM0191 G29A heavy chain variable region	QVQLVQSGAEVKKPGSSVKVSKASGYTFTGYV MHWVRQAPGQGLEWMGFIIPIFGTANYAQKFQ RVTITSDKSTTTAYMELSSLRSEDTAVYYCARGA GYNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: <u>262</u> ~~B00~~ 2	BKM0192 VH	BKM0192 T31A heavy chain variable region	QVQLVQSGAEVKKPGSSVKVSKASGYTFTGYV MHWVRQAPGQGLEWMGFIIPIFGTANYAQKFQ RVTITSDKSTTTAYMELSSLRSEDTAVYYCARGA GYNFDGAYRFFDFWGQGTTLTVSS
SEQ ID NO: <u>263</u> ~~B00~~ 3	BKM0193 VH	BKM0193 G29a T31A heavy chain variable region	QVQLVQSGAEVKKPGSSVKVSKASGYTFTGYV MHWVRQAPGQGLEWMGFIIPIFGTANYAQKF

			QGRVTITSDKSTTTAYMELSSLRSEDNAVYYCAR GAGYNFDGAYRFFDFWGQGTLLTVSS
SEQ ID NO: ~~B004~~ <u>26</u> 4	BKM0194 VH	BKM0194 N28G heavy chain variable region	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTGYV MHWVRQAPGQGLEWMGFIIPIFGTANYAQKFQG RVTITSDKSTTTAYMELSSLRSEDNAVYYCARGA GYNFDGAYRFFDFWGQGTLLTVSS
SEQ ID NO: ~~B005~~ <u>26</u> 5	BKM0195 VH	BKM0195 N30S heavy chain variable region	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTGYV MHWVRQAPGQGLEWMGFIIPIFGTANYAQKFQG RVTITSDKSTTTAYMELSSLRSEDNAVYYCARGA GYNFDGAYRFFDFWGQGTLLTVSS
SEQ ID NO: ~~B006~~ <u>26</u> 6	BKM0196 VH	BKM0196 N28G N30S heavy chain variable region	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTGYV MHWVRQAPGQGLEWMGFIIPIFGTANYAQKFQG RVTITSDKSTTTAYMELSSLRSEDNAVYYCARGA GYNFDGAYRFFDFWGQGTLLTVSS
SEQ ID NO: 255	mJOVI.1-L	JOVI.1 light chain variable region	DVVMTQSPLSLPVSLGDQASISCRSSQRLVHSNG NTYLHWY LQKPGQSPKLLIYRVSNRFPGVDRFS SGSGTDFTLKISRVEAEDLGIYFCSQSTHVPYTF GGGTKLEIK
SEQ ID NO: 256	h1JOVI.1-L	JOVI.1 light chain variable region humanized variant 1	DVVMTQSPLSLPVTGPGEPAISCRSSQRLVHSNGN TYLHWY LQKPGQSPQLLIYRVSNRFPGVDRFSG SGSGTDFTLKISRVEAEDVGVYFCSQSTHVPYTFG GGTKVEIK
SEQ ID NO: 257	h2JOVI.1-L	JOVI.1 light chain variable region humanized variant 2	EVVMTQSPGTLSPGERATLSCRSSQRLVHSNG NTYLHWYQQKPGQAPRLIYRVSNRFPGIPDRFS SGSGTDFTLTISRLEPEDFAVYFCSQSTHVPYTF GGGTKVEIK
SEQ ID NO: 258	h3JOVI.1-L	JOVI.1 light chain variable region humanized variant 3	DVVMTQSPLSLPVTLGQPASISCRSSQRLVHSNGN TYLHWYQQRPQGQSPRLIYRVSNRFPGVDRFSG SGSGTDFTLKISRVEAEDVGVYFCSQSTHVPYTFG GGTKVEIK
SEQ ID NO: 259	h4JOVI.1-L	JOVI.1 light chain variable region humanized variant 4	DVVMTQTPLSLPVTGPGEPAISCRSSQRLVHSNGN TYLHWY LQKPGQSPQLLIYRVSNRFPGVDRFSG SGSGTDFTLKISRVEAEDVGVYFCSQSTHVPYTFG GGTKVEIK
SEQ ID NO: 260	h5JOVI.1-L	JOVI.1 light chain variable region humanized variant 5	DVVMTQTPLSLSVTPGQPASISCRSSQRLVHSNGN TYLHWY LQKPGQSPQLLIYRVSNRFPGVDRFSG SGSGTDFTLKISRVEAEDVGVYFCSQSTHVPYTFG GGTKVEIK
SEQ ID NO: 7357	L1 germlined- VL	JOVI.1 light chain variable region humanized L1	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGN TYHWYQQRPQGQSPRLIYRVSNRFPGVDRFSGS GSGTDFTLKISRVEAEDVGVYFCSQSTHVPYTFG GGTKVEIK
SEQ ID NO: 7358	L2 germlined- VL	JOVI.1 light chain variable region humanized L2	DVVMTQSPLSLPVTLGQPASISCRSSQRLVHSNGN TYLHWYQQRPQGQSPRLIYKVSNRDSGVDRFSG SGSGTDFTLKISRVEAEDVGVYFCSQSTHVPYTFG GGTKVEIK
SEQ ID NO: 7359	L3 germlined- VL	JOVI.1 light chain variable region humanized L3	DVVMTQSPLSLPVTLGQPASISCRSSQRLVHSNGN TYLHWYQQRPQGQSPRLIYRVSNRFPGVDRFSG SGSGTDFTLKISRVEAEDVGVYFCMQSTHWPYTF GGGTKVEIK
SEQ ID NO: 7360	L1/L2/L3 germlined- VL	JOVI.1 light chain variable region humanized L1/L2/L3	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGN TYHWYQQRPQGQSPRLIYKVSNRDSGVDRFSGS GSGTDFTLKISRVEAEDVGVYFCMQSTHWPYTFG GGTKVEIK

SEQ ID NO: ~~B007~~ <u>2</u> <u>67</u>	BKM0191 VL	BKM0191 G29A light chain variable region	DVVMQTQSPLSLPVTLGQPASISCRSSQRLVHSN ANTYLHWYQQRPGQSPRLLIYRVSNRFPGVDP RFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTH VPYTFGGGGTKVEIK
SEQ ID NO: ~~B008~~ <u>2</u> <u>68</u>	BKM0192 VL	BKM0192 T31A light chain variable region	DVVMQTQSPLSLPVTLGQPASISCRSSQRLVHSN GNAYLHWYQQRPGQSPRLLIYRVSNRFPGVDP RFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTH VPYTFGGGGTKVEIK
SEQ ID NO: ~~B009~~ <u>2</u> <u>69</u>	BKM0193 VL	BKM0193 G29a T31A light chain variable region	DVVMQTQSPLSLPVTLGQPASISCRSSQRLVHSN ANAYLHWYQQRPGQSPRLLIYRVSNRFPGVDP RFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTH VPYTFGGGGTKVEIK
SEQ ID NO: ~~B010~~ <u>2</u> <u>70</u>	BKM0194 VL	BKM0194 N28G light chain variable region	DVVMQTQSPLSLPVTLGQPASISCRSSQRLVHSG GNTYLHWYQQRPGQSPRLLIYRVSNRFPGVDP RFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTH VPYTFGGGGTKVEIK
SEQ ID NO: ~~B011~~ <u>2</u> <u>71</u>	BKM0195 VL	BKM0195 N30S light chain variable region	DVVMQTQSPLSLPVTLGQPASISCRSSQRLVHSN GSTYLHWYQQRPGQSPRLLIYRVSNRFPGVDP RFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTH VPYTFGGGGTKVEIK
SEQ ID NO: ~~B012~~ <u>2</u> <u>72</u>	BKM0196 VL	BKM0196 N28G N30S light chain variable region	DVVMQTQSPLSLPVTLGQPASISCRSSQRLVHSG GSTYLHWYQQRPGQSPRLLIYRVSNRFPGVDP RFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTH VPYTFGGGGTKVEIK

Table 5. Exemplary TRBC1-targeting antigen binding domains/antibody molecules

SEQ ID NO	Ab ID	Description	Sequence
SEQ ID NO: 6154	Ch(anti-TRBC1) HC N297A	Anti-TRBC1 heavy chain	EVRLQQSGPDLIKPGASVKMSCKASGYTFTGYVM HWVKQRPGQGLEWIGFINPYNDIQSNERFRGKA TLTSDKSSTTAYMELSSLTSEDSAVYYCARGAGYN FDGAYRFFDFWGQGTTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYASTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPCREEMTKNQVSLWCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSL SPGK
SEQ ID NO: 6155	Ch(anti-TRBC1) HC	Anti-TRBC1 heavy chain	EVRLQQSGPDLIKPGASVKMSCKASGYTFTGYVM HWVKQRPGQGLEWIGFINPYNDIQSNERFRGKA TLTSDKSSTTAYMELSSLTSEDSAVYYCARGAGYN FDGAYRFFDFWGQGTTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPCREE

JVD4-VH	QVQLVQ SGAEVK KPGASV KVSCKA SGYPFH (SEQ ID NO: 7397)	GYVMH (SEQ ID NO: 7346)	WVRQAP GQGLEW MG (SEQ ID NO: 208)	FINPYND DIQSNER FRG (SEQ ID NO: 201)	RVTMTS DKSTTTA YMELSSL RSEDTA VYYCAR (SEQ ID NO: 209)	GNGKNF DGAYRF FDF (SEQ ID NO: 7398)	WGQGTL VTVSS (SEQ ID NO: 210)
JVD5-VH	QVQLVQ SGAEVK KPGASV KVSCKA SGYTYP (SEQ ID NO: 7399)	GYVMH (SEQ ID NO: 7346)	WVRQAP GQGLEW MG (SEQ ID NO: 208)	FINPYND DIQSNER FRG (SEQ ID NO: 201)	RVTMTS DKSTTTA YMELSSL RSEDTA VYYCAR (SEQ ID NO: 209)	GNGKWF DGAYRF FDF (SEQ ID NO: 7400)	WGQGTL VTVSS (SEQ ID NO: 210)
JVD6-VH	QVQLVQ SGAEVK KPGASV KVSCKA SNQNFH (SEQ ID NO: ~~7402~~ ~~7401~~)	GYHMH (SEQ ID NO: 7401)	WVRQAP GQGLEW MG (SEQ ID NO: 208)	FINPYND DIQSNER FRG (SEQ ID NO: 201)	RVTMTS DKSTTTA YMELSSL RSEDTA VYYCAR (SEQ ID NO: 209)	GNGKWF DGAYRF FDF (SEQ ID NO: 7403)	WGQGTL VTVSS (SEQ ID NO: 210)
JVD7-VH	QVQLVQ SGAEVK KPGASV KVSCKA SSQNFH (SEQ ID NO: 7404)	GFYMH (SEQ ID NO: 7405)	WVRQAP GQGLEW MG (SEQ ID NO: 208)	FINPYND DIQSNER FRG (SEQ ID NO: 201)	RVTMTS DKSTTTA YMELSSL RSEDTA VYYCAR (SEQ ID NO: 209)	GNGKWF DGAYRF FDF (SEQ ID NO: 7403)	WGQGTL VTVSS (SEQ ID NO: 210)
JVD8-VH	QVQLVQ SGAEVK KPGASV KVSCKA SYQDFH (SEQ ID NO: 7406)	GYKMH (SEQ ID NO: 7407)	WVRQAP GQGLEW MG (SEQ ID NO: 208)	FINPYND DIQSNER FRG (SEQ ID NO: 201)	RVTMTS DKSTTTA YMELSSL RSEDTA VYYCAR (SEQ ID NO: 209)	GNGKWF DGAYRF FDF (SEQ ID NO: 7403)	WGQGTL VTVSS (SEQ ID NO: 210)
JVD9-VH	QVQLVQ SGAEVK KPGASV KVSCKA SGYNFH (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 RSEDTA VYYCAR (SEQ ID NO: 209)	GNGKWF DGAYRF FDF (SEQ ID NO: 7403)	WGQGTL VTVSS (SEQ ID NO: 210)
BKM0 097 anti- TRBC 2 VH; BJM1	QVQLVQ SGAEVK KPGASV KVSCKA STSGFH	GYPMH (SEQ ID NO: 7422)	WVRQAP GQGLEW MG (SEQ ID NO: 208)	FINPYND DIQSNER FRG (SEQ ID NO: 201)	RVTMTS DKSTTTA YMELSSL RSEDTA VYYCAR (SEQ	GNGKWF DGAYRF FDF (SEQ ID NO: 7403)	WGQGTL VTVSS (SEQ ID NO: 210)

thereto. In some embodiments, the antigen binding domain that binds to NKp30 comprises one or more framework regions (e.g., VHFWR1, VHFWR2, VHFWR3, VHFWR4, VLFWR1, VLFWR2, VLFWR3, and/or VLFWR4) disclosed in Table 7, Table 18, or Table 8, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antigen binding domain that binds to NKp30 comprises a VH and/or a VL disclosed in Table 9, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antigen binding domain that binds to NKp30 comprises an amino acid sequence disclosed in Table 10, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[00387] In some embodiments, the antigen binding domain that binds to NKp30 comprises one or more CDRs (e.g., VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and/or VLCDR3) disclosed in Table 8A and/or 8B, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antigen binding domain that binds to NKp30 comprises one or more framework regions (e.g., VHFWR1, VHFWR2, VHFWR3, VHFWR4, VLFWR1, VLFWR2, VLFWR3, and/or VLFWR4) disclosed in Table 8A and/or 8B, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antigen binding domain that binds to NKp30 comprises a VH and/or a VL disclosed in Table 9, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[00388] In some embodiments, the antigen binding domain that binds to NKp30 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.

[00389] In some embodiments, the VHCDR1, VHCDR2, and VHCDR3 comprise the amino acid sequences of SEQ ID NOs: 7313, 6001, and 7315, 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: 7313, 6001, and 6002, 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: 7313, 6008, and 6009, 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: 7313, 7385, and 7315, 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: 7313, 7318, and 6009, 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: ~~C019, C021, and C023~~[375, 377, and 379](#), 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: ~~C033, C035, and C037~~389, 391, and 393, 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: ~~C047, C049, and C051~~403, 405, and 407, 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: ~~C061, C063, and C065~~417, 419, and 421, 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: ~~C075, C077, and C079~~431, 433, and 435, 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: ~~C089, C091, and C093~~445, 447, and 449, 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: ~~C103, C105, and C107~~459, 461, and 463, 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: ~~C116, C118, and C120~~472, 474, and 476, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[00390] In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of SEQ ID NOs: 7326, 7327, and 7329, 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: 6063, 6064, and 7293, 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: 6070, 6071, and 6072, 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: 6070, 6064, and 7321, 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: ~~C026, C028, and C030~~382, 384, and 386, 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: ~~C040, C042, and C044~~396, 398, and 400, 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: ~~C054, C056, and C058~~410, 412, and 414, 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: ~~C068, C070, and C072~~[424, 426, and 428](#), 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: ~~C082, C084, and C086~~[438, 440, and 442](#), 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: ~~C096, C098, and C100~~[452, 454, and 456](#), 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: ~~C110, C112, and C113~~[466, 468, and 469](#), 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: ~~C123, C125, and C127~~[479, 481, and 483](#), respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[00391] In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 comprise the amino acid sequences of SEQ ID NOs: 7313, 6001, 7315, 7326, 7327, and 7329, 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: 7313, 6001, 6002, 6063, 6064, and 7293, 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: 7313, 6008, 6009, 6070, 6071, and 6072, 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: 7313, 7385, 7315, 6070, 6064, and 7321, 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: 7313, 7318, 6009, 6070, 6064, and 7321, 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: ~~C019, C021, C023~~[375, 377, 379, C026, C028, and C030](#)[382, 384, and 386](#), 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: ~~C033, C035, C037~~[389, 391, 393, C040, C042, and C044](#)[396, 398, and 400](#), 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: ~~C047, C049, C051~~[403, 405, 407, C054, C056, and C058](#)[410, 412, and 414](#), 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: ~~C061, C063, C065~~[417, 419, 421](#), ~~C068, C070, and C072~~[424, 426, and 428](#), 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: ~~C075, C077, C079~~[431, 433, 435](#), ~~C082, C084, and C086~~[438, 440, and 442](#), 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: ~~C089, C091, C093~~[445, 447, 449](#), ~~C096, C098, and C100~~[452, 454, and 456](#), 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: ~~C103, C105, C107~~459, 461, 463, C110, C112, and C113466, 468, and 469, 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: ~~C116, C118, C120~~472, 474, 476, C123, C125, and C127479, 481, and 483, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[00392] In some embodiments, the VH comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7298 or 7300-7304 (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: 7299 or 7305-7309 (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: 7302 and 7305, 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: 7302 and 7309, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[00393] 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 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 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 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 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 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL comprise the amino acid sequences of SEQ ID NOs: 7297 and 7296, 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: 6122 and 6136, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[00394] In some embodiments, the antigen binding domain that binds to NKp30 comprises the amino acid sequence of SEQ ID NO: 7310 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the antigen binding domain that binds to NKp30 comprises the amino acid sequence of SEQ ID NO: 7311 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the antigen binding domain that binds to NKp30 comprises the amino acid sequence of SEQ ID NO: 6187, 6188, 6189 or 6190 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[00395] In some embodiments, the antigen binding domain that targets NKp30 comprises a VH comprising a heavy chain complementarity determining region 1 (VHCDR1) amino acid sequence of

	SGFSIN (SEQ ID NO: 6026)		ID NO: 6027)	ID NO: 6001)	AVYYCA R (SEQ ID NO: 6028)		
9G1- HC_5	EIQLVES GGGLVQ PGGSLRL SCAVSGF SIN (SEQ ID NO: 6030)	TGGYHW N (SEQ ID NO: 6000)	WVRQAP GKGLEW VG (SEQ ID NO: 6032)	YIYSSGS TSYNPSL KS (SEQ ID NO: 6001)	RFTISRD TAKNSF YLQMNS LRAEDT AVYYCA R (SEQ ID NO: 6033)	GNWHYF DF (SEQ ID NO: 6002)	WGQGT MVTVSS (SEQ ID NO: 6034)
9G1- HC_6	QIQLVQS GAEVKK PGASVK VSCKVS GFSIN (SEQ ID NO: 6035)	TGGYHW N (SEQ ID NO: 6000)	WVRQAP GQGLEW MG (SEQ ID NO: 6036)	YIYSSGS TSYNPSL KS (SEQ ID NO: 6001)	RVTMTR DTSTNTF YMELSSL RSEDTA VYYCAR (SEQ ID NO: 6037)	GNWHYF DF (SEQ ID NO: 6002)	WGQGT MVTVSS (SEQ ID NO: 6038)
15H6- HC_1	QIQLQES GPGLVK PSQTL TCTVSGF SIN (SEQ ID NO: 6039)	TGGYHW N (SEQ ID NO: 6007)	WIRQHP GKGLEW IG (SEQ ID NO: 6040)	YIYSSGT TRYNPSL KS (SEQ ID NO: 6008)	LVTISRD TSKNQFS LKLSSVT AADTAV YYCAR (SEQ ID NO: 6041)	GNWHYF DY (SEQ ID NO: 6009)	WGQGT LVTVSS (SEQ ID NO: 6042)
15H6- HC_2	QIQLQES GPGLVK PSETLSL TCTVSGF SIN (SEQ ID NO: 6043)	TGGYHW N (SEQ ID NO: 6007)	WIRQPA GKGLEW IG (SEQ ID NO: 6044)	YIYSSGT TRYNPSL KS (SEQ ID NO: 6008)	RVTMSR DTSKNQ FSLKLSS VTAADT AVYYCA R (SEQ ID NO: 6045)	GNWHYF DY (SEQ ID NO: 6009)	WGQGT LVTVSS (SEQ ID NO: 6046)
15H6- HC_3	EIQLLES GGGLVQ PGGSLRL SCAVSGF SIN (SEQ ID NO: 6047)	TGGYHW N (SEQ ID NO: 6007)	WVRQAP GKGLEW VG (SEQ ID NO: 6048)	YIYSSGT TRYNPSL KS (SEQ ID NO: 6008)	RFTISRD TSKNTFY LQMNSL RAEDTA VYYCAR (SEQ ID NO: 6049)	GNWHYF DY (SEQ ID NO: 6009)	WGQGT LVTVSS (SEQ ID NO: 6050)
15H6- HC_4	EIQLVES GGGLVK PGGSLRL SCAVSGF SIN (SEQ ID NO: 6051)	TGGYHW N (SEQ ID NO: 6007)	WIRQAP GKGLEW VG (SEQ ID NO: 6052)	YIYSSGT TRYNPSL KS (SEQ ID NO: 6008)	RFTISRD TAKNSF YLQMNS LRAEDT AVYYCA R (SEQ ID NO: 6053)	GNWHYF DY (SEQ ID NO: 6009)	WGQGT LVTVSS (SEQ ID NO: 6054)
15H6- HC_5	QIQLVQS GAEVKK PGASV	TGGYHW N (SEQ	WVRQAP GQGLEW MG (SEQ	YIYSSGT TRYNPSL KS	RVTMTR DTSTNTF YMELS	GNWHYF DY	WGQGT LVTVSS

	(SEQ ID NO: 7373)				R (SEQ ID NO: 6024)		
9G1-HC_4	QIQLVQS GAEVKK PGSSVKV SCKVSGF SINTG (SEQ ID NO: 7374)	GYHWN (SEQ ID NO: 7313)	WVRQAP GQGLEW MG (SEQ ID NO: 6027)	YIYSSGS TSYNPSL KS (SEQ ID NO: 6001)	RVTITRD TSTNTFY MELSSLR SEDNAV YYCAR (SEQ ID NO: 6028)	GNWHYF DF (SEQ ID NO: 6002)	WGQGT MVTVSS (SEQ ID NO: 6029)
9G1-HC_5	EIQLVES GGGLVQ PGGSLRL SCAVSGF SINTG (SEQ ID NO: 7375)	GYHWN (SEQ ID NO: 7313)	WVRQAP GKGLEW VG (SEQ ID NO: 6032)	YIYSSGS TSYNPSL KS (SEQ ID NO: 6001)	RFTISRD TAKNSF YLQMNS LRAEDT AVYYCA R (SEQ ID NO: 6033)	GNWHYF DF (SEQ ID NO: 6002)	WGQGT MVTVSS (SEQ ID NO: 6034)
9G1-HC_6	QIQLVQS GAEVKK PGASVK VCKVVS GFSINTG (SEQ ID NO: 7376)	GYHWN (SEQ ID NO: 7313)	WVRQAP GQGLEW MG (SEQ ID NO: 6036)	YIYSSGS TSYNPSL KS (SEQ ID NO: 6001)	RVTMTR DTSTNTF YMESSL RSEDNA VYYCAR (SEQ ID NO: 6037)	GNWHYF DF (SEQ ID NO: 6002)	WGQGT MVTVSS (SEQ ID NO: 6038)
15H6-HC_1	QIQLQES GPGLVK PSQTLST TCTVSGF SINTG (SEQ ID NO: 7372)	GYHWN (SEQ ID NO: 7313)	WIRQHP GKGLEW IG (SEQ ID NO: 6040)	YIYSSGT TRYNPSL KS (SEQ ID NO: 6008)	LVTISRD TSKNQFS LKLSSVT AADNAV YYCAR (SEQ ID NO: 6041)	GNWHYF DY (SEQ ID NO: 6009)	WGQGTL VTVSS (SEQ ID NO: 6042)
15H6-HC_2	QIQLQES GPGLVK PSETLSL TCTVSGF SINTG (SEQ ID NO: 7371)	GYHWN (SEQ ID NO: 7313)	WIRQPA GKGLEW IG (SEQ ID NO: 6044)	YIYSSGT TRYNPSL KS (SEQ ID NO: 6008)	RVTMSR DTSKNQ FSLKLSS VTAADT AVYYCA R (SEQ ID NO: 6045)	GNWHYF DY (SEQ ID NO: 6009)	WGQGTL VTVSS (SEQ ID NO: 6046)
15H6-HC_3	EIQLLES GGGLVQ PGGSLRL SCAVSGF SINTG (SEQ ID NO: 7373)	GYHWN (SEQ ID NO: 7313)	WVRQAP GKGLEW VG (SEQ ID NO: 6048)	YIYSSGT TRYNPSL KS (SEQ ID NO: 6008)	RFTISRD TSKNTFY LQMNSL RAEDTA VYYCAR (SEQ ID NO: 6049)	GNWHYF DY (SEQ ID NO: 6009)	WGQGTL VTVSS (SEQ ID NO: 6050)
15H6-HC_4	QIQLVES GGGLVK PGGSLRL SCAVS	GYHWN (SEQ ID NO: 7313)	WIRQAP GKGLEW VG (SEQ	YIYSSGT TRYNPSL KS	RFTISRD TAKNSF YLQMNS LRAEDT	GNWHYF DY (SEQ ID NO: 6009)	WGQGTL VTVSS (SEQ ID NO: 6054)

15E1-LC	SFTLTQP PLVSVA VGQVATI TC (SEQ ID NO: 7325)	SGEKLSD KYVH (SEQ ID NO: 7326)	WYQQKP GRAPVM VIY (SEQ ID NO: 6067)	ENDRRPS (SEQ ID NO: 7327)	GIPDQFS GSNSGNI ASLTISK AQAGDE ADYFC (SEQ ID NO: 7328)	QFWDST NSAV (SEQ ID NO: 7329)	FGGGTQ LTVL (SEQ ID NO: 6080)
15E1_Humanized variant_VL1	SSETTQP PSVSVSP GQTASIT C (SEQ ID NO: 7335)	SGEKLSD KYVH (SEQ ID NO: 7326)	WYQQKP GQSPVM VIY (SEQ ID NO: 6106)	ENDRRPS (SEQ ID NO: 7327)	GIPERFS GSNSGN TATLTIS GTQAMD EADYFC (SEQ ID NO: 7336)	QFWDST NSAV (SEQ ID NO: 7329)	FGGGTQ LTVL (SEQ ID NO: 6080)
15E1_Humanized variant_VL2	SSETTQP HSVSVA TAQMAR ITC (SEQ ID NO: 6089)	SGEKLSD KYVH (SEQ ID NO: 7326)	WYQQKP GQDPVM VIY (SEQ ID NO: 6090)	ENDRRPS (SEQ ID NO: 7327)	GIPERFS GSNPGN TATLTIS RIEAGDE ADYFC (SEQ ID NO: 7337)	QFWDST NSAV (SEQ ID NO: 7329)	FGGGTQ LTVL (SEQ ID NO: 6080)
15E1_Humanized variant_VL3	QSVTTQP PSASGTP GQRTVIS C (SEQ ID NO: 6081)	SGEKLSD KYVH (SEQ ID NO: 7326)	WYQQLP GTAPKM LIY (SEQ ID NO: 6078)	ENDRRPS (SEQ ID NO: 7327)	GVPDRFS GSNSGNS ASLAISG LRSEDEA DYFC (SEQ ID NO: 7338)	QFWDST NSAV (SEQ ID NO: 7329)	FGGGTQ LTVL (SEQ ID NO: 6080)
15E1_Humanized variant_VL4	QSVTTQP PSVSGAP GQRTVIS C (SEQ ID NO: 6077)	SGEKLSD KYVH (SEQ ID NO: 7326)	WYQQLP GTAPKM LIY (SEQ ID NO: 6078)	ENDRRPS (SEQ ID NO: 7327)	GVPDRFS GSNSGNS ASLAITG LQAEDE ADYFC (SEQ ID NO: 7339)	QFWDST NSAV (SEQ ID NO: 7329)	FGGGTQ LTVL (SEQ ID NO: 6080)
15E1_Humanized variant_VL5	DSVTTQS PLSLPVT LGQPASI SC (SEQ ID NO: 7340)	SGEKLSD KYVH (SEQ ID NO: 7326)	WYQQR GQSPRM LIY (SEQ ID NO: 7341)	ENDRRPS (SEQ ID NO: 7327)	GVPDRFS GSNSGN DATLKIS RVEAED VGIFYFC (SEQ ID NO: 7342)	QFWDST NSAV (SEQ ID NO: 7329)	FGGGTK VEIK (SEQ ID NO: 233)

Table 8A. Exemplary heavy chain CDRs and FWRs of NKp30-targeting antigen binding domains

Ab ID	VHFWR1	VHCDR1	VHFWR2	VHCDR2	VHFWR3	VHCDR3	VHFWR4
BKM0138	EIQLES GGGLVQ PGGSLRL SCAVS	<u>ITTTGYH</u> <u>WN</u> (SEQ ID NO: <u>375C019</u>)	WVRQAP GKGLEW VG (SEQ	<u>YIYSSGS</u> <u>TSYNPSL</u> <u>KS</u> (SEQ	RFTISR TSKNTFY LQMNSL RAEDT	<u>GDWHYF</u> <u>DY</u> (SEQ ID	WGQGT MVTVSS (SEQ ID

	GFS (SEQ ID NO: 374 ~~C018~~)		ID NO: 376 ~~C020~~)	ID NO: 377 ~~C021~~)	AVYYCA R (SEQ ID NO: 378 ~~C022~~)	NO: 379 ~~C023~~)	NO: 380 ~~C024~~)
BKM0 139	EIQLES GGGLVQ PGGSLRL SCAVSGF S (SEQ ID NO: 388 ~~C032~~)	<u>ITTTGYH</u> <u>WN</u> (SEQ ID NO: 389 ~~C033~~)	WVRQAP GKGLEW VG (SEQ ID NO: 390 ~~C034~~)	<u>YIYSSGS</u> <u>TSYNPSL</u> <u>KS</u> (SEQ ID NO: 391 ~~C035~~)	RFTISRD TSKNTFY LQMNSL RAEDTA VYYCAR (SEQ ID NO: 392 ~~C036~~)	<u>GDWHYF</u> <u>DY</u> (SEQ ID NO: 393 ~~C037~~)	WGQGT MVTVSS (SEQ ID NO: 394 ~~C038~~)
BKM0 140	EIQLES GGGLVQ PGGSLRL SCAVSGF S (SEQ ID NO: 402 ~~C046~~)	<u>ITTTGYH</u> <u>WN</u> (SEQ ID NO: 403 ~~C047~~)	WVRQAP GKGLEW VG (SEQ ID NO: 404 ~~C048~~)	<u>YIYSSGS</u> <u>TSYNPSL</u> <u>KS</u> (SEQ ID NO: 405 ~~C049~~)	RFTISRD TSKNTFY LQMNSL RAEDTA VYYCAR (SEQ ID NO: 406 ~~C050~~)	<u>GDWHYF</u> <u>DY</u> (SEQ ID NO: 407 ~~C051~~)	WGQGT MVTVSS (SEQ ID NO: 408 ~~C052~~)
BKM0 141	EIQLES GGGLVQ PGGSLRL SCAVSGF S (SEQ ID NO: 416 ~~C060~~)	<u>ITTTGYH</u> <u>WN</u> (SEQ ID NO: 417 ~~C061~~)	WVRQAP GKGLEW VG (SEQ ID NO: 418 ~~C062~~)	<u>YIYSSGS</u> <u>TSYNPSL</u> <u>KS</u> (SEQ ID NO: 419 ~~C063~~)	RFTISRD TSKNTFY LQMNSL RAEDTA VYYCAR (SEQ ID NO: 420 ~~C064~~)	<u>GDWHYF</u> <u>DY</u> (SEQ ID NO: 421 ~~C065~~)	WGQGT MVTVSS (SEQ ID NO: 422 ~~C066~~)
BKM0 142	EIQLES GGGLVQ PGGSLRL SCAVSGF S (SEQ ID NO: 430 ~~C074~~)	<u>ITTTGYH</u> <u>WN</u> (SEQ ID NO: 431 ~~C075~~)	WVRQAP GKGLEW VG (SEQ ID NO: 432 ~~C076~~)	<u>YIYSSGS</u> <u>TSYAPSL</u> <u>KS</u> (SEQ ID NO: 433 ~~C077~~)	RFTISRD TSKNTFY LQMNSL RAEDTA VYYCAR (SEQ ID NO: 434 ~~C078~~)	<u>GDWHYF</u> <u>DY</u> (SEQ ID NO: 435 ~~C079~~)	WGQGT MVTVSS (SEQ ID NO: 436 ~~C080~~)
BKM0 143	EIQLES GGGLVQ PGGSLRL SCAVSGF S (SEQ ID NO: 444 ~~C088~~)	<u>ITTTGYH</u> <u>WN</u> (SEQ ID NO: 445 ~~C089~~)	WVRQAP GKGLEW VG (SEQ ID NO: 446 ~~C090~~)	<u>YIYSSGS</u> <u>TSYAPSL</u> <u>KS</u> (SEQ ID NO: 447 ~~C091~~)	RFTISRD TSKNTFY LQMNSL RAEDTA VYYCAR (SEQ ID NO: 448 ~~C092~~)	<u>GDWHYF</u> <u>DY</u> (SEQ ID NO: 449 ~~C093~~)	WGQGT MVTVSS (SEQ ID NO: 450 ~~C094~~)
BKM0 144	EIQLES GGGLVQ PGGSLRL SCAVSGF S (SEQ ID NO: 458 ~~C102~~)	<u>ITTTGYH</u> <u>WN</u> (SEQ ID NO: 459 ~~C103~~)	WVRQAP GKGLEW VG (SEQ ID NO: 460 ~~C104~~)	<u>YIYSSGS</u> <u>TSYAPSL</u> <u>KS</u> (SEQ ID NO: 461 ~~C105~~)	RFTISRD TSKNTFY LQMNSL RAEDTA VYYCAR (SEQ ID NO: 462 ~~C106~~)	<u>GDWHYF</u> <u>DY</u> (SEQ ID NO: 463 ~~C107~~)	WGQGT MVTVSS (SEQ ID NO: 464 ~~C108~~)
BKM0 145	EIQLES GGGLVQ	<u>ITTTGYH</u> <u>WN</u> (SEQ	WVRQAP GKGLEW	<u>YIYSSGS</u> <u>TSYAPSL</u>	RFTISRD TSKNTF	<u>GDWHYF</u> <u>DY</u>	WGQGT MVTVSS

	PGGSLRL SCAVSGF S (SEQ ID NO: 471 ~~C115~~)	ID NO: 472 ~~C116~~)	VG (SEQ ID NO: 473 ~~C117~~)	<u>KS</u> (SEQ ID NO: 474 ~~C118~~)	YLQMNSL RAEDTAV YYCAR (SEQ ID NO: 475 ~~C119~~)	(SEQ ID NO: 476 ~~C120~~)	(SEQ ID NO: 477 ~~C121~~)
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Table 8B. Exemplary light chain CDRs and FWRs of NKp30-targeting antigen binding domains

Ab ID	VLFWR1	VLCDR1	VLFWR2	VLCDR2	VLFWR3	VLCDR3	VLFWR4
BKM0 138	DSVTTQS PLSLPVT L GQPASISC (SEQ ID NO: 381 ~~C025~~)	<u>S</u> GEKLS <u>D</u> <u>KYVH</u> (SEQ ID NO: 382 ~~C026~~)	WYQQR P GQSPRML IY (SEQ ID NO: 383 ~~C027~~)	<u>EN</u> DRRPS (SEQ ID NO: 384 ~~C028~~)	GVPDRFS GSNSGND ATLKISR VEAEDVG VYFC (SEQ ID NO: 385 ~~C029~~)	<u>QF</u> WDSTA <u>SAV</u> (SEQ ID NO: 386 ~~C030~~)	FGGGTKV EIK (SEQ ID NO: 387 ~~C031~~)
BKM0 139	DSVTTQS PLSLPVT L GQPASISC (SEQ ID NO: 395 ~~C039~~)	<u>S</u> GEKLS <u>D</u> <u>KYVH</u> (SEQ ID NO: 396 ~~C040~~)	WYQQR P GQSPRML IY (SEQ ID NO: 397 ~~C041~~)	<u>EN</u> DRRPS (SEQ ID NO: 398 ~~C042~~)	GVPDRFS GSNSGND ATLKISR VEAEDVG VYFC (SEQ ID NO: 399 ~~C043~~)	<u>QF</u> WASTN <u>SAV</u> (SEQ ID NO: 400 ~~C044~~)	FGGGTKV EIK (SEQ ID NO: 401 ~~C045~~)
BKM0 140	SSETTQPP SVSVSPG QTASITC (SEQ ID NO: 409 ~~C053~~)	<u>S</u> GEKLS <u>D</u> <u>KYVH</u> (SEQ ID NO: 410 ~~C054~~)	WYQQKP P GQSPVMV IY (SEQ ID NO: 411 ~~C055~~)	<u>EN</u> DRRPS (SEQ ID NO: 412 ~~C056~~)	GIPERFSG SNSGNTA TLTISGTQ AMDEAD YFC (SEQ ID NO: 413 ~~C057~~)	<u>QF</u> WASTN <u>SAV</u> (SEQ ID NO: 414 ~~C058~~)	FGGGTQL TVL (SEQ ID NO: 415 ~~C059~~)
BKM0 141	SSETTQPP SVSVSPG QTASITC (SEQ ID NO: 423 ~~C067~~)	<u>S</u> GEKLS <u>D</u> <u>KYVH</u> (SEQ ID NO: 424 ~~C068~~)	WYQQKP P GQSPVMV IY (SEQ ID NO: 425 ~~C069~~)	<u>EN</u> DRRPS (SEQ ID NO: 426 ~~C070~~)	GIPERFSG SNSGNTA TLTISGTQ AMDEAD YFC (SEQ ID NO: 427 ~~C071~~)	<u>QF</u> WDSTA <u>SAV</u> (SEQ ID NO: 428 ~~C072~~)	FGGGTQL TVL (SEQ ID NO: 429 ~~C073~~)
BKM0 142	DSVTTQS PLSLPVT L GQPASISC (SEQ ID NO: 437 ~~C081~~)	<u>S</u> GEKLS <u>D</u> <u>KYVH</u> (SEQ ID NO: 438 ~~C082~~)	WYQQR P GQSPRML IY (SEQ ID NO: 439 ~~C083~~)	<u>EN</u> DRRPS (SEQ ID NO: 440 ~~C084~~)	GVPDRFS GSNSGND ATLKISR VEAEDVG VYFC (SEQ ID NO: 441 ~~C085~~)	<u>QF</u> WDSTN <u>SAV</u> (SEQ ID NO: 442 ~~C086~~)	FGGGTKV EIK (SEQ ID NO: 443 ~~C087~~)
BKM0 143	SSETTQPP SVSVSPG QTASITC (SEQ ID NO: 451 ~~C095~~)	<u>S</u> GEKLS <u>D</u> <u>KYVH</u> (SEQ ID NO: 452 ~~C096~~)	WYQQKP P GQSPVMV IY (SEQ ID NO: 453 ~~C097~~)	<u>EN</u> DRRPS (SEQ ID NO: 454 ~~C098~~)	GIPERFSG SNSGNTA TLTISGTQ AMDEAD YFC (SEQ ID NO: 455 ~~C099~~)	<u>QF</u> WDSTN <u>SAV</u> (SEQ ID NO: 456 ~~C100~~)	FGGGTQL TVL (SEQ ID NO: 457 ~~C101~~)

BKM0 144	DSVTTQS PLSLPVT LGQPASI SC (SEQ ID NO: 465 ~~C109~~)	<u>SGEKLSD</u> <u>KYVH</u> (SEQ ID NO: 466 ~~C110~~)	WYQQR GQSPRM LIY (SEQ ID NO: 467 ~~C111~~)	<u>ENDRRPS</u> (SEQ ID NO: 468 ~~C112~~)	GVPDRFS GSNSGN DATLKIS RVEAED VGVEFC (SEQ ID NO: 441 ~~C085~~)	<u>QFWAST</u> <u>ASAV</u> (SEQ ID NO: 469 ~~C113~~)	FGGGTK VEIK (SEQ ID NO: 470 ~~C114~~)
BKM0 145	SSETTQP PSVSVSP GQTASIT C (SEQ ID NO: 478 ~~C122~~)	<u>SGEKLSD</u> <u>KYVH</u> (SEQ ID NO: 479 ~~C123~~)	WYQQKP GQSPVM VIY (SEQ ID NO: 480 ~~C124~~)	<u>ENDRRPS</u> (SEQ ID NO: 481 ~~C125~~)	GIPERFS GSNSGNT ATLTISG TQAMDE ADYFC (SEQ ID NO: 482 ~~C126~~)	<u>QFWAST</u> <u>ASAV</u> (SEQ ID NO: 483 ~~C127~~)	FGGGTQL TVL (SEQ ID NO: 484 ~~C128~~)

Table 9. 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	QIQLQESGPGLVKPSQSLSLTCSVTGFSINTGGYHW NWIRQFPGKKLEWMGYIYSSGSTSYNPSLKSRI RDTSKNQFFLQLNSVTTEDTATYYCARGNWHYFD FWGQGTMTVTVSS
SEQ ID NO: 6122	15H6-HC	15H6 heavy chain variable region	QIQLQESGPGLVKPSQSLSLTCSVTGFSINTGGYHW NWIRQFPGKKLEWMGYIYSSGSTRYNPSLKSRI RDTSKNQFFLQLNSVTPEDTATYYCTRGNWHYFD YWGQGTMLVAVSS
SEQ ID NO: 6123	9G1-HC_1	9G1 heavy chain variable region humanized variant 1	QIQLQESGPGLVKPSETLSLTCTVSGFSINTGGYHW NWIRQAPGKGLEWIGYIYSSGSTSYNPSLKSRTM SRDTSKNQFSLKLSSVTAADTAVYYCARGNWHYF DFWGQGTMTVTVSS
SEQ ID NO: 6124	9G1-HC_2	9G1 heavy chain variable region humanized variant 2	QIQLQESGPGLVKPSQTLSTCTVSGFSINTGGYHW NWIRQHPGKGLEWIGYIYSSGSTSYNPSLKSRLTIS RDTSKNQFSLKLSSVTAADTAVYYCARGNWHYFD FWGQGTMTVTVSS
SEQ ID NO: 6125	9G1-HC_3	9G1 heavy chain variable region humanized variant 3	EIQLLESGGGLVQPGGSLRLSCAVSGFSINTGGYH WNWVRQAPGKGLEWVGYYIYSSGSTSYNPSLKS TISRDTSKNTFYLMNSLRAEDTAVYYCARGNWH YFDFWGQGTMTVTVSS
SEQ ID NO: 6126	9G1-HC_4	9G1 heavy chain variable region humanized variant 4	QIQLVQSGAEVKKPGSSVKVCKVSGFSINTGGYH WNWVRQAPGQGLEWMGYIYSSGSTSYNPSLKS VTITRDTSTNTFYMELSSLRSEDATAVYYCARGN HYFDFWGQGTMTVTVSS
SEQ ID NO: 6127	9G1-HC_5	9G1 heavy chain variable region humanized variant 5	EIQLVESGGGLVQPGGSLRLSCAVSGFSINTGGYH WNWVRQAPGKGLEWVGYYIYSSGSTSYNPSLKS TISRDTAKNSFYLMNSLRAEDTAVYYCARGNWH YFDFWGQGTMTVTVSS
SEQ ID NO: 6128	9G1-HC_6	9G1 heavy chain variable region humanized variant 6	QIQLVQSGAEVKKPGASVKVCKVSGFSINTGGYH WNWVRQAPGQGLEWMGYIYSSGSTSYNPSLKS VTMTTRDTSTNTFYMELSSLRSEDATAVYYCARGN HYFDFWGQGTMTVTVSS
SEQ ID NO: 6129	15H6-HC_1	15H6 heavy chain variable	QIQLQESGPGLVKPSQTLSTCTVSGFSINTGGYHW NWIRQHPGKGLEWIGYIYSSGSTRYNPSLKS

SEQ ID NO: 7300	15E1_ Humanized variant_VH 1	15E1 heavy chain variable region humanized variant 1	QIQLQESGPGLVKPSQTLSTCTVSGFSITTTGY WNWIRQHPGKGLEWIGYIYSSGSTSYNPSLKS VTISRDTSKNQFSLKLSSVTAADTAVYYCARGD WHYFDYWGQGTMTVTVSS
SEQ ID NO: 7301	15E1_ Humanized variant_VH 2	15E1 heavy chain variable region humanized variant 2	QIQLVESGGGLVKPGGSLRLSCAVSGFSITTTGY HWNWIRQAPGKGLEWVGYYIYSSGSTSYNPSLKS RFTISRDTAKNSFYLMNSLRAEDTAVYYCARG DWHYFDYWGQGTMTVTVSS
SEQ ID NO: 7302	15E1_ Humanized variant_VH 3 (BJM0407 VH and BJM0411 VH)	15E1 heavy chain variable region humanized variant 3	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYIYSSGSTSYNPSLK SRFTISRDTSKNTFYLMNSLRAEDTAVYYCAR GDWHYFDYWGQGTMTVTVSS
SEQ ID NO: 7303	15E1_ Humanized variant_VH 4	15E1 heavy chain variable region humanized variant 4	EIQLVESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYIYSSGSTSYNPSLK SRFTISRDTAKNSFYLMNSLRAEDTAVYYCAR GDWHYFDYWGQGTMTVTVSS
SEQ ID NO: 7304	15E1_ Humanized variant_VH 5	15E1 heavy chain variable region humanized variant 5	QIQLVQSGAEVKKPGASVKVSCVSGFSITTTGY HWNWVRQAPGQGLEWMGYIYSSGSTSYNPSLK SRVTMTTRDTSTNTFYMELSSLRSEDVAVYYCAR GDWHYFDYWGQGTMTVTVSS
SEQ ID NO: 7305	15E1_ Humanized variant_VL 1 (BJM0407 VL)	15E1 light chain variable region humanized variant 1	SSETTQPPSVSVSPGQTASITCSGEKLSDKYVHW YQQKPGQSPVMVIYENDRRPSGIPERFSGSNS TATLTISGTQAMDEADYFCQFWDSTNSAVFGGG TQLTVL
SEQ ID NO: 7306	15E1_ Humanized variant_VL 2	15E1 light chain variable region humanized variant 2	SSETTQPHSVSVATAQMARITCSGEKLSDKYVH WYQQKPGQDPVMVIYENDRRPSGIPERFSGSNP GNTATLTISRIEAGDEADYFCQFWDSTNSAVFG GGTQLTVL
SEQ ID NO: 7307	15E1_ Humanized variant_VL 3	15E1 light chain variable region humanized variant 3	QSVTTQPPSASGTPGQRVTISCSGEKLSDKYVH WYQQLPGTAPKMLIYENDRRPSGVPDRFSGSNS GNSASLAISGLRSEDEADYFCQFWDSTNSAVFG GGTQLTVL
SEQ ID NO: 7308	15E1_ Humanized variant_VL 4	15E1 light chain variable region humanized variant 4	QSVTTQPPSVSGAPGQRVTISCSGEKLSDKYVH WYQQLPGTAPKMLIYENDRRPSGVPDRFSGSNS GNSASLAITGLQAEDEADYFCQFWDSTNSAVFG GGTQLTVL
SEQ ID NO: 7309	15E1_ Humanized variant_VL 5 (BJM0411 VL)	15E1 light chain variable region humanized variant 5	DSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVH WYQQRPQGSPRMLIYENDRRPSGVPDRFSGSNS GNDATLKISRVEAEDVGVYFCQFWDSTNSAVFG GGTKVEIK
SEQ ID NO: ~~C0043~~ 57	BKM0138 VH	BKM0138 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYIYSSGSTSYNPSLK SRFTISRDTSKNTFYLMNSLRAEDTAVYYCAR GDWHYFDYWGQGTMTVTVSS

SEQ ID NO: ~~C002~~ <u>3</u> <u>58</u>	BKM0139 VH	BKM0139 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYNPSLK SRFTISRDTSKNTFYLMQNSLRAEDTAVYYCAR GDWHYFDYWGQGTMTVSS
SEQ ID NO: ~~C003~~ <u>3</u> <u>59</u>	BKM0140 VH	BKM0140 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYNPSLK SRFTISRDTSKNTFYLMQNSLRAEDTAVYYCAR GDWHYFDYWGQGTMTVSS
SEQ ID NO: ~~C004~~ <u>3</u> <u>60</u>	BKM0141 VH	BKM0141 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYNPSLK SRFTISRDTSKNTFYLMQNSLRAEDTAVYYCAR GDWHYFDYWGQGTMTVSS
SEQ ID NO: ~~C005~~ <u>3</u> <u>61</u>	BKM0142 VH	BKM0142 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYAPSLK SRFTISRDTSKNTFYLMQNSLRAEDTAVYYCAR GDWHYFDYWGQGTMTVSS
SEQ ID NO: ~~C006~~ <u>3</u> <u>62</u>	BKM0143 VH	BKM0143 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYAPSLK SRFTISRDTSKNTFYLMQNSLRAEDTAVYYCAR GDWHYFDYWGQGTMTVSS
SEQ ID NO: ~~C007~~ <u>3</u> <u>63</u>	BKM0144 VH	BKM0144 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYAPSLK SRFTISRDTSKNTFYLMQNSLRAEDTAVYYCAR GDWHYFDYWGQGTMTVSS
SEQ ID NO: ~~C008~~ <u>3</u> <u>64</u>	BKM0145 VH	BKM0145 heavy chain variable region	EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYAPSLK SRFTISRDTSKNTFYLMQNSLRAEDTAVYYCAR GDWHYFDYWGQGTMTVSS
SEQ ID NO: ~~C009~~ <u>3</u> <u>65</u>	BKM0138 VL	BKM0138 light chain variable region	DSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVH WYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNS GNDATLKISRVEAEDVGVYFCQFWDSTASAVFG GGTKVEIK
SEQ ID NO: ~~C010~~ <u>3</u> <u>66</u>	BKM0139 VL	BKM0139 light chain variable region	DSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVH WYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNS GNDATLKISRVEAEDVGVYFCQFWASTNSAVFG GGTKVEIK
SEQ ID NO: ~~C011~~ <u>3</u> <u>67</u>	BKM0140 VL	BKM0140 light chain variable region	SSETTQPPSVSVSPGQTASITCSGEKLSDKYVHW YQKPGQSPVMVIYENDRRPSGIPERFSGSNSGN TATLTISGTQAMDEADYFCQFWASTNSAVFGGG TQLTVL
SEQ ID NO: ~~C012~~ <u>3</u> <u>68</u>	BKM0141 VL	BKM0141 light chain variable region	SSETTQPPSVSVSPGQTASITCSGEKLSDKYVHW YQKPGQSPVMVIYENDRRPSGIPERFSGSNSGN TATLTISGTQAMDEADYFCQFWASTNSAVFGGG TQLTVL
SEQ ID NO: ~~C013~~ <u>3</u> <u>69</u>	BKM0142 VL	BKM0142 light chain variable region	DSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVH WYQQRPGQSPRMLIYENDRRPSGVPDRFSGSNS GNDATLKISRVEAEDVGVYFCQFWDSTNSAVFG GGTKVEIK
SEQ ID NO: ~~C014~~ <u>3</u> <u>70</u>	BKM0143 VL	BKM0143 light chain variable region	SSETTQPPSVSVSPGQTASITCSGEKLSDKYVHW YQKPGQSPVMVIYENDRRPSGIPERFSGSNSGN TATLTISGTQAMDEADYFCQFWASTNSAVFGGG TQLTVL

SEQ ID NO: ~~C015~~ 37 1	BKM0144 VL	BKM0144 light chain variable region	DSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVHW YQQRPGQSPRMLIYENDRRPSGVPDRFSGNSGND ATLKISRVEAEDVGVYFCQFWASTASAVFGGGTK VEIK
SEQ ID NO: ~~C016~~ 37 2	BKM0145 VL	BKM0145 light chain variable region	SSETTQPPSVSVSPGQTASITCSGEKLSDKYVHWY QQKPGQSPVMVIYENDRRPSGIPERFSGNSGNTA TLTISGTQAMDEADYFCQFWASTASAVFGGGTQL TVL

Table 10. Exemplary NKp30-targeting antigen binding domains/antibody molecules

SEQ ID NO	Ab ID	Description	Sequence
SEQ ID NO: 6148	Ch(anti- NKp30 9G1)HC N297A	9G1 heavy chain	QIQLQESGPGLVKPSQSLSLTCSVTGFSINTGGYHW NWIRQFPGKKLEWMGYIYSSGSTSYNPSLKSRI SDTTSKNQFFLQLNSVTTEDTATYYCARGNWHYFD FWGQGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSLGTQTYICNVNHKPSNTK VDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYASTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 6149	Ch(anti- NKp30 9G1)HC	9G1 heavy chain	QIQLQESGPGLVKPSQSLSLTCSVTGFSINTGGYHW NWIRQFPGKKLEWMGYIYSSGSTSYNPSLKSRI SDTTSKNQFFLQLNSVTTEDTATYYCARGNWHYFD FWGQGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSLGTQTYICNVNHKPSNTK VDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSREEMTKNQVSLSCAVKGFYPSDIAVEWES NGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 6150	Ch(anti- NKp30 9G1)LC	9G1 light chain	SYTLTQPPLLSVALGHKATITCSGERLSDKYVHWY QQKPGRAPVMVIYENDKRPSGIPDQFSGSNSGNTA TLTISKAQAGYEADYYCQSWDSTNSAVFGSGTQL TVLGQPKANPTVTLFPPSSEELQANKATLVCLISDF YPGAVTVAWKADGSPVKAGVETTKPSKQSNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV PTECS
SEQ ID NO: 6151	Ch(anti- NKp30 15H6)HC N297A	15H6 heavy chain	QIQLQESGPGLVKPSQSLSLTCSVTGFSINTGGYHW NWIRQFPGKKLEWMGYIYSSGTRYNPSLKSRI SDTTSKNQFFLQLNSVTPEDTATYYCTRGNWHYFD YWGQGTLVAVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSLGTQTYI

SEQ ID NO: 6190	anti-NKp30 15H6 scFv (VL-VH)	Hamster anti- NKp30 scFv of 15H6 in VL to VH orientation	SYTLTQPPSLSVAPGQKATHCSGENLSDKYVHWY QQKPGRAPVMVIYENKRPSPGIPDQFSGSNSGNIAT LTISKAQPGSEADYYCHYWESINSVVFSGTHLTV LGGGGSGGGSGGGSGGGSGGGSGGIQLQESGPGLVK PSQSLSLTCSVTGFSINTGGYHWNWIRQFPGKKLE WMGYIYSSGTTRYNPSLKSRSITRDTSKNQFFLQL NSVTPEDTATYYCTRGNWHYFDYWGQGTLVAVS S
SEQ ID NO: 7310	BJM0859 lambda scFv		EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHW NWVRQAPGKGLEWVGYYSSGSTSYNPSLKSRTFI SRDTSKNTFYLMNSLRAEDTAVYYCARGDWHY FDYWGQGTMTVTVSSGGGGSGGGSGGGSGGGG SSSETTQPPSVSVSPGQTASITCSGEKLSDKYVHWY QQKPGQSPVMVIYENDRRPSGIPERFSGSNSGNTA TLTISGTQAMDEADYFCQFWNSTNSAVFGGGTQL TVL
SEQ ID NO: 7311	BJM0860 kappa scFv		EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHW NWVRQAPGKGLEWVGYYSSGSTSYNPSLKSRTFI SRDTSKNTFYLMNSLRAEDTAVYYCARGDWHY FDYWGQGTMTVTVSSGGGGSGGGSGGGSGGGG SDSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVHW YQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGND ATLKISRVEAEDVGVYFCQFWNSTNSAVFGGGTK VEIK
SEQ ID NO: ~~C01737~~ 3	BKM0138 scFv		EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHW NWVRQAPGKGLEWVGYYSSGSTSYNPSLKSRTFI SRDTSKNTFYLMNSLRAEDTAVYYCARGDWHY FDYWGQGTMTVTVSSGGGGSGGGSGGGSGGGG SDSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVHW YQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGND ATLKISRVEAEDVGVYFCQFWNSTASAVFGGGTK VEIK
SEQ ID NO: ~~C01848~~ 5	BKM0139 scFv		EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHW NWVRQAPGKGLEWVGYYSSGSTSYNPSLKSRTFI SRDTSKNTFYLMNSLRAEDTAVYYCARGDWHY FDYWGQGTMTVTVSSGGGGSGGGSGGGSGGGG SDSVTTQSPLSLPVTLGQPASISCSGEKLSDKYVHW YQQRPGQSPRMLIYENDRRPSGVPDRFSGSNSGND ATLKISRVEAEDVGVYFCQFWASTNSAVFGGGTK VEIK
SEQ ID NO: 486 ~~C01~~ 9	BKM0140 scFv		EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHW NWVRQAPGKGLEWVGYYSSGSTSYNPSLKSRTFI SRDTSKNTFYLMNSLRAEDTAVYYCARGDWHY FDYWGQGTMTVTVSSGGGGSGGGSGGGSGGGG SSSETTQPPSVSVSPGQTASITCSGEKLSDKYVHWY QQKPGQSPVMVIYENDRRPSGIPERFSGSNSGNTA TLTISGTQAMDEADYFCQFWASTNSAVFGGGTQL TVL
SEQ ID NO: 487 ~~C02~~ 0	BKM0141 scFv		EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGYHW NWVRQAPGKGLEWVGYYSSGSTSYNPSLKSRTFI SRDTSKNTFYLMNSLRAEDTAVYYCARGDWHY FDYWGQGTMTVTVSSGGGGSGGGSGGGSGGGG SSSETTQPPSVSVSPGQTASITCSGEKLSDKYVHWY QQKPGQSPVMVIYENDRRPSGIPE

			RFSGSNSGNTATLTISGTQAMDEADYFCQFWDS TASAVFGGGTQLTVL
SEQ ID NO: ~~488~~ ~~21~~	BKM0142 scFv		EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYAPSLK SRFTISRDTSKNTFYLMNSLRAEDTAVYYCAR GDWHYFDYWGGQGTMTVSSGGGGSGGGGSGG GGSGGGGSDSVTTQSPLSLPVTLGQPASISCSGE KLSDKYVHWYQQRPGQSPRMLIYENDRRPSGV PDRFSGSNSGNDATLKISRVEAEDVGVYFCQFW DSTNSAVFGGGTKVEIK
SEQ ID NO: ~~489~~ ~~22~~	BKM0143 scFv		EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYAPSLK SRFTISRDTSKNTFYLMNSLRAEDTAVYYCAR GDWHYFDYWGGQGTMTVSSGGGGSGGGGSGG GGSGGGGSSSETTQPPSVSVSPGQTASITCSGEK LSDKYVHWYQQKPGQSPVMVIYENDRRPSGIPE RFSGSNSGNTATLTISGTQAMDEADYFCQFWDS TNSAVFGGGTQLTVL
SEQ ID NO: ~~490~~ ~~23~~	BKM0144 scFv		EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYAPSLK SRFTISRDTSKNTFYLMNSLRAEDTAVYYCAR GDWHYFDYWGGQGTMTVSSGGGGSGGGGSGG GGSGGGGSDSVTTQSPLSLPVTLGQPASISCSGE KLSDKYVHWYQQRPGQSPRMLIYENDRRPSGV PDRFSGSNSGNDATLKISRVEAEDVGVYFCQFW ASTASAVFGGGTKVEIK
SEQ ID NO: ~~491~~ ~~24~~	BKM0145 scFv		EIQLLESGGGLVQPGGSLRLSCAVSGFSITTTGY HWNWVRQAPGKGLEWVGYYSSGSTSYAPSLK SRFTISRDTSKNTFYLMNSLRAEDTAVYYCAR GDWHYFDYWGGQGTMTVSSGGGGSGGGGSGG GGSGGGGSSSETTQPPSVSVSPGQTASITCSGEK LSDKYVHWYQQKPGQSPVMVIYENDRRPSGIPE RFSGSNSGNTATLTISGTQAMDEADYFCQFWAS TASAVFGGGTQLTVL

[00465] In some embodiments, the NK cell engager is an antigen binding domain that binds to NKp46 (e.g., NKp46 present, e.g., expressed or displayed, on the surface of an NK cell) and comprises any CDR amino acid sequence, framework region (FWR) amino acid sequence, or variable region amino acid sequence disclosed in Table 15. In some embodiments, binding of the NK cell engager, e.g., antigen binding domain that binds to NKp46, to the NK cell activates the NK cell. An antigen binding domain that binds to NKp46 (e.g., NKp46 present, e.g., expressed or displayed, on the surface of an NK cell) may be said to target NKp46, the NK cell, or both.

[00466] In some embodiments, the NK cell engager is an antigen binding domain that binds to NKG2D (e.g., NKG2D present, e.g., expressed or displayed, on the surface of an NK cell) and comprises any CDR amino acid sequence, framework region (FWR) amino acid sequence, or variable region amino acid sequence disclosed in Table 15. In some embodiments, binding of the NK cell engager, e.g., antigen binding domain that binds to NKG2D, to the NK cell activates the NK cell. An antigen binding domain that binds to NKG2D (e.g., NKG2D present, e.g., expressed or displayed, on

does not appreciably activate the lymphoma cell or lymphocyte, e.g., T cell, (e.g., as measured by T cell proliferation, expression of a T cell activation marker (e.g., CD69 or CD25), and/or expression of a cytokine (e.g., TNF α and IFN γ). In some embodiments, the multifunctional molecule does not activate NK cells or does not substantially activate NK cells in the absence of a TRBC1-expressing cell.

[00961] In some embodiments, the second antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 7, 8, 8A, 8B, 9, 10, 18, and 25, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the second antigen binding domain 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, wherein the VHCDR1, VHCDR2, and VHCDR3 of the second antigen binding domain comprise the amino acid sequences of: SEQ ID NOs: 7313, 6001, and 7315, respectively; SEQ ID NOs: 7313, 6001, and 6002, respectively; SEQ ID NOs: 7313, 6008, and 6009, respectively; SEQ ID NOs: 7313, 7385, and 7315, respectively; SEQ ID NOs: 7313, 7318, and 6009, respectively; SEQ ID NOs: ~~C019, C021, and C023~~375, 377, and 379, respectively; SEQ ID NOs: ~~C033, C035, and C037~~389, 391, and 393, respectively; SEQ ID NOs: ~~C047, C049, and C051~~403, 405, and 407, respectively; SEQ ID NOs: ~~C061, C063, and C065~~417, 419, and 421, respectively; SEQ ID NOs: ~~C075, C077, and C079~~431, 433, and 435, respectively; SEQ ID NOs: ~~C089, C091, and C093~~445, 447, and 449, respectively; SEQ ID NOs: ~~C103, C105, and C107~~459, 461, and 463, respectively; or SEQ ID NOs: ~~C116, C118, and C120~~472, 474, and 476, respectively. In some embodiments, the VLCDR1, VLCDR2, and VLCDR3 of the second antigen binding domain comprise the amino acid sequences of: SEQ ID NOs: 7326, 7327, and 7329, respectively; SEQ ID NOs: 6063, 6064, and 7293, respectively; SEQ ID NOs: 6070, 6071, and 6072, respectively; SEQ ID NOs: 6070, 6064, and 7321, respectively; SEQ ID NOs: ~~C026, C028, and C030~~382, 384, and 386, respectively; SEQ ID NOs: ~~C040, C042, and C044~~396, 398, and 400, respectively; SEQ ID NOs: ~~C054, C056, and C058~~410, 412, and 414, respectively; SEQ ID NOs: ~~C068, C070, and C072~~424, 426, and 428, respectively; SEQ ID NOs: ~~C082, C084, and C086~~438, 440, and 442, respectively; SEQ ID NOs: ~~C096, C098, and C100~~452, 454, and 456, respectively; SEQ ID NOs: ~~C110, C112, and C113~~466, 468, and 469, respectively; SEQ ID NOs: ~~C123, C125, and C127~~479, 481, and 483, respectively.

[00962] In some embodiments, the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 of the second antigen binding domain comprise the amino acid sequences of: SEQ ID NOs: 7313, 6001, 7315, 7326, 7327, and 7329, respectively; SEQ ID NOs: 7313, 6001, 6002, 6063, 6064, and 7293, respectively; SEQ ID NOs: 7313, 6008, 6009, 6070, 6071, and 6072, respectively; SEQ ID NOs: 7313, 7385, 7315, 6070, 6064, and 7321, respectively; SEQ ID NOs: 7313, 7318, 6009, 6070, 6064, and 7321, respectively; SEQ ID NOs: ~~C019, C021, C023~~375, 377, 379, ~~C026, C028, and~~

~~C030~~382, 384, and 386, respectively; SEQ ID NOs: ~~C033, C035, C037~~389, 391, 393, ~~C040, C042,~~
~~and C044~~396, 398, and 400, respectively; SEQ ID NOs: ~~C047, C049, C051~~403, 405, 407, ~~C054,~~
~~C056, and C058~~410, 412, and 414, respectively; SEQ ID NOs: ~~C061, C063, C065~~417, 419, 421,
~~C068, C070, and C072~~424, 426, and 428, respectively; SEQ ID NOs: ~~C075, C077, C079~~431, 433,
435, ~~C082, C084, and C086~~438, 440, and 442, respectively; SEQ ID NOs: ~~C089, C091, C093~~445,
447, 449, ~~C096, C098, and C100~~452, 454, and 456, respectively; SEQ ID NOs: ~~C103, C105,~~
~~C107~~459, 461, 463, ~~C110~~;

~~C112, and C113~~466, 468, and 469, respectively; or SEQ ID NOs: ~~C116, C118, C120~~472, 474, 476, ~~C123, C125, and C127~~479, 481, and 483, respectively.

[00963] In some embodiments, the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7302, 7298, 7300, 7301, 7303, and 7304 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7309, 7305, 7299, 7306-7308 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6121 or 6123-6128 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7294 or 6137-6141 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6122 or 6129-6134 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6136 or 6142-6147 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: ~~C001-C008~~357-364 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: ~~C009-C016~~365-372 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the VH and VL of the second antigen binding domain comprise the amino acid sequences of: SEQ ID NOs: 7302 and 7309, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or SEQ ID NOs: 7302 and 7305, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the second antigen binding domain comprise the amino acid sequences of: SEQ ID NO: 7311 or 7310 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); SEQ ID NO: 6187 or 6188 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); SEQ ID NO: 6189 or 6190 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); any of SEQ ID NOs: ~~C017-C024~~373 and 485-491.

[00964] In some embodiments, the multifunctional molecule binds to TRBC2 monovalently. In some embodiments, the multifunctional molecule comprises a configuration shown in any of FIGS. 30A-30D, optionally wherein: (i) the multifunctional antibody molecule comprises an anti-TRBC2 Fab and an anti-NKp30 scFv, e.g., comprises a configuration shown in FIG. 30A; (ii) the multifunctional antibody molecule comprises an anti-TRBC2 Fab and an anti-NKp30 Fab, e.g., comprises a configuration shown in FIG. 30B; (iii) the multifunctional antibody molecule comprises an anti-NKp30 Fab and an anti-TRBC2 scFv, e.g., comprises a configuration shown in FIG. 30C; or

7382, 7380, and 7384 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the multifunctional molecule comprises: (i) 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: 7302 (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); (ii) 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); or (iii) SEQ ID NOs: 7379, 7380, and 7384 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[00969] In some embodiments, the multifunctional molecule comprises: a heavy chain constant region variant, e.g., an Fc region variant, that comprises one or more mutations that result in reduced or ablated affinity for at least one Fc receptor, optionally wherein the one or more mutations result in reduced or ablated antibody dependent cell-mediated cytotoxicity (ADCC), Antibody-dependent cellular phagocytosis (ADCP), or complement dependent cytotoxicity (CDC). In some embodiments, the Fc region variant comprises one or more mutations disclosed in Table 20, optionally wherein the Fc region variant comprises an N297A mutation.

Exemplary Embodiment 3

[00970] In an aspect, the disclosure features a multifunctional molecule, comprising:

(i) a first antigen binding domain that binds to T cell receptor beta chain constant domain 1 (TRBC1), and

(ii) a second antigen binding domain that binds to NKp30,

wherein the first antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 3A-3B or 4 (e.g., any of SEQ ID NOs: ~~261-356~~~~B001-B095~~), or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[00971] In some embodiments, the second antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed herein.

[00972] In another aspect, the disclosure features a multifunctional molecule, comprising:

(i) a first antigen binding domain that binds to T cell receptor beta chain constant domain 1 (TRBC1), and

(ii) a second antigen binding domain that binds to NKp30,

wherein the second antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 8A-8B, 9, or 10 (e.g., any of SEQ ID NOs: ~~C001-C128~~~~357-484~~): , or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[00973] In some embodiments, the first antigen binding domain comprises one or more CDRs,

framework regions, variable regions, or antigen binding domains disclosed herein.

[00974] In an aspect, the disclosure features a multifunctional molecule, comprising:

(i) a first antigen binding domain that binds to T cell receptor beta chain constant domain 1 (TRBC1), and

(ii) a second antigen binding domain that binds to NKp30,

wherein the first antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 3A-3B or 4 (e.g., any of SEQ ID NOs: [261-356](#)~~B001-B095~~), or a sequence having at least 85%, 90%, 95%, or 99% identity thereto; and

wherein the second antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 8A-8B, 9, or 10 (e.g., any of SEQ ID NOs ~~C001-C128~~[357-484](#)): , or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

Exemplary Embodiment 4

[00975] In one aspect, provided herein is an antibody molecule that binds to TRBC2, comprising one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 21-25, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antibody molecule that binds to TRBC2 comprises one or more CDRs (e.g., VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and/or VLCDR3) disclosed in Table 21 or Table 22, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antibody molecule 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 21 or Table 22, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antibody molecule that binds to TRBC2 comprises a VH and/or a VL disclosed in Table 23, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the antibody molecule that binds to TRBC2 comprises an amino acid sequence disclosed in Table 24, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[00976] In one aspect, provided herein is an antibody molecule that binds to NKp30, comprising one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 7, 8, 8A, 8B, 9, 10, 18, and 25, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[00977] In one aspect, provided herein is an antibody molecule that binds to TRBC1, comprising one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 2, 3, 3A, 3B, 4, 5, 6 and 19, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[00978] In some embodiments, the antibody molecule comprises a heavy chain constant region variant, e.g., an Fc region variant, that comprises one or more mutations that result in reduced or

sequences of:

SEQ ID NOs: 7313, 6001, and 7315, respectively;

SEQ ID NOs: 7313, 6001, and 6002, respectively;

SEQ ID NOs: 7313, 6008, and 6009, respectively;

SEQ ID NOs: 7313, 7385, and 7315, respectively; or

SEQ ID NOs: 7313, 7318, and 6009, respectively;

SEQ ID NOs: ~~C019, C021, and C023~~375, 377, and 379, respectively;

SEQ ID NOs: ~~C033, C035, and C037~~389, 391, and 393, respectively;

SEQ ID NOs: ~~C047, C049, and C051~~403, 405, and 407, respectively;

SEQ ID NOs: ~~C061, C063, and C065~~417, 419, and 421, respectively;

SEQ ID NOs: ~~C075, C077, and C079~~431, 433, and 435, respectively;

SEQ ID NOs: ~~C089, C091, and C093~~445, 447, and 449, respectively;

SEQ ID NOs: ~~C103, C105, and C107~~459, 461, and 463, respectively; or

SEQ ID NOs: ~~C116, C118, and C120~~472, 474, and 476, respectively.

[001191] A11. The multifunctional molecule of embodiment A10, wherein the VLCDR1, VLCDR2, and VLCDR3 of the second antigen binding domain comprise the amino acid sequences of:

SEQ ID NOs: 7326, 7327, and 7329, respectively;

SEQ ID NOs: 6063, 6064, and 7293, respectively;

SEQ ID NOs: 6070, 6071, and 6072, respectively; or

SEQ ID NOs: 6070, 6064, and 7321, respectively;

SEQ ID NOs: ~~C026, C028, and C030~~382, 384, and 386, respectively;

SEQ ID NOs: ~~C040, C042, and C044~~396, 398, and 400, respectively;

SEQ ID NOs: ~~C054, C056, and C058~~410, 412, and 414, respectively;

SEQ ID NOs: ~~C068, C070, and C072~~424, 426, and 428, respectively;

SEQ ID NOs: ~~C082, C084, and C086~~438, 440, and 442, respectively;

SEQ ID NOs: ~~C096, C098, and C100~~452, 454, and 456, respectively;

SEQ ID NOs: ~~C110, C112, and C113~~466, 468, and 469, respectively;

SEQ ID NOs: ~~C123, C125, and C127~~479, 481, and 483, respectively.

[001192] A12. The multifunctional molecule of embodiment A10 or A11, wherein the VHCDR1, VHCDR2, VHCDR3, VLCDR1, VLCDR2, and VLCDR3 of the second antigen binding domain comprise the amino acid sequences of:

SEQ ID NOs: 7313, 6001, 7315, 7326, 7327, and 7329, respectively;

SEQ ID NOs: 7313, 6001, 6002, 6063, 6064, and 7293, respectively;

SEQ ID NOs: 7313, 6008, 6009, 6070, 6071, and 6072, respectively;

SEQ ID NOs: 7313, 7385, 7315, 6070, 6064, and 7321, respectively; or

SEQ ID NOs: 7313, 7318, 6009, 6070, 6064, and 7321, respectively;

SEQ ID NOs: ~~C019, C021, C023~~375, 377, 379, ~~C026, C028, and C030~~382, 384, and 386, respectively;

SEQ ID NOs: ~~C033, C035, C037~~389, 391, 393, ~~C040, C042, and C044~~396, 398, and 400, respectively;
 SEQ ID NOs: ~~C047, C049, C051~~403, 405, 407, ~~C054, C056, and C058~~410, 412, and 414, respectively;
 SEQ ID NOs: ~~C061, C063, C065~~417, 419, 421, ~~C068, C070, and C072~~424, 426, and 428, respectively;
 SEQ ID NOs: ~~C075, C077, C079~~431, 433, 435, ~~C082, C084, and C086~~438, 440, and 442, respectively;
 SEQ ID NOs: ~~C089, C091, C093~~445, 447, 449, ~~C096, C098, and C100~~452, 454, and 456, respectively;
 SEQ ID NOs: ~~C103, C105, C107~~459, 461, 463, ~~C110, C112, and C113~~466, 468, and 469, respectively; or
 SEQ ID NOs: ~~C116, C118, C120~~472, 474, 476, ~~C123, C125, and C127~~479, 481, and 483, respectively.

[001193] A13. The multifunctional molecule of any of embodiments A10-A12, wherein:

- (i) the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7302, 7298, 7300, 7301, 7303, and 7304 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7309, 7305, 7299, and 7306-7308 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto);
- (ii) the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6121 or 6123-6128 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7294 or 6137-6141 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or
- (iii) the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6122 or 6129-6134 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6136 or 6142-6147 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or
- (iv) the VH of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: ~~C001-C008~~357-364 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto) and/or the VL of the second antigen binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: ~~C009-C016~~365-372 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[001194] A14. The multifunctional molecule of any of embodiments A10-A13, wherein the VH and VL of the second antigen binding domain comprise the amino acid sequences of:

SEQ ID NOs: 7302 and 7309, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or

SEQ ID NOs: 7302 and 7305, respectively (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[001195] A15. The multifunctional molecule of any of embodiments A10-A14, wherein the second antigen binding domain comprise the amino acid sequences of:

SEQ ID NO: 7311 or 7310 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto);

SEQ ID NO: 6187 or 6188 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or SEQ ID NO: 6189 or 6190 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or any of SEQ ID NOs: ~~C017-C024~~373 and 485-491.

[001196] A16. The multifunctional molecule of any of embodiments A1-A15, wherein the multifunctional molecule binds to TRBC2 monovalently.

[001197] A17. The multifunctional molecule of any of embodiments A1-A16, wherein the multifunctional molecule comprises a configuration shown in any of FIGs. 30A-30D, optionally wherein:

- (i) the multifunctional antibody molecule comprises an anti-TRBC2 Fab and an anti-NKp30 scFv, e.g., comprises a configuration shown in FIG. 30A;
- (ii) the multifunctional antibody molecule comprises an anti-TRBC2 Fab and an anti-NKp30 Fab, e.g., comprises a configuration shown in FIG. 30B;
- (iii) the multifunctional antibody molecule comprises an anti-NKp30 Fab and an anti-TRBC2 scFv, e.g., comprises a configuration shown in FIG. 30C; or
- (iv) the multifunctional antibody molecule comprises an anti-TRBC2 scFv and an anti-NKp30 scFv, e.g., comprises a configuration shown in FIG. 30D.

[001198] A18. The multifunctional molecule of any of embodiments A1-A17, further comprising a dimerization module comprising one or more immunoglobulin chain constant regions (e.g., Fc regions) comprising one or more of: a paired cavity-protuberance ("knob-in-a hole"), an electrostatic interaction, or a strand-exchange.

[001199] A19. The multifunctional molecule of any of embodiments A1-A18, comprising an anti-TRBC2 amino acid sequence disclosed in any of Tables 21-25, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto, and/or an anti-NKp30 amino acid sequence disclosed in any of Tables 7, 8, 8A, 8B, 9, 10, 18, and 25, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[001200] A20. The multifunctional molecule of any of embodiments A1-A19, comprising:

- (i) an anti-TRBC2 VH of SEQ ID NO: 7420 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), an anti-TRBC2 VL of SEQ ID NO: 7419 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), an anti-NKp30 VH of SEQ ID NO: 7302 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), and an anti-NKp30 VL of SEQ ID NO: 7309 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto);
- (ii) an anti-TRBC2 VH of SEQ ID NO: 7420 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), an anti-TRBC2 VL of SEQ ID NO: 7419 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), and an anti-NKp30 scFv of SEQ ID NO: 7311 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or

[001201] A21. The multifunctional molecule of any of embodiments A1-A19, comprising:

- (i) an anti-TRBC2 VH of SEQ ID NO: 7423 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), an anti-TRBC2 VL of SEQ ID NO: 7419 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), an anti-NKp30 VH of SEQ ID NO: 7302 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), and an anti-NKp30 VL of SEQ ID NO: 7309 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto);
- (ii) an anti-TRBC2 VH of SEQ ID NO: 7423 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), an anti-TRBC2 VL of SEQ ID NO: 7419 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto), and an anti-NKp30 scFv of SEQ ID NO: 7311 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto); or
- (iii) SEQ ID NOs: 7440, 7439, and 7383 (or a sequence having at least 85%, 90%, 95%, or 99% identity thereto).

[001202] A22. A multifunctional molecule, comprising:

- (i) a first antigen binding domain that binds to T cell receptor beta chain constant domain 1 (TRBC1), and
- (ii) a second antigen binding domain that binds to NKp30,

wherein the first antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 3A-3B or 4 (e.g., any of SEQ ID NOs: [261-356B001-B095](#)), or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[001203] A23. The multifunctional molecule of embodiment A22, wherein the second antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed herein.

[001204] A24. A multifunctional molecule, comprising:

- (i) a first antigen binding domain that binds to T cell receptor beta chain constant domain 1 (TRBC1), and
- (ii) a second antigen binding domain that binds to NKp30,

wherein the second antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 8A-8B, 9, or 10 (e.g., any of SEQ ID NOs: [C001-C128357-484](#)): , or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[001205] A25. The multifunctional molecule of embodiment A24, wherein the first antigen binding domain comprises one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed herein.

[001206] A26. An antibody molecule that binds to TRBC2, comprising one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 21-25, or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[001207] A27. An antibody molecule that binds to TRBC1, comprising one or more CDRs, framework regions, variable regions, or antigen binding domains disclosed in any of Tables 3A-3B or

4 (e.g., any of SEQ ID NOs: [261-356](#)~~B001-B095~~), or a sequence having at least 85%, 90%, 95%, or 99% identity thereto.

[001208] A28. The multifunctional molecule of any of embodiments A1-A25 or the antibody molecule of embodiment A26 or A27, further comprising a heavy chain constant region variant, e.g., an Fc region variant, that comprises one or more mutations that result in reduced or ablated affinity for at least one Fc receptor, optionally wherein the one or more mutations result in reduced or ablated antibody dependent cell-mediated cytotoxicity (ADCC), Antibody-dependent cellular phagocytosis (ADCP), or complement dependent cytotoxicity (CDC).

[001209] A29. The multifunctional molecule of any of embodiments A1-A25 and A28, or the antibody molecule of any of embodiments A26-A28, wherein the Fc region variant comprises one or more mutations disclosed in Table 20, optionally wherein the Fc region variant comprises an N297A mutation.

[001210] A30. A nucleic acid molecule encoding the multifunctional molecule of any of embodiments A1-A25, A28, and A29, or the antibody molecule of any of embodiments A26-A29.

[001211] A31. A vector, e.g., an expression vector, comprising the nucleic acid molecule of embodiment A30.

[001212] A32. A cell comprising the nucleic acid molecule of embodiment A30 or the vector of embodiment A31.

[001213] A33. A method of making, e.g., producing, the multifunctional molecule of any of embodiments A1-A25, A28, and A29 or the antibody molecule of any of embodiments A26-A29, comprising culturing the cell of embodiment A32, under suitable conditions, e.g., conditions suitable for gene expression and/or homo- or heterodimerization.

[001214] A34. A pharmaceutical composition comprising the multifunctional molecule of any of embodiments A1-A25, A28, and A29 or the antibody molecule of any of embodiments A26-A29 and a pharmaceutically acceptable carrier, excipient, or stabilizer.

[001215] A35. A method of treating a cancer, comprising administering to a subject in need thereof the multifunctional molecule of any of embodiments A1-A25, A28, and A29, wherein the multifunctional molecule is administered in an amount effective to treat the cancer.

[001216] A36. The method of embodiment A35, further comprising identifying, evaluating, or selecting a subject in need of treatment, wherein identifying, evaluating, or selecting comprises determining (e.g., directly determining or indirectly determining, e.g., obtaining information regarding) whether a subject has cancer cells that express a T cell receptor comprising TRBC1 or TRBC2.

[001217] A37. The method of embodiment A35, further comprising, responsive to determining that a subject has cancer cells that express a T cell receptor comprising TRBC1 or TRBC2: optionally, selecting the subject for treatment with a multifunctional molecule comprising an antigen