

FIG. 1

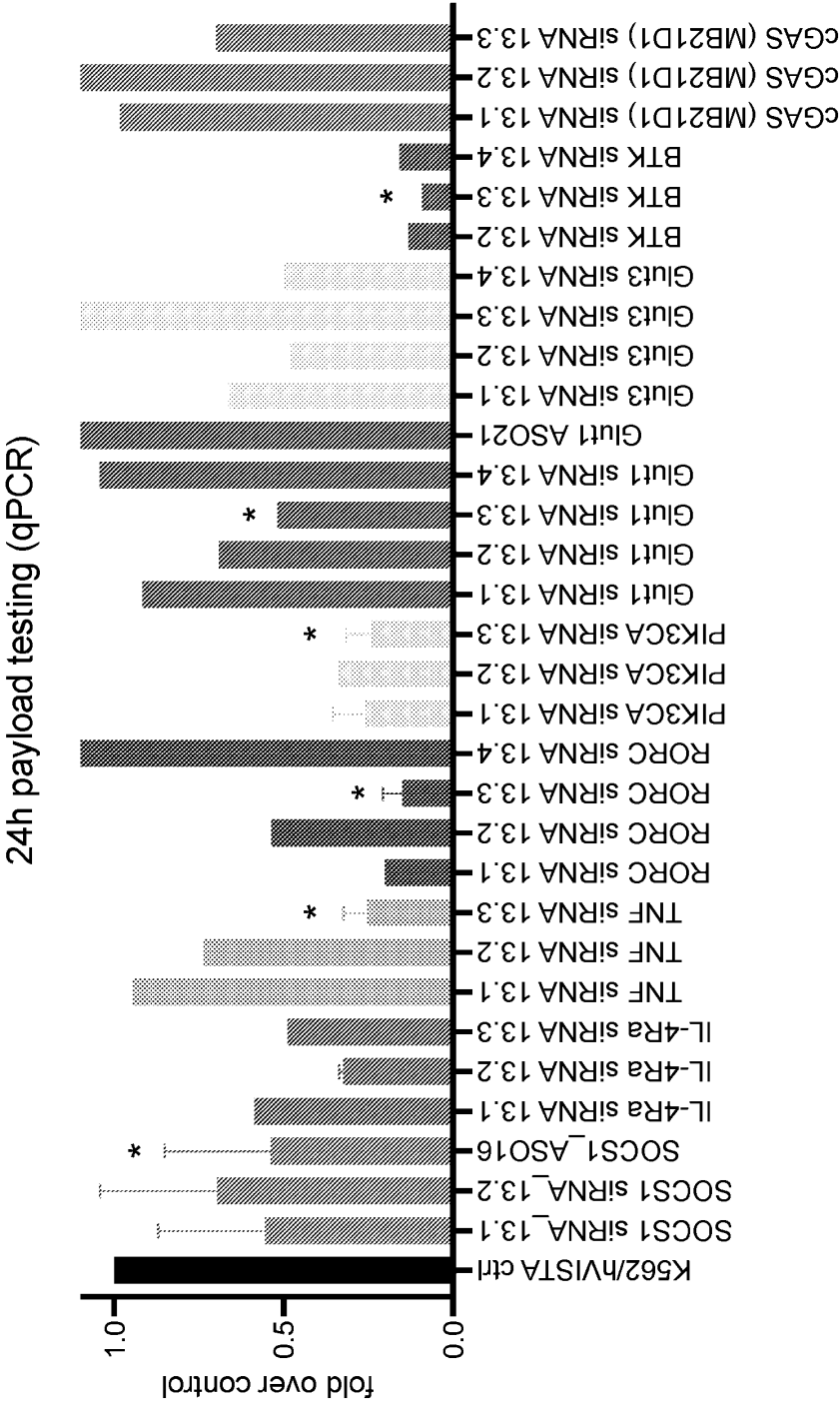


Figure 1. Immunologically relevant siRNAs and ASO payloads have been identified and tested. K562-VISTA cells were transfected with 200 nM siRNA (or ASO) alone, and target knockdown was analyzed by qRT-PCR using the ddct method and reported as fold over control. Scrambled siRNA or ASO controls were also ordered from IDT. Payloads marked with (*) were selected for conjugation to a delivery vehicle (anti-VISTA Mab INX201).

FIG. 2

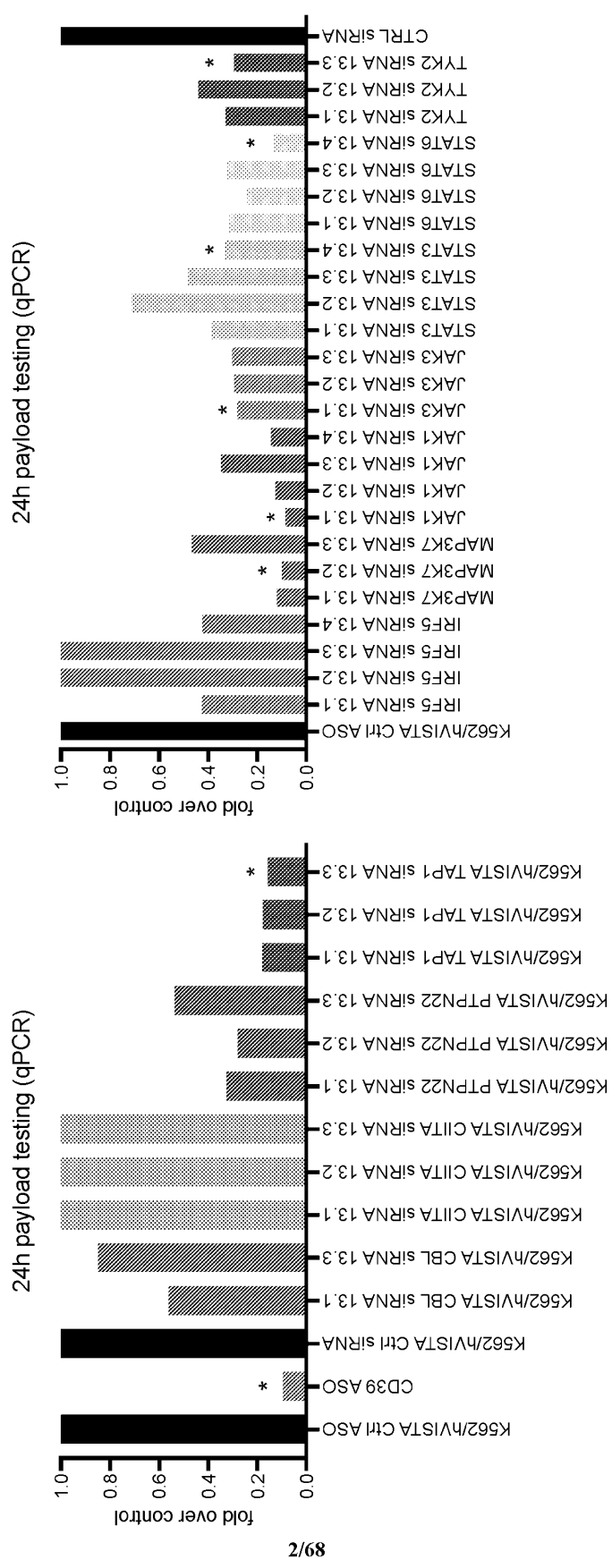


Figure 2. Additional immunologically relevant siRNAs and ASO payloads have been identified and tested. K562-VISTA cells were transfected with 200 nM siRNA (or ASO) alone, and target knockdown was analyzed by qRT-PCR using the ddct method and reported as fold over control. Scrambled siRNA or ASO controls were also ordered from IDT. Payloads marked with (*) were selected for conjugation to a delivery vehicle (anti-VISTA Mab INX201). Only CD39 ARC is described in this report from the second round of payloads; other ARC's conjugation is planned/ongoing.

FIG. 3

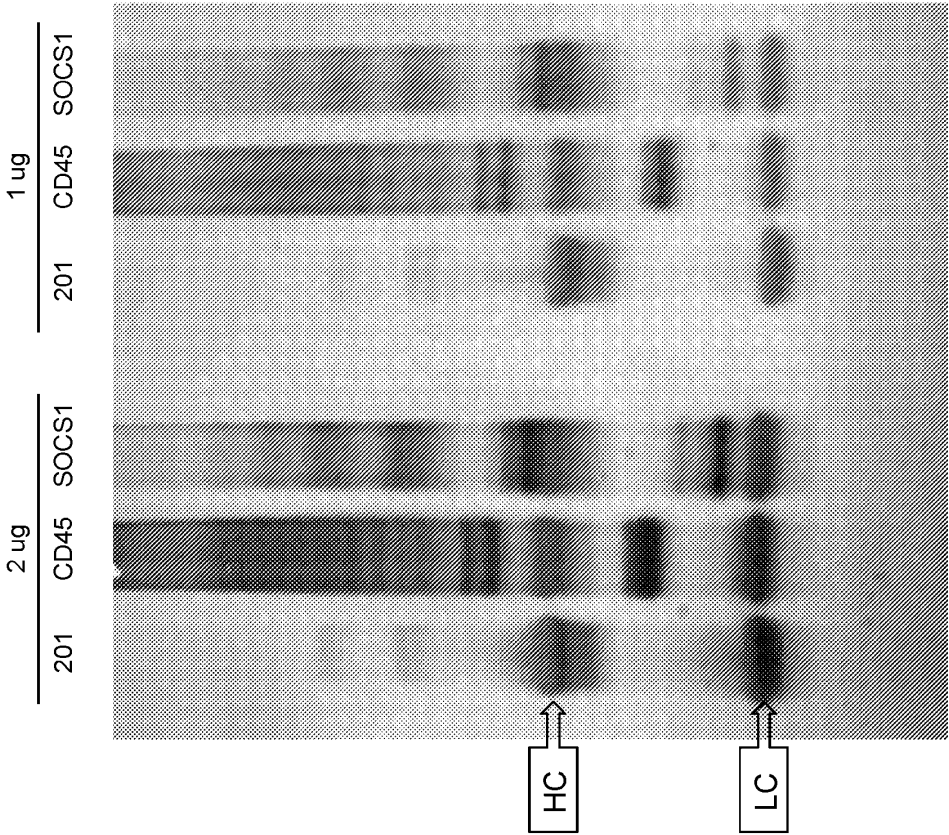


Figure 3. SDS-PAGE of the more ... reducing SDS-PAGE followed by silver stain. Lane labels: 201 – free INX201 anti-VISTA Mab; CD45 – ARC with CD45 siRNA; SOCS1 – ARC with SOCS1 ASO; a discrete pattern of multiple conjugates is observed, confirming efficient conjugation. The HC or LC shift with siRNA is more profound than ASO, based on the molecular weight of the payload (~17 vs. ~6 kDa).

FIG. 4A

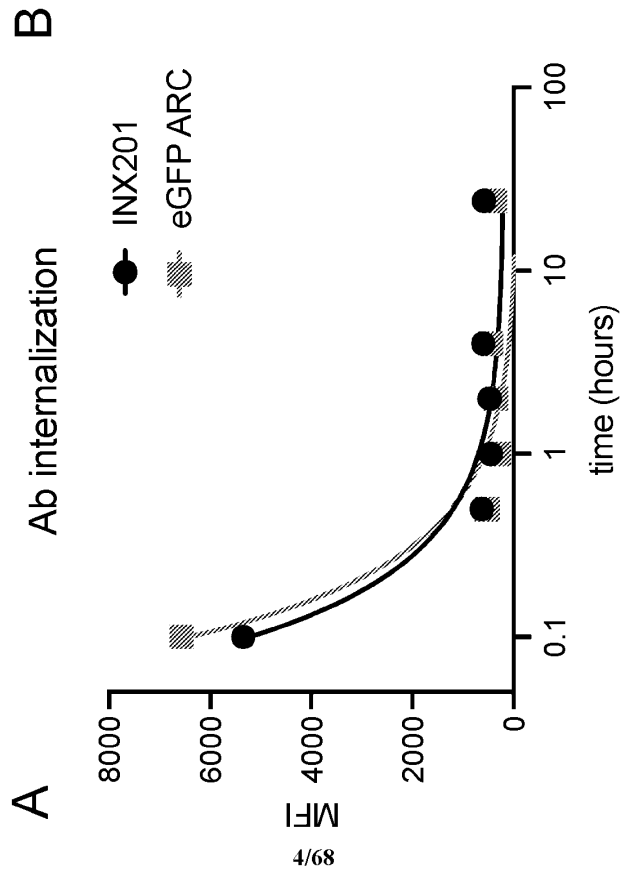


FIG. 4B

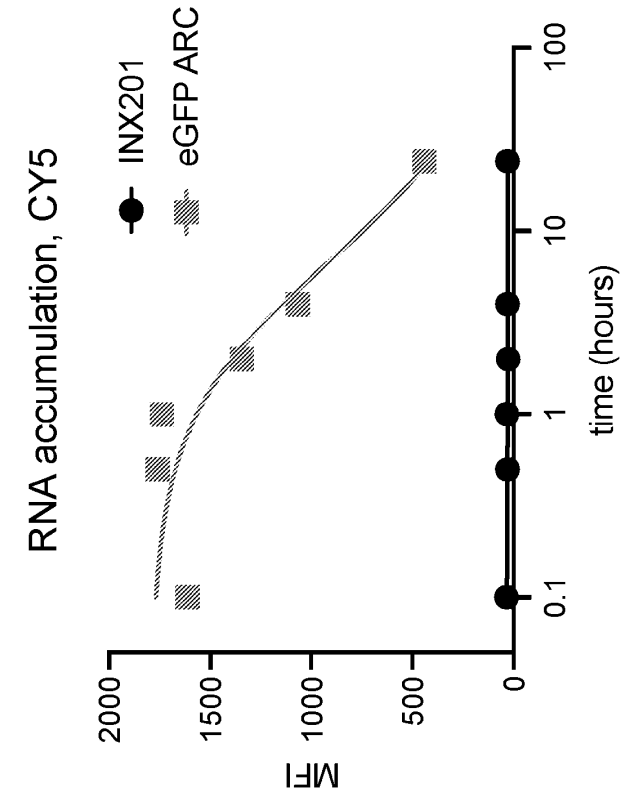


Figure 4A-4B. ARC efficient binding and internalization from the surface and intracellular retention of siRNA inside K562-VISTA cells. Free INX201 (line with circles) or eGFP ARC (line with squares) were used at 200 nM. A) Time course of antibody binding and internalization B) RNA accumulation assay, measured by Cy5. MFI – mean fluorescent intensity; representative of two independent experiments shown.

FIG. 5A

FIG. 5B

FIG. 5C

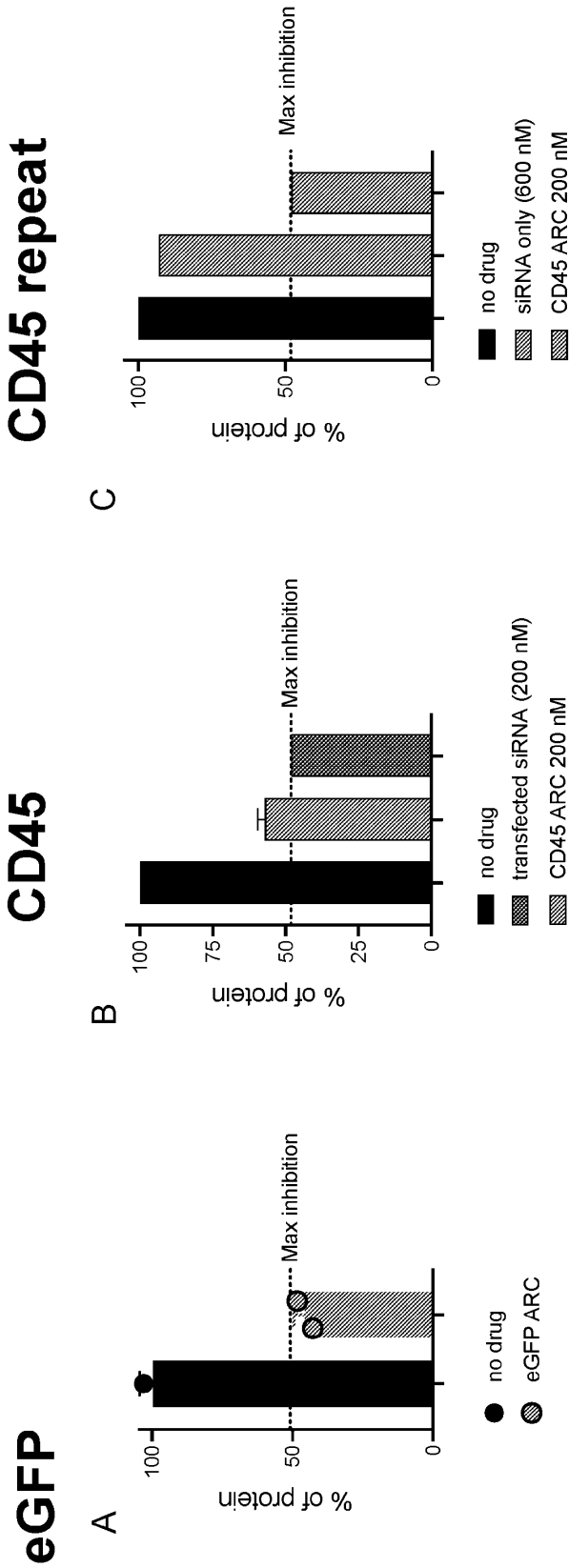


Figure 5A-C. INX201 ARC's knockdown protein expression is equivalent to transfection *in vitro*. K562-VISTA WT cells or eGFP+ cell pools were used for this study. A) cells were treated for 28 hours with no drug (left bar) or 200 nM eGFP ARC (right bar). The maximal levels of eGFP protein knockdown were established by transfecting eGFP siRNA into the same cells (~50%, measured at 24 hours). ARC-mediated knockdown was similar to the maximal possible knockdown levels (based on siRNA sequence). B) Dash line represents the maximal level of CD45 protein knockdown expected, based on the payload (siRNA) potency, which is 50%, as measured from free transfected CD45 siRNA at 48 hours (right bar); cells treated for 72 hours with 200 nM eGFP ARC (middle bar) or with no drug (left bar). C) CD45 levels measured in a repeat experiment. Cells were treated for 72 hours with no drug (left bar), free siRNA, no transfection (middle bar), and 200 nM ARC (right bar).

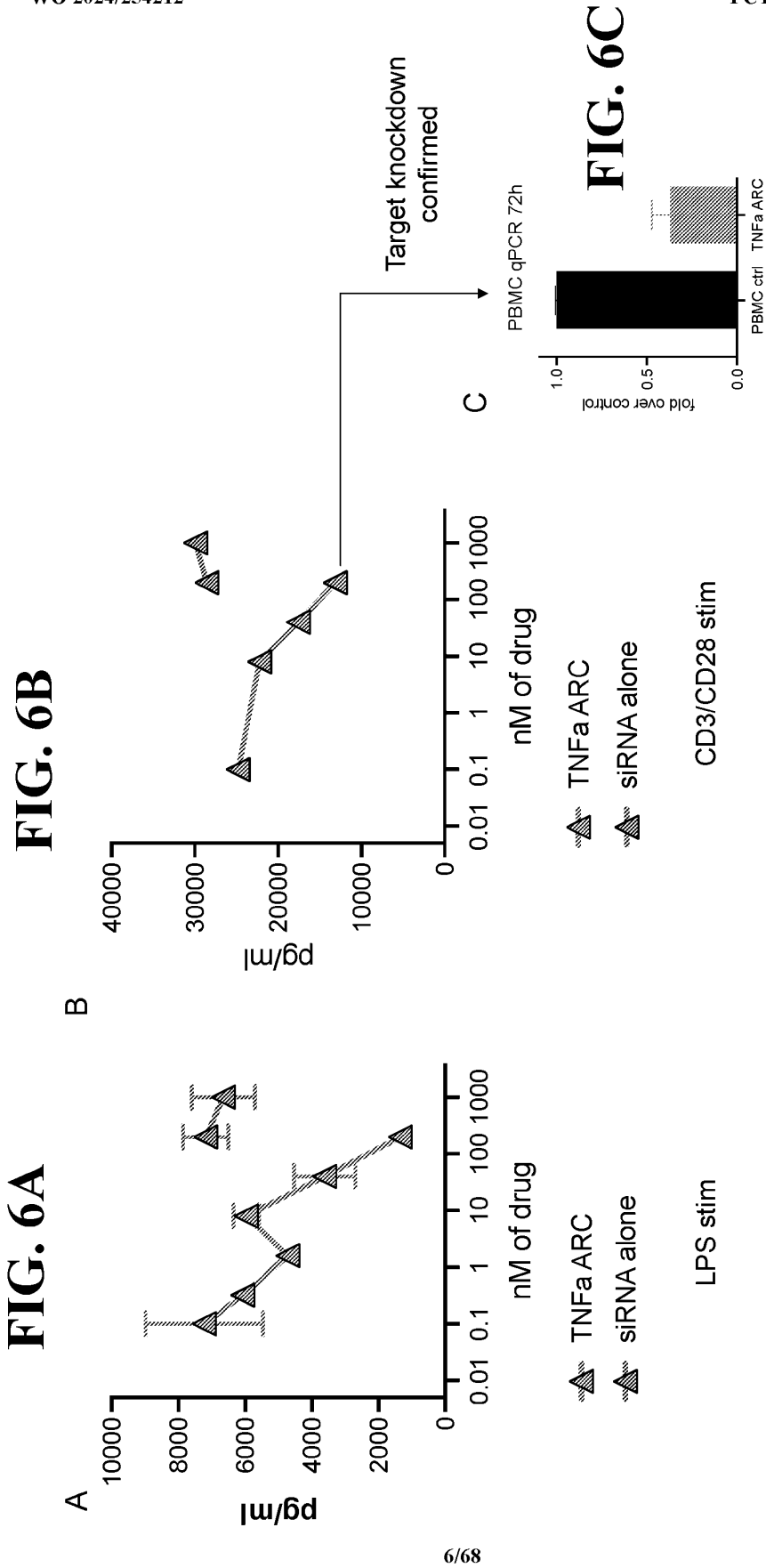


Figure 6A-C. INX201 ARCs inhibit TNFα from PBMC. Human PBMCs were activated with (A) 10 ng/ml LPS or (B) anti-CD3/CD28 beads, bead to T cell ratio 1:2, and treated with TNFα ARC (0-200 nM) or free RNA (200-1000 nM) for 48 hours (LPS) or 72 hours (beads). There was an efficient dose-dependent reduction in TNFα levels with ARC but not free siRNA. C) qRT-PCR performed from ARC-treated versus untreated PBMCs, collected at 72 hours, confirmed efficient target knockdown; no ARC was visualized as 0.1 nM (due to log scale).

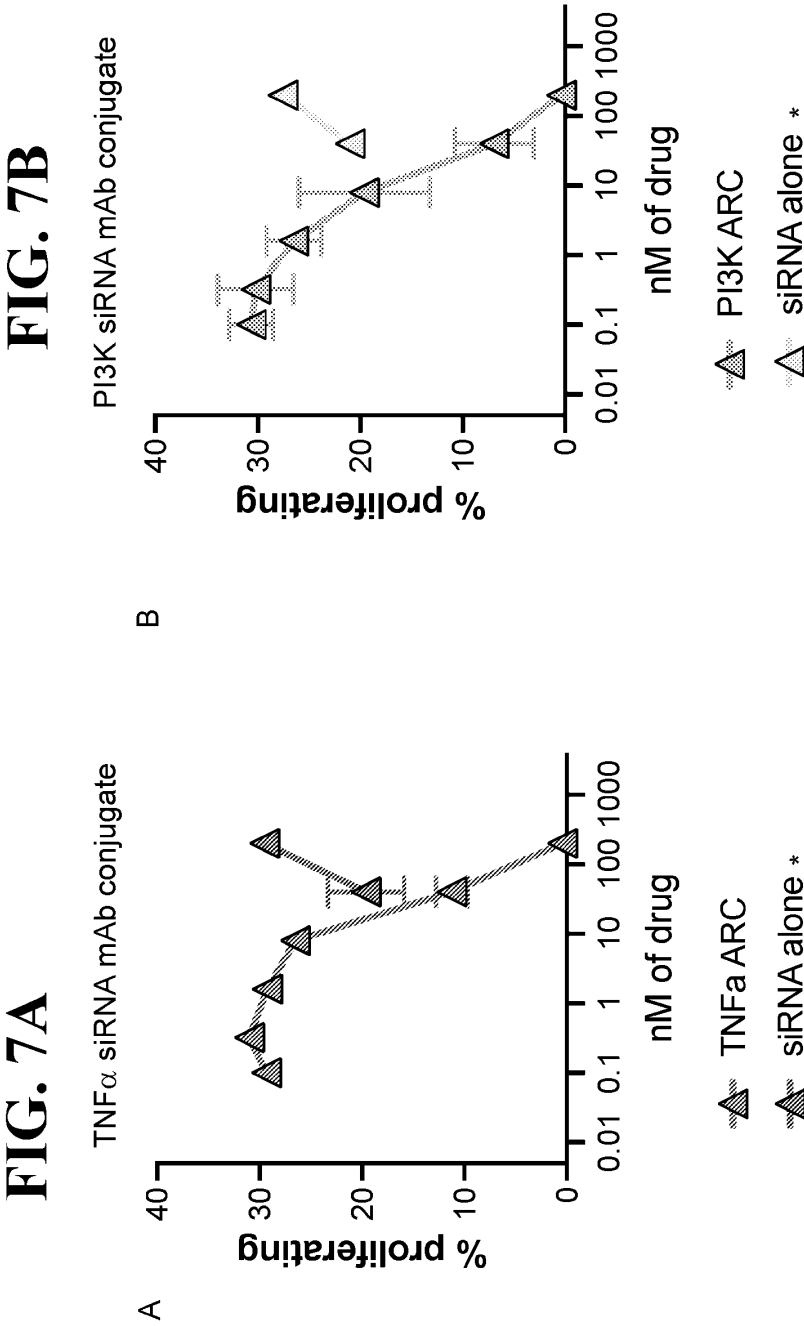
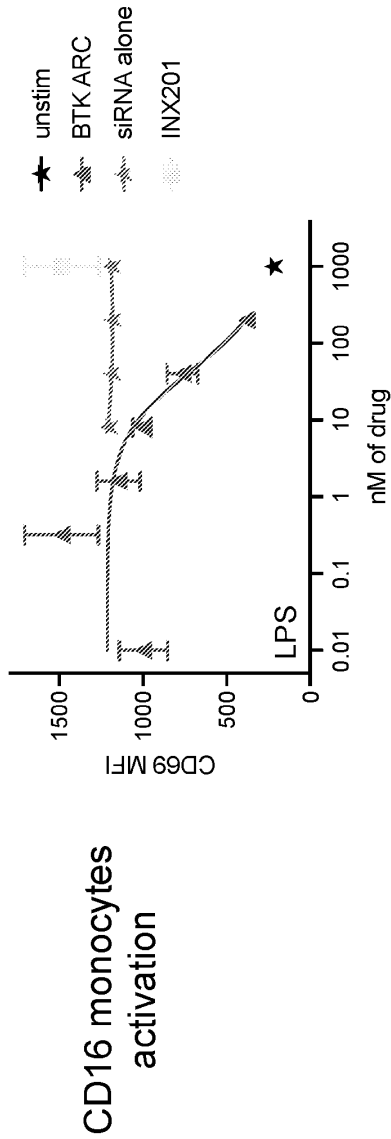


Figure 7A-B. INX201 ARCs slow down the proliferation of T cells. Human PBMCs were activated with anti-CD3/CD28 beads, bead to T cell ratio 1:2, and treated with (A) TNFa ARC (0-200 nM) or free RNA (200-1000 nM) or (B) PI3K ARC (0-200 nM) or free RNA (200-1000 nM) for 72 hours. There was an efficient dose-dependent reduction in newly proliferating T cells with ARC but not free siRNA treatments. Proliferation was analyzed by cell trace violet dilution, visualized by flow cytometry; no ARC was visualized as 0.1 nM (due to log scale). The curves were generated from inhibitor vs. response three-parameter non-linear regression analysis (GraphPad Prism 9). A single technical replicate per concentration point was used.

FIG. 8A

A



B

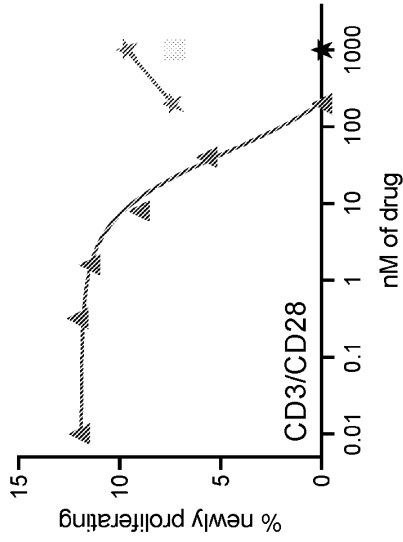


FIG. 8B

Figure 8A-B. Reduced PBMC activation by INX201-BTK ARC. Human PBMCs were activated with (A) 10 ng/ml LPS or (B) anti-CD3/CD28 beads, bead to T cell ratio 1:2, and treated with BTK ARC (0-200 nM, triangles) or free RNA (200-1000 nM, stars), or free INX201 (square) for 48 hours (LPS) or 72 hours (beads). The curves were generated from inhibitor vs. response three-parameter non-linear regression analysis (GraphPad Prism 9). CD69 levels were measured in A; % newly proliferating cells in B; A single technical replicate per concentration point was used; no ARC was visualized as 0.1 nM (due to log scale); unstim – unstimulated cells; MFI – mean fluorescent intensity.

FIG. 9A

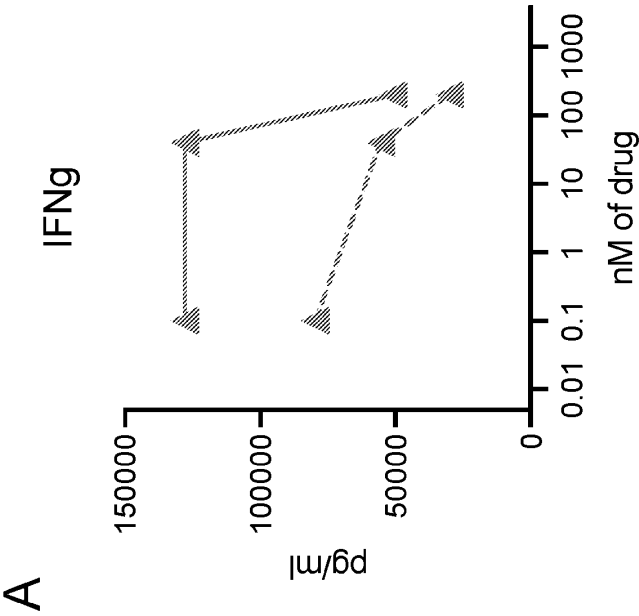


FIG. 9B

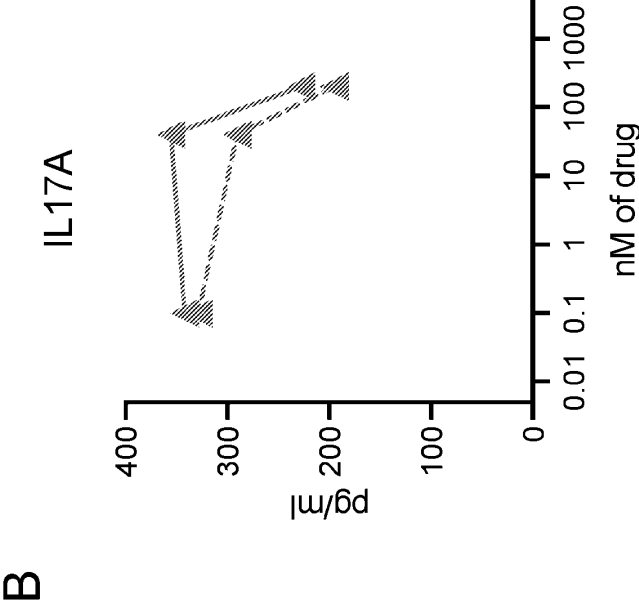


Figure 9A-B. Reduced cytokine production by INX201-Glut1 ARC. Purified human T cells were activated with anti-CD3/CD28 beads, bead to a T cell ratio 1:2, and treated with Glut1 ARC (0-200 nM) for 72 hours. A single technical replicate per concentration point was used. Two human donors were tested: donor1 – solid line, donor 2 – dashed line; no ARC was visualized as 0.1 nM (due to log scale). A) IFN γ and B) IL17A were measured by Luminex.

FIG. 10A

FIG. 10B

FIG. 10C

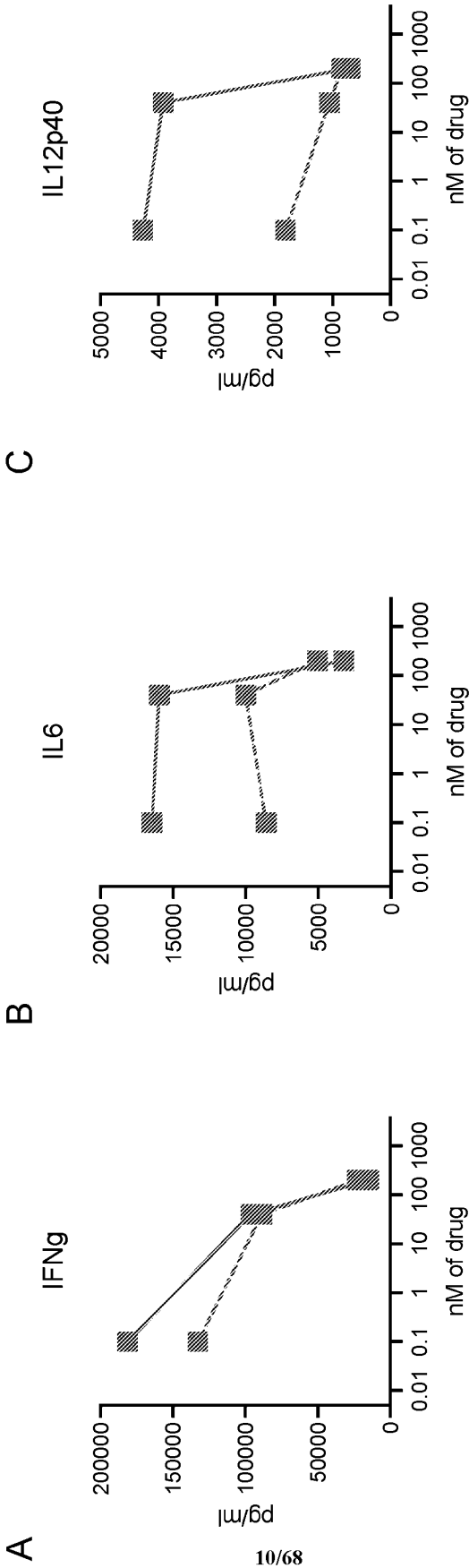


Figure 10A-C. Reduced cytokine production by INX201-Glut1 ARC. Purified human T cells were activated with anti-CD3/CD28 beads, bead to a T cell ratio 1:2, and treated with RORC ARC (0-200 nM) for 72 hours. A single technical replicate per concentration point was used. Two human donors were tested: donor1 – solid line, donor 2 – dashed line; no ARC was visualized as 0.1 nM (due to log scale). A) IFN γ , B) IL6, and C) IL12p40 were measured by Luminex.

FIG. 11

CD39 ASO mAb conjugate

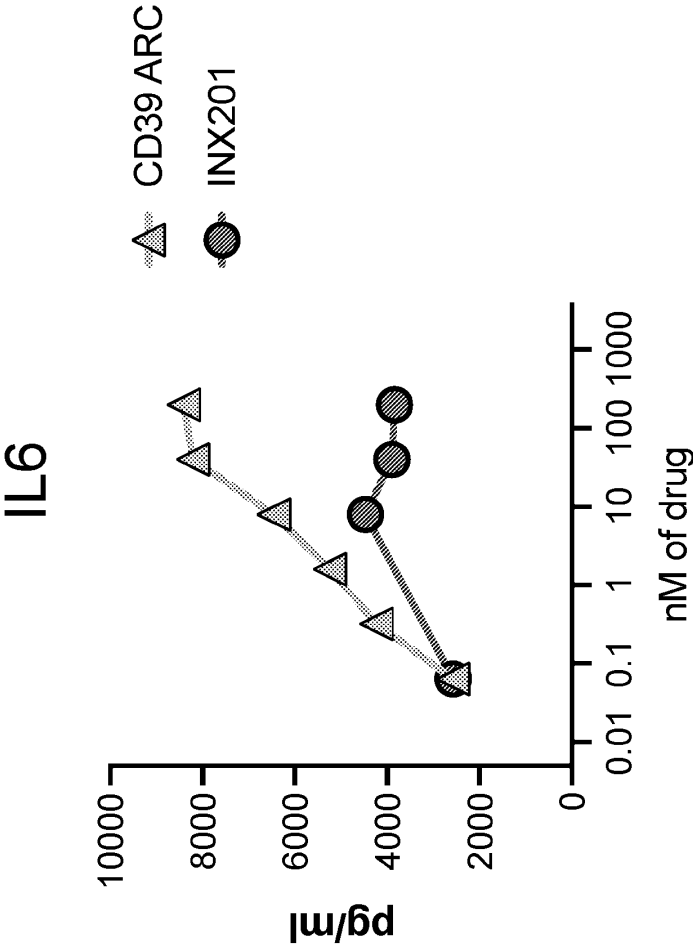


Figure 11. INX201-CD39 ASO ARCs targeting enhances immune responses in human PBMC. Human PBMCs were activated with anti-CD3/CD28 beads and treated with CD39 ARC (0-200 nM, triangles) or free INX201 (0-200 nM, circles) for 72 hours. The curves were generated from inhibitor vs. response three-parameter non-linear regression analysis (GraphPad Prism 9). A single technical replicate per concentration point was used; no ARC was visualized as 0.1 nM (due to the log scale).

FIG. 12A

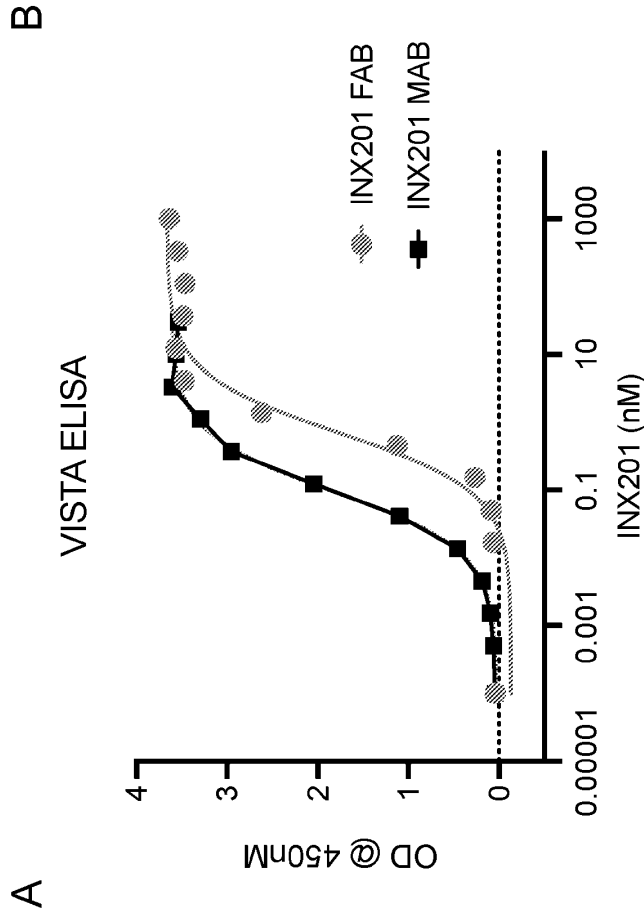


FIG. 12B

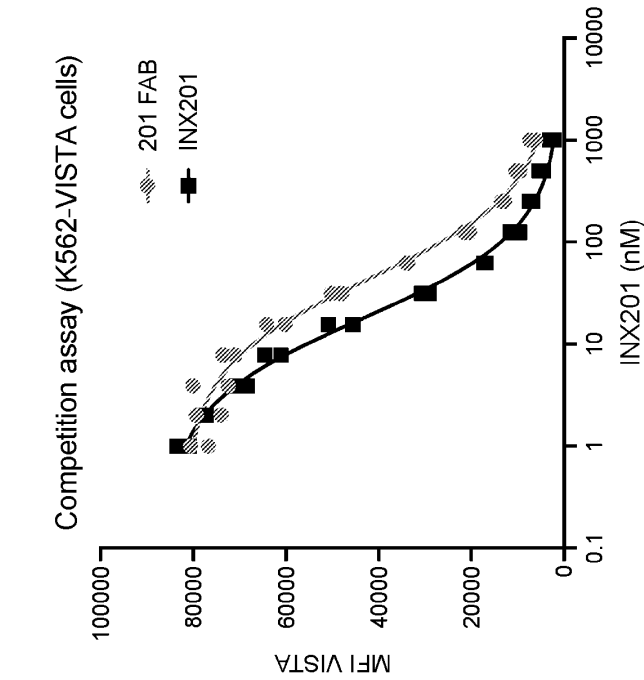


Figure 12A-B. Platform optimization: anti-VISTA Fab can be used instead of Mab. A) Comparison of binding to human VISTA ECD between INX201 Mab (squares) and INX201 Fab (circles) by ELISA. B) K562-VISTA cell-based competition assay, where the pre-bound increasing concentrations of INX201 Mab (squares) or INX201 Fab (circles) block available VISTA on the cell surface (hence reduced VISTA MFI measurement by INX201-AF488; the curves were generated from inhibitor vs. response three-parameter non-linear regression analysis (GraphPad Prism 9). n=2 technical replicate per concentration point was used; no Ab was visualized as 0.0001 nM (due to log scale).

FIG. 13

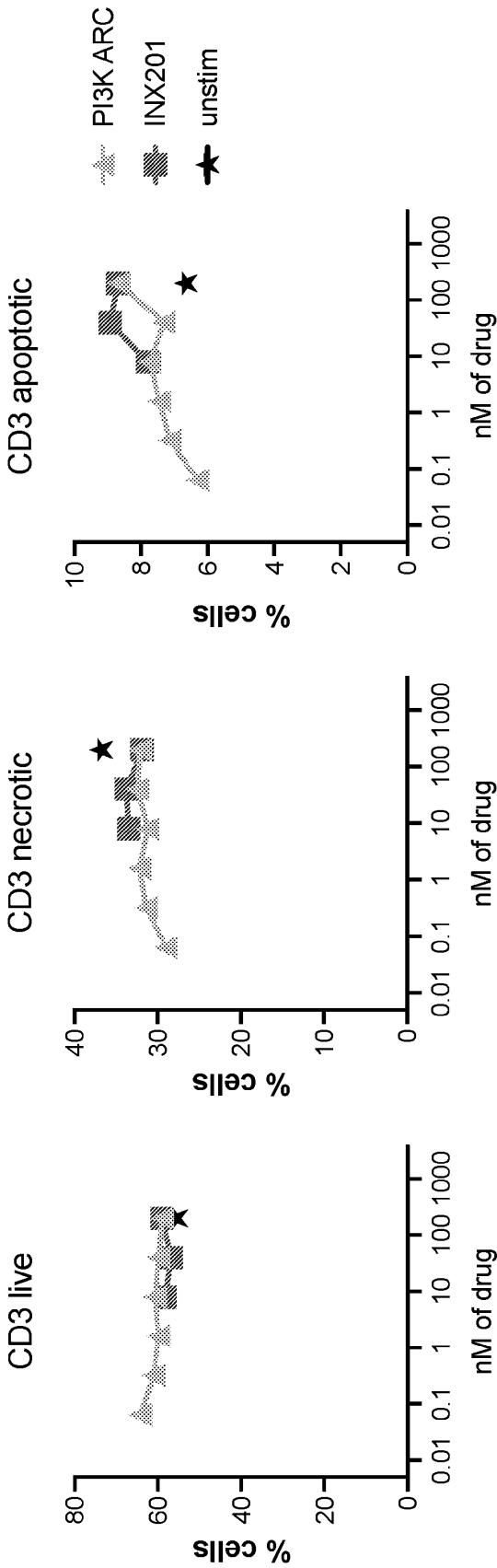


Figure 13. ARC does not impact t cell viability. Human PBMCs were activated with anti-CD3/CD28 beads and treated with PI3K ARC (0-200 nM, triangles) or free INX201 (0-200 nM, squares) for 72 hours. The curves were generated from inhibitor vs. response three-parameter non-linear regression analysis (GraphPad Prism 9). A single technical replicate per concentration point was used; no ARC was visualized as 0.1 nM (due to the log scale); unstim - unstimulated cells.

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
GA1	Mouse IgG1/kappa	LLDSGLYCC LVVEIRHHH SEHRVH	GYTLTDYN (SEQ ID NO:100)	INLNVAIT (SEQ ID NO:101)	ARGGYRTY YAMDY (SEQ ID NO:102)	ENIYSN (SEQ ID NO:103)	AAT (SEQ ID NO:104)	QHFWGTP RT (SEQ ID NO:105)	EVQLQQGAEVLKPG ASVKISCKASGYTLTD YNMDWVKQSHGKSL EWIGHNINVAITTYN QKFKGKATLTVDKSS TAYMEIRLSLTSEDYAV YTCARGGYRTYTYAM DYWGQGTSTVYS (SEQ ID NO:106)	AKTTPSPYYPLAPGSAAT NSMVTGLCLVKGYFPEVPT VTWNSGSLSGVHTFPAVL QSDLYTLSSVTVPSSTWPS ETVTCNVAAHPASSTKVDK IVPRDCGCKPCTVPEVSS VFHPKPKDVLITLTTPKVT GVPSRFSGSGSGTQ YSLKINSLSQSEDFGS DDVEVHTAQTQPREQFN STFRSVCSELPIMHQDWLN GKEFKCRVNSAAFPAPKEKT ISKTKLNPKS (SEQ ID NO:107)	DIQMTQSPASLSVS VGEVTVITTCRASENI YSNLAWYQQKQKG SPQLLVYAATNLAD GVPSRFSGSGSGTQ YSLKINSLSQSEDFGS YYCQHFWGTPRTFG GGTKLEIK (SEQ ID NO:108)	RADAAPTYSI FPSPSEQLTSG GASVVCFLNN FYPKDNVKKW KIDGSEKQNG VINSWTDQD SKDSTYSMS TLTLTKDEYER HNSYTCEATH KISTSPVKNF NRNEC (SEQ ID NO:109)
			GYTLTDYN (SEQ ID NO:110)	INLNVAIT (SEQ ID NO:111)	ARGGYRTY YAMDY (SEQ ID NO:112)	ENIYSN (SEQ ID NO:113)	AAT (SEQ ID NO:114)	QHFWGTP RT (SEQ ID NO:115)	EVQLQQGAEVLKPG ASVKISCKASGYTLTD YNMDWVKQSHGKSL EWIGHNINVAITTYN QKFKGKATLTVDKSS TAYMEIRLSLTSEDYAV YTCARGGYRTYTYAM DYWGQGTSTVYS (SEQ ID NO:116)	ASTKGPSVFPLAPCSRSTSE STAALGCLVKDYEPEPTVS WNSGALTSGVHTFPAVLQ SSGLYSLSVTVPSNFGT QTYTCNVVDHHPKNTKVDK TVERRKCCVCPCPAPPA GPSVFLFPPPKKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEOFNSTFRVSVLTVVHQ DWLNGKEYCKCKVSNKGLP APIETKSTKTKGQPREPQVY TLPPSRREEMTKNQSLTCL VKGFPYSDIAVEWESNGQ PENNYKTTTPMILDSGFF LYSKLTVDKSRWQQGNV SCSMVHEALHNYHTQKSL LSPGK (SEQ ID NO:117)	DIQMTQSPASLSVS VGEVTVITTCRASENI YSNLAWYQQKQKG SPQLLVYAATNLAD GVPSRFSGSGSGTQ YSLKINSLSQSEDFGS YYCQHFWGTPRTFG GGTKLEIK (SEQ ID NO:118)	RTVAAPSVFIF PPSEQLKSG TASVVCCLNN FYPREKRVQ WKVDNALQS GNSQESVTEQ DSKSDSTYLS TLTLKADYEK HKVYACEVTH QGLSPVTKSF NRGEC (SEQ ID NO:119)
GA1- IgG2	Human IgG2/kappa	LLDSGLYCC LVVEIRHHH SEHRVH	GYTLTDYN (SEQ ID NO:110)	INLNVAIT (SEQ ID NO:111)	ARGGYRTY YAMDY (SEQ ID NO:112)	ENIYSN (SEQ ID NO:113)	AAT (SEQ ID NO:114)	QHFWGTP RT (SEQ ID NO:115)	EVQLQQGAEVLKPG ASVKISCKASGYTLTD YNMDWVKQSHGKSL EWIGHNINVAITTYN QKFKGKATLTVDKSS TAYMEIRLSLTSEDYAV YTCARGGYRTYTYAM DYWGQGTSTVYS (SEQ ID NO:116)	ASTKGPSVFPLAPCSRSTSE STAALGCLVKDYEPEPTVS WNSGALTSGVHTFPAVLQ SSGLYSLSVTVPSNFGT QTYTCNVVDHHPKNTKVDK TVERRKCCVCPCPAPPA GPSVFLFPPPKKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEOFNSTFRVSVLTVVHQ DWLNGKEYCKCKVSNKGLP APIETKSTKTKGQPREPQVY TLPPSRREEMTKNQSLTCL VKGFPYSDIAVEWESNGQ PENNYKTTTPMILDSGFF LYSKLTVDKSRWQQGNV SCSMVHEALHNYHTQKSL LSPGK (SEQ ID NO:117)	DIQMTQSPASLSVS VGEVTVITTCRASENI YSNLAWYQQKQKG SPQLLVYAATNLAD GVPSRFSGSGSGTQ YSLKINSLSQSEDFGS YYCQHFWGTPRTFG GGTKLEIK (SEQ ID NO:118)	DIVLTQSPAS LAVSLGQRATI SCRASQSVST STFSYMHVY QOKPGQPPK LUKYASNLES GYPARFSGSG SGTDFTLNIHP VEEEDTATY CQHSWEIPT FGGKLEIK (SEQ ID NO:119)
			GYSTGYT (SEQ ID NO:120)	INPYNGGI (SEQ ID NO:121)	ARRTLRPYF FDY (SEQ ID NO:122)	QSVSTSTFSY (SEQ ID NO:123)	YAS (SEQ ID NO:124)	QHSWEIPT T (SEQ ID NO:125)	EVQLQQSGPELVKPGTSM KISKASQSYFTGYTMINW VRQSHGKNI EWIGLINPYN GGINYNQKFKARATLTVDK SSSTAYMELLSITSEDSAV YCARRTLRLPYFDYWGGQ TTLTVSS (SEQ ID NO:127)	DIQMTQSPASLSVS VGEVTVITTCRASENI YSNLAWYQQKQKG SPQLLVYAATNLAD GVPSRFSGSGSGTQ YSLKINSLSQSEDFGS YYCQHFWGTPRTFG GGTKLEIK (SEQ ID NO:118)	DIVLTQSPASLSVS VGEVTVITTCRASENI YSNLAWYQQKQKG SPQLLVYAATNLAD GVPSRFSGSGSGTQ YSLKINSLSQSEDFGS YYCQHFWGTPRTFG GGTKLEIK (SEQ ID NO:118)	DIVLTQSPAS LAVSLGQRATI SCRASQSVST STFSYMHVY QOKPGQPPK LUKYASNLES GYPARFSGSG SGTDFTLNIHP VEEEDTATY CQHSWEIPT FGGKLEIK (SEQ ID NO:129)
GG8	Mouse IgG1/?	LLDSGLYCC LVVEIRHHH SEHRVH; GHVDITYK TWYRSRG EVQTC	GYSTGYT (SEQ ID NO:120)	INPYNGGI (SEQ ID NO:121)	ARRTLRPYF FDY (SEQ ID NO:122)	QSVSTSTFSY (SEQ ID NO:123)	YAS (SEQ ID NO:124)	QHSWEIPT T (SEQ ID NO:125)	EVQLQQSGPELVKPGTSM KISKASQSYFTGYTMINW VRQSHGKNI EWIGLINPYN GGINYNQKFKARATLTVDK SSSTAYMELLSITSEDSAV YCARRTLRLPYFDYWGGQ TTLTVSS (SEQ ID NO:127)	DIQMTQSPASLSVS VGEVTVITTCRASENI YSNLAWYQQKQKG SPQLLVYAATNLAD GVPSRFSGSGSGTQ YSLKINSLSQSEDFGS YYCQHFWGTPRTFG GGTKLEIK (SEQ ID NO:118)	DIVLTQSPASLSVS VGEVTVITTCRASENI YSNLAWYQQKQKG SPQLLVYAATNLAD GVPSRFSGSGSGTQ YSLKINSLSQSEDFGS YYCQHFWGTPRTFG GGTKLEIK (SEQ ID NO:118)	DIVLTQSPAS LAVSLGQRATI SCRASQSVST STFSYMHVY QOKPGQPPK LUKYASNLES GYPARFSGSG SGTDFTLNIHP VEEEDTATY CQHSWEIPT FGGKLEIK (SEQ ID NO:129)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
GG8- IgG2	Human IgG2/ κ appa	LLDGLYCC LVVEIRHHH SEHRVH;	GYSFTGYT (SEQ ID NO:130)	INPYNGGI (SEQ ID NO:131)	ARRTLRPYF FDY (SEQ ID NO:132)	QSVSTSTFSY (SEQ ID NO:133)	YAS (SEQ ID NO:134)	QHSWEIPY T (SEQ ID NO:135)	EVQLQSGGPELVKPG TSMKISCKASGYFTG YTMNHWVRQSHGKNL EWGLINPYNGGINYN QKFKARATLTVDKSSS TAYMELSLTSEDSAV YYCARRTLRLPYFDY WGCGTTLTVSS (SEQ ID NO:136)	ASTKGPSVFPLAPCSRSTSE STAALGCLVLYDYPFPTVVS WNSGALTSGVHTFPAVLQ SSGLYSLSSVTVFSSNFGT QTYTCNVDHKPSNTKVDK TVERKCCVECPCPAPPA GPSVFLPPPKPKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEQFNSTFRVVSIVLVVHQ DWLNGKEYKCKVSNKGLP APIETKSTKTKGQPREPQVY TLPSPREEMTKNQVSLTCL VKGPFPSDIAVEWESNGQ PENNYKTPPMILDSGFF LYSKLTVDKSRWQQGNV SCSVIMHEALHNHYTQKSLS LSPGK (SEQ ID NO:137)	DIVLTQSPASLAVSL GQRATISCRASQSV STSTFSYMHWHYQQ KPGQPKLLIKYASN LESGVPARFSGSGS TTLTSKADYEK GTDFITLIHPVEED TATYYCQHSWEIPY TFGGGTKLEIK (SEQ ID NO:138)	RTVAAPSVEIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKSDTYSLS TTLTSKADYEK HKYACEVTH QQLSPVTKSF NRGEC (SEQ ID NO:139)
		GHDVTFYK TWYRSRRG EVQTC							EVKLESGGGLVQPG GSLKLSCAASGDFSR YWMWSVWRQAPGKG LEWIGEVYPDSTINYN TPSLKDKFIHSRDNAK NTLYLQMIKVRSEDTA LYYCARGRDYWGQ GTSVTYSS (SEQ ID NO:146)	ASTKGPSVFPLAPCSRSTSE STAALGCLVLYDYPFPTVVS WNSGALTSGVHTFPAVLQ SSGLYSLSSVTVFSSNFGT QTYTCNVDHKPSNTKVDK TVERKCCVECPCPAPPA GPSVFLPPPKPKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEQFNSTFRVVSIVLVVHQ DWLNGKEYKCKVSNKGLP APIETKSTKTKGQPREPQVY TLPSPREEMTKNQVSLTCL VKGPFPSDIAVEWESNGQ PENNYKTPPMILDSGFF LYSKLTVDKSRWQQGNV SCSVIMHEALHNHYTQKSLS LSPGK (SEQ ID NO:147)	DIQMTQSPASLSAS VGTEVTTTCRASGNI HNILSWYHQKQK SPQLLVYNKTLAD GVPSRFSGSGGTQ YSLKINSLOPEDGS YYCQNFWSPTPTFG SGTKLEIK (SEQ ID NO:148)	RTVAAPSVEIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKSDTYSLS TTLTSKADYEK HKYACEVTH QQLSPVTKSF NRGEC (SEQ ID NO:149)
IE8	Mouse IgG1/?	LLDGLYCC LVVEIR	GFDFSRYW (SEQ ID NO:140)	VYPDSSII (SEQ ID NO:141)	ARGRGDY (SEQ ID NO:142)	GNIHNY (SEQ ID NO:143)	NAK (SEQ ID NO:144)	QNFWSPTF T (SEQ ID NO:145)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
IE8-IgG2	Human IgG2/kappa	LLDSGLYCC LVVEIR	GFDFSRYW (SEQ ID NO:150)	VYPDSSTI (SEQ ID NO:151)	ARGRGDY (SEQ ID NO:152)	GNIHNY (SEQ ID NO:153)	NAK (SEQ ID NO:154)	QNFWSPTF T (SEQ ID NO:155)	EVKLLSEGGGLVQPG GSLKLSCAASGFDFSR YWMWVVRQAPGKG LEWIGEVYDPSSTINY TPSLKDKFHSIRDNAK NTLYLQMIKYRSEDTA LYYCARGRGDYWGQ GTSVTYSS (SEQ ID NO:156)	ASTKGPSVFPLAPSRSTSE STAALGCLVKDYFPEPTVVS WNSGALTSGVHTFPAVLQ SSGLYSLSSVTVFSSNFGT QTYTCNVDHKPSNTKVDK TVERKCCVECPCPAPPA GPSVFLPPPKPKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEQFNSTFRVSVLTVVHQ DWLNGKEYKCKVSNKGLP APIETKSTKTKQPREPQVY TLPPSREEMTKNQVSLTCL VKGPFPSDIAVEWESNGQ PENNYKTPPMILDSGSGFF LYSKLTVDKSRWQQGNVF SCSVIMHEALHNHYTQKSLS LSPGK (SEQ ID NO:157)	DIQMTQSPASLSAS VGTEVTTICRASGNI HNYLSWYHQKQK SPQLLVYNAKTLAD GVPSRFSGSGGTQ YSLKINSIQPEDFGS YYCQNFWSPTPTFG SGTKLEIK (SEQ ID NO:158)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSSTYLS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:159)
IE8-IgG2- C127S	Human mutated IgG2/kappa	LLDSGLYCC LVVEIR	GFDFSRYW (SEQ ID NO:160)	VYPDSSTI (SEQ ID NO:161)	ARGRGDY (SEQ ID NO:162)	GNIHNY (SEQ ID NO:163)	NAK (SEQ ID NO:164)	QNFWSPTF T (SEQ ID NO:165)	EVKLLSEGGGLVQPG GSLKLSCAASGFDFSR YWMWVVRQAPGKG LEWIGEVYDPSSTINY TPSLKDKFHSIRDNAK NTLYLQMIKYRSEDTA LYYCARGRGDYWGQ GTSVTYSS (SEQ ID NO:166)	ASTKGPSVFPLAPSRSTSE STAALGCLVKDYFPEPTVVS WNSGALTSGVHTFPAVLQ SSGLYSLSSVTVFSSNFGT QTYTCNVDHKPSNTKVDK TVERKCCVECPCPAPPA GPSVFLPPPKPKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEQFNSTFRVSVLTVVHQ DWLNGKEYKCKVSNKGLP APIETKSTKTKQPREPQVY TLPPSREEMTKNQVSLTCL VKGPFPSDIAVEWESNGQ PENNYKTPPMILDSGSGFF LYSKLTVDKSRWQQGNVF SCSVIMHEALHNHYTQKSLS LSPGK (SEQ ID NO:167)	DIQMTQSPASLSAS VGTEVTTICRASGNI HNYLSWYHQKQK SPQLLVYNAKTLAD GVPSRFSGSGGTQ YSLKINSIQPEDFGS YYCQNFWSPTPTFG SGTKLEIK (SEQ ID NO:168)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSSTYLS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:169)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (Imgt)	Heavy-chain cdr2 (Imgt)	Heavy-chain cdr3 (Imgt)	Light-chain cdr1 (Imgt)	Light-chain cdr2 (Imgt)	Light-chain cdr3 (Imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB100	Human IgG1/kappa	Group 1	GYSFTSYW (SEQ ID NO:170)	IYPGDSOT (SEQ ID NO:171)	ARDVSSFYGY SPMFEDY (SEQ ID NO:172)	QSVSSY (SEQ ID NO:173)	DAS (SEQ ID NO:174)	QQRSNWP LT (SEQ ID NO:175)	EVQLVDSGAEVKKPG ESLKISCKGSGYSFTSY WIGWVRQMPGKGLE WIMGIYIPGDSOTRYS PSFQGQVTSADKSSIS TAYLQWSSLKASDTA MYYCARDVSSFYGY PMFEDYWGQGLTVTV SS (SEQ ID NO:176)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHTCPCAP ELLGGPSVFLPPPKKDTLM ISRTPETVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYCKVSNK ALPAIEKTIKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVMHEALHNHYTQK SLISPGK (SEQ ID NO:177)	EVLTQSPATLSLSPG ERATLSCRASQSVSS YLAWYQQKPGQAP RLIYDASNRATGIP ARFSGSGSTDFLT ISSLEPEDFAVYYCQ QRSNWPLTFGQGT KVEIK (SEQ ID NO:178)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSSTYLS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:179)
			GYSFTSYW (SEQ ID NO:180)	IYPGDSOT (SEQ ID NO:181)	ARDVSSFYGY YSALLDY (SEQ ID NO:182)	QSVSSY (SEQ ID NO:183)	GAS (SEQ ID NO:184)	QQYGSSPL T (SEQ ID NO:185)	EVQLVDSGAEVKKPG ESLKISCKGSGYSFTSY WIGWVRQMPGKGLE WIMGIYIPGDSOTRYS PSFQGQVTSADKSSIS TAYLQWSSLKASDTA MYYCARDVSSFYGY ALLDYWGQGLTVTVS S (SEQ ID NO:186)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHTCPCAP ELLGGPSVFLPPPKKDTLM ISRTPETVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYCKVSNK ALPAIEKTIKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVMHEALHNHYTQK SLISPGK (SEQ ID NO:187)	EVLTQSPGTLSLSPG ERATLSCRASQSVSS YLAWYQQKPGQAP PRLLIYGASSRATGIP DRFSGSGSTDFLT ISRLEPEDFAVYYCQ QYGSPLTFGGGTK VEIK (SEQ ID NO:188)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSSTYLS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:189)
VSTB101	Human IgG1/kappa	VSTB101 Group 1										

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB102	Human IgG1/kappa	Group 1	GYSFTSYW (SEQ ID NO:190)	IYPGDSOT (SEQ ID NO:191)	ARDSYSFYGH TPVLDY (SEQ ID NO:192)	QSVSSSY (SEQ ID NO:193)	GAS (SEQ ID NO:194)	QQYGSST T (SEQ ID NO:195)			
								EVQLVQSGAEVKKPG ESLKISCKGSGYSTSY WIGWVRQMPGKGLE WIMGIYVPGDSOTRYS PSFQGGVTSADKSI TAYLQWSSLKASDTA MYCARDSDSYFYGHT PVLIDYWGQGLTVTS S (SEQ ID NO:196)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLFPPPKKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTTTPVLDSGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSISPGK (SEQ ID NO:197)	EIVLTQSPGTLSLSPG ERATLSCRASQSVSS SVLAHWYQQKPGCA PRLLIYGASRATGIP DRFSGSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSTFTGQGTK VEIK (SEQ ID NO:198)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSYSTLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:199)
VSTB103 INX904	Human IgG1/kappa	Group 1	GYSFTSYW (SEQ ID NO:200)	IYPGDSOT (SEQ ID NO:201)	ARDDALYGG YILDY (SEQ ID NO:202)	QSVLYSSNNK NY (SEQ ID NO:203)	WAS (SEQ ID NO:204)	QQYSTPLT (SEQ ID NO:205)			
								EVQLVQSGAEVKKPG ESLKISCKGSGYSTSY WIGWVRQMPGKGLE WIMGIYVPGDSOTRYS PSFQGGVTSADKSI TAYLQWSSLKASDTA MYCARDSDSYFYGHT PVLIDYWGQGLTVTS SLSISPGK (SEQ ID NO:206)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLFPPPKKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTTTPVLDSGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSISPGK (SEQ ID NO:207)	DIVMTQSPDSLAVS LGERATINCKSSQSV LYSSNNKYNLAHWYQ QKPGQPKLIYWA STRSGVPDRFSGS GGSGDTFTLTISLQA EDVAVYYCCQYYST PLTFGGGTKEIK (SEQ ID NO:208)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSYSTLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:209)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB104	Human IgG1/kappa	Group 1	GYSFTSYW (SEQ ID NO:210)	IYPGDSDT (SEQ ID NO:211)	ARDANSYS AASIFDY (SEQ ID NO:212)	QSVLYSSNNK NY (SEQ ID NO:213)	WAS (SEQ ID NO:214)	QQYSTPLT (SEQ ID NO:215)	EVQLVQSGAEVKKPG ESLKISCKGSGYSTSY WIGWVRQMPGKGLE WIMGIYVPGDSITRYS PSFGQGVTSADKSI TAYLQWSSLIKASDTA MYTCARDANISFYSA SIFDYWGQGLTVTS S (SEQ ID NO:216)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHTCPCAP ELLGPGSVFLPPPKKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSISKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVIMHEALHNHYTQK SLSISPGK (SEQ ID NO:217)	DIVMTQSPDLSAVS LGERATINCKSSQSV LYSNNKNYLAWYQ QKPGQPKLIYWIA STRESGVPRFSGS GSGTDFTLTISLQA EDVAVYYCQYYST PLTFGGGTKEIK (SEQ ID NO:218)	RTVAAPSFIIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQSL GNSQESVTEQ DSKSDSTYSLSS TLTISKADYEK HKVYACEVTH QQLSPTVKSF NRGEC (SEQ ID NO:219)
									QQQLVQSGAEVKKPG SSVYVSKCAGSGTFS YAIWVRQAPGQGLE WIMGGIPIGTANYA QKFGGRVTTADESTS TAYMELSLRSEDTA YYCARSSYGVWSYED YWGQGLTVTS (SEQ ID NO:226)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHTCPCAP ELLGPGSVFLPPPKKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSISKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVIMHEALHNHYTQK SLSISPGK (SEQ ID NO:227)	DIQMTQSPSSLSAS VGDRVITTCRASQSI ATNLNMYQQKPGK APKLIYAASLIQSG VPSRFSGSGSGTDFT LTISLQPEDFATYYC QQINDRPIITFGQGT KVEIK (SEQ ID NO:228)	RTVAAPSFIIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQSL GNSQESVTEQ DSKSDSTYSLSS TLTISKADYEK HKVYACEVTH QQLSPTVKSF NRGEC (SEQ ID NO:229)
VSTB105	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:220)	IPIPIGTA (SEQ ID NO:221)	ARSSYGVSY EDY (SEQ ID NO:222)	QSIATN (SEQ ID NO:223)	AAS (SEQ ID NO:224)	QQNDRPI T (SEQ ID NO:225)	QQQLVQSGAEVKKPG SSVYVSKCAGSGTFS YAIWVRQAPGQGLE WIMGGIPIGTANYA QKFGGRVTTADESTS TAYMELSLRSEDTA YYCARSSYGVWSYED YWGQGLTVTS (SEQ ID NO:226)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHTCPCAP ELLGPGSVFLPPPKKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSISKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVIMHEALHNHYTQK SLSISPGK (SEQ ID NO:227)	DIQMTQSPSSLSAS VGDRVITTCRASQSI ATNLNMYQQKPGK APKLIYAASLIQSG VPSRFSGSGSGTDFT LTISLQPEDFATYYC QQINDRPIITFGQGT KVEIK (SEQ ID NO:228)	RTVAAPSFIIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQSL GNSQESVTEQ DSKSDSTYSLSS TLTISKADYEK HKVYACEVTH QQLSPTVKSF NRGEC (SEQ ID NO:229)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB106 INX915	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:230)	IIPIFGTA (SEQ ID NO:231)	ARSSYGWSY EFDY (SEQ ID NO:232)	QSIRTD (SEQ ID NO:233)	SAS (SEQ ID NO:234)	QQNERTPIT (SEQ ID NO:235)	QVQLVQSGAEVKKPG SSVKVSCASGGTFSS YAIWVWRQAPGGGLE YAIWVWRQAPGGGLE WMGGIPIFGTANYA TAYMELSSLRSEDTAV YICARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:236)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLFPPPKKDTLM VRFNWYYDGVEVHNATK KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPNENYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVMHEALHNHYTQK SLISLSPGK (SEQ ID NO:237)	DIQMTQSPSSLSAS VGDRVITTCRASQSI RTDLNHWYQQKPKGK RTDLNHWYQQKPKGK APKLLYSASSLQSG VPSRFSGSGSDTDFT LTISLQPEDFATYYC QQNERTPTTFGQGT KVEIK (SEQ ID NO:238)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSYSTLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:239)
									QVQLVQSGAEVKKPG SSVKVSCASGGTFSS YAIWVWRQAPGGGLE YAIWVWRQAPGGGLE WMGGIPIFGTANYA OKEQGRVITTADETS TAYMELSSLRSEDTAV YICARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:246)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLFPPPKKDTLM VRFNWYYDGVEVHNATK KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPNENYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVMHEALHNHYTQK SLISLSPGK (SEQ ID NO:247)	DIQMTQSPSSLSAS VGDRVITTCRASQSI NNDLNHWYQQKPKGK APKLLIYAASSLQSG VPSRFSGSGSDTDFT LTISLQPEDFATYYC QQNIRATPTTFGQGT KVEIK (SEQ ID NO:248)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSYSTLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:249)
VSTB107 INX916	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:240)	IIPIFGTA (SEQ ID NO:241)	ARSSYGWSY EFDY (SEQ ID NO:242)	QSINND (SEQ ID NO:243)	AAS (SEQ ID NO:244)	QQNIRATP T (SEQ ID NO:245)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB108	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:250)	IIPIFGTA (SEQ ID NO:251)	ARNTFGWSG ELDY (SEQ ID NO:252)	QSIISR (SEQ ID NO:253)	SAS (SEQ ID NO:254)	QQNHDPIT T (SEQ ID NO:255)	QVQLVQSGAEVKKPG SSVKVSKASGGTFSS YAIWVWRQAPGGGLE YAIWVWRQAPGGGLE WMGGIPIFGTANYA QKFGGRVITTADETS TAYMELSLRSEDTAV YYCARNTFGWSGELD YWGQGTLVTVSS (SEQ ID NO:256)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGGPSVFLPPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNATK KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISLSPGK (SEQ ID NO:257)	DIQMTQSPSLSAS VGDRVITTCRASQSI SNRLNWYQQKPGK APKLLYSASSLQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQNHNPITFGQG TKVEIK (SEQ ID NO:258)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDSTYLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:259)
									QVQLVQSGAEVKKPG SSVKVSKASGGTFSS YAIWVWRQAPGGGLE YAIWVWRQAPGGGLE WMGGIPIFGTANYA QKFGGRVITTADETS TAYMELSLRSEDTAV YYCARNTFGWSGELD YWGQGTLVTVSS (SEQ ID NO:266)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGGPSVFLPPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNATK KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISLSPGK (SEQ ID NO:267)	DIQMTQSPSLSAS VGDRVITTCRASQSI ATYLNWYQQKPGK APKLLIYAASSLQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQNHNPITFGQGT KVEIK (SEQ ID NO:268)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDSTYLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:269)
VSTB109	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:260)	IIPIFGTA (SEQ ID NO:261)	ARSSYGWSY EFDY (SEQ ID NO:262)	QSIATY (SEQ ID NO:263)	AAS (SEQ ID NO:264)	QQNHNPIT T (SEQ ID NO:265)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB110 INX917	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:270)	IIPIFGTA (SEQ ID NO:271)	ARHSGWVA ELDY (SEQ ID NO:272)	QSINTD (SEQ ID NO:273)	AAS (SEQ ID NO:274)	QQGASDPI T (SEQ ID NO:275)	QVQLVQSGAEVKKPG SSVKVSCASGGTFSS YAIWVRQAPGQGLE WMGGIPIFGTANYA QKFGGRVITADESTS TAYMELSLRSEDTAV YYCARHISIGWVAELD YWGGQGLTVTVSS (SEQ ID NO:276)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGGPSVFLPPPKKDTLM VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYCKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISLSPGK (SEQ ID NO:277)	DIQMTQSPSLSAS VGDRVITTCRASQSI NTDLNHWYQQKPKG APKLLIYAASLIQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQGASDPITFGQGT KVEIK (SEQ ID NO:278)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVONALQS GNSQESVTEQ DSKDSYSLSS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:279)
									QVQLVQSGAEVKKPG SSVKVSCASGGTFSS YAIWVRQAPGQGLE WMGGIPIFGTANYA QKFGGRVITADESTS TAYMELSLRSEDTAV YYCARHISIGWVAELD YWGGQGLTVTVSS (SEQ ID NO:286)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGGPSVFLPPPKKDTLM VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYCKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISLSPGK (SEQ ID NO:287)	DIQMTQSPSLSAS VGDRVITTCRASQSI NTDLNHWYQQKPKG APKLLIYAASLIQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQNRGSPITFGQGT KVEIK (SEQ ID NO:288)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVONALQS GNSQESVTEQ DSKDSYSLSS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:289)
VSTB111	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:280)	IIPIFGTA (SEQ ID NO:281)	ARSSYGWSY EFDY (SEQ ID NO:282)	QSINTD (SEQ ID NO:283)	AAS (SEQ ID NO:284)	QQNRGSP T (SEQ ID NO:285)	QVQLVQSGAEVKKPG SSVKVSCASGGTFSS YAIWVRQAPGQGLE WMGGIPIFGTANYA QKFGGRVITADESTS TAYMELSLRSEDTAV YYCARSSYGWSYEFD YWGGQGLTVTVSS (SEQ ID NO:286)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGGPSVFLPPPKKDTLM VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYCKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISLSPGK (SEQ ID NO:287)	DIQMTQSPSLSAS VGDRVITTCRASQSI NTDLNHWYQQKPKG APKLLIYAASLIQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQNRGSPITFGQGT KVEIK (SEQ ID NO:288)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVONALQS GNSQESVTEQ DSKDSYSLSS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:289)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB113 INX918	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:290)	IIPIFGTA (SEQ ID NO:291)	ARHSIGWVA ELDY (SEQ ID NO:292)	QSIATD (SEQ ID NO:293)	AAS (SEQ ID NO:294)	QQAHWYP LT (SEQ ID NO:295)	QVQLVQSGAEVKKPG SSVKVSCASGGTFSS YAIWVWROAPGGGLE WMGGIPIFGTANYA TAYMELSLRSEDSTAV YYCARHSIGWVAELD YWGGQGLTVTVSS (SEQ ID NO:296)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGSPVFLFPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNATK KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISPGK (SEQ ID NO:297)	DIQMTQSPSLSAS VGDRVITTCRASQSI ATSLNMYQQKPGK APKLLIYASLSQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQAHWYPLTFGGG TKVEIK (SEQ ID NO:298)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYLSL TTLTKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:299)
			GGTFSSYA (SEQ ID NO:300)	IIPIFGTA (SEQ ID NO:301)	ARHSIGWVA ELDY (SEQ ID NO:302)	QSIATS (SEQ ID NO:303)	YAS (SEQ ID NO:304)	QQGAYPL T (SEQ ID NO:305)	QVQLVQSGAEVKKPG SSVKVSCASGGTFSS YAIWVWROAPGGGLE WMGGIPIFGTANYA TAYMELSLRSEDSTAV YYCARHSIGWVAELD YWGGQGLTVTVSS (SEQ ID NO:306)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGSPVFLFPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNATK KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISPGK (SEQ ID NO:307)	DIQMTQSPSLSAS VGDRVITTCRASQSI ATSLNMYQQKPGK APKLLIYASLSQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQAHWYPLTFGGG TKVEIK (SEQ ID NO:308)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYLSL TTLTKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:309)
VSTB114	Human IgG1/kappa	Group 1										

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB115 INX919	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:310)	IIPIFGTA (SEQ ID NO:311)	ARSSYGWSY EFDY (SEQ ID NO:312)	QSIRTY (SEQ ID NO:313)	AAS (SEQ ID NO:314)	QQAYSNPI T (SEQ ID NO:315)	QVQLVQSGAEVKKPG SSVKVSKASGGTFSS YAIWVWRQAPGGGLE YAIWVWRQAPGGGLE WMGGIPIFGTANYA WMGGIPIFGTANYA TAYMELSLRSEDSTAV TAYMELSLRSEDSTAV YYCARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:316)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVYPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGGPSVFLPPPKKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYCKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLISLSPGK (SEQ ID NO:317)	DIQMTQSPSLSAS VGDRVITTCRASQSI RTYLNWYQQKPKG DSDKSTYSLS TLLSKADYEK APKLLYAASLIQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQAYSNPITFGQGT KVEIK (SEQ ID NO:318)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYSLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:319)
									QVQLVQSGAEVKKPG SSVKVSKASGGTFSS YAIWVWRQAPGGGLE YAIWVWRQAPGGGLE WMGGIPIFGTANYA WMGGIPIFGTANYA TAYMELSLRSEDSTAV TAYMELSLRSEDSTAV YYCARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:326)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVYPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGGPSVFLPPPKKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYCKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLISLSPGK (SEQ ID NO:327)	DIQMTQSPSLSAS VGDRVITTCRASQSI RTYLNWYQQKPKG DSDKSTYSLS TLLSKADYEK APKLLYAASLIQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQARDTPTFGQGT KVEIK (SEQ ID NO:328)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYSLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:329)
VSTB116	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:320)	IIPIFGTA (SEQ ID NO:321)	ARSSYGWSY EFDY (SEQ ID NO:322)	QSINTN (SEQ ID NO:323)	AAS (SEQ ID NO:324)	QQARDTPI T (SEQ ID NO:325)	QVQLVQSGAEVKKPG SSVKVSKASGGTFSS YAIWVWRQAPGGGLE YAIWVWRQAPGGGLE WMGGIPIFGTANYA WMGGIPIFGTANYA TAYMELSLRSEDSTAV TAYMELSLRSEDSTAV YYCARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:326)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVYPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGGPSVFLPPPKKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYCKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLISLSPGK (SEQ ID NO:327)	DIQMTQSPSLSAS VGDRVITTCRASQSI RTYLNWYQQKPKG DSDKSTYSLS TLLSKADYEK APKLLYAASLIQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQARDTPTFGQGT KVEIK (SEQ ID NO:328)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYSLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:329)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB49	Human IgG1/kappa	Group 1	GYTFPSHT (SEQ ID NO:330)	IYPFDST (SEQ ID NO:331)	ARGIRGYTM DY (SEQ ID NO:332)	ESVDNYGLSF (SEQ ID NO:333)	GAS (SEQ ID NO:334)	QQSKEVPY T (SEQ ID NO:335)	QVQLVQSGAEVKKPG ASVKVSCKASGYTPS HTHWVROAPGQRL WMGSHYFIDSTYNQ KFKDRVITTRDTSAST AYMELSLRSEDTAAY YCARGIRGYTMDYW GGGTLTVYSS (SEQ ID NO:336)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPSVFLPPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCVIMHEALHNHYTQK SLISLSPGK (SEQ ID NO:337)	DVVMQTQSPSLPVT LGQPASISCRASESV DNYGLSFMNWFQQ RPGQSPRRILYIGAS NQSGVGPDRFSGSG SGTDFTLKSRVEAE DIVGVYCCQSQKEVP YTFGGGTGLEIK (SEQ ID NO:338)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSSTYLSL TTLTKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:339)
		Group 2	GYTFINVG (SEQ ID NO:340)	INPYTGEP (SEQ ID NO:341)	AREGYGVNIF PY (SEQ ID NO:342)	ESVDTYANSL (SEQ ID NO:343)	RAS (SEQ ID NO:344)	QQTNEDPR T (SEQ ID NO:345)	QVQLVQSGSELKKPG ASVKVSCKASGYTFTN YGLNWVRQAPGQGL EWMGWINPYTGEPT YADDFKGRFVSLDTS VSTAYLQICSLKAEDT AVYYCAREGYGVNIFP YWGQGTLVTVSS (SEQ ID NO:346)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPSVFLPPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCVIMHEALHNHYTQK SLISLSPGK (SEQ ID NO:347)	DIVMTQTPLSLSVTP GQPASISCRASESD TYANSLIMHWYLQK PGQPPQLLIYRASNL ESGVPDRFSGSGSG TDFTLKSRVEAEADV GVVYCCQQTIEDPR FGQGTGLEIK (SEQ ID NO:348)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSSTYLSL TTLTKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:349)
VSTB50 INX500	Human IgG1/kappa	NLTLDLGL and VQTGKDAP SNC										

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB51	Human IgG1/kappa	Group 1	GFTFSYV (SEQ ID NO:350)	ISNSGSYT (SEQ ID NO:351)	ARDTVLSPFD Y (SEQ ID NO:352)	SSISY (SEQ ID NO:353)	DTS (SEQ ID NO:354)	HQRSFT (SEQ ID NO:355)	EVQLVESGGGLVQPG GSLRLSCAASGFTFSY TMSWVRQAPGKGLE WYATISNGSYTYLD SVKGRFTISRDNKNS LYLQMNSLRRAEDTAV YYCARDTVLSPEFYW GGGTVTVSS (SEQ ID NO:356)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLPPPKPKDTLM ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCVIMHEALHNYTQK SLISPGK (SEQ ID NO:357)	EIVLTQSPDFQSVTP KEKVTITCSATSSISY MHWYQQKPDQSP KLKIDTSELASGVPS RFSGSGSGTDFTLTIT NSLEAEDAATYYCH QRRSFTFGQGTKLEIK (SEQ ID NO:358)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDTYSLS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:359)
									QVQLVQSGAEVKKPG SSYKVSVKASGGTFSN YWIGWVRQAPGQGL EWMEGIYPGGGFTY NEKEGRTVITADEST STAYMEISLSRSEDTA VYYCARYSRDESDYS MDFWGGQGLTVTVSS (SEQ ID NO:366)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLPPPKPKDTLM ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCVIMHEALHNYTQK SLISPGK (SEQ ID NO:367)	DVVMQTQSPSLPVT LGQPASISCKSSQSL LYSNKITYLNWFQQ RPGQSPRLIYLVSK LDGVPDRFESGSGS GTDFTLKSRVEAED VGVVYVCVQATHPPQ TFGGGTKLEIK (SEQ ID NO:368)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDTYSLS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:369)
VSTB52	Human IgG1/kappa		GGTFSNYW (SEQ ID NO:360)	IYPGGGFT (SEQ ID NO:361)	ARYYRSDEY SMDF (SEQ ID NO:362)	QSLYSNGKT Y (SEQ ID NO:363)	LVS (SEQ ID NO:364)	VQATHFPQ T (SEQ ID NO:365)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB53 INX905	Human IgG1/kappa	Group 1	GYTFHYT (SEQ ID NO:370)	IIPSSGYS (SEQ ID NO:371)	ARGAYDDYY DYVAMDY (SEQ ID NO:372)	QTVVHSGN TY (SEQ ID NO:373)	KVS (SEQ ID NO:374)	FAQSHVPW T (SEQ ID NO:375)	QVQLVQSGAEVKKPG ASVKVSKASGYTFTH YTHWVRQAPGQGLE WIMGYIIPSSGYSYN QKFRDVTMTTRDTST STVYMELSSLRSEDTA VYYCARGAYDDYYDY YAMDYWGQGLTVTV SS (SEQ ID NO:376)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLPPPKKDTLM ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSISKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSISPGK (SEQ ID NO:377)	DIVMTQSPILSPVTP GEPASISCRSQTIQ HSNGNTYLEWYLOK PGQSPQLLYKVSNR FSGVPDRFSGSGG TDFTLKISRVEADV GVYYCFQASHVFW TFGGQTKLEIK (SEQ ID NO:378)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYSLSS TLLSKADYEK HKVYACEVTH QGILSPVTKSF NRGEC (SEQ ID NO:379)
									QVQLVQSGAEVKKPG ASVKVSKASGYNIKD TYMHWVRQAPGQGL LEWMGRIDPTHTGYVI YDPKEQGRVTMTTRDT STSTVYMELSSLRSED TAVVYCARDREDPYW FLDWVGQGLTVTVSS (SEQ ID NO:386)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLPPPKKDTLM ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSISKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSISPGK (SEQ ID NO:387)	DIVMTQSPILSPVTP GQPASISCRASESVE YYGTSLMQWYLOK PGQSPQLLYDAFN VESGVPDRFSGSGS GTDFTLKSRVEADV VGYYVCCQSRKVP WTFGGQTKLEIK (SEQ ID NO:388)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYSLSS TLLSKADYEK HKVYACEVTH QGILSPVTKSF NRGEC (SEQ ID NO:389)
VSTB54 INX906	Human IgG1/kappa	Group 2	GYNIKOTY (SEQ ID NO:380)	IDPTHGWV (SEQ ID NO:381)	ARDREDPYW FLDV (SEQ ID NO:382)	ESVEYVGTSL (SEQ ID NO:383)	DAF (SEQ ID NO:384)	QGSRKVP WT (SEQ ID NO:385)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
		Group											
VSTB55	Human IgG1/kappa		GYSIASDVV (SEQ ID NO:390)	ISYSGST (SEQ ID NO:391)	ARITTVPTG SYGVDF (SEQ ID NO:392)	SSVNF (SEQ ID NO:393)	DTS (SEQ ID NO:394)	QQWSNYP FT (SEQ ID NO:395)		QVQLQESGFLVNP ETLSLTCAVSGYASD YVNWIRQPGKGL EWIGYSYSGSTSNP SINSRVTISVDTSKNQ FSLKLSSTVAADTA YCARITTVPTGSYG VDFWGGQGTIVTSS (SEQ ID NO:396)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTPVPS SLG TQTYCNVNHKPSNTKVDK KVEPKSCDKTHCTCP CAP ELLGPGSVFLPPKPKD TLM ISRTPETCVVDVSHED PE VKFNWYVDGVEVHNAK T KPREEQYNSTRYRVSV LTV LHQDWLNGKEYCKVSN K ALPAIEKTSISKAGQPR EP QVYTLPPSRDELTKNQ VSL TCLVKGFPYSDIAVEW ESN GQPENNYKTTTPPVLD SGS FFLYSKLTVDKSRWQQ GN VFCSVMHEALHNHYTQ K SLSLSPGK (SEQ ID NO:397)	EIVLTQSPDFQSVTP KEKVTITCSGSSVN FMVWYQQKPDQSP KLIKDTSNLASGVP SRFSGSGDFTFLTI NSLEAEADAATYYCQ QWSNYPFTFGQGT KLEIK (SEQ ID NO:398)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ SNSQESVTEQ DSKDSYSLSS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:399)
										QVQLVQSGAEVKKPG ASVKVSCKASGYFTTS YWIHWVRQAPGQG LEWMGYIIPNTLTD YNQKFKDRVTMTRO TSYSTVYMELSSLRSE DTAVVYCARLDGDYD YALDYWGQGTIVTSS S (SEQ ID NO:406)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTPVPS SLG TQTYCNVNHKPSNTKVDK KVEPKSCDKTHCTCP CAP ELLGPGSVFLPPKPKD TLM ISRTPETCVVDVSHED PE VKFNWYVDGVEVHNAK T KPREEQYNSTRYRVSV LTV LHQDWLNGKEYCKVSN K ALPAIEKTSISKAGQPR EP QVYTLPPSRDELTKNQ VSL TCLVKGFPYSDIAVEW ESN GQPENNYKTTTPPVLD SGS FFLYSKLTVDKSRWQQ GN VFCSVMHEALHNHYTQ K SLSLSPGK (SEQ ID NO:407)	DIVMTQTPLSLSVTP GQPASISCRASESVE YGTGTFMQLWYLLQK PGQPPQLLYTASNV ESGVPDRFSGSGG TDFTLKISRVEAEDV GVVYCCQSRKVPYT FGQGTGLEIK (SEQ ID NO:408)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ SNSQESVTEQ DSKDSYSLSS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:409)
VSTB56 INX901	Human IgG1/kappa	Group 2	GYTFTSYW (SEQ ID NO:400)	IIPNTLHT (SEQ ID NO:401)	ARLDGDYD ALDY (SEQ ID NO:402)	ESVEYGTGF (SEQ ID NO:403)	TAS (SEQ ID NO:404)	QQSRKVPY T (SEQ ID NO:405)					

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
V5TB57	Human IgG1/kappa							EVQLVESGGGLVQPG GSLRLSCAASGFTSTY AMSWVRQAPGKGLK WYATISGSGSDTYYP DTVKGRFTISRDNAK NSLYLQMINSRAEDT AVYYCARPTYYGFSY FDYWGQGLTLTVSS (SEQ ID NO:416)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHTCPPAP ELLGSPSVFLPPKPKDTLM ISRTPETVCVVVDVSHEDPE VKFNWYVDGVEVHNART KPREEQYNSTRYRVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCVIMHEALHNHYTQK SLSISPGK (SEQ ID NO:417)	DIQLTQSPFSLASV GDRVITTCASSSVS YMIHWYQQKPKGA PKLLYSTSNLASGVP SRFSGSGSTFTFLTI SSLQPEDFATYYCH QWRTPYTFGQGTKL EIK(SEQ ID NO:418)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREKVKQ WKVDNALQKS GNSQESVTEQ DSKDYTSLS TLLSKADYEK HKVYACEVTH QGILSPVTKSF NRGEC (SEQ ID NO:419)
								QVQLQESGGPLVKRPS ETLSLTCTVSGFSLTNY GVHWIRQPPGKGLK WIGVWIRGGNTDYN AAFMRSRTISVDTSK NOFSLKLSVTAADTA VYYCARSMVSYTVDY WGQGLTLTVSS (SEQ ID NO:426)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHTCPPAP ELLGSPSVFLPPKPKDTLM ISRTPETVCVVVDVSHEDPE VKFNWYVDGVEVHNART KPREEQYNSTRYRVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCVIMHEALHNHYTQK SLSISPGK (SEQ ID NO:427)	EIVLTQSPDFQSVTP KEKVITTCASSSVS MHWYQQKPDQSP KLIKDTSNLASGVP SRFSGSGSTFTFLTI NSLEAEDAATYYCQ QWSSYPPTFGQGTK LEIK (SEQ ID NO:428)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREKVKQ WKVDNALQKS GNSQESVTEQ DSKDYTSLS TLLSKADYEK HKVYACEVTH QGILSPVTKSF NRGEC (SEQ ID NO:429)
V5TB58	Human IgG1/kappa										

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB59	Human IgG1/kappa	Group 1	GYTFDYW (SEQ ID NO:430)	IETSLNYP (SEQ ID NO:431)	ARWGIYGNP WFAY (SEQ ID NO:432)	ESVDYVNSF (SEQ ID NO:433)	RAS (SEQ ID NO:434)	QQSNEDPY (SEQ ID NO:435)	QVQLVQSGAEVKKPG ASVKVSCASGYTFD YWMHWVRQAPGQ GLEWMGAIETSLNYP TSTSTVYMEISLRSE DTAVYYCARWGIYGNP PWFAFWGRGTLTVT SS	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTPVPS TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCP ELLGSPSVFLPPPKKDTLM ISRTPETCVVDVSHEDPE VKFNWYVDGVEVHNART KPREEQYNSTYRVVSVLT LHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVIMHEALHNHYTQK SISLSPGK	DIVMITQTPLSLVTP GQPASISCRASESD SVVNSFVHWYLRKP GQPPQLLYRASNL SGVPDRFSGSGSGT DFTLKSRVEAEVDG VYYCQQSNEDPYTE GQGTGLEIK (SEQ ID NO:438)	RTVAAPSVEIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSYSLSS TLTISKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:439)
								T		ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTPVPS TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCP ELLGSPSVFLPPPKKDTLM ISRTPETCVVDVSHEDPE VKFNWYVDGVEVHNART KPREEQYNSTYRVVSVLT LHQDWLNGKEYKCKVSNK ALPAIEKTIKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVIMHEALHNHYTQK SISLSPGK	DIVMITQTPLSLVTP GQPASISCRASESD SVVNSFVHWYLRKP GQPPQLLYRASNL SGVPDRFSGSGSG TDFTLKSRVEAEVD GVYYCQQSHEDPYT FGQGTGLEIK (SEQ ID NO:448)	RTVAAPSVEIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSYSLSS TLTISKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:449)
VSTB60 Group 2	Human IgG1/kappa	Group 2	GYTFINYG (SEQ ID NO:440)	INTYTGES (SEQ ID NO:441)	ARDYYGIYVS AY (SEQ ID NO:442)	ESVDNYANS F (SEQ ID NO:443)	RAS (SEQ ID NO:444)	QQSHEDPY T (SEQ ID NO:445)	QVQLVQSGSELKKPG ASVKVSCASGYTFIN YGMTWVRQAPGQGG LEWMGWINTYTGES TYADDFKGRVFSLD SVSTAYLIQICSLKAEDT AVYYCARDYGYIYVSA YWGQGTLLTVSS			
			NLTLDLSGL and VQTGKDAP SNC									

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB61	Human IgG1/kappa		GYTFISHW (SEQ ID NO:450)	INPRDGR (SEQ ID NO:451)	ARGDFHYGD YFWYFDV (SEQ ID NO:452)	QNVHGA (SEQ ID NO:453)	MAS (SEQ ID NO:454)	LOHWNYLT (SEQ ID NO:455)	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS HWIMHWVRQAPGQ GLEWMGEINPRDGR TNYNEKFRTRVMTNR DTSTSTVYMEISLSRS EDTAVVYCARGDHY GDYFWYFDVWGQGT LVTYSS (SEQ ID NO:456)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHCTCPAP ELLGGPSVFLPPKPKDITLM ISRTPETVCVVVDVSHEDPE VKFNWYVDGVEVHNART KPREEQYNSTYRVSVLTV LHQDWLNGKEYCKVSNK ALPAIEKTSKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVMHEALHNHYTQK SISLSPGK (SEQ ID NO:457)	DIQMTQSPSLSAS VGDRVTITCKASQN VHGAVAWYQQKP DSDKSTYSLSS TTLTKADYEK HKYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:459)	RTVAAPSVEIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSDKSTYSLSS TTLTKADYEK HKYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:469)
VSTB62	Human IgG1/kappa		GYTFTHYW (SEQ ID NO:460)	IYPGDGDT (SEQ ID NO:461)	ARRDYDYG Y (SEQ ID NO:462)	SSVSH (SEQ ID NO:463)	LTS (SEQ ID NO:464)	QQYQTYPP T (SEQ ID NO:465)	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTH YWIQWVRQAPGQGL EWIMGAIPGCGDTR YTQKFRGRTVMTNRT STSTVYMEISLSRSED TAVVYCARRDYDYG YWGQGTITVTVSS (SEQ ID NO:466)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHCTCPAP ELLGGPSVFLPPKPKDITLM ISRTPETVCVVVDVSHEDPE VKFNWYVDGVEVHNART KPREEQYNSTYRVSVLTV LHQDWLNGKEYCKVSNK ALPAIEKTSKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVMHEALHNHYTQK SISLSPGK (SEQ ID NO:467)	EIVLTQSPDFQSVTP KEKVTITCSASSVS HMVWYQQKPDQS PKLLIKITSNLAGVP SRFSGSGGTDFTLTIT NSLEAEADAITYCYQ QYQTYPTPEGQGT LEIK (SEQ ID NO:468)	RTVAAPSVEIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSDKSTYSLSS TTLTKADYEK HKYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:469)

FIGURE 14

[illegible]

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB65	Human IgG1/kappa	Group 1	GYFTSYW (SEQ ID NO:490)	INPSNGLT (SEQ ID NO:491)	ARSYDYGD YYAMDY (SEQ ID NO:492)	QSIHSHNGN TY (SEQ ID NO:493)	KVS (SEQ ID NO:494)	QAASHVPW (SEQ ID NO:495)	QVQLVQSGAEVKKPG ASVKVSKASGYTFTS YWIHWVRQAPGQGL EWMGEINPSNGLTY NEKFRNRVTMTSDTS TSTVYMEISLSRSEDY AVYYCARSYDYDGDY YAMDYWGQGLTVV SS (SEQ ID NO:496)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLPPPKPKDTLM ISRTPETVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTRYRVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSISKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVMHEALHNHYTQK SISLSPGK (SEQ ID NO:497)	DIVMTQSPSLSPVT GEPASISCRSQIV HSNGNTYLEWYLOK PGQSPQLLYKVSNR FSGVPDRFSGSGG TDFTLKISRVEAEDV GVYYCFQASHVFW TFGGQTKLEIK (SEQ ID NO:498)	RTVAAPSVEIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQKS GNSQESVTEQ DSKSDTSYLS TLTLSKADYEK HKVYACEVTH QQLSPVTKSF NRGEC (SEQ ID NO:499)
								T				
VSTB66 INX907	Human IgG1/kappa	Group 2	GYPFTGYF (SEQ ID NO:500)	INPYNGGT (SEQ ID NO:501)	ARWTFDGLF MDY (SEQ ID NO:502)	ENVDKYGISF (SEQ ID NO:503)	ATS (SEQ ID NO:504)	QQSKEDPY T (SEQ ID NO:505)	QVQLVQSGAEVKKPG ASVKVSKASGYPTFG YFMHWVRQAPGQG LEWMGRINPYNGGT VYNQENDRVTMTTR DTSTVYMEISLSRS EDTAVVYCARWYTFDG LFMDYWGQGLTVV SS (SEQ ID NO:506)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLPPPKPKDTLM ISRTPETVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTRYRVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSISKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVMHEALHNHYTQK SISLSPGK (SEQ ID NO:507)	DVVMTQSPSLSPVT LGQPASISCRASENV DKYGISFMNWFQQ RPGQSPRLIYATSN QSGGVPDRFSGSGS GTDFTLKISRVEAED VGYYCQCSKEDPY TFGGQTKLEIK (SEQ ID NO:508)	RTVAAPSVEIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQKS GNSQESVTEQ DSKSDTSYLS TLTLSKADYEK HKVYACEVTH QQLSPVTKSF NRGEC (SEQ ID NO:509)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB67 INX909	Human IgG1/kappa	Group 1	DYIESSYW (SEQ ID NO:510)	IFPGSGGT (SEQ ID NO:511)	ARAIYDYD MYFYDS (SEQ ID NO:512)	QDISSY (SEQ ID NO:513)	YTS (SEQ ID NO:514)	QHVNLTLP WT (SEQ ID NO:515)	QVQLVQSGAEVKKPG ASVKVCSKASDYIFSS YWIQWVRQAPGGQL EWMGEIFFPGSGGTNY NEKFKGRVTMTSDTS TSTVYMELSLRSEDIT AVYYCARAIYDYDYM SYFYDSWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVYPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHITCPCPAP ELLGPGSVFLPPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSISPGK (SEQ ID NO:517)	DIQMTQSPSLSAS VGDRVITTCRASQDI SSYLINWYQQKPGK VPKLLIYTSRLHSG VPSRFSGSGSDTDFT LTISLQPEDVATYY CQHVNLTLPWTFGQ GTKLEIK (SEQ ID NO:518)	RTVAAPSVFIF PPSDEQLKSGT ASVVCLLNNFY PREAKVQWIK VDNALSGNS QESVTEQDSK DSTYLSLSLTLL SKADYEHKV YACEVTHOGL SSPVTKSFNRG EC (SEQ ID NO:519)
									QVQLVQSGAEVKKPG ASVKVCSKASGYTFID YTMNHWVRQAPGQRL EWMGLINPYNGGTT YNQKFKGRVTITRDT ASTAYMELSLRSEDIT AVYYCARHYGNYNW YFDVWGCGTIVTVSS (SEQ ID NO:526)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVYPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHITCPCPAP ELLGPGSVFLPPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSISPGK (SEQ ID NO:527)	DIQLTQSPFELSAY GDRVITTCASQYV NTAVAWYQQKPGK APKLLIYASRYVTG VPSRFSGSGSGTEFT LTISLQPEDFATYYC QQHFTTTPTEFGGT KLEIK (SEQ ID NO:528)	RTVAAPSVFIF PPSDEQLKSG TASVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSYSLSS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:529)
VSTB68	Human IgG1/kappa		GYTFIDYT (SEQ ID NO:520)	INPYNGG T (SEQ ID NO:521)	ARHYGNYN WYFDV (SEQ ID NO:522)	QYVNTA (SEQ ID NO:523)	SAS (SEQ ID NO:524)	QQHFTTPI T (SEQ ID NO:525)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB69	Human IgG1/kappa											
VSTB70	Human IgG1/kappa											

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB71	Human IgG1/kappa		GYVFSRSW (SEQ ID NO:550)	IYPGDGDT (SEQ ID NO:551)	ARRWFL (SEQ ID NO:552)	QSLNSGDQ KSY (SEQ ID NO:553)	GAS (SEQ ID NO:554)	QNDHSYPL T (SEQ ID NO:555)	QVQLVQSGAEVKKPG SSVKVCSKASGYFESR SWINWVRQAPGQGL EWMGRYPGDGDTN YNGKFKGRVTITADES TSTAYWEISSLRSEDT AVYYCARRWFLWGQ GTLTVSS (SEQ ID NO:556)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSFVFLPPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYCKVSNK ALPAIEKTIISKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCVIMHEALHNHYTQK SLISLSPGK (SEQ ID NO:557)	DIVMTQSPDSLAVS LGERATINCKSSQL LNSGDKSYLAWY QQPFGQPKPLNG ASTRESGVPDRFSGS GSGTDFTLTISLQA EDVAVYYCQNDHSY PLTGGQTKLEIK (SEQ ID NO:558)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYSLSS TLTISKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:559)
									EVQLVESGGGLVQPG GSLRLSCAASGFTFSY AMSWVRQAPGKGL WVAEISSGSGHTYP DVTYGRFTISRDAK NSLYQMNSLRRAEDT AVYYCARRGNLYDGP YWGQGTLVVSS (SEQ ID NO:566)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSFVFLPPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYCKVSNK ALPAIEKTIISKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCVIMHEALHNHYTQK SLISLSPGK (SEQ ID NO:567)	EIVLTQSPATLSLSPG ERATLSCASSSVSH MYWYQQKPGQAP RLIYDTISKLASGPA RFGSGSGTDFTLTIS SLEPEDFAVYYCCQ WNFYPTFGQGTKL EIK (SEQ ID NO:568)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYSLSS TLTISKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:569)
VSTB72	Human IgG1/kappa		GFTFSYA (SEQ ID NO:560)	RSSGGSHT (SEQ ID NO:561)	ARRGNLYDG PY (SEQ ID NO:562)	SSVSH (SEQ ID NO:563)	DTS (SEQ ID NO:564)	QQWNFYP FT (SEQ ID NO:565)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB73 INX910	Human IgG1/kappa	Group 2	GYFTDYV (SEQ ID NO:570)	Y INPGSGNT (SEQ ID NO:571)	ARVLVSVMID Y (SEQ ID NO:572)	SSINY (SEQ ID NO:573)	DTS (SEQ ID NO:574)	HQRSSYPW T (SEQ ID NO:575)	QVQLVQSGAEVKKPG ASVKVSCASGYTFD YVISWVRQAPGGGLE WMGEHPGSGNTYY EKFGRVMTMDTST STYVMELSLSRSEDTA VYYCARVLVSVMIDY WGGGTLTIVSS (SEQ ID NO:576)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLFPPPKKDTLM VKFNWYVDGVEVHNATK KPREQYNSTYRVVSVLTV LHQDWLNGKEYCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHHEALHNHYTQK SLISLSPGK (SEQ ID NO:577)	EIVLTQSPDFQSVTP KEKVTITCSASSINY ITWYQQKPKDQSPKL LIKDTSKLASGVPSR FSGSGSGTDFTLTIN SLEAEADAATYYCHQ RSSYPMTFGQGTRL EIK (SEQ ID NO:578)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVONALQS GNSQESVTEQ DSKSDTSYLS TLLTSKADYEK HKVYACEVTH QGILSSPVTKSF NRGEC (SEQ ID NO:579)
									QMQLVQSGPEVKRP GTSVYVSCASGYTFT DYNIQWVRQARGQR LEWIGDINPKYDSTRY NQKEGRVITTRDMS TSTAYMELSLSRSED AVYYCAADGSSAMID YWGQGTTVTVSS (SEQ ID NO:586)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLFPPPKKDTLM VKFNWYVDGVEVHNATK KPREQYNSTYRVVSVLTV LHQDWLNGKEYCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHHEALHNHYTQK SLISLSPGK (SEQ ID NO:587)	DIVMTQSPDSLAVS LGERATINCKSSQSL LNSGHNKYNLAWY QQKPGQPKLLYG ASTRESGVPDRFSGS GSGTDTFTLTISLQA EDVAVYYCQNDHR YPLTFGGQGTKLEIK (SEQ ID NO:588)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVONALQS GNSQESVTEQ DSKSDTSYLS TLLTSKADYEK HKVYACEVTH QGILSSPVTKSF NRGEC (SEQ ID NO:589)
VSTB74	Human IgG1/kappa Group 4	Group 4	GYFTDYN (SEQ ID NO:580)	INPKYDST (SEQ ID NO:581)	AADGSSAM DY (SEQ ID NO:582)	QSLNSGHQ KNY (SEQ ID NO:583)	GAS (SEQ ID NO:584)	QNDHRYPL T (SEQ ID NO:585)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB75	Human IgG1/kappa								QVQLVQSGAEVKKPG SSVKVCKASGFIK YVHWVRQAPGGGLE WMGWIDPENGNTY DPKFQGRVTTTAD STAYMELSLRSED VYTCARDYGYFDY GGGTLTVYSS (SEQ ID NO:596)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHCTCPAP ELLGSPSVFLPPPKPD ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSISKAGQPR QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSLSPGK (SEQ ID NO:597)	DVVMVTQSPAFLSVT PGEKVITTCAGSSV IMVWYQDKPDQA PKLLIKSTNLSAGVP SRFSGSGSDTFTFT ISSLEAEDAATYYCQ QRRSYPHTEGQGTK LEIK (SEQ ID NO:598)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDSTYLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:599)
									QVQLVQSGAEVKKPG ASVKVCKASGYTFD YWINWVRQAPGGGL EWMGNVPSHSYTN NQEFDKRVITMTDTS TSTVYMEELSRSED AVYVCARGGYRPPY AMDYWGQGTGTVTVS S (SEQ ID NO:606)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHCTCPAP ELLGSPSVFLPPPKPD ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSISKAGQPR QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSLSPGK (SEQ ID NO:607)	AIQLTQSPSSLASV GDRVITTCASENIY GALNWKQPKPKA PKLIYGATNLAAGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QNVLTSTPTFGQGT KLEIK (SEQ ID NO:608)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDSTYLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:609)
VSTB76 INX911	Human IgG1/kappa	Group 2	GYTFDYYW (SEQ ID NO:600)	IYPSHSYT (SEQ ID NO:601)	ARGGYRYP YAMDY (SEQ ID NO:602)	ENIYGA (SEQ ID NO:603)	GAT (SEQ ID NO:604)	QNVLTPT (SEQ ID NO:605)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB78	Human IgG1/kappa	Group 2	GYFTNWV (SEQ ID NO:610)	INPSSGYT (SEQ ID NO:611)	ARDGGSVLF GY (SEQ ID NO:612)	QSLNSGIRK NY (SEQ ID NO:613)	SAS (SEQ ID NO:614)	KQSNLYT (SEQ ID NO:615)	QVQLVQSGAEVKKPG ASVKVSKASGYTFN YWMHWVRQAPGQ GLEWMGVNPSGGYT EYNQKFKDQRTMTNR EDTAVYYCARDGGSV LFCYWGGGTTVTYSS (SEQ ID NO:616)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPGSFVLPFPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCVIMHEALHNHYTQK SLISLSPGK (SEQ ID NO:617)	DIVMTQSPDLSAVS LGERATINCKSSQSL LNSGIRKNYLAWYQ QKPGQPKLLYSAS TRESGVPDFRFGSG SGTDFTLTSSLQAE DIVAVYCKQSYNLY TFGGQTKLEIK (SEQ ID NO:618)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVONALQS GNSQESVTEQ DSKSDTYSLS TLLSKADYEK HKVYACEVTH QGILSPVTKSF NRGEC (SEQ ID NO:619)
VSTB79	Human IgG1/kappa		AYSITSDY A (SEQ ID NO:620)	ITYSGST (SEQ ID NO:621)	ARSFGEY (SEQ ID NO:622)	QSIGTS (SEQ ID NO:623)	YAS (SEQ ID NO:624)	QQINSWP TT (SEQ ID NO:625)	QVQLQESGPGLVKPS ETLSLTCAVSAYSITSD YAWNWIRQPPGKGL EWIGITYSGSTRYNP SIKSRVTISVDTSKNQ FSKLSSVTAADTAVY YCARSEFGYWGGGTT VTYSS (SEQ ID NO:626)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPGSFVLPFPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCVIMHEALHNHYTQK SLISLSPGK (SEQ ID NO:627)	EIVMTQSPATLSVP GERATISCRASQSIG TSIHVYQKPKGQA PRLLIYASEISGIPA RESGSGSEFTLTIS SLQSEDFAVYCCQI NSWPTTFGGQTKLE IK (SEQ ID NO:628)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVONALQS GNSQESVTEQ DSKSDTYSLS TLLSKADYEK HKVYACEVTH QGILSPVTKSF NRGEC (SEQ ID NO:629)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB80	Human IgG1/kappa											
VSTB81	Human IgG1/kappa											

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB82	Human IgG1/kappa							QVQLQESGGLVNP ETLSLTCAVSGYSD YAWNWIRQPGKGL EWIGFTYSGSTNYP SLKSRVTSVSDTSKQ FSLSKSSVTAADTA YCARSHYGSTYWF VWVGQGTIVTVSS (SEQ ID NO:656)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHCTCPAP ELLGSPSVFLPPKPKDTLM ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QYVTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISLSPGK (SEQ ID NO:657)	DIVMTQTPLSLSVTP GQPASISCRASESVE YGTSLMQWYLOK TTLTSKADYEK PGQSPQLLIYAASN VESGVDPDRFSGSGS GTDFTLKISRVEAED VGVYVCOQTRKVP WTEGQGTRLLEIK (SEQ ID NO:658)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDSTYLS TTLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:659)
VSTB83	Human IgG1/kappa							QVQLVQSGAEVKKPG ASVKVSKASGYFTTS YDINWVRQAPGQGL EWMGWYTPGDGYTE YNEKERGRVMTTRDT STSTVYMELSLRSED TAVVYCARWGYGSYA MDYWGQGTTLTVYSS (SEQ ID NO:666)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKYDK KVEPKSCDKTHCTCPAP ELLGSPSVFLPPKPKDTLM ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QYVTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISLSPGK (SEQ ID NO:667)	DIVMTQSPSLSPVTP GEPASISCRSSQSLV HSNGNTYHWYIQ KPGQSPQLLIYKVS RESGVDPRESGSGS GTDFTLKISRVEAED VGVYVCSQSTHVPP TFGQGTLEIK (SEQ ID NO:668)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDSTYLS TTLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:669)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB84 INX912	Human IgG1/kappa	Group 2	GYFTSYW (SEQ ID NO:670)	INPSTGY (SEQ ID NO:671)	ARSYDYDG GAWFAY (SEQ ID NO:672)	ESVEYGTSL (SEQ ID NO:673)	AAS (SEQ ID NO:674)	QQSRKVPS T (SEQ ID NO:675)	QVQLVQSGAEVKKPG ASVKVSKASGYTFTS YWMHWVRQAPGQ GLEWMGVNPSGYP GYNQKFKDRVTMT DTSTSTVYIELSLRS EDTAVVYCARSYDY DGGAWFAYWGQGT TVTYS (SEQ ID NO:676)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTPVSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPAP ELLGPSVFLPPPKKDTLM VKFNWYVDGVEVHNAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISLSPGK (SEQ ID NO:677)	DIVMTQTPLSLVTP GQPASISCRASESVE YGTSLMQWYLOK PGQPPQLLIYAASN VESGVPRDFSGSGS GTDFTLKISRVEAED VGVYCCQSRKVPS TFGGQTKLEIK (SEQ ID NO:678)	RTVAAPSVFIF PPSDEQLKSG TASVACLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDTYSLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:679)
									QVQLVQSGAEVKKPG ASVKVSKASGYTFTD YAMHWVRQAPGQG LEWMGVNIDTYGNT NYNQKFKGRVTMT DTSTSTVYIELSLRS DDTAIVYCARGGGD ALDYWGCGTIVTVSS (SEQ ID NO:686)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTPVSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPAP ELLGPSVFLPPPKKDTLM VKFNWYVDGVEVHNAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLISLSPGK (SEQ ID NO:687)	DIQMTQSPSSLSAS VGDRVITTCRASQS VSNDRVWVYQQKPG KAPKLLIYASNRYI GVPSRFGSGSGTD FTFTISLQPEDIATY YCCQQGYSLRTFGQ GTKLEIK (SEQ ID NO:688)	RTVAAPSVFIF PPSDEQLKSG TASVACLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDTYSLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:689)
VSTB85 INX913	Human IgG1/kappa	Group 1	GYFTDYA (SEQ ID NO:680)	IDTYYGNT (SEQ ID NO:681)	ARGGGDALD Y (SEQ ID NO:682)	QSVND (SEQ ID NO:683)	YAS (SEQ ID NO:684)	QQGYTSLR T (SEQ ID NO:685)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB87	Human IgG1/kappa		GYSITSGYS (SEQ ID NO:690)	IHYIGIT (SEQ ID NO:691)	AREDDYDYG VFAY (SEQ ID NO:692)	QSSNN (SEQ ID NO:693)	YAS (SEQ ID NO:694)	QQNSWP HT (SEQ ID NO:695)	QVQLQESGGLVKPS ETLSLTCAVSGYSITSG YSWHWIRQPPGKGL EWIGYHYIGITNNIP SLKSRVTSVSDTSKNQ FSKLSSVTAADTAAY YCARDDYDYGVFAY WGGGTLTIVSS (SEQ ID NO:696)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPSVFLPPPKKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSLSPGK (SEQ ID NO:697)	EIVLTQSPATLSLSPG ERATLSCRASQISN NIHWYQQKPGAP RLIYYASQSIGIPA RFSGSGSGTDFTLTIS SLEPEDFAVYYCQQ SNVWPHFTGQGTKL EIK (SEQ ID NO:698)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDTYSLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:699)
									QVQLQESGGLVKPS ETLSLTCTVSGFSLTNY DISWIRQPPGKGLEW IGVIMTGGGTNYNSA FMSRVTSVSDTSKNQF SLKLSVTAADTAAYY CAREGLLLPLYWGQG TLTVSS (SEQ ID NO:706)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPSVFLPPPKKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSLSPGK (SEQ ID NO:707)	DIQMTQSPSLSAS VGDRVITTCRASQN VGTNVAWYQQKPG KVPKLLIYASRYYS GVPSRFGSGSGTD FTLTISLQPEDVAITY YCCQQYNSTYPLTFGQ GTKLEIK (SEQ ID NO:708)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDTYSLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:709)
VSTB88	Human IgG1/kappa		GFSLTNYD (SEQ ID NO:700)	IWTGGGT (SEQ ID NO:701)	AREGLLLPLY (SEQ ID NO:702)	QNVGTN (SEQ ID NO:703)	SAS (SEQ ID NO:704)	QQYNSPL T (SEQ ID NO:705)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB89	Human IgG1/kappa		GYTFNFG (SEQ ID NO:710)	INTYTGEP (SEQ ID NO:711)	ARGAYYGS RVWFAY (SEQ ID NO:712)	QNLVHSGN TV (SEQ ID NO:713)	KVS (SEQ ID NO:714)	SQSSHVPYT (SEQ ID NO:715)	QVQLVQSGSELKPG ASVKVCKASGYTFN FGMNWVRQAPGQG LEWNGWINTYGE TYADDFKGRVFLDT SVSTAYLQICLKAEDT AVYYCARGAYYGS VWFAYWGQGLTVV SS (SEQ ID NO:716)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKVDK KVEPKSCDKTHCTCPAP ELLGPSVFLPPPKKDTLM ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSIAKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSISPGK (SEQ ID NO:717)	DIVMTQSPISLPVTP GEPASICTSSQNLV HSNGNTYLIHWYIQ KPGQSPQLLYKVN RFSGVPDRFSGSGS GTDFTLKISRVEAED VGVYCSQSHVPI TFGGQTKLEIK (SEQ ID NO:718)	RTVAAPSVFIF PPSDEQLKSG TASVACLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSYSLSS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:719)
									QVQLQESGPGLVKPS ETLSITCTVSGFSLTSS GVHWIRQPPKRGLE WIGVWISGNTDYN AAFIKRVTSIVDTSKN QFSLKLSYTAADTAV YYCAREDDYDWDYFD VWVGQGTITVTS (SEQ ID NO:726)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYCNVNHKPSNTKVDK KVEPKSCDKTHCTCPAP ELLGPSVFLPPPKKDTLM ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTSIAKAGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSWMHEALHNHYTQK SLSISPGK (SEQ ID NO:727)	DIVMTQSPISLPVTP GQPASISCRASESVE YYGTSLMQWYLQK PGQPPQLLIYAASN VKSGVPDRFSGSGS GTDFTLKISRVEAED VGVYCCQSRKVP WTFGGQTKLEIK (SEQ ID NO:728)	RTVAAPSVFIF PPSDEQLKSG TASVACLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSYSLSS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:729)
VSTB90	Human IgG1/kappa		GFSLTSSG (SEQ ID NO:720)	IWGGNT (SEQ ID NO:721)	AREDDYDWD YFDV (SEQ ID NO:722)	ESVEYGTSL (SEQ ID NO:723)	AAS (SEQ ID NO:724)	QGSRKVP WT (SEQ ID NO:725)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB91	Human IgG1/kappa								QVQLVQSGAEVKKPG ASVKVSKASGYTFA NFWMHVWRQAPGQ GLEWWMGAIPEGNSDT GYNCKFKGRVTMTNR DTSTSTVYMEISSLRS EDTAVYVCARELTGY YFDYWGCGTLVTYSS (SEQ ID NO:730)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPSVFLFPPKPKDTLM ISRTPETVTVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEDYNSTYRVVSVLTV LHQDWLNGKEYCKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SIISLPK (SEQ ID NO:731)	EIVLTQSPATLSLSPG ERATLSCATSSVY MHWYQOKPGQAP RLIYSSSNLASGIPA RFSGSGSGTDFTLTIS SLEPEDFAVYCHQ WSGHFTFGQGTKLE IK (SEQ ID NO:732)	RTVAAPSVFIF PPSDEQLKSG TASVCLINN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDYSTYLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:733)
									QVQLVQSGAEVKKPG ASVKVSKASGYTFA NFWMHVWRQAPGQ GLEWWMGAIPEGNSDT GYNCKFKGRVTMTNR DTSTSTVYMEISSLRS EDTAVYVCARELTGY YFDYWGCGTLVTYSS (SEQ ID NO:736)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPSVFLFPPKPKDTLM ISRTPETVTVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEDYNSTYRVVSVLTV LHQDWLNGKEYCKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SIISLPK (SEQ ID NO:747)	EIVLTQSPATLSLSPG ERATLSCATSSVY MHWYQOKPGQAP RLIYSSSNLASGIPA RFSGSGSGTDFTLTIS SLEPEDFAVYCHQ WSGHFTFGQGTKLE IK (SEQ ID NO:738)	RTVAAPSVFIF PPSDEQLKSG TASVCLINN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDYSTYLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:748)
VSTB92 INX908	Human IgG1/kappa	Group 1							QVQLVQSGAEVKKPG ASVKVSKASGYTFA NFWMHVWRQAPGQRL EWMGDVPPGGGHSY NEKFKGRVITTRDTSA STAYMEISSLRSIEDTA VYVCARRFDYGGYFF DYWGCGTLVTYSS SIISLPK (SEQ ID NO:746)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPSVFLFPPKPKDTLM ISRTPETVTVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEDYNSTYRVVSVLTV LHQDWLNGKEYCKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GGPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SIISLPK (SEQ ID NO:747)	EIVLTQSPATLSLSPG ERATLSCATSSVY MHWYQOKPGQAP RLIYSSSNLASGIPA RFSGSGSGTDFTLTIS SLEPEDFAVYCHQ WSGHFTFGQGTKLE IK (SEQ ID NO:738)	RTVAAPSVFIF PPSDEQLKSG TASVCLINN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDYSTYLS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:749)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB93	Human IgG1/kappa							QVQLQESGPGLVKPS ETLSLTCTVSGFSITNY DISWIQPPGKGLGW IGWIWTTGGTNVNSA FMSRVTISVDTSKNQF SLKLSVTAADTAAYYY CARDSPYFCGYWYG QGTITVTVSS (SEQ ID NO:756)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPGSFVLPKPKDITLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVIMHEALHNHYTQK SLSISPGK (SEQ ID NO:757)	DIVMITQTLISLVTP GQPASISCRSSQSLV HSGNTYLIHWYIQ KPGQSPQLLYKVN RFSGVPDRFSGSGS GTDFTLKISRVEAD VGYYCSQSTHP WTEGQGTKLEIK (SEQ ID NO:758)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSYSLSS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:759)
								QVQLQESGPGLVKPS ETLSLTCAVSGYSITSD YAWMTWIRQPPGKGL EWIGYMMYSGSASY NPSLKGRVTISVDTSK NQFSLKLSVTAADTA VYYCARFDHYGGRFD YWGQGTTVTVSS (SEQ ID NO:766)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPGSFVLPKPKDITLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVIMHEALHNHYTQK SLSISPGK (SEQ ID NO:767)	AIQLTQSPSSLSASV GDRVTTTCASSSVS YHWYQQKPKGAP KLLIYEISKLAGVPS RESGSGSGTDFLTIS SLQPEDFATYYCQQ WNYPLFTFGQGTKL EIK (SEQ ID NO:768)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKDSYSLSS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:769)
VSTB94	Human IgG1/kappa										

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB95 INX903	Human IgG1/kappa	PVDKGHDV TF and RRPIRDLTF QDL	GFTRNVG (SEQ ID NO:770)	IISGGSYT (SEQ ID NO:771)	ARYDHDGD YYAMDY (SEQ ID NO:772)	QSVHSNGN TY (SEQ ID NO:773)	KVS (SEQ ID NO:774)	FQGSHPV WT (SEQ ID NO:775)	EVQLVESGGGLVQPG GSLRLSCAASGFTFRN YGM5WVRQAPGKGL EWVASISGGSYYTPY DSVKGRFTISRDNKAK NSLYLQMINSLRAEDT AVYYCARIYDHDGDY YAMDYWGQGTTVTV SS	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLFPPPKKDTLM ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFPSDIAVEWESN GGPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHHEALHNHYTQK SLSISPGK (SEQ ID NO:777)	DIVMITQSPILSPVTP GEPASISCRSSQIV HSNGNTYLEWYLOK PGQSPQLIKYVSNR FSGVPDRFSGSGG TDTFLKISRVEADV GVYYCFQGSHPVW TFGGQTKLEIK (SEQ ID NO:778)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDSTYLS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:779)
									QVQLVQSGAEVKKPG SSYKVSCKASGYFTFS YDINWVRQAPGQGL EWMGRHYPGDGSKY NEKEGRVITTDADKST STAYMEISLSRSEDTA VYYCAREGITPFAYW GGGTITVYSS (SEQ ID NO:786)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLFPPPKKDTLM ISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFPSDIAVEWESN GGPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHHEALHNHYTQK SLSISPGK (SEQ ID NO:787)	AIQLTQSPSSLSASV GDRVITTCRAKSKIS KYLAWYQQKPGKA PKLIYSGSTLQSGV PSRFSGSGSGTDFTL TISSLPEDFATYYC QQHNEYFPWTEGGG TKLEIK (SEQ ID NO:788)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSKSDSTYLS TLLTSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:789)
VSTB96	Human IgG1/kappa		(SEQ ID NO:780)	(SEQ ID NO:781)	(SEQ ID NO:782)	(SEQ ID NO:783)	(SEQ ID NO:784)	(SEQ ID NO:785)				

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB97 INX914	Human IgG1/kappa	Group 1						QVQLVQSGAEVKKPG SSVKVSKASGGTFSS YAIWVWROAPGGGLE YMWGIIPIFGTANYA WMGIIPIFGTANYA TAYMELSLRSEDSTAV YYCARSSYGVWSYEDF YWGQGTLVTVSS (SEQ ID NO:796)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVYPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLPPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNNAKT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVMHEALHNHYTQK SLISPGK (SEQ ID NO:797)	DIQMTQSPSLSAS VGDRVITTCRASQSI SSYLNWYQQKPGK DSDKSTYSLSS TLLSKADYEK APKLLYAASSLQSG VPSRFSGSGSDTFT LTISLQPEDFATYYC QQSYSTPLTFGQGT KVEIK (SEQ ID NO:798)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYSLSS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:799)
VSTB98	Human IgG1/kappa	Group 1						QVQLVQSGAEVKKPG SSVKVSKASGGTFSS YAIWVWROAPGGGLE YMWGIIPIFGTANYA WMGIIPIFGTANYA TAYMELSLRSEDSTAV YYCARSTVGWWSYEDF YWGQGTLVTVSS (SEQ ID NO:806)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSVTVYPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSVFLPPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNNAKT KPREQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSVMHEALHNHYTQK SLISPGK (SEQ ID NO:807)	DIQMTQSPSLSAS VGDRVITTCRASQSI SSYLNWYQQKPGK DSDKSTYSLSS TLLSKADYEK APKLLYAASSLQSG VPSRFSGSGSDTFT LTISLQPEDFATYYC QQSYSTPLTFGQGT KVEIK (SEQ ID NO:808)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVDNALQ GNSQESVTEQ DSDKSTYSLSS TLLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:809)

FIGURE 14

mAb ID	Description	Epitope Sequence/ Epitope Group	Heavy-chain cdr1 (imgt)	Heavy-chain cdr2 (imgt)	Heavy-chain cdr3 (imgt)	Light-chain cdr1 (imgt)	Light-chain cdr2 (imgt)	Light-chain cdr3 (imgt)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB99	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:810)	IIPIFGTA (SEQ ID NO:811)	ARHVLGWVL ELDY (SEQ ID NO:812)	QSISSY (SEQ ID NO:813)	AAS (SEQ ID NO:814)	QQSYSTPLT (SEQ ID NO:815)	QVQLVQSGAEVKKPG SSVKVSCKASGGTFSS YAIWVROAPGGGLE YIMGGIPIFGTANYA QKFGGRVITTADESTS TAYMELSSLRSEDTAV YYCARHVLGWVLELD YWGQGLTVYSS (SEQ ID NO:816)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVTVPSSSLG TQTYICNVNHKPSNTKYDK KVEPKSCDKTHCTCPCPAP ELLGPGSFLFPPKPKDTLM ISRTPETVTCVVVDVSHEDPE VKFNWYVDGVEVHNKAT KPREEQYNSTYRVVSVLTV LHQDQLNGKEYCKCKVSNK ALPAIEKTIISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGN VFCSYVMHEALHNHYTQK SISISPGK (SEQ ID NO:817)	DIQMTQSPSLSAS VGDRVITTCRASQSI SSYLINWYQQKPGK SSYLINWYQQKPGK APKLLYAASSLQSG VPSRFGSGSGTDFT LTISLQPEDFATYYC QQSYSTPLTFGQGT KVEIK (SEQ ID NO:818)	RTVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQ WKVONALQS GNQESVTEQ DSKDSYLSLS TLTISKADYEK HKVYACEVTH QGILSSPVTKSF NRGEC (SEQ ID NO:819)

FIGURE 14

mAb ID	Description	Epitope Sequence	CDR1	CDR2	CDR3	CDR4	CDR5	CDR6	CDR7	CDR8	CDR9	CDR10	CDR11	CDR12	CDR13	CDR14	CDR15	CDR16	CDR17	CDR18	CDR19	CDR20	CDR21	CDR22	CDR23	CDR24	CDR25	CDR26	CDR27	CDR28	CDR29	CDR30	CDR31	CDR32	CDR33	CDR34	CDR35	CDR36	CDR37	CDR38	CDR39	CDR40	CDR41	CDR42	CDR43	CDR44	CDR45	CDR46	CDR47	CDR48	CDR49	CDR50	CDR51	CDR52	CDR53	CDR54	CDR55	CDR56	CDR57	CDR58	CDR59	CDR60	CDR61	CDR62	CDR63	CDR64	CDR65	CDR66	CDR67	CDR68	CDR69	CDR70	CDR71	CDR72	CDR73	CDR74	CDR75	CDR76	CDR77	CDR78	CDR79	CDR80	CDR81	CDR82	CDR83	CDR84	CDR85	CDR86	CDR87	CDR88	CDR89	CDR90	CDR91	CDR92	CDR93	CDR94	CDR95	CDR96	CDR97	CDR98	CDR99	CDR100	CDR101	CDR102	CDR103	CDR104	CDR105	CDR106	CDR107	CDR108	CDR109	CDR110	CDR111	CDR112	CDR113	CDR114	CDR115	CDR116	CDR117	CDR118	CDR119	CDR120	CDR121	CDR122	CDR123	CDR124	CDR125	CDR126	CDR127	CDR128	CDR129	CDR130	CDR131	CDR132	CDR133	CDR134	CDR135	CDR136	CDR137	CDR138	CDR139	CDR140	CDR141	CDR142	CDR143	CDR144	CDR145	CDR146	CDR147	CDR148	CDR149	CDR150	CDR151	CDR152	CDR153	CDR154	CDR155	CDR156	CDR157	CDR158	CDR159	CDR160	CDR161	CDR162	CDR163	CDR164	CDR165	CDR166	CDR167	CDR168	CDR169	CDR170	CDR171	CDR172	CDR173	CDR174	CDR175	CDR176	CDR177	CDR178	CDR179	CDR180	CDR181	CDR182	CDR183	CDR184	CDR185	CDR186	CDR187	CDR188	CDR189	CDR190	CDR191	CDR192	CDR193	CDR194	CDR195	CDR196	CDR197	CDR198	CDR199	CDR200	CDR201	CDR202	CDR203	CDR204	CDR205	CDR206	CDR207	CDR208	CDR209	CDR210	CDR211	CDR212	CDR213	CDR214	CDR215	CDR216	CDR217	CDR218	CDR219	CDR220	CDR221	CDR222	CDR223	CDR224	CDR225	CDR226	CDR227	CDR228	CDR229	CDR230	CDR231	CDR232	CDR233	CDR234	CDR235	CDR236	CDR237	CDR238	CDR239	CDR240	CDR241	CDR242	CDR243	CDR244	CDR245	CDR246	CDR247	CDR248	CDR249	CDR250	CDR251	CDR252	CDR253	CDR254	CDR255	CDR256	CDR257	CDR258	CDR259	CDR260	CDR261	CDR262	CDR263	CDR264	CDR265	CDR266	CDR267	CDR268	CDR269	CDR270	CDR271	CDR272	CDR273	CDR274	CDR275	CDR276	CDR277	CDR278	CDR279	CDR280	CDR281	CDR282	CDR283	CDR284	CDR285	CDR286	CDR287	CDR288	CDR289	CDR290	CDR291	CDR292	CDR293	CDR294	CDR295	CDR296	CDR297	CDR298	CDR299	CDR300	CDR301	CDR302	CDR303	CDR304	CDR305	CDR306	CDR307	CDR308	CDR309	CDR310	CDR311	CDR312	CDR313	CDR314	CDR315	CDR316	CDR317	CDR318	CDR319	CDR320	CDR321	CDR322	CDR323	CDR324	CDR325	CDR326	CDR327	CDR328	CDR329	CDR330	CDR331	CDR332	CDR333	CDR334	CDR335	CDR336	CDR337	CDR338	CDR339	CDR340	CDR341	CDR342	CDR343	CDR344	CDR345	CDR346	CDR347	CDR348	CDR349	CDR350	CDR351	CDR352	CDR353	CDR354	CDR355	CDR356	CDR357	CDR358	CDR359	CDR360	CDR361	CDR362	CDR363	CDR364	CDR365	CDR366	CDR367	CDR368	CDR369	CDR370	CDR371	CDR372	CDR373	CDR374	CDR375	CDR376	CDR377	CDR378	CDR379	CDR380	CDR381	CDR382	CDR383	CDR384	CDR385	CDR386	CDR387	CDR388	CDR389	CDR390	CDR391	CDR392	CDR393	CDR394	CDR395	CDR396	CDR397	CDR398	CDR399	CDR400	CDR401	CDR402	CDR403	CDR404	CDR405	CDR406	CDR407	CDR408	CDR409	CDR410	CDR411	CDR412	CDR413	CDR414	CDR415	CDR416	CDR417	CDR418	CDR419	CDR420	CDR421	CDR422	CDR423	CDR424	CDR425	CDR426	CDR427	CDR428	CDR429	CDR430	CDR431	CDR432	CDR433	CDR434	CDR435	CDR436	CDR437	CDR438	CDR439	CDR440	CDR441	CDR442	CDR443	CDR444	CDR445	CDR446	CDR447	CDR448	CDR449	CDR450	CDR451	CDR452	CDR453	CDR454	CDR455	CDR456	CDR457	CDR458	CDR459	CDR460	CDR461	CDR462	CDR463	CDR464	CDR465	CDR466	CDR467	CDR468	CDR469	CDR470	CDR471	CDR472	CDR473	CDR474	CDR475	CDR476	CDR477	CDR478	CDR479	CDR480	CDR481	CDR482	CDR483	CDR484	CDR485	CDR486	CDR487	CDR488	CDR489	CDR490	CDR491	CDR492	CDR493	CDR494	CDR495	CDR496	CDR497	CDR498	CDR499	CDR500	CDR501	CDR502	CDR503	CDR504	CDR505	CDR506	CDR507	CDR508	CDR509	CDR510	CDR511	CDR512	CDR513	CDR514	CDR515	CDR516	CDR517	CDR518	CDR519	CDR520	CDR521	CDR522	CDR523	CDR524	CDR525	CDR526	CDR527	CDR528	CDR529	CDR530	CDR531	CDR532	CDR533	CDR534	CDR535	CDR536	CDR537	CDR538	CDR539	CDR540	CDR541	CDR542	CDR543	CDR544	CDR545	CDR546	CDR547	CDR548	CDR549	CDR550	CDR551	CDR552	CDR553	CDR554	CDR555	CDR556	CDR557	CDR558	CDR559	CDR560	CDR561	CDR562	CDR563	CDR564	CDR565	CDR566	CDR567	CDR568	CDR569	CDR570	CDR571	CDR572	CDR573	CDR574	CDR575	CDR576	CDR577	CDR578	CDR579	CDR580	CDR581	CDR582	CDR583	CDR584	CDR585	CDR586	CDR587	CDR588	CDR589	CDR590	CDR591	CDR592	CDR593	CDR594	CDR595	CDR596	CDR597	CDR598	CDR599	CDR600	CDR601	CDR602	CDR603	CDR604	CDR605	CDR606	CDR607	CDR608	CDR609	CDR610	CDR611	CDR612	CDR613	CDR614	CDR615	CDR616	CDR617	CDR618	CDR619	CDR620	CDR621	CDR622	CDR623	CDR624	CDR625	CDR626	CDR627	CDR628	CDR629	CDR630	CDR631	CDR632	CDR633	CDR634	CDR635	CDR636	CDR637	CDR638	CDR639	CDR640	CDR641	CDR642	CDR643	CDR644	CDR645	CDR646	CDR647	CDR648	CDR649	CDR650	CDR651	CDR652	CDR653	CDR654	CDR655	CDR656	CDR657	CDR658	CDR659	CDR660	CDR661	CDR662	CDR663	CDR664	CDR665	CDR666	CDR667	CDR668	CDR669	CDR670	CDR671	CDR672	CDR673	CDR674	CDR675	CDR676	CDR677	CDR678	CDR679	CDR680	CDR681	CDR682	CDR683	CDR684	CDR685	CDR686	CDR687	CDR688	CDR689	CDR690	CDR691	CDR692	CDR693	CDR694	CDR695	CDR696	CDR697	CDR698	CDR699	CDR700	CDR701	CDR702	CDR703	CDR704	CDR705	CDR706	CDR707	CDR708	CDR709	CDR710	CDR711	CDR712	CDR713	CDR714	CDR715	CDR716	CDR717	CDR718	CDR719	CDR720	CDR721	CDR722	CDR723	CDR724	CDR725	CDR726	CDR727	CDR728	CDR729	CDR730	CDR731	CDR732	CDR733	CDR734	CDR735	CDR736	CDR737	CDR738	CDR739	CDR740	CDR741	CDR742	CDR743	CDR744	CDR745	CDR746	CDR747	CDR748	CDR749	CDR750	CDR751	CDR752	CDR753	CDR754	CDR755	CDR756	CDR757	CDR758	CDR759	CDR760	CDR761	CDR762	CDR763	CDR764	CDR765	CDR766	CDR767	CDR768	CDR769	CDR770	CDR771	CDR772	CDR773	CDR774	CDR775	CDR776	CDR777	CDR778	CDR779	CDR780	CDR781	CDR782	CDR783	CDR784	CDR785	CDR786	CDR787	CDR788	CDR789	CDR790	CDR791	CDR792	CDR793	CDR794	CDR795	CDR796	CDR797	CDR798	CDR799	CDR800	CDR801	CDR802	CDR803	CDR804	CDR805	CDR806	CDR807	CDR808	CDR809	CDR810	CDR811	CDR812	CDR813	CDR814	CDR815	CDR816	CDR817	CDR818	CDR819	CDR820	CDR821	CDR822	CDR823	CDR824	CDR825	CDR826	CDR827	CDR828	CDR829	CDR830	CDR831	CDR832	CDR833	CDR834	CDR835	CDR836	CDR837	CDR838	CDR839	CDR840	CDR841	CDR842	CDR843	CDR844	CDR845	CDR846	CDR847	CDR848	CDR849	CDR850	CDR851	CDR852	CDR853	CDR854	CDR855	CDR856	CDR857	CDR858	CDR859	CDR860	CDR861	CDR862	CDR863	CDR864	CDR865	CDR866	CDR867	CDR868	CDR869	CDR870	CDR871	CDR872	CDR873	CDR874	CDR875	CDR876	CDR877	CDR878	CDR879	CDR880	CDR881	CDR882	CDR883	CDR884	CDR885	CDR886	CDR887	CDR888	CDR889	CDR890	CDR891	CDR892	CDR893	CDR894	CDR895	CDR896	CDR897	CDR898	CDR899	CDR900	CDR901	CDR902	CDR903	CDR904	CDR905	CDR906	CDR907	CDR908	CDR909	CDR910	CDR911	CDR912	CDR913	CDR914	CDR915	CDR916	CDR917	CDR918	CDR919	CDR920	CDR921	CDR922	CDR923	CDR924	CDR925	CDR926	CDR927	CDR928	CDR929	CDR930	CDR931	CDR932	CDR933	CDR934	CDR935	CDR936	CDR937	CDR938	CDR939	CDR940	CDR941	CDR942	CDR943	CDR944	CDR945	CDR946	CDR947	CDR948	CDR949	CDR950	CDR951	CDR952	CDR953	CDR954	CDR955	CDR956	CDR957	CDR958	CDR959	CDR960	CDR961	CDR962	CDR963	CDR964	CDR965	CDR966	CDR967	CDR968	CDR969	CDR970	CDR971	CDR972	CDR973	CDR974	CDR975	CDR976	CDR977	CDR978	CDR979	CDR980	CDR981	CDR982	CDR983	CDR984	CDR985	CDR986	CDR987	CDR988	CDR989	CDR990	CDR991	CDR992	CDR993	CDR994	CDR995	CDR996	CDR997	CDR998	CDR999	CDR1000	CDR1001	CDR1002	CDR1003	CDR1004	CDR1005	CDR1006	CDR1007	CDR1008	CDR1009	CDR1010	CDR1011	CDR1012	CDR1013	CDR1014	CDR1015	CDR1016	CDR1017	CDR1018	CDR1019	CDR1020	CDR1021	CDR1022	CDR1023	CDR1024	CDR1025	CDR1026	CDR1027	CDR1028	CDR1029	CDR1030	CDR1031	CDR1032	CDR1033	CDR1034	CDR1035	CDR1036	CDR1037	CDR1038	CDR1039	CDR1040	CDR1041	CDR1042	CDR1043	CDR1044	CDR1045	CDR1046	CDR1047	CDR1048	CDR1049	CDR1050	CDR1051	CDR1052	CDR1053	CDR1054	CDR1055	CDR1056	CDR1057	CDR1058	CDR1059	CDR1060	CDR1061	CDR1062	CDR1063	CDR1064	CDR1065	CDR1066	CDR1067	CDR1068	CDR1069	CDR1070	CDR1071	CDR1072	CDR1073	CDR1074	CDR1075	CDR1076	CDR1077	CDR1078	CDR1079	CDR1080	CDR1081	CDR1082	CDR1083	CDR1084	CDR1085	CDR1086	CDR1087	CDR1088	CDR1089	CDR1090	CDR1091	CDR1092	CDR1093	CDR1094	CDR1095	CDR1096	CDR1097	CDR1098	CDR1099	CDR1100	CDR1101	CDR1102	CDR1103	CDR1104	CDR1105	CDR1106	CDR1107	CDR1108	CDR1109	CDR1110	CDR1111	CDR1112	CDR1113	CDR1114	CDR1115	CDR1116	CDR1117	CDR1118	CDR1119	CDR1120	CDR1121	CDR1122	CDR1123	CDR1124	CDR1125	CDR1126	CDR1127	CDR1128	CDR1129	CDR1130	CDR1131	CDR1132	CDR1133	CDR1134	CDR1135	CDR1136	CDR1137	CDR1138	CDR1139	CDR1140	CDR1141	CDR1142	CDR1143	CDR1144	CDR1145	CDR1146	CDR1147	CDR1148	CDR1149	CDR1150	CDR1151	CDR1152	CDR1153	CDR1154	CDR1155	CDR1156	CDR1157	CDR1158	CDR1159	CDR1160	CDR1161	CDR1162	CDR1163	CDR1164	CDR1165	CDR1166	CDR1167	CDR1168	CDR1169	CDR1170	CDR1171	CDR1172	CDR1173	CDR1174	CDR1175	CDR1176	CDR1177	CDR1178	CDR1179	CDR1180	CDR1181	CDR1182	CDR1183	CDR1184	CDR1185	CDR1186	CDR1187	CDR1188	CDR1189	CDR1190	CDR1191	CDR1192	CDR1193	CDR1194	CDR1195	CDR1196	CDR1197	CDR1198	CDR1199	CDR1200	CDR1201	CDR1202	CDR1203	CDR1204	CDR1205	CDR1206	CDR1207	CDR1208	CDR1209	CDR1210
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FIGURE 14

mAb ID	Description	Epitope Sequence	285-297-299-301-303-305-307-309-311-313-315-317-319-321-323-325-327-329-331-333-335-337-339-341-343-345-347-349-351-353-355-357-359-361-363-365-367-369-371-373-375-377-379-381-383-385-387-389-391-393-395-397-399-401-403-405-407-409-411-413-415-417-419-421-423-425-427-429-431-433-435-437-439-441-443-445-447-449-451-453-455-457-459-461-463-465-467-469-471-473-475-477-479-481-483-485-487-489-491-493-495-497-499-501-503-505-507-509-511-513-515-517-519-521-523-525-527-529-531-533-535-537-539-541-543-545-547-549-551-553-555-557-559-561-563-565-567-569-571-573-575-577-579-581-583-585-587-589-591-593-595-597-599-601-603-605-607-609-611-613-615-617-619-621-623-625-627-629-631-633-635-637-639-641-643-645-647-649-651-653-655-657-659-661-663-665-667-669-671-673-675-677-679-681-683-685-687-689-691-693-695-697-699-701-703-705-707-709-711-713-715-717-719-721-723-725-727-729-731-733-735-737-739-741-743-745-747-749-751-753-755-757-759-761-763-765-767-769-771-773-775-777-779-781-783-785-787-789-791-793-795-797-799-801-803-805-807-809-811-813-815-817-819-821-823-825-827-829-831-833-835-837-839-841-843-845-847-849-851-853-855-857-859-861-863-865-867-869-871-873-875-877-879-881-883-885-887-889-891-893-895-897-899-901-903-905-907-909-911-913-915-917-919-921-923-925-927-929-931-933-935-937-939-941-943-945-947-949-951-953-955-957-959-961-963-965-967-969-971-973-975-977-979-981-983-985-987-989-991-993-995-997-999-1001-1003-1005-1007-1009-1011-1013-1015-1017-1019-1021-1023-1025-1027-1029-1031-1033-1035-1037-1039-1041-1043-1045-1047-1049-1051-1053-1055-1057-1059-1061-1063-1065-1067-1069-1071-1073-1075-1077-1079-1081-1083-1085-1087-1089-1091-1093-1095-1097-1099-1101-1103-1105-1107-1109-1111-1113-1115-1117-1119-1121-1123-1125-1127-1129-1131-1133-1135-1137-1139-1141-1143-1145-1147-1149-1151-1153-1155-1157-1159-1161-1163-1165-1167-1169-1171-1173-1175-1177-1179-1181-1183-1185-1187-1189-1191-1193-1195-1197-1199-1201-1203-1205-1207-1209-1211-1213-1215-1217-1219-1221-1223-1225-1227-1229-1231-1233-1235-1237-1239-1241-1243-1245-1247-1249-1251-1253-1255-1257-1259-1261-1263-1265-1267-1269-1271-1273-1275-1277-1279-1281-1283-1285-1287-1289-1291-1293-1295-1297-1299-1301-1303-1305-1307-1309-1311-1313-1315-1317-1319-1321-1323-1325-1327-1329-1331-1333-1335-1337-1339-1341-1343-1345-1347-1349-1351-1353-1355-1357-1359-1361-1363-1365-1367-1369-1371-1373-1375-1377-1379-1381-1383-1385-1387-1389-1391-1393-1395-1397-1399-1401-1403-1405-1407-1409-1411-1413-1415-1417-1419-1421-1423-1425-1427-1429-1431-1433-1435-1437-1439-1441-1443-1445-1447-1449-1451-1453-1455-1457-1459-1461-1463-1465-1467-1469-1471-1473-1475-1477-1479-1481-1483-1485-1487-1489-1491-1493-1495-1497-1499-1501-1503-1505-1507-1509-1511-1513-1515-1517-1519-1521-1523-1525-1527-1529-1531-1533-1535-1537-1539-1541-1543-1545-1547-1549-1551-1553-1555-1557-1559-1561-1563-1565-1567-1569-1571-1573-1575-1577-1579-1581-1583-1585-1587-1589-1591-1593-1595-1597-1599-1601-1603-1605-1607-1609-1611-1613-1615-1617-1619-1621-1623-1625-1627-1629-1631-1633-1635-1637-1639-1641-1643-1645-1647-1649-1651-1653-1655-1657-1659-1661-1663-1665-1667-1669-1671-1673-1675-1677-1679-1681-1683-1685-1687-1689-1691-1693-1695-1697-1699-1701-1703-1705-1707-1709-1711-1713-1715-1717-1719-1721-1723-1725-1727-1729-1731-1733-1735-1737-1739-1741-1743-1745-1747-1749-1751-1753-1755-1757-1759-1761-1763-1765-1767-1769-1771-1773-1775-1777-1779-1781-1783-1785-1787-1789-1791-1793-1795-1797-1799-1801-1803-1805-1807-1809-1811-1813-1815-1817-1819-1821-1823-1825-1827-1829-1831-1833-1835-1837-1839-1841-1843-1845-1847-1849-1851-1853-1855-1857-1859-1861-1863-1865-1867-1869-1871-1873-1875-1877-1879-1881-1883-1885-1887-1889-1891-1893-1895-1897-1899-1901-1903-1905-1907-1909-1911-1913-1915-1917-1919-1921-1923-1925-1927-1929-1931-1933-1935-1937-1939-1941-1943-1945-1947-1949-1951-1953-1955-1957-1959-1961-1963-1965-1967-1969-1971-1973-1975-1977-1979-1981-1983-1985-1987-1989-1991-1993-1995-1997-1999-2001-2003-2005-2007-2009-2011-2013-2015-2017-2019-2021-2023-2025-2027-2029-2031-2033-2035-2037-2039-2041-2043-2045-2047-2049-2051-2053-2055-2057-2059-2061-20
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FIGURE 14

mAb ID	Description	Epitope Sequence	385-430	431-476	477-522	523-568	569-614	615-660	661-706	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB.02	Human IgG1/kappa		385F-430F 431F-469F	385E-430E 432F-509F	385G-430G 432F-509F	385H-430H 432F-509F	385I-430I 432F-509F	385J-430J 432F-509F	385K-430K 432F-509F	EVQLVDSGAEVHQGKSELVSGSGFTSVWGMMV DMPKGLGEMGVPEGGDTFTYSPSGGGVTSADK RTATLQMSLSASDITAMTYCARSDYFQHTPALDY WGDTLVYS	ASTGSPVFLAPSSTSGGTAAGCLGVDPPEPTVSWNSGALTSGV HTPAVLDSGLYSLSVTVPSSSLGTQTYCNVNHHPKNTVDKVEPK SCDKHTCPCPAPPELLGGPVLEPRPKDITLMISRTPREYTCVVDSHSE DPEVMFNTYDGVGVNNAKTIPREQDNTSTYRAVSIVTLVQDMNLG KPKCKYKMKALPAPEKTSKANGQPREQVITLPPSRDELTMGVSLTC LVGGPPSDVAEWEWSNGDEPNWYITTPVLDSDGSFFLSLTYGSRW QSGNFTSCVWHEALHHNTQKSLSPK	RTVAAPSVHPPSDGLKSGTASVVC LNNFYPREAVQVQVKVMDLSDGNS QESVTCDDKSDSTYLSSTLTLSKADE HKHYACLVTHQGLSPVTSNHRGE C	
VSTB.03	Human IgG1/kappa		385F-430F 431F-469F	385E-430E 432F-509F	385G-430G 432F-509F	385H-430H 432F-509F	385I-430I 432F-509F	385J-430J 432F-509F	385K-430K 432F-509F	EVQLVDSGAEVHQGKSELVSGSGFTSVWGMMV DMPKGLGEMGVPEGGDTFTYSPSGGGVTSADK RTATLQMSLSASDITAMTYCARSDYFQHTPALDY WGDTLVYS	ASTGSPVFLAPSSTSGGTAAGCLGVDPPEPTVSWNSGALTSGV HTPAVLDSGLYSLSVTVPSSSLGTQTYCNVNHHPKNTVDKVEPK SCDKHTCPCPAPPELLGGPVLEPRPKDITLMISRTPREYTCVVDSHSE DPEVMFNTYDGVGVNNAKTIPREQDNTSTYRAVSIVTLVQDMNLG KPKCKYKMKALPAPEKTSKANGQPREQVITLPPSRDELTMGVSLTC LVGGPPSDVAEWEWSNGDEPNWYITTPVLDSDGSFFLSLTYGSRW QSGNFTSCVWHEALHHNTQKSLSPK	RTVAAPSVHPPSDGLKSGTASVVC LNNFYPREAVQVQVKVMDLSDGNS QESVTCDDKSDSTYLSSTLTLSKADE HKHYACLVTHQGLSPVTSNHRGE C	
VSTB.04	Human IgG1/kappa		385F-430F 431F-469F	385E-430E 432F-509F	385G-430G 432F-509F	385H-430H 432F-509F	385I-430I 432F-509F	385J-430J 432F-509F	385K-430K 432F-509F	EVQLVDSGAEVHQGKSELVSGSGFTSVWGMMV DMPKGLGEMGVPEGGDTFTYSPSGGGVTSADK RTATLQMSLSASDITAMTYCARSDYFQHTPALDY WGDTLVYS	ASTGSPVFLAPSSTSGGTAAGCLGVDPPEPTVSWNSGALTSGV HTPAVLDSGLYSLSVTVPSSSLGTQTYCNVNHHPKNTVDKVEPK SCDKHTCPCPAPPELLGGPVLEPRPKDITLMISRTPREYTCVVDSHSE DPEVMFNTYDGVGVNNAKTIPREQDNTSTYRAVSIVTLVQDMNLG KPKCKYKMKALPAPEKTSKANGQPREQVITLPPSRDELTMGVSLTC LVGGPPSDVAEWEWSNGDEPNWYITTPVLDSDGSFFLSLTYGSRW QSGNFTSCVWHEALHHNTQKSLSPK	RTVAAPSVHPPSDGLKSGTASVVC LNNFYPREAVQVQVKVMDLSDGNS QESVTCDDKSDSTYLSSTLTLSKADE HKHYACLVTHQGLSPVTSNHRGE C	
VSTB.05	Human IgG1/kappa		385F-430F 431F-469F	385E-430E 432F-509F	385G-430G 432F-509F	385H-430H 432F-509F	385I-430I 432F-509F	385J-430J 432F-509F	385K-430K 432F-509F	EVQLVDSGAEVHQGKSELVSGSGFTSVWGMMV DMPKGLGEMGVPEGGDTFTYSPSGGGVTSADK RTATLQMSLSASDITAMTYCARSDYFQHTPALDY WGDTLVYS	ASTGSPVFLAPSSTSGGTAAGCLGVDPPEPTVSWNSGALTSGV HTPAVLDSGLYSLSVTVPSSSLGTQTYCNVNHHPKNTVDKVEPK SCDKHTCPCPAPPELLGGPVLEPRPKDITLMISRTPREYTCVVDSHSE DPEVMFNTYDGVGVNNAKTIPREQDNTSTYRAVSIVTLVQDMNLG KPKCKYKMKALPAPEKTSKANGQPREQVITLPPSRDELTMGVSLTC LVGGPPSDVAEWEWSNGDEPNWYITTPVLDSDGSFFLSLTYGSRW QSGNFTSCVWHEALHHNTQKSLSPK	RTVAAPSVHPPSDGLKSGTASVVC LNNFYPREAVQVQVKVMDLSDGNS QESVTCDDKSDSTYLSSTLTLSKADE HKHYACLVTHQGLSPVTSNHRGE C	
VSTB.06	Human IgG1/kappa		385F-430F 431F-469F	385E-430E 432F-509F	385G-430G 432F-509F	385H-430H 432F-509F	385I-430I 432F-509F	385J-430J 432F-509F	385K-430K 432F-509F	EVQLVDSGAEVHQGKSELVSGSGFTSVWGMMV DMPKGLGEMGVPEGGDTFTYSPSGGGVTSADK RTATLQMSLSASDITAMTYCARSDYFQHTPALDY WGDTLVYS	ASTGSPVFLAPSSTSGGTAAGCLGVDPPEPTVSWNSGALTSGV HTPAVLDSGLYSLSVTVPSSSLGTQTYCNVNHHPKNTVDKVEPK SCDKHTCPCPAPPELLGGPVLEPRPKDITLMISRTPREYTCVVDSHSE DPEVMFNTYDGVGVNNAKTIPREQDNTSTYRAVSIVTLVQDMNLG KPKCKYKMKALPAPEKTSKANGQPREQVITLPPSRDELTMGVSLTC LVGGPPSDVAEWEWSNGDEPNWYITTPVLDSDGSFFLSLTYGSRW QSGNFTSCVWHEALHHNTQKSLSPK	RTVAAPSVHPPSDGLKSGTASVVC LNNFYPREAVQVQVKVMDLSDGNS QESVTCDDKSDSTYLSSTLTLSKADE HKHYACLVTHQGLSPVTSNHRGE C	

FIGURE 14

Ab ID	Description	Epitope Sequence	Weight (kDa)	Charge (pI)	Mass (kDa)	Charge (pI)	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
S1D107	Human IgG1/kappa		657-725	657-725	657-725	657-725	QVQLVQSGAEVMPGSSVIVSKASGSGTSSYASWY RQAPCGLEWMGIGIHPTGTANYAQRFQGRVITTADE STSTAMELSSLRSEDVAVYCARISGWAEIDVWG GGTVVYS	ASTGSPVFLAPSMSKTSGGTAALGCLVQDYDFPEPTVSWNSGALTSY HTPAVLDSGLYSLSSVTVYPSSSLGTQTYCNVNHPSKNTVDKVEPK SCDHTCPCPAPPELLGSPVFLPPKPDITLMISRTPEVTCVVVDVSH DPEVFNHYVDGVEVHNAKTPKEQINSTRVAVSVTLVHDMNLG KEYCKYKSMALPAPEKTSKAGQPEPQVITTPSRIELTNQVQLT KLVGEPFDIAVEWESNGDENNYKTPPVLDSDGSEFFYSALTYSKRSY QDGNFSCVMEALHNHTYKLSLSPPGK	IQDMTQSPSLASVGDRTVITRQAQSDINMLNW VQIQPGAPAKLITVAASLSQSPVSRPSFSGSGTDF TITSLSDPEATYYCDQNNHPITFGGTVEIK	RTVAAPSVFHPDQELQAGTASVVC LUMNPYPREAQVQKVKMDLQSNIS QSVYEQDKQDSTYSLSTLTLSKADE KHKVAACEVTHQGLSPVTSNHRGE C
			657-725	657-725	657-725	657-725	QVQLVQSGAEVMPGSSVIVSKASGSGTSSYASWY RQAPCGLEWMGIGIHPTGTANYAQRFQGRVITTADE STSTAMELSSLRSEDVAVYCARISGWAEIDVWG GGTVVYS	ASTGSPVFLAPSMSKTSGGTAALGCLVQDYDFPEPTVSWNSGALTSY HTPAVLDSGLYSLSSVTVYPSSSLGTQTYCNVNHPSKNTVDKVEPK SCDHTCPCPAPPELLGSPVFLPPKPDITLMISRTPEVTCVVVDVSH DPEVFNHYVDGVEVHNAKTPKEQINSTRVAVSVTLVHDMNLG KEYCKYKSMALPAPEKTSKAGQPEPQVITTPSRIELTNQVQLT KLVGEPFDIAVEWESNGDENNYKTPPVLDSDGSEFFYSALTYSKRSY QDGNFSCVMEALHNHTYKLSLSPPGK	IQDMTQSPSLASVGDRTVITRQAQSDINMLNW VQIQPGAPAKLITVAASLSQSPVSRPSFSGSGTDF TITSLSDPEATYYCDQNNHPITFGGTVEIK	RTVAAPSVFHPDQELQAGTASVVC LUMNPYPREAQVQKVKMDLQSNIS QSVYEQDKQDSTYSLSTLTLSKADE KHKVAACEVTHQGLSPVTSNHRGE C
S1D108	Human IgG1/kappa		657-725	657-725	657-725	657-725	QVQLVQSGAEVMPGSSVIVSKASGSGTSSYASWY RQAPCGLEWMGIGIHPTGTANYAQRFQGRVITTADE STSTAMELSSLRSEDVAVYCARISGWAEIDVWG GGTVVYS	ASTGSPVFLAPSMSKTSGGTAALGCLVQDYDFPEPTVSWNSGALTSY HTPAVLDSGLYSLSSVTVYPSSSLGTQTYCNVNHPSKNTVDKVEPK SCDHTCPCPAPPELLGSPVFLPPKPDITLMISRTPEVTCVVVDVSH DPEVFNHYVDGVEVHNAKTPKEQINSTRVAVSVTLVHDMNLG KEYCKYKSMALPAPEKTSKAGQPEPQVITTPSRIELTNQVQLT KLVGEPFDIAVEWESNGDENNYKTPPVLDSDGSEFFYSALTYSKRSY QDGNFSCVMEALHNHTYKLSLSPPGK	IQDMTQSPSLASVGDRTVITRQAQSDINMLNW VQIQPGAPAKLITVAASLSQSPVSRPSFSGSGTDF TITSLSDPEATYYCDQNNHPITFGGTVEIK	RTVAAPSVFHPDQELQAGTASVVC LUMNPYPREAQVQKVKMDLQSNIS QSVYEQDKQDSTYSLSTLTLSKADE KHKVAACEVTHQGLSPVTSNHRGE C
			657-725	657-725	657-725	657-725	QVQLVQSGAEVMPGSSVIVSKASGSGTSSYASWY RQAPCGLEWMGIGIHPTGTANYAQRFQGRVITTADE STSTAMELSSLRSEDVAVYCARISGWAEIDVWG GGTVVYS	ASTGSPVFLAPSMSKTSGGTAALGCLVQDYDFPEPTVSWNSGALTSY HTPAVLDSGLYSLSSVTVYPSSSLGTQTYCNVNHPSKNTVDKVEPK SCDHTCPCPAPPELLGSPVFLPPKPDITLMISRTPEVTCVVVDVSH DPEVFNHYVDGVEVHNAKTPKEQINSTRVAVSVTLVHDMNLG KEYCKYKSMALPAPEKTSKAGQPEPQVITTPSRIELTNQVQLT KLVGEPFDIAVEWESNGDENNYKTPPVLDSDGSEFFYSALTYSKRSY QDGNFSCVMEALHNHTYKLSLSPPGK	IQDMTQSPSLASVGDRTVITRQAQSDINMLNW VQIQPGAPAKLITVAASLSQSPVSRPSFSGSGTDF TITSLSDPEATYYCDQNNHPITFGGTVEIK	RTVAAPSVFHPDQELQAGTASVVC LUMNPYPREAQVQKVKMDLQSNIS QSVYEQDKQDSTYSLSTLTLSKADE KHKVAACEVTHQGLSPVTSNHRGE C
S1D109	Human IgG1/kappa		657-725	657-725	657-725	657-725	QVQLVQSGAEVMPGSSVIVSKASGSGTSSYASWY RQAPCGLEWMGIGIHPTGTANYAQRFQGRVITTADE STSTAMELSSLRSEDVAVYCARISGWAEIDVWG GGTVVYS	ASTGSPVFLAPSMSKTSGGTAALGCLVQDYDFPEPTVSWNSGALTSY HTPAVLDSGLYSLSSVTVYPSSSLGTQTYCNVNHPSKNTVDKVEPK SCDHTCPCPAPPELLGSPVFLPPKPDITLMISRTPEVTCVVVDVSH DPEVFNHYVDGVEVHNAKTPKEQINSTRVAVSVTLVHDMNLG KEYCKYKSMALPAPEKTSKAGQPEPQVITTPSRIELTNQVQLT KLVGEPFDIAVEWESNGDENNYKTPPVLDSDGSEFFYSALTYSKRSY QDGNFSCVMEALHNHTYKLSLSPPGK	IQDMTQSPSLASVGDRTVITRQAQSDINMLNW VQIQPGAPAKLITVAASLSQSPVSRPSFSGSGTDF TITSLSDPEATYYCDQNNHPITFGGTVEIK	RTVAAPSVFHPDQELQAGTASVVC LUMNPYPREAQVQKVKMDLQSNIS QSVYEQDKQDSTYSLSTLTLSKADE KHKVAACEVTHQGLSPVTSNHRGE C
			657-725	657-725	657-725	657-725	QVQLVQSGAEVMPGSSVIVSKASGSGTSSYASWY RQAPCGLEWMGIGIHPTGTANYAQRFQGRVITTADE STSTAMELSSLRSEDVAVYCARISGWAEIDVWG GGTVVYS	ASTGSPVFLAPSMSKTSGGTAALGCLVQDYDFPEPTVSWNSGALTSY HTPAVLDSGLYSLSSVTVYPSSSLGTQTYCNVNHPSKNTVDKVEPK SCDHTCPCPAPPELLGSPVFLPPKPDITLMISRTPEVTCVVVDVSH DPEVFNHYVDGVEVHNAKTPKEQINSTRVAVSVTLVHDMNLG KEYCKYKSMALPAPEKTSKAGQPEPQVITTPSRIELTNQVQLT KLVGEPFDIAVEWESNGDENNYKTPPVLDSDGSEFFYSALTYSKRSY QDGNFSCVMEALHNHTYKLSLSPPGK	IQDMTQSPSLASVGDRTVITRQAQSDINMLNW VQIQPGAPAKLITVAASLSQSPVSRPSFSGSGTDF TITSLSDPEATYYCDQNNHPITFGGTVEIK	RTVAAPSVFHPDQELQAGTASVVC LUMNPYPREAQVQKVKMDLQSNIS QSVYEQDKQDSTYSLSTLTLSKADE KHKVAACEVTHQGLSPVTSNHRGE C
S1D110	Human IgG1/kappa		657-725	657-725	657-725	657-725	QVQLVQSGAEVMPGSSVIVSKASGSGTSSYASWY RQAPCGLEWMGIGIHPTGTANYAQRFQGRVITTADE STSTAMELSSLRSEDVAVYCARISGWAEIDVWG GGTVVYS	ASTGSPVFLAPSMSKTSGGTAALGCLVQDYDFPEPTVSWNSGALTSY HTPAVLDSGLYSLSSVTVYPSSSLGTQTYCNVNHPSKNTVDKVEPK SCDHTCPCPAPPELLGSPVFLPPKPDITLMISRTPEVTCVVVDVSH DPEVFNHYVDGVEVHNAKTPKEQINSTRVAVSVTLVHDMNLG KEYCKYKSMALPAPEKTSKAGQPEPQVITTPSRIELTNQVQLT KLVGEPFDIAVEWESNGDENNYKTPPVLDSDGSEFFYSALTYSKRSY QDGNFSCVMEALHNHTYKLSLSPPGK	IQDMTQSPSLASVGDRTVITRQAQSDINMLNW VQIQPGAPAKLITVAASLSQSPVSRPSFSGSGTDF TITSLSDPEATYYCDQNNHPITFGGTVEIK	RTVAAPSVFHPDQELQAGTASVVC LUMNPYPREAQVQKVKMDLQSNIS QSVYEQDKQDSTYSLSTLTLSKADE KHKVAACEVTHQGLSPVTSNHRGE C
			657-725	657-725	657-725	657-725	QVQLVQSGAEVMPGSSVIVSKASGSGTSSYASWY RQAPCGLEWMGIGIHPTGTANYAQRFQGRVITTADE STSTAMELSSLRSEDVAVYCARISGWAEIDVWG GGTVVYS	ASTGSPVFLAPSMSKTSGGTAALGCLVQDYDFPEPTVSWNSGALTSY HTPAVLDSGLYSLSSVTVYPSSSLGTQTYCNVNHPSKNTVDKVEPK SCDHTCPCPAPPELLGSPVFLPPKPDITLMISRTPEVTCVVVDVSH DPEVFNHYVDGVEVHNAKTPKEQINSTRVAVSVTLVHDMNLG KEYCKYKSMALPAPEKTSKAGQPEPQVITTPSRIELTNQVQLT KLVGEPFDIAVEWESNGDENNYKTPPVLDSDGSEFFYSALTYSKRSY QDGNFSCVMEALHNHTYKLSLSPPGK	IQDMTQSPSLASVGDRTVITRQAQSDINMLNW VQIQPGAPAKLITVAASLSQSPVSRPSFSGSGTDF TITSLSDPEATYYCDQNNHPITFGGTVEIK	RTVAAPSVFHPDQELQAGTASVVC LUMNPYPREAQVQKVKMDLQSNIS QSVYEQDKQDSTYSLSTLTLSKADE KHKVAACEVTHQGLSPVTSNHRGE C
S1D111	Human IgG1/kappa		657-725	657-725	657-725	657-725	QVQLVQSGAEVMPGSSVIVSKASGSGTSSYASWY RQAPCGLEWMGIGIHPTGTANYAQRFQGRVITTADE STSTAMELSSLRSEDVAVYCARISGWAEIDVWG GGTVVYS	ASTGSPVFLAPSMSKTSGGTAALGCLVQDYDFPEPTVSWNSGALTSY HTPAVLDSGLYSLSSVTVYPSSSLGTQTYCNVNHPSKNTVDKVEPK SCDHTCPCPAPPELLGSPVFLPPKPDITLMISRTPEVTCVVVDVSH DPEVFNHYVDGVEVHNAKTPKEQINSTRVAVSVTLVHDMNLG KEYCKYKSMALPAPEKTSKAGQPEPQVITTPSRIELTNQVQLT KLVGEPFDIAVEWESNGDENNYKTPPVLDSDGSEFFYSALTYSKRSY QDGNFSCVMEALHNHTYKLSLSPPGK	IQDMTQSPSLASVGDRTVITRQAQSDINMLNW VQIQPGAPAKLITVAASLSQSPVSRPSFSGSGTDF TITSLSDPEATYYCDQNNHPITFGGTVEIK	RTVAAPSVFHPDQELQAGTASVVC LUMNPYPREAQVQKVKMDLQSNIS QSVYEQDKQDSTYSLSTLTLSKADE KHKVAACEVTHQGLSPVTSNHRGE C
			657-725	657-725	657-725	657-725	QVQLVQSGAEVMPGSSVIVSKASGSGTSSYASWY RQAPCGLEWMGIGIHPTGTANYAQRFQGRVITTADE STSTAMELSSLRSEDVAVYCARISGWAEIDVWG GGTVVYS	ASTGSPVFLAPSMSKTSGGTAALGCLVQDYDFPEPTVSWNSGALTSY HTPAVLDSGLYSLSSVTVYPSSSLGTQTYCNVNHPSKNTVDKVEPK SCDHTCPCPAPPELLGSPVFLPPKPDITLMISRTPEVTCVVVDVSH DPEVFNHYVDGVEVHNAKTPKEQINSTRVAVSVTLVHDMNLG KEYCKYKSMALPAPEKTSKAGQPEPQVITTPSRIELTNQVQLT KLVGEPFDIAVEWESNGDENNYKTPPVLDSDGSEFFYSALTYSKRSY QDGNFSCVMEALHNHTYKLSLSPPGK	IQDMTQSPSLASVGDRTVITRQAQSDINMLNW VQIQPGAPAKLITVAASLSQSPVSRPSFSGSGTDF TITSLSDPEATYYCDQNNHPITFGGTVEIK	RTVAAPSVFHPDQELQAGTASVVC LUMNPYPREAQVQKVKMDLQSNIS QSVYEQDKQDSTYSLSTLTLSKADE KHKVAACEVTHQGLSPVTSNHRGE C

FIGURE 14

mAb ID	Description	Epitope Sequence	Accession	Accession	Accession	Accession	Accession	Accession	Accession	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB114	Human IgG1/Igappa	VSTB114-14	6851-6869	6855-6863	6859-6867	6863-6871	6867-6875	6871-6879	6875-6883	QVQLVQSGAEVMPGSSGVKVKSCAGSETSSYASVW RQAPGQLEWVGRIHIGTAMFAADGKGRVITTADE STSYAMFELSRLSEDTAVYVCARSGWVALEDPWG QGTIVTSS	ASTGKPSVPLAPSKSTSGGTAAALGCLVDYFREPVTYVWNSGALTSGV HFPALQSSGYSLSLSVTVPSSSLGTQTYCNVNHKPSNTVDMKVEPK SDCKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH DPEWENYVGVGVENHAKTPREEQYNTSYRVSUTLVTHQDNLG IWEKCVSKMALPAPIETKSKAGQREPKQVTPPSRDELTMKQVSLC LWVGFPDSIAHVEWMSGDPENNYKITPPVLDSDGSFYSALTVKMSRW QDGNFSCVMIHEALHNHTQKLSLSPGK	RTVAAPSVFIFPQDQSLGTSASVVC LNNIPPREAKVQWVKVINALDGSN QESVTEQDSKDSYLSLTLTKADYVE KHKVACEVTHGELSPTVTKSMRGE C	
VSTB115	Human IgG1/Igappa	VSTB115-15	6877-6885	6881-6889	6885-6893	6889-6897	6893-6901	6897-6905	6901-6909	QVQLVQSGAEVMPGSSGVKVKSCAGSETSSYASVW RQAPGQLEWVGRIHIGTAMFAADGKGRVITTADE STSYAMFELSRLSEDTAVYVCARSGWVALEDPWG QGTIVTSS	ASTGKPSVPLAPSKSTSGGTAAALGCLVDYFREPVTYVWNSGALTSGV HFPALQSSGYSLSLSVTVPSSSLGTQTYCNVNHKPSNTVDMKVEPK SDCKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH DPEWENYVGVGVENHAKTPREEQYNTSYRVSUTLVTHQDNLG IWEKCVSKMALPAPIETKSKAGQREPKQVTPPSRDELTMKQVSLC LWVGFPDSIAHVEWMSGDPENNYKITPPVLDSDGSFYSALTVKMSRW QDGNFSCVMIHEALHNHTQKLSLSPGK	RTVAAPSVFIFPQDQSLGTSASVVC LNNIPPREAKVQWVKVINALDGSN QESVTEQDSKDSYLSLTLTKADYVE KHKVACEVTHGELSPTVTKSMRGE C	
VSTB116	Human IgG1/Igappa	VSTB116-16	6877-6885	6881-6889	6885-6893	6889-6897	6893-6901	6897-6905	6901-6909	QVQLVQSGAEVMPGSSGVKVKSCAGSETSSYASVW RQAPGQLEWVGRIHIGTAMFAADGKGRVITTADE STSYAMFELSRLSEDTAVYVCARSGWVALEDPWG QGTIVTSS	ASTGKPSVPLAPSKSTSGGTAAALGCLVDYFREPVTYVWNSGALTSGV HFPALQSSGYSLSLSVTVPSSSLGTQTYCNVNHKPSNTVDMKVEPK SDCKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH DPEWENYVGVGVENHAKTPREEQYNTSYRVSUTLVTHQDNLG IWEKCVSKMALPAPIETKSKAGQREPKQVTPPSRDELTMKQVSLC LWVGFPDSIAHVEWMSGDPENNYKITPPVLDSDGSFYSALTVKMSRW QDGNFSCVMIHEALHNHTQKLSLSPGK	RTVAAPSVFIFPQDQSLGTSASVVC LNNIPPREAKVQWVKVINALDGSN QESVTEQDSKDSYLSLTLTKADYVE KHKVACEVTHGELSPTVTKSMRGE C	
VSTB119	Human IgG1/Igappa	VSTB119-19	6851-6869	6855-6863	6859-6867	6863-6871	6867-6875	6871-6879	6875-6883	QVQLVQSGAEVMPGSSGVKVKSCAGSETTFRTHHW RQAPGQLEWVGSIYFIDSTYINIKRKRVITTRDTS ASTAMFELSRLSEDTAVYVCARSGWVALEDPWGQ TLTVSS	ASTGKPSVPLAPSKSTSGGTAAALGCLVDYFREPVTYVWNSGALTSGV HFPALQSSGYSLSLSVTVPSSSLGTQTYCNVNHKPSNTVDMKVEPK SDCKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH DPEWENYVGVGVENHAKTPREEQYNTSYRVSUTLVTHQDNLG IWEKCVSKMALPAPIETKSKAGQREPKQVTPPSRDELTMKQVSLC LWVGFPDSIAHVEWMSGDPENNYKITPPVLDSDGSFYSALTVKMSRW QDGNFSCVMIHEALHNHTQKLSLSPGK	RTVAAPSVFIFPQDQSLGTSASVVC LNNIPPREAKVQWVKVINALDGSN QESVTEQDSKDSYLSLTLTKADYVE KHKVACEVTHGELSPTVTKSMRGE C	
VSTB120	Human IgG1/Igappa	VSTB120-20	6851-6869	6855-6863	6859-6867	6863-6871	6867-6875	6871-6879	6875-6883	QVQLVQSGAEVMPGSSGVKVKSCAGSETTFRTHHW RQAPGQLEWVGSIYFIDSTYINIKRKRVITTRDTS ASTAMFELSRLSEDTAVYVCARSGWVALEDPWGQ TLTVSS	ASTGKPSVPLAPSKSTSGGTAAALGCLVDYFREPVTYVWNSGALTSGV HFPALQSSGYSLSLSVTVPSSSLGTQTYCNVNHKPSNTVDMKVEPK SDCKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH DPEWENYVGVGVENHAKTPREEQYNTSYRVSUTLVTHQDNLG IWEKCVSKMALPAPIETKSKAGQREPKQVTPPSRDELTMKQVSLC LWVGFPDSIAHVEWMSGDPENNYKITPPVLDSDGSFYSALTVKMSRW QDGNFSCVMIHEALHNHTQKLSLSPGK	RTVAAPSVFIFPQDQSLGTSASVVC LNNIPPREAKVQWVKVINALDGSN QESVTEQDSKDSYLSLTLTKADYVE KHKVACEVTHGELSPTVTKSMRGE C	
VSTB121	Human IgG1/Igappa	VSTB121-21	6851-6869	6855-6863	6859-6867	6863-6871	6867-6875	6871-6879	6875-6883	QVQLVQSGAEVMPGSSGVKVKSCAGSETTFRTHHW RQAPGQLEWVGSIYFIDSTYINIKRKRVITTRDTS ASTAMFELSRLSEDTAVYVCARSGWVALEDPWGQ TLTVSS	ASTGKPSVPLAPSKSTSGGTAAALGCLVDYFREPVTYVWNSGALTSGV HFPALQSSGYSLSLSVTVPSSSLGTQTYCNVNHKPSNTVDMKVEPK SDCKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH DPEWENYVGVGVENHAKTPREEQYNTSYRVSUTLVTHQDNLG IWEKCVSKMALPAPIETKSKAGQREPKQVTPPSRDELTMKQVSLC LWVGFPDSIAHVEWMSGDPENNYKITPPVLDSDGSFYSALTVKMSRW QDGNFSCVMIHEALHNHTQKLSLSPGK	RTVAAPSVFIFPQDQSLGTSASVVC LNNIPPREAKVQWVKVINALDGSN QESVTEQDSKDSYLSLTLTKADYVE KHKVACEVTHGELSPTVTKSMRGE C	

FIGURE 14

[illegible]

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[illegible]

FIGURE 14

[illegible]

FIGURE 14

[illegible]

FIGURE 14

UniProt ID	Description	Epitope Sequence	Accession	Weight (kDa)	PI	CD1	CD2	CD3	CD4	CD5	CD6	CD7	CD8	CD9	CD10	CD11	CD12	CD13	CD14	CD15	CD16	CD17	CD18	CD19	CD20	CD21	CD22	CD23	CD24	CD25	CD26	CD27	CD28	CD29	CD30	CD31	CD32	CD33	CD34	CD35	CD36	CD37	CD38	CD39	CD40	CD41	CD42	CD43	CD44	CD45	CD46	CD47	CD48	CD49	CD50	CD51	CD52	CD53	CD54	CD55	CD56	CD57	CD58	CD59	CD60	CD61	CD62	CD63	CD64	CD65	CD66	CD67	CD68	CD69	CD70	CD71	CD72	CD73	CD74	CD75	CD76	CD77	CD78	CD79	CD80	CD81	CD82	CD83	CD84	CD85	CD86	CD87	CD88	CD89	CD90	CD91	CD92	CD93	CD94	CD95	CD96	CD97	CD98	CD99	CD100	CD101	CD102	CD103	CD104	CD105	CD106	CD107	CD108	CD109	CD110	CD111	CD112	CD113	CD114	CD115	CD116	CD117	CD118	CD119	CD120	CD121	CD122	CD123	CD124	CD125	CD126	CD127	CD128	CD129	CD130	CD131	CD132	CD133	CD134	CD135	CD136	CD137	CD138	CD139	CD140	CD141	CD142	CD143	CD144	CD145	CD146	CD147	CD148	CD149	CD150	CD151	CD152	CD153	CD154	CD155	CD156	CD157	CD158	CD159	CD160	CD161	CD162	CD163	CD164	CD165	CD166	CD167	CD168	CD169	CD170	CD171	CD172	CD173	CD174	CD175	CD176	CD177	CD178	CD179	CD180	CD181	CD182	CD183	CD184	CD185	CD186	CD187	CD188	CD189	CD190	CD191	CD192	CD193	CD194	CD195	CD196	CD197	CD198	CD199	CD200	CD201	CD202	CD203	CD204	CD205	CD206	CD207	CD208	CD209	CD210	CD211	CD212	CD213	CD214	CD215	CD216	CD217	CD218	CD219	CD220	CD221	CD222	CD223	CD224	CD225	CD226	CD227	CD228	CD229	CD230	CD231	CD232	CD233	CD234	CD235	CD236	CD237	CD238	CD239	CD240	CD241	CD242	CD243	CD244	CD245	CD246	CD247	CD248	CD249	CD250	CD251	CD252	CD253	CD254	CD255	CD256	CD257	CD258	CD259	CD260	CD261	CD262	CD263	CD264	CD265	CD266	CD267	CD268	CD269	CD270	CD271	CD272	CD273	CD274	CD275	CD276	CD277	CD278	CD279	CD280	CD281	CD282	CD283	CD284	CD285	CD286	CD287	CD288	CD289	CD290	CD291	CD292	CD293	CD294	CD295	CD296	CD297	CD298	CD299	CD300	CD301	CD302	CD303	CD304	CD305	CD306	CD307	CD308	CD309	CD310	CD311	CD312	CD313	CD314	CD315	CD316	CD317	CD318	CD319	CD320	CD321	CD322	CD323	CD324	CD325	CD326	CD327	CD328	CD329	CD330	CD331	CD332	CD333	CD334	CD335	CD336	CD337	CD338	CD339	CD340	CD341	CD342	CD343	CD344	CD345	CD346	CD347	CD348	CD349	CD350	CD351	CD352	CD353	CD354	CD355	CD356	CD357	CD358	CD359	CD360	CD361	CD362	CD363	CD364	CD365	CD366	CD367	CD368	CD369	CD370	CD371	CD372	CD373	CD374	CD375	CD376	CD377	CD378	CD379	CD380	CD381	CD382	CD383	CD384	CD385	CD386	CD387	CD388	CD389	CD390	CD391	CD392	CD393	CD394	CD395	CD396	CD397	CD398	CD399	CD400	CD401	CD402	CD403	CD404	CD405	CD406	CD407	CD408	CD409	CD410	CD411	CD412	CD413	CD414	CD415	CD416	CD417	CD418	CD419	CD420	CD421	CD422	CD423	CD424	CD425	CD426	CD427	CD428	CD429	CD430	CD431	CD432	CD433	CD434	CD435	CD436	CD437	CD438	CD439	CD440	CD441	CD442	CD443	CD444	CD445	CD446	CD447	CD448	CD449	CD450	CD451	CD452	CD453	CD454	CD455	CD456	CD457	CD458	CD459	CD460
UniProt ID	Description	Epitope Sequence	Accession	Weight (kDa)	PI	CD1	CD2	CD3	CD4	CD5	CD6	CD7	CD8	CD9	CD10	CD11	CD12	CD13	CD14	CD15	CD16	CD17	CD18	CD19	CD20	CD21	CD22	CD23	CD24	CD25	CD26	CD27	CD28	CD29	CD30	CD31	CD32	CD33	CD34	CD35	CD36	CD37	CD38	CD39	CD40	CD41	CD42	CD43	CD44	CD45	CD46	CD47	CD48	CD49	CD50	CD51	CD52	CD53	CD54	CD55	CD56	CD57	CD58	CD59	CD60	CD61	CD62	CD63	CD64	CD65	CD66	CD67	CD68	CD69	CD70	CD71	CD72	CD73	CD74	CD75	CD76	CD77	CD78	CD79	CD80	CD81	CD82	CD83	CD84	CD85	CD86	CD87	CD88	CD89	CD90	CD91	CD92	CD93	CD94	CD95	CD96	CD97	CD98	CD99	CD100	CD101	CD102	CD103	CD104	CD105	CD106	CD107	CD108	CD109	CD110	CD111	CD112	CD113	CD114	CD115	CD116	CD117	CD118	CD119	CD120	CD121	CD122	CD123	CD124	CD125	CD126	CD127	CD128	CD129	CD130	CD131	CD132	CD133	CD134	CD135	CD136	CD137	CD138	CD139	CD140	CD141	CD142	CD143	CD144	CD145	CD146	CD147	CD148	CD149	CD150	CD151	CD152	CD153	CD154	CD155	CD156	CD157	CD158	CD159	CD160	CD161	CD162	CD163	CD164	CD165	CD166	CD167	CD168	CD169	CD170	CD171	CD172	CD173	CD174	CD175	CD176	CD177	CD178	CD179	CD180	CD181	CD182	CD183	CD184	CD185	CD186	CD187	CD188	CD189	CD190	CD191	CD192	CD193	CD194	CD195	CD196	CD197	CD198	CD199	CD200	CD201	CD202	CD203	CD204	CD205	CD206	CD207	CD208	CD209	CD210	CD211	CD212	CD213	CD214	CD215	CD216	CD217	CD218	CD219	CD220	CD221	CD222	CD223	CD224	CD225	CD226	CD227	CD228	CD229	CD230	CD231	CD232	CD233	CD234	CD235	CD236	CD237	CD238	CD239	CD240	CD241	CD242	CD243	CD244	CD245	CD246	CD247	CD248	CD249	CD250	CD251	CD252	CD253	CD254	CD255	CD256	CD257	CD258	CD259	CD260	CD261	CD262	CD263	CD264	CD265	CD266	CD267	CD268	CD269	CD270	CD271	CD272	CD273	CD274	CD275	CD276	CD277	CD278	CD279	CD280	CD281	CD282	CD283	CD284	CD285	CD286	CD287	CD288	CD289	CD290	CD291	CD292	CD293	CD294	CD295	CD296	CD297	CD298	CD299	CD300	CD301	CD302	CD303	CD304	CD305	CD306	CD307	CD308	CD309	CD310	CD311	CD312	CD313	CD314	CD315	CD316	CD317	CD318	CD319	CD320	CD321	CD322	CD323	CD324	CD325	CD326	CD327	CD328	CD329	CD330	CD331	CD332	CD333	CD334	CD335	CD336	CD337	CD338	CD339	CD340	CD341	CD342	CD343	CD344	CD345	CD346	CD347	CD348	CD349	CD350	CD351	CD352	CD353	CD354	CD355	CD356	CD357	CD358	CD359	CD360	CD361	CD362	CD363	CD364	CD365	CD366	CD367	CD368	CD369	CD370	CD371	CD372	CD373	CD374	CD375	CD376	CD377	CD378	CD379	CD380	CD381	CD382	CD383	CD384	CD385	CD386	CD387	CD388	CD389	CD390	CD391	CD392	CD393	CD394	CD395	CD396	CD397	CD398	CD399	CD400	CD401	CD402	CD403	CD404	CD405	CD406	CD407	CD408	CD409	CD410	CD411	CD412	CD413	CD414	CD415	CD416	CD417	CD418	CD419	CD420	CD421	CD422	CD423	CD424	CD425	CD426	CD427	CD428	CD429	CD430	CD431	CD432	CD433	CD434	CD435	CD436	CD437	CD438	CD439	CD440	CD441	CD442	CD443	CD444	CD445	CD446	CD447	CD448	CD449	CD450	CD451	CD452	CD453	CD454	CD455	CD456	CD457	CD458	CD459	CD460
UniProt ID	Description	Epitope Sequence	Accession	Weight (kDa)	PI	CD1	CD2	CD3	CD4	CD5	CD6	CD7	CD8	CD9	CD10	CD11	CD12	CD13	CD14	CD15	CD16	CD17	CD18	CD19	CD20	CD21	CD22	CD23	CD24	CD25	CD26	CD27	CD28	CD29	CD30	CD31	CD32	CD33	CD34	CD35	CD36	CD37	CD38	CD39	CD40	CD41	CD42	CD43	CD44	CD45	CD46	CD47	CD48	CD49	CD50	CD51	CD52	CD53	CD54	CD55	CD56	CD57	CD58	CD59	CD60	CD61	CD62	CD63	CD64	CD65	CD66	CD67	CD68	CD69	CD70	CD71	CD72	CD73	CD74	CD75	CD76	CD77	CD78	CD79	CD80	CD81	CD82	CD83	CD84	CD85	CD86	CD87	CD88	CD89	CD90	CD91	CD92	CD93	CD94	CD95	CD96	CD97	CD98	CD99	CD100	CD101	CD102	CD103	CD104	CD105	CD106	CD107	CD108	CD109	CD110	CD111	CD112	CD113	CD114	CD115	CD116	CD117	CD118	CD119	CD120	CD121	CD122	CD123	CD124	CD125	CD126	CD127	CD128	CD129	CD130	CD131	CD132	CD133	CD134	CD135	CD136	CD137	CD138	CD139	CD140	CD141	CD142	CD143	CD144	CD145	CD146	CD147	CD148	CD149	CD150	CD151	CD152	CD153	CD154	CD155	CD156	CD157	CD158	CD159	CD160	CD161	CD162	CD163	CD164	CD165	CD166	CD167	CD168	CD169	CD170	CD171	CD172	CD173	CD174	CD175	CD176	CD177	CD178	CD179	CD180	CD181	CD182	CD183	CD184	CD185	CD186	CD187	CD188	CD189	CD190	CD191	CD192	CD193	CD194	CD195	CD196	CD197	CD198	CD199	CD200	CD201	CD202	CD203	CD204	CD205	CD206	CD207	CD208	CD209	CD210	CD211	CD212	CD213	CD214	CD215	CD216	CD217	CD218	CD219	CD220	CD221	CD222	CD223	CD224	CD225	CD226	CD227	CD228	CD229	CD230	CD231	CD232	CD233	CD234	CD235	CD236	CD237	CD238	CD239	CD240	CD241	CD242	CD243	CD244	CD245	CD246	CD247	CD248	CD249	CD250	CD251	CD252	CD253	CD254	CD255	CD256	CD257	CD258	CD259	CD260	CD261	CD262	CD263	CD264	CD265	CD266	CD267	CD268	CD269	CD270	CD271	CD272	CD273	CD274	CD275	CD276	CD277	CD278	CD279	CD280	CD281	CD282	CD283	CD284	CD285	CD286	CD287	CD288	CD289	CD290	CD291	CD292	CD293	CD294	CD295	CD296	CD297	CD298	CD299	CD300	CD301	CD302	CD303	CD304	CD305	CD306	CD307	CD308	CD309	CD310	CD311	CD312	CD313	CD314	CD315	CD316	CD317	CD318	CD319	CD320	CD321	CD322	CD323	CD324	CD325	CD326	CD327	CD328	CD329	CD330	CD331	CD332	CD333	CD334	CD335	CD336	CD337	CD338	CD339	CD340	CD341	CD342	CD343	CD344	CD345	CD346	CD347	CD348	CD349	CD350	CD351	CD352	CD353	CD354	CD355	CD356	CD357	CD358	CD359	CD360	CD361	CD362	CD363	CD364	CD365	CD366	CD367	CD368	CD369	CD370	CD371	CD372	CD373	CD374	CD375	CD376	CD377	CD378	CD379	CD380	CD381	CD382	CD383	CD384	CD385	CD386	CD387	CD388	CD389	CD390	CD391	CD392	CD393	CD394	CD395	CD396	CD397	CD398	CD399	CD400	CD401	CD402	CD403	CD404	CD405	CD406	CD407	CD408	CD409	CD410	CD411	CD412	CD413	CD414	CD415	CD416	CD417	CD418	CD419	CD420	CD421	CD422	CD423	CD424	CD425	CD426	CD427	CD428	CD429	CD430	CD431	CD432	CD433	CD434	CD435	CD436	CD437	CD438	CD439	CD440	CD441	CD442	CD443	CD444	CD445	CD446	CD447	CD448	CD449	CD450	CD451	CD452	CD453	CD454	CD455	CD456	CD457	CD458	CD459	CD460
UniProt ID	Description	Epitope Sequence	Accession	Weight (kDa)	PI	CD1	CD2	CD3	CD4	CD5	CD6	CD7	CD8	CD9	CD10	CD11	CD12	CD13																																																																																																																																																																																																																																																																																																																																																																																																																																																															

FIGURE 14

mAb ID	Description	Epitope Sequence	385-430	431-476	477-522	523-568	569-614	615-660	Heavy-chain Variable	Heavy-chain Constant	Light-chain Variable	Light-chain Constant
VSTB86	Human IgG1/kappa		65772399	65772400	65772401	65772402	65772403	65772404	QVQLVQSGAEVWPSSVYVPSSELTQTYCNVNHPSMTVDKVEPK SCKDTHCPDCAPELGGPVLEPRPKDITLMISRTPTCTVVDVDSHE DPEVMFNTYDGVVFNAAKTIPREQVNSTYRVASVTVLQDMNLNG KTKCKKSMKALPAPEKTSKANGDPEQVYVLPAPRELTNMGVSLTC LUGPFPDVAIVEMSGDEPNMYITPPVLDSDGSFFLSALTYSKRW QSGNIFSCSVNHEALHHNTQKSLSPKRC	ASTGSPVFRAPSSKSTSGGTAAGCLVQDYFPEVTVSNVSGALTSGV HTPFAVLDSSGLYSLSSVTVPPSSSLGTQTYCNVNHPSMTVDKVEPK SCKDTHCPDCAPELGGPVLEPRPKDITLMISRTPTCTVVDVDSHE DPEVMFNTYDGVVFNAAKTIPREQVNSTYRVASVTVLQDMNLNG KTKCKKSMKALPAPEKTSKANGDPEQVYVLPAPRELTNMGVSLTC LUGPFPDVAIVEMSGDEPNMYITPPVLDSDGSFFLSALTYSKRW QSGNIFSCSVNHEALHHNTQKSLSPKRC	AQQLTQSPSLASVSGDRVTTTORAQSSSLNMY QDQPGKAPALLTAASLSQSGVPRFSGSGSDTFT ITSSLOPEDATITTCQDPSITRTTGGTNEIK	RTVAAPSVHPPSDEQLKGTASV/C LNNYPREAQVQVQKMDLSDGNS QESVTCDDKSDSTYLSSTLTLLBAADYE HKHYACEVTHQGLSPVTSNHRGE C
VSTB87	Human IgG1/kappa		65772426	65772427	65772428	65772429	65772430	65772431	QVQLVQSGAEVWPSSVYVPSSELTQTYCNVNHPSMTVDKVEPK SCKDTHCPDCAPELGGPVLEPRPKDITLMISRTPTCTVVDVDSHE DPEVMFNTYDGVVFNAAKTIPREQVNSTYRVASVTVLQDMNLNG KTKCKKSMKALPAPEKTSKANGDPEQVYVLPAPRELTNMGVSLTC LUGPFPDVAIVEMSGDEPNMYITPPVLDSDGSFFLSALTYSKRW QSGNIFSCSVNHEALHHNTQKSLSPKRC	ASTGSPVFRAPSSKSTSGGTAAGCLVQDYFPEVTVSNVSGALTSGV HTPFAVLDSSGLYSLSSVTVPPSSSLGTQTYCNVNHPSMTVDKVEPK SCKDTHCPDCAPELGGPVLEPRPKDITLMISRTPTCTVVDVDSHE DPEVMFNTYDGVVFNAAKTIPREQVNSTYRVASVTVLQDMNLNG KTKCKKSMKALPAPEKTSKANGDPEQVYVLPAPRELTNMGVSLTC LUGPFPDVAIVEMSGDEPNMYITPPVLDSDGSFFLSALTYSKRW QSGNIFSCSVNHEALHHNTQKSLSPKRC	AQQLTQSPSLASVSGDRVTTTORAQSSSLNMY QDQPGKAPALLTAASLSQSGVPRFSGSGSDTFT ITSSLOPEDATITTCQDPSITRTTGGTNEIK	RTVAAPSVHPPSDEQLKGTASV/C LNNYPREAQVQVQKMDLSDGNS QESVTCDDKSDSTYLSSTLTLLBAADYE HKHYACEVTHQGLSPVTSNHRGE C
VSTB88	Human IgG1/kappa		65772458	65772459	65772460	65772461	65772462	65772463	QVQLVQSGAEVWPSSVYVPSSELTQTYCNVNHPSMTVDKVEPK SCKDTHCPDCAPELGGPVLEPRPKDITLMISRTPTCTVVDVDSHE DPEVMFNTYDGVVFNAAKTIPREQVNSTYRVASVTVLQDMNLNG KTKCKKSMKALPAPEKTSKANGDPEQVYVLPAPRELTNMGVSLTC LUGPFPDVAIVEMSGDEPNMYITPPVLDSDGSFFLSALTYSKRW QSGNIFSCSVNHEALHHNTQKSLSPKRC	ASTGSPVFRAPSSKSTSGGTAAGCLVQDYFPEVTVSNVSGALTSGV HTPFAVLDSSGLYSLSSVTVPPSSSLGTQTYCNVNHPSMTVDKVEPK SCKDTHCPDCAPELGGPVLEPRPKDITLMISRTPTCTVVDVDSHE DPEVMFNTYDGVVFNAAKTIPREQVNSTYRVASVTVLQDMNLNG KTKCKKSMKALPAPEKTSKANGDPEQVYVLPAPRELTNMGVSLTC LUGPFPDVAIVEMSGDEPNMYITPPVLDSDGSFFLSALTYSKRW QSGNIFSCSVNHEALHHNTQKSLSPKRC	AQQLTQSPSLASVSGDRVTTTORAQSSSLNMY QDQPGKAPALLTAASLSQSGVPRFSGSGSDTFT ITSSLOPEDATITTCQDPSITRTTGGTNEIK	RTVAAPSVHPPSDEQLKGTASV/C LNNYPREAQVQVQKMDLSDGNS QESVTCDDKSDSTYLSSTLTLLBAADYE HKHYACEVTHQGLSPVTSNHRGE C
VSTB89	Human IgG1/kappa		65772486-88	65772489	65772490	65772491	65772492	65772493	QVQLVQSGAEVWPSSVYVPSSELTQTYCNVNHPSMTVDKVEPK SCKDTHCPDCAPELGGPVLEPRPKDITLMISRTPTCTVVDVDSHE DPEVMFNTYDGVVFNAAKTIPREQVNSTYRVASVTVLQDMNLNG KTKCKKSMKALPAPEKTSKANGDPEQVYVLPAPRELTNMGVSLTC LUGPFPDVAIVEMSGDEPNMYITPPVLDSDGSFFLSALTYSKRW QSGNIFSCSVNHEALHHNTQKSLSPKRC	ASTGSPVFRAPSSKSTSGGTAAGCLVQDYFPEVTVSNVSGALTSGV HTPFAVLDSSGLYSLSSVTVPPSSSLGTQTYCNVNHPSMTVDKVEPK SCKDTHCPDCAPELGGPVLEPRPKDITLMISRTPTCTVVDVDSHE DPEVMFNTYDGVVFNAAKTIPREQVNSTYRVASVTVLQDMNLNG KTKCKKSMKALPAPEKTSKANGDPEQVYVLPAPRELTNMGVSLTC LUGPFPDVAIVEMSGDEPNMYITPPVLDSDGSFFLSALTYSKRW QSGNIFSCSVNHEALHHNTQKSLSPKRC	AQQLTQSPSLASVSGDRVTTTORAQSSSLNMY QDQPGKAPALLTAASLSQSGVPRFSGSGSDTFT ITSSLOPEDATITTCQDPSITRTTGGTNEIK	RTVAAPSVHPPSDEQLKGTASV/C LNNYPREAQVQVQKMDLSDGNS QESVTCDDKSDSTYLSSTLTLLBAADYE HKHYACEVTHQGLSPVTSNHRGE C

FIG. 15

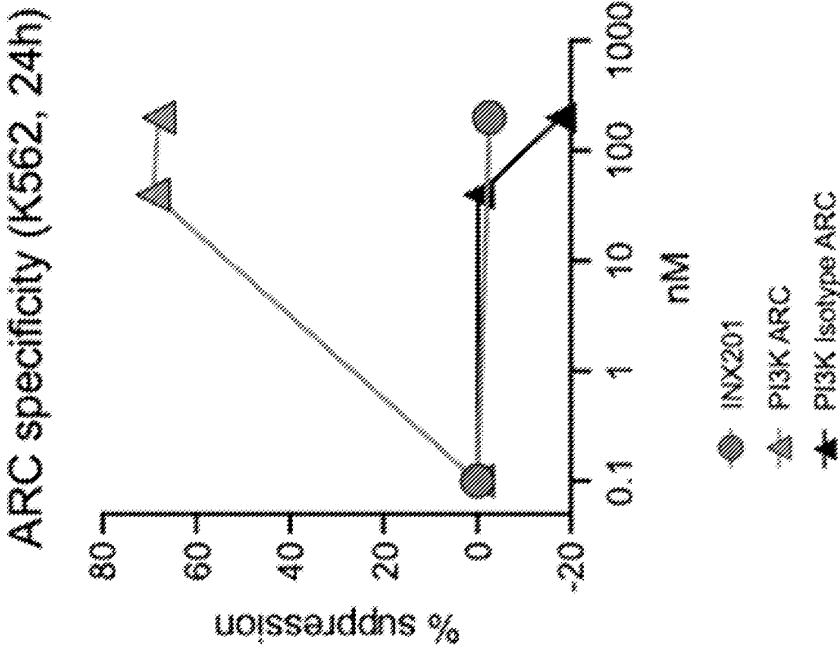
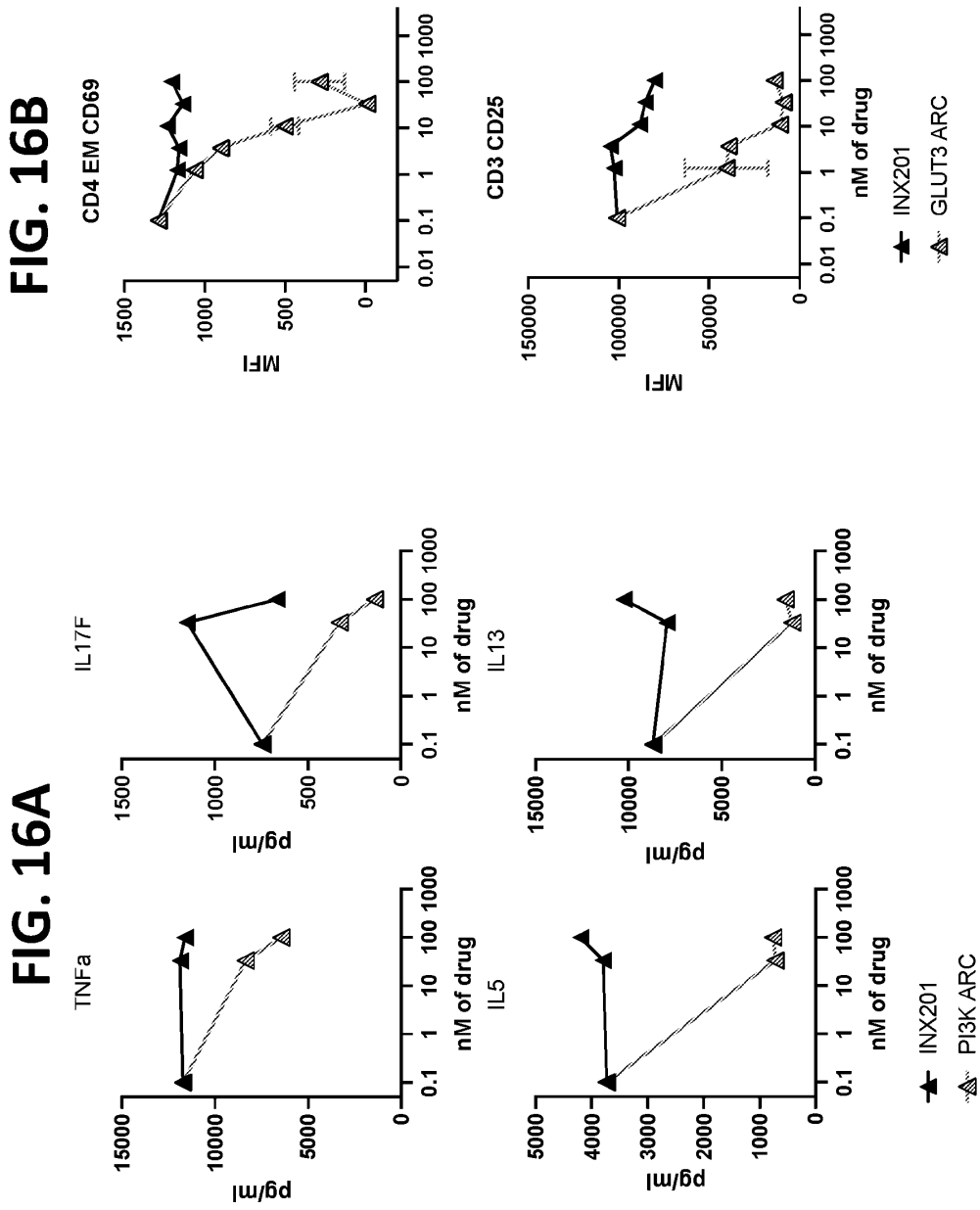


Figure 15. INX201 (anti-VISTA) PI3K ARC, but not isotype control IgG1 PI3K ARC specifically knockdown PI3K. K562-VISTA cells were transfected with 40-200 nM INX201-PI3K ARC or isotype control IgG1-PI3K ARC, and target knockdown was analyzed by qRT-PCR using the ddct method and reported as % target suppression, where 0% suppression were INX201 alone samples; PI3K ARC: anti-human VISTA mAb conjugated to PI3K siRNA; PI3K isotype ARC: IgG control conjugated to PI3K siRNA; INX201, mAb unconjugated: naked anti-human VISTA mAb. A single technical replicate per concentration point was used.



Figures 16A and 16B. Human PI3K and GLUT3 ARCs are functional *in vitro*. Human PBMCs were activated with anti-CD3/CD28 beads for 72 hours, bead to T cell ratio 1:2, and treated with (A) PI3K ARC or free INX201 (0-200 nM), or (B) GLUT3 ARC or free INX201 (0-200 nM). The curves were generated from inhibitor vs. response three-parameter non-linear regression analysis (GraphPad Prism 10). IL5/IL13/TNFα/IL17F cytokine levels were measured by Luminex. CD69 levels were measured in live CD45+/HLA-DR-/CD56-/CD3+/CD4+/CD45RA-/CD27- T effector memory cells; CD25 levels are measured in live CD45+/HLA-DR-/CD56-/CD3 cells. A single technical replicate per concentration point was used in A; n=2 technical replicate per concentration point was used in B; no ARC was visualized as 0.1 nM (due to log scale); MFI – mean fluorescent intensity. Data represented as mean ± SEM, where appropriate.

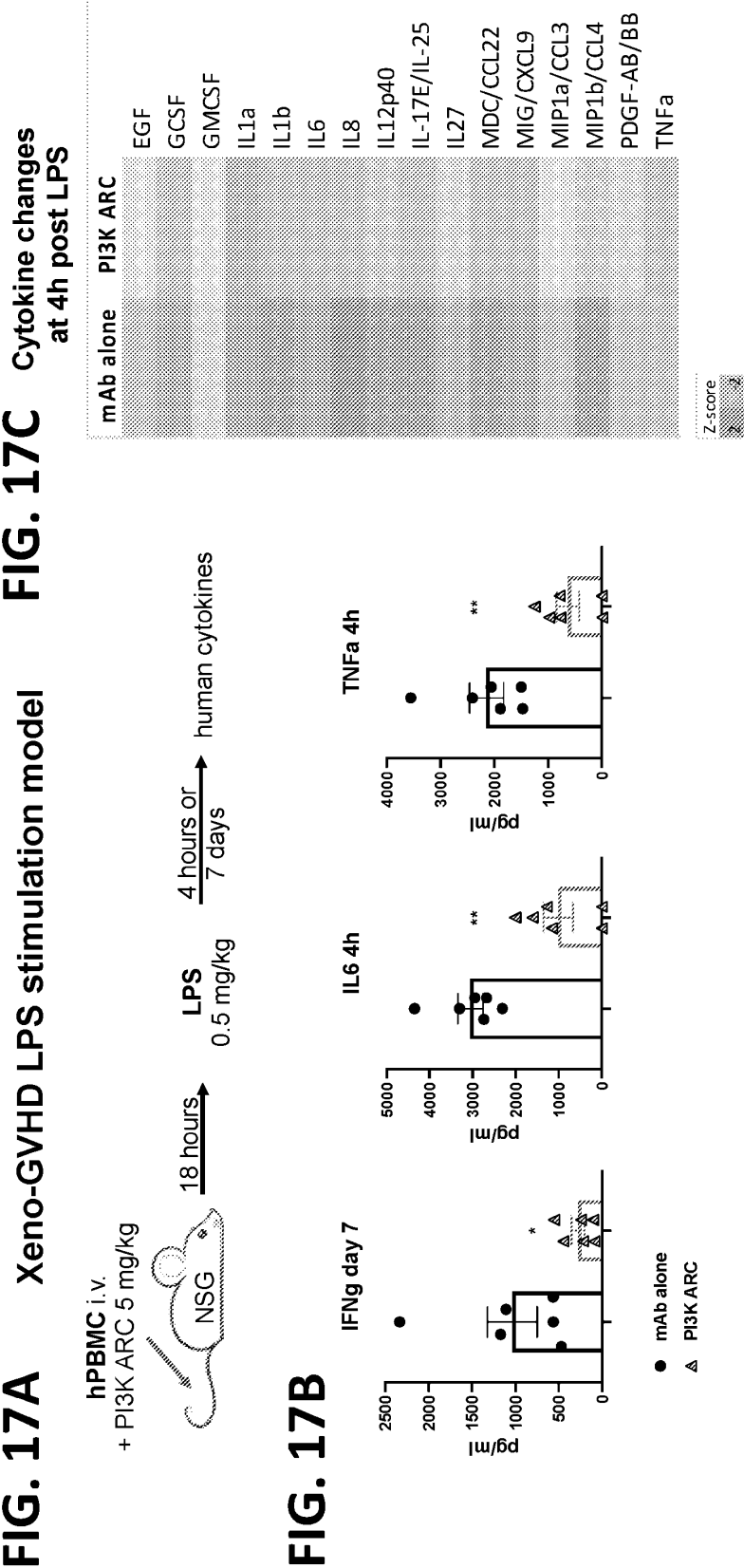


FIG. 18

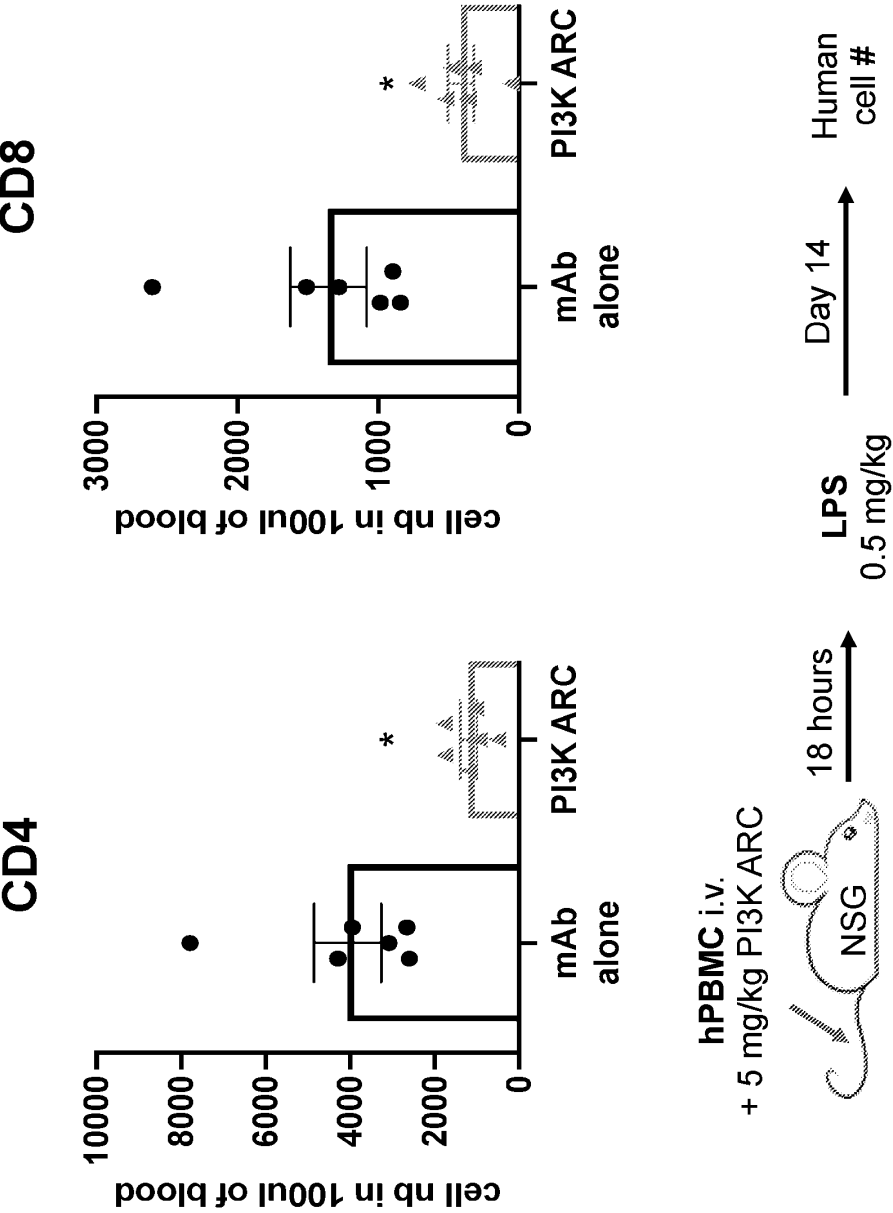


Figure 18. PI3K ARC diminishes LPS induced T cell proliferation in vivo. NSG mice were injected i.v. with PI3K ARC (triangles, n=6) or INX201 (circles, n=6) at 5 mg/Kg together with human PBMC transfer. 18 hours after injection mice were stimulated with 0.5 mg/kg LPS, intraperitoneally. Changes in blood T cell numbers at day 14, (n=6 mice per group) are shown for both CD4 and CD8. Statistical analysis was performed by Student's t-test. Data represented as mean $\pm$ SEM, * - $p < 0.05$.

FIG. 19

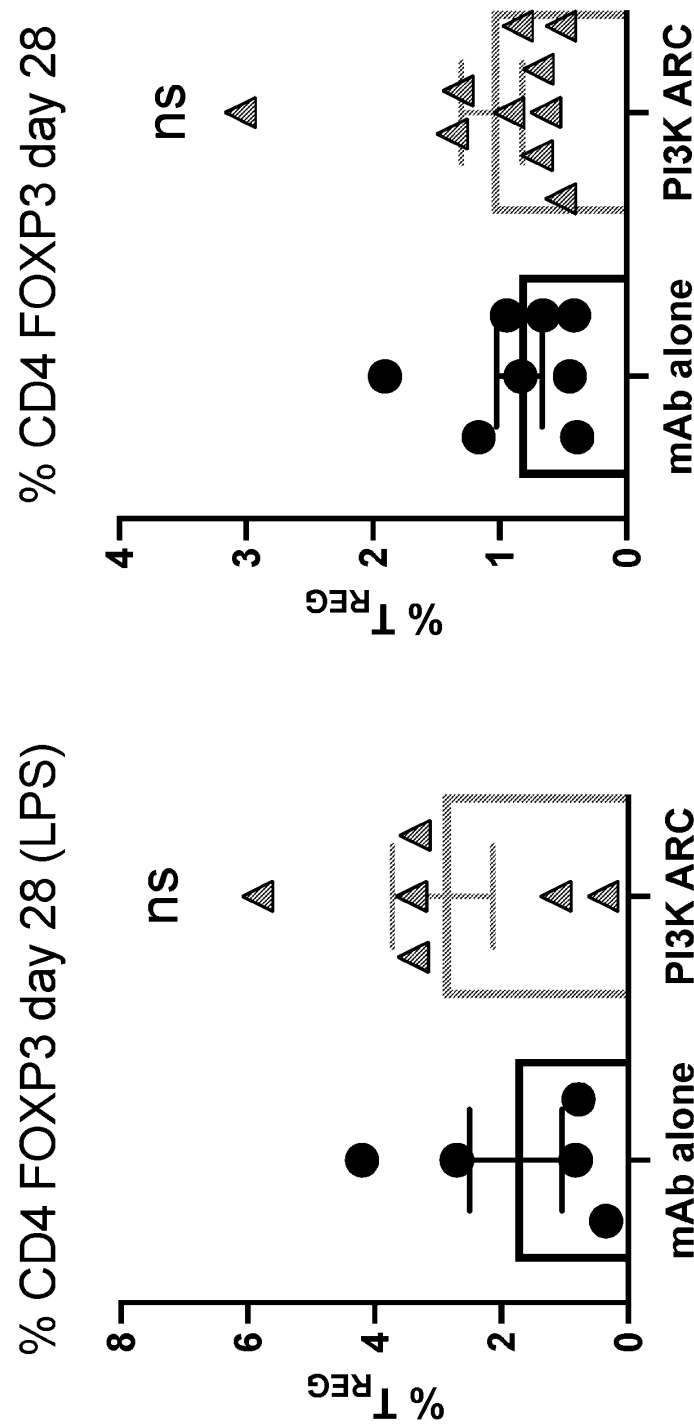


Figure 19. PI3K ARC does not reduce percent of regulatory T cells *in vivo*. NSG mice were injected i.v. with PI3K ARC (triangles, n=10) or INX201 (circles, n=8) at 5 mg/Kg together with human PBMC transfer (right graph). In separate groups of mice, 18 hours after PBMC injection mice were stimulated with 0.5 mg/kg LPS, intraperitoneally (n=6 for both INX201 and PI3K ARC groups, left graph). Blood samples were processed on day 28. Percent changes in Treg are shown. Statistical analysis was performed by Student's t-test. Data represented as mean ± SEM ns – not significant.

FIG. 20

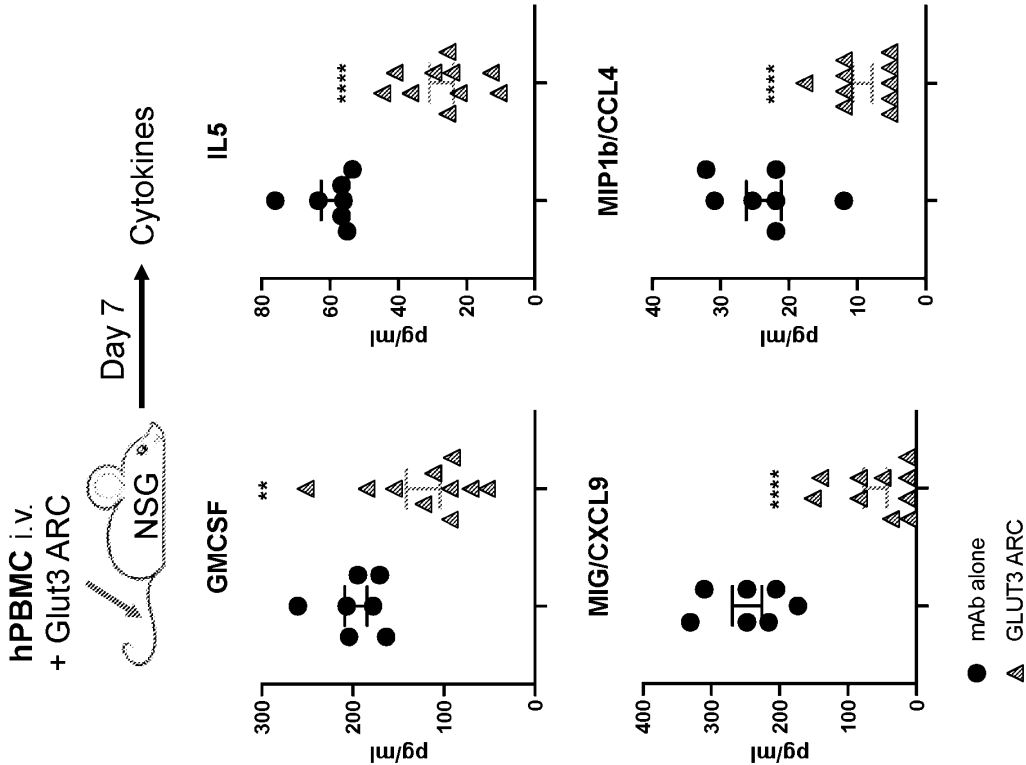


Figure 20. GLUT3 ARC reduces inflammatory cytokine responses in xeno-GvHD. NSG mice were injected i.v. with PI3K ARC (triangles, n=10) or INX201 (circles, n=8) at 5 mg/Kg together with human PBMc transfer. Changes in plasma human cytokine levels on day 7 are shown. Statistical analysis was performed by Student's t-test. Data represented as mean ± SEM. **, ** - p < 0.01; ****, **** - p < 0.0001.