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(54) **ANTI-HUMAN VISTA ANTIBODIES AND USE THEREOF**

(71) Applicants: **ImmuNext, Inc.**, Lebanon, NH (US); **THE TRUSTEES OF DARTMOUTH COLLEGE**, HANOVER, NH (US)

(72) Inventors: **Sabrina DELONG**, Lebanon, NH (US); **Michael MOLLOY**, Enfield, NH (US); **Catherine CARRIERE**, Lebanon, NH (US); **Jay ROTHSTEIN**, Norwich, VT (US); **Isabelle LEMERCIER**, Enfield, NH (US)

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A61K 39/00	(2006.01)
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A61K 45/06	(2006.01)
A61P 1/00	(2006.01)
A61P 1/16	(2006.01)
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A61P 17/06	(2006.01)
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(52) **U.S. Cl.**

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(57) **ABSTRACT**

The invention provides agonistic anti-human VISTA antibodies and antibody fragments. These agonist antibodies and antibody fragments may be used to potentiate or enhance or mimic VISTA's suppressive effects on T cell immunity and thereby suppress T cell immunity. These agonist antibodies and antibody fragments are especially useful in the treatment of autoimmunity, allergy, inflammatory conditions, GVHD, sepsis and transplant recipients. Screening assays for identifying these agonists are also provided.

Specification includes a Sequence Listing.

FIG. 1A

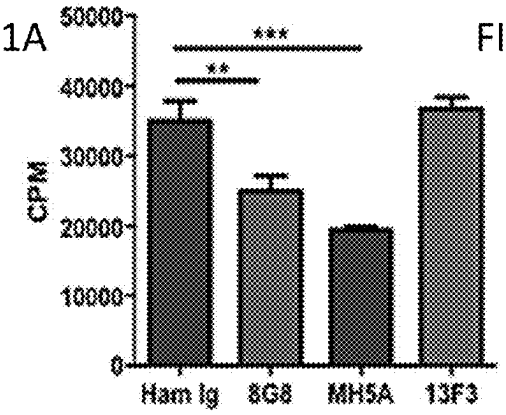


FIG. 1B

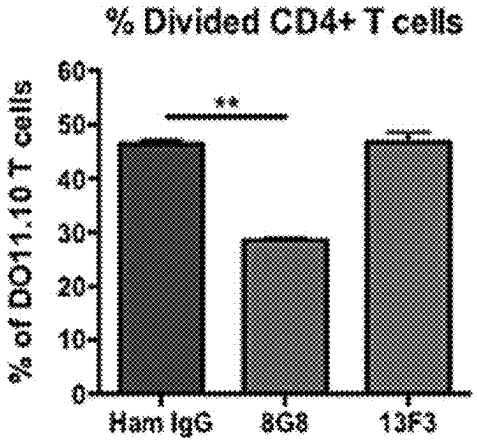


FIG. 1C

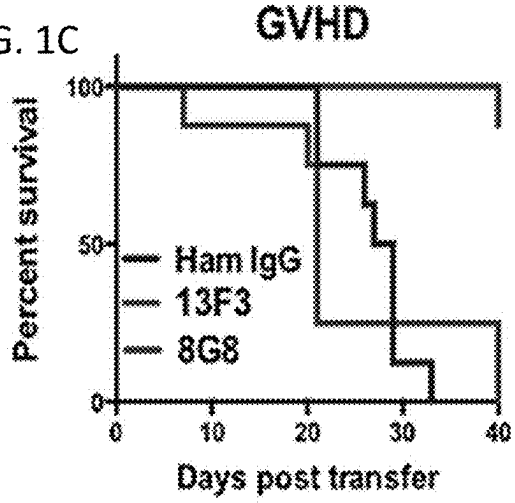


FIG. 1D

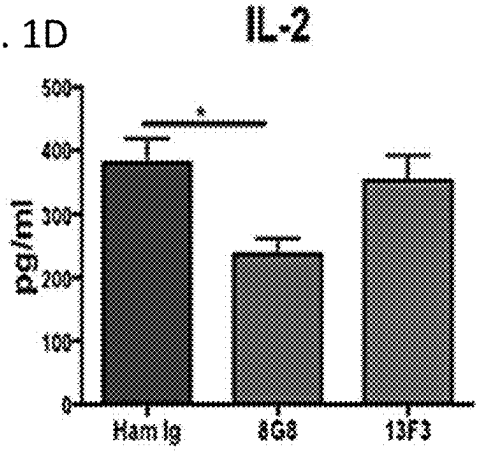


Figure 1A-1D. *In vitro* and *in vivo* screening assays can be used to identify suppressive VISTA mAb.

FIG. 2A

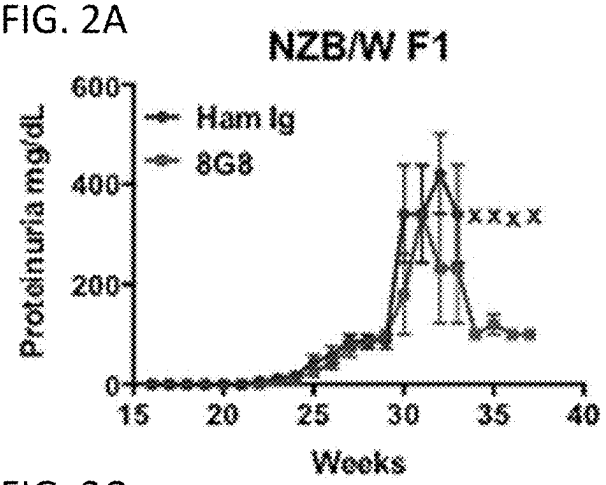


FIG. 2B

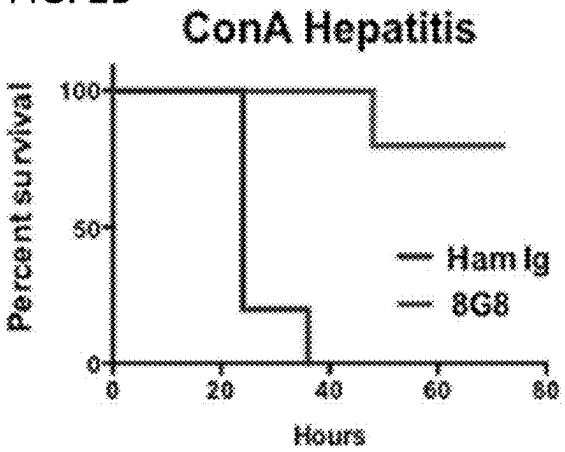


FIG. 2C

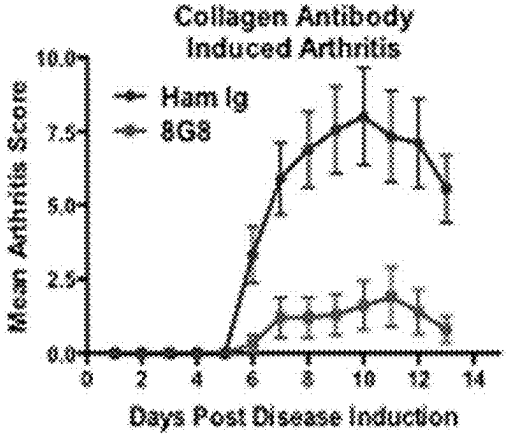


FIG. 2D

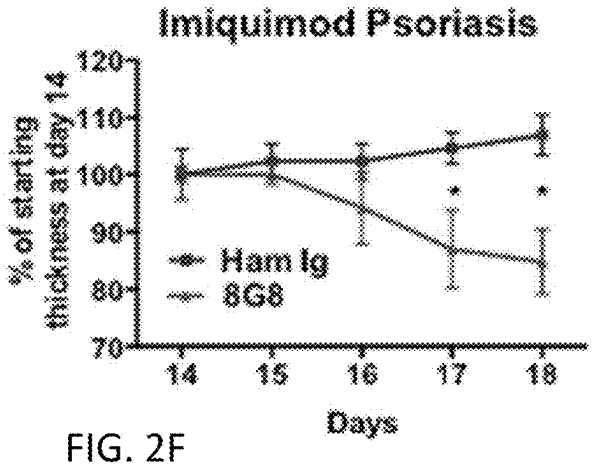


FIG. 2E

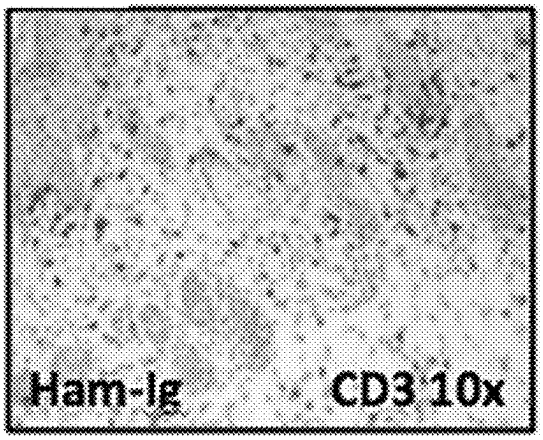
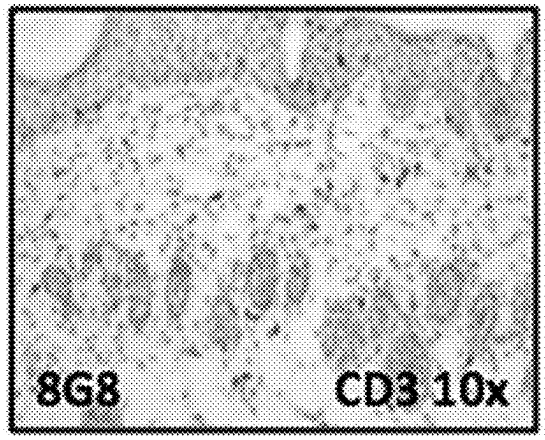


FIG. 2F



Figures 2A-2F. VISTA suppresses multiple models of autoimmune disease.

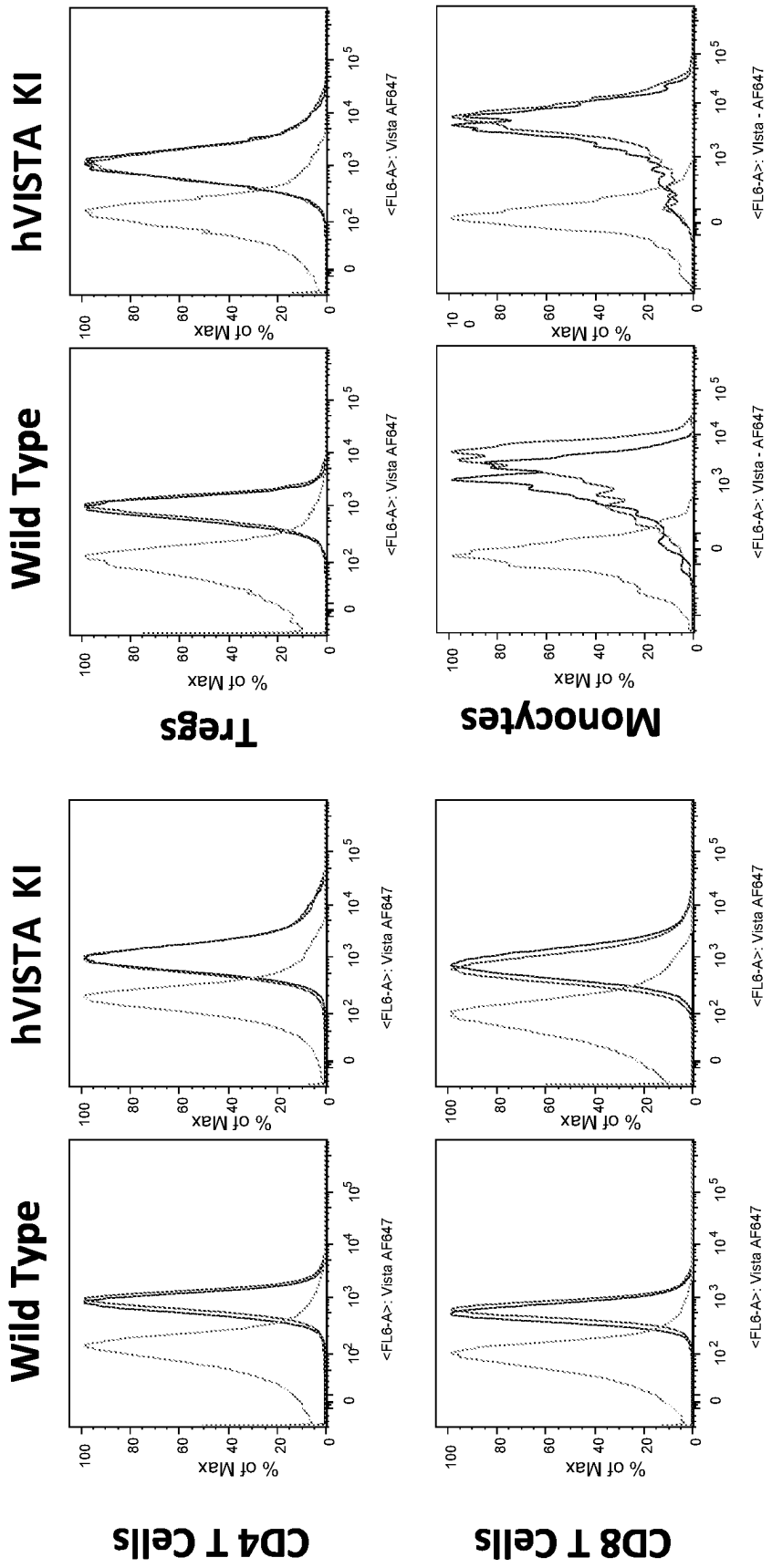


Figure 3. Expression of VISTA in WT and hV-KI mice.

FIGURE 4A

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)	INLNYAIT (SEQ ID NO:101)	ARGGYRYTY YAMDY (SEQ ID NO:102)	ENIYSN (SEQ ID NO:103)	AAT (SEQ ID NO:104)	QHFWGTP RT (SEQ ID NO:105)	EVQLQQFGAELVKPG ASVKISCKASGYTLTD YNMDWVKQSHGKSL EWIGHINLNYAITTYN QKFKGKATLTVDKSSS TAYMELRSLTSEDTAV YYCARGGYRYTYYAM DYWGQGTSVTVSS (SEQ ID NO:106)	AKTTPPSVYPLAPGSAAQT NSMVTLGCLVKGYFPEPVT VTWNSGSLSSGVHTFPAVL QSDLYTLSSSVTVPSSTWPS ETVTCNVAHPASSTKVDKK IVPRDCGCKPCICTVPEVSS VFIFPPKPKDVLTITLTPKVT CVVVDISKDDPEVQFSWFV DDVEVHTAQTQPREEQFN STFRSVSELPIMHQDWLN GKEFKCRVNSAAFPAPIEKT ISKTKLNPKS (SEQ ID NO:107)	DIQMTQSPASLSVS VGETVTITCRASENI YSNLAWYQQKQGK SPQLLVYAATNLAD GVPSRFSGSGSGTQ YSLKINSLQSEDFGS YYCQHFWGTPRTFG GGTKLEIK (SEQ ID NO:108)	RADAAPTVSI FPPSSEQLTSG GASVVCFLNN FYPKDINVKW KIDGSERQNG VLNSWTDQD SKDSTYSMSS TLTLTKDEYER HNSYTCEATH KTSTSPIVKSF NRNEC (SEQ ID NO:109)
GA1-IgG2	Human IgG2/kappa	LLDSGLYCC LVVEIRHHH SEHRVH	GYTLTDYN (SEQ ID NO:110)	INLNYAIT (SEQ ID NO:111)	ARGGYRYTY YAMDY (SEQ ID NO:112)	ENIYSN (SEQ ID NO:113)	AAT (SEQ ID NO:114)	QHFWGTP RT (SEQ ID NO:115)	EVQLQQFGAELVKPG ASVKISCKASGYTLTD YNMDWVKQSHGKSL EWIGHINLNYAITTYN QKFKGKATLTVDKSSS TAYMELRSLTSEDTAV YYCARGGYRYTYYAM DYWGQGTSVTVSS (SEQ ID NO:116)	ASTKGPSVFPLAPCSRSTSE STAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKVDK TVERKCCVECPPCPAPPVA GPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVVHQ DWLNGKEYKCKVSNKGLP APIEKTISKTKGQPREPQVY TLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQ PENNYKTTPPMLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLS LSPGK (SEQ ID NO:117)	DIQMTQSPASLSVS VGETVTITCRASENI YSNLAWYQQKQGK SPQLLVYAATNLAD GVPSRFSGSGSGTQ YSLKINSLQSEDFGS YYCQHFWGTPRTFG GGTKLEIK (SEQ ID NO:118)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:119)
GG8	Mouse IgG1/?	LLDSGLYCC LVVEIRHHH SEHRVH; GHDVTFYK TWYRSSRG EVQTC	GYSFTGYT (SEQ ID NO:120)	INPYNGGI (SEQ ID NO:121)	ARRTLLRPYF FDY (SEQ ID NO:122)	QSVSTSTFSY (SEQ ID NO:123)	YAS (SEQ ID NO:124)	QHSWEIPY T (SEQ ID NO:125)	EVQLQQSGPELVKPG TSMKISCKASGYSFTG YTMNWVRQSHGKNL EWIGLINPYNGGINYN QKFKARATLTVDKSSS TAYMELLSLTSEDSAV YYCARRTLLRPYFFDY WGQGTTLTVSS (SEQ ID NO:126)	EVQLQQSGPELVKPGTSM KISCKASGYSFTGYTMNW VRQSHGKNLEWIGLINPYN GGINYNQKFKARATLTVDK SSSTAYMELLSLTSEDSAVY YCARRTLLRPYFFDYWGQG TTLTVSS (SEQ ID NO:127)	DIVLTQSPASLAVSL GQRATISCRASQSV STSTFSYMHWYQQ KPGQPPKLLIKYASN LESGVPARFSGSGS GTDFTLNIHPVEEED TATYYCQHSWEIPY TFGGGTKLEIK (SEQ ID NO:128)	DIVLTQSPAS LAVSLGQRATI SCRASQSVST STFSYMHWY QQKPGQPPK LLIKYASNLES GVPARFSGSG SGTDFTLNIHP VEEEDTATYY CQHSWEIPYT FGGGTKLEIK (SEQ ID NO:129)

FIGURE 4B

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/kappa	LLDSGLYCC LVVEIRHHH SEHRVH; GHDVTFYK TWYRSSRG EVQTC	GYSFTGYT (SEQ ID NO:130)	INPYNGGI (SEQ ID NO:131)	ARRTLLRPYF FDY (SEQ ID NO:132)	QSVSTSTFSY (SEQ ID NO:133)	YAS (SEQ ID NO:134)	QHSWEIPY T (SEQ ID NO:135)	EVQLQQSGPELVKPG TSMKISCKASGYSFTG YTMNWVRQSHGKNL EWIGLINPYNGGINYN QKFKARATLTVDKSSS TAYMELLSLTSEDSAV YYCARRTLLRPYFFDY WGQGTTLTVSS (SEQ ID NO:136)	ASTKGPSVFPLAPCSRSTSE STAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKVDK TVERKCCVECPPCPAPPVA GPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVVHQ DWLNGKEYKCKVSNKGLP APIEKTISKTKGQPREPQVY TLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQ PENNYKTTPPMLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLS LSPGK (SEQ ID NO:137)	DIVLTQSPASLAVSL GQRATISCRASQSV STSTFSYMHWYQQ KPGQPPKLLIKYASN LESGVPARFSGSGS GTDFTLNIHPVEEED TATYYCQHSWEIPY TFGGGTKLEIK (SEQ ID NO:138)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:139)
IE8	Mouse IgG1/?	LLDSGLYCC LVVEIR	GFDFSRYW (SEQ ID NO:140)	VYPDSSTI (SEQ ID NO:141)	ARGRGDY (SEQ ID NO:142)	GNIHNY (SEQ ID NO:143)	NAK (SEQ ID NO:144)	QNFWSTPF T (SEQ ID NO:145)	EVKLLESGGGLVQPG GSLKLSCAASGFDFSR YWMSWVRQAPGKG LEWIGEVYPDSSTINY TPSLKDKFIISRDNAK NTLYLQMIKVRSEDTA LYYCARGRGDYWGQ GTSVTVSS (SEQ ID NO:146)	ASTKGPSVFPLAPCSRSTSE STAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKVDK TVERKCCVECPPCPAPPVA GPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVVHQ DWLNGKEYKCKVSNKGLP APIEKTISKTKGQPREPQVY TLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQ PENNYKTTPPMLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLS LSPGK (SEQ ID NO:147)	DIQMTQSPASLSAS VGETVTITCRASGNI HNYLSWYHQKQGK SPQLLVYNAKTLAD GVPSRFSGSGSGTQ YSLKINSLQPEDFGS YYCQNFWSTPFTFG SGTKLEIK (SEQ ID NO:148)	RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:149)

FIGURE 4C

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)	QNFWSTPF T (SEQ ID NO:155)	EVKLLESGGGLVQPG GSLKLSCAASGFDFSR YWMSWVRQAPGKG LEWIGEVYPDSSTINY TPSLKDKFIISRDNAK NTLYLQMIKVRSEDTA LYYCARGRGDYWGQ GTSVTVSS (SEQ ID NO:156)	ASTKGPSVFPLAPCSRSTSE STAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKVDK TVERKCCVECPPCPAPPVA GPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVVHQ DWLNGKEYKCKVSNKGLP APIEKTISKTKGQPREPQVY TLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQ PENNYKTTPPMLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLS LSPGK (SEQ ID NO:157)	DIQMTQSPASLSAS VGETVTITCRASGNI HNYLSWYHQKQGK SPQLLVYNAKTLAD GVPSRFSGSGSGTQ YSLKINSLQPEDFGS YYCQNFWSTPFTFG SGTKLEIK (SEQ ID NO:158)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK 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)	QNFWSTPF T (SEQ ID NO:165)	EVKLLESGGGLVQPG GSLKLSCAASGFDFSR YWMSWVRQAPGKG LEWIGEVYPDSSTINY TPSLKDKFIISRDNAK NTLYLQMIKVRSEDTA LYYCARGRGDYWGQ GTSVTVSS (SEQ ID NO:166)	ASTKGPSVFPLAPSSRSTSE STAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSNFGT QTYTCNVDHKPSNTKVDK TVERKCCVECPPCPAPPVA GPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVQF NWYVDGVEVHNAKTKPR EEQFNSTFRVVSVLTVVHQ DWLNGKEYKCKVSNKGLP APIEKTISKTKGQPREPQVY TLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQ PENNYKTTPPMLDSDGSFF LYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLS LSPGK (SEQ ID NO:167)	DIQMTQSPASLSAS VGETVTITCRASGNI HNYLSWYHQKQGK SPQLLVYNAKTLAD GVPSRFSGSGSGTQ YSLKINSLQPEDFGS YYCQNFWSTPFTFG SGTKLEIK (SEQ ID NO:168)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:169)

FIGURE 4D

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)	IYPGDSDT (SEQ ID NO:171)	ARDVSSFYGY SPMFDY (SEQ ID NO:172)	QSVSSY (SEQ ID NO:173)	DAS (SEQ ID NO:174)	QQRSNWP LT (SEQ ID NO:175)	EVQLVQSGAEVKKPG ESLKISCKGSGYSFTSY WIGWVRQMPGKGLE WMGIIYPGDSDTRYS PSFQGQVTISADKSIS TAYLQWSSLKASDTA MYYCARDVSSFYGYS PMFDYWGQGTLVTV SS (SEQ ID NO:176)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK ((SEQ ID NO:177)	EIVLTQSPATLSLSPG ERATLSCRASQSVSS YLAWYQQKPGQAP RLLIYDASNRATGIP ARFSGSGSGTDFTLT ISSLEPEDFAVYYCQ QRSNWPLTFGQGT KVEIK (SEQ ID NO:178)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:179)
VSTB101	Human IgG1/kappa	VSTB101 Group 1	GYSFTSYW (SEQ ID NO:180)	IYPGDSDT (SEQ ID NO:181)	ARDAHSFYG YSALLDY (SEQ ID NO:182)	QSVSSSY (SEQ ID NO:183)	GAS (SEQ ID NO:184)	QQYGSSPL T (SEQ ID NO:185)	EVQLVQSGAEVKKPG ESLKISCKGSGYSFTSY WIGWVRQMPGKGLE WMGIIYPGDSDTRYS PSFQGQVTISADKSIS TAYLQWSSLKASDTA MYYCARDAHSFYGYS ALLDYWGQGTLVTVS S (SEQ ID NO:186)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:187)	EIVLTQSPGTLSLSPG ERATLSCRASQSVSS SYLAWYQQKPGQA PRLLIYGASSRATGIP DRFSGSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSPLTFGQGTK VEIK (SEQ ID NO:188)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:189)

FIGURE 4E

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
VSTB102	Human IgG1/kappa	Group 1	GYSFTSYW (SEQ ID NO:190)	IYPGDSDT (SEQ ID NO:191)	ARDSYSFYGH TPVLDY (SEQ ID NO:192)	QSVSSSY (SEQ ID NO:193)	GAS (SEQ ID NO:194)	QQYGSSPL T (SEQ ID NO:195)	EVQLVQSGAEVKKPG ESLKISCKGSGYSFTSY WIGWVRQMPGKGLE WMGIIYPGDSDTRYS PSFQGQVTISADKSIS TAYLQWSSLKASDTA MYYCARDSYSFYGHT PVLDYWGQGTLVTVS S (SEQ ID NO:196)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:197)	EIVLTQSPGTLSLSPG ERATLSCRASQSVSS SYLAWYQQKPGQA PRLLIYGASSRATGIP DRFSGSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSPLTFGQGTK VEIK (SEQ ID NO:198)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:199)
VSTB103 INX904	Human IgG1/kappa	VSTB101 Group 1	GYSFTSYW (SEQ ID NO:200)	IYPGDSDT (SEQ ID NO:201)	ARDDALYGG YYLDY (SEQ ID NO:202)	QSVLYSSNNK NY (SEQ ID NO:203)	WAS (SEQ ID NO:204)	QQYYSTPLT (SEQ ID NO:205)	EVQLVQSGAEVKKPG ESLKISCKGSGYSFTSY WIGWVRQMPGKGLE WMGIIYPGDSDTRYS PSFQGQVTISADKSIS TAYLQWSSLKASDTA MYYCARDDALYGGYY LDYWGQGTLVTVSS (SEQ ID NO:206)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:207)	DIVMTQSPDSLAVS LGERATINCKSSQSV LYSSNNKNYLAWYQ QKPGQPPKLLIYWA STRESGVPDRFSGS GSGTDFTLTISSLQA EDVAVYYCQQYYST PLTFGQGTKVEIK ((SEQ ID NO:208)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:209)

FIGURE 4F

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)	ARDANSFYS AASIFDY (SEQ ID NO:212)	QSVLYSSNNK NY (SEQ ID NO:213)	WAS (SEQ ID NO:214)	QQYYSTPLT (SEQ ID NO:215)	EVQLVQSGAEVKKPG ESLKISCKGSGYSFTSY WIGWVRQMPGKGLE WMGIIYPGDSDTRYS PSFQGQVTISADKSIS TAYLQWSSLKASDTA MYYCARDANSFYSAA SIFDYWGQGTLVTVS S (SEQ ID NO:216)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:217)	DIVMTQSPDSLAVS LGERATINCKSSQSV LYSSNNKNYLAWYQ QKPGQPPKLLIYWA STRESGVPDRFSGS GSGTDFTLTISSLQA EDVAVYYCQQYYST PLTFGQGTKVEIK (SEQ ID NO:218)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:219)
VSTB105	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:220)	IIPIFGTA (SEQ ID NO:221)	ARSSYGWSY EFDY (SEQ ID NO:222)	QSIATN (SEQ ID NO:223)	AAS (SEQ ID NO:224)	QQNDDRPI T (SEQ ID NO:225)	QVQLVQSGAEVKKPG SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:226)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK ((SEQ ID NO:227)	DIQMTQSPSSLSAS VGDRVTITCRASQSI ATNLNWYQQKPGK APKLLIYAASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQNDDRPITFGQGT KVEIK (SEQ ID NO:228)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:229)

FIGURE 4G

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 SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:236)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:237)	DIQMTQSPSSLSAS VGDRVTITCRASQSI RTDLNWYQQKPGK APKLLIYSASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQNERTPITFGQGT KVEIK (SEQ ID NO:238)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:239)
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)	QQNRATPI T (SEQ ID NO:245)	QVQLVQSGAEVKKPG SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:246)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:247)	DIQMTQSPSSLSAS VGDRVTITCRASQSI NNDLNWYQQKPGK APKLLIYAASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQNRATPITFGQGT KVEIK (SEQ ID NO:248)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:249)

FIGURE 4H

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)	ARNTFGWSGELDY (SEQ ID NO:252)	QSISNR (SEQ ID NO:253)	SAS (SEQ ID NO:254)	QQNHDNPIT (SEQ ID NO:255)	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARNTFGWSGELDYWGQGTLVTVSS (SEQ ID NO:256)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:257)	DIQMTQSPSSLSASVGDRVTITCRASQSISNRLNWYQQKPGKAPKLLIYSASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNHDNPITFGQGTKVEIK (SEQ ID NO:258)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:259)
VSTB109	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:260)	IIPIFGTA (SEQ ID NO:261)	ARSSYGWSYEFDY (SEQ ID NO:262)	QSIATY (SEQ ID NO:263)	AAS (SEQ ID NO:264)	QQNHNRPIT (SEQ ID NO:265)	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSSYGWSYEFDYWGQGTLVTVSS (SEQ ID NO:266)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:267)	DIQMTQSPSSLSASVGDRVTITCRASQSIATYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNHNRPITFGQGTKVEIK (SEQ ID NO:268)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:269)

FIGURE 4I

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)	ARHSIGWVA ELDY (SEQ ID NO:272)	QSINTD (SEQ ID NO:273)	AAS (SEQ ID NO:274)	QQGASDPI T (SEQ ID NO:275)	QVQLVQSGAEVKKPG SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARHSIGWVAELD YWGQGTLVTVSS (SEQ ID NO:276)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:277)	DIQMTQSPSSLSAS VGDRVTITCRASQSI NTDLNWYQQKPGK APKLLIYAASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQGASDPITFGQGT KVEIK (SEQ ID NO:278)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:279)
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)	QQNRGSPI T (SEQ ID NO:285)	QVQLVQSGAEVKKPG SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:286)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:287)	DIQMTQSPSSLSAS VGDRVTITCRASQSI NTDLNWYQQKPGK APKLLIYAASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQNRGSPITFGQGT KVEIK (SEQ ID NO:288)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:289)

FIGURE 4J

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 SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARHSIGWVAELD YWGQGTLVTVSS (SEQ ID NO:296)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:297)	DIQMTQSPSSLSAS VGDRVTITCRASQSI ATDLNWYQQKPGK APKLLIYAASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQAHWYPLTFGQG TKVEIK (SEQ ID NO:298)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:299)
VSTB114	Human IgG1/kappa	Group 1	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)	QQGAYYPL T (SEQ ID NO:305)	QVQLVQSGAEVKKPG SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARHSIGWVAELD YWGQGTLVTVSS (SEQ ID NO:306)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:307)	DIQMTQSPSSLSAS VGDRVTITCRASQSI ATSLNWYQQKPGK APKLLIYYASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQGAYYPLTFGQGT KVEIK (SEQ ID NO:308)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:309)

FIGURE 4K

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 SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:316)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:317)	DIQMTQSPSSLSAS VGDRVTITCRASQSI RTYLNWYQQKPGK APKLLIYAASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQAYSNPITFGQGT KVEIK (SEQ ID NO:318)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:319)
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 SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:326)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:327)	DIQMTQSPSSLSAS VGDRVTITCRASQSI NTNLNWYQQKPGK APKLLIYAASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQARDTPITFGQGT KVEIK (SEQ ID NO:328)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:329)

FIGURE 4L

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)	IYPFIDST (SEQ ID NO:331)	ARGIRGYTMDY (SEQ ID NO:332)	ESVDNYGLSF (SEQ ID NO:333)	GAS (SEQ ID NO:334)	QQSKEVPYT (SEQ ID NO:335)	QVQLVQSGAEVKKPGASVKVSCKASGYTFPSHTIHWVRQAPGQRLEWMGSIYPFIDSTIYNQKFKDRVTITRDTSASTAYMELSSLRSEDTAVYYCARGIRGYTMDYWGQGTLVTVSS (SEQ ID NO:336)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:337)	DVVMTQSPLSLPVTLGQPASISCRASESVDNYGLSFMNWFQQRPGQSPRRLIYGASNQGSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSKEVPYTFGQGTKLEIK (SEQ ID NO:338)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:339)
VSTB50 INX500	Human IgG1/kappa	NLTLLDSGL and VQTGKDAP SNC Group 2	GYTFTNYG (SEQ ID NO:340)	INPYTGEP (SEQ ID NO:341)	AREGYGNYIFPY (SEQ ID NO:342)	ESVDTYANSL (SEQ ID NO:343)	RAS (SEQ ID NO:344)	QQTNEDPRT (SEQ ID NO:345)	QVQLVQSGSELKKPGASVKVSCKASGYTFTNYGLNWVRQAPGQGLEWMGWINPYTGEPTYADDFKGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCAREGYGNYIFPYWGQGTLVTVSS (SEQ ID NO:346)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:347)	DIVMTQTPLSLSVTPGQPASISCRASESVDTYANSLMHWYLQKPGQPPQLLIYRASNLESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQTNEDPRTFGQGTKLEIK (SEQ ID NO:348)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:349)

FIGURE 4M

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	GFTFSSYT (SEQ ID NO:350)	ISNSGSYT (SEQ ID NO:351)	ARDTVLSPFDY (SEQ ID NO:352)	SSISY (SEQ ID NO:353)	DTS (SEQ ID NO:354)	HQRSSFT (SEQ ID NO:355)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMSWVRQAPGKGLEWVATISNSGSYTYYLDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTVLSPFDYWGQGTTVTVSS (SEQ ID NO:356)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:357)	EIVLTQSPDFQSVTPKEKVTITCSATSSISYMHWYQQKPDQSPKLLIKDTSELASGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQRSSFTFGQGTKLEIK (SEQ ID NO:358)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:359)
VSTB52	Human IgG1/kappa		GGTFSNYW (SEQ ID NO:360)	IYPGGGFT (SEQ ID NO:361)	ARYYRSDEDYSMDF (SEQ ID NO:362)	QSLLYSNGKTY (SEQ ID NO:363)	LVS (SEQ ID NO:364)	VQATHFPQT (SEQ ID NO:365)	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNYWIGWVRQAPGQGLEWMGEIYPGGGFTHYNEKFKGRVTITADESTSTAYMELSSLRSEDTAVYYCARYYRSDEDYSMDFWGQGTLVTVSS (SEQ ID NO:366)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:367)	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSNGKTYLNWFQQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCVQATHFPQTFGQGTKLEIK (SEQ ID NO:368)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:369)

FIGURE 4N

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	GYTFTHYT (SEQ ID NO:370)	IIPSSGYS (SEQ ID NO:371)	ARGAYDDYY DYYAMDY (SEQ ID NO:372)	QTIVHSNGN TY (SEQ ID NO:373)	KVS (SEQ ID NO:374)	FQASHVPW T (SEQ ID NO:375)	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTH YTIHWVRQAPGQGLE WMGYIIPSSGYSEYN QKFKDRVTMTRDTST STVYMELSSLRSEDTA VYYCARGAYDDYYDY YAMDYWGQGTLVTV SS (SEQ ID NO:376)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:377)	DIVMTQSPLSLPVTP GEPASISCRSSQTIV HSNGNTYLEWYLQK PGQSPQLLIYKVSNR FSGVPDRFSGSGSG TDFTLKISRVEAEDV GVYYCFQASHVPW TFGQGTKLEIK (SEQ ID NO:378)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:379)
VSTB54 INX906	Human IgG1/kappa	Group 2	GYNIKDTY (SEQ ID NO:380)	IDPTHGYV (SEQ ID NO:381)	ARDRFDPYW FLDV (SEQ ID NO:382)	ESVEYYGTSL (SEQ ID NO:383)	DAF (SEQ ID NO:384)	QQSRKVP WT (SEQ ID NO:385)	QVQLVQSGAEVKKPG ASVKVSCKASGYNIKD TYMHWVRQAPGQG LEWMGRIDPTHGYVI YDPKFQGRVTMTRDT STSTVYMELSSLRSED TAVYYCARDRFDPYW FLDVWGQGTLVTVSS (SEQ ID NO:386)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:387)	DIVMTQTPLSLSVTP GQPASISCRASESVE YYGTSLMQWYLQK PGQSPQLLIYDAFN VESGVPDRFSGSGS GTDFTLKISRVEAED VGVYYCQQSRKVP WTFGQGTKLEIK (SEQ ID NO:388)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:389)

FIGURE 4O

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
VSTB55	Human IgG1/kappa		GYSIASDYV (SEQ ID NO:390)	ISYSGST (SEQ ID NO:391)	ARITTVVPTG SYYGVDF (SEQ ID NO:392)	SSVNF (SEQ ID NO:393)	DTS (SEQ ID NO:394)	QQWSNYP FT (SEQ ID NO:395)	QVQLQESGPGLVKPS ETLSLTCAVSGYSIASD YVWNWIRQPPGKGL EWIGYISYSGSTSNNP SLNSRVTISVDTSKNQ FSLKLSSVTAADTAVY YCARITTVVPTGSYYG VDFWGQGTTVTVSS (SEQ ID NO:396)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:397)	EIVLTQSPDFQSVTP KEKVTITCSGSSSVN FMYWYQQKPDQSP KLLIKDTSNLASGVP SRFSGSGSGTDFTLTI NSLEAEDAATYYCQ QWSNYPFTFGQGT KLEIK (SEQ ID NO:398)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:399)
VSTB56 INX901	Human IgG1/kappa	Group 2	GYTFTSYW (SEQ ID NO:400)	IIPNTLHT (SEQ ID NO:401)	ARLDGDYDY ALDY (SEQ ID NO:402)	ESVEYYGTSF (SEQ ID NO:403)	TAS (SEQ ID NO:404)	QQSRKVPY T (SEQ ID NO:405)	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YWLHWVRQAPGQG LEWMGYIIPNTLHTD YNQKFKDRVTMTRD TSTSTVYMELSSLRSE DTAVYYCARLDGDYD YALDYWGQGTLVTVS S (SEQ ID NO:406)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:407)	DIVMTQTPLSLSVTP GQPASISCRASESVE YYGTSFMQWYLQK PGQPPQLLIYTASNV ESGVPDRFSGSGSG TDFTLKISRVEAEDV GVYYCQQSRKVPYT FGQGTKLEIK (SEQ ID NO:408)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:409)

FIGURE 4P

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
VSTB57	Human IgG1/kappa		GFTFSTYA (SEQ ID NO:410)	ISSGGSDT (SEQ ID NO:411)	ARPTYYGIFS YFDY (SEQ ID NO:412)	SSVSY (SEQ ID NO:413)	STS (SEQ ID NO:414)	HQWRTYPT (SEQ ID NO:415)	EVQLVESGGGLVQPG GSLRLSCAASGFTFSTY AMSWVRQAPGKGLE WVATISSGGSDTYYP DTVKGRFTISRDNAK NSLYLQMNSLRAEDT AVYYCARPTYYGIFSY FDYWGQGTLVTVSS (SEQ ID NO:416)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:417)	DIQLTQSPSFLSASV GDRVTITCSASSSVS YMHWYQQKPGKA PKLLIYSTSNLASGVP SRFSGSGSGTEFTLTI SSLQPEDFATYYCH QWRTYPTFGQGTKL EIK(SEQ ID NO:418)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:419)
VSTB58	Human IgG1/kappa		GFSLT NYG (SEQ ID NO:420)	IWRGG NT (SEQ ID NO:421)	ARSMV SYTVDY (SEQ ID NO:422)	SSVSY (SEQ ID NO:423)	DTS (SEQ ID NO:424)	QQWS SYPPT (SEQ ID NO:425)	QVQLQESGPGLVKPS ETLSLTCTVSGFSLTNY GVHWIRQPPGKGLE WIGVIWRGGNTDYN AAFMSRVTISVDTSK NQFSLKLSSVTAADTA VYYCARSMVSYTVDY WGQGTLVTVSS (SEQ ID NO:426)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:427)	EIVLTQSPDFQSVTP KEKVTITCSASSSVSY MHWYQQKPDQSP KLLIKDTSNLASGVP SRFSGSGSGTDFTLTI NSLEAEDAATYYCQ QWSSYPPTFGQGTK LEIK (SEQ ID NO:428)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:429)

FIGURE 4Q

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	GYTFTDYW (SEQ ID NO:430)	IETSLNYP (SEQ ID NO:431)	ARWGIYGNP WFAY (SEQ ID NO:432)	ESVDSYVNSF (SEQ ID NO:433)	RAS (SEQ ID NO:434)	QQSNEDPY (SEQ ID NO:435) T	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTD YWMHWVRQAPGQ GLEWMGAIETSLNYP SYNQKFKGRVTMTRD TSTSTVYMELSSLRSE DTAVYYCARWGIYGN PWFAYWGRGTLVTV (SEQ ID NO:436) SS	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:437)	DIVMTQTPLSLSVTP GQPASISCRASESVD SYVNSFVHWYLQKP GQPPQLLIYRASNLE SGVPDRFSGSGSGT DFTLKISRVEAEDVG VYYCQQSNEDPYTF GQGTKLEIK (SEQ ID NO:438)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:439)
VSTB60 Group 2	Human IgG1/kappa	NLTLLDSGL and VQTGKDAP SNC Group 2	GYTFTNYG (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 ASVKVSCKASGYTFTN YGMTWVRQAPGQG LEWMGWINTYTGES TYADDFKGRFVFSLDT SVSTAYLQICSLKAEDT AVYYCARDYYGIYVSA YWGQGTLVTVSS (SEQ ID NO:446)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:447)	DIVMTQTPLSLSVTP GQPASISCRASESVD NYANSFMHWYLQK PGQSPQLLIYRASNL ESGVPDRFSGSGSG TDFTLKISRVEAEDV GVYYCQQSHEDPYT FGQGTKLEIK (SEQ ID NO:448)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:449)

FIGURE 4R

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		GYTFTSHW (SEQ ID NO:450)	INPRDGRT (SEQ ID NO:451)	ARGDFHYGD YFWYFDV (SEQ ID NO:452)	QNVHGA (SEQ ID NO:453)	MAS (SEQ ID NO:454)	LQHWNYLT (SEQ ID NO:455)	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS HWMHWVRQAPGQ GLEWMGEINPRDGR TNYNEKFKTRVTMTR DTSTSTVYMELSSLRS EDTAVYYCARGDFHY GDYFWYFDVWGQGT LVTVSS (SEQ ID NO:456)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:457)	DIQMTQSPSSLSAS VGDRVTITCKASQN VHGAVAWYQQKP GKVPKLLIYMASNR PTGVPSRFSGSGSG TDFTLTISSLQPEDV ATYYCLQHWNYLTF GQGTKLEIK (SEQ ID NO:458)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:459)
VSTB62	Human IgG1/kappa		GYTFTHYW (SEQ ID NO:460)	IYPGDGDT (SEQ ID NO:461)	ARRDYDYGD Y (SEQ ID NO:462)	SSVSH (SEQ ID NO:463)	LTS (SEQ ID NO:464)	QQYQTYPP T (SEQ ID NO:465)	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTH YWIQWVRQAPGQGL EWMGAIYPGDGDTR YTQKFKGRVTMTRDT STSTVYMELSSLRSED TAVYYCARRDYDYGD YWGQGTTVTVSS (SEQ ID NO:466)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:467)	EIVLTQSPDFQSVTP KEKVTITCSASSSVS HMYWYQQKPDQS PKLLIKLTSNLASGVP SRFSGSGSGTDFTLTI NSLEAEDAATYYCQ QYQTYPPTFGQGTR LEIK (SEQ ID NO:468)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:469)

FIGURE 4S

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
VSTB63 INX902	Human IgG1/kappa	Group 2	GFSITSDFA (SEQ ID NO:470)	ITYSGFT (SEQ ID NO:471)	ARQEYGNYV WYFDV (SEQ ID NO:472)	ESVEYYGTSL (SEQ ID NO:473)	AAS (SEQ ID NO:474)	QQSRKVP WT (SEQ ID NO:475)	QVQLQESGPGLVKPS ETLSLTCAVSGFSITSD FAWNWIRQPPGKGL EWIGYITYSGFTNYNP SLESRVTISVDTSKNQ FSLKLSSVTAADTAVY YCARQEYGNYVWYF DVWGQGTLVTVSS (SEQ ID NO:476)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:477)	DIVMTQTPLSLSVTP GQPASISCRASESVE YYGTSLLQWYLQKP GQPPQLLIYAASNV ESGVPDRFSGSGSG TDFTLKISRVEAEDV GVYYCQQSRKVPW TFGQGTKLEIK (SEQ ID NO:478)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:479)
VSTB64	Human IgG1/kappa		GYSITSGYF (SEQ ID NO:480)	MGYDGRI (SEQ ID NO:481)	AREGDYYGS GFAYW (SEQ ID NO:482)	QNVNTN (SEQ ID NO:483)	SAS (SEQ ID NO:484)	QQYNNYPL T (SEQ ID NO:485)	QVQLQESGPGLVKPS ETLSLTCAVSGYSITSG YFWNWIRQPPGKGL EWIGYMGYDGRIFYS PSLKNRVTISVDTSKN QFSLKLSSVTAADTAV YYCAREGDYYGSGFA YWGQGTLVTVSS (SEQ ID NO:486)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:487)	DIQMTQSPSSLSAS VGDRVTITCKASQN VNTNLAWYQQKPG KVPKLLIYSASYRYS GVPSRFSGSGSGTD FTLTISSLQPEDVATY YCQQYNNYPLTFGQ GTKLEIK (SEQ ID NO:488)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:489)

FIGURE 4T

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	GYTFTSYW (SEQ ID NO:490)	INPSNGLT (SEQ ID NO:491)	ARSYDYDGD YYAMDY (SEQ ID NO:492)	QSIVHSNGN TY (SEQ ID NO:493)	KVS (SEQ ID NO:494)	FQASHVPW (SEQ ID NO:495) T	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YWIHWVRQAPGQGL EWMGEINPSNGLTNY NEKFRNRVTMTRDTS TSTVYMELSSLRSEDT AVYYCARSYDYDGDY YAMDYWGQGTLVTV SS (SEQ ID NO:496)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:497)	DIVMTQSPLSLPVTP GEPASISCRSTQSIV HSNGNTYLEWYLQK PGQSPQLLIYKVSNR FSGVPDRFSGSGSG TDFTLKISRVEAEDV GVYYCFQASHVPW TFGQGTKLEIK (SEQ ID NO:498)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:499)
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 ASVKVSCKASGYPFTG YFMHWVRQAPGQG LEWMGRINPYNGGT VYNQNFNDRVTMTR DTSTSTVYMELSSLRS EDTAVYYCARWTFDG LFMDYWGQGTTVTV SS (SEQ ID NO:506)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:507)	DVVMTQSPLSLPVT LGQPASISCRASENV DKYGISFMNWFQQ RPGQSPRRLIYATSN QGSGVPDRFSGSGS GTDFTLKISRVEAED VGVYYCQQSKEDPY TFGQGTKLEIK (SEQ ID NO:508)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:509)

FIGURE 4U

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	DYIFSSYW (SEQ ID NO:510)	IFPGSGGT (SEQ ID NO:511)	ARAIYYDYD MYYFDS (SEQ ID NO:512)	QDISSY (SEQ ID NO:513)	YTS (SEQ ID NO:514)	QHVNTLP WT (SEQ ID NO:515)	QVQLVQSGAEVKKPG ASVKVSCKASDYIFSS YWIQWVRQAPGQGL EWMGEIFPGSGGTNY NEKFKGRVTMTRDTS TSTVYMELSSLRSEDT AVYYCARAIYYDYDM YYFDSWGQGTTVTVS S (SEQ ID NO:516)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:517)	DIQMTQSPSSLSAS VGDRVTITCRASQDI SSYLNWYQQKPGK VPKLLIYYTSRLHSG VPSRFSGSGSGTDFT LTISSLQPEDVATYY CQHVNTLPWTFGQ GTKLEIK (SEQ ID NO:518)	RTVAAPSVFIF PPSDEQLKSGT ASVVCLLNNFY PREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTLTL SKADYEKHKV YACEVTHQGL SSPVTKSFNRG EC (SEQ ID NO:519)
VSTB68	Human IgG1/kappa		GYTFTDYT (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)	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTD YTMNWVRQAPGQRL EWMGLINPYNGGTT YNQKFKGRVTITRDTS ASTAYMELSSLRSEDT AVYYCARHYGNYNW YFDVWGQGTTVTVSS (SEQ ID NO:526)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:527)	DIQLTQSPSFLSASV GDRVTITCKASQYV NTAVAWYQQKPGK APKLLIYSASYRYTG VPSRFSGSGSGTEFT LTISSLQPEDFATYYC QQHFTTPITFGQGT KLEIK (SEQ ID NO:528)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:529)

FIGURE 4V

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		GYTFTNYG (SEQ ID NO:530)	INTYTGEP (SEQ ID NO:531)	ARNYGNYVAY (SEQ ID NO:532)	QDINSY (SEQ ID NO:533)	RAN (SEQ ID NO:534)	LQYDEFPLT (SEQ ID NO:535)	QVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCARNYGNYVAYWGQGTTVTVSS (SEQ ID NO:536)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:537)	DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKSLIYRANRLVDGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQYDEFPLTFGQGTRLEIK (SEQ ID NO:538)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:539)
VSTB70	Human IgG1/kappa	Group 1	GYTFSNYW (SEQ ID NO:540)	ILPGSGNV (SEQ ID NO:541)	ATPPHYYGYDYYDVNY (SEQ ID NO:542)	QSLLDSDGKTY (SEQ ID NO:543)	LVS (SEQ ID NO:544)	WQGTHFPQT (SEQ ID NO:545)	EVQLVQSGAEVKKPGATVKISCKVSGYTFSNYWIEWVQQAPGKGLEWMGEILPGSGNVHYNEKFKGRVTITADTSTDTAYMELSSLRSEDTAVYYCATPPHYYGYDYYDVNYWGQGTLVTVSS (SEQ ID NO:546)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:547)	DVVMTQSPLSLPVTLGQPASISCKSSQSLLDSDGKTYLNWFQQRPGQSPRRLIYLVSELDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPQTFGQGTKLEIK (SEQ ID NO:548)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:549)

FIGURE 4W

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)	QSLLNSGDQKSY (SEQ ID NO:553)	GAS (SEQ ID NO:554)	QNDHSYPLT (SEQ ID NO:555)	QVQLVQSGAEVKKPGSSVKVSCKASGYVFSRSWINWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTITADESTSTAYMELSSLRSEDTAVYYCARRWFLWGQGTLVTVSS (SEQ ID NO:556)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:557)	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGDQKSYLAWYQQKPGQPPKLLIYGASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQNDHSYPLTFGQGTKLEIK (SEQ ID NO:558)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:559)
VSTB72	Human IgG1/kappa		GFTFSSYA (SEQ ID NO:560)	ISSGGSHT (SEQ ID NO:561)	ARRGNLYDGPY (SEQ ID NO:562)	SSVSH (SEQ ID NO:563)	DTS (SEQ ID NO:564)	QQWNFYPFT (SEQ ID NO:565)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVAEISSGGSHTYYPDTVTGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARRGNLYDGPYWGQGTLVTVSS (SEQ ID NO:566)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:567)	EIVLTQSPATLSLSPGERATLSCSASSSVSHMYWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQWNFYPFTFGQGTKLEIK (SEQ ID NO:568)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:569)

FIGURE 4X

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	GYTFTDYV (SEQ ID NO:570)	IYPGSGNT (SEQ ID NO:571)	ARVLVSVMDY (SEQ ID NO:572)	SSINY (SEQ ID NO:573)	DTS (SEQ ID NO:574)	HQRSSYPWT (SEQ ID NO:575)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYVISWVRQAPGQGLEWMGEIYPGSGNTYYYEKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARVLVSVMDYWGQGTLVTVSS (SEQ ID NO:576)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:577)	EIVLTQSPDFQSVTPKEKVTITCSASSSINYITWYQQKPDQSPKLLIKDTSKLASGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQRSSYPWTFGQGTRLEIK (SEQ ID NO:578)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:579)
VSTB74	Human IgG1/kappa Group 4	Group 4	GYIFTDYN (SEQ ID NO:580)	INPKYDST (SEQ ID NO:581)	AADGSSAMDY (SEQ ID NO:582)	QSLLNSGHQKNY (SEQ ID NO:583)	GAS (SEQ ID NO:584)	QNDHRYPLT (SEQ ID NO:585)	QMQLVQSGPEVKKPGTSVKVSCKASGYIFTDYNIDWVRQARGQRLEWIGDINPKYDSTRYNQKFKGRVTITRDMSTSTAYMELSSLRSEDTAVYYCAADGSSAMDYWGQGTTVTVSS (SEQ ID NO:586)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:587)	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGHQKNYLAWYQQKPGQPPKLLIYGASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQNDHRYPLTFGQGTKLEIK (SEQ ID NO:588)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:589)

FIGURE 4Y

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		GFNIKDYY (SEQ ID NO:590)	IDPENGNT (SEQ ID NO:591)	ARDYGYFDYW (SEQ ID NO:592)	SSVIY (SEQ ID NO:593)	STS (SEQ ID NO:594)	QQRSSYPHT (SEQ ID NO:595)	QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDYYIHWVRQAPGQGLEWMGWIDPENGNTIYDPKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDYGYFDYWGQGTLVTVSS (SEQ ID NO:596)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:597)	DVVMTQSPAFLSVTPGEKVTITCSAGSSVIYMYWYQQKPDQAPKLLIKSTSNLASGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQRSSYPHTFGQGTKLEIK (SEQ ID NO:598)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:599)
VSTB76 INX911	Human IgG1/kappa	Group 2	GYTFTDYW (SEQ ID NO:600)	IYPSHSYT (SEQ ID NO:601)	ARGGYRYPYYAMDY (SEQ ID NO:602)	ENIYGA (SEQ ID NO:603)	GAT (SEQ ID NO:604)	QNVLSTPYT (SEQ ID NO:605)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYWINWVRQAPGQGLEWMGNIYPSHSYTNYNQEFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGYRYPYYAMDYWGQGTTVTVSS (SEQ ID NO:606)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:607)	AIQLTQSPSSLSASVGDRVTITCGASENIYGALNWYQQKPGKAPKLLIYGATNLADGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQNVLSTPYTFGQGTKLEIK (SEQ ID NO:608)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:609)

FIGURE 4Z

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	GYTFTNYW (SEQ ID NO:610)	INPSSGYT (SEQ ID NO:611)	ARDGGSVLFGY (SEQ ID NO:612)	QSLLNSGIRKNY (SEQ ID NO:613)	SAS (SEQ ID NO:614)	KQSYNLYT (SEQ ID NO:615)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLEWMGYINPSSGYTEYNQKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDGGSVLFGYWGQGTTVTVSS (SEQ ID NO:616)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:617)	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGIRKNYLAWYQQKPGQPPKLLIYSASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLYTFGQGTKLEIK (SEQ ID NO:618)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:619)
VSTB79	Human IgG1/kappa		AYSITSDYA (SEQ ID NO:620)	ITYSGST (SEQ ID NO:621)	ARSFGY (SEQ ID NO:622)	QSIGTS (SEQ ID NO:623)	YAS (SEQ ID NO:624)	QQINSWPTT (SEQ ID NO:625)	QVQLQESGPGLVKPSETLSLTCAVSAYSITSDYAWNWIRQPPGKGLEWIGYITYSGSTRYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSFGYWGQGTTVTVSS (SEQ ID NO:626)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:627)	EIVMTQSPATLSVSPGERATLSCRASQSIGTSIHWYQQKPGQAPRLLIYYASESISGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQINSWPTTFGQGTKLEIK (SEQ ID NO:628)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:629)

FIGURE 4AA

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		GFNIKDYY (SEQ ID NO:630)	IDPENGDT (SEQ ID NO:631)	ARDMGSSYVY (SEQ ID NO:632)	SSVIY (SEQ ID NO:633)	STS (SEQ ID NO:634)	QQRSSYPFT (SEQ ID NO:635)	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQGLEWMGWIDPENGDTEYAPKFQDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDMGSSYVYWGRGTLVTVSS (SEQ ID NO:636)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:637)	DVVMTQSPAFLSVTPGEKVTITCSASSSVIYMHWYQQKPDQAPKLLIKSTSNLASGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQRSSYPFTFGQGTKLEIK (SEQ ID NO:638)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:639)
VSTB81	Human IgG1/kappa	Group 1	GFSLSTSGMG (SEQ ID NO:640)	IYWDDDK (SEQ ID NO:641)	ARRPDYFGSSYVD (SEQ ID NO:642)	ESVDTYGNSF (SEQ ID NO:643)	LAS (SEQ ID NO:644)	QQNNEDPWT (SEQ ID NO:645)	QVTLKESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKALEWLAHIYWDDDKRYNPSLKSRLTISKDTSKNQVVLTMTNMDPVDTATYYCARRPDYFGSSYVDWGQGTTVTVSS (SEQ ID NO:646)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:647)	DIVMTQTPLSLSVTPGQPASISCRASESVDTYGNSFMHWYLQKPGQPPQLLIYLASNLDFGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQNNEDPWTFGQGTKLEIK (SEQ ID NO:648)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:649)

FIGURE 4BB

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
VSTB82	Human IgG1/kappa		GYSITSDYA (SEQ ID NO:650)	ITYSGST (SEQ ID NO:651)	ARSHYGSTY WYFDV (SEQ ID NO:652)	ESVEYYGTSL (SEQ ID NO:653)	AAS (SEQ ID NO:654)	QQTRKVP WT (SEQ ID NO:6565)	QVQLQESGPGLVKPS ETLSLTCAVSGYSITSD YAWNWIRQPPGKGL EWIGFITYSGSTNYNP SLKSRVTISVDTSKNQ FSLKLSSVTAADTAVY YCARSHYGSTYWYFD VWGQGTTVTVSS (SEQ ID NO:656)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:657)	DIVMTQTPLSLSVTP GQPASISCRASESVE YYGTSLMQWYLQK PGQSPQLLIYAASN VESGVPDRFSGSGS GTDFTLKISRVEAED VGVYYCQQTRKVP WTFGQGTRLEIK (SEQ ID NO:658)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:659)
VSTB83	Human IgG1/kappa		GYTFTSYD (SEQ ID NO:660)	IYPGDGYT (SEQ ID NO:661)	ARWGYGSYA MDY (SEQ ID NO:662)	QSLVHSNGN TY (SEQ ID NO:664)	KVS (SEQ ID NO:664)	SQSTHVPP T (SEQ ID NO:665)	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YDINWVRQAPGQGL EWMGWIYPGDGYTE YNEKFRGRVTMTRDT STSTVYMELSSLRSED TAVYYCARWGYGSYA MDYWGQGTLVTVSS (SEQ ID NO:666)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:667)	DIVMTQSPLSLPVTP GEPASISCRSSQSLV HSNGNTYLHWYLQ KPGQSPQLLIYKVSN RFSGVPDRFSGSGS GTDFTLKISRVEAED VGVYYCSQSTHVPP TFGQGTKLEIK (SEQ ID NO:668)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:669)

FIGURE 4CC

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	GYTFTSYW (SEQ ID NO:670)	INPSTGYP (SEQ ID NO:671)	ARSYYDYDG GAWFAY (SEQ ID NO:672)	ESVEYYGTSL (SEQ ID NO:673)	AAS (SEQ ID NO:674)	QQSRKVPS T (SEQ ID NO:675)	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTS YWMHWVRQAPGQ GLEWMGYINPSTGYP GYNQKFKDRVTMTR DTSTSTVYMELSSLRS EDTAVYYCARSYYDY DGGAWFAYWGQGT TVTVSS (SEQ ID NO:676)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:677)	DIVMTQTPLSLSVTP GQPASISCRASESVE YYGTSLMQWYLQK PGQPPQLLIYAASN VESGVPDRFSGSGS GTDFTLKISRVEAED VGVYYCQQSRKVPS TFGQGTKLEIK (SEQ ID NO:678)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:679)
VSTB85 INX913	Human IgG1/kappa	Group 1	GYTFTDYA (SEQ ID NO:680)	IDTYYGNT (SEQ ID NO:681)	ARGGGDALD Y (SEQ ID NO:682)	QSVSND (SEQ ID NO:683)	YAS (SEQ ID NO:684)	QQGYTSLR T (SEQ ID NO:685)	QVQLVQSGAEVKKPG ASVKVSCKASGYTFTD YAMHWVRQAPGQG LEWMGVIDTYYGNT NYNQKFKGRVTMTR DTSISTAYMELSRLRS DDTAVYYCARGGGD ALDYWGQGTTVTVSS (SEQ ID NO:686)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:687)	DIQMTQSPSSLSAS VGDRVTITCKASQS VSNDVVWYQQKPG KAPKLLIYYASNRYI GVPSRFSGSGSGTD FTFTISSLQPEDIATY YCQQGYTSLRTFGQ GTKLEIK (SEQ ID NO:688)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:689)

FIGURE 4DD

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)	AREDYDYDG VFAY (SEQ ID NO:692)	QSISNN (SEQ ID NO:693)	YAS (SEQ ID NO:694)	QQSNSWP HT (SEQ ID NO:695)	QVQLQESGPGLVKPS ETLSLTCAVSGYSITSG YSWHWIRQPPGKGL EWIGYIHYIGITNNNP SLKSRVTISVDTSKNQ FSLKLSSVTAADTAVY YCAREDYDYDGVFAY WGQGTLVTVSS (SEQ ID NO:696)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:697)	EIVLTQSPATLSLSPG ERATLSCRASQSISN NLHWYQQKPGQAP RLLIYYASQSISGIPA RFSGSGSGTDFTLTIS SLEPEDFAVYYCQQ SNSWPHTFGQGTKL EIK (SEQ ID NO:698)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:699)
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)	QQYNSYPL T (SEQ ID NO:705)	QVQLQESGPGLVKPS ETLSLTCTVSGFSLTNY DISWIRQPPGKGLEW IGVIWTGGGTNYNSA FMSRVTISVDTSKNQF SLKLSSVTAADTAVYY CAREGLLLPLYWGQG TLVTVSS (SEQ ID NO:706)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:707)	DIQMTQSPSSLSAS VGDRVTITCKASQN VGTNVAWYQQKPG KVPKLLIYSASYRYS GVPSRFSGSGSGTD FTLTISSLQPEDVATY YCQQYNSYPLTFGQ GTKLEIK (SEQ ID NO:708)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:709)

FIGURE 4EE

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		GYTFTNFG (SEQ ID NO:710)	INTYTGEP (SEQ ID NO:711)	ARGAYYYGS RVWFAY (SEQ ID NO:712)	QNLVHSNGN TY (SEQ ID NO:713)	KVS (SEQ ID NO:714)	SQSSHVPYT (SEQ ID NO:715)	QVQLVQSGSELKKPG ASVKVSCKASGYTFTN FGMNWVRQAPGQG LEWMGWINTYTGEP TYADDFKGRFVFSLDT SVSTAYLQICSLKAEDT AVYYCARGAYYYGSR VWFAYWGQGTLVTV SS (SEQ ID NO:716)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:717)	DIVMTQSPLSLPVTP GEPASISCTSSQNLV HSNGNTYLHWYLQ KPGQSPQLLIYKVSN RFSGVPDRFSGSGS GTDFTLKISRVEAED VGVYYCSQSSHVPY TFGQGTKLEIK (SEQ ID NO:718)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:719)
VSTB90	Human IgG1/kappa		GFSLTSSG (SEQ ID NO:720)	IWSGGNT (SEQ ID NO:721)	AREDYDYDW YFDV (SEQ ID NO:722)	ESVEYYGTSL (SEQ ID NO:723)	AAS (SEQ ID NO:724)	QQSRKVP WT (SEQ ID NO:725)	QVQLQESGPGLVKPS ETLSLTCTVSGFSLTSS GVHWIRQPPGKGLE WIGVIWSGGNTDYN AAFISRVTISVDTSKN QFSLKLSSVTAADTAV YYCAREDYDYDWYFD VWGQGTTVTVSS (SEQ ID NO:726)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:727)	DIVMTQTPLSLSVTP GQPASISCRASESVE YYGTSLMQWYLQK PGQPPQLLIYAASN VKSGVPDRFSGSGS GTDFTLKISRVEAED VGVYYCQQSRKVP WTFGQGTKLEIK (SEQ ID NO:728)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:729)

FIGURE 4FF

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		GYTFANFW (SEQ ID NO:730)	IFPGNSDT (SEQ ID NO:731)	ARELTGTYYFDY (SEQ ID NO:732)	SSVSY (SEQ ID NO:733)	SSS (SEQ ID NO:734)	HQWSGHFT (SEQ ID NO:735)	QVQLVQSGAEVKKPGASVKVSCKASGYTFANFWMHWVRQAPGQGLEWMGAIFPGNSDTGYNQKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARELTGTYYFDYWGQGTLVTVSS (SEQ ID NO:736)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:737)	EIVLTQSPATLSLSPGERATLSCSATSSVSYMHWYQQKPGQAPRLLIYSSSNLASGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCHQWSGHFTFGQGTKLEIK (SEQ ID NO:738)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:739)
VSTB92 INX908	Human IgG1/kappa	Group 1	GYTFANYL (SEQ ID NO:740)	IYPGGGFI (SEQ ID NO:741)	ARRFDYGGYFFDY (SEQ ID NO:742)	QSIVHSNGNIY (SEQ ID NO:743)	KVS (SEQ ID NO:744)	FQGSHVPWT (SEQ ID NO:745)	QVQLVQSGAEVKKPGASVKVSCKASGYTFANYLIGWVRQAPGQRLEWMGDIYPGGGFISYNEKFKGRVTITRDTSASTAYMELSSLRSEDTAVYYCARRFDYGGYFFDYWGQGTLVTVSS (SEQ ID NO:746)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:747)	DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNIYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKLEIK (SEQ ID NO:748)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:749)

FIGURE 4GG

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
VSTB93	Human IgG1/kappa		GFSITNYD (SEQ ID NO:750)	IWTGGGT (SEQ ID NO:751)	ARDRSPYFGYDY (SEQ ID NO:752)	QSLVHSNGNTY (SEQ ID NO:753)	KVS (SEQ ID NO:754)	SQSTHVPWT (SEQ ID NO:755)	QVQLQESGPGLVKPETLSLTCTVSGFSITNYDISWIRQPPGKGLEWIGVIWTGGGTNYNSAFMSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRSPYFGYDYWGQGTTVTVSS (SEQ ID NO:756)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:757)	DIVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPWTFGQGTKLEIK (SEQ ID NO:758)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:759)
VSTB94	Human IgG1/kappa		GYSITSDYA (SEQ ID NO:760)	MMYSGSA (SEQ ID NO:761)	ARFDHYYGRFDY (SEQ ID NO:762)	SSVSY (SEQ ID NO:763)	EIS (SEQ ID NO:764)	QQWNYPLFT (SEQ ID NO:765)	QVQLQESGPGLVKPETLSLTCAVSGYSITSDYAWTWIRQPPGKGLEWIGYMMYSGSASYNPSLKGRVTISVDTSKNQFSLKLSSVTAADTAVYYCARFDHYYGRFDYWGQGTTVTVSS (SEQ ID NO:766)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:767)	AIQLTQSPSSLSASVGDRVTITCSASSSVSYIHWYQQKPGKAPKLLIYEISKLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQWNYPLFTFGQGTKLEIK (SEQ ID NO:768)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:769)

FIGURE 4HH

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 Group 1	GFTFRNYG (SEQ ID NO:770)	IISGGSYT (SEQ ID NO:771)	ARIYDHDGD YYAMDY (SEQ ID NO:772)	QSIVHSNGN TY (SEQ ID NO:773)	KVS (SEQ ID NO:774)	FQGSHVP WT (SEQ ID NO:775)	EVQLVESGGGLVQPG GSLRLSCAASGFTFRN YGMSWVRQAPGKGL EWVASIISGGSYTYYP DSVKGRFTISRDNAK NSLYLQMNSLRAEDT AVYYCARIYDHDGDY YAMDYWGQGTTVTV SS (SEQ ID NO:776)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:777)	DIVMTQSPLSLPVTP GEPASISCRSSQSIV HSNGNTYLEWYLQK PGQSPQLLIYKVSNR FSGVPDRFSGSGSG TDFTLKISRVEAEDV GVYYCFQGSHVPW TFGQGTKLEIK (SEQ ID NO:778)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:779)
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)	QVQLVQSGAEVKKPG SSVKVSCKASGYTFTS YDINWVRQAPGQGL EWMGRIYPGDGSTKY NEKFKGRVTITADKST STAYMELSSLRSEDTA VYYCAREGITPFAYW GQGTTVTVSS (SEQ ID NO:786)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:787)	AIQLTQSPSSLSASV GDRVTITCRASKSIS KYLAWYQQKPGKA PKLLIYSGSTLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQHNEYPWTFGQG TKLEIK (SEQ ID NO:788)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:789)

FIGURE 4II

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
VSTB97 INX914	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:790)	IIPIFGTA (SEQ ID NO:791)	ARSSYGWSY EFDY (SEQ ID NO:792)	QSISSY (SEQ ID NO:793)	AAS (SEQ ID NO:794)	QQSYSTPLT (SEQ ID NO:795)	QVQLVQSGAEVKKPG SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARSSYGWSYEFD YWGQGTLVTVSS (SEQ ID NO:796)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:797)	DIQMTQSPSSLSAS VGDRVTITCRASQSI SSYLNWYQQKPGK APKLLIYAASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQSYSTPLTFGQGT KVEIK (SEQ ID NO:798)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:799)
VSTB98	Human IgG1/kappa	Group 1	GGTFSSYA (SEQ ID NO:800)	IIPIFGTA (SEQ ID NO:801)	ARSTVGWSY EFDY (SEQ ID NO:802)	QSISSY (SEQ ID NO:803)	AAS (SEQ ID NO:804)	QQSYSTPLT (SEQ ID NO:805)	QVQLVQSGAEVKKPG SSVKVSCKASGGTFSS YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARSTVGWSYEFD YWGQGTLVTVSS (SEQ ID NO:806)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:807)	DIQMTQSPSSLSAS VGDRVTITCRASQSI SSYLNWYQQKPGK APKLLIYAASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQSYSTPLTFGQGT KVEIK (SEQ ID NO:808)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:809)

FIGURE 4JJ

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 YAISWVRQAPGQGLE WMGGIIPIFGTANYA QKFQGRVTITADESTS TAYMELSSLRSEDTAV YYCARHVLGWVLELD YWGQGTLVTVSS (SEQ ID NO:816)	ASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQK SLSLSPGK (SEQ ID NO:817)	DIQMTQSPSSLSAS VGDRVTITCRASQSI SSYLNWYQQKPGK APKLLIYAASSLQSG VPSRFSGSGSGTDFT LTISSLQPEDFATYYC QQSYSTPLTFGQGT KVEIK (SEQ ID NO:818)	RTVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ WKVDNALQS GNSQESVTEQ DSKDSTYSLSS TLTLSKADYEK HKVYACEVTH QGLSSPVTKSF NRGEC (SEQ ID NO:819)

FIGURE 4KK

mAb ID	Description	Epitope Sequence	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	LLDSGLYCCLVVE IRHHHSEHRVH	GYTLTDYN	INLNYAIT	ARGGYRYTYYA MDY	ENIYSN	AAT	QHFWGT PRT	EVQLQQFGAELVKPGASVKISCKASGY TLTDYNMDWVKQSHGKSLEWIGHIN LNYAITTYNQKFKGKATLTVDKSSSTA YMELRSLTSEDTAVYYCARGGYRYTYY AMDYWGQGTSVTVSS	AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPE PVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVP SSTWPSETVTCNVAHPASSTKVDKKIVPRDCGCKP CICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFR SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTIS KTKLNPKS	DIQMTQSPASLSVSVGETVTITCRA SENIYSNLAWYQQKQGKSPQLLVY AATNLADGVPSRFSGSGSGTQYSLK INSLQSEDFGSYYCQHFWGTPRTFG GGTKLEIK	RADAAPTVSIFPPSSEQLTS GGASVVCFLNNFYPKDIN VKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLT LTKDEYERHNSYTCEATHK TSTSPIVKSFNRNEC
GA1-IgG2	Human IgG2/kappa	LLDSGLYCCLVVE IRHHHSEHRVH	GYTLTDYN	INLNYAIT	ARGGYRYTYYA MDY	ENIYSN	AAT	QHFWGT PRT	EVQLQQFGAELVKPGASVKISCKASGY TLTDYNMDWVKQSHGKSLEWIGHIN LNYAITTYNQKFKGKATLTVDKSSSTA YMELRSLTSEDTAVYYCARGGYRYTYY AMDYWGQGTSVTVSS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	DIQMTQSPASLSVSVGETVTITCRA SENIYSNLAWYQQKQGKSPQLLVY AATNLADGVPSRFSGSGSGTQYSLK INSLQSEDFGSYYCQHFWGTPRTFG GGTKLEIK	RTVAAPSVFIFPPSDEQLKS GTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
GG8	Mouse IgG1/?	LLDSGLYCCLVVE IRHHHSEHRVH; GHDVTFYKTWY RSSRGEVQTC	GYSFTGYT	INPYNGGI	ARRTLLRPYFFD Y	QSVSTSTFS Y	YAS	QHSWEIP YT	EVQLQQSGPELVKPGTSMKISCKASGY SFTGYTMNWVRQSHGKNLEWIGLIN PYNGGINYNQKFKARATLTVDKSSSTA YMELLSLTSEDSAVYYCARRTLLRPYFF DYWGQGTTLTVSS		DIVLTQSPASLAVSLGQRATISCRAS QSVSTSTFSYMHWYQQKPGQPPKL LIKYASNLESGVPARFSGSGSGTDFT LNIHPVEEEDTATYYCQHSWEIPYTF GGGTKLEIK	
GG8-IgG2	Human IgG2/kappa	LLDSGLYCCLVVE IRHHHSEHRVH; GHDVTFYKTWY RSSRGEVQTC	GYSFTGYT	INPYNGGI	ARRTLLRPYFFD Y	QSVSTSTFS Y	YAS	QHSWEIP YT	EVQLQQSGPELVKPGTSMKISCKASGY SFTGYTMNWVRQSHGKNLEWIGLIN PYNGGINYNQKFKARATLTVDKSSSTA YMELLSLTSEDSAVYYCARRTLLRPYFF DYWGQGTTLTVSS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPP CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEK TISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	DIVLTQSPASLAVSLGQRATISCRAS QSVSTSTFSYMHWYQQKPGQPPKL LIKYASNLESGVPARFSGSGSGTDFT LNIHPVEEEDTATYYCQHSWEIPYTF GGGTKLEIK	RTVAAPSVFIFPPSDEQLKS GTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGL SSPVTKSFNRGEC

FIGURE 4LL

mAb ID	Description	Epitope Sequence	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	Mouse IgG1/?	LLDSGLYCCLVVEIR	GFDFSRYW	VYPDSSTI	ARGRGDY	GNIHNY	NAK	QNFWSTPFT	EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEVYPDSSTINYTPSLKDKFIISRDNAKNTLYLQMIKVRSEDTALYYCARGRGDYWGQGTSVTVSS		DIQMTQSPASLSASVGETVTITCRASGNIHNYLSWYHQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQNFWSTPFTFGSGTKLEIK	
IE8-IgG2	Human IgG2/kappa	LLDSGLYCCLVVEIR	GFDFSRYW	VYPDSSTI	ARGRGDY	GNIHNY	NAK	QNFWSTPFT	EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEVYPDSSTINYTPSLKDKFIISRDNAKNTLYLQMIKVRSEDTALYYCARGRGDYWGQGTSVTVSS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPASLSASVGETVTITCRASGNIHNYLSWYHQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQNFWSTPFTFGSGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
IE8-IgG2-C127S	Human mutated IgG2/kappa	LLDSGLYCCLVVEIR	GFDFSRYW	VYPDSSTI	ARGRGDY	GNIHNY	NAK	QNFWSTPFT	EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEVYPDSSTINYTPSLKDKFIISRDNAKNTLYLQMIKVRSEDTALYYCARGRGDYWGQGTSVTVSS	ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPASLSASVGETVTITCRASGNIHNYLSWYHQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQNFWSTPFTFGSGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB100	Human IgG1/kappa		GYSFTSYW	IYPGDSDT	ARDVSSFYGYSPMFDY	QSVSSY	DAS	QQRSNWPLT	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARDVSSFYGYSPMFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPLTFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB101	Human IgG1/kappa		GYSFTSYW	IYPGDSDT	ARDAHSFYGYSALLDY	QSVSSSY	GAS	QQYGSSPLT	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARDAHSFYGYSALLDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4MM

mAb ID	Description	Epitope Sequence	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
VSTB102	Human IgG1/kappa		GYSFTSYW	IYPGDSDT	ARDSYSFYGHTPVLDY	QSVSSSY	GAS	QQYGSSPLT	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARDSYSFYGHTPVLDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB103	Human IgG1/kappa		GYSFTSYW	IYPGDSDT	ARDDALYGGYYLDY	QSVLYSSNNKNY	WAS	QQYYSTPLT	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARDDALYGGYYLDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB104	Human IgG1/kappa		GYSFTSYW	IYPGDSDT	ARDANSFYSAASIFDY	QSVLYSSNNKNY	WAS	QQYYSTPLT	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARDANSFYSAASIFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB105	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARSSYGWSYEFDY	QSIATN	AAS	QQNDDRPIT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSSYGWSYEFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSIATNLNWYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNDDRPITFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB106	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARSSYGWSYEFDY	QSIRTD	SAS	QQNERTPIT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSSYGWSYEFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSIRTDLNWYQQKPGKAPKLLIYSASLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNERTPITFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4NN

mAb ID	Description	Epitope Sequence	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
VSTB107	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARSSYGWSYEFDY	QSINND	AAS	QQNRATPIT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSSYGWSYEFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSINNDLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNRATPITFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB108	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARNTFGWSGELDY	QSISNR	SAS	QQNHDNPIT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARNTFGWSGELDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSISNRLNWYQQKPGKAPKLLIYSASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNHDNPITFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB109	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARSSYGWSYEFDY	QSIATY	AAS	QQNHNRPIT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSSYGWSYEFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSIATYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNHNRPITFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB110	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARHSIGWVAELDY	QSINTD	AAS	QQGASDPIT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARHSIGWVAELDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSINTDLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGASDPITFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB111	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARSSYGWSYEFDY	QSINTD	AAS	QQNRGSPIT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSSYGWSYEFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSINTDLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNRGSPITFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4OO

mAb ID	Description	Epitope Sequence	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	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARHSIGWVAELDY	QSIATD	AAS	QQAHWYPLT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARHSIGWVAELDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSIATDLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAHWYPLTFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB114	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARHSIGWVAELDY	QSIATS	YAS	QQGAYYPLT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARHSIGWVAELDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSIATSLNWYQQKPGKAPKLLIYYASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGAYYPLTFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB115	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARSSYGWSYEFDY	QSIRTY	AAS	QQAYSNPIT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSSYGWSYEFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSIRTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAYSNPITFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB116	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARSSYGWSYEFDY	QSINTN	AAS	QQARDTPIT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSSYGWSYEFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSINTNLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQARDTPITFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB49	Human IgG1/kappa		GYTFPSHT	IYPFIDST	ARGIRGYTMDY	ESVDNYGLSF	GAS	QQSKEVPYT	QVQLVQSGAEVKKPGASVKVSCKASGYTFPSHTIHWVRQAPGQRLEWMGSIYPFIDSTIYNQKFKDRVTITRDTSASTAYMELSSLRSEDTAVYYCARGIRGYTMDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DVVMTQSPLSLPVTLGQPASISCRASESVDNYGLSFMNWFQQRPGQSPRRLIYGASNQGSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSKEVPYTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4PP

mAb ID	Description	Epitope Sequence	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
VSTB50	Human IgG1/kappa	NLTLLDSGL and VQTGKDAPSNC	GYTFTNYG	INPYTGEP	AREGYGNYIFPY	ESVDTYANSL	RAS	QQTNEDPRT	QVQLVQSGSELKKPGASVKVSCKASGYTFTNYGLNWVRQAPGQGLEWMGWINPYTGEPTYADDFKGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCAREGYGNYIFPYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRASESVDTYANSLMHWYLQKPGQPPQLLIYRASNLESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQTNEDPRTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB51	Human IgG1/kappa		GFTFSSYT	ISNSGSYT	ARDTVLSPFDY	SSISY	DTS	HQRSSFT	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMSWVRQAPGKGLEWVATISNSGSYTYYLDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTVLSPFDYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPDFQSVTPKEKVTITCSATSSISYMHWYQQKPDQSPKLLIKDTSELASGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQRSSFTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB52	Human IgG1/kappa		GGTFSNYW	IYPGGGFT	ARYYRSDEDYSMDF	QSLLYSNGKTY	LVS	VQATHFPQT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNYWIGWVRQAPGQGLEWMGEIYPGGGFTHYNEKFKGRVTITADESTSTAYMELSSLRSEDTAVYYCARYYRSDEDYSMDFWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DVVMTQSPLSLPVTLGQPASISCKSSQSLLYSNGKTYLNWFQQRPGQSPRRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCVQATHFPQTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB53	Human IgG1/kappa		GYTFTHYT	IIPSSGYS	ARGAYDDYYDYYAMDY	QTIVHSNGNTY	KVS	FQASHVPWT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTHYTIHWVRQAPGQGLEWMGYIIPSSGYSEYNQKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGAYDDYYDYYAMDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPLSLPVTPGEPASISCRSSQTIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQASHVPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB54	Human IgG1/kappa		GYNIKDTY	IDPTHGYV	ARDRFDPYWFLDV	ESVEYYGTSL	DAF	QQSRKVPWT	QVQLVQSGAEVKKPGASVKVSCKASGYNIKDTYMHWVRQAPGQGLEWMGRIDPTHGYVIYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDRFDPYWFLDVWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRASESVEYYGTSLMQWYLQKPGQSPQLLIYDAFNVESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSRKVPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4QQ

mAb ID	Description	Epitope Sequence	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
VSTB55	Human IgG1/kappa		GYSIASDYV	ISYSGST	ARITTVVPTGSYYGVDF	SSVNF	DTS	QQWSNYPFT	QVQLQESGPGLVKPSETLSLTCAVSGYSIASDYVWNWIRQPPGKGLEWIGYISYSGSTSNNPSLNSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARITTVVPTGSYYGVDFWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPDFQSVTPKEKVTITCSGSSSVNFMYWYQQKPDQSPKLLIKDTSNLASGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQWSNYPFTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB56	Human IgG1/kappa		GYTFTSYW	IIPNTLHT	ARLDGDYDYALDY	ESVEYYGTSF	TAS	QQSRKVPYT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWLHWVRQAPGQGLEWMGYIIPNTLHTDYNQKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARLDGDYDYALDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRASESVEYYGTSFMQWYLQKPGQPPQLLIYTASNVESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSRKVPYTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB57	Human IgG1/kappa		GFTFSTYA	ISSGGSDT	ARPTYYGIFSYFDY	SSVSY	STS	HQWRTYPT	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVATISSGGSDTYYPDTVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARPTYYGIFSYFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQLTQSPSFLSASVGDRVTITCSASSSVSYMHWYQQKPGKAPKLLIYSTSNLASGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCHQWRTYPTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB58	Human IgG1/kappa		GFSLTNYG	IWRGGNT	ARSMVSYTVDY	SSVSY	DTS	QQWSSYPPT	QVQLQESGPGLVKPSETLSLTCTVSGFSLTNYGVHWIRQPPGKGLEWIGVIWRGGNTDYNAAFMSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSMVSYTVDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPDFQSVTPKEKVTITCSASSSVSYMHWYQQKPDQSPKLLIKDTSNLASGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQWSSYPPTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB59	Human IgG1/kappa		GYTFTDYW	IETSLNYP	ARWGIYGNPWFAY	ESVDSYVNSF	RAS	QQSNEDPYT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYWMHWVRQAPGQGLEWMGAIETSLNYPSYNQKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARWGIYGNPWFAYWGRGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRASESVDSYVNSFVHWYLQKPGQPPQLLIYRASNLESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSNEDPYTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4RR

mAb ID	Description	Epitope Sequence	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
VSTB60	Human IgG1/kappa	NLTLLDSGL and VQTGKDAPSNC	GYTFTNYG	INTYTGES	ARDYYGIYVSAY	ESVDNYANSF	RAS	QQSHEDPYT	QVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMTWVRQAPGQGLEWMGWINTYTGESTYADDFKGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCARDYYGIYVSAYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRASESVDNYANSFMHWYLQKPGQSPQLLIYRASNLESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSHEDPYTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB61	Human IgG1/kappa		GYTFTSHW	INPRDGRT	ARGDFHYGDYFWYFDV	QNVHGA	MAS	LQHWNYLT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSHWMHWVRQAPGQGLEWMGEINPRDGRTNYNEKFKTRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGDFHYGDYFWYFDVWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCKASQNVHGAVAWYQQKPGKVPKLLIYMASNRPTGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCLQHWNYLTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB62	Human IgG1/kappa		GYTFTHYW	IYPGDGDT	ARRDYDYGDY	SSVSH	LTS	QQYQTYPPT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTHYWIQWVRQAPGQGLEWMGAIYPGDGDTRYTQKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARRDYDYGDYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPDFQSVTPKEKVTITCSASSSVSHMYWYQQKPDQSPKLLIKLTSNLASGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQYQTYPPTFGQGTRLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB63	Human IgG1/kappa		GFSITSDFA	ITYSGFT	ARQEYGNYVWYFDV	ESVEYYGTSL	AAS	QQSRKVPWT	QVQLQESGPGLVKPSETLSLTCAVSGFSITSDFAWNWIRQPPGKGLEWIGYITYSGFTNYNPSLESRVTISVDTSKNQFSLKLSSVTAADTAVYYCARQEYGNYVWYFDVWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRASESVEYYGTSLLQWYLQKPGQPPQLLIYAASNVESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSRKVPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB64	Human IgG1/kappa		GYSITSGYF	MGYDGRI	AREGDYYGSGFAYW	QNVNTN	SAS	QQYNNYPLT	QVQLQESGPGLVKPSETLSLTCAVSGYSITSGYFWNWIRQPPGKGLEWIGYMGYDGRIFYSPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGDYYGSGFAYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCKASQNVNTNLAWYQQKPGKVPKLLIYSASYRYSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQQYNNYPLTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4SS

mAb ID	Description	Epitope Sequence	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		GYTFTSYW	INPSNGLT	ARSYDYDGDYYAMDY	QSIVHSNGNTY	KVS	FQASHVPWT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWIHWVRQAPGQGLEWMGEINPSNGLTNYNEKFRNRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSYDYDGDYYAMDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPLSLPVTPGEPASISCRSTQSIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQASHVPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB66	Human IgG1/kappa		GYPFTGYF	INPYNGGT	ARWTFDGLFMDY	ENVDKYGISF	ATS	QQSKEDPYT	QVQLVQSGAEVKKPGASVKVSCKASGYPFTGYFMHWVRQAPGQGLEWMGRINPYNGGTVYNQNFNDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARWTFDGLFMDYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DVVMTQSPLSLPVTLGQPASISCRASENVDKYGISFMNWFQQRPGQSPRRLIYATSNQGSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSKEDPYTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB67	Human IgG1/kappa		DYIFSSYW	IFPGSGGT	ARAIYYDYDMYYFDS	QDISSY	YTS	QHVNTLPWT	QVQLVQSGAEVKKPGASVKVSCKASDYIFSSYWIQWVRQAPGQGLEWMGEIFPGSGGTNYNEKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARAIYYDYDMYYFDSWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQDISSYLNWYQQKPGKVPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQHVNTLPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB68	Human IgG1/kappa		GYTFTDYT	INPYNGGT	ARHYGNYNWYFDV	QYVNTA	SAS	QQHFTTPIT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYTMNWVRQAPGQRLEWMGLINPYNGGTTYNQKFKGRVTITRDTSASTAYMELSSLRSEDTAVYYCARHYGNYNWYFDVWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQLTQSPSFLSASVGDRVTITCKASQYVNTAVAWYQQKPGKAPKLLIYSASYRYTGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQHFTTPITFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB69	Human IgG1/kappa		GYTFTNYG	INTYTGEP	ARNYGNYVAY	QDINSY	RAN	LQYDEFPLT	QVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCARNYGNYVAYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKSLIYRANRLVDGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQYDEFPLTFGQGTRLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4TT

mAb ID	Description	Epitope Sequence	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
VSTB70	Human IgG1/kappa		GYTFSNYW	ILPGSGNV	ATPPHYYGYDYYDVNY	QSLLDSDGKTY	LVS	WQGTHFPQT	EVQLVQSGAEVKKPGATVKISCKVSGYTFSNYWIEWVQQAPGKGLEWMGEILPGSGNVHYNEKFKGRVTITADTSTDTAYMELSSLRSEDTAVYYCATPPHYYGYDYYDVNYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DVVMTQSPLSLPVTLGQPASISCKSSQSLLDSDGKTYLNWFQQRPGQSPRRLIYLVSELDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPQTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB71	Human IgG1/kappa		GYVFSRSW	IYPGDGDT	ARRWFL	QSLLNSGDQKSY	GAS	QNDHSYPLT	QVQLVQSGAEVKKPGSSVKVSCKASGYVFSRSWINWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTITADESTSTAYMELSSLRSEDTAVYYCARRWFLWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGDQKSYLAWYQQKPGQPPKLLIYGASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQNDHSYPLTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB72	Human IgG1/kappa		GFTFSSYA	ISSGGSHT	ARRGNLYDGPY	SSVSH	DTS	QQWNFYPFT	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVAEISSGGSHTYYPDTVTGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARRGNLYDGPYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPATLSLSPGERATLSCSASSSVSHMYWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQWNFYPFTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB73	Human IgG1/kappa		GYTFTDYV	IYPGSGNT	ARVLVSVMDY	SSINY	DTS	HQRSSYPWT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYVISWVRQAPGQGLEWMGEIYPGSGNTYYYEKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARVLVSVMDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPDFQSVTPKEKVTITCSASSSINYITWYQQKPDQSPKLLIKDTSKLASGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQRSSYPWTFGQGTRLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB74	Human IgG1/kappa		GYIFTDYN	INPKYDST	AADGSSAMDY	QSLLNSGHQKNY	GAS	QNDHRYPLT	QMQLVQSGPEVKKPGTSVKVSCKASGYIFTDYNIDWVRQARGQRLEWIGDINPKYDSTRYNQKFKGRVTITRDMSTSTAYMELSSLRSEDTAVYYCAADGSSAMDYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGHQKNYLAWYQQKPGQPPKLLIYGASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQNDHRYPLTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4UU

mAb ID	Description	Epitope Sequence	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		GFNIKDYY	IDPENGNT	ARDYGYFDYW	SSVIY	STS	QQRSSYPHT	QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDYYIHWVRQAPGQGLEWMGWIDPENGNTIYDPKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDYGYFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DVVMTQSPAFLSVTPGEKVTITCSAGSSVIYMYWYQQKPDQAPKLLIKSTSNLASGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQRSSYPHTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB76	Human IgG1/kappa		GYTFTDYW	IYPSHSYT	ARGGYRYPYYAMDY	ENIYGA	GAT	QNVLSTPYT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYWINWVRQAPGQGLEWMGNIYPSHSYTNYNQEFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGYRYPYYAMDYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	AIQLTQSPSSLSASVGDRVTITCGASENIYGALNWYQQKPGKAPKLLIYGATNLADGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQNVLSTPYTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB78	Human IgG1/kappa		GYTFTNYW	INPSSGYT	ARDGGSVLFGY	QSLLNSGIRKNY	SAS	KQSYNLYT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLEWMGYINPSSGYTEYNQKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDGGSVLFGYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGIRKNYLAWYQQKPGQPPKLLIYSASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLYTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB79	Human IgG1/kappa		AYSITSDYA	ITYSGST	ARSFGY	QSIGTS	YAS	QQINSWPTT	QVQLQESGPGLVKPSETLSLTCAVSAYSITSDYAWNWIRQPPGKGLEWIGYITYSGSTRYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSFGYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVMTQSPATLSVSPGERATLSCRASQSIGTSIHWYQQKPGQAPRLLIYYASESISGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQINSWPTTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB80	Human IgG1/kappa		GFNIKDYY	IDPENGDT	ARDMGSSYVY	SSVIY	STS	QQRSSYPFT	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQGLEWMGWIDPENGDTEYAPKFQDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDMGSSYVYWGRGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DVVMTQSPAFLSVTPGEKVTITCSASSSVIYMHWYQQKPDQAPKLLIKSTSNLASGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQRSSYPFTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4VV

mAb ID	Description	Epitope Sequence	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
VSTB81	Human IgG1/kappa		GFSLSTSGMG	IYWDDDK	ARRPDYFGSSYVD	ESVDTYGNSF	LAS	QQNNEDPWT	QVTLKESGPALVKPTQTLTLTCTFSGFSLSTSGMGVSWIRQPPGKALEWLAHIYWDDDKRYNPSLKSRLTISKDTSKNQVVLTMTNMDPVDTATYYCARRPDYFGSSYVDWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRASESVDTYGNSFMHWYLQKPGQPPQLLIYLASNLDFGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQNNEDPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB82	Human IgG1/kappa		GYSITSDYA	ITYSGST	ARSHYGSTYWYFDV	ESVEYYGTSL	AAS	QQTRKVPWT	QVQLQESGPGLVKPSETLSLTCAVSGYSITSDYAWNWIRQPPGKGLEWIGFITYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARSHYGSTYWYFDVWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRASESVEYYGTSLMQWYLQKPGQSPQLLIYAASNVESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQTRKVPWTFGQGTRLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB83	Human IgG1/kappa		GYTFTSYD	IYPGDGYT	ARWGYGSYAMDY	QSLVHSNGNTY	KVS	SQSTHVPPT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGWIYPGDGYTEYNEKFRGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARWGYGSYAMDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPPTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB84	Human IgG1/kappa		GYTFTSYW	INPSTGYP	ARSYYDYDGGAWFAY	ESVEYYGTSL	AAS	QQSRKVPST	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQGLEWMGYINPSTGYPGYNQKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSYYDYDGGAWFAYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRASESVEYYGTSLMQWYLQKPGQPPQLLIYAASNVESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSRKVPSTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB85	Human IgG1/kappa		GYTFTDYA	IDTYYGNT	ARGGGDALDY	QSVSND	YAS	QQGYTSLRT	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAMHWVRQAPGQGLEWMGVIDTYYGNTNYNQKFKGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGGDALDYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCKASQSVSNDVVWYQQKPGKAPKLLIYYASNRYIGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQGYTSLRTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4WW

mAb ID	Description	Epitope Sequence	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	IHYIGIT	AREDYDYDGVFAY	QSISNN	YAS	QQSNSWPHT	QVQLQESGPGLVKPSETLSLTCAVSGYSITSGYSWHWIRQPPGKGLEWIGYIHYIGITNNNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREDYDYDGVFAYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPATLSLSPGERATLSCRASQSISNNLHWYQQKPGQAPRLLIYYASQSISGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSNSWPHTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB88	Human IgG1/kappa		GFSLTNYD	IWTGGGT	AREGLLLPLY	QNVGTN	SAS	QQYNSYPLT	QVQLQESGPGLVKPSETLSLTCTVSGFSLTNYDISWIRQPPGKGLEWIGVIWTGGGTNYNSAFMSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREGLLLPLYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCKASQNVGTNVAWYQQKPGKVPKLLIYSASYRYSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQQYNSYPLTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB89	Human IgG1/kappa		GYTFTNFG	INTYTGEP	ARGAYYYGSRVWFAY	QNLVHSNGNTY	KVS	SQSSHVPYT	QVQLVQSGSELKKPGASVKVSCKASGYTFTNFGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCARGAYYYGSRVWFAYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPLSLPVTPGEPASISCTSSQNLVHSNGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSSHVPYTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB90	Human IgG1/kappa		GFSLTSSG	IWSGGNT	AREDYDYDWYFDV	ESVEYYGTSL	AAS	QQSRKVPWT	QVQLQESGPGLVKPSETLSLTCTVSGFSLTSSGVHWIRQPPGKGLEWIGVIWSGGNTDYNAAFISRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREDYDYDWYFDVWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRASESVEYYGTSLMQWYLQKPGQPPQLLIYAASNVKSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSRKVPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB91	Human IgG1/kappa		GYTFANFW	IFPGNSDT	ARELTGTYYFDY	SSVSY	SSS	HQWSGHFT	QVQLVQSGAEVKKPGASVKVSCKASGYTFANFWMHWVRQAPGQGLEWMGAIFPGNSDTGYNQKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARELTGTYYFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	EIVLTQSPATLSLSPGERATLSCSATSSVSYMHWYQQKPGQAPRLLIYSSSNLASGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCHQWSGHFTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4XX

mAb ID	Description	Epitope Sequence	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
VSTB92	Human IgG1/kappa		GYTFANYL	IYPGGGFI	ARRFDYGGYFFDY	QSIVHSNGNIY	KVS	FQGSHVPWT	QVQLVQSGAEVKKPGASVKVSCKASGYTFANYLIGWVRQAPGQRLEWMGDIYPGGGFISYNEKFKGRVTITRDTSASTAYMELSSLRSEDTAVYYCARRFDYGGYFFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNIYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB93	Human IgG1/kappa		GFSITNYD	IWTGGGT	ARDRSPYFGYDY	QSLVHSNGNTY	KVS	SQSTHVPWT	QVQLQESGPGLVKPSETLSLTCTVSGFSITNYDISWIRQPPGKGLEWIGVIWTGGGTNYNSAFMSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDRSPYFGYDYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQTPLSLSVTPGQPASISCRSSQSLVHSNGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB94	Human IgG1/kappa		GYSITSDYA	MMYSGSA	ARFDHYYGRFDY	SSVSY	EIS	QQWNYPLFT	QVQLQESGPGLVKPSETLSLTCAVSGYSITSDYAWTWIRQPPGKGLEWIGYMMYSGSASYNPSLKGRVTISVDTSKNQFSLKLSSVTAADTAVYYCARFDHYYGRFDYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	AIQLTQSPSSLSASVGDRVTITCSASSSVSYIHWYQQKPGKAPKLLIYEISKLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQWNYPLFTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB95	Human IgG1/kappa	PVDKGHDVTF and RRPIRDLTFQDL	GFTFRNYG	IISGGSYT	ARIYDHDGDYYAMDY	QSIVHSNGNTY	KVS	FQGSHVPWT	EVQLVESGGGLVQPGGSLRLSCAASGFTFRNYGMSWVRQAPGKGLEWVASIISGGSYTYYPDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARIYDHDGDYYAMDYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIVMTQSPLSLPVTPGEPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHVPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB96	Human IgG1/kappa		GYTFTSYD	IYPGDGST	AREGITPFAY	KSISKY	SGS	QQHNEYPWT	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGRIYPGDGSTKYNEKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCAREGITPFAYWGQGTTVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	AIQLTQSPSSLSASVGDRVTITCRASKSISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPWTFGQGTKLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 4YY

mAb ID	Description	Epitope Sequence	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
VSTB97	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARSSYGWSYEFDY	QSISSY	AAS	QQSYSTPLT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSSYGWSYEFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB98	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARSTVGWSYEFDY	QSISSY	AAS	QQSYSTPLT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSTVGWSYEFDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
VSTB99	Human IgG1/kappa		GGTFSSYA	IIPIFGTA	ARHVLGWVLELDY	QSISSY	AAS	QQSYSTPLT	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARHVLGWVLELDYWGQGTLVTVSS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGQGTKVEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 5

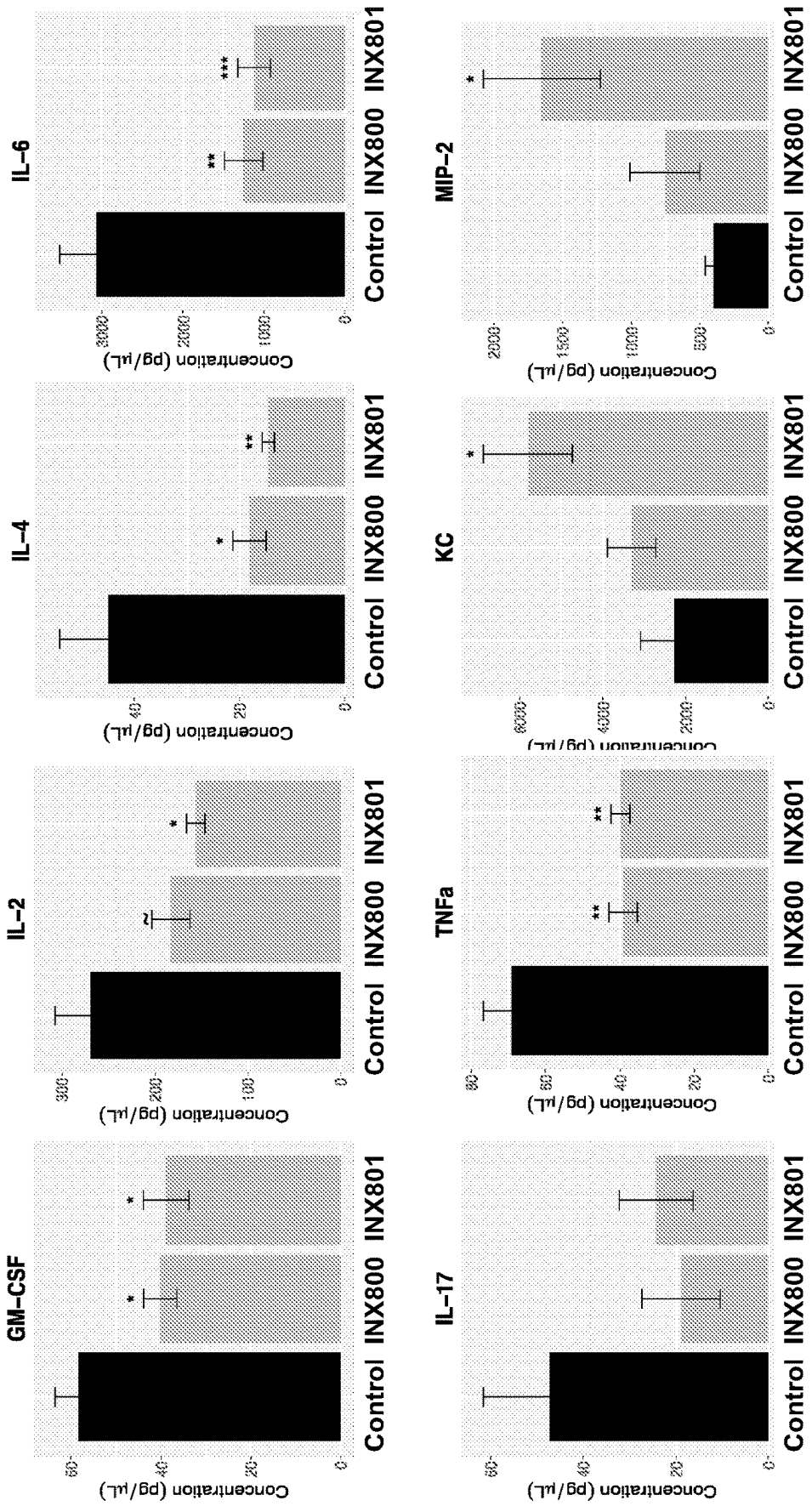

GM-CSF
IL-2
IL-4
IL-6
IL-17
TNFa
KC
MIP-2
Concentration (pg/μL)
Control
INX800
INX801

FIGURE 6:

Effects Of Agonist Anti-Human VISTA Abs In A GVHD Animal Model.

.

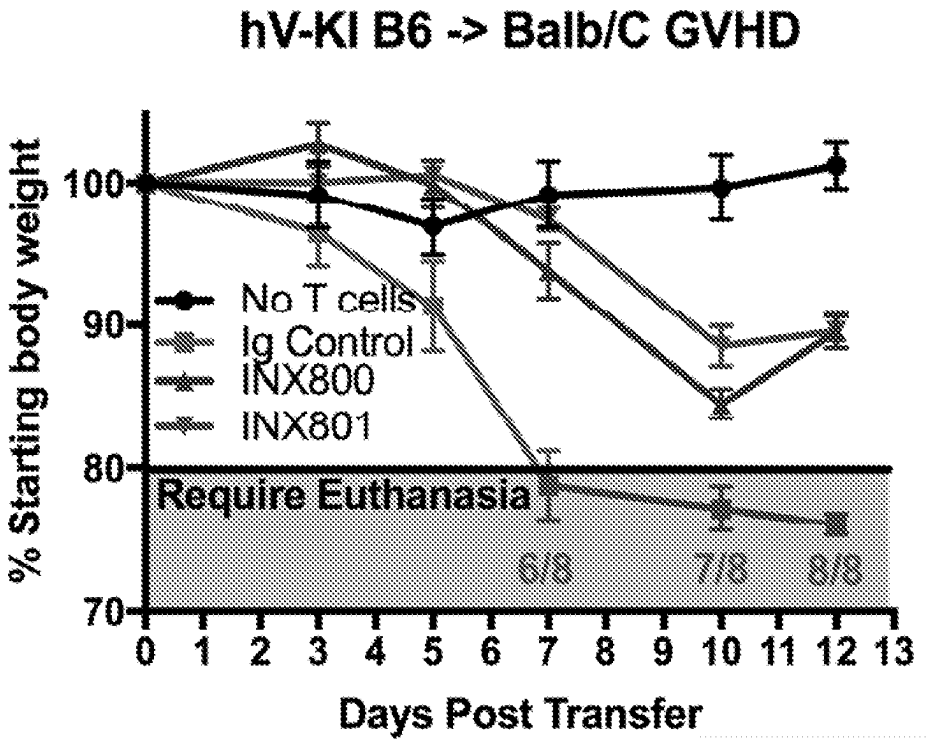


FIGURE 7
Agonist VISTA Antibodies SuppressCD3 driven T cell response

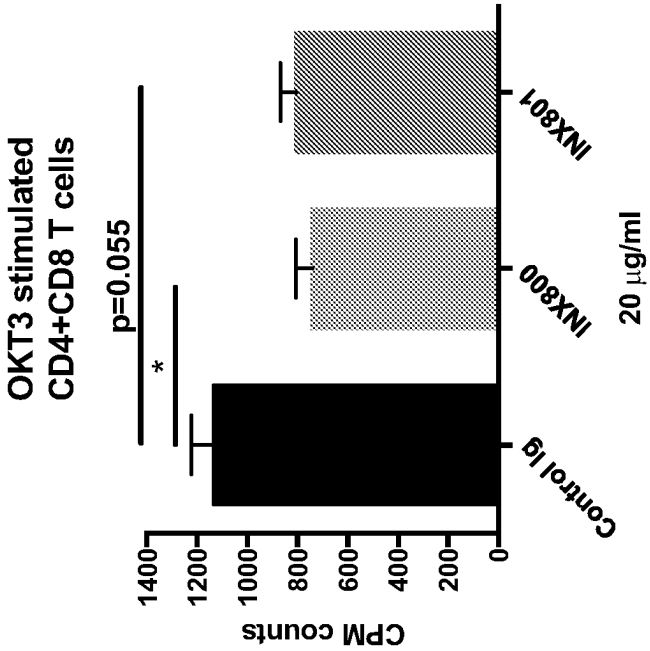


FIGURE 8

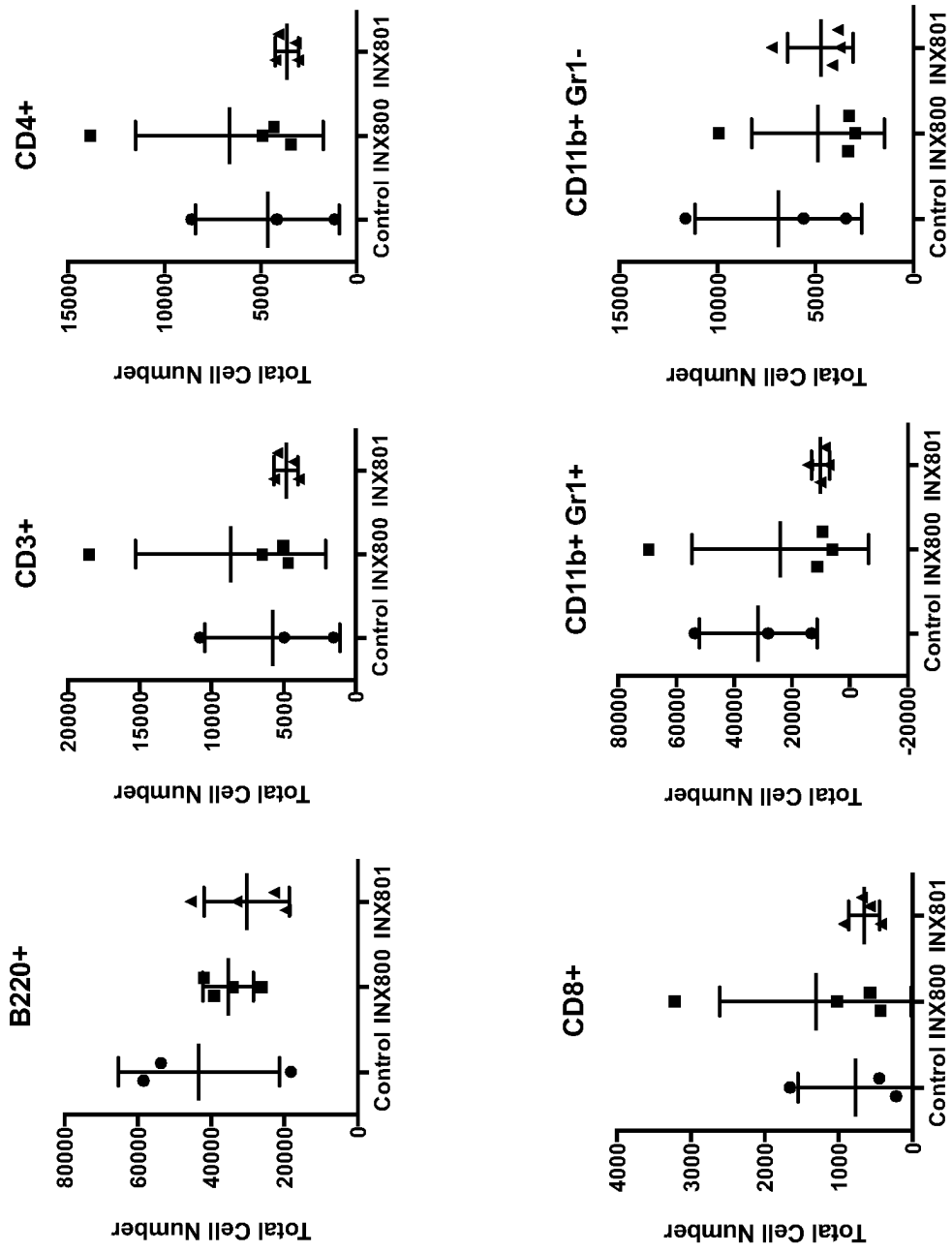

B220+
CD3+
CD4+
CD8+
CD11b+ Gr1+
CD11b+ Gr1-
Total Cell Number
Control INX800 INX801

FIGURE 9: Effects of VISTA Abs in ConA Assay and on Select Proinflammatory Cytokines and Markers

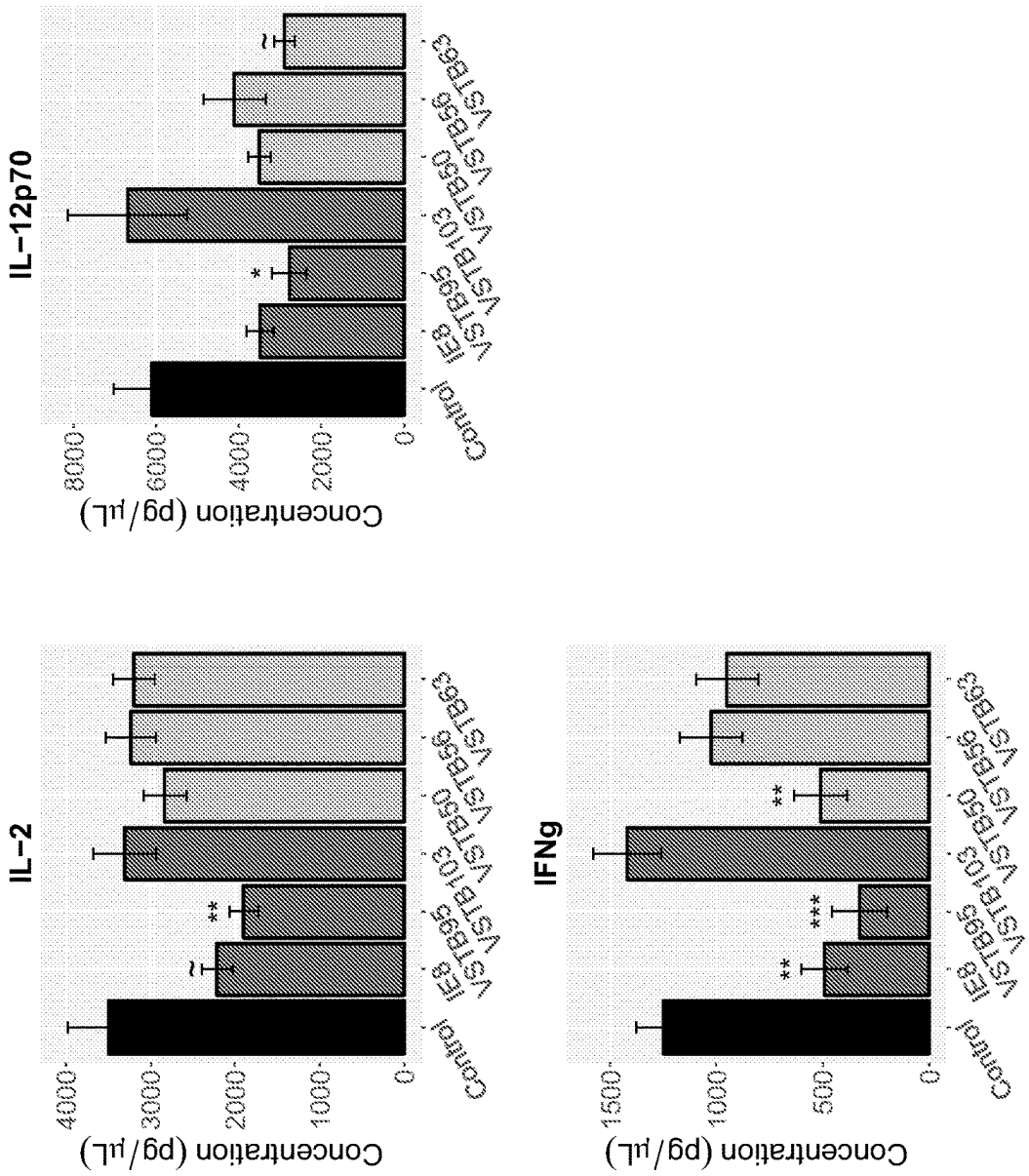


FIGURE 10

FIG. 10A

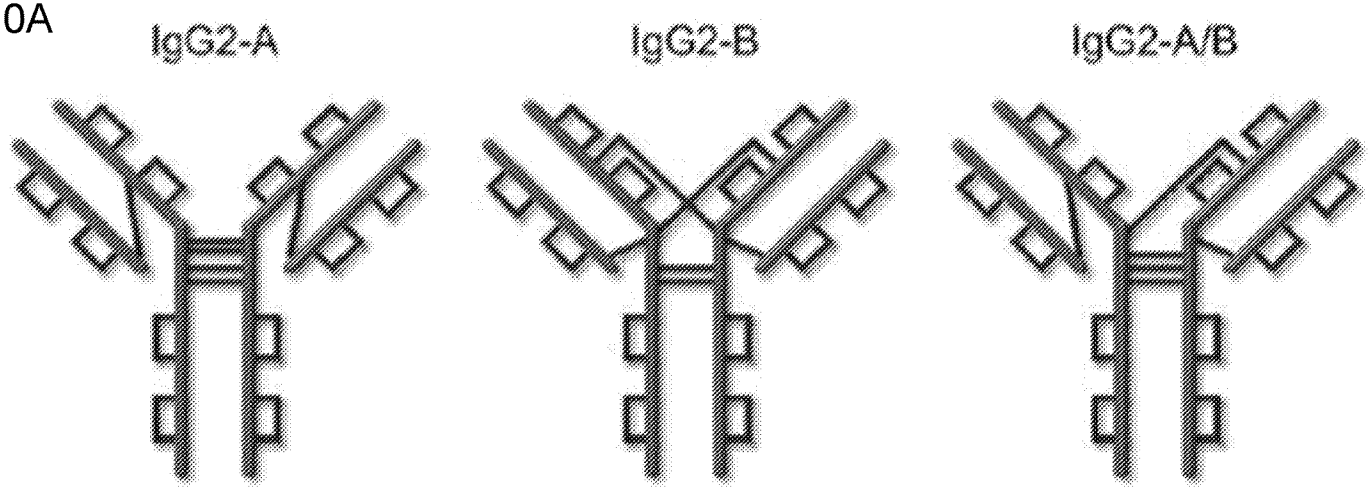


FIG. 10B

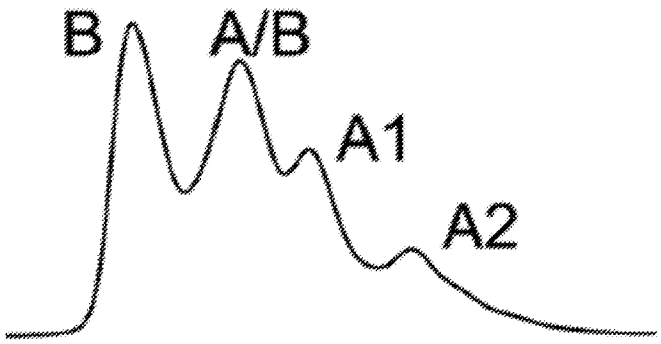


FIG. 10C

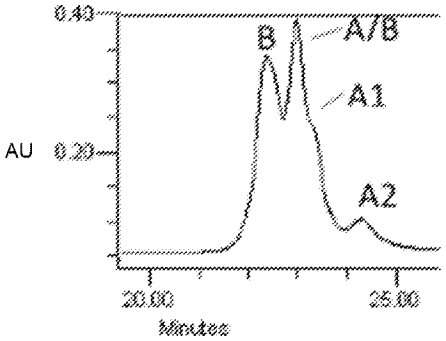


Figure 10: IgG2 Isoforms.

FIGURE 11

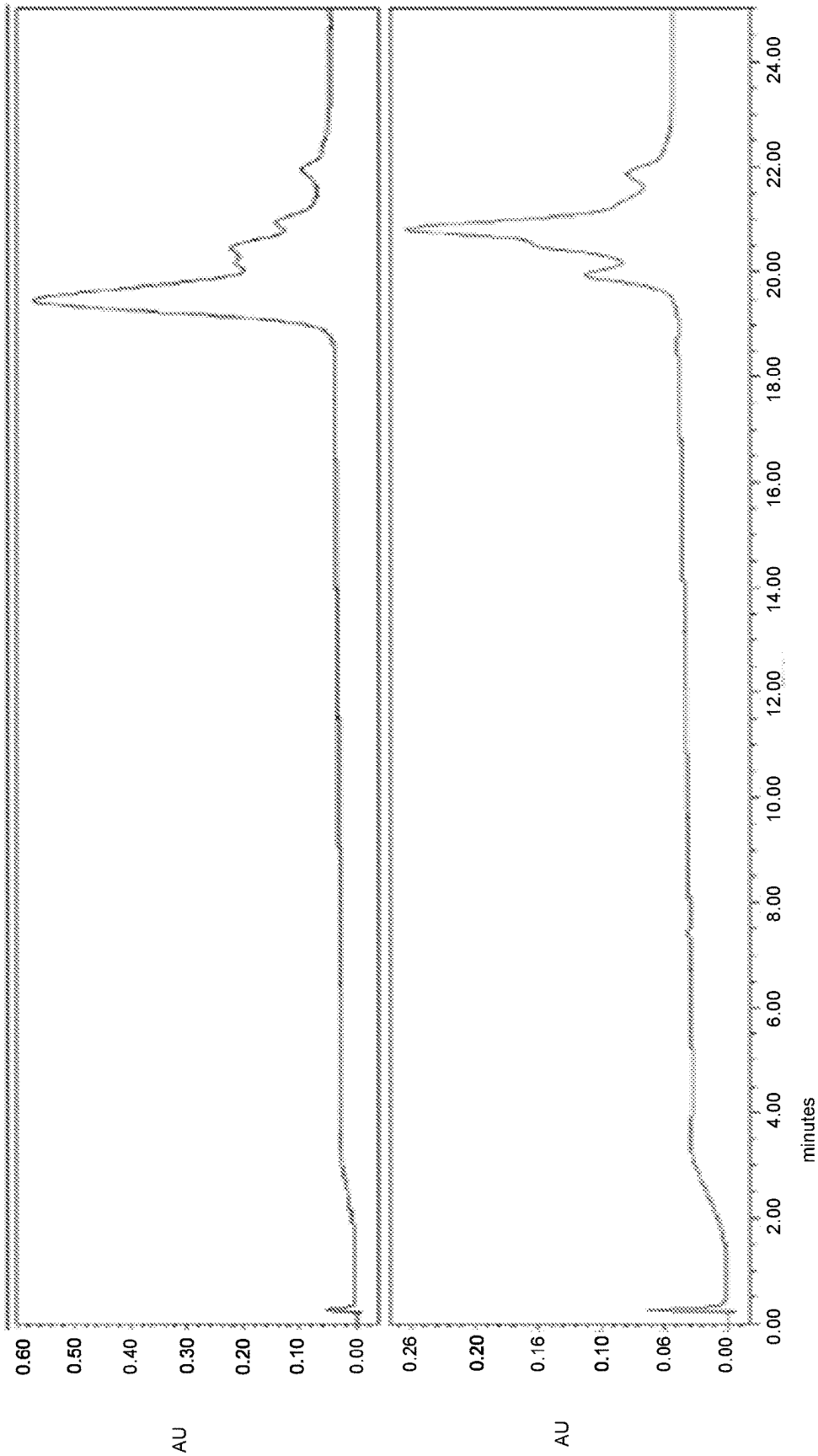


Figure 11: Chemical enrichment of IgG2 A or B isoforms.

FIGURE 12

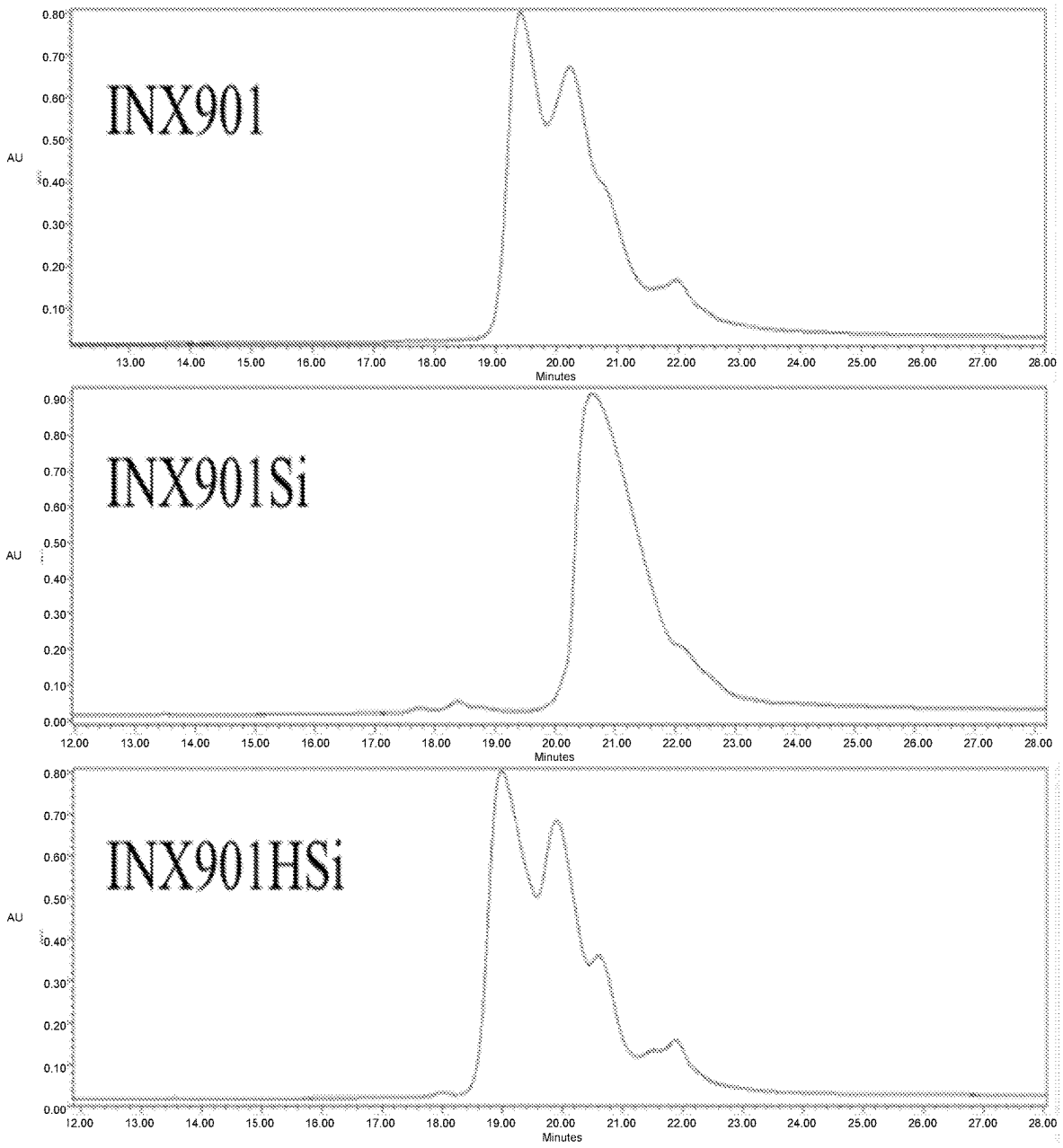


Figure 12: Comparison of INX901 Fc-silent variants with respect to disulfide shuffling.

FIGURE 13

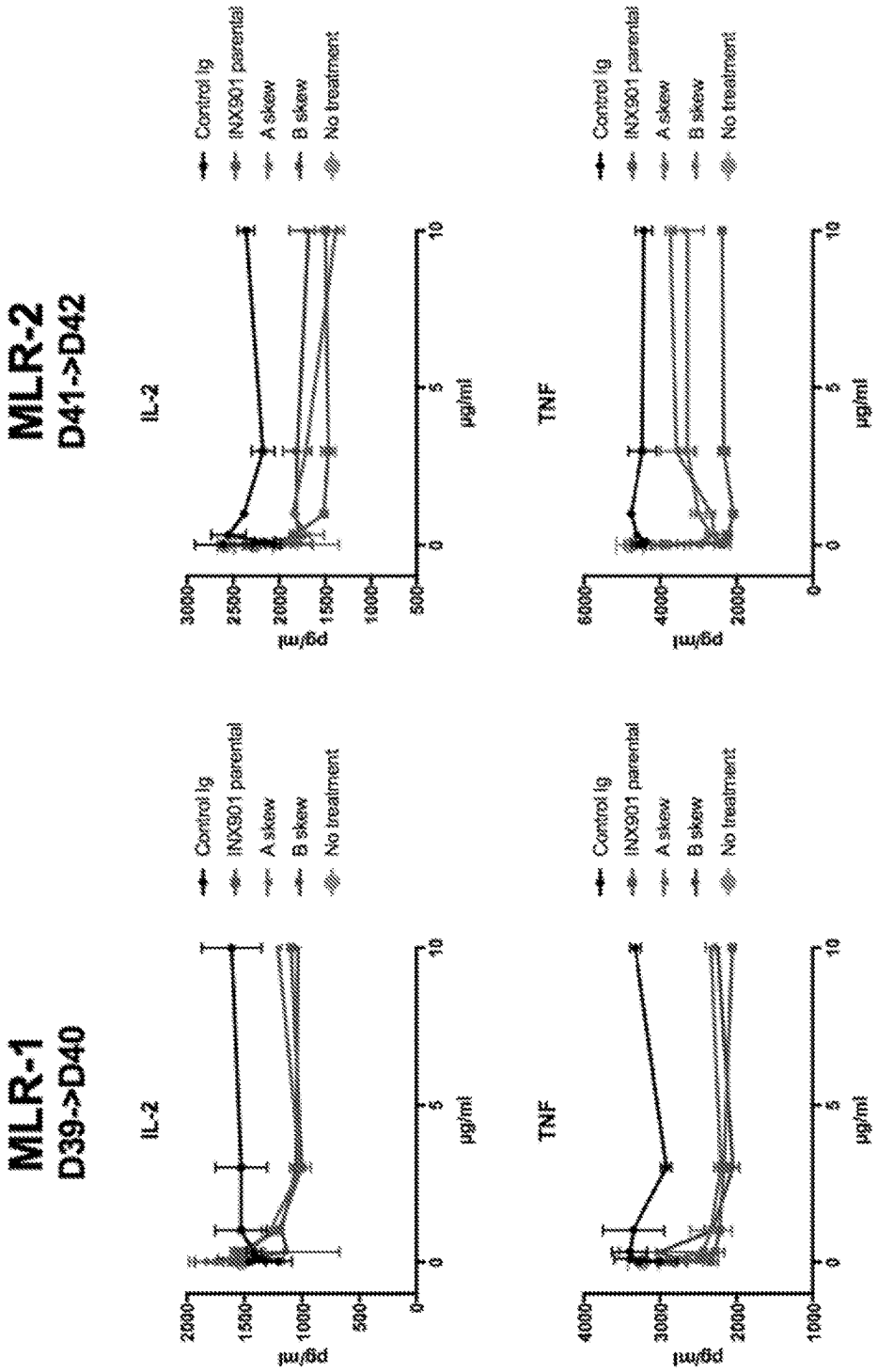


Figure 13. Biochemically skewed INX901 forms can still reduce cytokine production in the MLR.

FIGURE 14

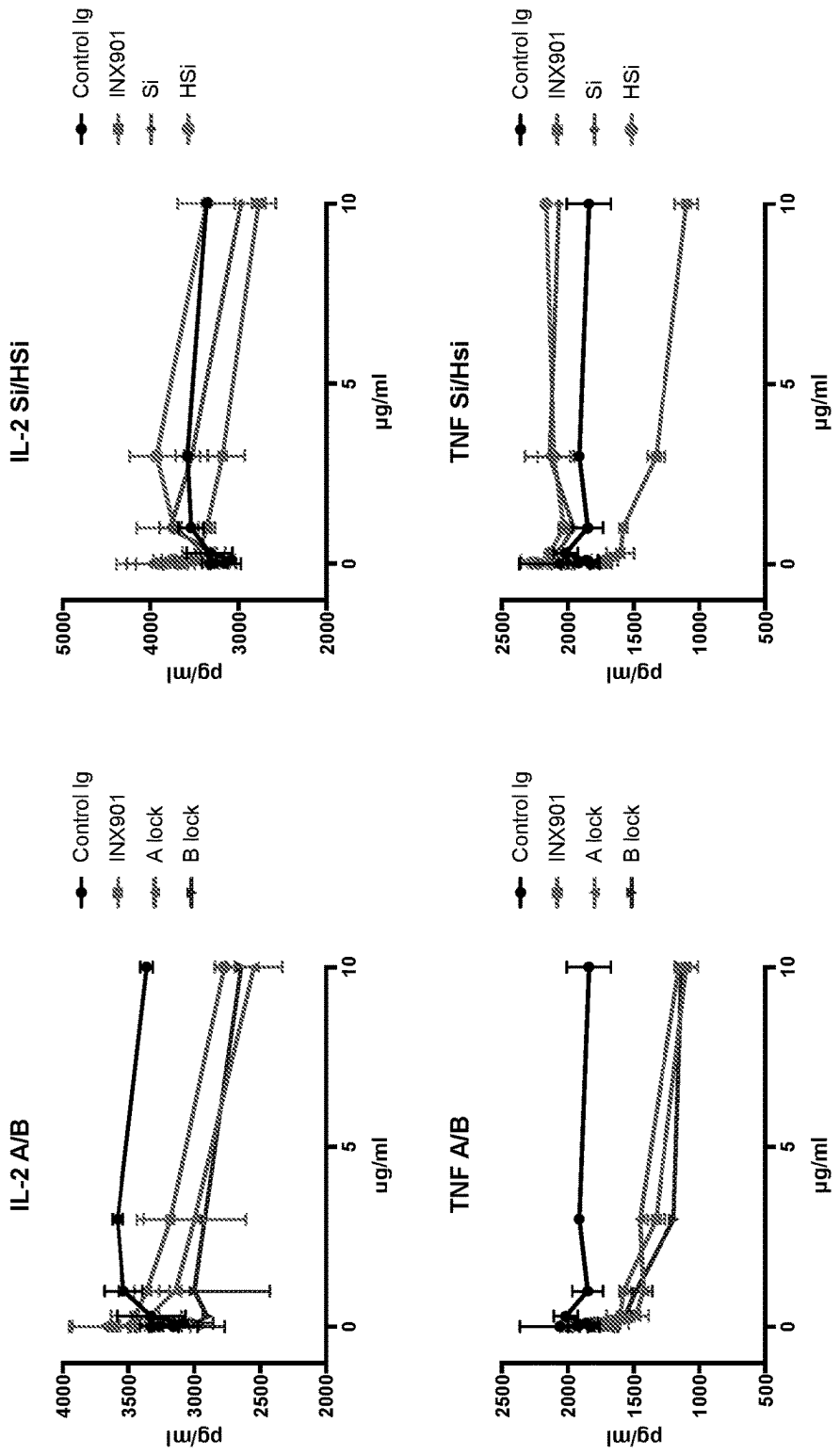


Figure 14. Genetically locked INX901 forms can still reduce cytokine production in the MLR, but Fc silent variants cannot.

FIGURE 15

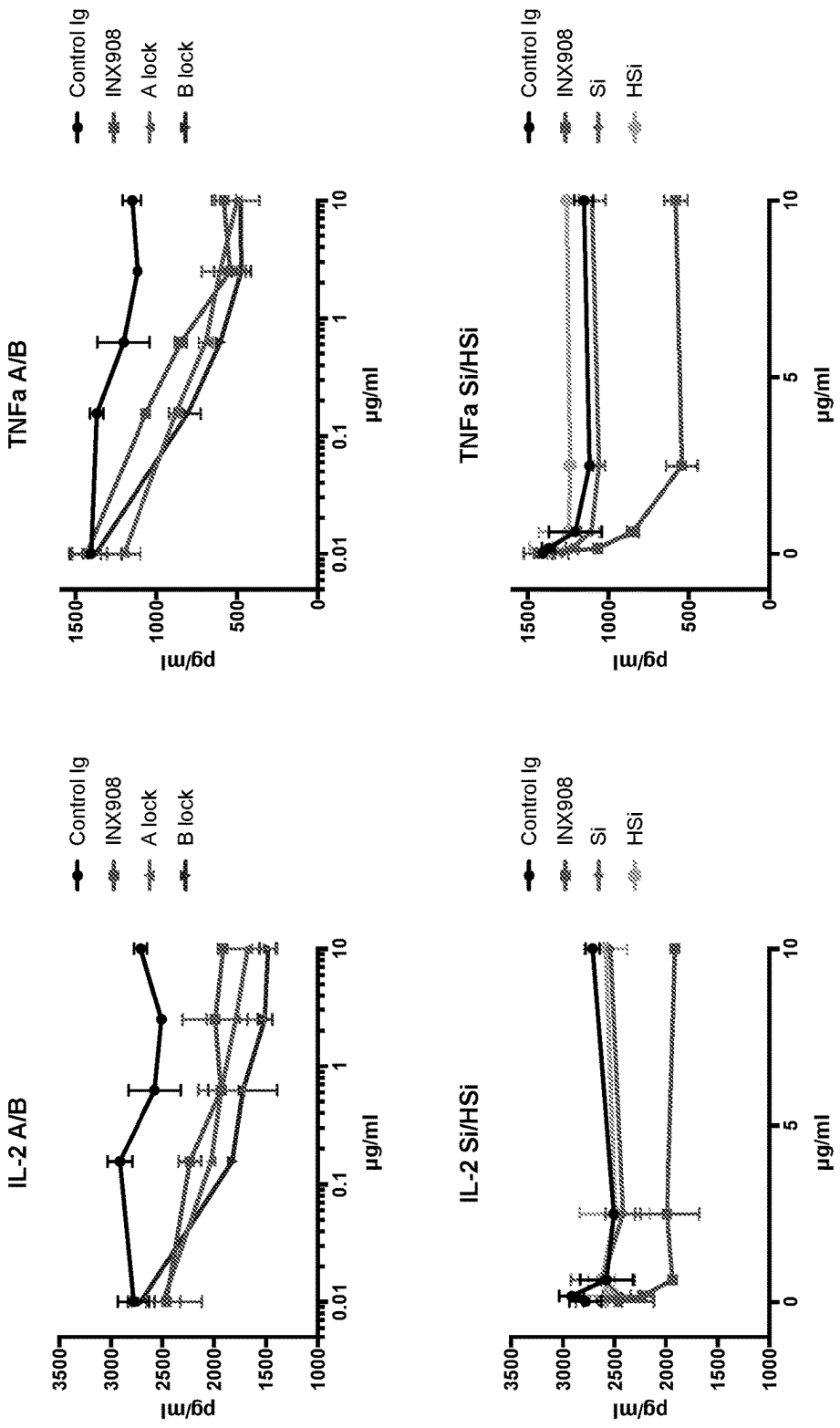


Figure 15. Genetically locked INX908 forms can still reduce cytokine production in the MLR, but Fc silent variants cannot

FIG 16

Pepscan uses peptide arrays to determine both linear and discontinuous epitopes

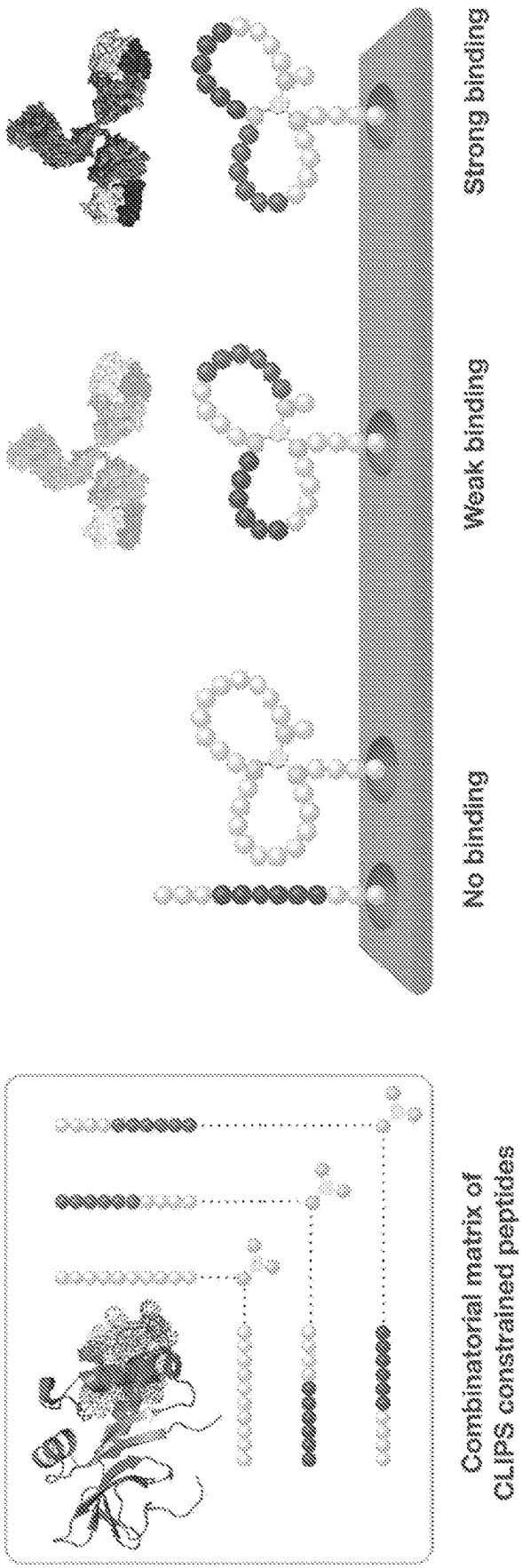


FIG 17 All suppressive INX abs bind same core seq

HDX/Crystal Results (Above ECD Sequence)
Bold indicates crystal support

Green = Potent Agonist
Red = Stability Issues (not potent)
1/2 = Competitive Binding Bin

Pepscan Results (Below ECD Sequence)
Bold indicates dominantly recognized core sequences
Underlined indicates strong linear epitope recognition
*Important residues

FIG 18: Epitope Mapping Summary

	mGVHD	NSG	MLR	CAIA	Epitope EQVT?
INX800	+/-	-		-	no
INX803	+				yes
INX804	+				yes
INX900	-	-	-	+	yes
INX901	+	+	+	+	yes
INX902	+	+	+	+	yes
INX903	+	+	+	+	yes
INX904	-	-			yes
INX905		+	+		yes
INX906	+	+	+	+	yes
INX907		-			yes
INX908	+	+	+	+	yes

FIG 19: VISTA Epitopes

HDX/Crystal Results

Bold indicates crystal support

VSTB112/95 (INX903[1])	LLGPVDKG**HDVTFY** TWYR$SR---**QTCSERRP**IRQLT**FQDLHLH** TMR **LVVEIRHHHSEHRVHGAMEL**
VSTB50/60 (INX900[2]) HDX only	NLTLLDSGL VQTGKDAPSNC
VISTA ECD	FKVATPYSLYVCPEGQNVTLTCRLLGPVDKGHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASDHHGNFSITMRNLTLLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQESE
INX800[1]	TCRLLGPVDKG HGGHQAA SASDHHGNFS **HHHSEHRVHGAM**
INX803[1] **INX804[2]**	**LTCRLLGPV** EVQTCSERRPIR HLHHGGHQAA SDHHGNFS HHHSEHRVHGAM
~~INX900[2]~~	LLGPVDKGHDVTFYK **EVQTCSERRPIR** LAQRHGLESASDHHG HHHSEHRVHGAM
~~INX901[2]~~ **INX904[1]** ~~INX907[2]~~ ~~INX902[2]~~ ~~INX906[2]~~ ~~INX908[1]~~	**(6/7/8) NVTLTCRLLGPV **(4/7) **EVQTCSERR** SDHHGNFS HHHSEH
~~INX903[1]~~	**EVQTCSERR** TFQDLHLHHGGHQAA CLVVEIRHHHSEH **
~~INX905[1]~~	TCRLLGPVDKG **EVQTCSERRPIR** SDHHG HHHSEHRVHGAM

Green = Potent Agonist

Red = Stability Issues (not potent)

1/2 = Competitive Binding Bin

Pepscan Results

Bold indicates dominantly recognized core sequences

Underlined indicates strong linear epitope recognition

*Important residues

FIGURE 20

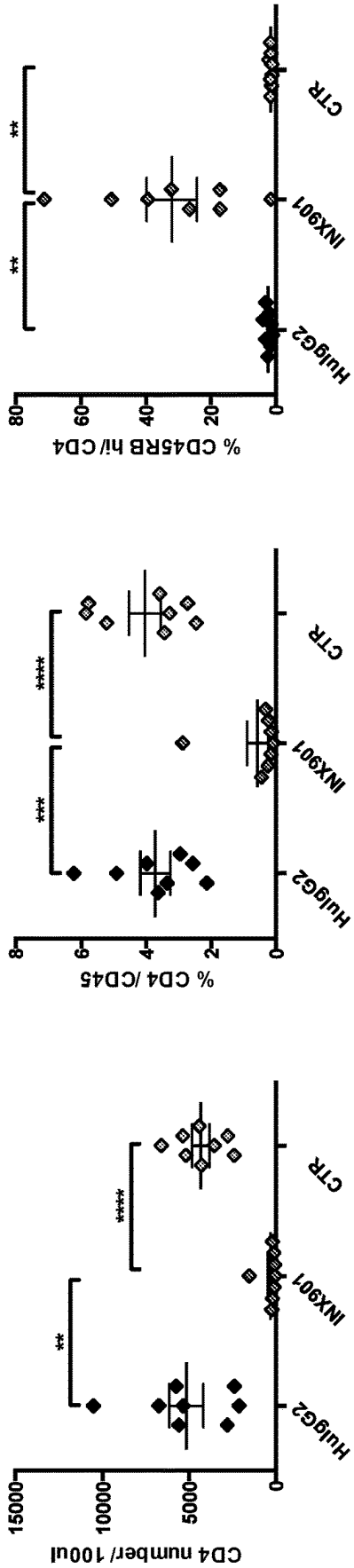


Figure 20: Changes in CD4 T cells in peripheral blood.

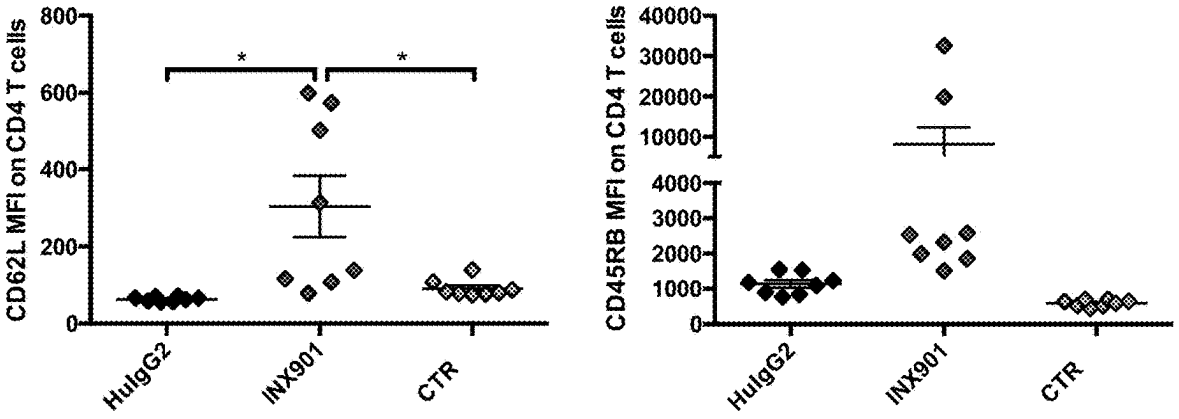


Figure 21: Changes in CD4 T cell activation status in peripheral blood.

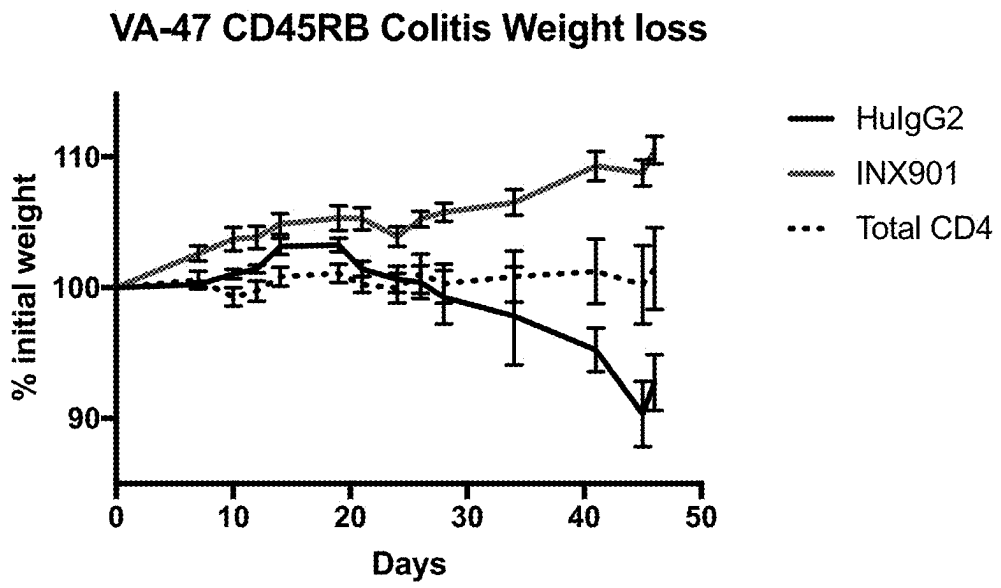


Figure 22: INX901 treatment prevents weight loss associated with colitis progression.

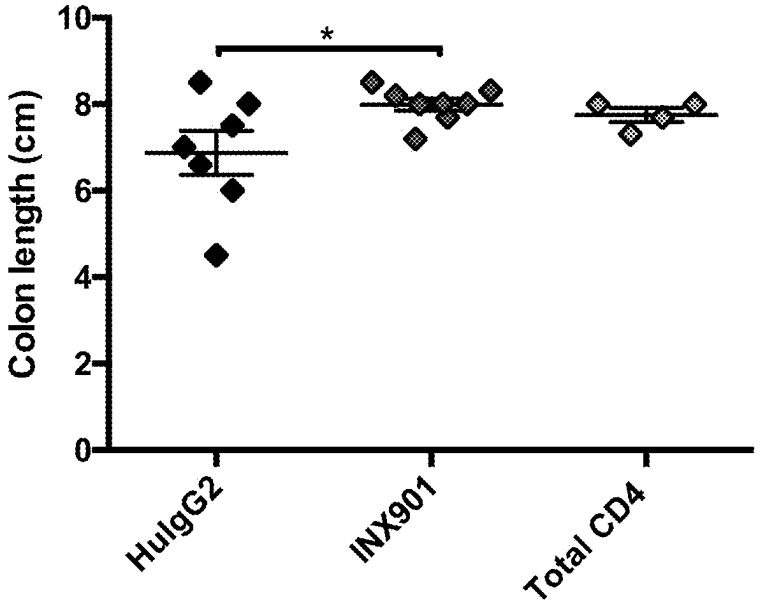


Figure 23: INX901 treatment prevented colon shortening.

FIGURE 24

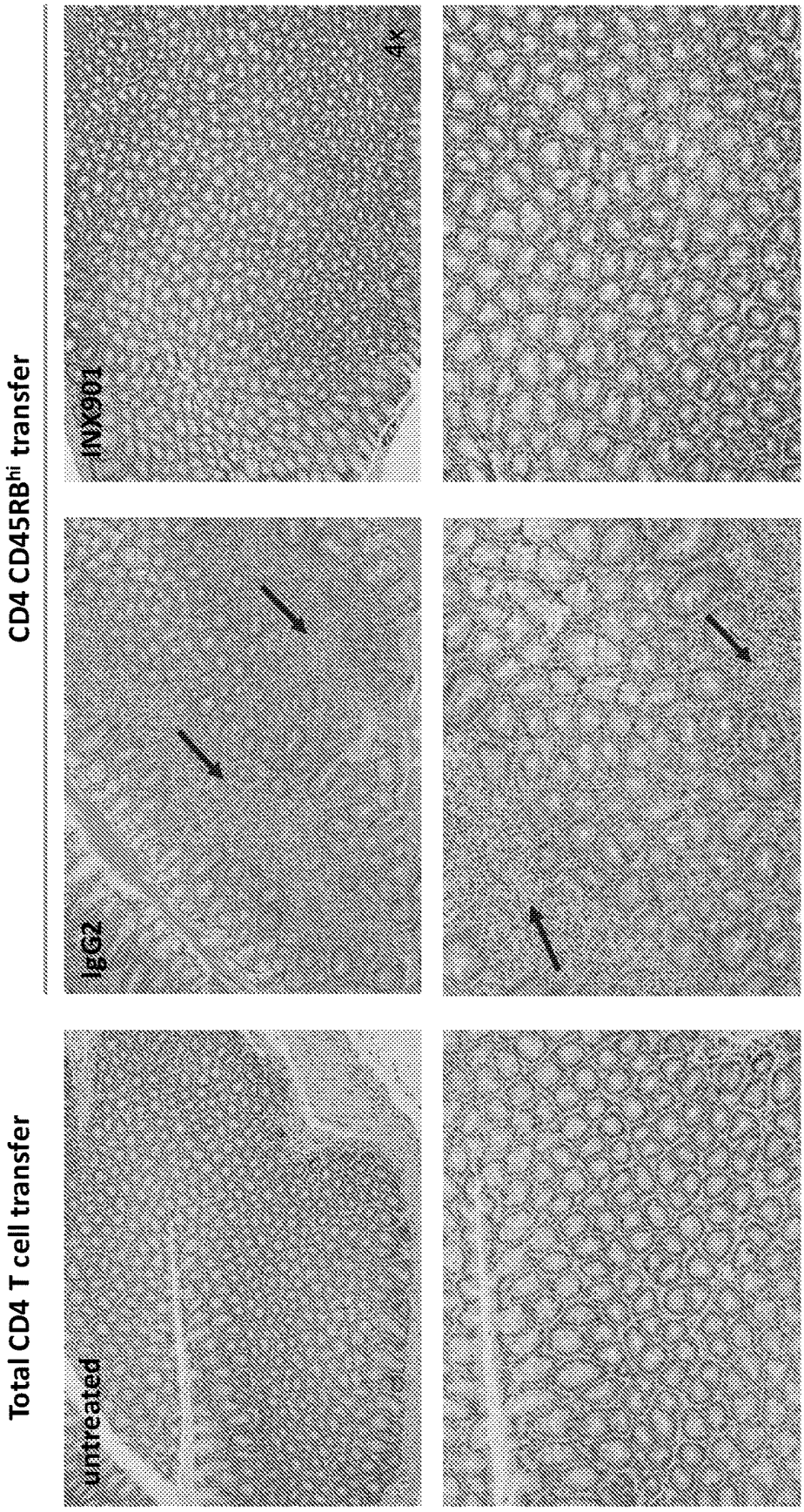


Figure 24: INX901 treatment prevented colitis development.

FIGURE 25

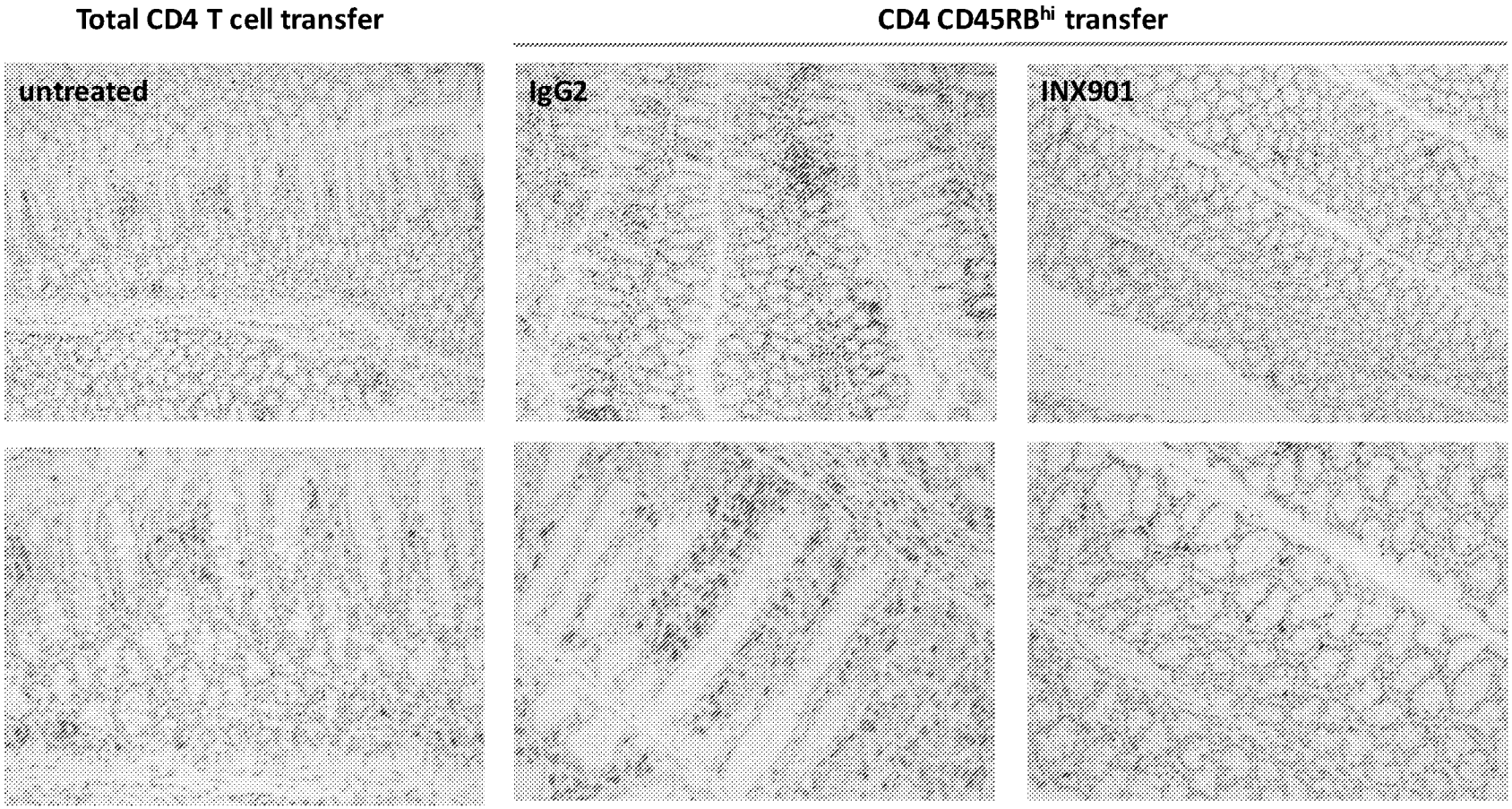


Figure 25: INX901 treatment prevented CD3+ T cell recruitment to the colon.

FIGURE 26

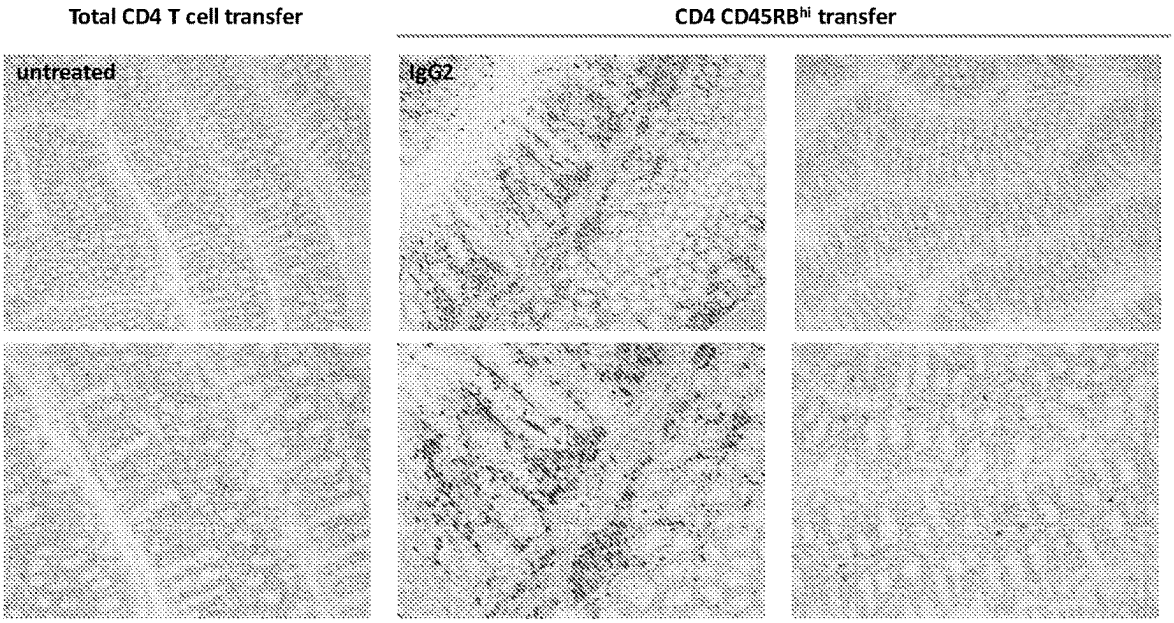


Figure 26: INX901 treatment prevented myeloid (CD11b+) cell recruitment to the colon.

FIGURE 27

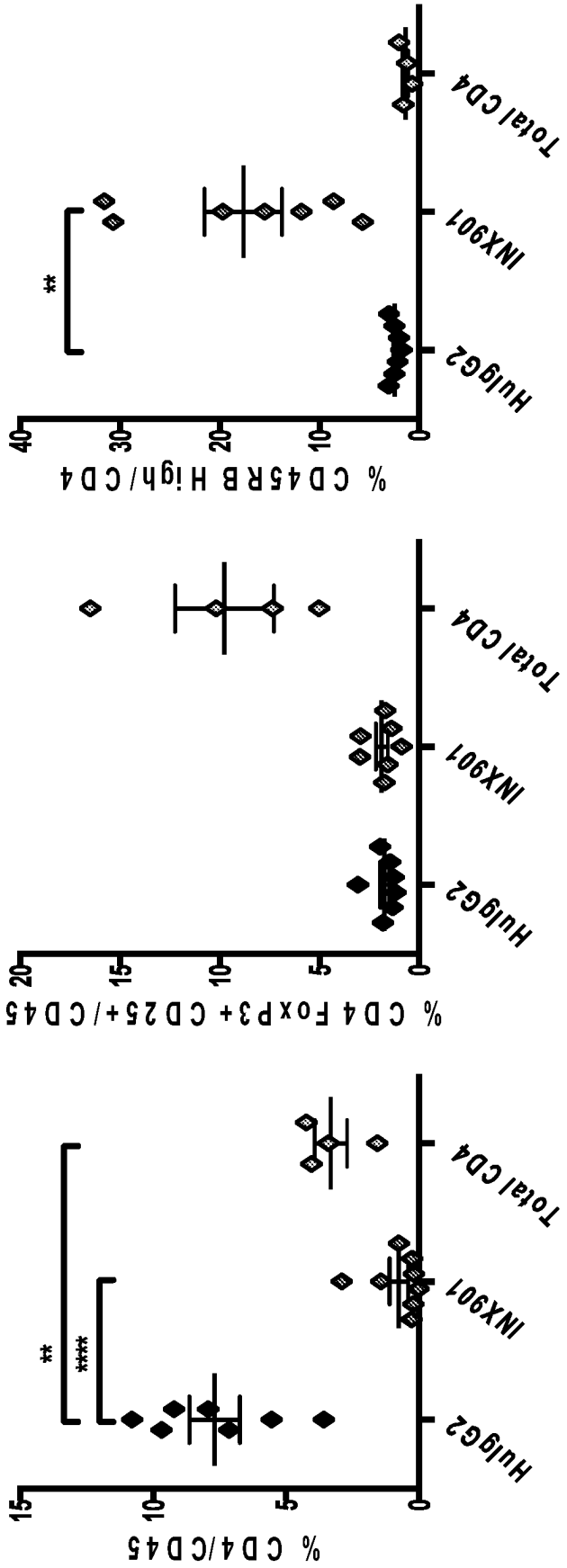
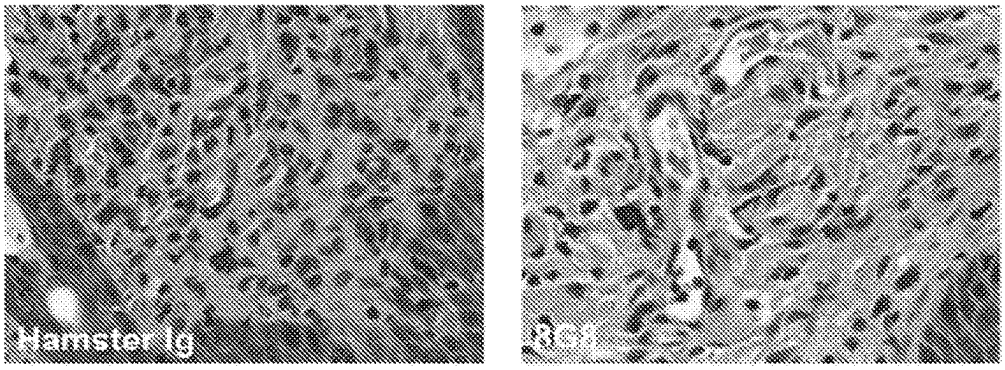


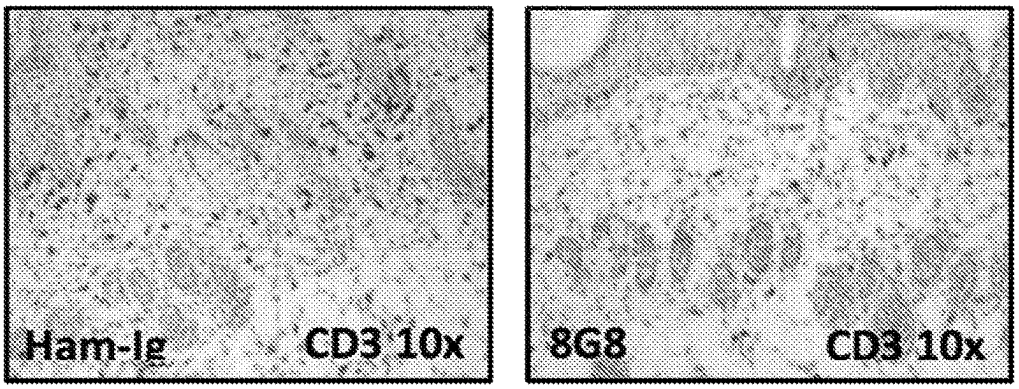
Figure 27: Changes in spleen CD4 T cells.

FIGURE 28



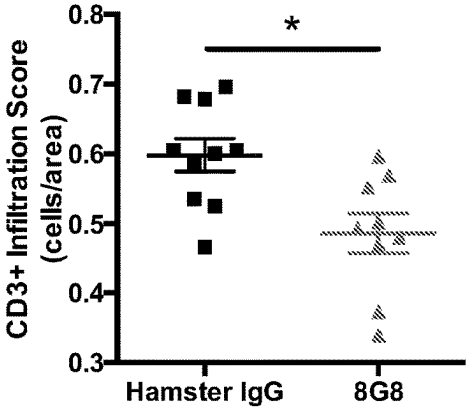
H&E Analysis of skin sections from the IMQD treated mice. The Hamster Ig image is on the left and the 8G8 treated group is on the right.

FIGURE 29



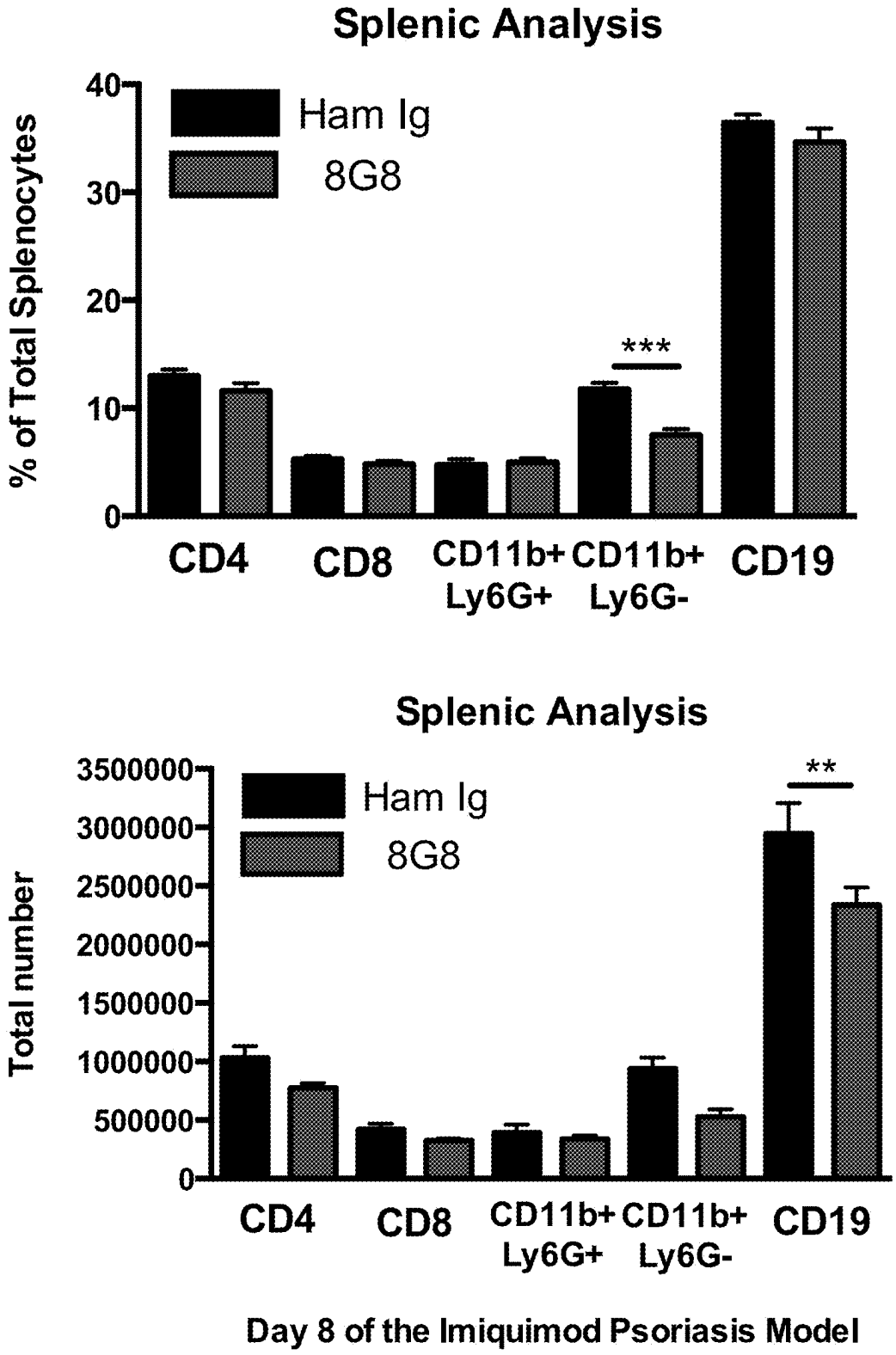
IH Analysis of skin sections from the IMQD treated mice. The Hamster Ig image is on the left and the 8G8 treated group is on the right.

FIGURE 30



Quantitative analysis of skin sections from the IMQD treated mice for CD3+ cells in the field of view.

FIGURE 31


Splenic Analysis
% of Total Splenocytes
40
30
20
10
0
Ham Ig
8G8
***
CD4
CD8
CD11b+ Ly6G+
CD11b+ Ly6G-
CD19
Splenic Analysis
Total number
3500000
3000000
2500000
2000000
1500000
1000000
500000
0
Ham Ig
8G8
**
CD4
CD8
CD11b+ Ly6G+
CD11b+ Ly6G-
CD19
Day 8 of the Imiquimod Psoriasis Model

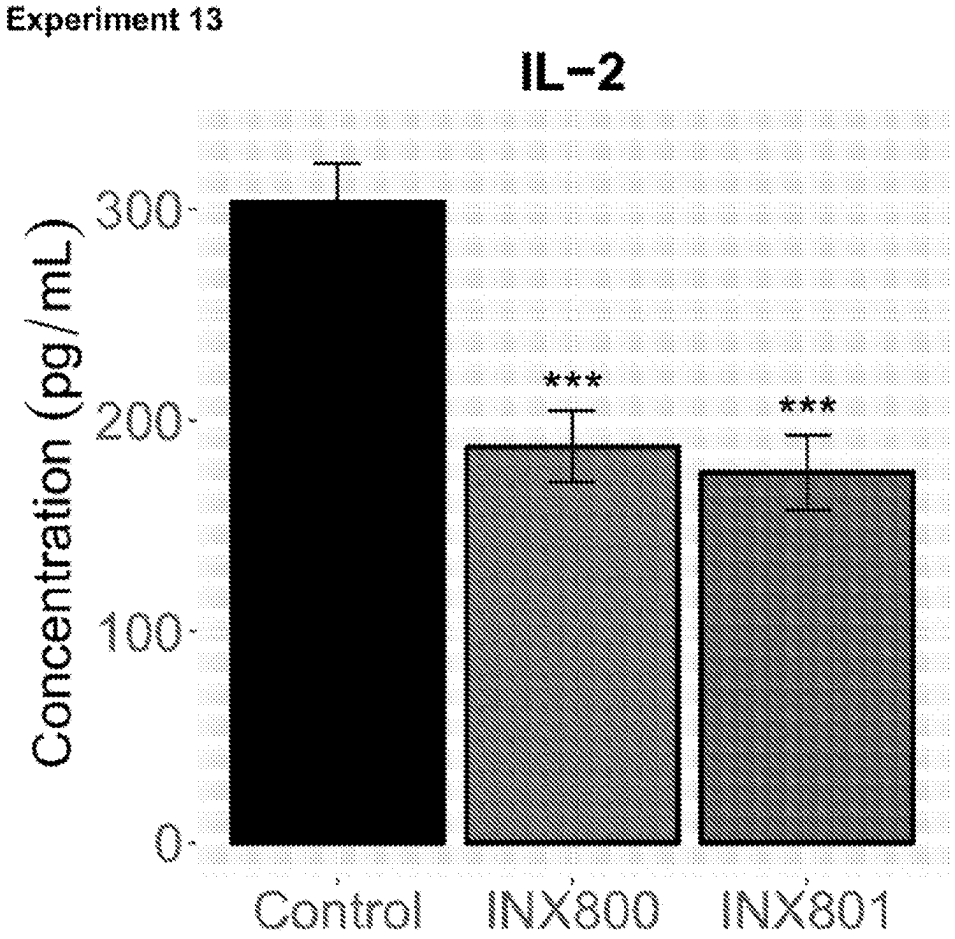

Experiment 13
IL-2
Concentration (pg/mL)
300
200
100
0
***
***
Control
INX800
INX801

FIGURE 32

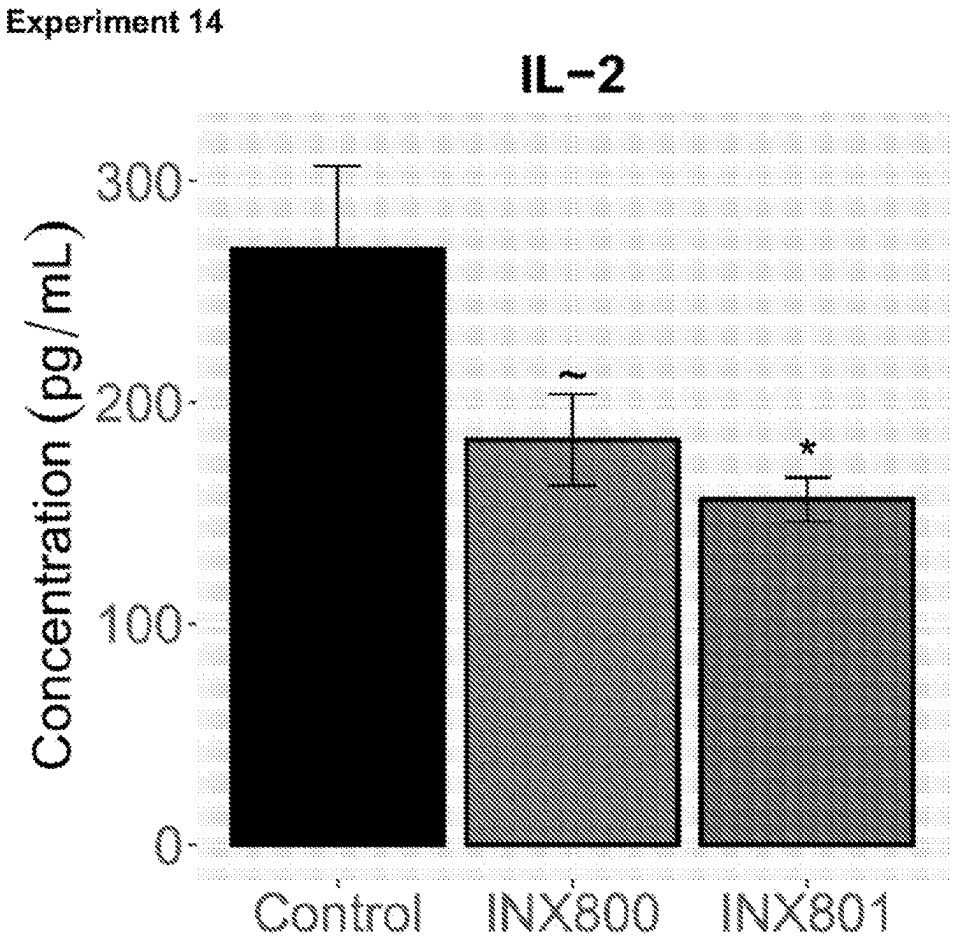

Experiment 14
IL-2
Concentration (pg/mL)
300
200
100
0
~
*
Control
INX800
INX801

FIGURE 33

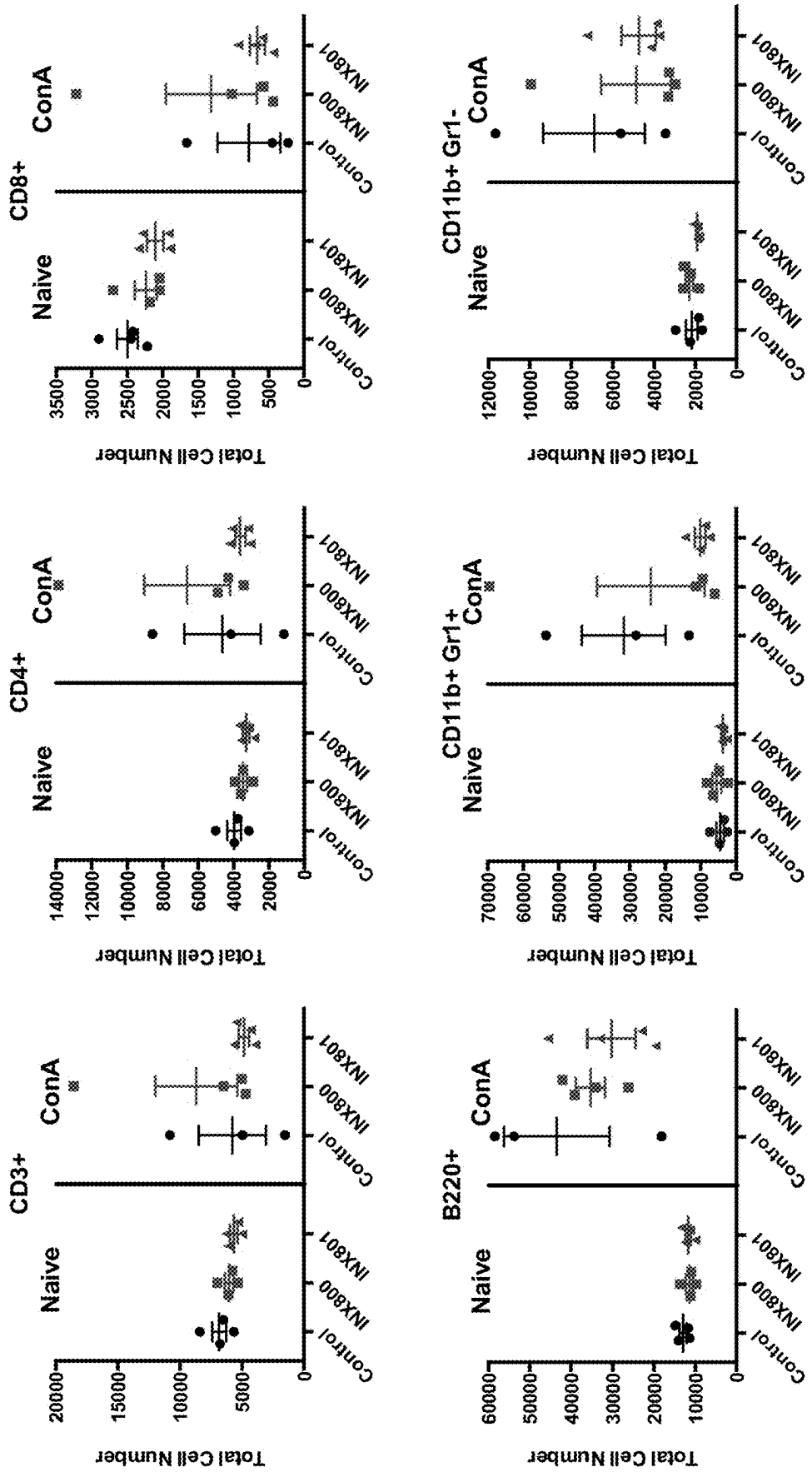


Figure 34. ALC counts from ConA-treated mice from Experiment 14 and naïve mice.

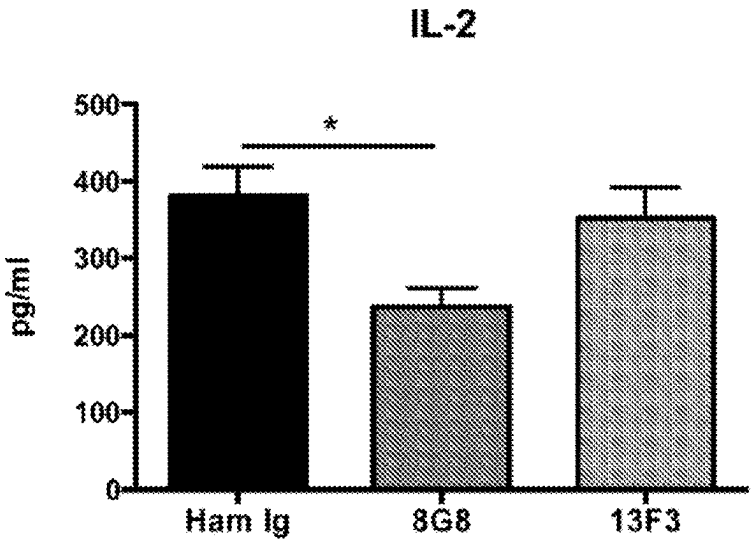
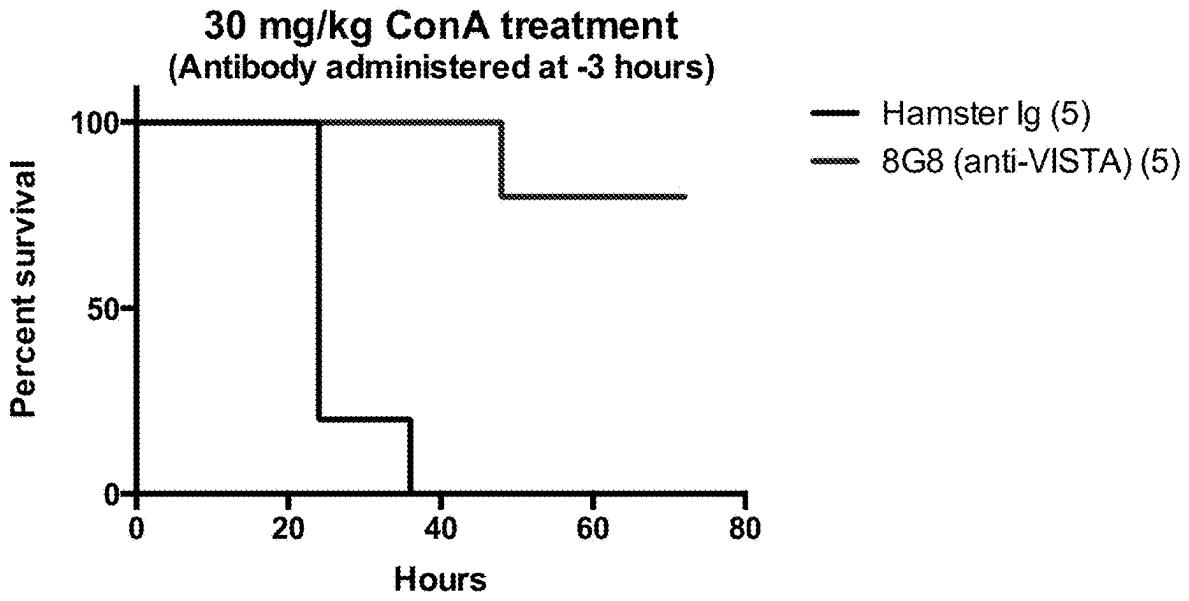


FIGURE 35

FIGURE 36



Kaplan Meier curves of the 30 mg/kg ConA treated mice.

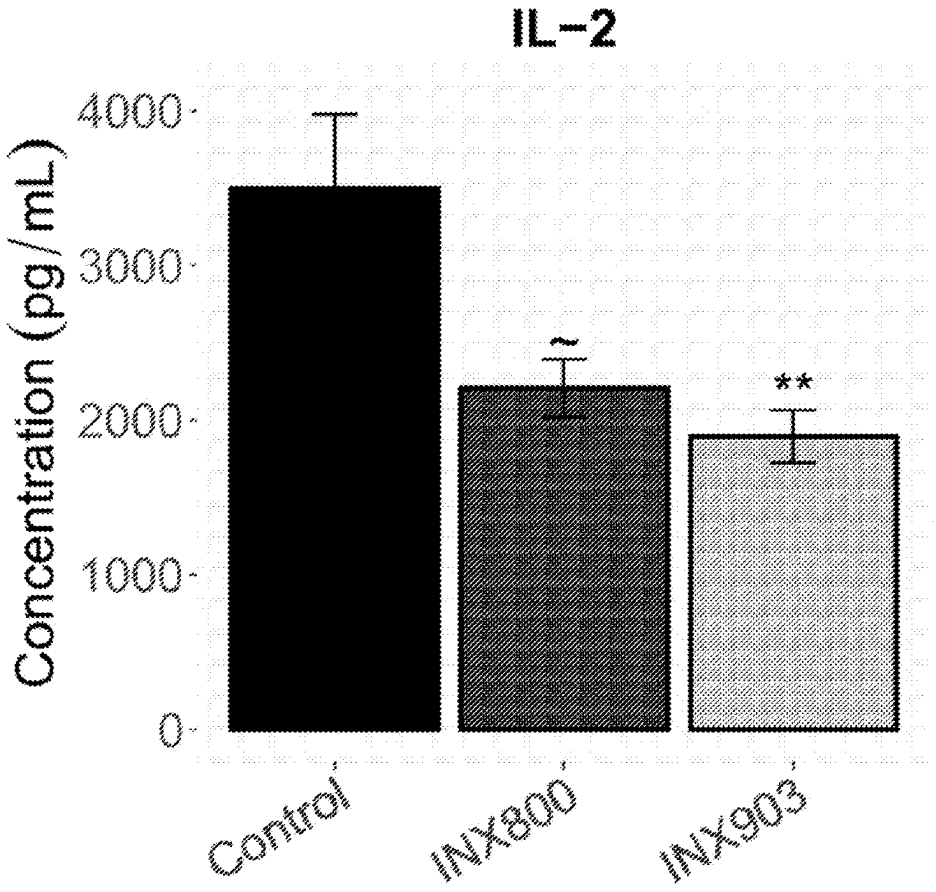

IL-2
Concentration (pg/mL)
4000
3000
2000
1000
0
~
**
Control
INX800
INX903

FIGURE 37

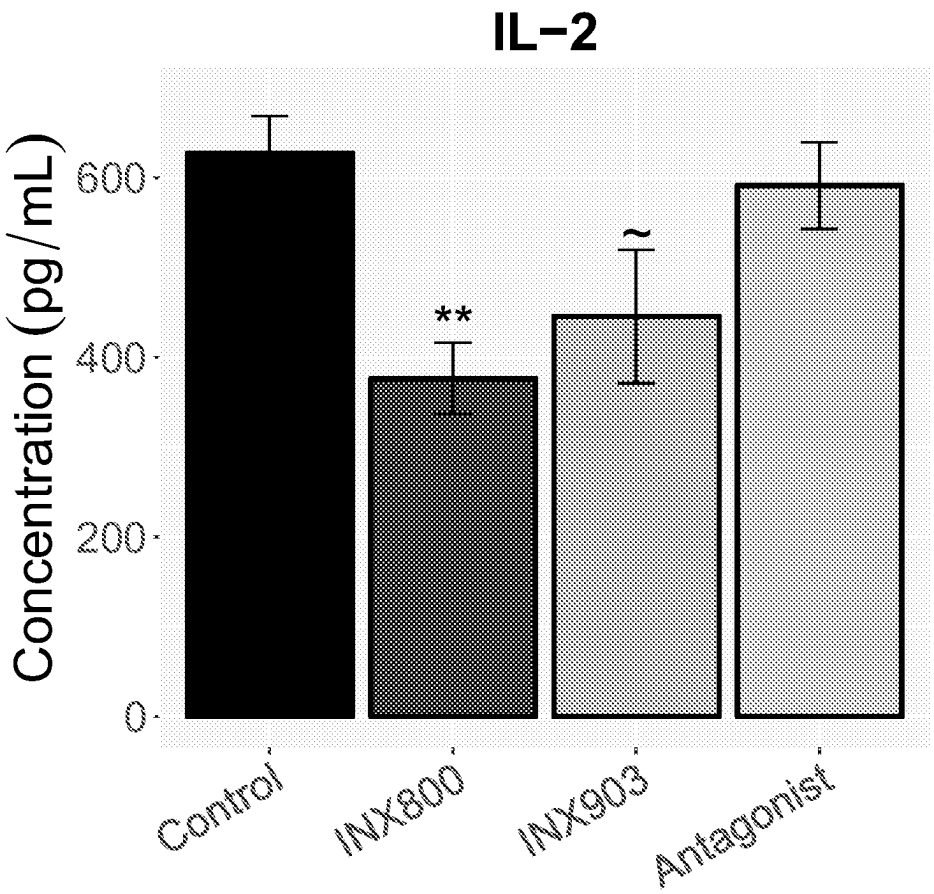

IL-2
Concentration (pg/mL)
600
400
200
0
**
~
Control
INX800
INX903
Antagonist

FIGURE 38A

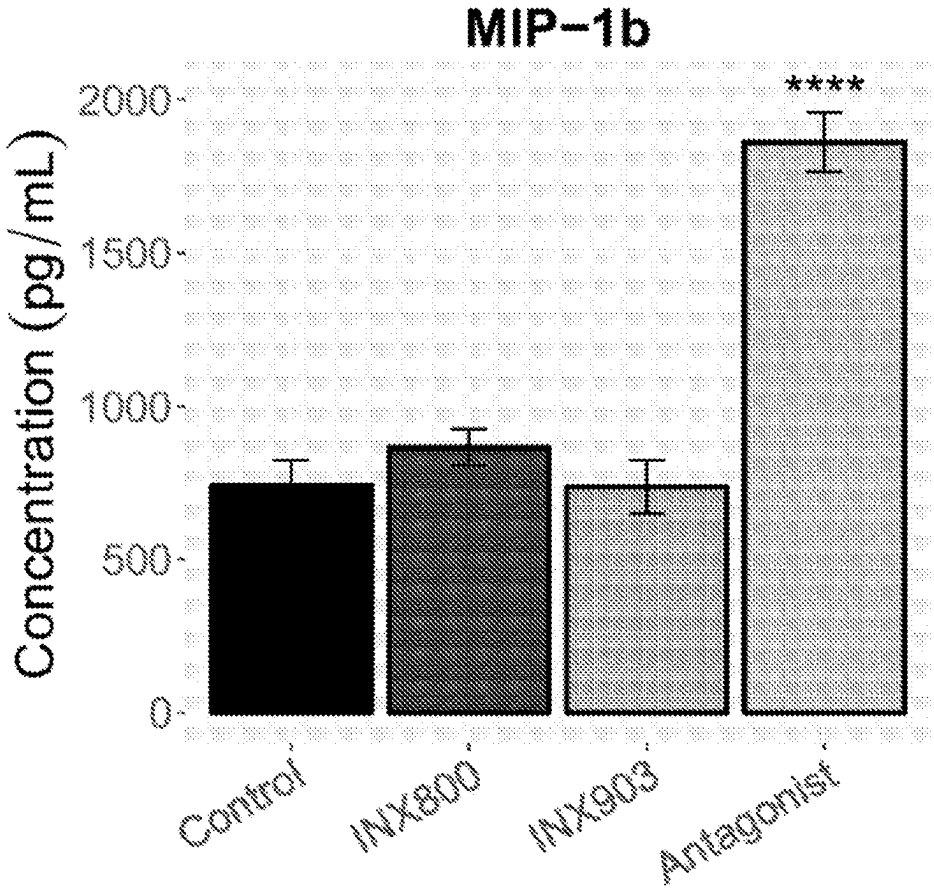
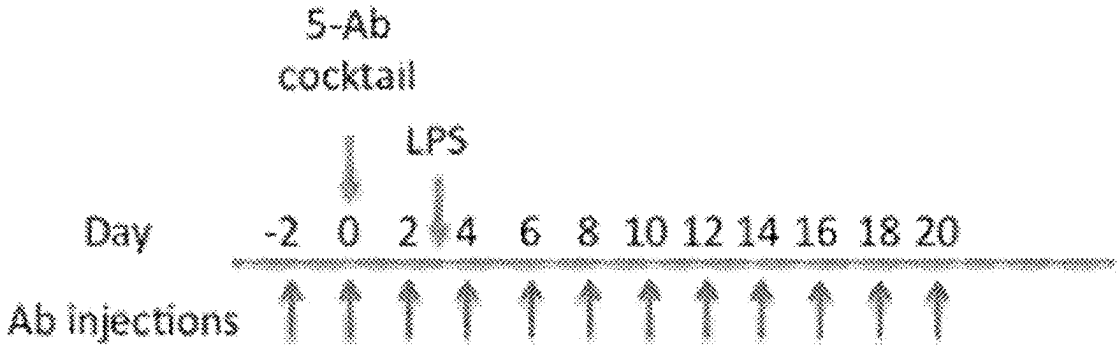

MIP-1b
Concentration (pg/mL)
2000
1500
1000
500
0
****
Control
INX800
INX903
Antagonist

FIGURE 38B

FIGURE 39



Experimental design.

FIGURE 40

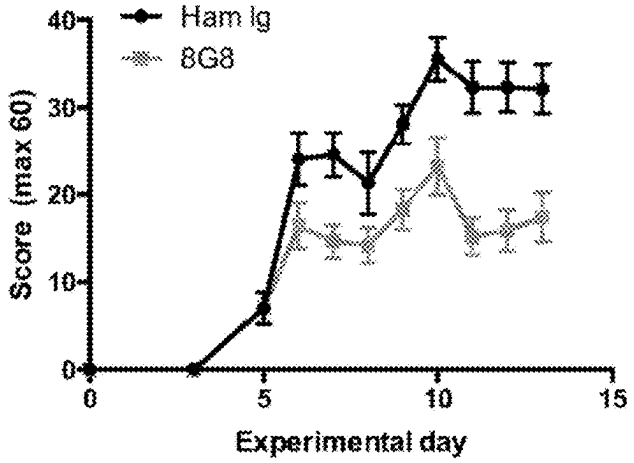
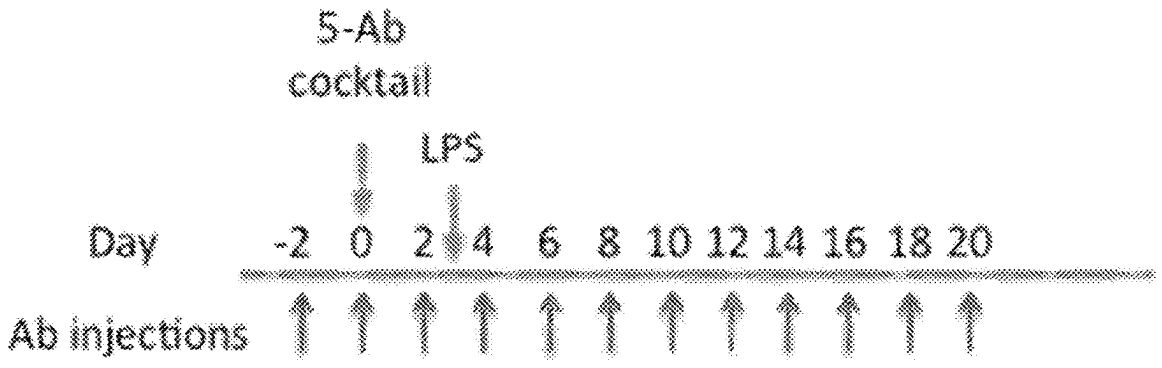


FIGURE 41



Experimental design.

FIGURE 42

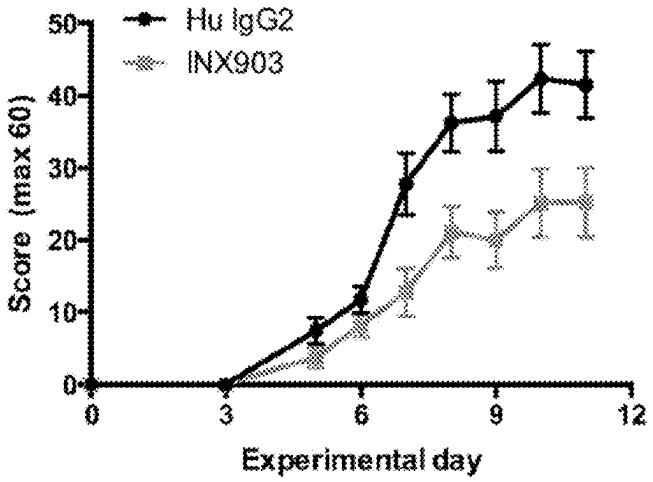


FIGURE 43

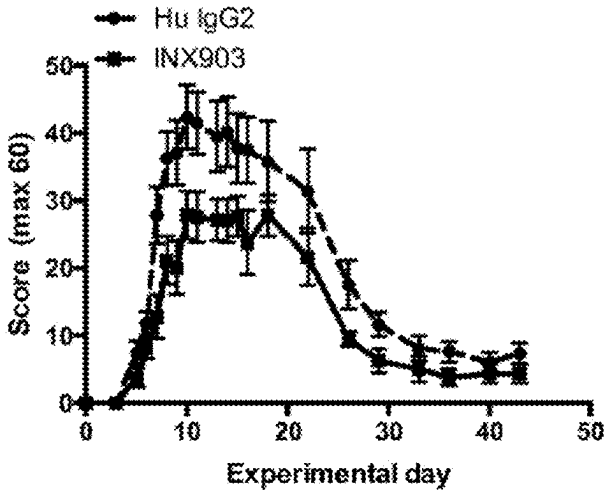

Hu IgG2
INX903
Score (max 60)
0
10
20
30
40
50
0
10
20
30
40
50
Experimental day

FIGURE 44

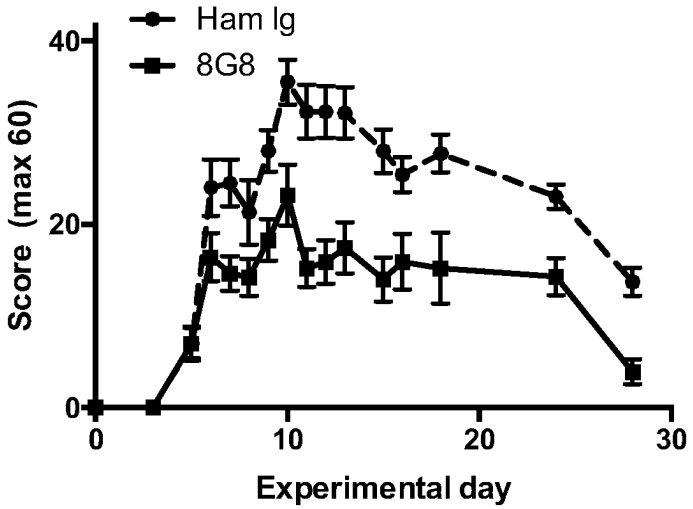
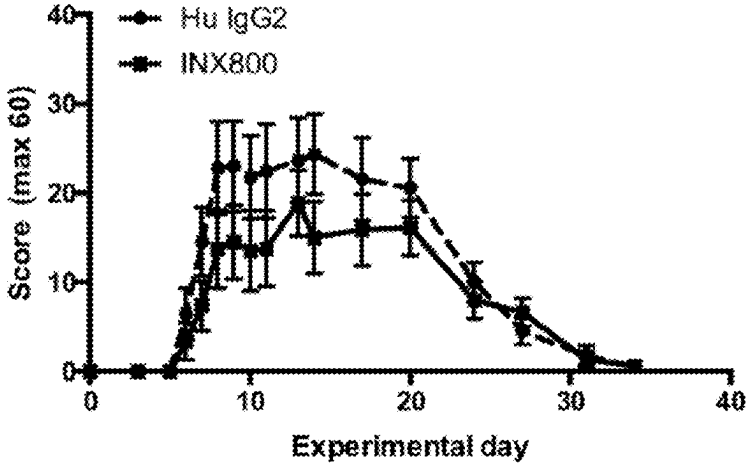


FIGURE 45



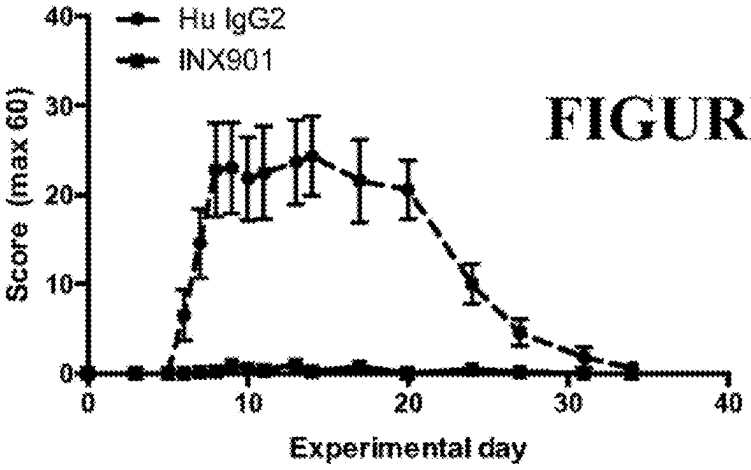


FIGURE 46

FIGURE 47

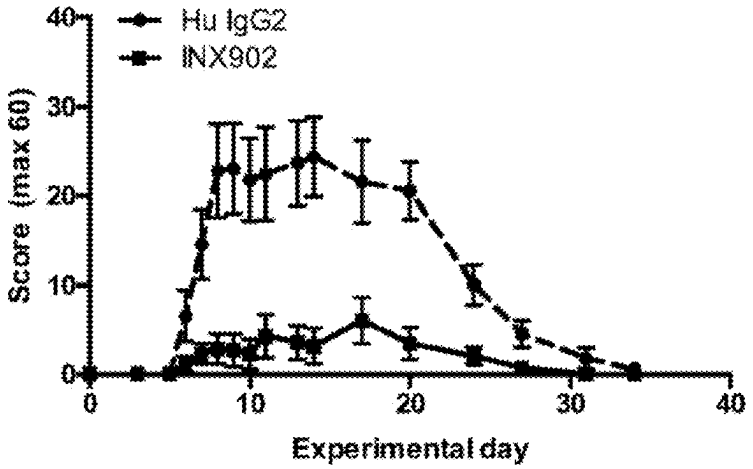
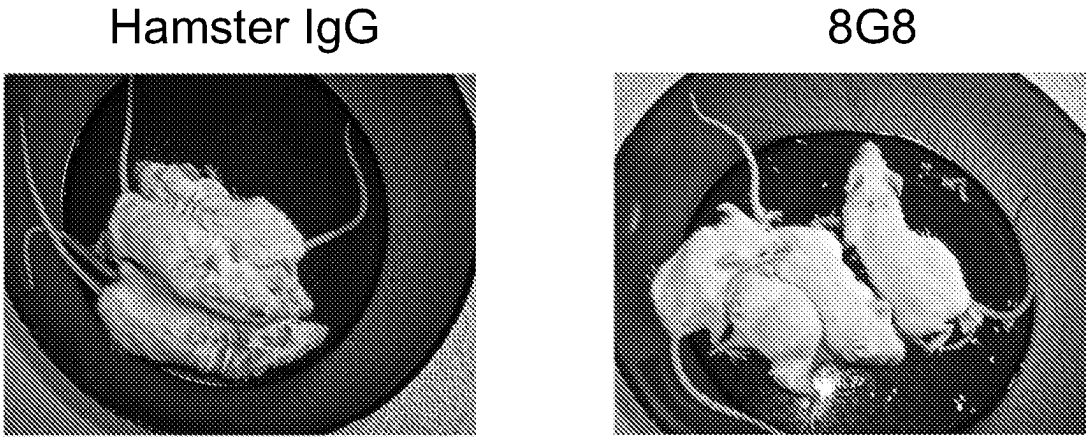
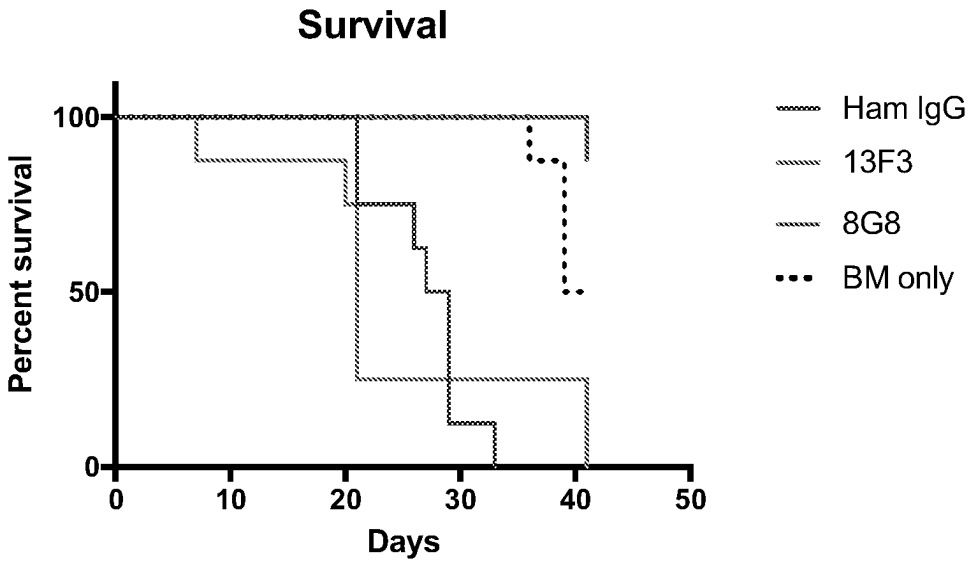

Hu IgG2
INX902
Score (max 60)
40
30
20
10
0
0
10
20
30
40
Experimental day

FIGURE 48A





Weights and survival of recipient mice treated with 8G8, 13F3, or control Hamster IgG antibodies in acute GvHD disease model

a) Mice appearance at D21
b) Survival.

FIGURE 48B

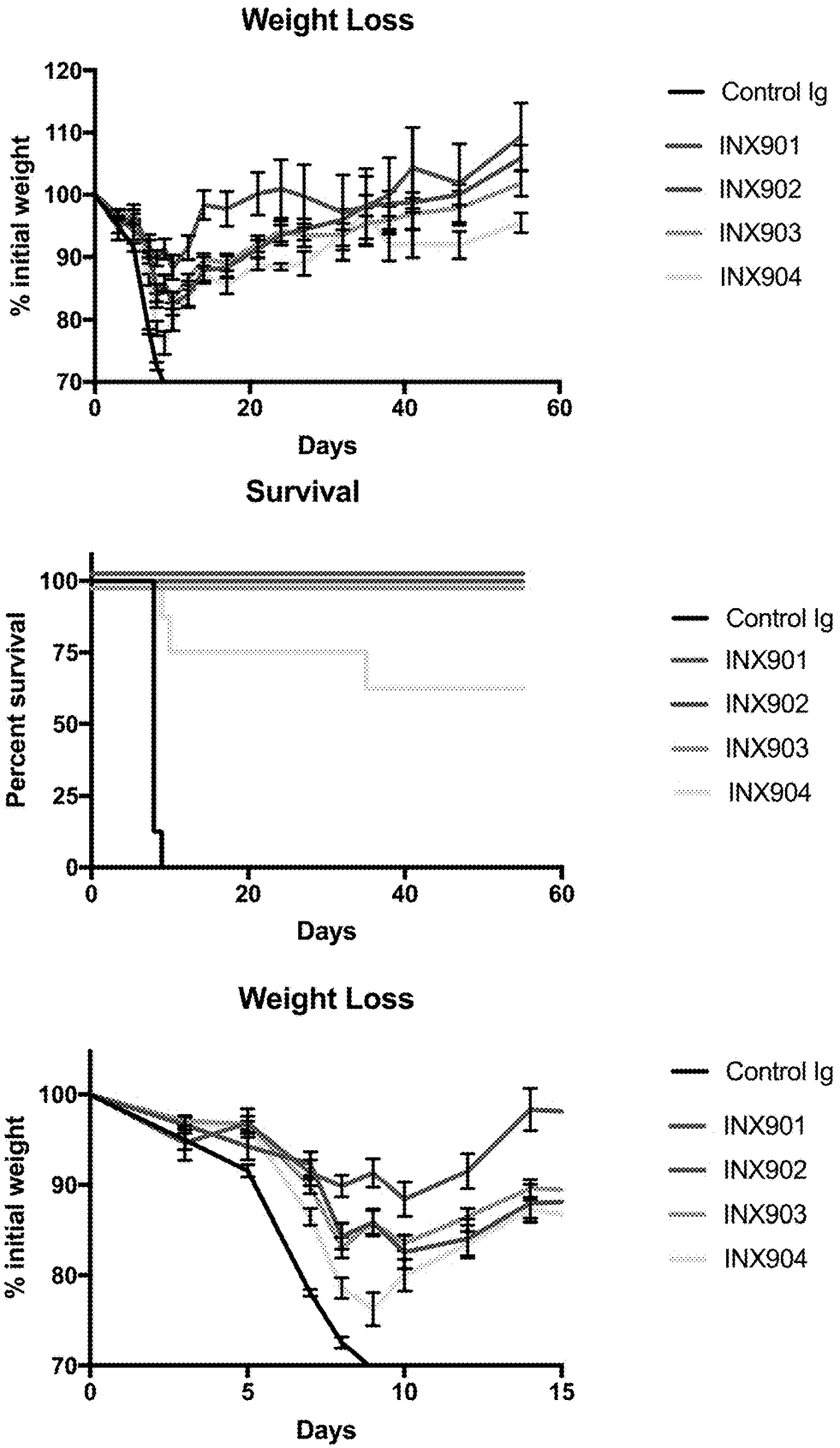

Weight Loss
% initial weight
120
110
100
90
80
70
0
20
40
60
Days
Control Ig
INX901
INX902
INX903
INX904
Survival
Percent survival
100
75
50
25
0
0
20
40
60
Days
Control Ig
INX901
INX902
INX903
INX904
Weight Loss
% initial weight
100
90
80
70
0
5
10
15
Days
Control Ig
INX901
INX902
INX903
INX904

FIGURE 49

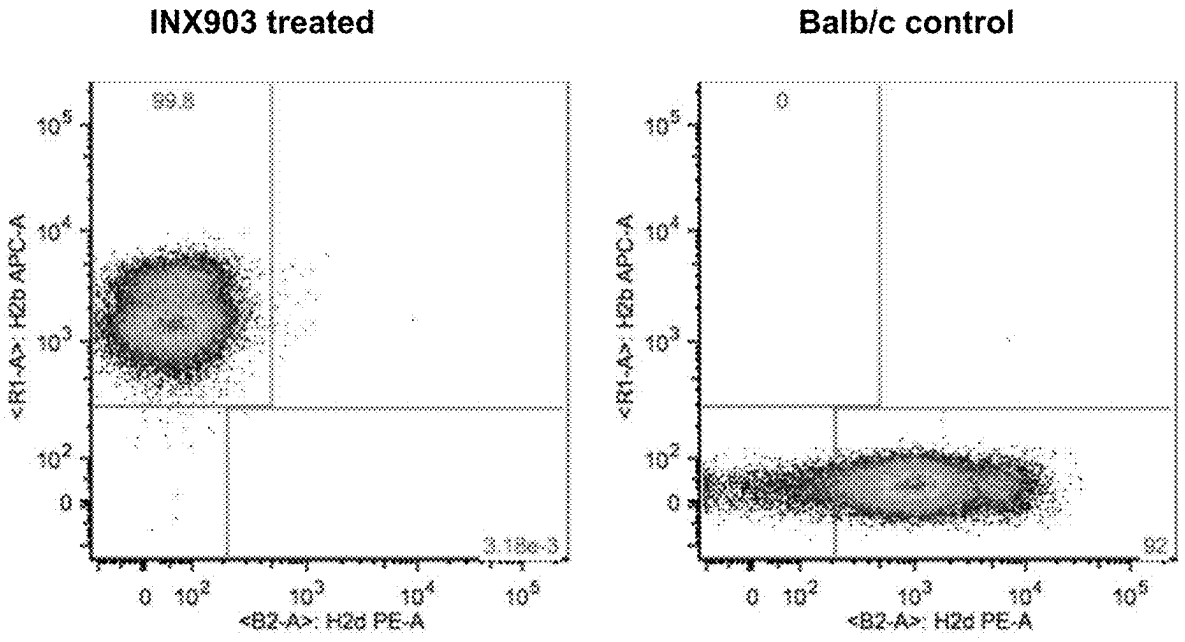
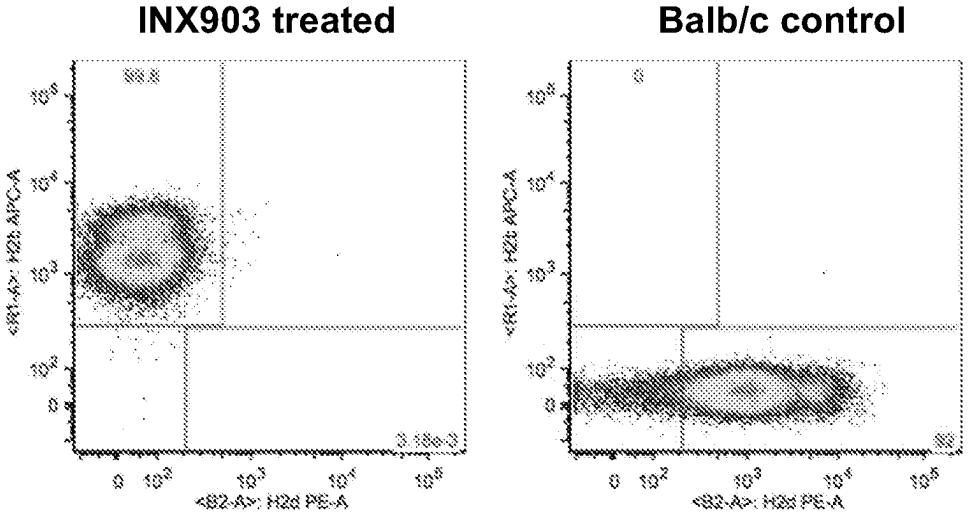

INX903 treated
Balb/c control
99.8
3.19e-3
0
92
<R1-A>: H2b APC-A
<B2-A>: H2d PE-A

FIGURE 50A

FIGURE 50A



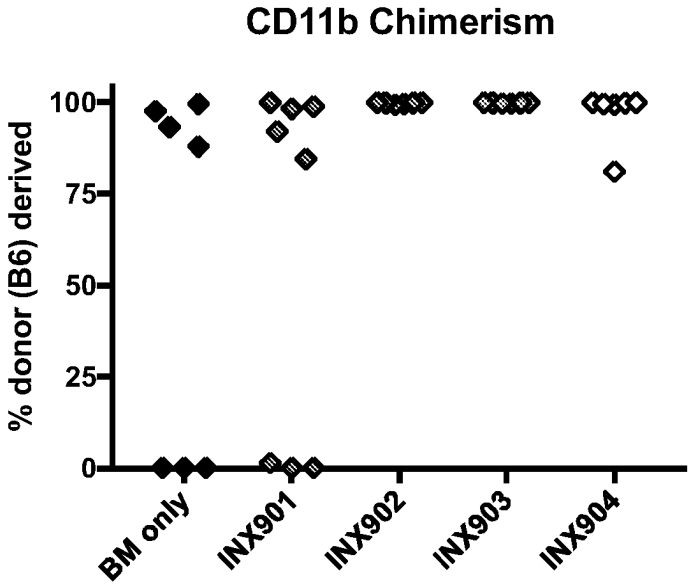


FIGURE 50B

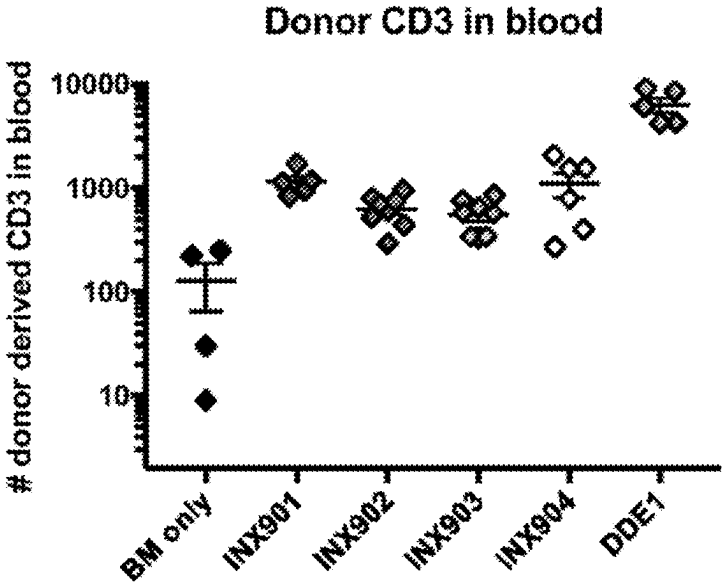

Donor CD3 in blood
donor derived CD3 in blood
10000
1000
100
10
BM only
INX901
INX902
INX903
INX904
DDE1

FIGURE 50C

FIGURE 51A

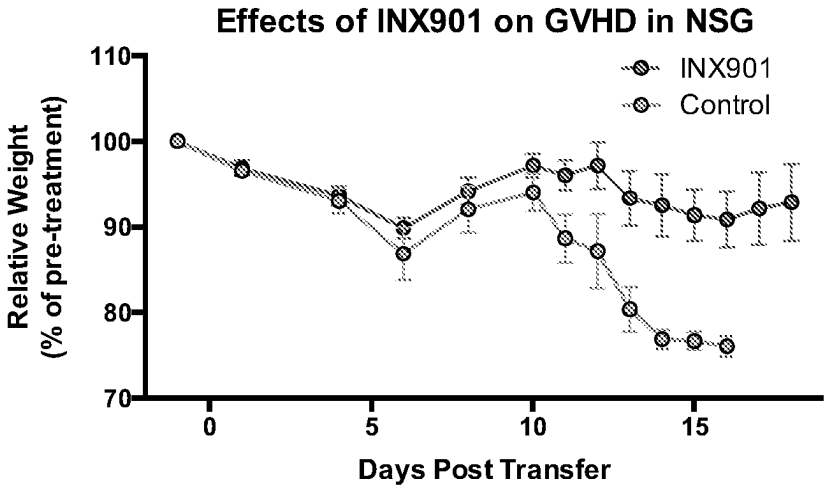
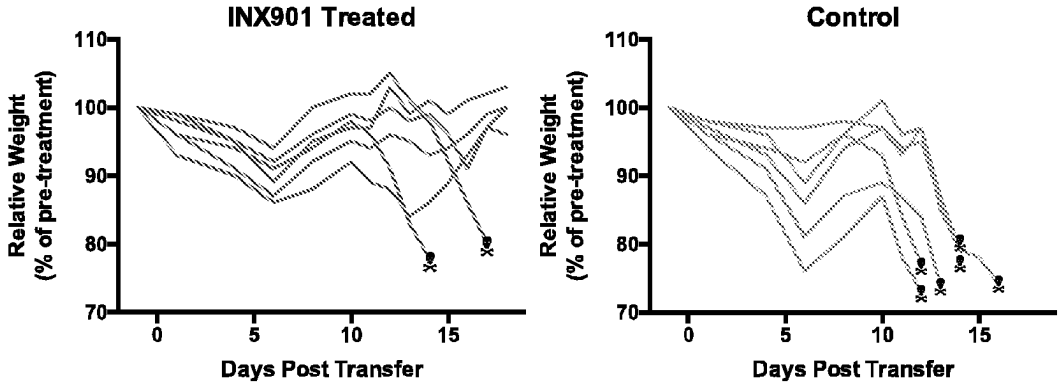
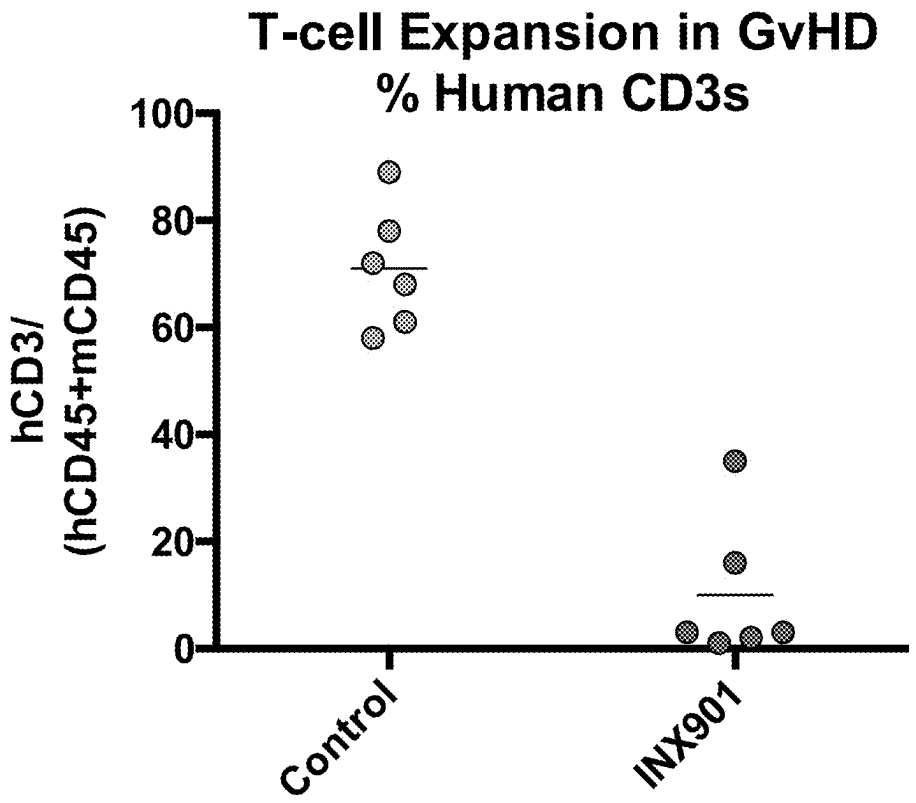


FIGURE 51B



Weights of NSG mice treated with INX901 or control AB in xeno-GvHD disease model

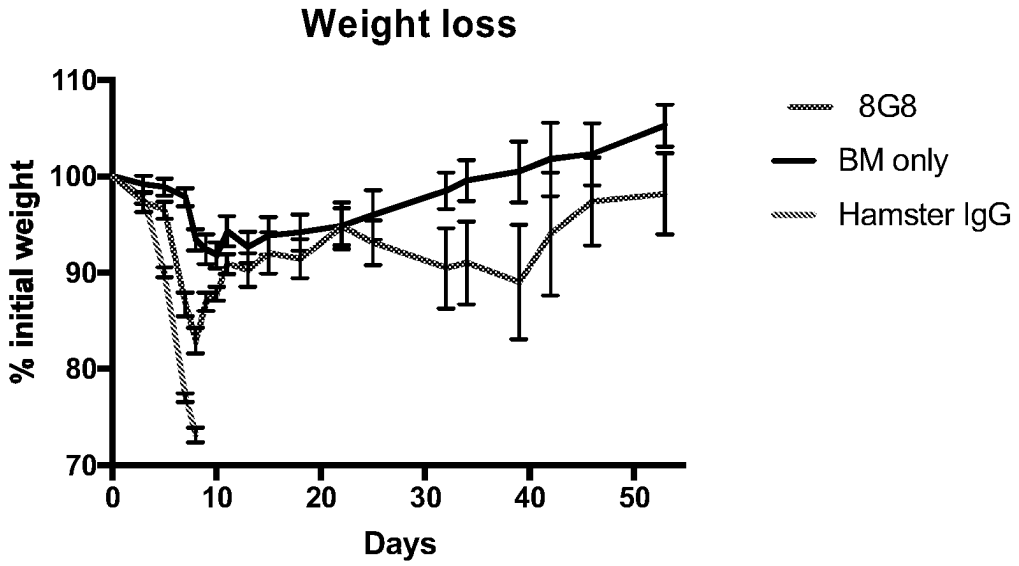
a) Means by group (N=6)
b) Weights of individual mice. Skull and crossbones indicate mice were either found dead or euthanized at the indicated date.

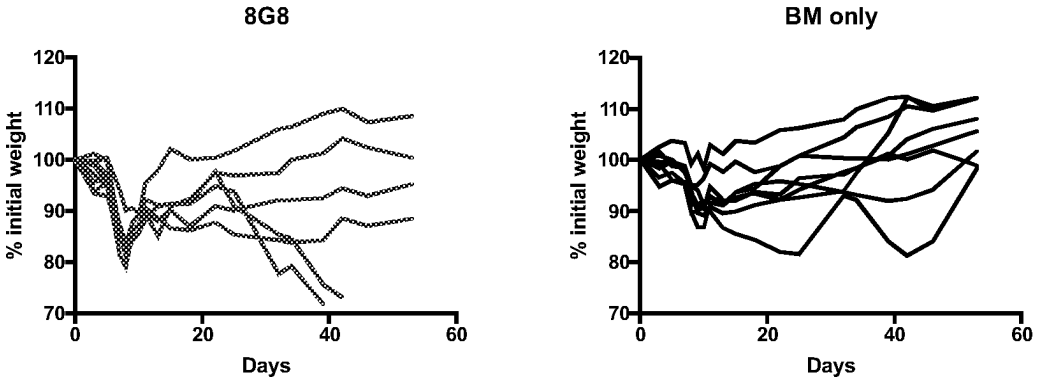


T-cell expansion in NSG mice treated with INX901 or control AB in xeno-GvHD disease model

FIGURE 52

FIGURE 53A





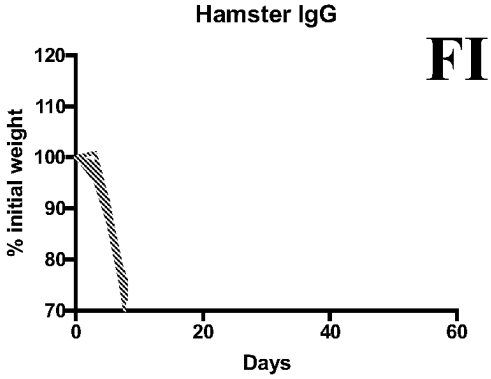
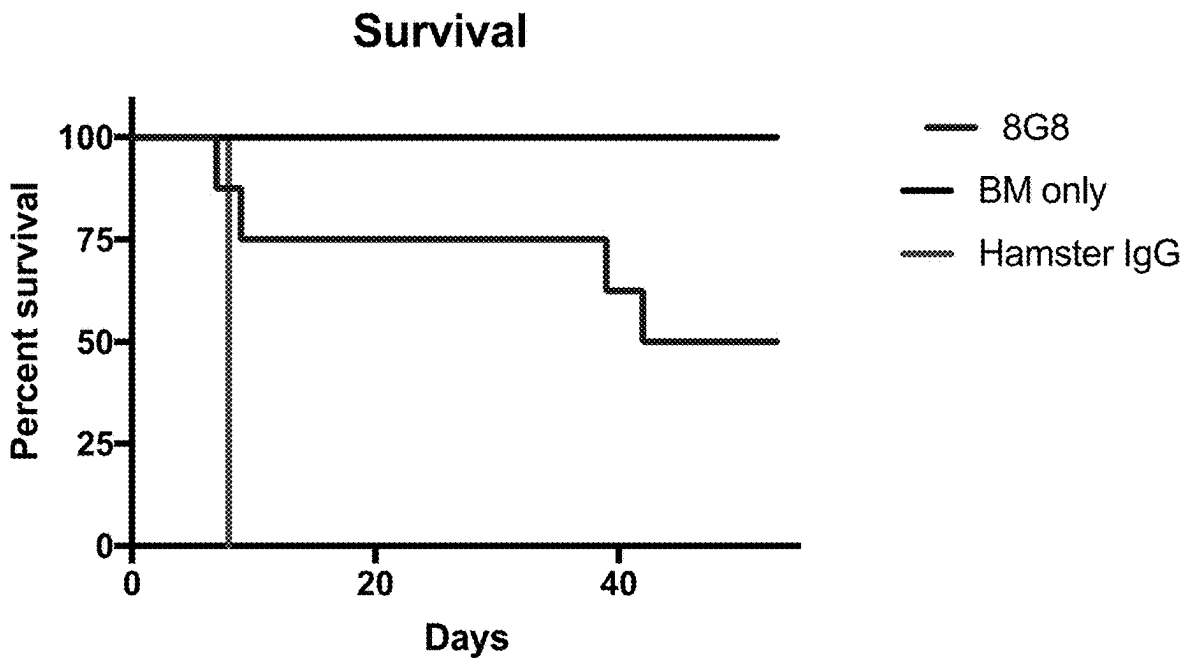


FIGURE 53B

c)



Weights and survival of recipient mice treated with 8G8 antibodies or control Hamster IgG in acute GvHD disease model

FIGURE 53C

FIGURE 54A

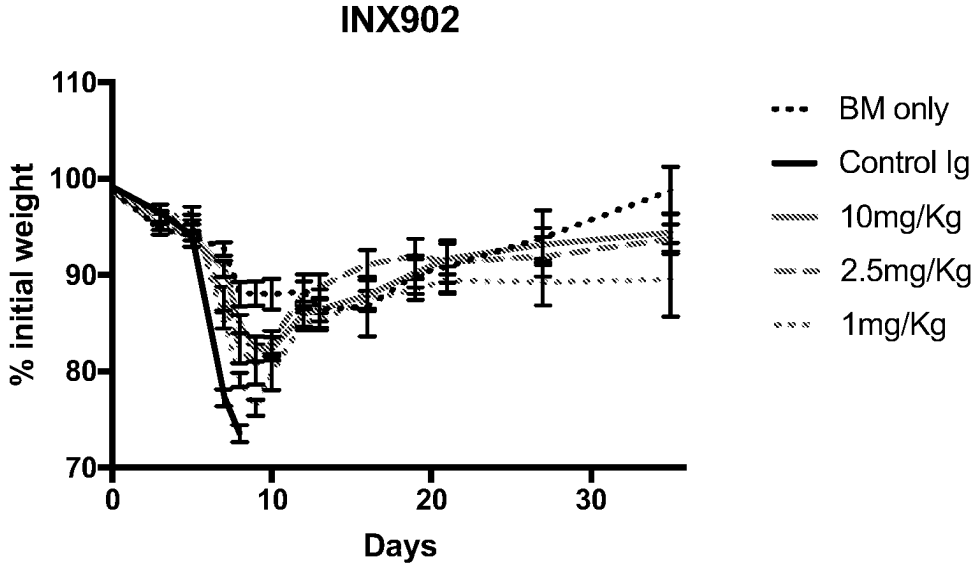
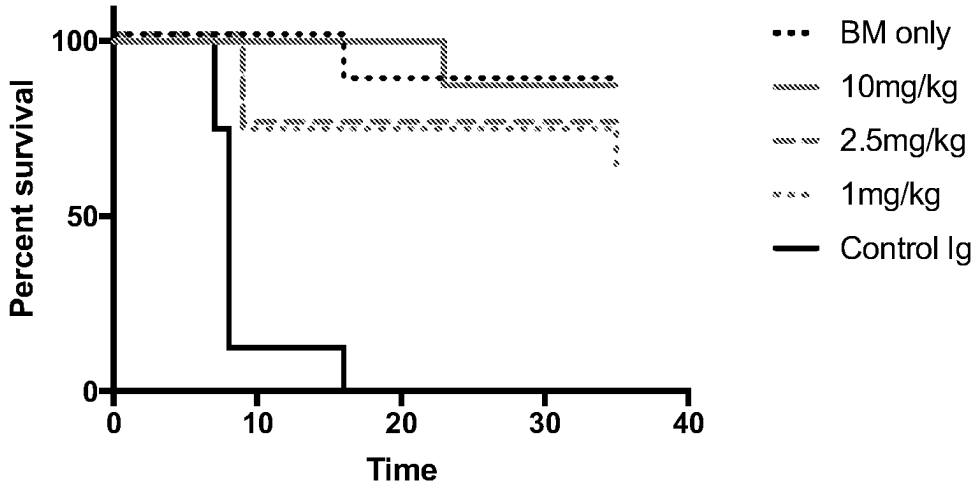


FIGURE 54B



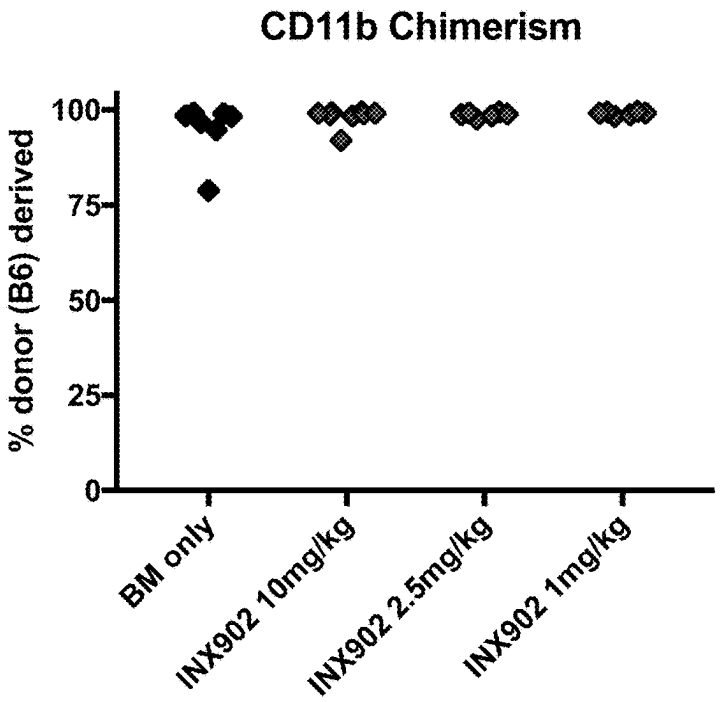


FIGURE 55A

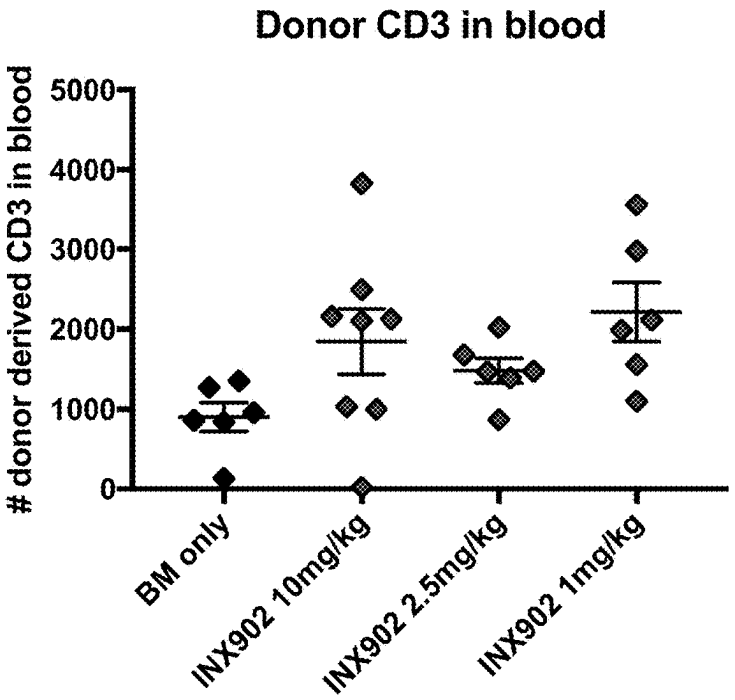


FIGURE 55B

Chimerism in surviving mice treated with various doses of INX902 or control Ig in acute GvHD disease model

FIGURE 56A

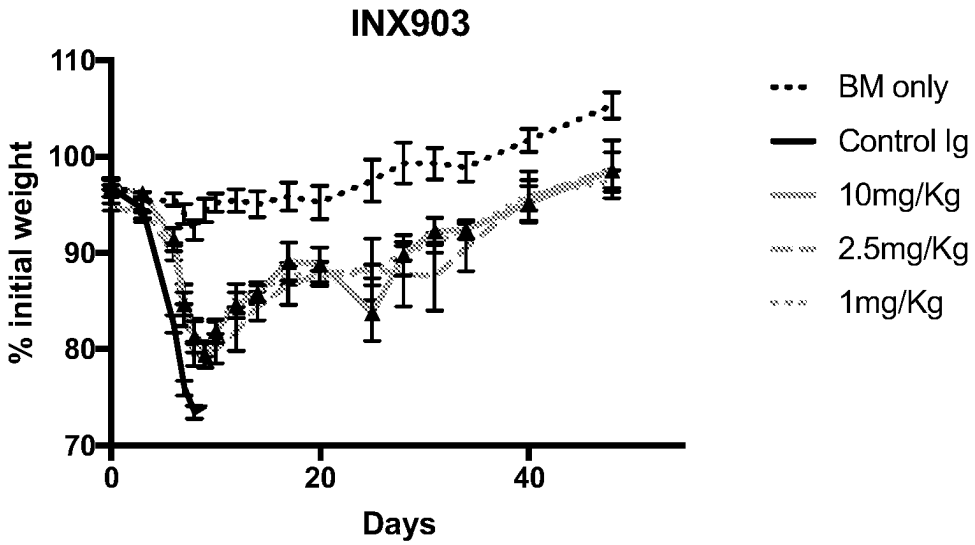

INX903
% initial weight
110
100
90
80
70
0
20
40
Days
BM only
Control Ig
10mg/Kg
2.5mg/Kg
1mg/Kg

FIGURE 56B

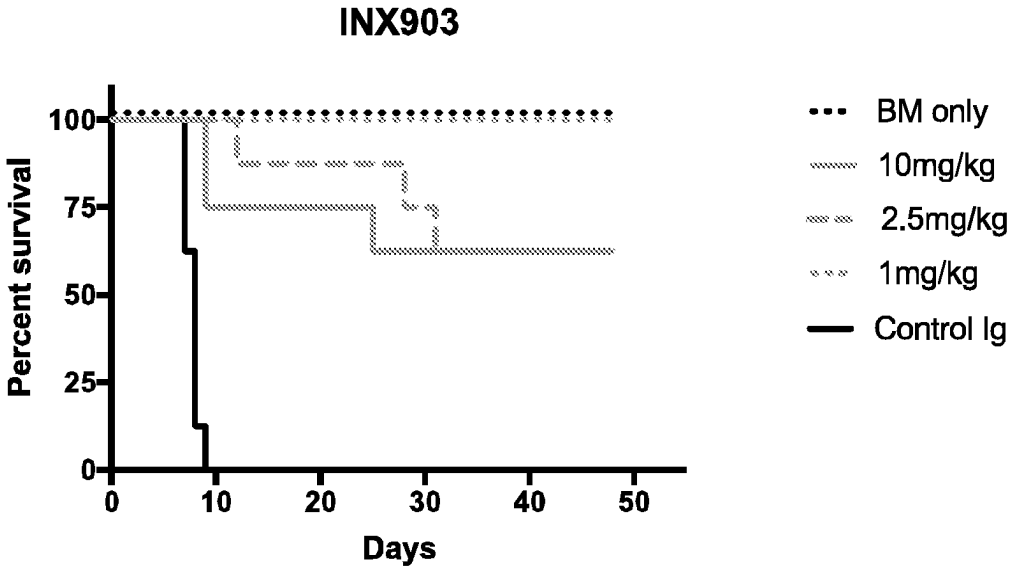
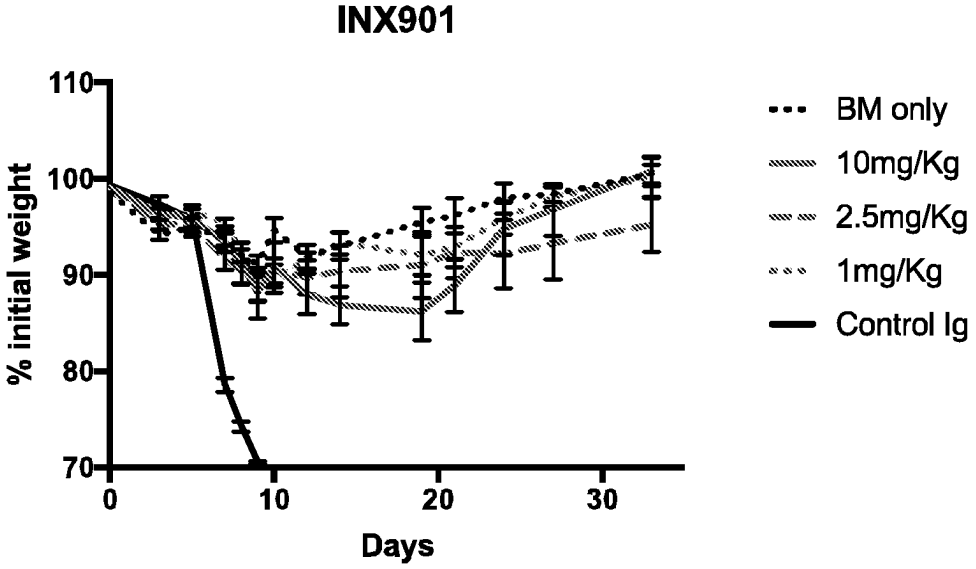


FIGURE 56C



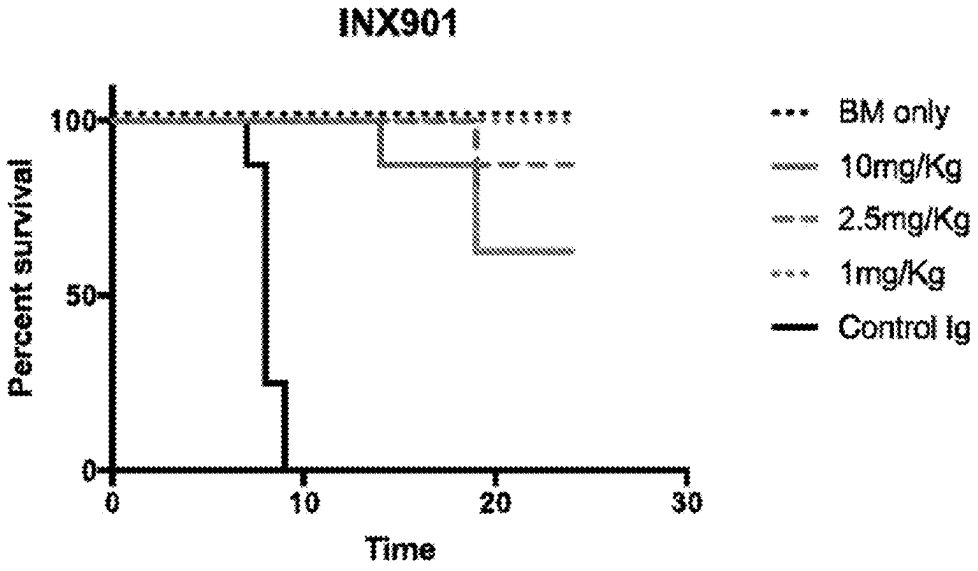
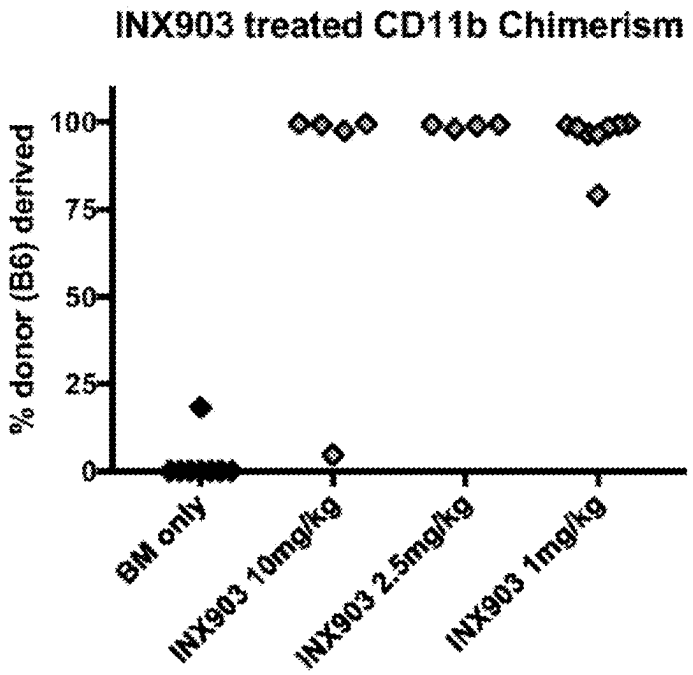

INX901
Percent survival
100
50
0
0
10
20
30
Time
BM only
10mg/Kg
2.5mg/Kg
1mg/Kg
Control Ig

FIGURE 56D

FIGURE 57A



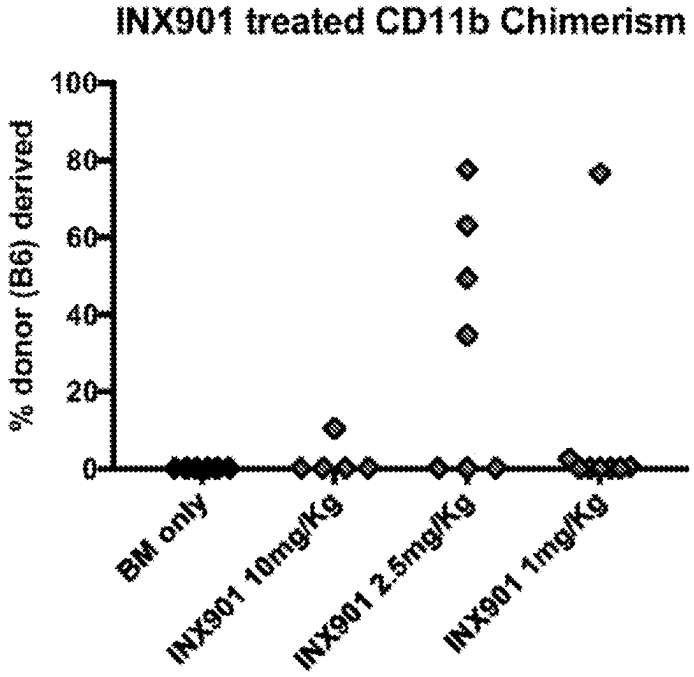


FIGURE 57B

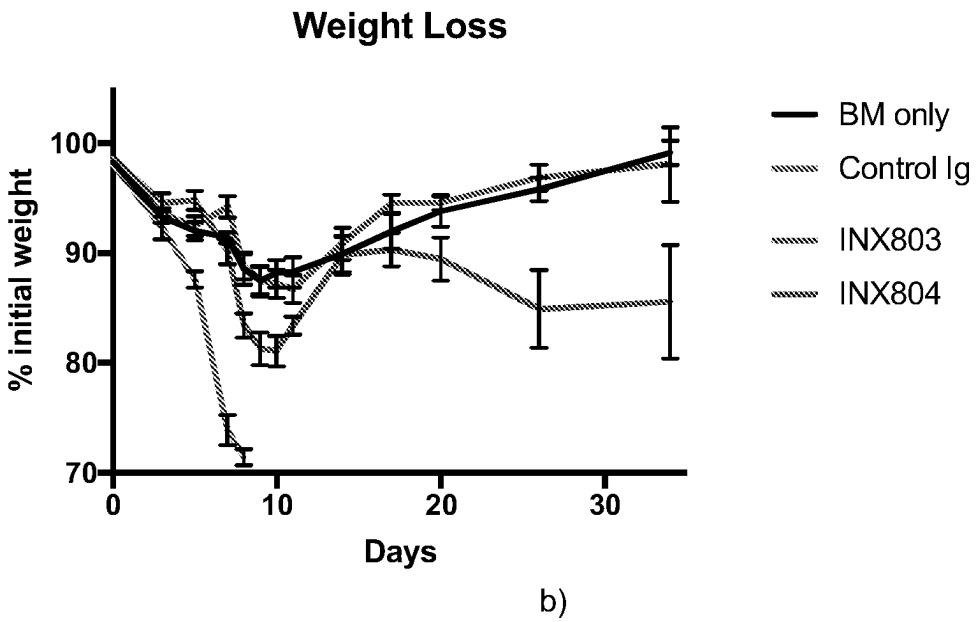

Weight Loss
% initial weight
100
90
80
70
0
10
20
30
Days
BM only
Control Ig
INX803
INX804
b)

FIGURE 58A

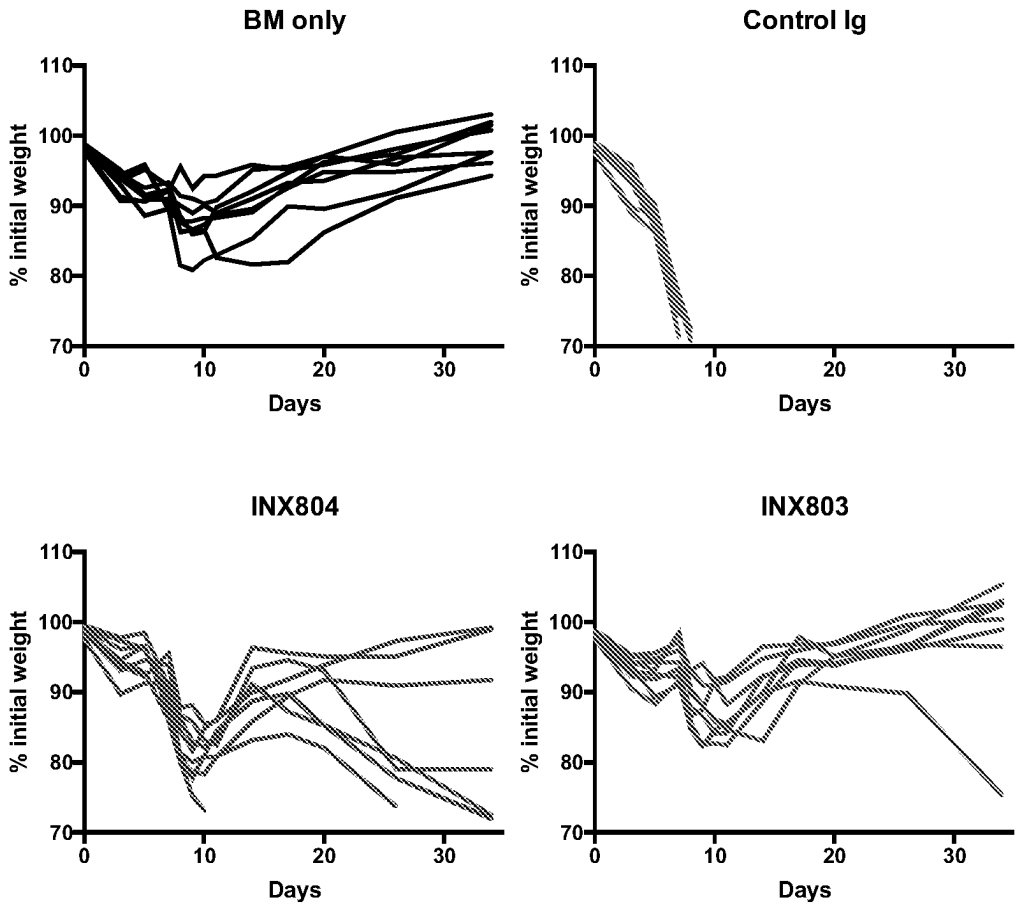
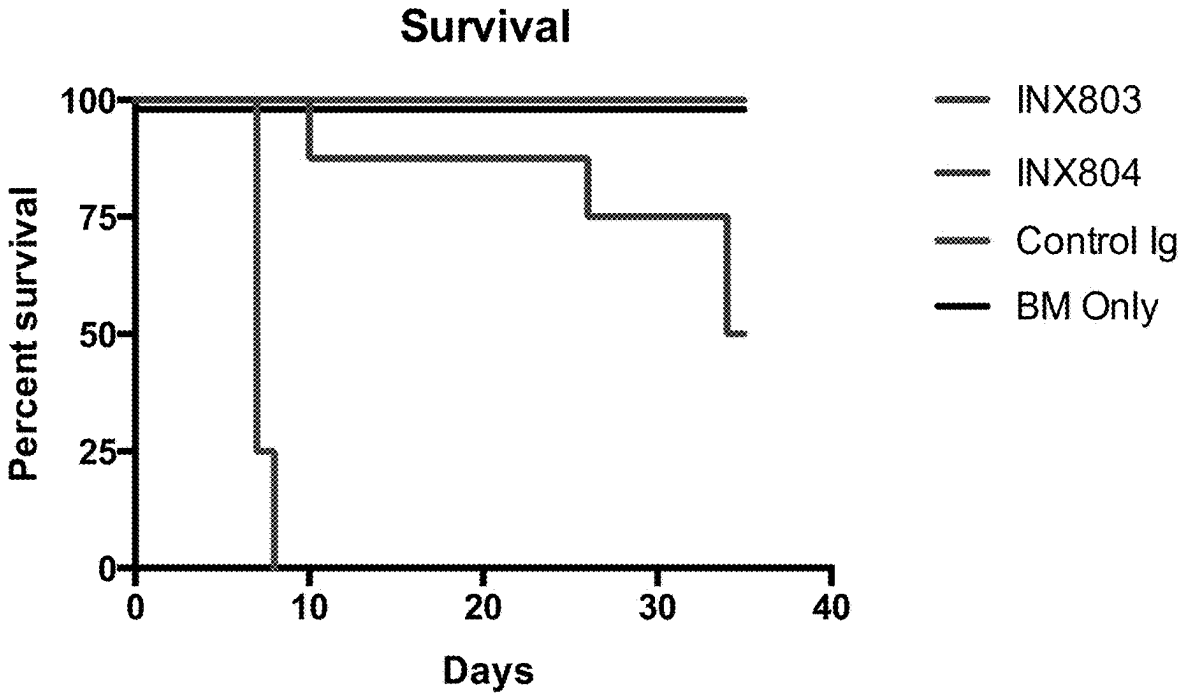
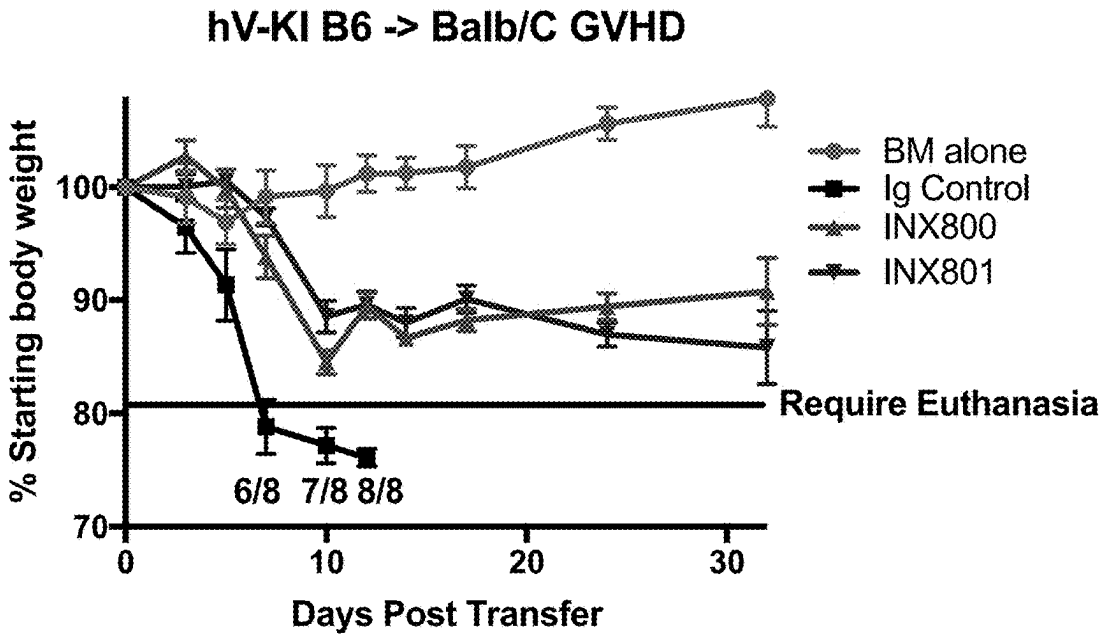

BM only
Control Ig
INX804
INX803
% initial weight
Days
110
100
90
80
70
0
10
20
30

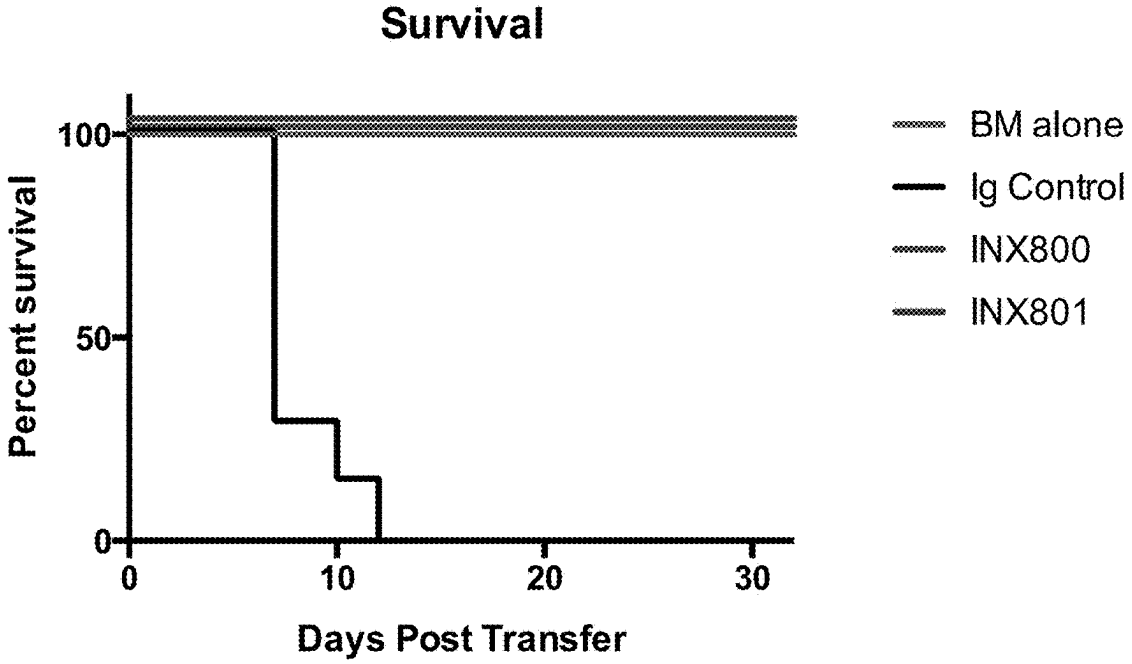
FIGURE 58B



Weights of recipient mice treated with INX antibodies or control Ig and survival in acute GvHD disease model

FIGURE 58C





Acute GvHD was induced by transfer of T cells and BM from hV-KI mice into irradiated Balb/c recipients.

FIGURE 59

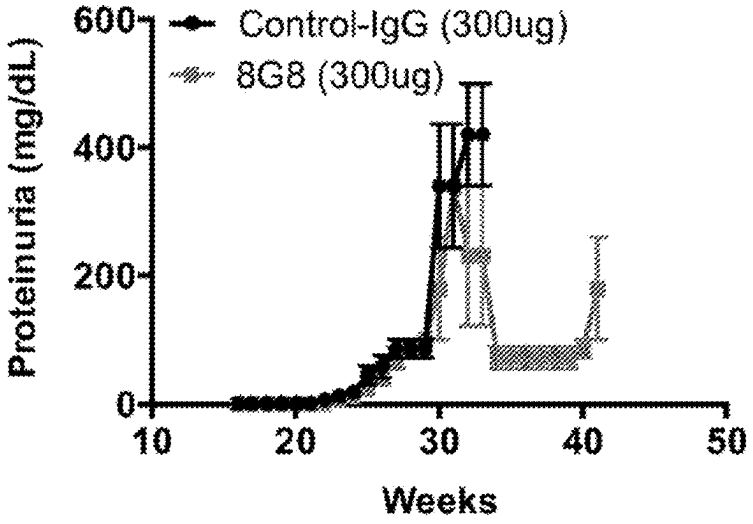

Control-IgG (300ug)
8G8 (300ug)
Proteinuria (mg/dL)
600
400
200
0
10
20
30
40
50
Weeks

FIGURE 60

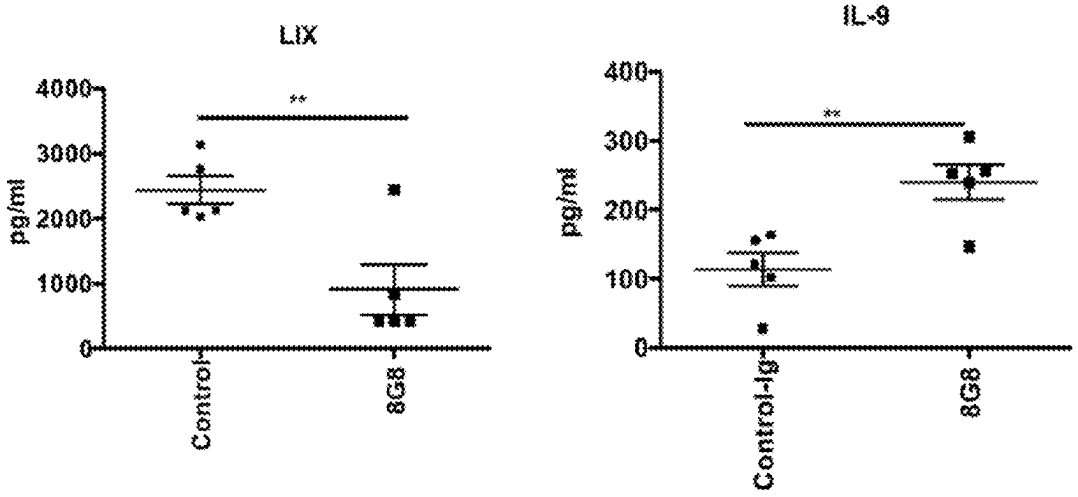

LIX
4000
3000
2000
1000
0
pg/ml
**
Control
8G8
IL-9
400
300
200
100
0
pg/ml
**
Control-Ig
8G8

FIGURE 61

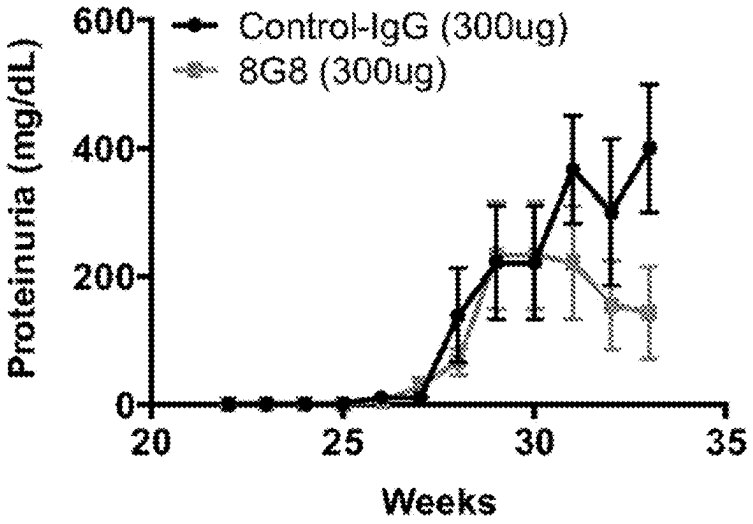

Control-IgG (300ug)
8G8 (300ug)
Proteinuria (mg/dL)
600
400
200
0
20
25
30
35
Weeks

FIGURE 62

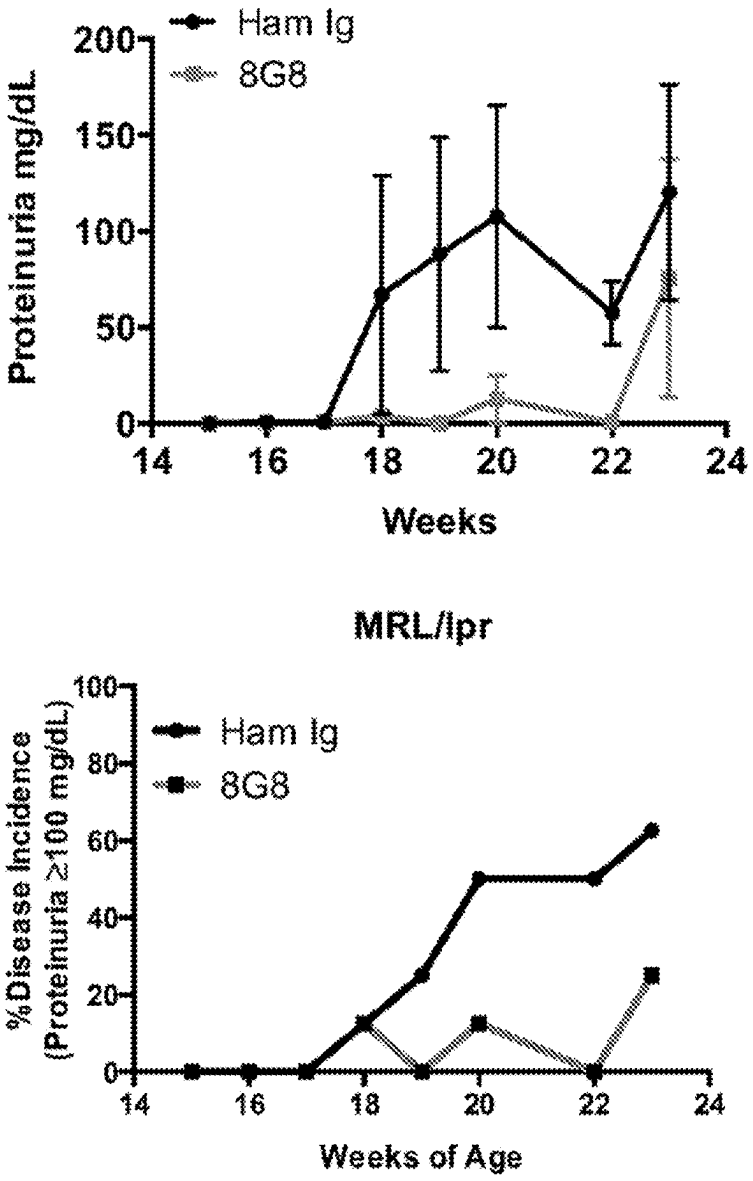

Ham Ig
8G8
Proteinuria mg/dL
200
150
100
50
0
14
16
18
20
22
24
Weeks
MRL/lpr
Ham Ig
8G8
% Disease Incidence
(Proteinuria ≥100 mg/dL)
100
80
60
40
20
0
14
16
18
20
22
24
Weeks of Age

FIGURE 63

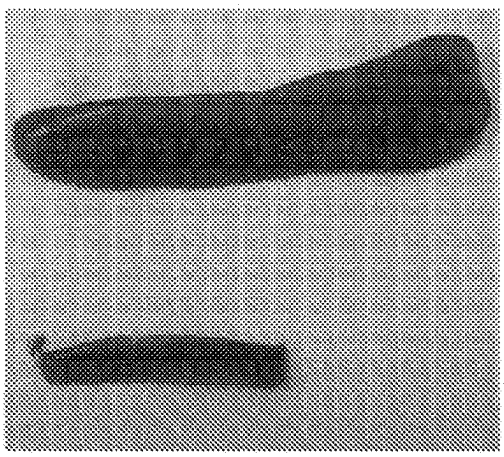


FIGURE 64

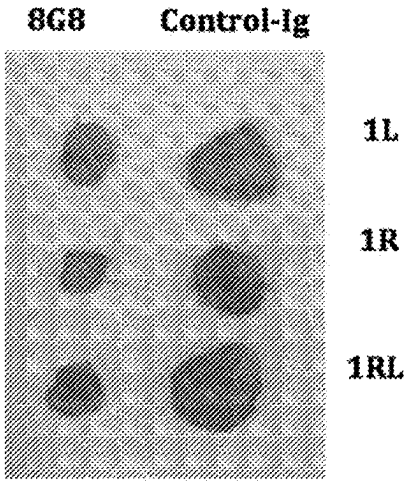


FIGURE 65

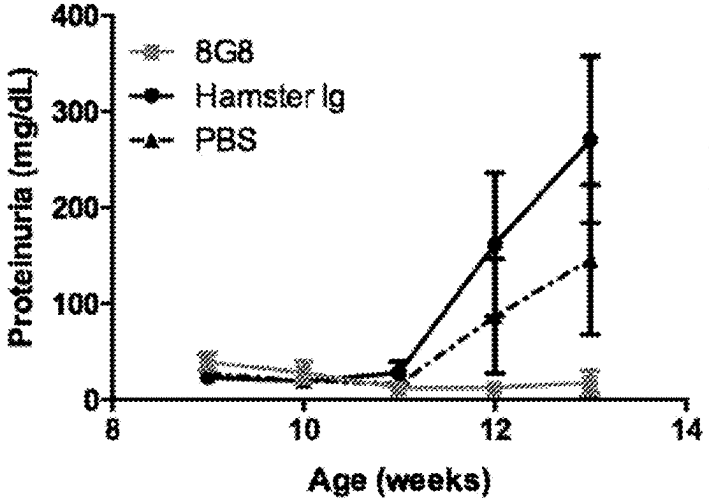


FIGURE 66A

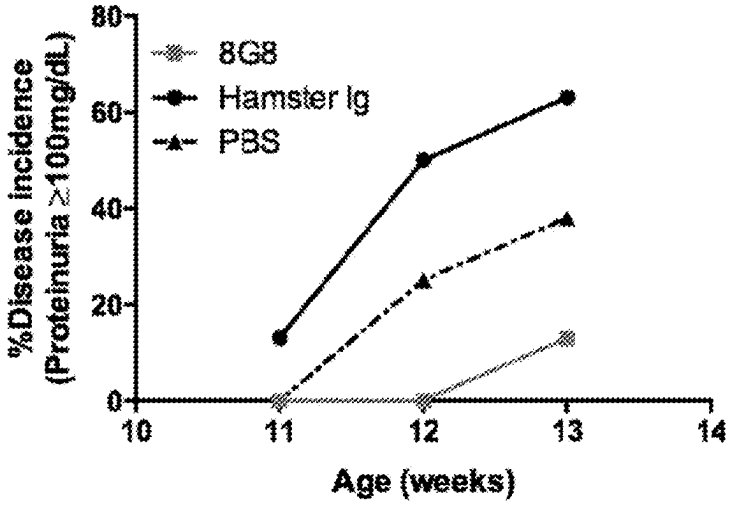


FIGURE 66B

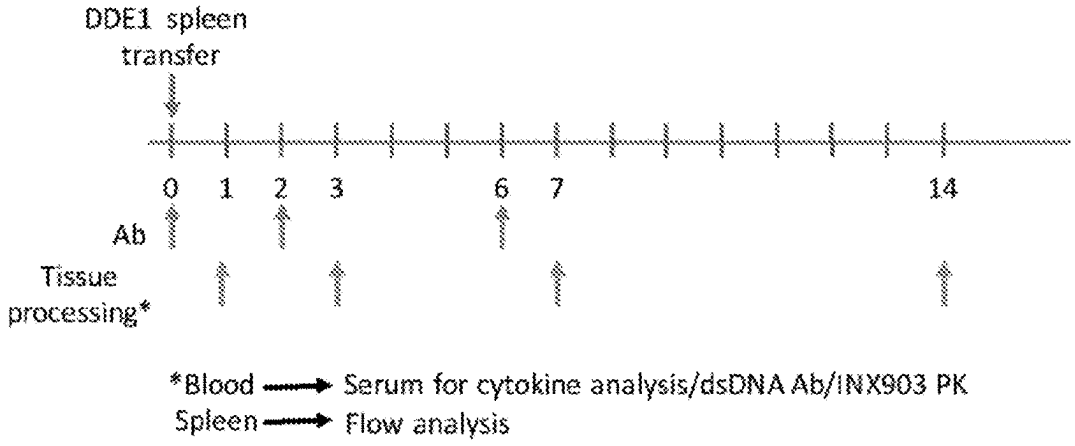
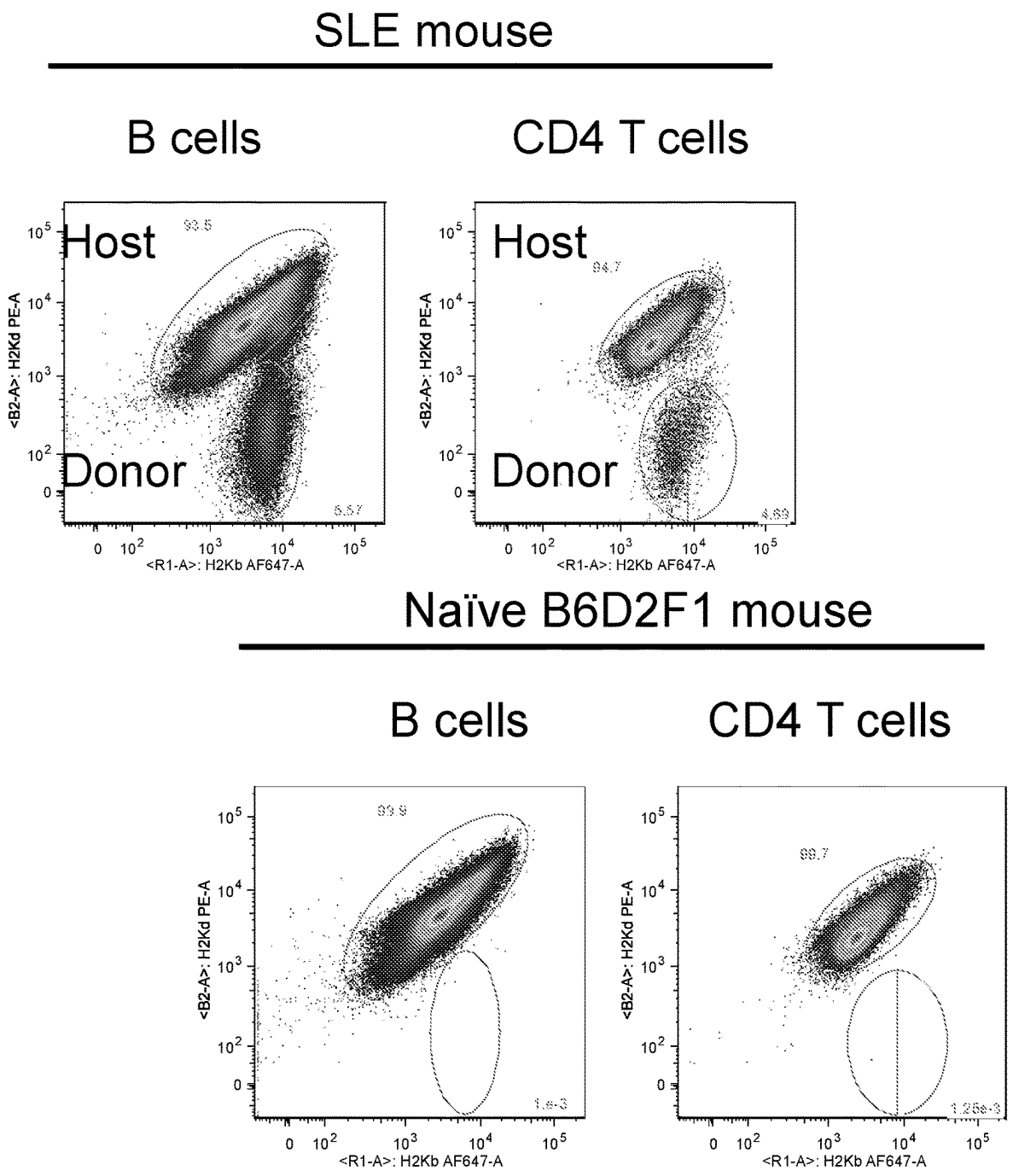

DDE1 spleen transfer
0
1
2
3
6
7
14
Ab
Tissue processing*
*Blood → Serum for cytokine analysis/dsDNA Ab/INX903 PK
Spleen → Flow analysis

FIGURE 67

FIGURE 68



Donor and host cell populations are distinguished by their MHC class I alleles.

FIGURE 69A

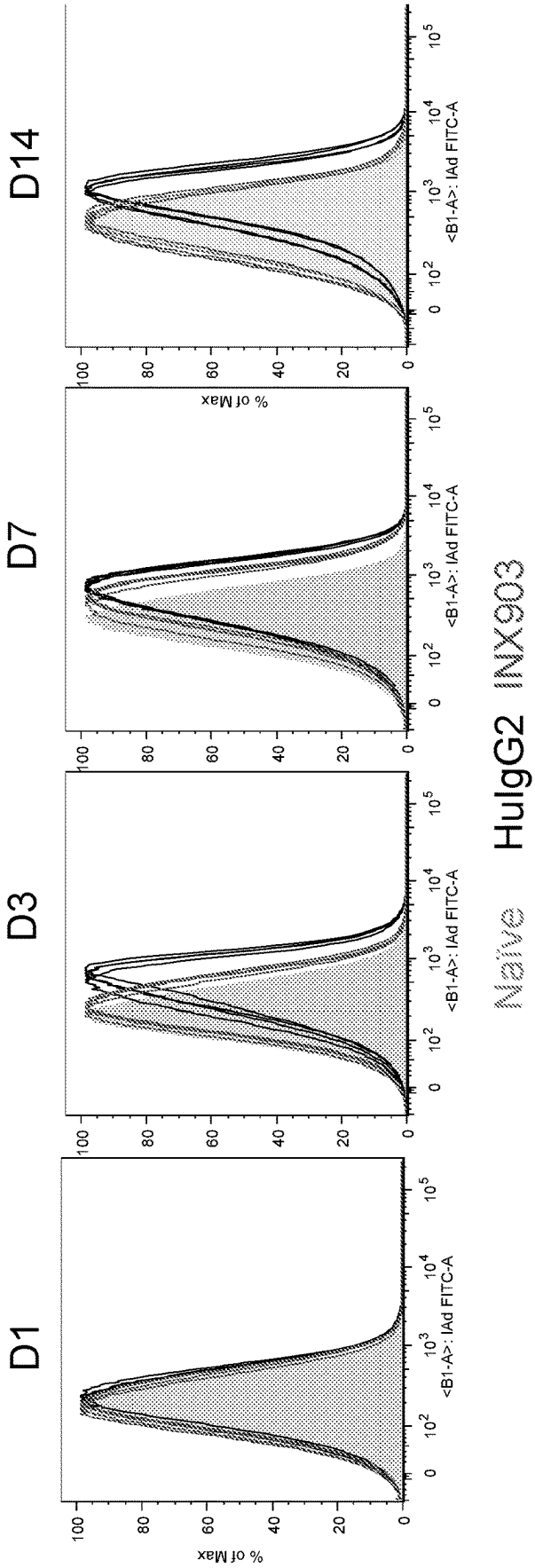
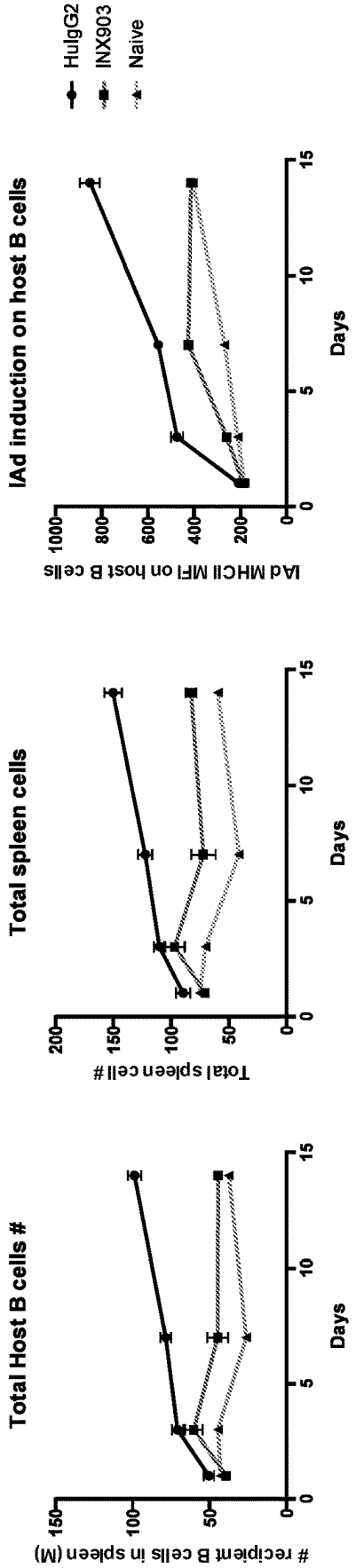


FIGURE 69B


Total Host B cells #
recipient B cells in spleen (M)
150
100
50
0
0
5
10
15
Days
Total spleen cells
Total spleen cell #
200
150
100
50
0
0
5
10
15
Days
IAd induction on host B cells
IAd MHCII MFI on host B cells
1000
800
600
400
200
0
0
5
10
15
Days
HuIgG2
INX903
Naive

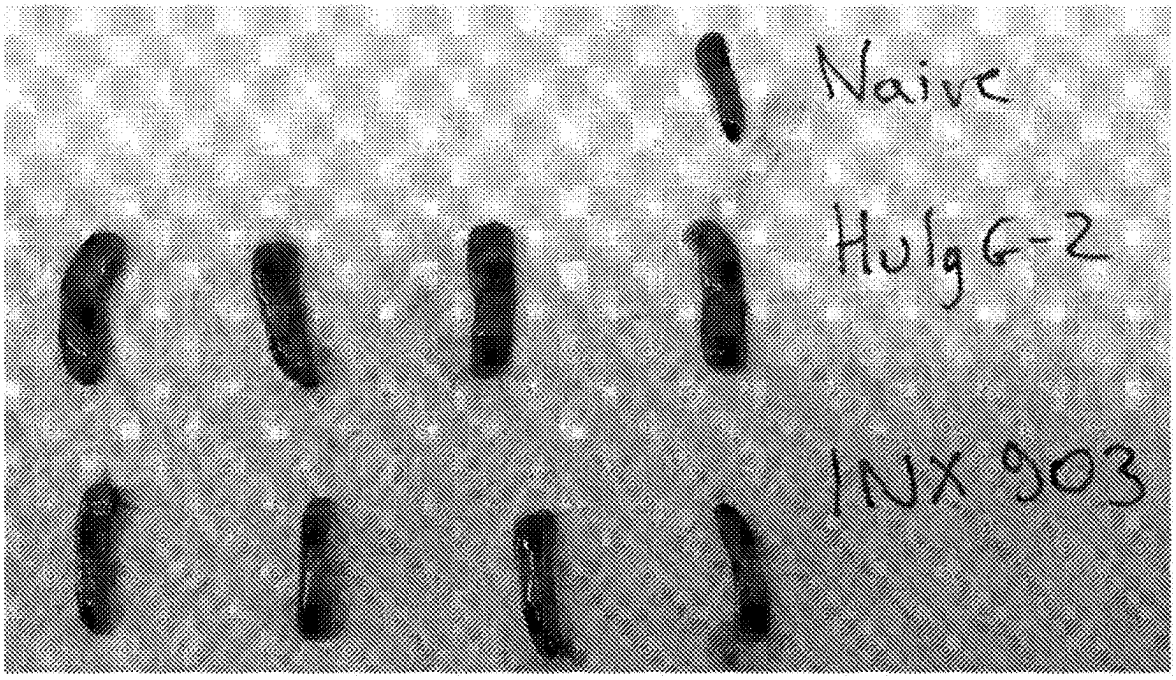
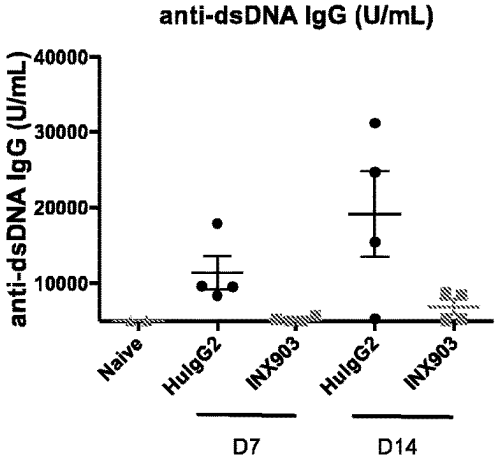


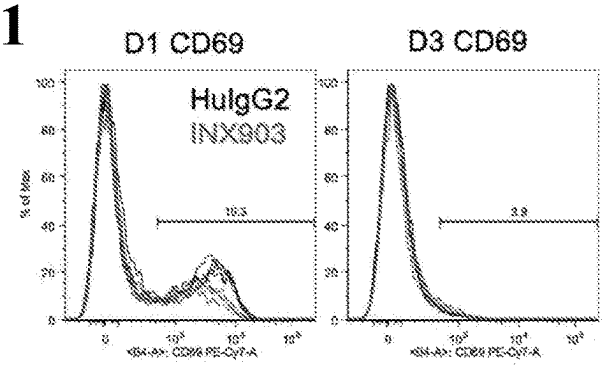
FIGURE 69C

FIGURE 70



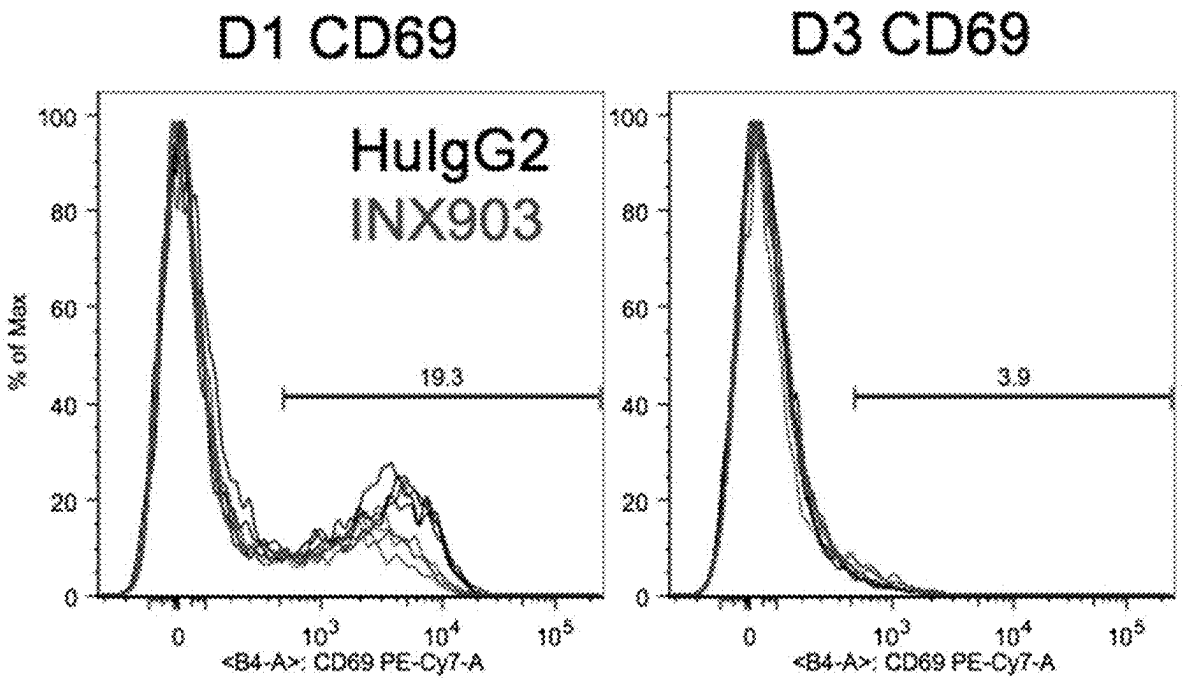
Autoantibodies anti-dsDNA production in SLE is prevented by INX903 treatment. Anti-dsDNA IgG titer in serum measured by ELISA in naïve (n=2), and HuIgG2 or INX903 treated mice at D7 and D14 (n=4, SEM).

FIGURE 71



Decreased CD69 expression at Day 1 in INX903-treated CD4 T cells (n=4).

FIGURE 71



Decreased CD69 expression at Day 1 in INX903-treated CD4 T cells (n=4).

FIGURE 72

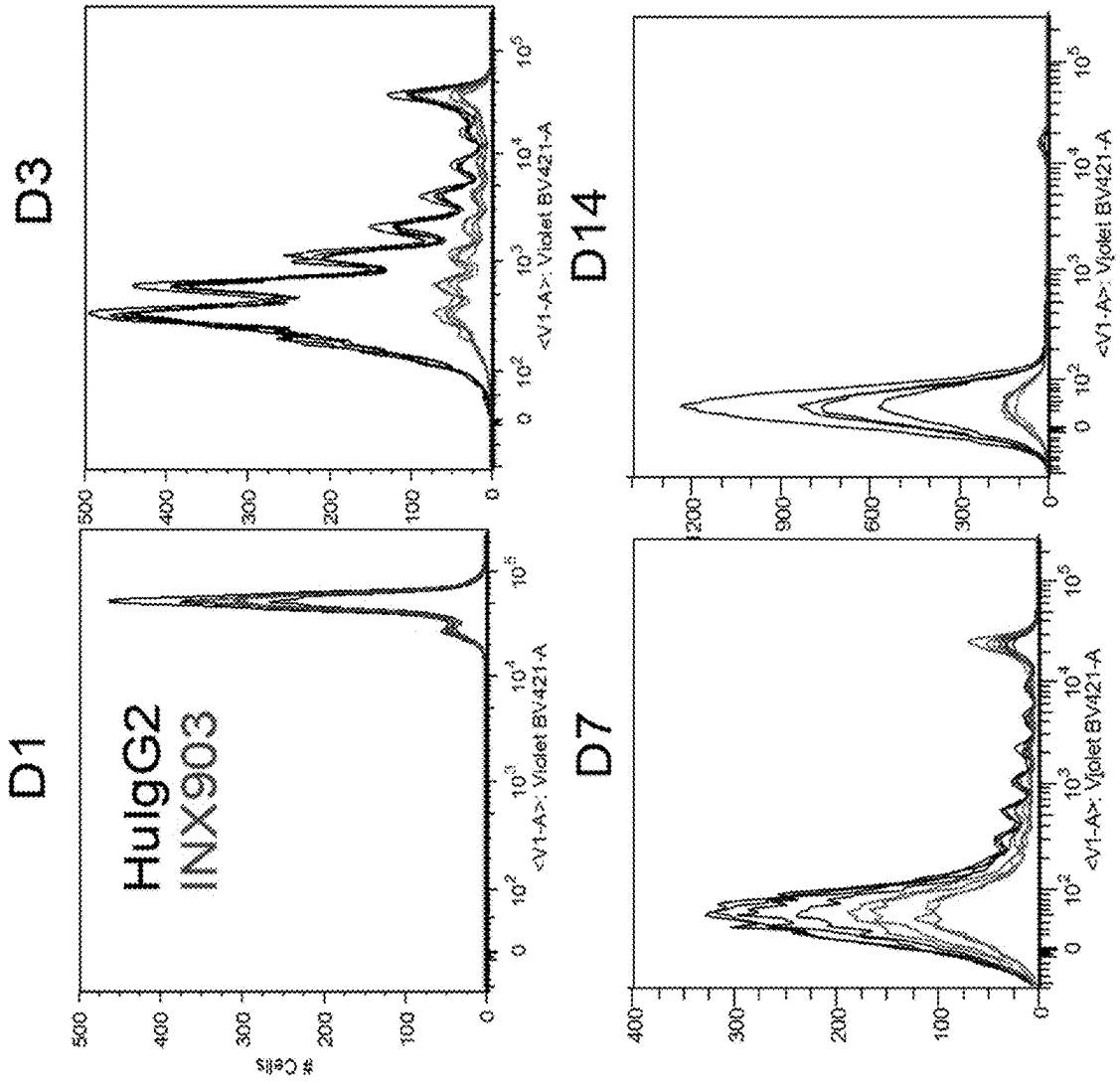
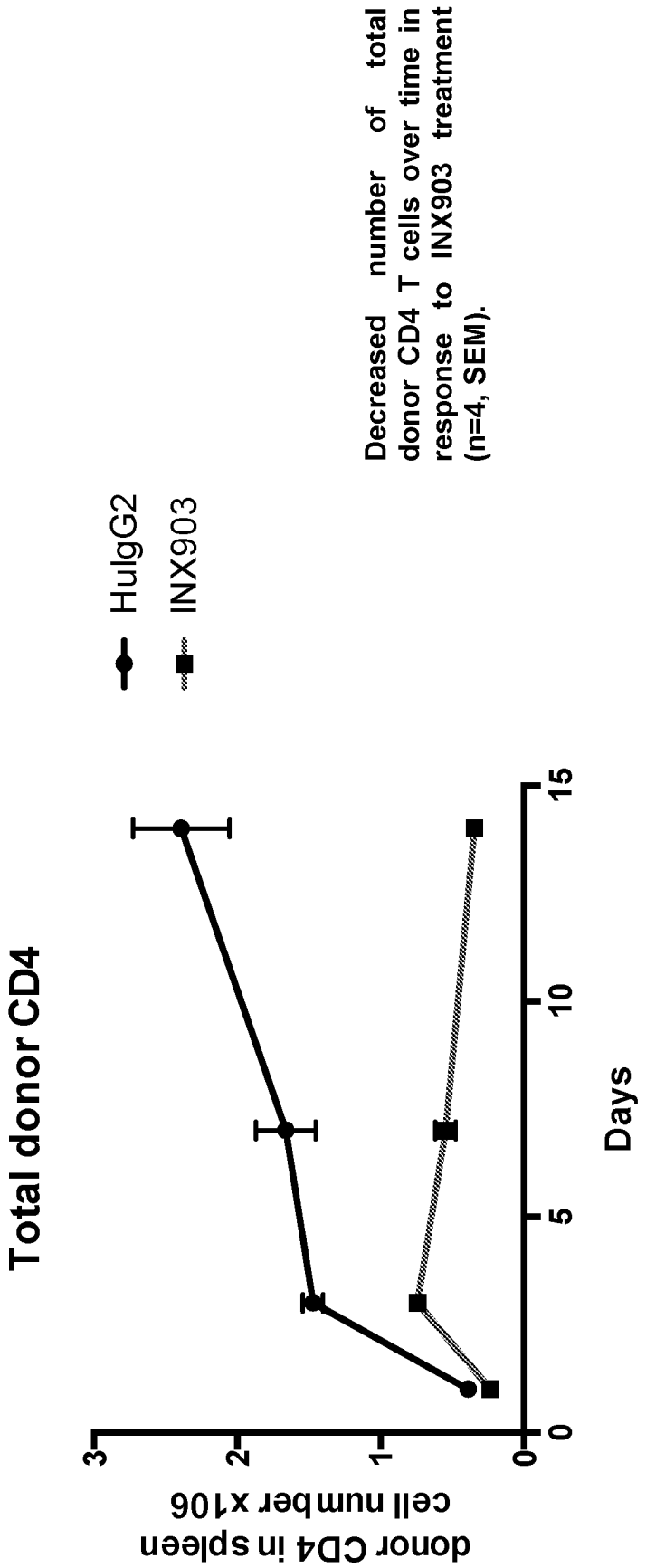
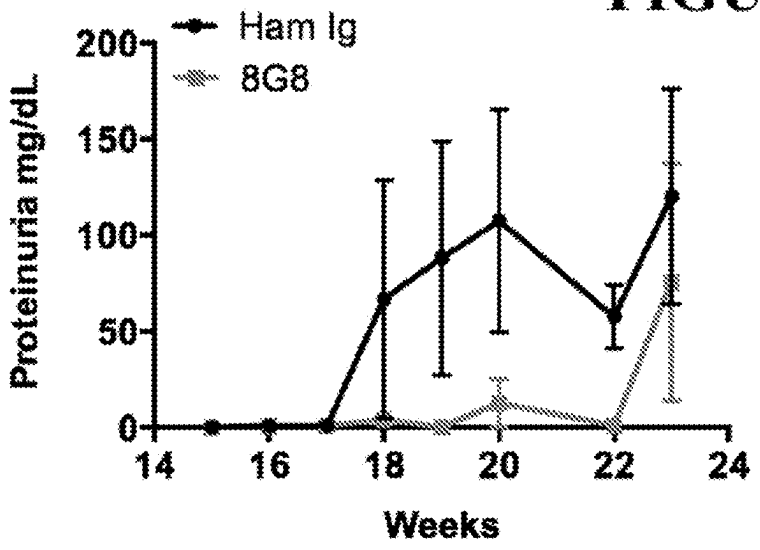


FIGURE 73



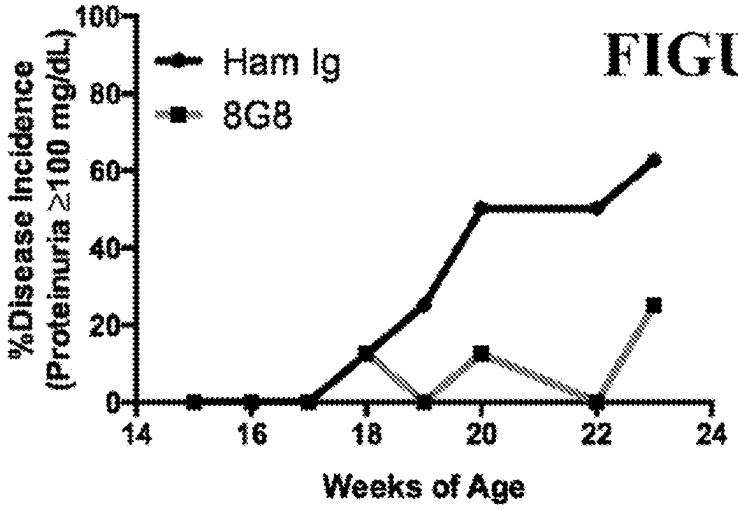
Decreased number of total donor CD4 T cells over time in response to INX903 treatment (n=4, SEM).

FIGURE 74A



MRL/lpr

FIGURE 74B



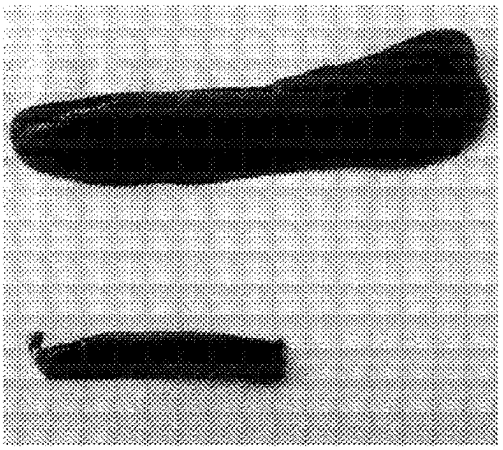


FIGURE 75

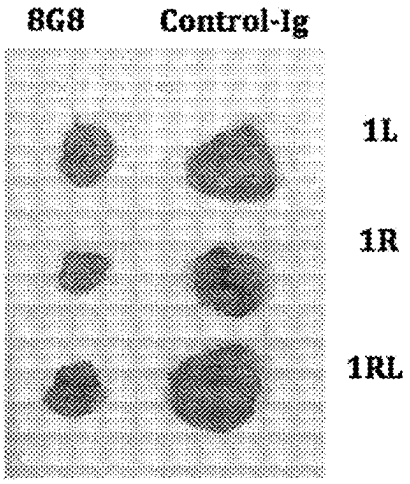


FIGURE 76

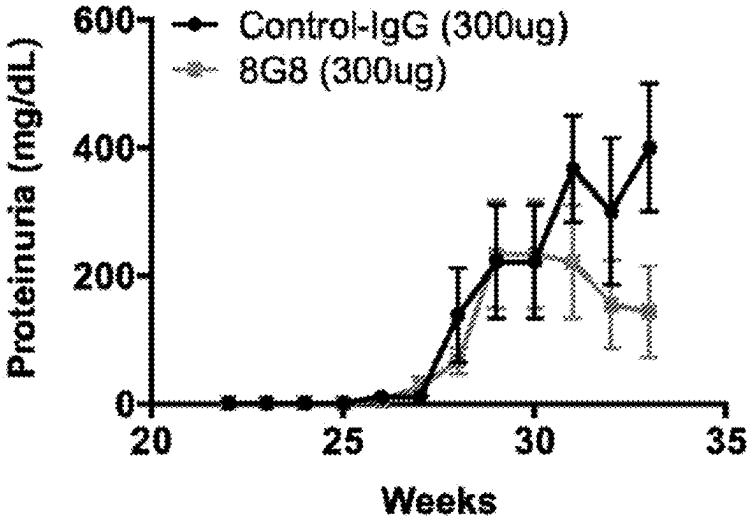
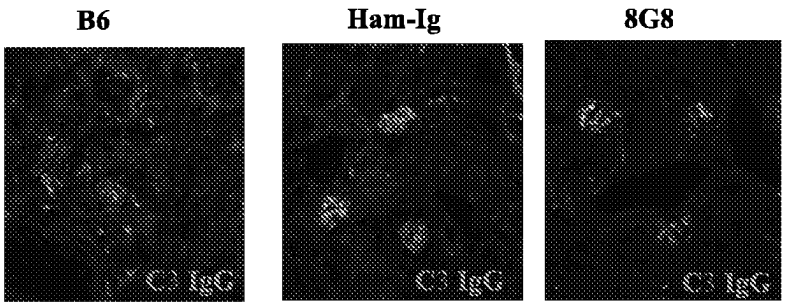


FIGURE 77

8G8 reduces proteinuria development in NZBWF-1 mice



8G8 exerts no impact on immune complex deposition in NZBWF-1 mice

FIGURE 78

ANTI-HUMAN VISTA ANTIBODIES AND USE THEREOF

RELATED APPLICATIONS

[0001] This application is a divisional of U.S. application Ser. No. 17/206,550, filed Mar. 19, 2021, which is a continuation of U.S. application Ser. No. 15/489,189 filed Apr. 17, 2017, which is a continuation of Int'l Appl. No. PCT/US2017/027800, filed Apr. 14, 2017, which claims priority to U.S. Provisional Application Nos. 62/323,193 filed Apr. 15, 2016, 62/343,355 filed May 31, 2016, 62/372,362 filed Aug. 9, 2016, 62/385,627 filed Sep. 9, 2016, 62/425,184 filed Nov. 22, 2016, 62/363,929 filed Jul. 19, 2016, 62/365,085 filed Jul. 21, 2016, 62/385,805 filed Sep. 9, 2016, 62/363,931 filed Jul. 19, 2016, 62/365,102 filed Jul. 21, 2016, 62/385,871 filed Sep. 9, 2016, 62/363,917 filed Jul. 19, 2016, 62/365,081 filed Jul. 21, 2016, 62/385,888 filed Sep. 9, 2016, 62/364,073 filed Jul. 19, 2016, 62/365,166 filed Jul. 21, 2016, 62/385,893 filed Sep. 9, 2016, 62/363,925 filed Jul. 19, 2016, 62/365,087 filed Jul. 21, 2016, 62/385,785 filed Sep. 9, 2016, 62/406,632 filed Oct. 11, 2016, each and all of which are incorporated herein by reference. This application relates to PCT application PCT/US17/27765 filed Apr. 14, 2017 "ANTI-HUMAN VISTA ANTIBODIES AND USE THEREOF" which is also being incorporated by reference and to which priority is also claimed.

[0002] This application includes as part of its disclosure a biological sequence listing text file named "1143260o002292.xml" having a size of 709,410 bytes that was created Oct. 10, 2024, which is incorporated by reference in its entirety.

FIELD

[0003] The invention in some embodiments relates to novel anti-human VISTA antibodies and antibody fragments, i.e., anti-human VISTA (V-region Immunoglobulin-containing Suppressor of T cell Activation(1)), ("VISTA") antibodies and antibody fragments. More specifically, the present application provides novel human VISTA agonists, i.e., anti-human VISTA antibodies and antibody fragments which agonize or promote the suppressive effects of human VISTA on immunity, particularly T cell immunity. Also, the invention relates to the use of such agonists to enhance or mimic the suppressive effects of VISTA on immunity such as its suppressive effects on $CD4^+$ or $CD8^+$ T cell proliferation, $CD4^+$ or $CD8^+$ T cell activation and its suppressive effect on the production of immune cytokines, particularly proinflammatory cytokines. Also the invention relates to the specific use of these agonistic antibodies and antibody fragments as prophylactics or therapeutics, especially in treating conditions wherein the prevention or inhibition of T cell immunity and the expression of proinflammatory cytokines is therapeutically beneficial such as autoimmunity, inflammation, allergic disorders, sepsis, GVHD or in alleviating the inflammatory side effects of some conditions such as cancer and more specifically IBD, psoriasis, GVHD, lupus, chronic infection and hepatotoxicity and rheumatoid arthritis.

BACKGROUND

[0004] Immune negative checkpoint regulator (NCR) pathways have proven to be extraordinary clinical targets in the treatment of human immune-related diseases. Blockade of two NCRs, CTLA-4 and PD-1, using monoclonal antibodies (mAbs) to enhance tumor immunity is revolutionizing the treatment of cancer and has established these pathways as clinically validated targets in human disease. Also soluble versions of NCR ligands that trigger NCR pathways have entered the clinic as immunosuppressive drugs to treat autoimmunity (i.e., AMP-110/B7-H4-Ig for Rheumatoid arthritis).

[0005] VISTA (see Ref 1), is an NCR ligand, whose closest phylogenetic relative is PD-L1. VISTA bears homology to PD-L1 but displays a unique expression pattern that is restricted to the hematopoietic compartment. Specifically, VISTA is constitutively and highly expressed on $CD11b^{high}$ myeloid cells, and expressed at lower levels on $CD4^+$ and $CD8^+$ T cells. Like PD-L1, VISTA is a ligand that profoundly suppresses immunity (Ref 1), and like PD-L1, blocking VISTA allows for the development of therapeutic immunity to cancer in pre-clinical oncology models (see Ref 2). Whereas blocking VISTA enhances immunity, especially $CD8^+$ and $CD4^+$ mediated T cell immunity, treatment with a soluble Ig fusion protein of the extracellular domain of VISTA (VISTA-Ig) suppresses immunity and has been shown to arrest the progression of multiple murine models of autoimmune disease.

[0006] Clear scientific evidence has shown that VISTA is a ligand that induces profound T cell suppression. Numerous antagonistic anti-human VISTA antibodies have been reported by different groups including Dartmouth College and Jannsen. These antibodies are useful in the treatment of conditions wherein the suppression of the immunosuppressive effects of VISTA on T cell immunity is desired such as cancer and infection. However, to the best of the inventors' knowledge no anti-human VISTA antibody or antibody fragment has been previously identified which agonizes the effects of human VISTA. Such agonistic anti-human VISTA antibodies and antibody fragments would be desirable in treating conditions wherein the suppression of immunity, particularly T cell immunity is desired and/or conditions wherein VISTA expression is aberrantly downregulated.

SUMMARY

[0007] It is an object of the invention to provide therapeutic and prophylactic methods for using antibodies and antibody fragments which specifically bind to human VISTA and variants thereof, e.g., chimeric, human, humanized or multispecific anti-human VISTA antibodies which specifically bind to human VISTA and which promote or mimic the effects of human VISTA on immunity.

[0008] It is a specific object of the invention to provide therapeutic and prophylactic methods of using an agonistic antibody or antibody fragment thereof comprising an antigen binding region that specifically binds to human VISTA wherein the agonistic antibody or antibody fragment binds to the same or overlapping epitope as any one of the anti-human VISTA antibodies having the CDR and variable heavy and light polypeptides shown in FIG. **4**.

[0009] It is a specific object of the invention to provide therapeutic and prophylactic methods of using an agonistic antibody or antibody fragment thereof comprising an antigen binding region that specifically binds to human VISTA wherein the antibodies or antibody fragments comprise variable heavy and light sequences having the CDR poly-

peptides of any one of the anti-human VISTA antibodies having the sequences shown in FIG. **4**.

[0010] It is a specific object of the invention to provide therapeutic and prophylactic methods using an agonistic antibody or antibody fragment thereof comprising an antigen binding region that specifically binds to human VISTA wherein the antibodies or antibody fragments comprise variable heavy and light sequences having the CDR polypeptides of an anti-human VISTA antibody selected from VSTB49-VSTB116.

[0011] It is a specific object of the invention to provide therapeutic and prophylactic methods of using an agonistic antibody or antibody fragment thereof comprising the CDRs of an anti-human VISTA antibody selected from VSTB49-VSTB116, which comprise a variable heavy and/or variable light polypeptide having at least 90%, 95%, or 96-99% sequence identity to the variable heavy and light polypeptide sequences of VSTB49-VSTB116.

[0012] It is a specific object of the invention to provide therapeutic and prophylactic methods of using an agonistic antibody or antibody fragment thereof comprising the same CDRs any one of VSTB49-VSTB116, which comprise a variable heavy and/or variable light polypeptide which is/are identical to the variable heavy and light polypeptide sequences of VSTB49-VSTB116.

[0013] It is a specific object of the invention to provide therapeutic and prophylactic methods of using an agonistic antibody or antibody fragment thereof which are chimeric, human, humanized, multispecific (e.g., bispecific) anti-human VISTA antibodies or antibody fragments comprising an antigen binding region that specifically binds to human VISTA which comprise variable heavy and light sequences having the CDR polypeptides as any one of the anti-human VISTA antibodies comprising the CDR and variable heavy and light polypeptides disclosed in FIG. **4**.

[0014] It is a specific object of the invention to provide therapeutic and prophylactic methods of using novel immunosuppressants, i.e., anti-human VISTA antibodies and antibody fragments, e.g., those containing human IgG2 constant domains or IgG2 Fc regions, optionally wherein the FcR binding capability of the human IgG2 constant domains or IgG2 Fc regions are maintained or are enhanced compared to the wild-type human IgG2 constant domains or IgG2 Fc regions, which agonize, elicit or mimic the effects of human VISTA on immunity, e.g., its suppressive effects on T cell activity, differentiation and proliferation and its suppressive effects on the expression of proinflammatory cytokines.

[0015] It is a specific object of the invention to provide therapeutic and prophylactic methods of using novel immunosuppressive antibodies and antibody fragments which enhance or mimic the suppressive effects of VISTA on T cell immunity, i.e., which suppress CD4+ or CD8+ T cell proliferation, CD4+ or CD8+ T cell activation and its suppression of the production of immune cytokines, particularly proinflammatory cytokines such as IL-2, IL-4, IL-6, IL-17, TNF-α, and/or GM-CSF(granulocyte-macrophage colony-stimulating factor), and its promoting effects on the expression of chemokines or chemoattractants such as KC (keratinocyte chemoattractant) or MIP-2(Macrophage inflammatory protein 2).

[0016] It is a specific object of the invention to provide therapeutic and prophylactic methods using novel immunosuppressive or agonistic anti-human VISTA antibodies and antibody fragments of specific epitopic specificity or which compete for binding to human VISTA with specific anti-human VISTA antibodies.

[0017] It is a specific object of the invention to provide therapeutic and prophylactic methods of using novel immunosuppressive or agonistic anti-human VISTA antibodies and antibody fragments of specific epitopic specificity or which compete for binding to human VISTA with specific anti-human VISTA antibodies which agonize (enhance, elicit or mimic) the suppressive effects of VISTA on immunity, e.g., its suppressive effects on T cell immunity, i.e., CD4+ or CD8+ T cell proliferation, CD4+ or CD8+ T cell activation, and/or which suppress the production of proinflammatory immune cytokines such as IL-2, IL-4, IL-6, IL-17, TNF-α, and/or GM-CSF(granulocyte-macrophage colony-stimulating factor), and its promoting effects on the expression of chemokines or chemoattractants such as KC (keratinocyte chemoattractant) or MIP-2(Macrophage inflammatory protein 2).

[0018] It is a specific object of the invention to provide therapeutic and prophylactic methods of using agonistic anti-human VISTA antibodies and antibody fragments as prophylactics or therapeutics, especially in treating conditions wherein preventing or inhibiting or reducing immune reactions is therapeutically desirable, and more particularly wherein the preventing or inhibiting or reducing T cell immunity, or more specifically CD4+ or CD8+ mediated T cell immunity is therapeutically beneficial such as autoimmunity, inflammation, allergic disorders, sepsis, GVHD, and/or in treating transplant or cell therapy recipients, e.g., CAR-T recipients, or in alleviating the inflammatory side effects of some conditions such as cancer.

[0019] It is another specific object of the invention to provide a diagnostic or therapeutic composition comprising a diagnostically or therapeutically effective amount of an agonist anti-human VISTA antibody according to the invention, e.g., one containing the same CDRs as any of the antibodies having the sequences shown in FIG. **4** which is suitable for use in human therapy, such as an intravenous, subcutaneous or intramuscular administrable composition.

[0020] It is another specific object of the invention to provide diagnostic or therapeutic methods which use an agonist antibody according to the invention in association with another immune agonist, e.g., a PD-1 or PD-L1 agonist, e.g., wherein the PD-1 or PD-L1 agonist is selected from an anti-PD-1 antibody or antibody fragment, an anti-PD-L1 antibody or antibody fragment, a PD-L1 polypeptide or fragment thereof which may be monovalent or multimeric, a PD-1 polypeptide or fragment thereof which may be monovalent or multimeric, or a complex or fusion protein comprising any of the foregoing.

[0021] It is another specific object of the invention to provide methods of contacting immune cells in vitro or in vivo with an agonist antibody according to the invention, e.g., human immune cells, e.g., wherein the contacted cells are infused into a human subject such as a subject who has an inflammatory, allergic or autoimmune condition, e.g., GVHD, chronic or acute hepatitis, RA, IBD, psoriasis, or lupus.

[0022] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated antibody or antibody

fragment thereof comprising an antigen binding region that specifically binds to human V-domain Ig Suppressor of T cell Activation (human VISTA), wherein the antibody or antibody fragment agonizes or promotes one or more of the effects of VISTA on immunity, e.g., a human IgG2 constant or human IgG2 Fc region optionally wherein the human IgG2 constant or Fc region of the antibody binds to Fc gamma receptors including human CD32A, e.g., wherein the IgG2 constant or Fc region comprises the native human IgG2 binding to one or more Fc receptors, optionally one or more of hFcγRI(CD64), FcγRIIA or hFcγRIIB, (CD32 or CD32A) and FcγRIIIA (CD16A) or FcγRIIIB (CD16B).

[0023] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic antibody or antibody fragment wherein the isolated antibody or antibody fragment competes with or binds to a VISTA epitope which includes or overlaps with the epitope bound by any of the anti-human VISTA antibodies having the sequences of FIG. **4**.

[0024] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic antibody or antibody fragment wherein the isolated antibody or antibody fragment competes with or binds to a VISTA epitope binds or interacts with one of more residues of an epitope comprising residues of LLDSGLYCCLVVEIRHHHSEHRVH (SEQ ID NO:92).

[0025] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic antibody or antibody fragment wherein the isolated antibody or antibody fragment competes with or binds to a VISTA epitope comprising one or more residues of 79EVQTCSERRPIR90 (SEQ ID NO:68), 48NVTLTCRLLGPV60, 153HHHSEHRVHGAM164, 52LTCRLLGPV60, 56LLGPVDKGHDVTFYK70, 113LAQRHGLESASDHHG127, 153HHHSEHRVHGAM164, 93TFQDLHLHHGGHQAA107, 146CLVVEIRHHHSEH158, 53TCRLLGPVDKG63, 123SDHHG127 and/or 153HHHSEHRVHGAM164.

[0026] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic antibody or antibody fragment wherein the isolated antibody or antibody fragment competes with or binds to a VISTA epitope comprising one or more residues of 79EVQTCSERRPIR90 (SEQ ID NO:68).

[0027] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic antibody or antibody fragment wherein the isolated antibody or antibody fragment promotes or enhances at least one effect of human VISTA on immunity, e.g. its suppressive effect on any one or more of T cell immunity, activation of monocytes, induction of T-cell proliferation; induction or suppression of cytokine expression, increased survival of monocytes, induction of antibody-dependent cell-mediated cytotoxicity (ADCC) in cells-expressing VISTA; and induction of antibody-dependent cellular phagocytosis (ADCP) in cells-expressing VISTA, e.g., wherein the isolated antibody or antibody fragment comprises an antigen binding region that specifically binds to human VISTA, wherein the antibody or antibody fragment comprises variable heavy and light sequences having the identical CDR polypeptides as any one of the anti-human VISTA antibodies having the CDR and variable heavy and light polypeptides shown in FIG. **4**, and/or comprises the same CDRs as an antibody selected from VSTB49-VSTB116 and/or comprises a variable heavy and/or variable light polypeptide having at least 90% sequence identity to those of an anti-human VISTA antibody selected from any one of VSTB49-VSTB116, wherein the variable heavy and light polypeptide sequences thereof are shown in FIG. **4** and/or comprises a variable heavy and/or variable light polypeptide having at least 95% sequence identity to those of an anti-human VISTA antibody selected from any one of VSTB49-VSTB116, wherein the variable heavy and light polypeptide sequences thereof are shown in FIG. **4** or comprises a variable heavy and/or variable light polypeptide having at least 96-99% sequence identity to those of an anti-human VISTA antibody selected from any one of VSTB49-VSTB116 and/or comprises a variable heavy and/or variable light polypeptide identical to those of an anti-human VISTA antibody selected from one of VSTB49-VSTB116, wherein the variable heavy and light polypeptide sequences thereof are shown in FIG. **4** and/or comprises a human constant domain, e.g., a human constant domain selected from IgG1, IgG2, IgG3 and IgG4, which optionally is modified, e.g., by deletion, substitution or addition mutations or any combination of the foregoing and/or wherein the isolated antibody or antibody fragment comprises or is a Fab, F(ab')2, or scFv antibody fragment.

[0028] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment wherein the isolated antibody or antibody fragment promotes or enhances at least one of the effects of human VISTA on immunity, e.g., selected from its suppressive effect T cell immunity, activation of monocytes, suppression of T-cell proliferation; induction or suppression of cytokine expression, increased survival of monocytes, suppression of antibody-dependent cell-mediated cytotoxicity (ADCC) in cells-expressing VISTA; and suppression of antibody-dependent cellular phagocytosis (ADCP) of cells-expressing VISTA, e.g., one comprising a human IgG2 constant or Fc region, e.g., wherein the isolated antibody or antibody fragment promotes or enhances the suppressive effect of human VISTA on immunity, e.g. its effect on any one or more of T cell immunity, activation of monocytes, T-cell proliferation; cytokine expression, survival of monocytes, antibody-dependent cell-mediated cytotoxicity (ADCC) in cells-expressing VISTA; and antibody-dependent cellular phagocytosis (ADCP) in cells-expressing VISTA.

[0029] It is another specific object of the invention to provide a method of treating or preventing an autoimmune,

allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment wherein the isolated antibody or antibody fragment inhibits T cell immunity and/or proinflammatory cytokine expression.

[0030] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment wherein the isolated antibody or antibody fragment comprises a human Fc region, e.g., human IgG1, IgG2, IgG3 and IgG4 or a chimera of any of the foregoing, and/or the isolated antibody or antibody fragment comprises a chimeric, human, multispecific or humanized antibody or antibody fragment and/or the isolated antibody or antibody fragment comprises a mutated human IgG2 constant domain or Fc region and/or the isolated antibody or antibody fragment comprises a human IgG2 constant domain or fragment thereof or an hIgG1, hIgG3, hIgG4, IgA, IgD, IgE, or IgM, wherein the entire or substantially the entire hinge and CH1 domains of said antibody and optionally the entire or substantially the entire light chain constant region have been replaced with the corresponding entire or substantially the entire light chain, and the hinge and CH1 domains ("H2 regions" or "H2 domains") of hIgG2 and/or the isolated antibody or antibody fragment (i) comprises an IgG2 Fc region wherein either or both of the heavy chain cysteine residue at position 127 and the light chain cysteine residue at position 214 (wherein numbering is according to Kabat) are deleted or changed to a different amino acid residue, resulting in an increase in the agonistic properties of the resultant modified antibody relative to an antibody wherein these residues are unchanged, (ii) the cysteine residue at position 214 in the H2 region of said antibody is mutated or substituted with another amino acid and/or one or more of the cysteine residues at positions 127, 232 or 233 of the heavy chain are deleted or substituted with another amino acid, (iii) it comprises a human IgG2 constant domain wherein at least one cysteine residue is deleted or changed to another amino acid, (iv) it competes with or binds to the same epitope on human VISTA as VSTB95 (variable heavy and light sequences shown in FIG. **4**).

[0031] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment wherein the isolated antibody or antibody fragment:

[0032] comprises the V_H CDRs of SEQ ID NO:100, 101 and 102 and the V_L CDRs of SEQ ID NO:103, 104 and 105;

[0033] comprises the V_H CDRs of SEQ ID NO:110, 111 and 112 and the V_L CDRs of SEQ ID NO:113, 114 and 115;

[0034] comprises the V_H CDRs of SEQ ID NO:120, 121 and 122 and the V_L CDRs of SEQ ID NO:123, 124 and 125;

[0035] comprises the V_H CDRs of SEQ ID NO:130, 131 and 132 and the V_L CDRs of SEQ ID NO:133, 134 and 135;

[0036] comprises the V_H CDRs of SEQ ID NO:140, 141 and 142 and the V_L CDRs of SEQ ID NO:143, 144 and 145;

[0037] comprises the V_H CDRs of SEQ ID NO:150, 151 and 152 and the V_L CDRs of SEQ ID NO:153, 154 and 155;

[0038] comprises the V_H CDRs of SEQ ID NO:160, 161 and 162 and the V_L CDRs of SEQ ID NO:163, 164 and 165;

[0039] comprises the V_H CDRs of SEQ ID NO:170, 171 and 172 and the V_L CDRs of SEQ ID NO:173, 174 and 175;

[0040] comprises the V_H CDRs of SEQ ID NO:180, 181 and 182 and the V_L CDRs of SEQ ID NO:183, 184 and 185;

[0041] comprises the V_H CDRs of SEQ ID NO:190, 191 and 192 and the V_L CDRs of SEQ ID NO:193, 194 and 195;

[0042] comprises the V_H CDRs of SEQ ID NO:200, 201 and 202 and the V_L CDRs of SEQ ID NO:203, 204 and 205;

[0043] comprises the V_H CDRs of SEQ ID NO:210, 211 and 212 and the V_L CDRs of SEQ ID NO:213, 214 and 215;

[0044] comprises the V_H CDRs of SEQ ID NO:220, 221 and 222 and the V_L CDRs of SEQ ID NO:223, 224 and 225;

[0045] comprises the V_H CDRs of SEQ ID NO:230, 231 and 232 and the V_L CDRs of SEQ ID NO:233, 234 and 235;

[0046] comprises the V_H CDRs of SEQ ID NO:240, 241 and 242 and the V_L CDRs of SEQ ID NO:243, 244 and 245;

[0047] comprises the V_H CDRs of SEQ ID NO:250, 251 and 252 and the V_L CDRs of SEQ ID NO:253, 254 and 255;

[0048] comprises the VH CDRs of SEQ ID NO:260, 261 and 262 and the V_L CDRs of SEQ ID NO:263, 264 and 265;

[0049] comprises the V_H CDRs of SEQ ID NO:270, 271 and 272 and the V_L CDRs of SEQ ID NO:273, 274 and 275;

[0050] comprises the V_H CDRs of SEQ ID NO:280, 281 and 282 and the V_L CDRs of SEQ ID NO:283, 284 and 285;

[0051] comprises the V_H CDRs of SEQ ID NO:290, 291 and 292 and the V_L CDRs of SEQ ID NO:293, 294 and 295;

[0052] comprises the V_H CDRs of SEQ ID NO:300, 301 and 302 and the V_L CDRs of SEQ ID NO:303, 304 and 305;

[0053] comprises the V_H CDRs of SEQ ID NO:310, 311 and 312 and the V_L CDRs of SEQ ID NO:313, 314 and 315;

[0054] comprises the V_H CDRs of SEQ ID NO:320, 321 and 322 and the V_L CDRs of SEQ ID NO:323, 324 and 325;

[0055] comprises the V_H CDRs of SEQ ID NO:330, 331 and 332 and the V_L CDRs of SEQ ID NO:333, 334 and 335;

[0056] comprises the V_H CDRs of SEQ ID NO:340, 341 and 342 and the V_L CDRs of SEQ ID NO:343, 344 and 345;

[0057] comprises the V_H CDRs of SEQ ID NO:350, 351 and 352 and the V_L CDRs of SEQ ID NO:353, 354 and 355;

[0058] comprises the V_H CDRs of SEQ ID NO:360, 361 and 362 and the V_L CDRs of SEQ ID NO:363, 364 and 365;

[0059] comprises the V_H CDRs of SEQ ID NO:370, 371 and 372 and the V_L CDRs of SEQ ID NO:373, 374 and 375;

[0060] comprises the V_H CDRs of SEQ ID NO:380, 381 and 382 and the V_L CDRs of SEQ ID NO:383, 384 and 385;

[0061] comprises the V_H CDRs of SEQ ID NO:390, 391 and 392 and the V_L CDRs of SEQ ID NO:393, 394 and 395;

[0062] comprises the V_H CDRs of SEQ ID NO:400, 401 and 402 and the V_L CDRs of SEQ ID NO:403, 404 and 405;

[0063] comprises the V_H CDRs of SEQ ID NO:410, 411 and 412 and the V_L CDRs of SEQ ID NO:413, 414 and 415;

[0064] comprises the V_H CDRs of SEQ ID NO:420, 421 and 422 and the V_L CDRs of SEQ ID NO:423, 424 and 425;

[0065] comprises the V_H CDRs of SEQ ID NO:430, 431 and 432 and the V_L CDRs of SEQ ID NO:433, 434 and 435;

[0066] comprises the V_H CDRs of SEQ ID NO:440, 441 and 442 and the V_L CDRs of SEQ ID NO:443, 444 and 445;

[0067] comprises the V_H CDRs of SEQ ID NO:450, 451 and 452 and the V_L CDRs of SEQ ID NO:453, 454 and 455;

[0068] comprises the V_H CDRs of SEQ ID NO:460, 461 and 462 and the V_L CDRs of SEQ ID NO:463, 464 and 465;

[0069] comprises the V_H CDRs of SEQ ID NO:470, 471 and 472 and the V_L CDRs of SEQ ID NO:473, 474 and 475;

[0070] comprises the V_H CDRs of SEQ ID NO:480, 481 and 482 and the V_L CDRs of SEQ ID NO:483, 484 and 485;

[0071] comprises the V_H CDRs of SEQ ID NO:490, 491 and 492 and the VL CDR polypeptides of SEQ ID NO:493, 494 and 495;

[0072] comprises the V_H CDRs of SEQ ID NO:500, 501 and 502 and the VL CDR polypeptides of SEQ ID NO:503, 504 and 505;

[0073] comprises the V_H CDRs of SEQ ID NO:510, 511 and 512 and the VL CDR polypeptides of SEQ ID NO:513, 514 and 515;

[0074] comprises the V_H CDRs of SEQ ID NO:520, 521 and 522 and the VL CDR polypeptides of SEQ ID NO:523, 524 and 525;

[0075] comprises the V_H CDRs of SEQ ID NO:530, 531 and 532 and the VL CDR polypeptides of SEQ ID NO:533, 534 and 535;

[0076] comprises the V_H CDRs of SEQ ID NO:540, 541 and 542 and the VL CDR polypeptides of SEQ ID NO:543, 544 and 545;

[0077] comprises the V_H CDRs of SEQ ID NO:550, 551 and 552 and the VL CDR polypeptides of SEQ ID NO:553, 554 and 555;

[0078] comprises the V_H CDRs of SEQ ID NO:560, 561 and 562 and the V_L CDRs of SEQ ID NO:563, 564 and 565;

[0079] comprises the V_H CDRs of SEQ ID NO:570, 571 and 572 and the V_L CDRs of SEQ ID NO:573, 574 and 575;

[0080] comprises the V_H CDRs of SEQ ID NO:580, 581 and 582 and the V_L CDRs of SEQ ID NO:583, 584 and 585;

[0081] comprises the V_H CDRs of SEQ ID NO:590, 591 and 592 and the V_L CDRs of SEQ ID NO:593, 594 and 595;

[0082] comprises the V_H CDRs of SEQ ID NO:600, 601 and 602 and the V_L CDRs of SEQ ID NO:603, 604 and 605;

[0083] comprises the V_H CDRs of SEQ ID NO:610, 611 and 612 and the V_L CDRs of SEQ ID NO:613, 614 and 615;

[0084] comprises the V_H CDRs of SEQ ID NO:620, 621 and 622 and the V_L CDRs of SEQ ID NO:623, 624 and 625;

[0085] comprises the V_H CDRs of SEQ ID NO:630, 631 and 632 and the V_L CDRs of SEQ ID NO:633, 634 and 635;

[0086] comprises the V_H CDRs of SEQ ID NO:640, 641 and 642 and the V_L CDRs of SEQ ID NO:643, 644 and 645;

[0087] comprises the V_H CDRs of SEQ ID NO:650, 651 and 652 and the V_L CDRs of SEQ ID NO:653, 654 and 655;

[0088] comprises the V_H CDRs of SEQ ID NO:660, 661 and 662 and the V_L CDRs of SEQ ID NO:663, 664 and 665;

[0089] comprises the V_H CDRs of SEQ ID NO:670, 671 and 672 and the V_L CDRs of SEQ ID NO:673, 674 and 675;

[0090] comprises the V_H CDRs of SEQ ID NO:680, 681 and 682 and the V_L CDRs of SEQ ID NO:683, 684 and 685;

[0091] comprises the V_H CDRs of SEQ ID NO:690, 691 and 692 and the V_L CDRs of SEQ ID NO:693, 694 and 695;

[0092] comprises the V_H CDRs of SEQ ID NO:700, 701 and 702 and the V_L CDRs of SEQ ID NO:703, 704 and 705;

[0093] comprises the V_H CDRs of SEQ ID NO:710, 711 and 712 and the V_L CDRs of SEQ ID NO:713, 714 and 715;

[0094] comprises the V_H CDRs of SEQ ID NO:720, 721 and 722 and the V_L CDRs of SEQ ID NO:723, 724 and 725;

[0095] comprises the V_H CDRs of SEQ ID NO:730, 731 and 732 and the V_L CDRs of SEQ ID NO:733, 734 and 735;

[0096] comprises the V_H CDRs of SEQ ID NO:740, 741 and 742 and the V_L CDRs of SEQ ID NO:743, 744 and 745;

[0097] comprises the V_H CDRs of SEQ ID NO:750, 751 and 752 and the V_L CDRs of SEQ ID NO:753, 754 and 755;

[0098] comprises the V_H CDRs of SEQ ID NO:760, 761 and 762 and the V_L CDRs of SEQ ID NO:763, 764 and 765;

[0099] comprises the V_H CDRs of SEQ ID NO:770, 771 and 772 and the V_L CDRs of SEQ ID NO:773, 774 and 775;

[0100] comprises the V_H CDRs of SEQ ID NO:780, 781 and 782 and the V_L CDRs of SEQ ID NO:783, 784 and 785;

[0101] comprises the V_H CDRs of SEQ ID NO:790, 791 and 792 and the V_L CDRs of SEQ ID NO:793, 794 and 795;

[0102] comprises the V_H CDRs of SEQ ID NO:800, 801 and 802 and the V_L CDRs of SEQ ID NO:803, 804 and 805;

[0103] comprises the V_H CDRs of SEQ ID NO:810, 811 and 812 and the V_L CDRs of SEQ ID NO: 813, 814 and 815.

[0104] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment wherein the isolated antibody or antibody fragment:

[0105] comprises the V_H polypeptide of SEQ ID NO:106 and the V_L polypeptide of SEQ ID NO:108;

[0106] comprises the V_H polypeptide of SEQ ID NO:116 and the V_L polypeptide of SEQ ID NO:118;

[0107] comprises the V_H polypeptide of SEQ ID NO:126 and the V_L polypeptide of SEQ ID NO:128;

[0108] comprises the V_H polypeptide of SEQ ID NO:136 and the V_L polypeptide f SEQ ID NO:138;

[0109] comprises the V_H polypeptide of SEQ ID NO:146 and the V_L polypeptide of SEQ ID NO:148;

[0110] comprises the V_H polypeptide of SEQ ID NO:156 and the V_L polypeptide of SEQ ID NO:158;

[0111] comprises the V_H polypeptide of SEQ ID NO:166 and the V_L polypeptide of SEQ ID NO:168;

[0112] comprises the V_H polypeptide of SEQ ID NO:176 and the V_L polypeptide of SEQ ID NO:178;

[0113] comprises the V_H polypeptide of SEQ ID NO:186 and the V_L polypeptide of SEQ ID NO:188;

[0114] comprises the V_H polypeptide of SEQ ID NO:196 and the V_L polypeptide of SEQ ID NO:198;

[0115] comprises the V_H polypeptide of SEQ ID NO:206 and the V_L polypeptide of SEQ ID NO:208;

[0116] comprises the V_H polypeptide of SEQ ID NO:216 and the V_L polypeptide of SEQ ID NO:218;

[0117] comprises the V_H polypeptide of SEQ ID NO:226 and the V_L polypeptide of SEQ ID NO:228;

[0118] comprises the V_H polypeptide of SEQ ID NO:236 and the V_L polypeptide of SEQ ID NO:238;

[0119] comprises the V_H polypeptide of SEQ ID NO:246 and the V_L polypeptide of SEQ ID NO:248;

[0120] comprises the V_H polypeptide of SEQ ID NO:256 and the V_L polypeptide of SEQ ID NO:258;

[0121] comprises the V_H polypeptide of SEQ ID NO:266 and the V_L polypeptide of SEQ ID NO:268;

[0122] comprises the V_H polypeptide of SEQ ID NO:276 and the VL polypeptide of SEQ ID NO:278;

[0123] comprises the V_H polypeptide of SEQ ID NO:286 and the V_L polypeptide of SEQ ID NO:288;

[0124] comprises the V_H polypeptide of SEQ ID NO:296 and the V_L polypeptide of SEQ ID NO:298;

[0125] comprises the V_H polypeptide of SEQ ID NO:306 and the V_L polypeptide of SEQ ID NO:308;

[0126] comprises the V_H polypeptide of SEQ ID NO:316 and the V_L polypeptide of SEQ ID NO:318;

[0127] comprises the V_H polypeptide of SEQ ID NO:326 and the V_L polypeptide of SEQ ID NO:328;

[0128] comprises the V_H polypeptide of SEQ ID NO:336 and the V_L polypeptide of SEQ ID NO:338;

[0129] comprises the V_H polypeptide of SEQ ID NO:346 and the V_L polypeptide of SEQ ID NO:348;

[0130] comprises the V_H polypeptide of SEQ ID NO:356 and the V_L polypeptide of SEQ ID NO:358;

[0131] comprises the V_H polypeptide of SEQ ID NO:366 and the V_L polypeptide of SEQ ID NO:368;

[0132] comprises the V_H polypeptide of SEQ ID NO:376 and the V_L polypeptide of SEQ ID NO:378;

[0133] comprises the V_H polypeptide of SEQ ID NO:386 and the V_L polypeptide of SEQ ID NO:388;

[0134] comprises the V_H polypeptide of SEQ ID NO:396 and the V_L polypeptide of SEQ ID NO:398;

[0135] comprises the V_H polypeptide of SEQ ID NO:406 and the V_L polypeptide of SEQ ID NO:408;

[0136] comprises the V_H polypeptide of SEQ ID NO:416 and the V_L polypeptide of SEQ ID NO:418;

[0137] comprises the V_H polypeptide of SEQ ID NO:426 and the V_L polypeptide of SEQ ID NO:428;

[0138] comprises the V_H polypeptide of SEQ ID NO:436 and the V_L polypeptide of SEQ ID NO:438;

[0139] comprises the V_H polypeptide of SEQ ID NO:446 and the V_L polypeptide of SEQ ID NO:448;

[0140] comprises the V_H polypeptide of SEQ ID NO:456 and the V_L polypeptide of SEQ ID NO:458;

[0141] comprises the V_H polypeptide of SEQ ID NO:466 and the V_L polypeptide of SEQ ID NO:468;

[0142] comprises the V_H polypeptide of SEQ ID NO:476 and the V_L polypeptide of SEQ ID NO:478;

[0143] comprises the V_H polypeptide of SEQ ID NO:486 and the V_L polypeptide of SEQ ID NO:488;

[0144] comprises the V_H polypeptide of SEQ ID NO:496 and the V_L polypeptide of SEQ ID NO:498;

[0145] comprises the V_H polypeptide of SEQ ID NO:506 and the V_L polypeptide of SEQ ID NO:508;

[0146] comprises the V_H polypeptide of SEQ ID NO:516 and the V_L polypeptide of SEQ ID NO:518;

[0147] comprises the V_H polypeptide of SEQ ID NO:526 and the V_L polypeptide of SEQ ID NO:528;

[0148] comprises the V_H polypeptide of SEQ ID NO:536 and the V_L polypeptide of SEQ ID NO:533, 534 and 535;

[0149] comprises the V_H polypeptide of SEQ ID NO:546 and the V_L polypeptide of SEQ ID NO:548;

[0150] comprises the V_H polypeptide of SEQ ID NO:556 and the V_L polypeptide of SEQ ID NO:558;

[0151] comprises the V_H polypeptide of SEQ ID NO:566 and the V_L polypeptide of SEQ ID NO:568;

[0152] comprises the V_H polypeptide of SEQ ID NO:576 and the V_L polypeptide of SEQ ID NO:578;

[0153] comprises the V_H polypeptide of SEQ ID NO:586 and the V_L polypeptide of SEQ ID NO:588;

[0154] comprises the V_H polypeptide of SEQ ID NO:596 and the V_L polypeptide of SEQ ID NO:598;

[0155] comprises the V_H polypeptide of SEQ ID NO:606 and the V_L polypeptide of SEQ ID NO:608;

[0156] comprises the V_H polypeptide of SEQ ID NO:616 and the V_L polypeptide of SEQ ID NO:618;

[0157] comprises the V_H polypeptide of SEQ ID NO:626 and the V_L polypeptide of SEQ ID NO:628;

[0158] comprises the V_H polypeptide of SEQ ID NO:636 and the V_L polypeptide of SEQ ID NO:638;

[0159] comprises the V_H polypeptide of SEQ ID NO:646 and the V_L polypeptide of SEQ ID NO:648;

[0160] comprises the V_H polypeptide of SEQ ID NO:656 and the V_L polypeptide of SEQ ID NO:658;

[0161] comprises the V_H polypeptide of SEQ ID NO:666 and the V_L polypeptide of SEQ ID NO:668;

[0162] comprises the V_H polypeptide of SEQ ID NO:676 and the V_L polypeptide of SEQ ID NO:678;

[0163] comprises the V_H polypeptide of SEQ ID NO:686 and the V_L polypeptide of SEQ ID NO:688;

[0164] comprises the V_H polypeptide of SEQ ID NO:696 and the V_L polypeptide of SEQ ID NO:698;

[0165] comprises the V_H polypeptide of SEQ ID NO:706 and the V_L polypeptide of SEQ ID NO:708;

[0166] comprises the V_H polypeptide of SEQ ID NO:716 and the V_L polypeptide of SEQ ID NO:718;

[0167] comprises the V_H polypeptide of SEQ ID NO:726 and the V_L polypeptide of SEQ ID NO:728;

[0168] comprises the V_H polypeptide of SEQ ID NO:736 and the V_L polypeptide of SEQ ID NO:738;

[0169] comprises the V_H polypeptide of SEQ ID NO:746 and the V_L polypeptide of SEQ ID NO:748;

[0170] comprises the V_H polypeptide of SEQ ID NO:756 and the V_L polypeptide of SEQ ID NO:758;

[0171] comprises the V_H polypeptide of SEQ ID NO:766 and the V_L polypeptide of SEQ ID NO:768;

[0172] comprises the V_H polypeptide of SEQ ID NO:776 and the V_L polypeptide of SEQ ID NO:778;

[0173] comprises the V_H polypeptide of SEQ ID NO:786 and the V_L polypeptide of SEQ ID NO:788;

[0174] comprises the V_H polypeptide of SEQ ID NO:796 and the V_L polypeptide of SEQ ID NO:798;

[0175] comprises the V_H polypeptide of SEQ ID NO:806 and the V_L polypeptide of SEQ ID NO:808; and

[0176] comprises the V_H polypeptide of SEQ ID NO:816 and the V_L polypeptide of SEQ ID NO: 818.

[0177] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody according to any of the foregoing which comprises a human IgG2 constant domain wherein optionally at least one cysteine residue is deleted or changed to another amino acid.

[0178] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing wherein the isolated antibody or antibody fragment comprises an agonistic anti-human VISTA antibody or antibody fragment which mediates any one or combination of at least one of the following immmunoinhibitory effects: (i) decreases immune response, (ii) decreases T cell activation, (iii) decreases cytotoxic T cell activity, (iv) decreases natural killer (NK) cell activity, (v) decreases T-cell activity, (vi) decreases pro-inflammatory cytokine secretion, (vii) decreases IL-2 secretion; (viii) decreases interferon-γ production, (ix) decreases Th1 response, (x) decreases Th2 response, (xi) increases cell number and/or activity of regulatory T cells, (xii) increases regulatory cell activity and/or one or more of myeloid derived suppressor cells (MDSCs), iMCs, mesenchymal stromal cells, TIE2-expressing monocytes, (xiii) increases regulatory cell activity and/or the activity of one or more of myeloid derived suppressor cells (MDSCs), iMCs, mesenchymal stromal cells, TIE2-expressing monocytes, (xiii) increases M2 macrophages, (xiv) increases M2 macrophage activity, (xv) increases N2 neutrophils, (xvi) increases N2 neutrophils activity, (xvii) increases inhibition of T cell activation, (xviii) increases inhibition of CTL activation, (xix) increases inhibition of NK cell activation, (xx) increases T cell exhaustion, (xxi) decreases T cell response, (xxii) decreases activity of cytotoxic cells, (xxiii) reduces antigen-specific memory responses, (xxiv) inhibits apoptosis or lysis of cells, (xxv) decreases cytotoxic or cytostatic effect on cells, (xxvi) reduces direct killing of cells, (xxvii) decreases Thl7 activity, and/or (xxviii) reduces complement dependent cytotoxicity and/or antibody dependent cell-mediated cytotoxicity, with the proviso that said anti-VISTA antibody or antigen-binding fragment may elicit an opposite effect to one or more of (i)-(xxviii) and optionally is used to treat autoimmunity, allergy, inflammation, transplant or sepsis.

[0179] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing in order to treat or prevent rheumatoid arthritis.

[0180] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing in order to treat or prevent GVHD.

[0181] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing in order to treat or prevent psoriasis.

[0182] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing in order to treat or prevent IBD or colitis or another inflammatory or autoimmune intestinal disorder.

[0183] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing in order to treat or prevent lupus.

[0184] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing in order to treat or prevent chronic or acute infection or inflammation or hepatotoxicity associated therewith, e.g., hepatitis A, B, C, D, E or G.

[0185] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing which method comprises the administration to a subject in need thereof at an agonistic antibody or antibody fragment which effects in vitro and/or in vivo any one or combination of at least one of the following immmunoinhibitory effects: (i) decreases immune response, (ii) decreases T cell activation, (iii) decreases cytotoxic T cell activity, (iv) decreases natural killer (NK) cell activity, (v) decreases T-cell activity, (vi) decreases pro-inflammatory cytokine secretion, (vii) decreases IL-2 secretion; (viii) decreases interferon-γ production, (ix) decreases Thl response, (x) decreases Th2 response, (xi) increases cell number and/or activity of regulatory T cells, (xii) increases regulatory cell activity and/or one or more of myeloid derived suppressor cells (MDSCs), iMCs, mesenchymal stromal cells, TIE2-expressing monocytes, (xiii) increases regulatory cell activity and/or the activity of one or more of myeloid derived suppressor cells (MDSCs), iMCs, mesenchymal stromal cells, TIE2-expressing monocytes, (xiii) increases M2 macrophages, (xiv) increases M2 macrophage activity, (xv) increases N2 neutrophils, (xvi) increases N2 neutrophils activity, (xvii) increases inhibition of T cell activation, (xviii) increases inhibition of CTL activation, (xix) increases inhibition of NK cell activation, (xx) increases T cell exhaustion, (xxi) decreases T cell response, (xxii) decreases activity of cytotoxic cells, (xxiii) reduces antigen-specific memory responses, (xxiv) inhibits apoptosis or lysis of cells, (xxv) decreases cytotoxic or cytostatic effect on cells, (xxvi) reduces direct killing of cells, (xxvii) decreases Thl7 activity, and/or (xxviii) reduces complement dependent cytotoxicity and/or antibody dependent cell-mediated cytotoxicity, with the proviso that said anti-VISTA antibody or antigen-binding fragment may elicit an opposite effect to one or more of (i)-(xxviii) and optionally is used to treat autoimmunity, allergy, inflammation, transplant or sepsis.

[0186] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing in the treatment or prevention of allergy, autoimmunity, transplant, gene therapy, inflammation, cancer, GVHD or sepsis, or to treat or prevent inflammatory, autoimmune, or allergic side effects associated with any of the foregoing therewith in a human subject.

[0187] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing further comprising the administration of another immunomodulatory antibody or fusion protein which is selected from immmunoinhibitory antibodies or fusion proteins targeting one or more of CTLA4, PD-1, PDL-1, LAG-3, TIM-3, BTLA, B7-H4, B7-H3, VISTA, and/or agonistic antibodies or fusion protein targeting one or more of CD40, CD137, OX40, GITR, CD27, CD28 or ICOS.

[0188] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing which includes assaying VISTA protein by the individual's cells or in bodily fluids prior, concurrent and/or after treatment, e.g., on hematopoietic cells and/or on hematopoietic cells selected from any one or more of myeloid lineage cells and/or a lymphocytes, monocyte or a neutrophils, T cells, B cells, a natural killer (NK) cells or a natural killer T (NKT) cells.

[0189] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing wherein the agonist anti-human VISTA antibody or fragment comprises the same CDRs as an antibody selected from VSTB49-VSTB116 and a human IgG2 Fc region which optionally may be mutated, optionally wherein the IgG2 constant or Fc region retains native FcR binding and/or the ability to bind CD32A and/or the agonist anti-human VISTA antibody or fragment comprises an affinity or K_D for human VISTA which is 50M or less as determined by surface plasmon resonance at 37° C. or the agonist anti-human VISTA antibody or fragment comprises an affinity or K_D for human VISTA which is 1 nM or less as determined by surface plasmon resonance at 37° C.

[0190] It is another specific object of the invention to provide a method of using an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing to elicit immunosuppression in vitro or in vivo.

[0191] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing which is selected from any of the antibodies having the variable sequences of FIG. **4**.

[0192] It is an object to further provide methods of treating or preventing autoimmunity, allergy and inflammation in a subject in need thereof, e.g., an individual with a an acute or chronic human autoimmune, allergic and inflammatory condition, by the administration of an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment wherein said immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment, e.g., wherein said immunosuppressive or agonistic anti-human VISTA anti-

body or antibody fragment agonizes at least one of the effects of human VISTA on immunity, e.g., its suppressive effects on T cell activity, differentiation and proliferation, cytokine levels and B cell immunity.

[0193] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing which is used to treat or prevent lupus or a lupus-like condition or lupus-like symptoms or a method of reversing, stabilizing and reducing the pathological symptoms associated with lupus or lupus-like conditions by the administration of an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment, e.g., "Systemic Lupus Erythematosus" or ("SLE"), cutaneous lor skin lupus, drug-induced lupus and neonatal lupus.

[0194] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing which is used to treat or prevent kidney inflammation, inflammatory kidney damage or proteinuria associated with an autoimmune or inflammatory condition in a subject in need thereof by the administration of an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment.

[0195] It is another specific object of the invention to provide a method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated agonistic anti-human VISTA antibody or antibody fragment according to any of the foregoing which is used to treat or prevent an inflammatory condition involving inflammation induced splenomegaly or lymphoproliferation in a subject in need thereof by the administration of an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment.

[0196] It is another specific object of the invention to provide a method of promoting IL-9 expression and/or reducing LIX/CXCL5 expression in a subject in need thereof by the administration of an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment according to the invention.

[0197] It is another specific object of the invention to provide a method of treating, inhibiting or preventing at least one of pathologic side effect of lupus or a lupus-like condition wherein said symptoms include proteinuria, autoantibodies, increased expression of cytokines and other factors associated with inflammation, inflammation of the kidneys, i.e., lupus nephritis, kidney damage increased blood pressure in the lungs, i.e., pulmonary hypertension, breathing difficulties, Inflammation of the nervous system and brain, inflammation in cranial blood vessels, hardening of the arteries or coronary artery disease, skin rash, skin lesions, hair loss or any combination of the foregoing by the administration of an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment according to the invention, optionally further including the administration of another drug used for the treatment of lupus which optionally is selected from corticosteroids, other anti-inflammatory agents, anti-malarial drugs, .anticoagulants, ACTH, other immunosuppressants such as methotrexate, cyclophosphamide, and other immunomodulatory antibodies such as belimumab.

[0198] It is another specific object of the invention to provide a method for preventing the development of GvHD complications, e.g., acute or chronic GVHD in a human patient which comprises administering to the human patient an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment according to the invention.

[0199] It is another specific object of the invention to provide a method for treating GvHD complications in a human patient, e.g., acute or chronic GVHD which comprises administering to the human patient an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment.

[0200] It is another specific object of the invention to provide a method for treating an organ, tissue or immune cells that are to be transplanted into a recipient in order to prevent an acute or chronic GvHD response by contacting said organ, tissue or immune cells that are to be transplanted into a recipient with an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment., e.g., wherein the transplanted cells, tissue or organ are allogeneic or xenogeneic, e.g., allogeneic bone marrow or hematopoietic cells or allogeneic precursors of bone marrow lineage cells and/or wherein said immunosuppressive or agonistic anti-human VISTA antibody or said antibody fragment is administered prior, concurrent or after transplant or a combination thereof and/or wherein the transplant comprises allogeneic cells which are administered to the patient to treat a malignant or genetic or other disease of the blood, e.g., aplastic anemia, myelofibrosis, or bone marrow failure following chemotherapy and radiation therapy.

[0201] It is another specific object of the invention to provide a method for reducing susceptibility to an opportunistic infection in a subject who is a bone marrow transplant recipient, comprising selecting a subject who has had an allogeneic bone marrow or hematopoietic stem cell transplant; and administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising a VISTA agonist antibody and an effective amount of an antigen of the opportunistic infection; wherein the pharmaceutical composition and the antigen reduce the susceptibility to the opportunistic infection in the subject, optionally further comprising administering or contacting the transplant cells, tissue or organ with an immunosuppressive drug and/or which further includes the administration or use of another drug which optionally is selected from TNF-alpha antagonists, IL-6 antagonists, hydroxychloroquine, corticosteroids, other anti-inflammatory agents, anticoagulants, ACTH, and other immunosuppressants such as methotrexate, cyclophosphamide, sulfasalazine, leflunomide, sodium aurothiomalate, cyclosporin, B cell depleting and inhibitory antibodies and other immunomodulatory antibodies.

[0202] It is another specific object of the invention to provide a method of treating or preventing treating or preventing psoriasis or another inflammatory skin condition, e.g., one involving the infiltration of immune cells, e.g., T cells, or a method of reversing, stabilizing and reducing the pathological symptoms associated with psoriasis or another inflammatory skin condition, e.g., one involving the infiltration of immune cells by the administration of an immunosuppressive or agonistic anti-human VISTA antibody or

antibody fragment according to the invention, optionally wherein said psoriasis or another inflammatory skin condition, e.g., one involving the infiltration of immune cells is selected from plaque psoriasis, pustular psoriasis, inverse psoriasis, guttate psoriasis, erythrodermic psoriasis, drug-induced psoriasis, or comprises plaque psoriasis.

[0203] It is another specific object of the invention to provide a method of treating or preventing inhibiting, reversing, or preventing the infiltration of $CD3^+$ T cells into a tissue wherein said infiltration is associated with the pathology of an autoimmune or inflammatory condition in a subject in need thereof by the administration of an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment.

[0204] It is another specific object of the invention to provide a method of treating, inhibiting or preventing at least one of pathologic side effect of psoriasis or another inflammatory skin condition wherein said symptoms include severe itching, skin plaques, redness, other skin discoloration or patchiness, rash, skin pustules, skin scaliness, nail pitting or discoloration or any combination of the foregoing by the administration of an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment optionally including the administration of another drug or used for the treatment of psoriasis or another inflammatory skin condition which optionally is selected from IL-12 antagonists, IL-17 antagonists, IL-23 antagonists, TNF-alpha antagonists, IL-6 antagonists, hydroxychloroquine, corticosteroids, other anti-inflammatory agents, ACTH, and other immunosuppressants such as methotrexate, cyclophosphamide, sulfasalazine, leflunomide, sodium aurothiomalate, cyclosporin, retinoids, vitamin D analogs, ciclosporin, hydroxycarbamide, fumarates such as dimethyl fumarate, and other immunomodulatory antibodies.

[0205] It is another specific object of the invention to provide a method of treating or preventing treating or preventing an arthritis or arthritis-like conditions or arthritis and arthritis-like symptoms or a method of reversing, stabilizing and reducing the pathological symptoms associated with arthritis and arthritis-like conditions by the administration of an immunosuppressives or agonistic anti-human VISTA antibody or antibody fragment, e.g., wherein arthritis and arthritis-like conditions are selected from rheumatoid arthritis ("RA"), psoriatic arthritis ("PA") and osteoarthritis ("OA").

[0206] It is another specific object of the invention to provide a method of treating or preventing treating or preventing joint inflammation, or joint pain associated with an autoimmune or inflammatory condition in a subject in need thereof by the administration of an immunosuppressives or agonistic anti-human VISTA antibody or antibody fragment.

[0207] It is another specific object of the invention to provide a method of treating, inhibiting or preventing at least one of pathologic side effect of arthritis or an arthritis-like conditions wherein said symptoms include joint damage, joint pain, lung or heart inflammation, low red blood cell count, fever, acute or chronic fatigue, vasculitis, fibrosis such as lung fibrosis, renal amyloidosis, atherosclerosis, myocardial infarction, stroke or any combination of the foregoing by the administration of an immunosuppressives or agonistic anti-human VISTA antibody or antibody fragment.

[0208] It is another specific object of the invention to provide a method for preventing or treating acute or chronic infection and inflammatory and/or cytokine responses associated with acute or chronic infection in a human patient which comprises administering to the human patient an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment.

[0209] It is another specific object of the invention to provide a method for preventing or treating acute or chronic hepatitis infection and inflammatory and/or cytokine responses associated with acute or chronic hepatitis infection in a human patient which comprises administering to the human patient an immunosuppressive or agonistic anti-human VISTA antibody or antibody fragment.

[0210] It is another specific object of the invention to provide a method for preventing or treating hepatotoxicity or liver damage e.g., associated with acute or chronic infection and inflammatory and/or cytokine responses associated with acute or chronic infection or cirrhosis or alcohol or drug abuse in a human patient which comprises administering to the human patient an agonistic anti-human VISTA antibody or antibody fragment, e.g., wherein the treated patient has hepatitis A, B, C, D, E or G.

[0211] It is another specific object of the invention to provide a therapeutic or prophylactic method according to any of the foregoing wherein the agonistic anti-VISTA antibody is administered by a systemic or non-systemic route mode of administration, e.g., the foregoing claims wherein the agonistic anti-VISTA antibody is administered by injection, topically, inhaled, or orally and/or the agonistic anti-VISTA antibody is administered by intravenous, subcutaneous, intraarterial, intramuscular, parenteral, spinal or epidermal administration (e.g., by injection or infusion) and/or the agonistic anti-VISTA antibody is administered by a systemic or non-systemic route mode of administration and/or the agonistic anti-VISTA antibody is administered by intravenous, subcutaneous, intraarterial, intramuscular, parenteral, spinal or epidermal administration (e.g., by injection or infusion).

[0212] It is another specific object of the invention to provide a therapeutic or prophylactic method, composition or an antibody or antibody fragment according to any of the foregoing wherein the agonistic anti-VISTA antibody is administered in association with another immune agonist, e.g., an agonistic anti-PD-1 antibody or antibody fragment, an agonistic anti-PD-L1 antibody or antibody fragment, an agonistic PD-L1 polypeptide or fragment thereof which may be monovalent or multimeric, an agonistic PD-1 polypeptide or fragment thereof which may be monovalent or multimeric, or a complex or fusion protein comprising any of the foregoing wherein these agonists may be administered separately or in combination and in either order.

[0213] It is another specific object of the invention to provide a therapeutic or prophylactic method or an antibody or antibody fragment according to any of the foregoing wherein the agonistic anti-VISTA antibody is human, humanized, multispecific or chimeric.

[0214] It is another specific object of the invention to provide a therapeutic or prophylactic method, composition or an antibody or antibody fragment according to any of the foregoing wherein the agonistic anti-VISTA comprises human IgG2 constant or Fc regions which optionally may be mutated.

[0215] It is another specific object of the invention to provide a therapeutic or prophylactic method or an antibody or antibody fragment according to any of the foregoing wherein the agonistic anti-VISTA antibody comprises a human IgG2 constant domain or fragment thereof or an hIgG1, hIgG3, hIgG4, IgA, IgD, IgE, or IgM, wherein the entire or substantially the entire hinge and CH1 domains of said antibody and optionally the entire or substantially the entire light chain constant region have been replaced with the corresponding entire or substantially the entire light chain, and the hinge and CH1 domains ("H2 regions" or "H2 domains") of hIgG2.

[0216] It is another specific object of the invention to provide a therapeutic or prophylactic method or an antibody or antibody fragment according to any of the foregoing wherein the agonistic anti-VISTA antibody comprises a human IgG2 constant domain or fragment thereof wherein either or both of the heavy chain cysteine residue at position 127 and the light chain cysteine residue at position 214 (wherein numbering is according to Kabat) are deleted or changed to a different amino acid residue, resulting in an increase in the agonistic properties of the resultant modified antibody relative to an antibody wherein these residues are unchanged and/or the VISTA agonist antibody comprises a human IgG2 constant domain or fragment thereof wherein the cysteine residue at position 214 in the H2 region of said antibody is mutated or substituted with another amino acid and/or one or more of the cysteine residues at positions 127, 232 or 233 of the heavy chain are deleted or substituted with another amino acid and/or the VISTA agonist antibody comprises a human IgG2 constant domain or fragment thereof wherein at least one cysteine residue is deleted or changed to another amino acid and/or the agonist comprises an antibody having the same CDRs as any of the antibodies in FIG. **4**.

[0217] It is another specific object of the invention to provide a therapeutic or prophylactic method according to any of the foregoing or an antibody or antibody fragment according to any of the foregoing wherein the agonistic anti-VISTA antibody competes with or binds to the same epitope on human VISTA as any of 1E8, GA1, GG8, or any of the other antibodies having the sequences shown in FIG. **4**.

[0218] It is another specific object of the invention to provide a therapeutic or prophylactic method according to any of the foregoing or an antibody or antibody fragment according to any of the foregoing wherein the agonistic anti-VISTA antibody binds to an epitope on human VISTA comprising one or more of the residues of the epitope on human VISTA bound by any of 1E8, GA1, GG8, INX800, INX01, INX802, INX900-919 or any of the other antibodies having the sequences shown in FIG. **4**.

BRIEF DESCRIPTION OF THE FIGURES

[0219] FIGS. **1**A-**1**D. This figure shows in vitro and in vivo screening assays which can be used to identify suppressive VISTA mAbs. 1A) Purified T cells were plated on top of anti-CD3 in the presence of the indicated mAb for 72 hours. Proliferation was measured by H3 incorporation. 1B) Purified DO11.10 T cells were stimulated by ISQ pulsed APCs for 6 days in the presence of the indicated antibody. Proliferation was measured through use of CTV dilution dye. C) GVHD was induced by transfer of C57BL/6 cells into irradiated BALB/c recipients. Mice were injected I.P. with 200 μg of antibody on day 0, 2 and 4 post transfer and survival was analyzed. D) Mice were treated with 10 mpk of the indicated antibody 3 hours prior to administration of ConA (15 mpk) and IL-2 was analyzed in plasma at 6 by Luminex.

[0220] FIG. **2**A-**2**F. This figure shows that agonist VISTA antibodies are immunosuppressive in multiple models of autoimmune disease. **2**A) NZB/W F1 mice were treated 3×/week with either 8G8 or Ham Ig (200 μg) starting at 25 weeks until the end of the experiment. "X" denotes time points where the control treated group had all been sacrificed. B) Mice were treated with 200 μg of antibody 3 hours prior to administration of 15 mg/kg (mpk) of ConA and survival was followed for 80 hours. **2**C) Mice were treated sequentially with Collagen II mAb followed by LPS and arthritis was measured by measuring for paw swelling. 8G8 and Ham-Ig were administered (200 μg) 3× every other day. **2**D) Imiquimod was applied to the ear of mice daily. At day 14, 8G8 or Ham-Ig (200 μg) were administered every other day and ear thickness was measured with calipers. **2**E, **2**F) Imiquimod was applied to the backs of mice daily. At day 9, mice were euthanized and skin was sectioned & stained for CD3 expression by IHC.

[0221] FIG. **3**. This figure shows the expression of VISTA in WT and hV-KI mice. CD4+ T cells, $CD8^+$ T cells, Tregs ($CD4^+$ $FoxP3^+$), and monocytes, $CD11b^+$, $Ly6C^+$, $Ly6G^-$ were isolated from the lymph nodes of WT and VISTA KI mice, and stained with αVISTA antibodies against mouse or human protein respectively.

[0222] FIGS. **4**A-**4**YY contains the sequences of different anti-human VISTA antibodies including those of INX800, INX801, and INX900-INX919.

[0223] FIG. **5** shows the effects of exemplary anti-human VISTA antibodies, i.e., INX800 and INX801 in a ConA hepatitis model which assesses the effects thereof on the expression of different cytokines, chemokines and chemoattractants.

[0224] FIG. **6** shows the effects of exemplary anti-human VISTA antibodies, i.e., INX800 and INX801 in an in vivo graft versus host disease (GVHD) animal model.

[0225] FIG. **7** shows the effects of exemplary agonistic anti-human VISTA antibodies, i.e., INX800 or INX801 on CD3-driven T cell immune responses.

[0226] FIG. **8** shows the effects of exemplary agonistic anti-human VISTA antibodies, i.e., INX800 or INX801 on the number of specific T cell populations or on total T cell numbers.

[0227] FIG. **9** compares the effects of exemplary anti-human VISTA antibodies in ConA assays and on the expression of select proinflammatory cytokines and inflammation markers, i.e., IL-2, γ interferon and IL-12p70.

[0228] FIGS. **10**A-**10**C: shows different IgG2 Isoforms. (**10**A) Disulfide shuffling leads to isoforms A and B, along with the transition for A/B (figure from Zhang, A. et al., 2015). (**10**B) Isoforms are distinguishable by RP-HPLC. (**10**C) Observed RP-HPLC chromatogram for INX901.

[0229] FIG. **11**: shows chemical enrichment of IgG2 A or B isoforms. (Black line, top) Chromatogram shows a dominant left-most peak defining the B-form. (Red line, bottom) Chromatogram shows a dominant right peak defining the A-form.

[0230] FIG. **12**: compares INX901 Fc-silent variants with respect to disulfide shuffling. (Top) INX901 on an IgG2 backbone exhibits an expected mixture of A, A/B, and B

isoforms. (Middle) INX901Si on a silent IgG1 backbone exists as a single isoform. (Bottom) INX901HSi possesses an IgG1 silent Fc region with a CH1/hinge from IgG2, which enables disulfide shuffling equivalent to native IgG2.

[0231] FIG. **13**. Biochemically skewed INX901 forms can still reduce cytokine production in the MLR. Supernatants from two separate MLRs were analyzed for cytokine production at the 72-hour time point by Luminex analysis. INX901 parental, A skew and B skew all reduced the production of TNFα and IL-2 in a dose dependent fashion.

[0232] FIG. **14**. Genetically locked INX901 forms can still reduce cytokine production in the MLR, but Fc silent variants cannot. Supernatants from each MLR were analyzed for cytokine production at the 72-hour time point by Luminex analysis. INX901 parental, A lock and B lock all reduced the production of TNFα and IL-2 in a dose dependent fashion. The Si and HSi variants, which contain mutations to silence the Fc domain, did not consistently suppress cytokine production.

[0233] FIG. **15**. Genetically locked INX908 forms can still reduce cytokine production in the MLR, but Fc silent variants cannot. Supernatants from each MLR were analyzed for cytokine production at the 72-hour time point by Luminex analysis. INX908 parental, A lock and B lock all reduced the production of TNFα and IL-2 in a dose dependent fashion. The Si and HSi variants, which contain mutations to silence the Fc domain, did not consistently suppress cytokine production.

[0234] FIG. **16**. This figure schematically describes the Pepscan® technology used to identify linear and discontinuous epitopes bound by agonist anti-human VISTA antibodies.

[0235] FIG. **17**: This figure shows that agonist anti-human VISTA antibodies bind to the same core sequence.

[0236] FIG. **18**: This figure summarizes the epitope analysis for different anti-human VISTA antibodies according to the invention.

[0237] FIG. **19**: This figure shows the epitopes bound by agonist anti-human VISTA antibodies and further identifies important residues involved in binding.

[0238] FIG. **20**: Changes in CD4 T cells in peripheral blood. Absolute numbers in 100 μl of blood (left graph); frequencies of CD45+ cells (center graph); frequencies of CD4+ cells (right graph) (n=8 per group, SEM, statistic unpaired T-test, no equal SD).

[0239] FIG. **21**: Changes in CD4 T cell activation status in peripheral blood. (n=8 per group, SEM, statistic unpaired T-test, no equal SD) (MFI: median fluorescence intensity).

[0240] FIG. **22**: INX901 treatment prevents weight loss associated with colitis progression. (n=8 per group, SEM).

[0241] FIG. **23**: INX901 treatment prevented colon shortening. (n=8 or 4 per group, SEM, statistic unpaired T-test, no equal SD).

[0242] FIG. **24**: INX901 treatment prevented colitis development. Representative pictures of H&E stained sections of the colon for each mouse group. Magnification: pictures on the top are at 4×, on the bottom at 20×. Arrows indicate areas with abundant inflammatory infiltrates. Note their complete absence in the INX901-treated colon sample.

[0243] FIG. **25** shows INX901 treatment prevented $CD3^+$ T cell recruitment to the colon. Representative pictures of CD3 stained sections of the colon for each mouse group. Magnification: pictures on the top are at 4×, on the bottom at 20×.

[0244] FIG. **26**: INX901 treatment prevented myeloid (CD11b+) cell recruitment to the colon. Representative pictures of CD11b stained sections of the colon for each mouse group. Magnification: pictures on the top are at 4×, on the bottom at 20×.

[0245] FIG. **27** shows changes in spleen CD4 T cells. Spleens were collected at day 46 (40 days post last antibody dosage) and analyzed by flow cytometry (n=8 or 4 per group, SEM, statistic unpaired T-test, no equal SD).

[0246] FIG. **28** shows H&E analysis of skin sections from the IMQD treated mice. The Hamster Ig image is on the left and the 8G8 treated group is on the right.

[0247] FIG. **29** shows IHC Analysis of skin sections from the IMQD treated mice. The Hamster Ig image is on the left and the 8G8 treated group is on the right.

[0248] FIG. **30** shows a quantitative analysis of skin sections from the IMQD treated mice for CD3+ cells in the field of view.

[0249] FIG. **31** shows a quantitative analysis of immunological populations in the spleen of Hamster Ig and 8G8 treated mice. Spleens were taken and analyzed at Day 8.

[0250] FIG. **32** shows Luminex analysis of IL-2 from a panel of 32 cytokines from the 6-hour time point of mice treated with Control-Ig, INX800 or INX801. Mice were pretreated at −3 hours with each of the indicated antibodies. At time 0, mice were dosed with 15 mg/kg of ConA, and then sacrificed and bled at the 6-hour time point.

[0251] FIG. **33** shows Luminex analysis of 32 cytokines from the 6-hour time point of mice treated with Control-Ig, INX800 or INX801. Mice were pretreated at −3 hours with each of the indicated antibodies. At time 0, mice were dosed with 15 mg/kg of ConA, and then sacrificed and bled at the 6-hour time point.

[0252] FIG. **34** shows ALC counts from ConA-treated mice from Experiment 14 and naïve mice. Mice were pretreated at −3 hours with each of the indicated antibodies at 10 mpk. At time 0, mice were dosed with 15 mg/kg of ConA (Experiment 14) or not dosed at all (naïve), and then bled at 6 hours for ALC counts by Flow cytometry

[0253] FIG. **35** shows Luminex analysis of serum IL-2 from a panel of 32 cytokines at the 6-hour time point of mice treated with Ham-Ig, 8G8 or 13F3. Mice were pretreated at −3 hours with each of the indicated antibodies. At time 0, mice were dosed with 15 mg/kg of ConA, and then sacrificed and bled at the 6-hour time point.

[0254] FIG. **36** shows Kaplan Meier curves of the 30 mg/kg ConA treated mice. Mice were pretreated at −3 hours with each of the indicated antibodies. At time 0, mice were dosed with 30 mg/kg of ConA, and then followed for survival analysis

[0255] FIG. **37** shows IL-2 expression in the plasma from the 6-hour time point of mice treated with Control-Ig, INX800 or INX903. Mice were pretreated at −3 hours with each of the indicated antibodies. At time 0, mice were dosed with 15 mg/kg of ConA, and then sacrificed and bled at the 6-hour time point.

[0256] FIG. **38**A-**38**B shows IL-2 and MIP-1β expression in the plasma from the 6-hour time point of mice treated with Control-Ig, INX800, INX903 or an Antagonist. Mice were pretreated at −3 hours with each of the indicated antibodies. At time 0, mice were dosed with 15 mg/kg of ConA, and then sacrificed and bled at the 6-hour time point.

[0257] FIG. **39** contains the experimental protocol for the CIA arthritis model.

[0258] FIG. **40** shows the effects of an agonistic anti-mouse VISTA antibody, 8G8, in a collagen-induced arthritis model. As shown treatment was initiated at day −2 and subsequently mice were dosed every other day. (n=10 in each group). 8G8 treatment significantly reduced disease severity (interaction term P<0.000005).

[0259] FIG. **41** contains the experimental protocol for a CIA arthritis model experiment in Example 9.

[0260] FIG. **42** shows the CAIA disease progression scoring for the experiment of Example 8. As shown treatment was initiated at day −2 and subsequently mice were dosed every other day. (n=10 in each group). 8G8 treatment significantly reduced disease severity (interaction term P<0.000005).

[0261] FIG. **43** shows CAIA disease progression scoring. Treatment was initiated at day −2 and subsequently mice were dosed every other day. (n=9 in control group and 8 in INX903 treated group; 1 mouse was removed from the control group as it never showed any signs of disease). INX903 treatment significantly reduced disease severity (interaction term P=0.01).

[0262] FIG. **44** shows CAIA disease progression scoring. Treatment was initiated at day −2 and subsequently mice were dosed every other day. (n=10 in each group). 8G8 treatment significantly reduced disease severity (interaction term P<0.0001).

[0263] FIG. **45** shows CAIA disease progression scoring with INX800 treatment. Treatment was initiated at day −2 and subsequently mice were dosed every other day. (n=9 in control group and 8 in INX800 treated group).

[0264] FIG. **46** shows CAIA disease progression scoring with INX901 treatment. Treatment was initiated at day −2 and subsequently mice were dosed every other day. (n=9 in control group and 10 in INX901 treated group).

[0265] FIG. **47** shows CAIA disease progression scoring with INX902 treatment.

[0266] Treatment was initiated at day −2 and subsequently mice were dosed every other day. (n=9 in control group and 7 in INX902 treated group).

[0267] FIGS. **48**A-**48**B show weights and survival of recipient mice treated with 8G8, 13F3, or control Hamster IgG antibodies in acute GvHD disease model.

[0268] FIG. **49** shows weights of recipient mice treated with INX anti-VISTA antibodies or control Ig and survival in acute GvHD disease model **49**A: Mean weight loss by group (N=5-8 mice per group) at the peak of disease; **49**B: Mean weight loss by group (N=5-8 mice per group); 49C: Survival.

[0269] FIGS. **50**A-**50**C shows chimerism and donor T-cell numbers in surviving mice treated with INX901, INX902, INX903 and INX904 or control Ig in acute GvHD disease model. **50**A) Representative plot of donor (H2Kb, vertical) or recipient (H2Kd, horizontal) expression in blood CD11b cells in α-human VISTA treated mice (left panel) or Balb/c control mice (right panel) **50**B) Percentage of donor derived CD11b in the blood of α-human VISTA treated mice. **50**C) donor derived T cells number in 25 μL of blood in chimeric α-human VISTA treated mice or in DDE1 control mice.

[0270] FIGS. **51**A-**51**B shows weights of NSG mice treated with INX901 or control AB in xeno-GvHD disease model. **51**A: Means by group (N=6) **51**B: weights of individual mice. Skull and crossbones indicate mice were either found dead or euthanized at the indicated date.

[0271] FIG. **52** shows T-cell expansion in NSG mice treated with INX901 or control AB in xeno-GvHD disease model The figure shows the values in % of total $CD45^+$ cells in the mouse peripheral circulation made up of human $CD3^+$ T-cells.

[0272] FIGS. **53**A-**53**C shows Weights and survival of recipient mice treated with 8G8 antibodies or control Hamster IgG in acute GvHD disease model; **53**A: Mean weight loss by group (N=8 mice per group); **53**B: Individual weight loss by group (N=8 mice per group); and **53**C: Survival.

[0273] FIGS. **54**A-**54**B shows weights of recipient mice treated with various doses of INX902 or control Ig and survival in acute GvHD disease model; **54**A shows mean weight loss by group (N=8 mice per group) for INX902 treated mice and **54**B shows survival for INX902 treated mice.

[0274] FIGS. **55**A-**55**B shows chimerism in surviving mice treated with various doses of INX902 or control Ig in acute GvHD disease model; **55**A shows Percentage of donor derived CD11b in the blood of INX902 treated mice and **55**B shows Donor derived T cells number in 25 μL of blood in INX902 treated mice or in DDE1 control mice.

[0275] FIG. **56**A-D shows weights of recipient mice treated with various doses of INX903 and INX901 antibodies or control Ig and survival in acute GvHD disease model; **56**A shows Mean weight loss by group (N=8 mice per group) and **56**B shows survival for INX903 treated mice; **56**C shows Mean weight loss by group (N=8 mice per group) for INX901 treated mice; and **56**D shows survival for INX901 treated mice.

[0276] FIGS. **57**A-**57**B shows chimerism in surviving mice treated with various doses of INX901 and INX901 or control Ig in acute GvHD disease model; **57**A: Percentage of donor derived CD11b in the blood of INX903 treated mice; **57**B: Percentage of donor derived CD11b in the blood of INX901 treated mice.

[0277] FIGS. **58**A-**58**C shows weights of recipient mice treated with INX antibodies or control Ig and survival in acute GvHD disease model; **58**A shows mean weight loss by group (N=8 mice per group); **58**B individual weight loss by group (N=8 mice per group) and 16C survival.

[0278] FIG. **59** shows acute GvHD was induced by transfer of T cells and BM from hV-KI mice into irradiated Balb/c recipients. Mice were tracked for disease by weight loss, with mice being sacrificed if more than 20% of the initial starting weight was lost.

[0279] FIG. **60** shows that the agonist anti-VISTA antibody 8G8 delays proteinuria onset in NZBWF-1 mice. In the experiments 16-week-old female NZBWF-1 mice were monitored weekly for proteinuria. Proteinuria values were recorded using chemstrips and quantified as mg/dL. At week 32, mice were treated with either 300 ug Control-IgG (black line, n=5) or 300 ug 8G8 (red line, n=5) by i.p injection three times a week. At week 33, mice treated with Control-IgG were sacrificed due to poor health.

[0280] FIG. **61** shows LIX/CXCL5 and IL-9 levels in the serum of Control-Ig and 8G8 treated NZBWF-1 mice were detected. Serum was collected at week 33 from Control-IgG (n=5) and 8G8 mice (n=5) and chemokines and cytokines were assessed on a 32 plex run using Bio-plex 200 Systems and analyzed by Bio Plex manager 6.0 software. Data is shown as the mean+/−SEM and statistical significance was determined by the unpaired Student t Test. In FIG. **7** **denotes significance (p<0.01) between groups.

[0281] FIG. **62** shows that 8G8 reduces proteinuria development in NZBWF-1 mice. In the experiments 22-week-old female NZBWF-1 mice were monitored weekly for proteinuria. Proteinuria values were recorded using chemstrips and quantified as mg/dL. On week 28, mice were treated with either 300 ug Control-IgG (black line, n=6) or 300 ug 8G8 (red line, n=6) by i.p injection three times a week.

[0282] FIG. **63** shows that the VISTA agonist 8G8 reduces proteinuria development in MRL/lpr mice in experiments wherein 15 week old female MRL/lpr mice were monitored weekly for proteinuria. Proteinuria values were recorded using chemstrips and quantified as mg/dL. On week 16, mice were treated with either 300 ug hamster-Ig (black line, n=8) or 300 ug 8G8 (red line, n=8) by i.p injection three times a week. Data at week 21 were discarded due to technical problems with the chemstrips. (A) Average proteinuria is shown with standard error bars. (B) Disease incidence at each time point was calculated as the percent of mice in each group that exhibited proteinuria at or greater than 100 mg/dL.

[0283] FIG. **64** shows that the VISTA agonist 8G8 (anti-mouse VISTA agonist antibody) reduces splenomegaly in MRL/lpr mice in experiments wherein spleens were harvested on week 23 from mice were treated with either 300 ug Control-Ig/hamster-Ig or 300 ug 8G8 by i.p injection three times a week. Splenomegaly was observed in Control-Ig treated mice compared to 8G8 treated mice. Shown here are representative spleens.

[0284] FIG. **65** shows that the VISTA agonist 8G8 (anti-mouse VISTA agonist antibody) reduces lymphoproliferation of cervical lymph nodes in MRL/lpr mice in experiments wherein cervical lymph nodes were harvested on week 23 from mice treated with either 300 ug Control-Ig/hamster-Ig or 300 ug 8G8 by i.p injection three times a week. Lymphoproliferation was observed in Control-Ig treated mice compared to 8G8 treated mice. Shown here are representative cervical lymph nodes.

[0285] FIGS. **66**A-**66**B shows that 8G8 (anti-mouse VISTA agonist antibody) reduces proteinuria development in MRL/lpr mice in experiments wherein 9 week old female MRL/lpr mice were monitored weekly for proteinuria. Proteinuria values were recorded using chemstrips and quantified as mg/dL. On week 11, mice were treated with either 200 uL PBS (dotted black line, n=8) or 10 mg/kg hamster-Ig (solid black line, n=8) or 10 mg/kg 8G8 (red line, n=8) by i.p injection three times a week. (66A) Average proteinuria is shown with standard error bars. (66B) Disease incidence at each time point was calculated as the percent of mice in each group that exhibited proteinuria at or greater than 100 mg/dL.

[0286] FIG. **67** shows experimental design for the DDE1 transfer experiment referenced in the example. INX903 (anti-human VISTA agonist Ab containing VSTB95 antibody variable regions (see FIG. **4**) and wild-type human IgG2 constant regions). In the experiments treatment was administered at days 0, 2, and 6 following DDE1 transfer. At each time point, 4 mice per group were analyzed plus 1 naïve mouse. Spleens were processed for flow cytometry, and serum was recovered from cardiac blood for detection of anti-dsDNA IgG by ELISA.

[0287] FIG. **68** contains results of DDE1 transfer experiments. The results indicate that donor and host cell populations are distinguishable by their MHC class I alleles. The host B6D2F1 cells express both H-2Kb and H-2Kd, whereas the donor DDE1 cells express only H-2Kb.

[0288] FIGS. **69**A-C contains further results of DDE1 transfer experiments. The figure shows that B cells activation during SLE progression is prevented by INX903 treatment. Panel A contains histograms plots of MHCII I^{Ad} expression on recipient B cells. Panel B shows the total number of recipient B cells and spleen cells over the course of the experiment and MHC class II IAd MFI on recipient B cell over the course of the experiment (n=4, SEM). Panel C shows the spleen size at day 14.

[0289] FIG. **70** contains further results of DDE1 transfer experiments. Particularly the results in the Figure show that anti-dsDNA autoantibody production in SLE is prevented by INX903 treatment. Anti-dsDNA IgG titer in serum measured by ELISA in naïve (n=2), and HulgG2 or INX903 treated mice at D7 and D14 (n=4, SEM).

[0290] FIG. **71** contains further results of DDE1 transfer experiments. The data in the Figure shows that shows that there is decreased CD69 expression at Day 1 in INX903-treated CD4 T cells (n=4).

[0291] FIG. **72** contains further results of DDE1 transfer experiments. The data in the figure show that there is a decreased number of CD4 T cells in INX903-treated mice, despite no changes in cell cycle (n=4).

[0292] FIG. **73** also shows decreased number of total donor CD4 T cells over time in response to INX903 treatment (n=4, SEM).

[0293] FIGS. **74**A-**74**B: shows that 8G8 reduces proteinuria development in MRL/lpr mice. As shown 15 week old female MRL/lpr mice were monitored weekly for proteinuria. Proteinuria values were recorded using chemstrips and quantified as mg/dL. On week 16, mice were treated with either 300 ug hamster-Ig (black line, n=8) or 300 ug 8G8 (red line, n=8) by i.p injection three times a week. Data at week 21 were discarded due to technical problems with the chemstrips. (74A) Average proteinuria is shown with standard error bars. (74B) Disease incidence at each time point was calculated as the percent of mice in each group that exhibited proteinuria at or greater than 100 mg/dL.

[0294] FIG. **75** shows that 8G8 administration reduces splenomegaly in MRL/lpr mice. Spleens were harvested on week 23 from mice were treated with either 300 ug Control-Ig/hamster-Ig or 300 ug 8G8 by i.p injection three times a week. Splenomegaly was observed in Control-Ig treated mice compared to 8G8 treated mice. Shown here are representative spleens.

[0295] FIG. **76** shows that 8G8 administration reduces lymphoproliferation of cervical lymph nodes in MRL/lpr mice. Cervical lymph nodes were harvested on week 23 from mice treated with either 300 ug Control-Ig/hamster-Ig or 300 ug 8G8 by i.p injection three times a week. Lymphoproliferation was observed in Control-Ig treated mice compared to 8G8 treated mice. Shown here are representative cervical lymph nodes.

[0296] FIG. **77** contains experimental results indicating that 8G8 administration reduces proteinuria development in NZBWF-1 mice.

[0297] FIG. **78** contains experimental results indicating that 8G8 administration does not affect immune complexes NZBWF-1 mice.

DETAILED DESCRIPTION

[0298] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as those commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein may be used in the invention or testing of the present invention, suitable methods and materials are described herein. The materials, methods and examples are illustrative only, and are not intended to be limiting. The nomenclatures utilized in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Standard techniques may be used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

[0299] As used in the description herein and throughout the claims that follow, the meaning of "a," "an," and "the" includes plural reference unless the context clearly dictates otherwise.

[0300] "Activating receptor," as used herein, refers broadly to immune cell receptors that bind antigen, complexed antigen (e.g., in the context of MHC molecules), Ig-fusion proteins, ligands, or antibodies. Activating receptors but are not limited to T cell receptors (TCRs), B cell receptors (BCRs), cytokine receptors, LPS receptors, complement receptors, and Fc receptors. For example, T cell receptors are present on T cells and are associated with CD3 molecules. T cell receptors are stimulated by antigen in the context of MHC molecules (as well as by polyclonal T cell activating reagents). T cell activation via the TCR results in numerous changes, e.g., protein phosphorylation, membrane lipid changes, ion fluxes, cyclic nucleotide alterations, RNA transcription changes, protein synthesis changes, and cell volume changes. For example, T cell receptors are present on T cells and are associated with CD3 molecules. T cell receptors are stimulated by antigen in the context of MHC molecules (as well as by polyclonal T cell activating reagents). T cell activation via the TCR results in numerous changes, e.g., protein phosphorylation, membrane lipid changes, ion fluxes, cyclic nucleotide alterations, RNA transcription changes, protein synthesis changes, and cell volume changes.

[0301] "Adjuvant" as used herein, refers to an agent used to stimulate the immune system and increase the response to a vaccine, without having any specific antigenic effect in itself.

[0302] "Agonist" herein refers to a molecule, generally an antibody or fusion proteins which enhances or mimics the effects of a specific molecule on immunity. Generally in the present application this will refer to anti-human VISTA agonist antibodies and antibody fragments which enhance or mimic the effects of human VISTA on immunity, particularly VISTA's suppressive effects on T cell immunity (CD4+ and/or CD8+ T cell immunity), the expression of proinflammatory cytokines and its effects of the expression of specific chemokines and chemoattractants.

[0303] "Aids in the diagnosis" or "aids in the detection" of a disease herein means that the expression level of a particular marker polypeptide or expressed RNA is detected alone or in association with one or more other markers in order to assess whether a subject has cells characteristic of a particular disease condition or the onset of a particular disease condition or comprises immune dysfunction such as immunosuppression characterized by VISTA expression or abnormal immune upregulation characterized by cells having reduced VISTA levels, such as during autoimmunity, inflammation or allergic responses, e.g., in individuals with chronic and non-chronic diseases.

[0304] "Allergic disease," as used herein, refers broadly to a disease involving allergic reactions. More specifically, an "allergic disease" is defined as a disease for which an allergen is identified, where there is a strong correlation between exposure to that allergen and the onset of pathological change, and where that pathological change has been proven to have an immunological mechanism. Herein, an immunological mechanism means that leukocytes show an immune response to allergen stimulation.

[0305] "Amino acid," as used herein refers broadly to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified (e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine.) Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid (i. e., a carbon that is bound to a hydrogen, a carboxyl group, an amino group), and an R group (e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium.) Analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid.

[0306] "Anergy" or "tolerance," or "prolonged antigen-specific T cell suppression" or "prolonged immunosuppression" as used herein refers broadly to refractivity to activating receptor-mediated stimulation. Refractivity is generally antigen-specific and persists after exposure to the tolerizing antigen has ceased. For example, anergy in T cells (as opposed to unresponsiveness) is characterized by lack of cytokine production, e.g., IL-2. T cell anergy occurs when T cells are exposed to antigen and receive a first signal (a T cell receptor or CD-3 mediated signal) in the absence of a second signal (a costimulatory signal). Under these conditions, reexposure of the cells to the same antigen (even if reexposure occurs in the presence of a costimulatory molecule) results in failure to produce cytokines and, thus, failure to proliferate. Anergic T cells can, however, mount responses to unrelated antigens and can proliferate if cultured with cytokines (e.g., IL-2). For example, T cell anergy can also be observed by the lack of IL-2 production by T lymphocytes as measured by ELISA or by a proliferation assay using an indicator cell line. Alternatively, a reporter gene construct can be used. For example, anergic T cells fail to initiate IL-2 gene transcription induced by a heterologous promoter under the control of the 5' IL-2 gene enhancer or by a multimer of the API sequence that can be found within the enhancer (Kang et al. (1992) Science 257: 1134). Modulation of a costimulatory signal results in modulation of effector function of an immune cell.

[0307] "Antagonist" herein refers to a molecule, generally an antibody or fusion proteins which blocks or reduces the effects of a specific molecule on immunity. Generally in the

present application this will refer to anti-human VISTA antagonist antibodies and antibody fragments which block or reduce the effects of human VISTA on immunity, particularly VISTA's suppressive effects on T cell immunity ($CD4^+$ and/or CD8+ T cell immunity), the expression of proinflammatory cytokines and VISTA's effects of the expression of specific chemokines and chemoattractants.

[0308] "Antibody", as used herein, refers broadly to an "antigen-binding portion" of an antibody (also used interchangeably with "antibody portion," "antigen-binding fragment," "antibody fragment"), as well as whole antibody molecules. The term "antigen-binding portion", as used herein, refers to one or more fragments of an antibody that retain the ability to specifically bind to an antigen (e.g., VISTA or specific portions thereof)). The term "antibody" as referred to herein includes whole polyclonal and monoclonal antibodies and any antigen-binding fragment (i. e., "antigen-binding portion") or single chains thereof as well as bispecific and multispecific antibodies, e.g., those that bind to multiple antigens or multiple antigen epitopes. An "antibody" refers to a glycoprotein comprising at least two heavy (H) chains and two light (L) chains interconnected by disulfide bonds, or an antigen-binding portion thereof. Each heavy chain is comprised of at least one heavy chain variable region (abbreviated herein as VH) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, C_H1, Cm and Cm—Each light chain is comprised of at least one light chain variable region (abbreviated herein as V_L) and a light chain constant region. The light chain constant region is comprised of one domain, CL—The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FRs). Each VH and VL is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (e.g., effector cells) and the first component (C1q) of the classical complement system. More generally, the term "antibody" is intended to include any polypeptide chain-containing molecular structure with a specific shape that fits to and recognizes an epitope, where one or more non-covalent binding interactions stabilize the complex between the molecular structure and the epitope. The archetypal antibody molecule is the immunoglobulin, and all types of immunoglobulins, IgG, IgM, IgA, IgE, IgD, etc., from all sources, e.g. human, rodent, rabbit, cow, sheep, pig, dog, other mammals, chicken, other avians, etc., are considered to be "antibodies."

[0309] The antigen-binding function of an antibody can be performed by fragments of a full-length antibody. Non-limiting examples of antigen-binding fragments encompassed within the term "antigen-binding portion" of an antibody include (a) a Fab fragment, a monovalent fragment consisting of the V_L, V_H, C_L and C_{H1} domains; (b) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (c) a Fd fragment consisting of the V_H and C_{H1} domains; (d) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody; (e) a dAb fragment (Ward, et al. (1989) *Nature* 341: 544-546), which consists of a V_H domain; and (f) an isolated complementarily determining region (CDR). Furthermore, although the two domains of the Fv fragment, V_L and V_H, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the V_L and V_H regions pair to form monovalent molecules (known as single chain Fv (scFv). See e.g., Bird, et al. (1988) *Science* 242: 423-426; Huston, et al. (1988) *Proc Natl. Acad. Sci. USA* 85: 5879-5883; and Osbourn, et al. (1998) *Nat. Biotechnol.* 16: 778. Single chain antibodies are also intended to be encompassed within the term "antigen-binding portion" of an antibody. Any V_H and V_L sequences of specific scFv can be linked to human immunoglobulin constant region cDNA or genomic sequences, in order to generate expression vectors encoding complete IgG molecules or other isotypes. VH and V_L can also be used in the generation of Fab, Fv, or other fragments of immunoglobulins using either protein chemistry or recombinant DNA technology. Other forms of single chain antibodies, such as diabodies are also encompassed. Diabodies are bivalent, bispecific antibodies in which V_H and V_L domains are expressed on a single polypeptide chain, but using a linker that is too short to allow for pairing between the two domains on the same chain, thereby forcing the domains to pair with complementary domains of another chain and creating two antigen-binding sites. See e.g. Holliger, et al. (1993) *Proc Natl. Acad. Sci. USA* 90: 6444-6448; Poljak, et al. (1994) *Structure* 2: 1121-1123. Still further, an antibody or antigen-binding portion thereof (antigen-binding fragment, antibody fragment, antibody portion) may be part of a larger immunoadhesion molecules, formed by covalent or noncovalent association of the antibody or antibody portion with one or more other proteins or peptides. Examples of immunoadhesion molecules include use of the streptavidin core region to make a tetrameric scFv molecule (Kipriyanov, et al. (1995) *Hum. Antibodies Hybridomas* 6: 93-101) and use of a cysteine residue, a marker peptide and a C-terminal polyhistidine tag to make bivalent and biotinylated scFv molecules. Kipriyanov, et al. (1994) *Mol. Immunol.* 31: 1047-1058. Antibody portions, such as Fab and $F(ab')_2$ fragments, can be prepared from whole antibodies using conventional techniques, such as papain or pepsin digestion, respectively, of whole antibodies. Moreover, antibodies, antibody portions and immunoadhesion molecules can be obtained using standard recombinant DNA techniques, as described herein. Antibodies may be polyclonal, monoclonal, xenogeneic, allogeneic, syngeneic, or modified forms thereof, e.g., humanized, chimeric, bispecific or multispecific antibodies.

[0310] "Antibody recognizing an antigen" and "an antibody specific for an antigen" is used interchangeably herein with the term "an antibody which binds specifically to an antigen" and refers to an immunoglobulin or fragment thereof that specifically binds an antigen.

[0311] "Antigen," as used herein, refers broadly to a molecule or a portion of a molecule capable of being bound by an antibody which is additionally capable of inducing an animal to produce an antibody capable of binding to an epitope of that antigen. An antigen may have one epitope, or have more than one epitope. The specific reaction referred to herein indicates that the antigen will react, in a highly selective manner, with its corresponding antibody and not with the multitude of other antibodies which may be evoked

by other antigens. In the case of a desired enhanced immune response to particular antigens of interest, antigens include, but are not limited to; infectious disease antigens for which a protective immune response may be elicited are exemplary.

[0312] "Antigen presenting cell," as used herein, refers broadly to professional antigen presenting cells (e.g., B lymphocytes, monocytes, dendritic cells, and Langerhans cells) as well as other antigen presenting cells (e.g., keratinocytes, endothelial cells, astrocytes, fibroblasts, and oligodendrocytes).

[0313] "Antisense nucleic acid molecule," as used herein, refers broadly to a nucleotide sequence which is complementary to a "sense" nucleic ac*id encoding a protein (e.g., complementary to the coding strand of a double-stranded cDNA molecule) complementary to an mRNA sequence or complementary to the coding strand of a gene. Accordingly, antisense nucleic acid molecules can hydrogen bond to sense nucleic acid molecules.

[0314] "Apoptosis," as used herein, refers broadly to programmed cell death which can be characterized using techniques which are known in the art. Apoptotic cell death can be characterized by cell shrinkage, membrane blebbing, and chromatin condensation culminating in cell fragmentation. Cells undergoing apoptosis also display a characteristic pattern of internucleosomal DNA cleavage.

[0315] "Autoimmunity" or "autoimmune disease or condition," as used herein, refers broadly to a disease or disorder arising from and directed against an individual's own tissues or a co-segregate or manifestation thereof or resulting condition therefrom, and includes. Herein autoimmune conditions include inflammatory or allergic conditions, e.g., chronic diseases characterized by a host immune reaction against self-antigens potentially associated with tissue destruction such as rheumatoid arthritis.

[0316] "B cell receptor" (BCR)," as used herein, refers broadly to the complex between membrane Ig (mIg) and other transmembrane polypeptides (e.g., IgA. and Ig) found on B cells. The signal transduction function of mIg is triggered by crosslinking of receptor molecules by oligomeric or multimeric antigens. B cells can also be activated by anti-immunoglobulin antibodies. Upon BCR activation, numerous changes occur in B cells, including tyrosine phosphorylation.

[0317] "Cancer," as used herein, refers broadly to any neoplastic disease (whether invasive or metastatic) characterized by abnormal and uncontrolled cell division causing malignant growth or tumor (e.g., unregulated cell growth.) The term "cancer" or "cancerous" as used herein should be understood to encompass any neoplastic disease (whether invasive, non-invasive or metastatic) which is characterized by abnormal and uncontrolled cell division causing malignant growth or tumor, non-limiting examples of which are described herein. This includes any physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer are exemplified in the working examples. Further cancers include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. More particular examples of such cancers include squamous cell cancer, lung cancer (including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, and squamous carcinoma of the lung), cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer (including gastrointestinal cancer), pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer, as well as B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL); small lymphocytic (SL) NHL; intermediate grade/follicular NHL; intermediate grade diffuse NHL; high grade immunoblastic NHL; high grade lymphoblastic NHL; high grade small non-cleaved cell NHL; bulky disease NHL; mantle cell lymphoma; AIDS-related lymphoma; and Waldenström's Macroglobulinemia); chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); Hairy cell leukemia; chronic myeloblasts leukemia; multiple myeloma and post-transplant lymphoproliferative disorder (PTLD). Other cancers amenable for treatment by the present invention include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include colorectal, bladder, ovarian, melanoma, squamous cell cancer, lung cancer (including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, and squamous carcinoma of the lung), cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer (including gastrointestinal cancer), pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer, as well as B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL); small lymphocytic (SL) NHL; intermediate grade/follicular NHL; intermediate grade diffuse NHL; high grade immunoblastic NHL; high grade lymphoblastic NHL; high grade small non-cleaved cell NHL; bulky disease NHL; mantle cell lymphoma; AIDS-related lymphoma; and Waldenström's Macroglobulinemia); chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); Hairy cell leukemia; chronic myeloblastic leukemia; and post-transplant lymphoproliferative disorder (PTLD), as well as abnormal vascular proliferation associated with phakomatoses, edema (such as that associated with brain tumors), and Meigs' syndrome. Preferably, the cancer is selected from the group consisting of colorectal cancer, breast cancer, colorectal cancer, rectal cancer, non-small cell lung cancer, non-Hodgkin's lymphoma (NHL), renal cell cancer, prostate cancer, liver cancer, pancreatic cancer, soft-tissue sarcoma, Kaposi's sarcoma, carcinoid carcinoma, head and neck cancer, melanoma, ovarian cancer, mesothelioma, and multiple myeloma. In an exemplary embodiment the cancer is an early or advanced (including metastatic) bladder, ovarian or melanoma. In another embodiment the cancer is colorectal cancer. The cancerous conditions amenable for treatment of the invention include cancers that express or do not express VISTA and further include non-metastatic or non-invasive as well as invasive or metastatic cancers wherein VISTA expression by immune, stromal or diseased cells suppress antitumor responses and anti-invasive immune responses. The method of the present invention is particularly suitable for the treatment of vascularized tumors. Cancers according to the invention include cancers that express or do not express VISTA and further include

non-metastatic or non-invasive as well as invasive or metastatic cancers wherein VISTA expression by immune, stromal or diseased cells suppress antitumor responses and anti-invasive immune responses, and those characterized by vascularized tumors.

[0318] "Chimeric antibody," as used herein, refers broadly to an antibody molecule in which the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen-binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, the variable region or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

[0319] "Coding region," as used herein, refers broadly to regions of a nucleotide sequence comprising codons which are translated into amino acid residues, whereas the term "noncoding region" refers to regions of a nucleotide sequence that are not translated into amino acids (e.g., 5' and 3' untranslated regions).

[0320] "Conservatively modified variants," as used herein, applies to both amino acid and nucleic acid sequences, and with respect to particular nucleic acid sequences, refers broadly to conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. "Silent variations" are one species of conservatively modified nucleic acid variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) may be modified to yield a functionally identical molecule.

[0321] "Complementarity determining region," "hypervariable region," or "CDR," as used herein, refers broadly to one or more of the hyper-variable or complementarily determining regions (CDRs) found in the variable regions of light or heavy chains of an antibody. See Kabat, et al. (1987) Sequences of Proteins of Immunological Interest National Institutes of Health, Bethesda, Md. These expressions include the hypervariable regions as defined by Kabat, et al. (1983) *Sequences of Proteins of Immunological Interest*, U. S. Dept. of Health and Human Services or the hypervariable loops in 3-dimensional structures of antibodies. Chothia and Lesk (1987) *J. Mol. Biol.* 196: 901-917. The CDRs in each chain are held in close proximity by framework regions and, with the CDRs from the other chain, contribute to the formation of the antigen-binding site. Within the CDRs there are select amino acids that have been described as the selectivity determining regions (SDRs) which represent the critical contact residues used by the CDR in the antibody-antigen interaction. (Kashmiri *Methods* 36: 25-34(2005)).

[0322] "Control amount," as used herein, refers broadly to a marker can be any amount or a range of amounts to be compared against a test amount of a marker. For example, a control amount of a marker may be the amount of a marker in a patient with a particular disease or condition or a person without such a disease or condition. A control amount can be either in absolute amount (e.g., microgram/ml) or a relative amount (e.g., relative intensity of signals).

[0323] "Costimulatory receptor," as used herein, refers broadly to receptors which transmit a costimulatory signal to an immune cell, e.g., CD28 or ICOS. As used herein, the term "inhibitory receptors" includes receptors which transmit a negative signal to an immune cell, e.g., a T cell or an NK cell.

[0324] "Costimulate," as used herein, refers broadly to the ability of a costimulatory molecule to provide a second, non-activating, receptor-mediated signal (a "costimulatory signal") that induces proliferation or effector function. For example, a costimulatory signal can result in cytokine secretion (e.g., in a T cell that has received a T cell-receptor-mediated signal) Immune cells that have received a cell receptor-mediated signal (e.g., via an activating receptor) may be referred to herein as "activated immune cells." With respect to T cells, transmission of a costimulatory signal to a T cell involves a signaling pathway that is not inhibited by cyclosporin A. In addition, a costimulatory signal can induce cytokine secretion (e.g., IL-2 and/or IL-10) in a T cell and/or can prevent the induction of unresponsiveness to antigen, the induction of anergy, or the induction of cell death in the T cell.

[0325] "Costimulatory polypeptide" or "costimulatory molecule" herein refers to a polypeptide that, upon interaction with a cell-surface molecule on T cells, modulates T cell responses.

[0326] "Costimulatory signaling" as used herein is the signaling activity resulting from the interaction between costimulatory polypeptides on antigen presenting cells and their receptors on T cells during antigen-specific T cell responses. Without wishing to be limited by a single hypothesis, the antigen-specific T cell response is believed to be mediated by two signals: 1) engagement of the T cell Receptor (TCR) with antigenic peptide presented in the context of MHC (signal 1), and 2) a second antigen-independent signal delivered by contact between different costimulatory receptor/ligand pairs (signal 2). Without wishing to be limited by a single hypothesis, this "second signal" is critical in determining the type of T cell response (activation vs inhibition) as well as the strength and duration of that response, and is regulated by both positive and negative signals from costimulatory molecules, such as the B7 family of proteins.

[0327] "B7" polypeptide herein means a member of the B7 family of proteins that costimulate T cells including, but not limited to B7-1, B7-2, B7-DC, B7-H5, B7-HI, B7-H2, B7-H3, B7-H4, B7-H6, B7-S3 and biologically active fragments and/or variants thereof. Representative biologically active fragments include the extracellular domain or fragments of the extracellular domain that costimulate T cells.

[0328] "Cytoplasmic domain," as used herein, refers broadly to the portion of a protein which extends into the cytoplasm of a cell.

[0329] "Diagnostic," as used herein, refers broadly to identifying the presence or nature of a pathologic condition. Diagnostic methods differ in their sensitivity and specificity. The "sensitivity" of a diagnostic assay is the percentage of diseased individuals who test positive (percent of "true positives"). Diseased individuals not detected by the assay are "false negatives." Subjects who are not diseased and who test negative in the assay are termed "true negatives." The

"specificity" of a diagnostic assay is 1 minus the false positive rate, where the "false positive" rate is defined as the proportion of those without the disease who test positive. While a particular diagnostic method may not provide a definitive diagnosis of a condition, it suffices if the method provides a positive indication that aids in diagnosis.

[0330] "Diagnosing," or "aiding in the diagnosis" as used herein refers broadly to classifying a disease or a symptom, and/or determining the likelihood that an individual has a disease condition (e.g., based on absence or presence of VISTA expression, and/or increased or decreased expression by immune, stromal and/or putative diseased cells); determining a severity of the disease, monitoring disease progression, forecasting an outcome of a disease and/or prospects of recovery. The term "detecting" may also optionally encompass any of the foregoing. Diagnosis of a disease according to the present invention may, in some embodiments, be affected by determining a level of a polynucleotide or a polypeptide of the present invention in a biological sample obtained from the subject, wherein the level determined can be correlated with predisposition to, or presence or absence of the disease. It should be noted that a "biological sample obtained from the subject" may also optionally comprise a sample that has not been physically removed from the subject.

[0331] "Effective amount," as used herein, refers broadly to the amount of a compound, antibody, antigen, or cells that, when administered to a patient for treating a disease, is sufficient to effect such treatment for the disease. The effective amount may be an amount effective for prophylaxis, and/or an amount effective for prevention. The effective amount may be an amount effective to reduce, an amount effective to prevent the incidence of signs/symptoms, to reduce the severity of the incidence of signs/symptoms, to eliminate the incidence of signs/symptoms, to slow the development of the incidence of signs/symptoms, to prevent the development of the incidence of signs/symptoms, and/or effect prophylaxis of the incidence of signs/symptoms. The "effective amount" may vary depending on the disease and its severity and the age, weight, medical history, susceptibility, and pre-existing conditions, of the patient to be treated. The term "effective amount" is synonymous with "therapeutically effective amount" for purposes of this invention.

[0332] "Extracellular domain" or "ECD" as used herein refers broadly to the portion of a protein that extends from the surface of a cell.

[0333] "Expression vector," as used herein, refers broadly to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention in vitro or in vivo, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, i. e., drive only transient expression in a cell. The term includes recombinant expression cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

[0334] "Family," as used herein, refers broadly to the polypeptide and nucleic acid molecules of the invention is intended to mean two or more polypeptide or nucleic acid molecules having a common structural domain or motif and having sufficient amino acid or nucleotide sequence homology as defined herein. Family members can be naturally or non-naturally occurring and can be from either the same or different species. For example, a family can contain a first polypeptide of human origin, as well as other, distinct polypeptides of human origin or alternatively, can contain homologues of non-human origin (e.g., monkey polypeptides.) Members of a family may also have common functional characteristics.

[0335] "Fc receptor" (FcRs) as used herein, refers broadly to cell surface receptors for the Fc portion of immunoglobulin molecules (Igs). Fc receptors are found on many cells which participate in immune responses. Among the human FcRs that have been identified so far are those which recognize IgG (designated FcγR), IgE (FceRI), IgA (FcaR), and polymerized IgM/A (FcεμR). FcRs are found in the following cell types: FceRI (mast cells), FceRll (many leukocytes), FcaR (neutrophils), and FcpR (glandular epithelium, hepatocytes). (Hogg Immunol. Today 9: 185-86 (1988)). The widely studied FcγRs are central in cellular immune defenses, and are responsible for stimulating the release of mediators of inflammation and hydrolytic enzymes involved in the pathogenesis of autoimmune disease. (Unkeless, Annu. Rev. Immunol. 6: 251-87 (1988)). The FcγRs provide a crucial link between effector cells and the lymphocytes that secrete Ig, since the macrophage/monocyte, polymorphonuclear leukocyte, and natural killer (NK) cell FcγRs confer an element of specific recognition mediated by IgG. Human leukocytes have at least three different types of FcγRs for IgG: hFcγRI(CD64) (found on monocytes/macrophages), hFcγRIIA or hFcγRIIB, (CD32 or CD32A) (found on monocytes, neutrophils, eosinophils, platelets, possibly B cells, and the K562 cell line) and FcγRIIIA (CD16A) or FcγRIIIB (CD16B) (found on NK cells, neutrophils, eosinophils, and macrophages).

[0336] "Framework region" or "FR," as used herein refers broadly to one or more of the framework regions within the variable regions of the light and heavy chains of an antibody. See Kabat, et al. *Sequences of Proteins of Immunological Interest* National Institutes of Health, Bethesda, Md (1987). These expressions include those amino acid sequence regions interposed between the CDRs within the variable regions of the light and heavy chains of an antibody.

[0337] "Graft versus Host Disease" (GVHD): as used herein refers to a common complication of allogeneic bone marrow transplantation or hematopoietic stem cells transplantation in which functional immune cells in the transplanted marrow recognize the recipient as "foreign" and produce an immune response to the host tissue. According to the 1959 Billingham Criteria, there are three criteria must be met in order for GVHD to occur: 1) Administration of an immunocompetent graft, with viable and functional immune cells; 2) the recipient is immunologically histoincompatible; 3) The recipient is immunocompromised and therefore cannot destroy or inactivate the transplanted cells. Clinically, graft-versus-host-disease is divided into acute and chronic forms. The acute or fulminant form of the disease (aGVHD) is normally observed within the first 100 days post-transplant, and is a major challenge to the effectiveness of transplants owing to the associated morbidity and mortality. The chronic form of graft-versus-host-disease (cGVHD) normally occurs after 100 days. The appearance of moderate to severe cases of cGVHD adversely influences long-term survival. After bone marrow transplantation, T cells present

in the graft, either as contaminants or intentionally introduced into the host, attack the tissues of the transplant recipient after perceiving host tissues as antigenically foreign. The T cells produce an excess of cytokines, including TNF alpha and interferon-gamma (IFNγ). A wide range of host antigens can initiate graft-versus-host-disease, among them the human leukocyte antigens (HLAs). However, graft-versus-host disease can occur even when HLA-identical siblings are the donors. Classically, acute graft-versus-host-disease is characterized by selective damage to the liver, skin and mucosa, and the gastrointestinal tract. Additional studies show that that graft-versus-host-disease targets organs including the immune system (such as the bone marrow and the thymus) itself, and the lungs in the form of idiopathic pneumonitis. Chronic graft-versus-host-disease also attacks the above organs, but over its long-term course can also cause damage to the connective tissue and exocrine glands.

[0338] "Heterologous," as used herein, refers broadly to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid (e.g., a promoter from one source and a coding region from another source.) Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

[0339] "High affinity," as used herein, refers broadly to an antibody or fusion protein having a KD of at least 10-6 M, more preferably 10-7 M, even more preferably at least 10-8 M and even more preferably at least 10-9 M, 10-10 M, 10-11 M, or 10-12 M for a target antigen or receptor. "High affinity" for an IgG antibody or fusion protein herein refers to an antibody having a KD of 10-6 M or less, more preferably 10-7 M or less, preferably 10-8 M or less, more preferably 10-9 M or less and even more preferably 10-10 M, 10-11 M, or 10-12 M or less for a target antigen or receptor. With particular respect to antibodies, "high affinity" binding can vary for different antibody isotypes. For example, "high affinity" binding for an IgM isotype refers to an antibody having a KD of 10-7 M or less, more preferably 10-8 M or less.

[0340] "Homology," as used herein, refers broadly to a degree of similarity between a nucleic acid sequence and a reference nucleic acid sequence or between a polypeptide sequence and a reference polypeptide sequence. Homology may be partial or complete. Complete homology indicates that the nucleic acid or amino acid sequences are identical. A partially homologous nucleic acid or amino acid sequence is one that is not identical to the reference nucleic acid or amino acid sequence. The degree of homology can be determined by sequence comparison, for example using BlastP software of the National Center of Biotechnology Information (NCBI) using default parameters. The term "sequence identity" may be used interchangeably with "homology."

[0341] "Host cell," as used herein, refers broadly to refer to a cell into which a nucleic acid molecule of the invention, such as a recombinant expression vector of the invention, has been introduced. Host cells may be prokaryotic cells (e.g., *E. coli*), or eukaryotic cells such as yeast, insect (e.g., SF9), amphibian, or mammalian cells such as CHO, HeLa, HEK-293, e.g., cultured cells, explants, and cells in vivo. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It should be understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

[0342] "Human monoclonal antibody" refers to antibodies displaying a single binding specificity which have variable regions in which both the framework and CDR regions are derived from human germline immunoglobulin sequences. In one embodiment, the human monoclonal antibodies are produced by a hybridoma which includes a B cell obtained from a transgenic nonhuman animal, e.g., a transgenic mouse, having a genome comprising a human heavy chain transgene and a light chain transgene fused to an immortalized cell. This includes fully human monoclonal antibodies and conjugates and variants thereof, e.g., which are bound to effector agents such as therapeutics or diagnostic agents.

[0343] "Humanized antibody," as used herein, refers broadly to include antibodies made by a non-human cell having variable and constant regions which have been altered to more closely resemble antibodies that would be made by a human cell. For example, by altering the non-human antibody amino acid sequence to incorporate amino acids found in human germline immunoglobulin sequences. The humanized antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo), for example in the CDRs. The term "humanized antibody", as used herein, also includes antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

[0344] "Hybridization," as used herein, refers broadly to the physical interaction of complementary (including partially complementary) polynucleotide strands by the formation of hydrogen bonds between complementary nucleotides when the strands are arranged antiparallel to each other.

[0345] "IgV domain" and "IgC domain" as used herein, refer broadly to Ig superfamily member domains. These domains correspond to structural units that have distinct folding patterns called Ig folds. Ig folds are comprised of a sandwich of two β sheets, each consisting of antiparallel β strands of 5-10 amino acids with a conserved disulfide bond between the two sheets in most, but not all, domains. IgC domains of Ig, TCR, and MHC molecules share the same types of sequence patterns and are called the CI set within the Ig superfamily. Other IgC domains fall within other sets. IgV domains also share sequence patter and are called V set domains. IgV domains are longer than C-domains and form an additional pair of β strands.

[0346] "Immune cell," as used herein, refers broadly to cells that are of hematopoietic origin and that play a role in the immune response. Immune cells include but are not limited to lymphocytes, such as B cells and T cells; natural killer cells; dendritic cells, and myeloid cells, such as monocytes, macrophages, eosinophils, mast cells, basophils, and granulocytes.

[0347] "Immunoassay," as used herein, refers broadly to an assay that uses an antibody to specifically bind an antigen. The immunoassay may be characterized by the use of specific binding properties of a particular antibody to isolate, target, and/or quantify the antigen.

[0348] "Immune related disease (or disorder or condition)" as used herein should be understood to encompass any disease disorder or condition selected from the group including but not limited to autoimmune diseases, inflammatory disorders and immune disorders associated with graft transplantation rejection, such as acute and chronic rejection of organ transplantation, allogenic stem cell transplantation, autologous stem cell transplantation, bone marrow transplantation, and graft versus host disease.

[0349] "Immune response," as used herein, refers broadly to T cell-mediated and/or B cell-mediated immune responses that are influenced by modulation of T cell costimulation. Exemplary immune responses include B cell responses (e.g., antibody production) T cell responses (e.g., cytokine production, and cellular cytotoxicity) and activation of cytokine responsive cells, e.g., macrophages. As used herein, the term "downmodulation" with reference to the immune response includes a diminution in any one or more immune responses, while the term "upmodulation" with reference to the immune response includes an increase in any one or more immune responses. It will be understood that upmodulation of one type of immune response may lead to a corresponding downmodulation in another type of immune response. For example, upmodulation of the production of certain cytokines (e.g., IL-10) can lead to downmodulation of cellular immune responses.

[0350] "Immunologic", "immunological" or "immune" response herein refer to the development of a humoral (antibody mediated) and/or a cellular (mediated by antigen-specific T cells or their secretion products) response directed against a peptide in a recipient patient. Such a response can be an active response induced by administration of immunogen or a passive response induced by administration of antibody or primed T-cells. Without wishing to be limited by a single hypothesis, a cellular immune response is elicited by the presentation of polypeptide epitopes in association with Class II or Class I MHC molecules to activate antigen-specific $CD4^+$ T helper cells and/or $CD8_+$ cytotoxic T cells, respectively. The response may also involve activation of monocytes, macrophages, NK cells, basophils, dendritic cells, astrocytes, microglia cells, eosinophils, activation or recruitment of neutrophils or other components of innate immunity. The presence of a cell-mediated immunological response can be determined by proliferation assays ($CD4^+$ T cells) or CTL (cytotoxic T lymphocyte) assays. The relative contributions of humoral and cellular responses to the protective or therapeutic effect of an immunogen can be distinguished by separately isolating antibodies and T cells from an immunized syngeneic animal and measuring protective or therapeutic effect in a second subject.

[0351] "Immunogenic agent" or "immunogen" is a moiety capable of inducing an immunological response against itself on administration to a mammal, optionally in conjunction with an adjuvant.

[0352] "Inflammatory disorders", "inflammatory conditions" and/or "inflammation", used interchangeably herein, refers broadly to chronic or acute inflammatory diseases, and expressly includes inflammatory autoimmune diseases and inflammatory allergic conditions. These conditions include by way of example inflammatory abnormalities characterized by dysregulated immune response to harmful stimuli, such as pathogens, damaged cells, or irritants. Inflammatory disorders underlie a vast variety of human diseases. Non-immune diseases with etiological origins in inflammatory processes include cancer, atherosclerosis, and ischemic heart disease. Examples of disorders associated with inflammation include: Chronic prostatitis, Glomerulonephritis, Hypersensitivities, Pelvic inflammatory disease, Reperfusion injury, Sarcoidosis, Vasculitis, Interstitial cystitis, normocomplementemic urticarial vasculitis, pericarditis, myositis, antisynthetase syndrome, scleritis, macrophage activation syndrome, Behget's Syndrome, PAPA Syndrome, Blau's Syndrome, gout, adult and juvenile Still's disease, cryropyrinopathy, Muckle-Wells syndrome, familial cold-induced auto-inflammatory syndrome, neonatal onset multisystemic inflammatory disease, familial Mediterranean fever, chronic infantile neurologic, cutaneous and articular syndrome, systemic juvenile idiopathic arthritis, Hyper IgD syndrome, Schnitzler's syndrome, TNF receptor-associated periodic syndrome (TRAPSP), gingivitis, periodontitis, hepatitis, cirrhosis, pancreatitis, myocarditis, vasculitis, gastritis, gout, gouty arthritis, and inflammatory skin disorders, selected from the group consisting of psoriasis, atopic dermatitis, eczema, rosacea, urticaria, and acne.

[0353] "Inhibitory signal," as used herein, refers broadly to a signal transmitted via an inhibitory receptor molecule on an immune cell. A signal antagonizes a signal via an activating receptor (e.g., via a TCR, CD3, BCR, or Fc molecule) and can result, e.g., in inhibition of: second messenger generation; proliferation; or effector function in the immune cell, e.g., reduced phagocytosis, antibody production, or cellular cytotoxicity, or the failure of the immune cell to produce mediators (e.g., cytokines (e.g., IL-2) and/or mediators of allergic responses); or the development of anergy.

[0354] "Isolated," as used herein, refers broadly to material removed from its original environment in which it naturally occurs, and thus is altered by the hand of man from its natural environment and includes "recombinant" polypeptides. Isolated material may be, for example, exogenous nucleic acid included in a vector system, exogenous nucleic acid contained within a host cell, or any material which has been removed from its original environment and thus altered by the hand of man (e.g., "isolated antibody"). For example, "isolated" or "purified," as used herein, refers broadly to a protein, DNA, antibody, RNA, or biologically active portion thereof, that is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the biological substance is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. As used herein the term "isolated" refers to a compound of interest (for example a polynucleotide or a polypeptide) that is in an environment different from that in which the compound naturally occurs e.g., separated from its natural milieu such as by concentrating a peptide to a concentration at which it is not found in nature. "Isolated" includes compounds that are within samples that are substantially enriched for the compound of interest and/or in which the compound of interest is partially or substantially purified.

[0355] "Isolated antibody", as used herein, is intended to refer to an antibody that is substantially free of other antibodies having different antigenic specificities (e.g., an

isolated antibody that specifically binds VISTA) is substantially free of antibodies that specifically bind antigens other than VISTA). Moreover, an isolated antibody may be substantially free of other cellular material and/or chemicals.

[0356] "Isotype" herein refers to the antibody class (e.g., IgM or IgG1) that is encoded by the heavy chain constant region genes.

[0357] "K-assoc" or "Ka", as used herein, refers broadly to the association rate of a particular antibody-antigen interaction, whereas the term "Kdiss" or "Kd," as used herein, refers to the dissociation rate of a particular antibody-antigen interaction.

[0358] The term "K_D", as used herein, is intended to refer to the dissociation constant, which is obtained from the ratio of Kd to Ka (i. e., Kd/Ka) and is expressed as a molar concentration (M). K_D values for antibodies can be determined using methods well established in the art such as plasmon resonance (BIAcore®), ELISA and KINEXA. A preferred method for determining the K_D of an antibody is by using surface Plasmon resonance, preferably using a biosensor system such as a BIAcore® system or by ELISA. Typically these methods are effected at 25° or 37° C. Antibodies for therapeutic usage generally will possess a KD when determined by surface Plasmon resonance of 50 nM or less or more typically 1 nM or less at 25° or 37° C.

[0359] "Label" or a "detectable moiety" as used herein, refers broadly to a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means.

[0360] "Low stringency," "medium stringency," "high stringency," or "very high stringency conditions," as used herein, refers broadly to conditions for nucleic acid hybridization and washing. Guidance for performing hybridization reactions can be found in Ausubel, et al., *Short Protocols in Molecular Biology* (5th Ed.) John Wiley & Sons, NY (2002). Exemplary specific hybridization conditions include but are not limited to: (1) low stringency hybridization conditions in 6× sodium chloride/sodium citrate (SSC) at about 45° C., followed by two washes in 0. 2×SSC, 0.1% SDS at least at 50° C. (the temperature of the washes can be increased to 55° C. for low stringency conditions); (2) medium stringency hybridization conditions in 6×SSC at about 45° C., followed by one or more washes in 0. 2×SSC, 0. 1% SDS at 60° C.; (3) high stringency hybridization conditions in 6×SSC at about 45° C. followed by one or more washes in 0. 2×. SSC, 0. 1% SDS at 65° C.; and (4) very high stringency hybridization conditions are 0. 5M sodium phosphate, 7% SDS at 65° C., followed by one or more washes at 0.2×SSC, and 1% SDS at 65° C.

[0361] "Lupus", as used herein, is intended to include all types of lupus. There are 4 types of lupus which are discussed below. "Lupus-like condition", as used herein, is intended to include inflammatory conditions with symptoms similar to lupus such as kidney inflammation, increased proteinuria, and splenomegaly. "Systemic Lupus Erythematosus" or ("SLE") the most common form of lupus which can be mild or severe and can affect major organ systems. This is the condition most people associate with "lupus". It is an autoimmune condition of unknown cause that may result in inflammation of the kidneys—called lupus nephritis—which can affect the body's ability to filter waste from the blood, and or if severe may result in kidney damage requiring dialysis or kidney transplant. Also SLE may result in an increase in blood pressure in the lungs—called pulmonary hypertension—can cause difficulty breathing. Further SLE may cause Inflammation of the nervous system and brain which can cause memory problems, confusion, headaches, and strokes. Further SLE may result in inflammation in the brain's blood vessels which can cause high fevers, seizures, and behavioral changes. Also SLE may result in hardening of the arteries or coronary artery disease—the buildup of deposits on coronary artery walls—can lead to a heart attack. "Skin Lupus" herein refers to lupus conditions that only affect the skin. There are three types of lupus that affect the skin chronic cutaneous lupus erythematosus (CCLE) (also known as Discoid Lupus Erythematosus [DLE]), subacute cutaneous lupus erythematosus (SCLE), and tumid lupus. Cutaneous Lupus Erythematosus or Discoid Lupus Erythematosus can cause many types of rashes and lesions (sores), the most common—called discoid rash—is raised, scaly and red, but not itchy. Areas of rash appear like disks, or circles. Another common example of cutaneous lupus is a rash over the cheeks and across the bridge of the nose, known as the butterfly rash. Other rashes or sores may appear on the face, neck, or scalp (areas of the skin that are exposed to sunlight or fluorescent light), or in the mouth, nose, or vagina. Hair loss and changes in the pigment, or color, of the skin are also symptoms of cutaneous lupus. Approximately 10 percent of people who have cutaneous lupus will develop systemic lupus. However, it is likely that these people already had systemic lupus, with the skin rash as their main symptom. "Drug-induced Lupus Erythematosus" is a condition caused by certain drugs which can cause lupus-like symptoms in people who do not have SLE. Generally, this form of lupus is temporary and usually subsides within months of the time that the medication is stopped. Medications known to induce lupus-like symptoms include the blood pressure medications hydralazine and methyldopa, a heart medication called procainamide, and a drug called D-penicillamine, which is used in cases of metal poisoning. Other causes of drug-induced lupus include minocycline (used to treat acne), Isoniazid—a treatment for tuberculosis and anti-TNF (used to treat rheumatoid arthritis). The symptoms of drug-induced lupus are similar to those of systemic lupus, however unlike SLE but it rarely affects major organs. Neonatal lupus is not a true form of lupus. It is a rare condition that affects infants of women who have lupus and is caused by antibodies from the mother acting upon the infant in the womb. At birth, the infant may have a skin rash, liver problems, or low blood cell counts but these symptoms generally disappear completely after several months with no lasting effects. Some infants with neonatal lupus can also have a serious heart defect.

[0362] "Mammal," as used herein, refers broadly to any and all warm-blooded vertebrate animals of the class Mammalia, including humans, characterized by a covering of hair on the skin and, in the female, milk-producing mammary glands for nourishing the young. Examples of mammals include but are not limited to alpacas, armadillos, capybaras, cats, camels, chimpanzees, chinchillas, cattle, dogs, goats, gorillas, hamsters, horses, humans, lemurs, llamas, mice, non-human primates, pigs, rats, sheep, shrews, squirrels, tapirs, and voles. Mammals include but are not limited to bovine, canine, equine, feline, murine, ovine, porcine, primate, and rodent species. Mammal also includes any and all those listed on the Mammal Species of the World maintained by the National Museum of Natural History, Smithsonian Institution in Washington D. C.

[0363] "Multispecific antibody" refers to an antibody with 2 or more antigen binding regions. This includes bispecific antibodies. These antigen binding regions may bind to different antigens or to different epitopes of the same antigen.

[0364] "Naturally-occurring nucleic acid molecule," as used herein, refers broadly refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

[0365] "Nucleic acid" or "nucleic acid sequence," as used herein, refers broadly to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

[0366] "Operatively linked", as used herein, refers broadly to when two DNA fragments are joined such that the amino acid sequences encoded by the two DNA fragments remain in-frame.

[0367] "Paratope," as used herein, refers broadly to the part of an antibody which recognizes an antigen (e.g., the antigen-binding site of an antibody.) Paratopes may be a small region (e.g., 15-22 amino acids) of the antibody's Fv region and may contain parts of the antibody's heavy and light chains. See Goldsby, et al. Antigens (Chapter 3) Immunology (5th Ed.) New York: W. H. Freeman and Company, pages 57-75.

[0368] "Patient," or "subject" or "recipient", "individual", or "treated individual" are used interchangeably herein, and refers broadly to any animal that is in need of treatment either to alleviate a disease state or to prevent the occurrence or reoccurrence of a disease state. Also, "Patient" as used herein, refers broadly to any animal that has risk factors, a history of disease, susceptibility, symptoms, and signs, was previously diagnosed, is at risk for, or is a member of a patient population for a disease. The patient may be a clinical patient such as a human or a veterinary patient such as a companion, domesticated, livestock, exotic, or zoo animal.

[0369] "Polypeptide," "peptide" and "protein," are used interchangeably and refer broadly to a polymer of amino acid residues s of any length, regardless of modification (e.g., phosphorylation or glycosylation). The terms apply to amino acid polymers in which one or more amino acid residue is an analog or mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer. Polypeptides can be modified, e.g., by the addition of carbohydrate residues to form glycoproteins. The terms "polypeptide," "peptide" and "protein" expressly include glycoproteins, as well as non-glycoproteins.

[0370] "Promoter," as used herein, refers broadly to an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation.

[0371] "Prophylactically effective amount," as used herein, refers broadly to the amount of a compound that, when administered to a patient for prophylaxis of a disease or prevention of the reoccurrence of a disease, is sufficient to effect such prophylaxis for the disease or reoccurrence. The prophylactically effective amount may be an amount effective to prevent the incidence of signs and/or symptoms. The "prophylactically effective amount" may vary depending on the disease and its severity and the age, weight, medical history, predisposition to conditions, preexisting conditions, of the patient to be treated.

[0372] "Prophylactic vaccine" and/or "Prophylactic vaccination" refers to a vaccine used to prevent a disease or symptoms associated with a disease such as cancer or an infectious condition.

[0373] "Prophylaxis," as used herein, refers broadly to a course of therapy where signs and/or symptoms are not present in the patient, are in remission, or were previously present in a patient. Prophylaxis includes preventing disease occurring subsequent to treatment of a disease in a patient. Further, prevention includes treating patients who may potentially develop the disease, especially patients who are susceptible to the disease (e.g., members of a patent population, those with risk factors, or at risk for developing the disease).

[0374] "Recombinant" as used herein, refers broadly with reference to a product, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all.

[0375] The term "recombinant human antibody", as used herein, includes all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as (a) antibodies isolated from an animal (e.g., a mouse) that is transgenic or transchromosomal for human immunoglobulin genes or a hybridoma prepared therefrom (described further below), (b) antibodies isolated from a host cell transformed to express the human antibody, e.g., from a transfectoma, (c) antibodies isolated from a recombinant, combinatorial human antibody library, and (d) antibodies prepared, expressed, created or isolated by any other means that involve splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies have variable regions in which the framework and CDR regions are derived from human germline immunoglobulin sequences. In certain embodiments, however, such recombinant human antibodies can be subjected to in vitro mutagenesis (or, when an animal transgenic for

human Ig sequences is used, in vivo somatic mutagenesis) and thus the amino acid sequences of the V_H and V_L regions of the recombinant antibodies are sequences that, while derived from and related to human germline VH and VL sequences, may not naturally exist within the human antibody germline repertoire in vivo.

[0376] "Signal sequence" or "signal peptide," as used herein, refers broadly to a peptide containing about 15 or more amino acids which occurs at the N-terminus of secretory and membrane bound polypeptides and which contains a large number of hydrophobic amino acid residues. For example, a signal sequence contains at least about 10-30 amino acid residues, preferably about 15-25 amino acid residues, more preferably about 18-20 amino acid residues, and even more preferably about 19 amino acid residues, and has at least about 35-65%, preferably about 38-50%, and more preferably about 40-45% hydrophobic amino acid residues (e.g., Valine, Leucine, Isoleucine or Phenylalanine). A "signal sequence," also referred to in the art as a "signal peptide," serves to direct a polypeptide containing such a sequence to a lipid bilayer, and is cleaved in secreted.

[0377] "Specifically (or selectively) binds" to an antibody or "specifically (or selectively) immunoreactive with," or "specifically interacts or binds," as used herein, refers broadly to a protein or peptide (or other epitope), refers, in some embodiments, to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologies. For example, under designated immunoassay conditions, the specified antibodies bind to a particular protein at least two times greater than the background (non-specific signal) and do not substantially bind in a significant amount to other proteins present in the sample. Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than about 10 to 100 times background.

[0378] "Specifically hybridizable" and "complementary" as used herein, refer broadly to a nucleic acid can form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. The binding free energy for a nucleic acid molecule with its complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., RNAi activity. Determination of binding free energies for nucleic acid molecules is well known in the art. (See, e.g., Turner, et al. *CSH Symp. Quant. Biol. L:* 123-33 (1987); Frier, et al. *PNAS* 83: 9373-77 1986); Turner, et al. *J. Am. Chem. Soc.* 109:3783-85 (1987)). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., about at least 5, 6, 7, 8, 9, 10 out of 10 being about at least 50%, 60%, 70%, 80%, 90%, and 100% complementary, inclusive). "Perfectly complementary" or 100% complementarity refers broadly all of the contiguous residues of a nucleic acid sequence hydrogen bonding with the same number of contiguous residues in a second nucleic acid sequence.

[0379] "Substantial complementarity" refers to polynucleotide strands exhibiting about at least 90% complementarity, excluding regions of the polynucleotide strands, such as overhangs, that are selected so as to be noncomplementary. Specific binding requires a sufficient degree of complementarity to avoid non-specific binding of the oligomeric compound to non-target sequences under conditions in which specific binding is desired, i. e., under physiological conditions in the case of in vivo assays or therapeutic treatment, or in the case of in vitro assays, under conditions in which the assays are performed. The non-target sequences typically may differ by at least 5 nucleotides.

[0380] "Signs" of disease, as used herein, refers broadly to any abnormality indicative of disease, discoverable on examination of the patient; an objective indication of disease, in contrast to a symptom, which is a subjective indication of disease.

[0381] "Solid support," "support," and "substrate," as used herein, refers broadly to any material that provides a solid or semi-solid structure with which another material can be attached including but not limited to smooth supports (e.g., metal, glass, plastic, silicon, and ceramic surfaces) as well as textured and porous materials.

[0382] "Soluble ectodomain (ECD)" or "ectodomain" or "soluble VISTA protein(s)/molecule(s)" of VISTA as used herein means non-cell-surface-bound VISTA molecules or any portion thereof, including, but not limited to: VISTA fusion proteins or VISTA ECD-Ig fusion proteins, wherein the extracellular domain of VISTA or fragment thereof is fused to an immunoglobulin (Ig) moiety rendering the fusion molecule soluble, or fragments and derivatives thereof, proteins with the extracellular domain of VISTA fused or joined with a portion of a biologically active or chemically active protein such as the papillomavirus E7 gene product, melanoma-associated antigen p97 or HIV env protein, or fragments and derivatives thereof; hybrid (chimeric) fusion proteins such as VISTA-Ig, or fragments and derivatives thereof. Such fusion proteins are described in greater detail below.

[0383] "Soluble VISTA protein(s)/molecule(s)" herein also include VISTA molecules with the transmembrane domain removed to render the protein soluble, or fragments and derivatives thereof; fragments, portions or derivatives thereof, and soluble VISTA mutant molecules. The soluble VISTA molecules used in the methods according to at least some embodiments of the invention may or may not include a signal (leader) peptide sequence.

[0384] "Subject" or "patient" or "individual" in the context of therapy or diagnosis herein includes any human or nonhuman animal. The term "nonhuman animal" includes all vertebrates, e.g., mammals and non-mammals, such as nonhuman primates, sheep, dogs, cats, horses, cows, chickens, amphibians, reptiles, etc., i.e., anyone suitable to be treated according to the present invention include, but are not limited to, avian and mammalian subjects, and are preferably mammalian. Any mammalian subject in need of being treated according to the present invention is suitable. Human subjects of both genders and at any stage of development (i. e., neonate, infant, juvenile, adolescent, and adult) can be treated according to the present invention. The present invention may also be carried out on animal subjects, particularly mammalian subjects such as mice, rats, dogs, cats, cattle, goats, sheep, and horses for veterinary purposes, and for drug screening and drug development purposes. "Subjects" is used interchangeably with "individuals" and "patients."

[0385] "Substantially free of chemical precursors or other chemicals," as used herein, refers broadly to preparations of VISTA protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the

language "substantially free of chemical precursors or other chemicals" includes preparations of VISTA protein having less than about 30% (by dry weight) of chemical precursors or non-VISTA chemicals, more preferably less than about 20% chemical precursors or non-VISTA chemicals, still more preferably less than about 10% chemical precursors or non-VISTA chemicals, and most preferably less than about 5% chemical precursors or non-VISTA chemicals.

[0386] "Symptoms" of disease as used herein, refers broadly to any morbid phenomenon or departure from the normal in structure, function, or sensation, experienced by the patient and indicative of disease.

[0387] "T cell," as used herein, refers broadly to CD4+ T cells and CD8+ T cells. The term T cell also includes both T helper 1 type T cells and T helper 2 type T cells.

[0388] "Therapy," "therapeutic," "treating," or "treatment", as used herein, refers broadly to treating a disease, arresting, or reducing the development of the disease or its clinical symptoms, and/or relieving the disease, causing regression of the disease or its clinical symptoms. Therapy encompasses prophylaxis, treatment, remedy, reduction, alleviation, and/or providing relief from a disease, signs, and/or symptoms of a disease. Therapy encompasses an alleviation of signs and/or symptoms in patients with ongoing disease signs and/or symptoms (e.g., inflammation, pain). Therapy also encompasses "prophylaxis". The term "reduced", for purpose of therapy, refers broadly to the clinical significant reduction in signs and/or symptoms. Therapy includes treating relapses or recurrent signs and/or symptoms (e.g., inflammation, pain). Therapy encompasses but is not limited to precluding the appearance of signs and/or symptoms anytime as well as reducing existing signs and/or symptoms and eliminating existing signs and/or symptoms. Therapy includes treating chronic disease ("maintenance") and acute disease. For example, treatment includes treating or preventing relapses or the recurrence of signs and/or symptoms (e.g., inflammation, pain).

[0389] "Treg cell" (sometimes also referred to as suppressor T cells or inducible Treg cells or iTregs) as used herein refers to a subpopulation of T cells which modulate the immune system and maintain tolerance to self-antigens and can abrogate autoimmune diseases. $Foxp3^+$ $CD4^+CD25^+$ regulatory T cells (Tregs) are critical in maintaining peripheral tolerance under normal conditions.

[0390] "Transmembrane domain," as used herein, refers broadly to an amino acid sequence of about 15 amino acid residues in length which spans the plasma membrane. More preferably, a transmembrane domain includes about at least 20, 25, 30, 35, 40, or 45 amino acid residues and spans the plasma membrane. Transmembrane domains are rich in hydrophobic residues, and typically have an a-helical structure. In an embodiment, at least 50%, 60%, 70%, 80%, 90%, 95% or more of the amino acids of a transmembrane domain are hydrophobic, e.g., leucines, isoleucines, tyrosines, or tryptophans. Transmembrane domains are described in, for example, Zagotta, et al. *Annu. Rev. Neurosci.* 19:235-263 (1996).

[0391] "Transgenic animal," as used herein, refers broadly to a non-human animal, preferably a mammal, more preferably a mouse, in which one or more of the cells of the animal includes a "transgene". The term "transgene" refers to exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, for example directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal.

[0392] "Unresponsiveness," as used herein, refers broadly to refractivity of immune cells to stimulation, e.g., and stimulation via an activating receptor or a cytokine. Unresponsiveness can occur, e.g., because of exposure to immunosuppressants or high doses of antigen.

[0393] "Variable region" or "VR," as used herein, refers broadly to the domains within each pair of light and heavy chains in an antibody that are involved directly in binding the antibody to the antigen. Each heavy chain has at one end a variable domain (V_H) followed by a number of constant domains. Each light chain has a variable domain (V_L) at one end and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain.

[0394] "Vector," as used herein, refers broadly to a nucleic acid molecule capable of transporting another nucleic acid molecule to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments may be ligated. Another type of vector is a viral vector, wherein additional DNA segments may be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Vectors are referred to herein as "recombinant expression vectors" or simply "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" may be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions. The techniques and procedures are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification. See, e.g., Sambrook, et al. *Molec. Cloning: Lab. Manual* [3rd Ed] Cold Spring Harbor Laboratory Press (2001). Standard techniques may be used for recombinant DNA, oligonucleotide synthesis, and tissue culture, and transformation (e.g., electroporation, lipofection). Enzymatic reactions and purification techniques may be performed according to manufacturer's specifications or as commonly accomplished in the art or as described herein.

[0395] Having defined certain terms and phrases used in the present application, the anti-VISTA antibodies and antigen binding antibody fragments and methods for the production and use thereof which are embraced by the invention are further described below.

[0396] The present invention relates to antibodies and antibody fragments comprising an antigen binding region that binds to a V-domain Ig Suppressor of T cell Activation (VISTA). VISTA is a checkpoint regulator that negatively

suppresses immune responses. See Wang et al., "VISTA, a novel mouse Ig superfamily ligand that negatively regulates T cell responses," *J. Exp. Med.,* 208(3) 577-92 (2011). This protein is expressed on normal human neutrophils, monocytes and T cells subsets. In addition, cynomolgus monkey cells express VISTA in a similar pattern to normal human cells. VISTA is also expressed in the peripheral blood cells e.g., of cancer patients.

[0397] The binding of an agonist anti-VISTA antibody or antibody fragment according to the invention will agonize, elicit or mimic at least one of the effects of VISTA on immunity thereby promoting at least one of the suppressive effects of VISTA on immunity, e.g., the suppression of T cell immunity or the suppression of the expression of specific proinflammatory cytokines or its promoting effect on the expression of certain chemoattractants and chemokines.

[0398] Such antibody fragments include by way of example Fab, $F(ab')_2$, and scFv antibody fragments. These antibody or antibody fragments can comprise an antibody constant region or fragment or variant thereof. Such antibodies and antibody fragments include those which bind to VISTA proteins expressed on hematopoietic and other cells, for example, myeloid cells and/or lymphocytes, monocytes, neutrophils, T cells, natural killer (NK) cells, natural killer T (NKT) cells, a tumor cell, and/or in the tumor microenvironment (TME). The tumor microenvironment is the cellular environment of the tumor. It can include surrounding immune cells, fibroblasts, blood vessels, other cells, signaling molecules, and the extracellular matrix.

[0399] The subject application provides novel agonist anti-human VISTA antibodies including those comprising the same CDRS as any of the anti-human VISTA antibodies having the sequences shown in FIG. **4**. While prior to the present invention a number of antagonist anti-human VISTA antibodies have been reported in the literature, no agonistic anti-human VISTA antibodies or antibody fragments have been reported.

[0400] As disclosed in the experimental examples which follow 2 chimeric anti-human VISTA antibodies were initially derived from an antagonistic murine anti-human VISTA antibody (1E8 having sequences in FIG. **4**) which respectively contain unmodified IgG2 human constant regions or IgG2 constant regions wherein the cysteine residue at position 127 of the kappa chain was changed to a serine residue. As shown in the Examples and the Figures referenced therein, both antibodies were found to agonize or mimic the suppressive effects of VISTA on immunity at least based on (i) their ability to decrease the expression of certain proinflammatory cytokines such as IL-2, IL-4, IL-6, IL-17, granulocyte macrophage colony stimulating factor (GM-CSF) and tumor necrosis factor-alpha (TNF-α) as well as reducing the expression of certain chemokines or chemoattractants such as KC (keratinocyte derived chemokine) or MIP-2 (Macrophage Inflammatory Protein-2); (ii) suppress T cell activity in GVHD model; and to (iii) suppress CD3-driven T cell responses.

[0401] Additionally after isolation of these 2 agonist antibodies another 10 chimeric agonist anti-human VISTA antibodies containing human IgG2 constant or Fc regions have been obtained. These antibodies were derived from the antibodies referred to herein as GG8, VSTB95 (INX903), VSTB103 (INX904), VSTB53 (INX905), VSTB92 (INX908), VSTB50(INX900), VSTB56(INX901), VSTB63 (INX902), VSTB54(INX906) and VSTB66(INX907)(having the sequences in FIG. **4**).

[0402] Particularly, these chimeric anti-human VISTA antibodies have the variable sequences shown in FIG. **4** and human IgG2 constant regions. As reported in Tables 1 and 2 infra these anti-human VISTA antibodies when assessed by use of antibody binning were found to bind to 2 different epitope groups designated Group 1 and Group 2. As noted in the FIG. **4** the epitope corresponding to Group 2 includes residues in 2 different peptides present in human VISTA, i.e., NLTLLDSGL and VQTGKDAPSNC. Also, as described in the examples infra the epitopic specificity of other agonist antibodies according to the invention has been determined by Pepscan© analysis.

[0403] As is indicated in the Tables 1 and 2 infra these 12 different anti-human VISTA antibodies were found to be immunosuppressive in at least one model of immunosuppression and many in several immunosuppression models. Particularly INX905, INX908, INX901, INX902 and INX906 were shown to be immunosuppressive in 2 different assays formats. While all of these antibodies were immunosuppressive and appear to elicit, promote or agonize the immunosuppressive effects of VISTA, INX901, INX902 and INX906 and INX908 appear to be the most immunosuppressive.

[0404] Also, other chimeric anti-human VISTA antibodies comprising human IgG2 constant domains containing the variable sequences of other anti-VISTA antibodies shown in FIG. **4** are to be screened for their immunosuppressive properties and their ability to agonize or mimic the immunosuppressive and other effects of human VISTA. Based on the results obtained to date this screening should identify other agonist anti-human VISTA antibodies. Additionally agonist anti-human VISTA antibodies according to the invention have been shown to be effective (immunosuppressive) in numerous autoimmune and inflammatory animal disease models including arthritis, lupus or SLE, GVHD, inflammatory bowel disease (IBD) or colitis, chronic and acute infectious disease or hepatotoxicity and psoriasis animal models. Based thereon the subject anti-human VISTA agonist antibodies should be well suited for use in therapeutic and prophylactic treatment of autoimmune, allergic and inflammatory conditions.

[0405] As noted chimeric IgG2 anti-human VISTA antibodies having the sequences shown in FIG. **4** were shown to be immunosuppressive in at least one model of immunosuppression. These antibodies moreover elicit these immunosuppressive effects in a specific immunomodulatory manner rather than by effecting the depletion of specific types of T cells or by depleting T cells in general.

[0406] As further shown in the examples surprisingly chimeric IgG2 agonistic anti-human VISTA antibodies containing a mutation in the hinge region elicited substantially the same suppressive effects on immunity, i.e., the mutation within in IgG2 constant region appeared to elicit no enhancement in suppression under the tested experimental conditions. Rather both the IgG2A and IgG2 B forms and mixtures thereof elicited the same immunosuppressive effects. Additionally, and also surprisingly, based on experiments disclosed in the examples it would appear that FcγR binding may contribute to the agonist properties of the subject anti-human VISTA antibodies. In particular it was found that the inclusion of silent IgG2 constant regions

ablated the immunosuppressive properties of the subject agonist antibodies. Based on these results it is hypothesized that one or more FcγRs may affect the agonistic properties of these antibodies and in particular it is hypothesized that FcγRIIA (CD32 or CD32A) or FcγRIIB (CD32B) binding may be involved in the agonist properties of the subject agonist antibodies.

[0407] Using these same methods it is expected that other agonist anti-human VISTA IgG2 antibodies may be obtained, e.g., others derived from anti-human VISTA antibodies having the sequences shown in FIG. **4**. As mentioned 12 agonist anti-human VISTA antibodies have been obtained to date including those having the sequences contained in FIG. **4**. Based on these results it is anticipated that other agonistic anti-human VISTA antibodies may be generated and shown to be immunosuppressive. Also it is anticipated that other agonistic anti-human VISTA antibodies may be generated which bind to the same or overlapping epitope and/or compete with any of the antibodies containing the sequences shown in FIG. **4**. In exemplary embodiments these antibodies will bind to the epitope corresponding to Group 1 or Group 2 antibodies or will compete for binding to human VISTA with such antibodies.

[0408] Methods for identifying the specific epitope(s) bound by an antibody are known in the art. In the working examples Applicants disclose the elucidation of the epitope bound by a number of anti-VISTA antibodies according to the invention. Thus, in exemplary embodiments agonist anti-human VISTA antibodies according to the invention will comprise IgG2 constant regions or fragments thereof, of the A form, B form or a mixture of the foregoing. In exemplary embodiments these antibodies will bind to one or more FcγRs, e.g., they will bind to the same FcγRs as an intact or wild-type human IgG2 Fc region. In other exemplary embodiments the antibody will bind to CD32 (CD32A and/or CD32B). This may be accomplished by the use of wild-type or modified IgG2 constant regions which bind to CD32 (CD32A and/or CD32B). Further, the agonist antibody may be modified to incorporate another polypeptide such as another Fc polypeptide or antigen binding region which binds to FcγRs such as CD32A and/or CD32B.

[0409] The IgG2 Fc or constant regions contained in the inventive agonist anti-human VISTA antibodies optionally may be modified, e.g., in order to alter effector function, e.g., to alter FcR binding, FcN binding, complement binding, glycosylation and the like. In particular, the IgG2 Fc or constant regions contained in the inventive agonist anti-human VISTA antibodies optionally may be modified by the conversion of the cysteine at position 27 or further optionally by the conversion of another cysteine residue or other residues, e.g., in the hinge region to another amino acid, e.g., a serine. Other potential Fc modifications are disclosed infra.

[0410] These VISTA agonist antibodies may be used in treating or preventing diseases conditions or for treating or reducing, ameliorating the pathological effects associated therewith, e.g., inflammation, in treating or preventing conditions wherein the suppression of T cell immunity or the expression of proinflammatory cytokines and or increased expression of chemokines and chemoattractants is therapeutically or prophylactically beneficial. These conditions include in particular autoimmunity, allergy, inflammatory disorders, sepsis, GVHD and for inhibiting unwanted T cell immune responses against transplanted cells, tissues or organs such as CAR-T cell or gene therapy constructs or cells containing.

[0411] As mentioned exemplary conditions which may be treated therapeutically or prophylactically using an agonist anti-human VISTA antibody according to the invention include autoimmune conditions, allergy conditions, inflammatory conditions, GVHD, transplant and sepsis. As mentioned, agonist anti-human VISTA antibodies according to the invention have been shown to be therapeutically effective and to be immunosuppressive in numerous animal disease models including arthritis, inflammatory bowel disease (IBD), lupus, GVHD, chronic acute infection/hepatotoxicity and psoriasis disease models. Therefore the inventive antibodies should be well suited for use in treating conditions wherein the suppression of immunity, especially T cell immunity is therapeutically desired.

A. Use of Agonistic Anti-Human Vista Antibodies and Fragments in Therapy and Diagnosis

[0412] Compositions containing agonists according to the invention may be used to inhibit T cell immunity and to treat conditions where this is therapeutically desirable such as autoimmunity, allergy or inflammatory conditions. These compositions will comprise an amount of an agonist antibody or antibody fragment according to the invention effective to suppress T cell activation or proliferation or cytokine expression or other effects of VISTA in a subject in need thereof. Such autoimmune, inflammatory and allergic conditions include for example arthritic conditions such as RA, psoriatic arthritis, psoriasis, scleroderma, multiple sclerosis, lupus, IBD, ITP, diabetes, GVHD, sarcoidosis, allergic asthma, hepatitis associated hepatotoxicity and for inhibiting unwanted T cell immune responses against transplanted cells, tissues or organs such as CAR-T cell or gene therapy constructs or cells containing and the like.

[0413] Specific conditions wherein the inventive antibodies may be used alone or in association with other therapeutics, especially other immunosuppressant molecules include acquired immune deficiency syndrome (AIDS), acquired splenic atrophy, acute anterior uveitis, Acute Disseminated Encephalomyelitis (ADEM), acute gouty arthritis, acute necrotizing hemorrhagic leukoencephalitis, acute or chronic sinusitis, acute purulent meningitis (or other central nervous system inflammatory disorders), acute serious inflammation, Addison's disease, adrenalitis, adult onset diabetes mellitus (Type II diabetes), adult-onset idiopathic hypoparathyroidism (AOIH), Agammaglobulinemia, agranulocytosis, vasculitides, including vasculitis, optionally, large vessel vasculitis, optionally, polymyalgia rheumatica and giant cell (Takayasu's) arthritis, allergic conditions, allergic contact dermatitis, allergic dermatitis, allergic granulomatous angiitis, allergic hypersensitivity disorders, allergic neuritis, allergic reaction, alopecia areata, alopecia totalis, Alport's syndrome, alveolitis, optionally allergic alveolitis or fibrosing alveolitis, Alzheimer's disease, amyloidosis, amylotrophic lateral sclerosis (ALS; Lou Gehrig's disease), an eosinophil-related disorder, optionally eosinophilia, anaphylaxis, ankylosing spondylitis, angiectasis, antibody-mediated nephritis, Anti-GBM/Anti-TBM nephritis, antigen-antibody complex-mediated diseases, antiglomerular basement membrane disease, anti-phospholipid antibody syndrome, antiphospholipid syndrome (APS), aphthae, aphthous stomatitis, aplastic anemia, arrhythmia, arterio-

sclerosis, arteriosclerotic disorders, arthritis, optionally rheumatoid arthritis such as acute arthritis, or chronic rheumatoid arthritis, arthritis chronica progrediente, arthritis deformans, ascariasis, aspergilloma, granulomas containing eosinophils, aspergillosis, aspermiogenese, asthma, optionally asthma bronchiale, bronchial asthma, or auto-immune asthma, ataxia telangiectasia, ataxic sclerosis, atherosclerosis, autism, autoimmune angioedema, autoimmune aplastic anemia, autoimmune atrophic gastritis, autoimmune diabetes, autoimmune disease of the testis and ovary including autoimmune orchitis and oophoritis, autoimmune disorders associated with collagen disease, autoimmune dysautonomia, autoimmune ear disease, optionally autoimmune inner ear disease (AGED), autoimmune endocrine diseases including thyroiditis such as autoimmune thyroiditis, autoimmune enteropathy syndrome, autoimmune gonadal failure, autoimmune hearing loss, autoimmune hemolysis, Autoimmune hepatitis, autoimmune hepatological disorder, autoimmune hyperlipidemia, autoimmune immunodeficiency, autoimmune inner ear disease (AIED), autoimmune myocarditis, autoimmune neutropenia, autoimmune pancreatitis, autoimmune polyendocrinopathies, autoimmune polyglandular syndrome type I, autoimmune retinopathy, autoimmune thrombocytopenic purpura (ATP), autoimmune thyroid disease, autoimmune urticaria, autoimmune-mediated gastrointestinal diseases, Axonal & neuronal neuropathies, Balo disease, Behçet's disease, benign familial and ischemia-reperfusion injury, benign lymphocytic angiitis, Berger's disease (IgA nephropathy), bird-fancier's lung, blindness, Boeck's disease, bronchiolitis obliterans (non-transplant) vs NSIP, bronchitis, bronchopneumonic aspergillosis, Bruton's syndrome, bullous pemphigoid, Caplan's syndrome, Cardiomyopathy, cardiovascular ischemia, Castleman's syndrome, Celiac disease, celiac sprue (gluten enteropathy), cerebellar degeneration, cerebral ischemia, and disease accompanying vascularization, Chagas disease, channelopathies, optionally epilepsy, channelopathies of the CNS, chorioretinitis, choroiditis, an autoimmune hematological disorder, chronic active hepatitis or autoimmune chronic active hepatitis, chronic contact dermatitis, chronic eosinophilic pneumonia, chronic fatigue syndrome, chronic hepatitis, chronic hypersensitivity pneumonitis, chronic inflammatory arthritis, Chronic inflammatory demyelinating polyneuropathy (CIDP), chronic intractable inflammation, chronic mucocutaneous candidiasis, chronic neuropathy, optionally IgM polyneuropathies or IgM-mediated neuropathy, chronic obstructive airway disease, chronic pulmonary inflammatory disease, Chronic recurrent multifocal osteomyelitis (CRMO), chronic thyroiditis (Hashimoto's thyroiditis) or subacute thyroiditis, Churg-Strauss syndrome, cicatricial pemphigoid/benign mucosal pemphigoid, CNS inflammatory disorders, CNS vasculitis, Coeliac disease, Cogan's syndrome, cold agglutinin disease, colitis polyposa, colitis such as ulcerative colitis, colitis ulcerosa, collagenous colitis, conditions involving infiltration of T cells and chronic inflammatory responses, congenital heart block, congenital rubella infection, Coombs positive anemia, coronary artery disease, Coxsackie myocarditis, CREST syndrome (calcinosis, Raynaud's phenomenon), Crohn's disease, cryoglobulinemia, Cushing's syndrome, cyclitis, optionally chronic cyclitis, heterochronic cyclitis, iridocyclitis, or Fuch's cyclitis, cystic fibrosis, cytokine-induced toxicity, deafness, degenerative arthritis, demyelinating diseases, optionally autoimmune demyelinating diseases, demyelinating neuropathies, dengue, dermatitis herpetiformis and atopic dermatitis, dermatitis including contact dermatitis, dermatomyositis, dermatoses with acute inflammatory components, Devic's disease (neuromyelitis optica), diabetic large-artery disorder, diabetic nephropathy, diabetic retinopathy, Diamond Blackfan anemia, diffuse interstitial pulmonary fibrosis, dilated cardiomyopathy, discoid lupus, diseases involving leukocyte diapedesis, Dressler's syndrome, Dupuytren's contracture, echovirus infection, eczema including allergic or atopic eczema, encephalitis such as Rasmussen's encephalitis and limbic and/or brainstem encephalitis, encephalomyelitis, optionally allergic encephalomyelitis or encephalomyelitis allergica and experimental allergic encephalomyelitis (EAE), endarterial hyperplasia, endocarditis, endocrine ophthalmopathy, endometriosis, endomyocardial fibrosis, endophthalmia phacoanaphylactica, endophthalmitis, enteritis allergica, eosinophilia-myalgia syndrome, eosinophilic fascitis, epidemic keratoconjunctivitis, epidermolysis bullosa acquisita (EBA), episclera, episcleritis, Epstein-Barr virus infection, erythema elevatum et diutinum, erythema multiforme, erythema nodosum leprosum, erythema nodosum, erythroblastosis fetalis, esophageal dysmotility, Essential mixed cryoglobulinemia, ethmoid, Evan's syndrome, Experimental Allergic Encephalomyelitis (EAE), Factor VIII deficiency, farmer's lung, febris rheumatica, Felty's syndrome, fibromyalgia, fibrosing alveolitis, filariasis, focal segmental glomerulosclerosis (FSGS), food poisoning, frontal, gastric atrophy, giant cell arthritis (temporal arthritis), giant cell hepatitis, giant cell polymyalgia, glomerulonephritides, glomerulonephritis (GN) with and without nephrotic syndrome such as chronic or acute glomerulonephritis (e.g., primary GN), Goodpasture's syndrome, gouty arthritis, granulocyte transfusion-associated syndromes, granulomatosis including lymphomatoid granulomatosis, granulomatosis with polyangiitis (GPA), granulomatous uveitis, Grave's disease, Guillain-Barre syndrome, gutatte psoriasis, hemoglobinuria paroxysmatica, Hamman-Rich's disease, Hashimoto's disease, Hashimoto's encephalitis, Hashimoto's thyroiditis, hemochromatosis, hemolytic anemia or immune hemolytic anemia including autoimmune hemolytic anemia (AIHA), hemolytic anemia, hemophilia A, Henoch-Schönlein purpura, Herpes gestationis, human immunodeficiency virus (HIV) infection, hyperalgesia, hypogammaglobulinemia, hypogonadism, hypoparathyroidism, idiopathic diabetes insipidus, idiopathic facial paralysis, idiopathic hypothyroidism, idiopathic IgA nephropathy, idiopathic membranous GN or idiopathic membranous nephropathy, idiopathic nephritic syndrome, idiopathic pulmonary fibrosis, idiopathic sprue, Idiopathic thrombocytopenic purpura (ITP), IgA nephropathy, IgE-mediated diseases, optionally anaphylaxis and allergic or atopic rhinitis, IgG4-related sclerosing disease, ileitis regionalis, immune complex nephritis, immune responses associated with acute and delayed hypersensitivity mediated by cytokines and T-lymphocytes, immune-mediated GN, immunoregulatory lipoproteins, including adult or acute respiratory distress syndrome (ARDS), Inclusion body myositis, infectious arthritis, infertility due to antispermatozoan antibodies, inflammation of all or part of the uvea, inflammatory bowel disease (IBD) inflammatory hyperproliferative skin diseases, inflammatory myopathy, insulin-dependent diabetes (type 1), insulitis, Interstitial cystitis, interstitial lung disease, interstitial lung fibrosis, iritis, ischemic re-perfusion

disorder, joint inflammation, Juvenile arthritis, juvenile dermatomyositis, juvenile diabetes, juvenile onset (Type I) diabetes mellitus, including pediatric insulin-dependent diabetes mellitus (IDDM), juvenile-onset rheumatoid arthritis, Kawasaki syndrome, keratoconjunctivitis sicca, kypanosomiasis, Lambert-Eaton syndrome, leishmaniasis, leprosy, leucopenia, leukocyte adhesion deficiency, Leukocytoclastic vasculitis, leukopenia, lichen planus, lichen sclerosus, ligneous conjunctivitis, linear IgA dermatosis, Linear IgA disease (LAD), Loffler's syndrome, lupoid hepatitis, lupus (including nephritis, cerebritis, pediatric, non-renal, extra-renal, discoid, alopecia), Lupus (SLE), lupus erythematosus disseminatus, Lyme arthritis, Lyme disease, lymphoid interstitial pneumonitis, malaria, male and female autoimmune infertility, maxillary, medium vessel vasculitis (including Kawasaki's disease and polyarteritis nodosa), membrano- or membranous proliferative GN (MPGN), including Type I and Type II, and rapidly progressive GN, membranous GN (membranous nephropathy), Meniere's disease, meningitis, microscopic colitis, microscopic polyangiitis, migraine, minimal change nephropathy, Mixed connective tissue disease (MCTD), mononucleosis infectiosa, Mooren's ulcer, Mucha-Habermann disease, multifocal motor neuropathy, multiple endocrine failure, multiple organ injury syndrome such as those secondary to septicemia, trauma or hemorrhage, multiple organ injury syndrome, multiple sclerosis (MS) such as spino-optical MS, multiple sclerosis, mumps, muscular disorders, myasthenia gravis such as thymoma-associated myasthenia gravis, myasthenia gravis, myocarditis, myositis, narcolepsy, necrotizing enterocolitis, and transmural colitis, and autoimmune inflammatory bowel disease, necrotizing, cutaneous, or hypersensitivity vasculitis, neonatal lupus syndrome (NLE), nephrosis, nephrotic syndrome, neurological disease, neuromyelitis optica (Devic's), neuromyelitis optica, neuromyotonia, neutropenia, non-cancerous lymphocytosis, nongranulomatous uveitis, non-malignant thymoma, ocular and orbital inflammatory disorders, ocular cicatricial pemphigoid, oophoritis, ophthalmia symphatica, opsoclonus myoclonus syndrome (OMS), opsoclonus or opsoclonus myoclonus syndrome (OMS), and sensory neuropathy, optic neuritis, orchitis granulomatosa, osteoarthritis, palindromic rheumatism, pancreatitis, pancytopenia, PANDAS (Pediatric Autoimmune Neuropsychiatric Disorders Associated with *Streptococcus*), paraneoplastic cerebellar degeneration, paraneoplastic syndrome, paraneoplastic syndromes, including neurologic paraneoplastic syndromes, optionally Lambert-Eaton myasthenic syndrome or Eaton-Lambert syndrome, parasitic diseases such as *Leishmania*, paroxysmal nocturnal hemoglobinuria (PNH), Parry Romberg syndrome, pars planitis (peripheral uveitis), Parsonnage-Turner syndrome, parvovirus infection, pemphigoid such as pemphigoid bullous and skin pemphigoid, pemphigus (including pemphigus vulgaris), pemphigus erythematosus, pemphigus *foliaceus*, pemphigus mucus-membrane pemphigoid, pemphigus, peptic ulcer, periodic paralysis, peripheral neuropathy, perivenous encephalomyelitis, pernicious anemia (anemia perniciosa), pernicious anemia, phacoantigenic uveitis, pneumonocirrhosis, POEMS syndrome, polyarteritis nodosa, Type I, II, & III, polyarthritis chronica primaria, polychondritis (e.g., refractory or relapsed polychondritis), polyendocrine autoimmune disease, polyendocrine failure, polyglandular syndromes, optionally autoimmune polyglandular syndromes (or polyglandular endocrinopathy syndromes), polymyalgia rheumatica, polymyositis, polymyositis/dermatomyositis, polyneuropathies, polyradiculitis *acuta*, post-cardiotomy syndrome, posterior uveitis, or autoimmune uveitis, postmyocardial infarction syndrome, postpericardiotomy syndrome, post-streptococcal nephritis, post-vaccination syndromes, presenile dementia, primary biliary cirrhosis, primary hypothyroidism, primary idiopathic myxedema, primary lymphocytosis, which includes monoclonal B cell lymphocytosis, optionally benign monoclonal gammopathy and monoclonal garnmopathy of undetermined significance, MGUS, primary myxedema, primary progressive MS (PPMS), and relapsing remitting MS (RRMS), primary sclerosing cholangitis, progesterone dermatitis, progressive systemic sclerosis, proliferative arthritis, psoriasis such as plaque psoriasis, psoriasis, psoriatic arthritis, pulmonary alveolar proteinosis, pulmonary infiltration eosinophilia, pure red cell anemia or aplasia (PRCA), pure red cell aplasia, purulent or nonpurulent sinusitis, pustular psoriasis and psoriasis of the nails, pyelitis, pyoderma gangrenosum, Quervain's thyroiditis, Raynaud's phenomenon, reactive arthritis, recurrent abortion, reduction in blood pressure response, reflex sympathetic dystrophy, refractory sprue, Reiter's disease or syndrome, relapsing polychondritis, reperfusion injury of myocardial or other tissues, reperfusion injury, respiratory distress syndrome, restless legs syndrome, retinal autoimmunity, retroperitoneal fibrosis, Reynaud's syndrome, rheumatic diseases, rheumatic fever, rheumatism, rheumatoid arthritis, rheumatoid spondylitis, rubella virus infection, Sampter's syndrome, sarcoidosis, schistosomiasis, Schmidt syndrome, SCID and Epstein-Barr virus-associated diseases, sclera, scleritis, sclerodactyl, scleroderma, optionally systemic scleroderma, sclerosing cholangitis, sclerosis disseminata, sclerosis such as systemic sclerosis, sensoneural hearing loss, seronegative spondyloarthritides, Sheehan's syndrome, Shulman's syndrome, silicosis, Sjögren's syndrome, sperm & testicular autoimmunity, sphenoid sinusitis, Stevens-Johnson syndrome, stiff-man (or stiff-person) syndrome, subacute bacterial endocarditis (SBE), subacute cutaneous lupus erythematosus, sudden hearing loss, Susac's syndrome, Sydenham's chorea, sympathetic ophthalmia, systemic lupus erythematosus (SLE) or systemic lupus erythematodes, cutaneous SLE, systemic necrotizing vasculitis, ANCA-associated vasculitis, optionally Churg-Strauss vasculitis or syndrome (CSS), tabes dorsalis, Takayasu's arteritis, telangiectasia, temporal arteritis/Giant cell arteritis, thromboangiitis ubiterans, thrombocytopenia, including thrombotic thrombocytopenic purpura (TTP) and autoimmune or immune-mediated thrombocytopenia such as idiopathic thrombocytopenic purpura (ITP) including chronic or acute ITP, thrombocytopenic purpura (TTP), thyrotoxicosis, tissue injury, Tolosa-Hunt syndrome, toxic epidermal necrolysis, toxic-shock syndrome, transfusion reaction, transient hypogammaglobulinemia of infancy, transverse myelitis, traverse myelitis, tropical pulmonary eosinophilia, tuberculosis, ulcerative colitis, undifferentiated connective tissue disease (UCTD), urticaria, optionally chronic allergic urticaria and chronic idiopathic urticaria, including chronic autoimmune urticaria, uveitis, anterior uveitis, uveoretinitis, valvulitis, vascular dysfunction, vasculitis, vertebral arthritis, vesiculobullous dermatosis, vitiligo, Wegener's granulomatosis (Granulomatosis with Polyangiitis (GPA)), Wiskott-Aldrich syndrome, or x-linked hyper IgM syndrome.

[0414] It should be understood that the disease conditions identified herein are intended to be exemplary and not exhaustive.

[0415] The subject agonists may be combined with other therapeutics which may be administered in the same or different compositions, at the same or different time and in either order. For example, the subject agonists may be administered in a therapeutic regimen that includes the administration of a PD-1 or PD-L1 agonist, CTLA4-Ig, a cytokine, a cytokine agonist or antagonist, or another receptor agonist or antagonist.

Downregulation of Immune Responses

[0416] Upregulating or enhancing the inhibitory function of a VISTA polypeptide may be used to downregulate immune responses. Downregulation can be in the form of inhibiting or blocking an immune response already in progress, or may involve preventing the induction of an immune response. The functions of activated immune cells can be inhibited by downregulating immune cell responses or by inducing specific anergy in immune cells, or both. For example, VISTA agonist antibodies may bind to the VISTA polypeptide which is expressed on various immune cells and thereby downmodulate the immune response. This agonist antibody may be monospecific or multispecific, e.g., it may comprise a bispecific antibody such as a BiTE. For example, such an antibody can comprise a VISTA antigen binding moiety and another antigen binding moiety, e.g., which targets a cell surface receptor on an immune cell, e.g., a T cell, a B cell, or a myeloid cell. Such an antibody, in addition to comprising a VISTA antigen binding site, may comprise a binding site which binds to a B cell antigen receptor, a T cell antigen receptor, or an Fc or other receptor, in order to target the molecule to a specific cell population. Selection of this second antigen for the bispecific antibody provides flexibility in selection of cell population to be targeted. VISTA agonist antibodies that promote or mimic VISTA activity may enhance the interaction of VISTA with its natural binding partners. As disclosed herein other human VISTA activating or agonist antibodies can be identified by their ability to inhibit T cell activity or proliferation and/or based on their immunosuppressive effects in vitro or inflammatory, allergic or autoimmune disease models.

[0417] A number of art-recognized readouts of cell activation can be employed to measure, e.g., cell proliferation or effector function (e.g., antibody production, cytokine production, phagocytosis) in the presence of the activating agent. The ability of a test antibody to agonize or promote the effects of human VISTA and thereby block this activation can be readily determined by measuring the ability of the agent to affect a decrease in proliferation or effector function being measured. Accordingly, the ability of a test antibody to be immunosuppressive and to block immune activation can be determined by measuring cytokine production and/or proliferation at different concentrations of antigen.

[0418] Tolerance may be induced against specific antigens by co-administering an antigen with a VISTA agonist antibody according to the invention. For example, tolerance may be induced to specific polypeptides Immune responses to allergens or foreign polypeptides to which an immune response is undesirable can be inhibited. For example, patients that receive Factor VIII frequently generate antibodies against this clotting factor. Co-administration of a VISTA agonist antibody according to the invention that stimulates or mimics VISTA activity or interaction with its natural binding partner, with recombinant factor VIII may suppress this undesired immune response.

[0419] A VISTA agonist antibody according to the invention may be used in combination with another agent that blocks the activity of costimulatory receptors on an immune cell or which agonizes the activity of another immunosuppressive receptor or ligand expressed on immune cells in order to downmodulate immune responses. Exemplary molecules include: PD-1, PDL-1 agonists, soluble forms of CTLA-4, anti-B7-1 antibodies, anti-B7-2 antibodies, antagonistic antibodies targeting one or more of LAG-3, TIM-3, BTLA, B7-H4, B7H3, et al. and/or agonistic antibodies targeting one or more of CD40, CD137, OX40, GITR, CD27, CD28 or ICOS or combinations thereof. These moieties can be combined in a single composition or compound, e.g., a bispecific antibody containing a VISTA agonist antibody according to the invention and further comprising another immune agonist antibody or it may comprise a fusion polypeptide containing a VISTA agonist antibody according to the invention which is fused to another immunosuppressive polypeptide or other active agent. Alternatively these moieties may be administered as separate or discrete entities (simultaneously or sequentially) in the same or different compositions to downregulate immune cell mediated immune responses in a subject.

[0420] Examples of specific immmunoinhibitory molecules that may be combined with VISTA agonist antibodies according to the invention include antibodies that block a costimulatory signal (e.g., against CD28 or ICOS), antibodies that activate an inhibitory signal via CTLA4, and/or antibodies against other immune cell markers (e.g., against CD40, CD40 ligand, or cytokines), fusion proteins (e.g., CTLA4-Fc or PD-1-Fc), and immunosuppressive drugs (e.g., rapamycin, cyclosporine A, or FK506).

[0421] In a further embodiment, bispecific antibodies containing VISTA agonist antibodies according to the invention are useful for targeting a specific cell population, e.g., using a marker found only on a certain type of cell, e.g., B lymphocytes, monocytes, dendritic cells, or Langerhans cells. Downregulating immune responses by activating VISTA activity or VISTA-immune cell interactions (and thus stimulating the negative signaling function of VISTA) is useful in downmodulating the immune response, e.g., in situations of tissue, skin and organ transplantation, in graft-versus-host disease (GVHD), or allergies, or in autoimmune and inflammatory diseases such as systemic lupus erythematosus, IBD, RA, psoriasis and multiple sclerosis. For example, blockage of immune cell function results in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by immune cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which promotes the activity of VISTA or the interaction of VISTA with its natural binding partner(s), on immune cells alone or in conjunction with another downmodulatory agent prior to or at the time of transplantation can inhibit the generation of a costimulatory signal. Moreover, promotion of VISTA activity may also be sufficient to anergize the immune cells, thereby inducing tolerance in a subject.

[0422] To achieve sufficient immunosuppression or tolerance in some diseases or in some subjects, it may necessary

to block the costimulatory function of other molecules. For example, it may be desirable to block the function of B7-1 and B7-2 by administering a soluble form of a combination of peptides having an activity of each of these antigens or blocking antibodies against these antigens (separately or together in a single composition) prior to or at the time of transplantation. Alternatively, it may be desirable to promote inhibitory activity of VISTA and to further inhibit a costimulatory activity of B7-1 and/or B7-2.

[0423] The subject anti-human VISTA agonist antibodies are especially useful in treating autoimmune disease. Many autoimmune disorders are the result of inappropriate activation of immune cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive immune cells may reduce or eliminate disease symptoms. Administration of the subject anti-human VISTA agonist antibodies that promote activity of VISTA or VISTA interaction with its natural binding partner(s), may induce antigen-specific tolerance of autoreactive immune cells which could lead to long-term relief from the disease. Additionally, co-administration of agents which block costimulation of immune cells by disrupting receptor-ligand interactions of B7 molecules with costimulatory receptors may be useful in inhibiting immune cell activation to prevent production of autoantibodies or cytokines which may be involved in the disease process.

[0424] Downregulation of an immune response via stimulation of VISTA activity or VISTA interaction with its natural binding partner(s) using the subject anti-human VISTA agonist antibodies may also be useful in treating an autoimmune attack of autologous tissues. Thus, conditions that are caused or exacerbated by autoimmune attack (e.g., heart disease, myocardial infarction or atherosclerosis) may be ameliorated or improved by increasing VISTA activity or VISTA binding to its natural binding partner. It is therefore within the scope of the invention to modulate conditions exacerbated by autoimmune attack, such as autoimmune disorders (as well as conditions such as heart disease, myocardial infarction, and atherosclerosis) by stimulating VISTA activity or VISTA interaction with its counter receptor using the subject anti-human VISTA agonist antibodies.

[0425] As mentioned previously the efficacy of agonist anti-human VISTA antibodies according to the invention for preventing or alleviating autoimmune and inflammatory disorders can be determined using a number of well-characterized animal models of human autoimmune and inflammatory diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis. See Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pages 840-856.

[0426] Inhibition of immune cell activation is further useful therapeutically in the treatment of allergies and allergic reactions, e.g., by inhibiting IgE production. The subject anti-human VISTA agonist antibodies which promote or mimic VISTA activity or VISTA interaction with its natural binding partner(s) can be administered to an allergic subject to inhibit immune cell-mediated allergic responses in the subject. Stimulation of VISTA activity or interaction with its natural binding partner(s), can be accompanied by exposure to allergen in conjunction with appropriate MHC molecules. Allergic reactions can be systemic or local in nature, depending on the route of entry of the allergen and the pattern of deposition of IgE on mast cells or basophils. Thus, immune cell-mediated allergic responses can be inhibited locally or systemically by administration of the subject anti-human VISTA agonist antibodies.

Selection of Anti-VISTA Antibodies that Bind to the Same Epitope

[0427] In certain embodiments, an agonistic anti-VISTA antibody according to the invention possesses desired functional properties such as modulation of immune stimulation and related functions. As shown in FIG. **4** and disclosed in the working examples, the epitopic specificity of a number of anti-human VISTA agonist antibodies according to the invention has been elucidated. As a number of antibodies which have been shown to bind to the same epitope have been found to be immunosuppressive it is expected that other VISTA agonist antibodies may be identified which bind to the same or overlapping epitope, i.e., they will interact with one or more of the amino acid residues of human VISTA polypeptide with which the exemplary VISTA agonist antibodies bind. Other antibodies with the same epitopic specificity may be selected and/or those which have the ability to cross-compete for binding to VISTA antigen with the desired antibodies. For example, the epitopic specificity of a desired antibody may be determined using a library of overlapping peptides comprising the entire VISTA polypeptide, e.g., 15-mers or an overlapping peptide library constituting a portion containing a desired epitope of VISTA and antibodies which bind to the same peptides or one or more residues thereof in the library are determined to bind the same linear or conformational epitope. In the examples the epitopic specificity was determined using Pepscan® methods which may be used to identify linear and conformational epitopes.

Modification of Agonist Antibodies According to the Invention

[0428] In addition or alternative to modifications made within the framework or CDR regions, antibodies according to at least some embodiments of the invention may be engineered to include modifications within the Fc region, typically to alter one or more functional properties of the antibody, such as serum half-life, complement fixation, Fc receptor binding, and/or antigen-dependent cellular cytotoxicity. Furthermore, an antibody according to at least some embodiments of the invention may be chemically modified (e.g., one or more chemical moieties can be attached to the antibody) or be modified to alter its glycosylation, again to alter one or more functional properties of the antibody. Such embodiments are described further below. The numbering of residues in the Fc region is that of the EU index of Kabat.

[0429] In one embodiment, the hinge region of CH1 is modified such that the number of cysteine residues in the hinge region is altered, e.g., increased or decreased. This approach is described further in U.S. Pat. No. 5,677,425 by Bodmer et al. The number of cysteine residues in the hinge region of CHI is altered to, for example, facilitate assembly of the light and heavy chains or to increase or decrease the stability of the antibody.

[0430] In another embodiment, the Fc hinge region of an antibody is mutated to decrease the biological half-life of the antibody. More specifically, one or more amino acid mutations are introduced into the CH2-CH3 domain interface

region of the Fc-hinge fragment such that the antibody has impaired Staphylococcal protein A (SpA) binding relative to native Fc-hinge domain SpA binding. This approach is described in further detail in U.S. Pat. No. 6,165,745 by Ward et al.

[0431] In another embodiment, the antibody is modified to increase its biological half-life. Various approaches are possible. For example, one or more of the following mutations can be introduced: T252L, T254S, and T256F, as described in U.S. Pat. No. 6,277,375 to Ward. Alternatively, to increase the biological half-life, the antibody can be altered within the CH1 or C_L region to contain a salvage receptor binding epitope taken from two loops of a CH2 domain of an Fc region of an IgG, as described in U.S. Pat. Nos. 5,869,046 and 6,121,022 by Presta et al.

[0432] In yet other embodiments, the Fc region is altered by replacing at least one amino acid residue with a different amino acid residue to alter the effector functions of the antibody. For example, one or more amino acids selected from amino acid residues 234, 235, 236, 237, 297, 318, 320 and 322 can be replaced with a different amino acid residue such that the antibody has an altered affinity for an effector ligand but retains the antigen-binding ability of the parent antibody. The effector ligand to which affinity is altered can be, for example, an Fc receptor or the Cl component of complement. This approach is described in further detail in U.S. Pat. Nos. 5,624,821 and 5,648,260, both by Winter et al.

[0433] In another example, one or more amino acids selected from amino acid residues 329, 331 and 322 can be replaced with a different amino acid residue such that the antibody has altered C1q binding and/or reduced or abolished complement dependent cytotoxicity (CDC). This approach is described in further detail in U.S. Pat. No. 6,194,551 by Idusogie et al.

[0434] In another example, one or more amino acid residues within amino acid positions 231 and 239 are altered to thereby alter the ability of the antibody to fix complement. This approach is described further in PCT Publication WO 94/29351 by Bodmer et al.

[0435] In yet another example, the Fc region is modified to increase the affinity of the antibody for an Fγ receptor by modifying one or more amino acids at the following positions: 238, 239, 248, 249, 252, 254, 255, 256, 258, 265, 267, 268, 269, 270, 272, 276, 278, 280, 283, 285, 286, 289, 290, 292, 293, 294, 295, 296, 298, 301, 303, 305, 307, 309, 312, 315, 320, 322, 324, 326, 327, 329, 330, 331, 333, 334, 335, 337, 338, 340, 360, 373, 376, 378, 382, 388, 389, 398, 414, 416, 419, 430, 434, 435, 437, 438 or 439. This approach is described further in PCT Publication WO 00/42072 by Presta. Moreover, the binding sites on human IgGI for FcγRI, FcγRII, FcγRIII and FcRn have been mapped and variants with improved binding have been described (see Shields, R. L. et al. (2001) *J. Biol. Chem.* 276:6591-6604). Specific mutations at positions 256, 290, 298, 333, 334 and 339 are shown to improve binding to FcγRIII. Additionally, the following combination mutants are shown to improve FcγRIII binding: T256A/S298A, S298A/E333A, S298A/K224A and S298A/E333A/K334A. Furthermore, mutations such as M252Y/S254T/T256E or M428L/N434S improve binding to FcRn and increase antibody circulation half-life (see Chan CA and Carter PJ (2010) *Nature Rev Immunol* 10:301-316).

[0436] In still another embodiment, the antibody can be modified to abrogate in vivo Fab arm exchange. Specifically, this process involves the exchange of IgG4 half-molecules (one heavy chain plus one light chain) between other IgG4 antibodies that effectively results in b specific antibodies which are functionally monovalent. Mutations to the hinge region and constant domains of the heavy chain can abrogate this exchange (see Aalberse, RC, Schuurman J., 2002, *Immunology* 105:9-19).

[0437] In still another embodiment, the glycosylation of an antibody is modified. For example, an aglycosylated antibody can be made (i.e., the antibody lacks glycosylation). Glycosylation can be altered to, for example, increase the affinity of the antibody for antigen. Such carbohydrate modifications can be accomplished by, for example, altering one or more sites of glycosylation within the antibody sequence. For example, one or more amino acid substitutions can be made that result in elimination of one or more variable region framework glycosylation sites to thereby eliminate glycosylation at that site. Such aglycosylation may increase the affinity of the antibody for antigen. Such an approach is described in further detail in U.S. Pat. Nos. 5,714,350 and 6,350,861 by Co et al.

[0438] Additionally or alternatively, an antibody can be made that has an altered type of glycosylation, such as a hypofucosylated antibody having reduced amounts of fucosyl residues or an antibody having increased bisecting GlcNac structures. Such altered glycosylation patterns have been demonstrated to increase the ADCC ability of antibodies. Such carbohydrate modifications can be accomplished by, for example, expressing the antibody in a host cell with altered glycosylation machinery. Cells with altered glycosylation machinery have been described in the art and can be used as host cells in which to express recombinant antibodies according to at least some embodiments of the invention to thereby produce an antibody with altered glycosylation. For example, the cell lines Ms704, Ms705, and Ms709 lack the fucosyltransferase gene, FUT8 (a (1,6) fucosyltransferase), such that antibodies expressed in the Ms704, Ms705, and Ms709 cell lines lack fucose on their carbohydrates. The Ms704, Ms705, and Ms709 FUT8 cell lines are created by the targeted disruption of the FUT8 gene in CHO/DG44 cells using two replacement vectors (see U.S. Patent Publication No. 20040110704 by Yamane et al. and Yamane-Ohnuki et al. (2004) *Biotechnol Bioeng* 87:614-22). As another example, EP 1,176,195 by Hanai et al. describes a cell line with a functionally disrupted FUT8 gene, which encodes a fucosyl transferase, such that antibodies expressed in such a cell line exhibit hypofucosylation by reducing or eliminating the a 1,6 bond-related enzyme. Hanai et al. also describe cell lines which have a low enzyme activity for adding fucose to the N-acetylglucosamine that binds to the Fc region of the antibody or does not have the enzyme activity, for example the rat myeloma cell line YB2/0 (ATCC CRL 1662). PCT Publication WO 03/035835 by Presta describes a variant CHO cell line, Lecl3 cells, with reduced ability to attach fucose to Asn(297)-linked carbohydrates, also resulting in hypofucosylation of antibodies expressed in that host cell (see also Shields, R. L. et al. (2002) *J. Biol. Chem.* 277:26733-26740). PCT Publication WO 99/54342 by Umana et al. describes cell lines engineered to express glycoprotein-modifying glycosyl transferases (e.g., P(1,4)-N-acetylglucosaminyltransferase Ill (GnTlll)) such that antibodies expressed in the engineered cell lines exhibit

increased bisecting GlcNac structures which results in increased ADCC activity of the antibodies (see also Umana et al. (1999) *Nat. Biotech.* 17: 176-180). Alternatively, the fucose residues of the antibody may be cleaved off using a fucosidase enzyme. For example, the fucosidase α-L-fucosidase removes fucosyl residues from antibodies (Tarentino, A. L. et al. (1975) *Biochem.* 14:5516-23).

[0439] Another modification of the antibodies herein that is contemplated by the invention is pegylation or the addition of other water soluble moieties, typically polymers, e.g., in order to enhance half-life. An antibody can be pegylated to, for example, increase the biological (e.g., serum) half-life of the antibody. To pegylate an antibody, the antibody, or fragment thereof, typically is reacted with polyethylene glycol (PEG), such as a reactive ester or aldehyde derivative of PEG, under conditions in which one or more PEG groups become attached to the antibody or antibody fragment. Preferably, the pegylation is carried out via an acylation reaction or an alkylation reaction with a reactive PEG molecule (or an analogous reactive water-soluble polymer). As used herein, the term "polyethylene glycol" is intended to encompass any of the forms of PEG that have been used to derivatize other proteins, such as mono (C_1-C_{10}) alkoxy- or aryloxy-polyethylene glycol or polyethylene glycol-maleimide. In certain embodiments, the antibody to be pegylated is an aglycosylated antibody. Methods for pegylating proteins are known in the art and can be applied to the antibodies according to at least some embodiments of the invention. See for example, EP 0 154 316 by Nishimura et al. and EP 0 401 384 by Ishikawa et al.

Methods of Engineering Antibodies

[0440] In certain embodiments, an agonist anti-VISTA antibody according to the invention having V_H and V_L sequences can be used to create new anti-VISTA antibodies, respectively, by modifying the V_H and/or V_L sequences, or the constant regions attached thereto. Thus, in another aspect according to at least some embodiments of the invention, the structural features of an anti-VISTA antibody according to at least some embodiments of the invention, are used to create structurally related anti-VISTA antibodies that retain at least one functional property of the antibodies according to at least some embodiments of the invention, such as binding to human VISTA. For example, one or more CDR regions of one VISTA antibody or mutations thereof can be combined recombinantly with known framework regions and/or other CDRs to create additional, recombinantly-engineered, anti-VISTA antibodies according to at least some embodiments of the invention, as discussed above. Other types of modifications include those described in the previous section. The starting material for the engineering method is one or more of the V_H and/or V_L sequences provided herein, or one or more CDR regions thereof. To create the engineered antibody, it is not necessary to actually prepare (i.e., express as a protein) an antibody having one or more of the V_H and/or VL sequences provided herein, or one or more CDR regions thereof. Rather, the information contained in the sequences is used as the starting material to create a "second generation" sequences derived from the original sequences and then the "second generation" sequences is prepared and expressed as a protein.

[0441] Standard molecular biology techniques can be used to prepare and express altered antibody sequence. Preferably, the anti-VISTA antibody encoded by the altered antibody sequences is one that retains one, some or all of the functional properties of the anti-VISTA antibodies, respectively, produced by methods and with sequences provided herein, which functional properties include binding to VISTA antigen with a specific K_D level or less and/or modulating immune responses and/or selectively binding to desired target cells such as for example, that express VISTA antigen.

[0442] The functional properties of the altered antibodies can be assessed using standard assays available in the art and/or described herein. In certain embodiments of the methods of engineering antibodies according to at least some embodiments of the invention, mutations can be introduced randomly or selectively along all or part of an anti-VISTA antibody coding sequence and the resulting modified anti-VISTA antibodies can be screened for binding activity and/or other desired functional properties.

[0443] Mutational methods have been described in the art. For example, PCT Publication WO 02/092780 by Short describes methods for creating and screening antibody mutations using saturation mutagenesis, synthetic ligation assembly, or a combination thereof. Alternatively, PCT Publication WO 03/074679 by Lazar et al. describes methods of using computational screening methods to optimize physiochemical properties of antibodies.

Nucleic Acid Molecules Encoding Antibodies

[0444] The invention further provides nucleic acids which encode an anti-VISTA antibody according to the invention, or a fragment or conjugate thereof. The nucleic acids may be present in whole cells, in a cell lysate, or in a partially purified or substantially pure form. A nucleic acid is "isolated" or "rendered substantially pure" when purified away from other cellular components or other contaminants, e.g., other cellular nucleic acids or proteins, by standard techniques, including alkaline/SDS treatment, CsCl banding, column chromatography, agarose gel electrophoresis and others well known in the art. See, F. Ausubel, et al., ed. (1987) *Current Protocols in Molecular Biology*, Greene Publishing and Wiley Interscience, New York. A nucleic acid according to at least some embodiments of the invention can be, for example, DNA or RNA and may or may not contain intronic sequences. In a preferred embodiment, the nucleic acid is a cDNA molecule.

[0445] Nucleic acids according to at least some embodiments of the invention can be obtained using standard molecular biology techniques. For antibodies expressed by hybridomas (e.g., hybridomas prepared from transgenic mice carrying human immunoglobulin genes as described further below), cDNAs encoding the light and heavy chains of the antibody made by the hybridoma can be obtained by standard PCR amplification or cDNA cloning techniques. For antibodies obtained from an immunoglobulin gene library (e.g., using phage display techniques), nucleic acid encoding the antibody can be recovered from the library.

[0446] Once DNA fragments encoding V_H and V_L segments are obtained, these DNA fragments can be further manipulated by standard recombinant DNA techniques, for example to convert the variable region genes to full-length antibody chain genes, to Fab fragment genes or to a scFv gene. In these manipulations, a V_L- or V_H-encoding DNA fragment is operatively linked to another DNA fragment encoding another protein, such as an antibody constant region or a flexible linker. As previously defined, "opera-

tively linked" means that that the two DNA fragments are joined such that the amino acid sequences encoded by the two DNA fragments remain in-frame.

[0447] The isolated DNA encoding the V_H region can be converted to a full-length heavy chain gene by operatively linking the V_H-encoding DNA to another DNA molecule encoding heavy chain constant regions (CH1, CH2 and CH3). The sequences of human heavy chain constant region genes are known in the art (see e.g., Kabat, E. A., el al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The heavy chain constant region can be an IgGI, IgG2, IgG3, IgG4, IgA, IgE, IgM or IgD constant region, but most preferably is an IgGI, IgG2 or IgG4 constant region. For a Fab fragment heavy chain gene, the VH-encoding DNA can be operatively linked to another DNA molecule encoding only the heavy chain C_H1 constant region.

[0448] The isolated DNA encoding the V_L region can be converted to a full-length light chain gene (as well as a Fab light chain gene) by operatively linking the V_L-encoding DNA to another DNA molecule encoding the light chain constant region, C_L—The sequences of human light chain constant region genes are known in the art (see e.g., Kabat, E. A., et al. (1991) *Sequences of Proteins of Immunological Interest*, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The light chain constant region can be a kappa (κ) or lambda (A) constant region, but most preferably is a K constant region.

[0449] To create a scFv gene, the V_H- and V_L-encoding DNA fragments are operatively linked to another fragment encoding a flexible linker, e.g., encoding the amino acid sequence (Gly4-Ser)3, such that the V_H and V_L sequences can be expressed as a contiguous single-chain protein, with the VLand V_H regions joined by the flexible linker (see e.g., Bird et al. (1988) *Science* 242:423-426; Huston et al. (1988) *Proc. Natl. Acad. Sci.,USA* 85:5879-5883; McCafferty et al., (1990) *Nature* 348:552-554).

Production of Anti-VISTA Monoclonal Antibodies

[0450] Anti-VISTA monoclonal antibodies (mAbs) and antigen-binding fragments according to the present invention can be produced by a variety of techniques, including conventional monoclonal antibody methodology e.g., the standard somatic cell hybridization technique of Kohler and Milstein (1975) *Nature* 256:495. Although somatic cell hybridization procedures are preferred, in principle, other techniques for producing monoclonal antibody can be employed e.g., viral or oncogenic transformation of B lymphocytes.

[0451] A preferred animal system for preparing hybridomas is the murine system. Hybridoma production in the mouse is a very well-established procedure. Immunization protocols and techniques for isolation of immunized splenocytes for fusion are known in the art. Fusion partners (e.g., murine myeloma cells) and fusion procedures are also known. Chimeric or humanized antibodies of the present invention can be prepared based on the sequence of a murine monoclonal antibody prepared as described above. DNA encoding the heavy and light chain immunoglobulins can be obtained from the murine hybridoma of interest and engineered to contain non-murine (e.g., human) immunoglobulin sequences using standard molecular biology techniques. For example, to create a chimeric antibody, the murine variable regions can be linked to human constant regions using methods known in the art (see e.g., U.S. Pat. No. 4,816,567 to Cabilly et al.). To create a humanized antibody, the murine CDR regions can be inserted into a human framework using methods known in the art (see e.g., U.S. Pat. No. 5,225,539 to Winter and U.S. Pat. Nos. 5,530,101; 5,585,089; 5,693,762 and 6,180,370 to Queen et al.).

[0452] According to at least some embodiments of the invention, the antibodies are human monoclonal antibodies. Such human monoclonal antibodies directed against VISTA can be generated using transgenic or transchromosomic mice carrying parts of the human immune system rather than the mouse system. These transgenic and transchromosomic mice include mice referred to herein as the HuMAb Mouse™ and KM Mouse™, respectively, and are collectively referred to herein as "human Ig mice." The HuMAb Mouse™ (Medarex Inc.) contains human immunoglobulin gene miniloci that encode unrearranged human heavy μ and γ and κ light chain immunoglobulin sequences, together with targeted mutations that inactivate the endogenous μ and κ chain loci (see e.g., Lonberg, et al. (1994) *Nature* 368 (6474): 856-859). Accordingly, the mice exhibit reduced expression of mouse IgM or κ and in response to immunization, the introduced human heavy and light chain transgenes undergo class switching and somatic mutation to generate high affinity human IgG κ monoclonal (Lonberg, N. et al. (1994), supra; reviewed in Lonberg, N. (1994) *Handbook of Experimental Pharmacology* 113:49-101; Lonberg, N. and Huszar, D. (1995) *Intern. Rev. Immunol.* 13: 65-93, and Harding, F. and Lonberg, N. (1995) *Ann. N. Y. Acad. Sci.* 764:536-546). The preparation and use of the HuMab Mouse®, and the genomic modifications carried by such mice, is further described in Taylor, L. et al. (1992) *Nucleic Acids Research* 20:6287-6295; Chen, J. et al. (1993) *International Immunology* 5:647-656; Tuaillon et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:3720-3724; Choi et al. (1993) *Nature Genetics* 4: 117-123; Chen, J. et al. (1993) *EMBO J.* 12: 821-830; Tuaillon et al. (1994) *J. Immunol.* 152:2912-2920; Taylor, L. et al. (1994) *International Immunology* 6:579-591; and Fishwild, D. et al. (1996) *Nature Biotechnology* 14: 845-851, the contents of all of which are hereby specifically incorporated by reference in their entirety. See further, U.S. Pat. Nos. 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,789,650; 5,877,397; 5,661,016; 5,814,318; 5,874,299; and 5,770,429; all to Lonberg and Kay; U.S. Pat. No. 5,545,807 to Surani et al.; PCT Publication Nos. WO 92/03918, WO 93/12227, WO 94/25585, WO 97/13852, WO 98/24884 and WO 99/45962, all to Lonberg and Kay; and PCT Publication No. WO 01/14424 to Korman et al.

[0453] In another embodiment, human antibodies according to at least some embodiments of the invention can be raised using a mouse that carries human immunoglobulin sequences on transgenes and transchomosomes, such as a mouse that carries a human heavy chain transgene and a human light chain transchromosome. Such mice, referred to herein as "KM Mice™", are described in detail in PCT Publication WO 02/43478 to Ishida et al.

[0454] Still further, alternative transgenic animal systems expressing human immunoglobulin genes are available in the art and can be used to raise anti-VISTA antibodies

according to at least some embodiments of the invention. For example, an alternative transgenic system referred to as the Xenomouse (Abgenix, Inc.) can be used; such mice are described in, for example, U.S. Pat. Nos. 5,939,598; 6,075,181; 6,114,598; 6, 150,584 and 6,162,963 to Kucherlapati et al.

[0455] Moreover, alternative transchromosomic animal systems expressing human immunoglobulin genes are available in the art and can be used to raise anti-VISTA antibodies according to at least some embodiments of the invention. For example, mice carrying both a human heavy chain transchromosome and a human light chain transchromosome, referred to as "TC mice" can be used; such mice are described in Tomizuka et al. (2000) *Proc. Natl. Acad Sci. USA* 97:722-727. Furthermore, cows carrying human heavy and light chain transchromosomes have been described in the art (Kuroiwa et al. (2002) *Nature Biotechnology* 20:889-894) and can be used to raise anti-VISTA antibodies according to at least some embodiments of the invention.

[0456] Human monoclonal antibodies according to at least some embodiments of the invention can also be prepared using phage display methods for screening libraries of human immunoglobulin genes. Such phage display methods for isolating human antibodies are established in the art. See for example: U.S. Pat. Nos. 5,223,409; 5,403,484; and U.S. Pat. No. 5,571,698 to Ladner et al.; U.S. Pat. Nos. 5,427,908 and 5,580,717 to Dower et al.; U.S. Pat. Nos. 5,969,108 and 6,172,197 to McCafferty et al.; and U.S. Pat. Nos. 5,885,793; 6,521,404; 6,544,731; 6,555,313; 6,582,915 and 6,593,081 to Griffiths et al.

[0457] Human monoclonal antibodies according to at least some embodiments of the invention can also be prepared using SCID mice into which human immune cells have been reconstituted such that a human antibody response can be generated upon immunization. Such mice are described in, for example, U.S. Pat. Nos. 5,476,996 and 5,698,767 to Wilson et al.

Immunization of Human Ig Mice

[0458] In some embodiments human Ig mice are used to raise human anti-VISTA antibodies according to the invention, e.g., by immunizing such mice with a purified or enriched preparation of VISTA antigen and/or recombinant VISTA, or VISTA fusion protein, as described by Lonberg, N. et al. (1994) *Nature* 368(6474): 856-859; Fishwild, D. et al. (1996) *Nature Biotechnology* 14: 845-851; and PCT Publication WO 98/24884 and WO 01/14424. Preferably, the mice will be 6-16 weeks of age upon the first infusion. For example, a purified or recombinant preparation (dose ranging from 0.5-500 μg) of VISTA antigen can be used to immunize the human Ig mice intraperitoneally.

[0459] In general transgenic mice respond when initially immunized intraperitoneally (IP) with antigen in complete Freund's adjuvant, followed by every other week IP immunizations (up to a total of 6) with antigen in incomplete Freund's adjuvant. However, adjuvants other than Freund's are also found to be effective. In addition, whole cells in the absence of adjuvant are found to be highly immunogenic. The immune response can be monitored over the course of the immunization protocol with plasma samples being obtained by retroorbital bleeds. The plasma can be screened by ELISA (as described below), and mice with sufficient titers of anti-VISTA human immunoglobulin can be used for fusions. Mice can be boosted intravenously with antigen 3 days before sacrifice and removal of the spleen. It is expected that 2-3 fusions for each immunization may need to be performed. Between 6 and 24 mice are typically immunized for each antigen. Usually both HCo7 and HCol2 strains are used. In addition, both HCo7 and HCol2 transgene can be bred together into a single mouse having two different human heavy chain transgenes (HCo7/HCo 12). Alternatively or additionally, the KM Mouse™ strain can be used. In an exemplary embodiment these mice will be engineered to selectively produce human IgG2 antibodies.

Generation of Hybridomas Producing Human Monoclonal Antibodies

[0460] In certain embodiments, hybridomas producing a human monoclonal anti-VISTA antibody according to the invention may be generated using splenocytes and/or lymph node cells from immunized mice can be isolated and fused to an appropriate immortalized cell line, such as a mouse myeloma cell line. The resulting hybridomas can be screened for the production of antigen-specific antibodies. For example, single cell suspensions of splenic lymphocytes from immunized mice can be fused to one-sixth the numbers of P3X63-Ag8.653 nonsecreting mouse myeloma cells (ATCC, CRL 1580) with 50% PEG. Cells are plated at approximately 2×10^5 in flat bottom microtiter plate, followed by a two week incubation in selective medium containing 20% fetal Clone Serum, 18% "653" conditioned media, 5% origen (IGEN), 4 mM L-glutamine, 1 mM sodium pyruvate, 5 mM HEPES, 0.055 mM 2-mercaptoethanol, 50 units/ml penicillin, 50 mg/ml streptomycin, 50 mg/ml gentamycin and IX HAT (Sigma; the HAT is added 24 hours after the fusion). After approximately two weeks, cells can be cultured in medium in which the HAT is replaced with HT. Individual wells can then be screened by ELISA for human monoclonal IgM and IgG antibodies. Once extensive hybridoma growth occurs, medium can be observed usually after 10-14 days. The antibody secreting hybridomas can be replated, screened again, and if still positive for human IgG, the monoclonal antibodies can be subcloned at least twice by limiting dilution. The stable subclones can then be cultured in vitro to generate small amounts of antibody in tissue culture medium for characterization.

[0461] To purify human monoclonal antibodies, selected hybridomas can be grown in two-liter spinner-flasks for monoclonal antibody purification. Supernatants can be filtered and concentrated before affinity chromatography with protein A-Sepharose (Pharmacia, Piscataway, N.J.). Eluted IgG can be checked by gel electrophoresis and high performance liquid chromatography to ensure purity. The buffer solution can be exchanged into PBS, and the concentration can be determined by OD280 using 1.43 extinction coefficient. The monoclonal antibodies can be aliquoted and stored at −80° C.

Generation of Transfectomas Producing Monoclonal Antibodies

[0462] In certain embodiments, an anti-VISTA antibody according to the invention can be produced in a host cell transfectoma using, for example, a combination of recombinant DNA techniques and gene transfection methods as is well known in the art (e.g., Morrison, S. (1985) *Science* 229:1202). For example, to express the antibodies, or antibody

fragments thereof, DNAs encoding partial or full-length light and heavy chains, can be obtained by standard molecular biology techniques (e.g., PCR amplification or cDNA cloning using a hybridoma that expresses the antibody of interest) and the DNAs can be inserted into expression vectors such that the genes are operatively linked to transcriptional and translational control sequences. In this context, the term "operatively linked" is intended to mean that an antibody gene is ligated into a vector such that transcriptional and translational control sequences within the vector serve their intended function of regulating the transcription and translation of the antibody gene. The expression vector and expression control sequences are chosen to be compatible with the expression host cell used. The antibody light chain gene and the antibody heavy chain gene can be inserted into separate vector or, more typically, both genes are inserted into the same expression vector. The antibody genes are inserted into the expression vector by standard methods (e.g., ligation of complementary restriction sites on the antibody gene fragment and vector, or blunt end ligation if no restriction sites are present). The light and heavy chain variable regions of the antibodies described herein can be used to create full-length antibody genes of any antibody isotype by inserting them into expression vectors already encoding heavy chain constant and light chain constant regions of the desired isotype such that the V_H segment is operatively linked to the C_H segments within the vector and the V_L segment is operatively linked to the C_L segment within the vector. Additionally or alternatively, the recombinant expression vector can encode a signal peptide that facilitates secretion of the antibody chain from a host cell. The antibody chain gene can be cloned into the vector such that the signal peptide is linked in-frame to the amino terminus of the antibody chain gene. The signal peptide can be an immunoglobulin signal peptide or a heterologous signal peptide (i.e., a signal peptide from a non-immunoglobulin protein).

Characterization of Antibody Binding to Antigen

[0463] In certain embodiments, the binding specificity of an agonistic anti-VISTA antibody according to the invention is determined by known antibody binding assay techniques such as ELISA. In an exemplary ELISA, microtiter plates are coated with a purified antigen, herein VISTA at 0.25 μg/ml in PBS, and then blocked with 5% bovine serum albumin in PBS. Dilutions of antibody (e.g., dilutions of plasma from -immunized mice) are added to each well and incubated for 1-2 hours at 37° C. The plates are washed with PBS/Tween and then incubated with secondary reagent (e.g., for human antibodies, a goat-anti-human IgG Fc-specific polyclonal reagent) conjugated to alkaline phosphatase for 1 hour at 37° C. After washing, the plates are developed with pNPP substrate (1 mg/ml), and analyzed at OD of 405-650. Preferably, mice which develop the highest titers will be used for fusions.

[0464] An ELISA assay as described above can also be used to screen for hybridomas that show positive reactivity with VISTA immunogen. Hybridomas that bind with high avidity to VISTA are subcloned and further characterized. One clone from each hybridoma, which retains the reactivity of the parent cells (by ELISA), can be chosen for making a 5-10 vial cell bank stored at −140° C., and for antibody purification.

[0465] To purify anti-VISTA antibodies, selected hybridomas can be grown in two-liter spinner-flasks for monoclonal antibody purification. Supernatants can be filtered and concentrated before affinity chromatography with protein A-Sepharose (Pharmacia, Piscataway, N.J.). Eluted IgG can be checked by gel electrophoresis and high performance liquid chromatography to ensure purity. The buffer solution can be exchanged into PBS, and the concentration can be determined by OD280 using 1.43 extinction coefficient. The monoclonal antibodies can be aliquoted and stored at −80° C.

[0466] To determine if the selected anti-VISTA monoclonal antibodies bind to unique epitopes, each antibody can be biotinylated using commercially available reagents (Pierce, Rockford, Il.). Competition studies using unlabeled monoclonal antibodies and biotinylated monoclonal antibodies can be performed using VISTA coated-ELISA plates as described above. Biotinylated mAb binding can be detected with a strep-avidin-alkaline phosphatase probe.

[0467] To determine the isotype of purified antibodies, isotype ELISAs can be performed using reagents specific for antibodies of a particular isotype, e.g., IgG2's. For example, to determine the isotype of a human monoclonal antibody, wells of microtiter plates can be coated with ˆg/ml of anti-human immunoglobulin overnight at 4° C. After blocking with 1% BSA, the plates are reacted with 1 mug/ml or less of test monoclonal antibodies or purified isotype controls, at ambient temperature for one to two hours. The wells can then be reacted with either human IgG1 or human IgM-specific alkaline phosphatase-conjugated probes. Plates are developed and analyzed as described above.

[0468] Anti-VISTA human IgGs can be further tested for reactivity with VISTA antigen, respectively, by Western blotting. Briefly, VISTA antigen can be prepared and subjected to sodium dodecyl sulfate polyacrylamide gel electrophoresis. After electrophoresis, the separated antigens are transferred to nitrocellulose membranes, blocked with 10% fetal calf serum, and probed with the monoclonal antibodies to be tested. Human IgG binding can be detected using anti-human IgG alkaline phosphatase and developed with BCIP/NBT substrate tablets (Sigma Chem. Co., St. Louis, Mo.).

[0469] In another aspect, the present invention features antibody-drug conjugates (ADCs), consisting of an antibody (or antibody fragment such as a single-chain variable fragment (scFv) linked to a payload drug (often cytotoxic). The antibody causes the ADC to bind to the target cancer cells. Often the ADC is then internalized by the cell and the drug is released into the cell. Because of the targeting, the side effects are lower and give a wider therapeutic window. Hydrophilic linkers (e.g., PEG4Mal) help prevent the drug being pumped out of resistant cancer cells through MDR (multiple drug resistance) transporters.

[0470] In another aspect, the present invention features immunoconjugates comprising an anti-VISTA antibody, or a fragment thereof, conjugated to a therapeutic agent, such as a cytotoxin, a drug (e.g., an immunosuppressant) or a radiotoxin. Such conjugates are referred to herein as "immunoconjugates". Immunoconjugates that include one or more cytotoxins are referred to as "immunotoxins." A cytotoxin or cytotoxic agent includes any agent that is detrimental to (e.g., kills) cells. Examples include Taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, teniposide, vincristine, vinblastine, colchicine,

doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents also include, for example, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thiotepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

[0471] Other examples of therapeutic cytotoxins that can be conjugated to an antibody according to at least some embodiments of the invention include duocarmycins, calicheamicin, maytansines and auristatins, and derivatives thereof. An example of a calicheamicin antibody conjugate is commercially available (Mylotarg™ Wyeth).

[0472] Cytotoxins can be conjugated to antibodies according to at least some embodiments of the invention using linker technology available in the art. Examples of linker types that have been used to conjugate a cytotoxin to an antibody include, but are not limited to, hydrazones, thioethers, esters, disulfides and peptide-containing linkers. A linker can be chosen that is, for example, susceptible to cleavage by low pH within the lysosomal compartment or susceptible to cleavage by proteases, such as proteases preferentially expressed in tumor tissue such as cathepsins (e.g., cathepsins B, C, D). For further discussion of types of cytotoxins, linkers and methods for conjugating therapeutic agents to antibodies, see also Saito, G. et al. (2003) *Adv. Drug Deliv. Rev.* 55: 199-215; Trail, P. A. et al. (2003) *Cancer Immunol. Immunother.* 52:328-337; Payne, G. (2003) *Cancer Cell* 3:207-212; Allen, T. M. (2002) *Nat. Rev. Cancer* 2:750-763; Pastan, I. and Kreitman, R. J. (2002) *Curr. Opin. Investig. Drugs* 3: 1089-1091; Senter, P. D. and Springer, C. J. (2001) *Adv. Drug Deliv. Rev.* 53:247-264.

[0473] Antibodies of the present invention also can be conjugated to a radioactive isotope to generate cytotoxic radiopharmaceuticals, also referred to as radioimmunoconjugates. Examples of radioactive isotopes that can be conjugated to antibodies for use diagnostically or therapeutically include, but are not limited to, iodine 131, indium 111, yttrium 90 and lutetium 177. Methods for preparing radioimmunoconjugates are established in the art.

[0474] Radioimmunoconjugates are commercially available, including Zevalin® (BiogenIDEC) and Bexxar®. (Corixa Pharmaceuticals), and similar methods can be used to prepare radioimmunoconjugates using the antibodies according to at least some embodiments of the invention.

[0475] The agonist anti-human VISTA antibodies and conjugates containing according to at least some embodiments of the invention can be used to modify a given biological response, and the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, an enzymatically active toxin, or active fragment thereof, such as abrin, ricin A, *pseudomonas* exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor or interferon-γ; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

[0476] Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in *Monoclonal Antibodies For Cancer Detection And Therapy*, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.,* 62: 119-58 (1982).

Bispecific Molecules

[0477] According to at least some embodiments the invention also encompasses multispecific anti-VISTA agonist antibodies. Multispecific antibodies are monoclonal antibodies that have binding specificities for at least two different sites. In another aspect, the present invention features bispecific molecules comprising an anti-VISTA antibody, or a fragment thereof, according to at least some embodiments of the invention. An antibody according to at least some embodiments of the invention, or antigen-binding portions thereof, can be derivatized or linked to another functional molecule, e.g., another peptide or protein (e.g., another antibody or ligand for a receptor) to generate a bispecific molecule that binds to at least two different binding sites or target molecules. The antibody according to at least some embodiments of the invention may in fact be derivatized or linked to more than one other functional molecule to generate multispecific molecules that bind to more than two different binding sites and/or target molecules; such multispecific molecules are also intended to be encompassed by the term "bispecific molecule" as used herein. To create a bispecific molecule according to at least some embodiments of the invention, an antibody can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other binding molecules, such as another antibody, antibody fragment, peptide or binding mimetic, such that a bispecific molecule results. In certain embodiments, one of the binding specificities of the bispecific antibodies is for VISTA and the other is for any other antigen. In certain embodiments, bispecific antibodies may bind to two different epitopes of VISTA. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express VISTA. Bispecific antibodies can be prepared as full length antibodies or antibody fragments.

[0478] A bispecific antibody according to at least some embodiments of the invention is an antibody which can bind simultaneously to two targets which are of different structure. Bispecific antibodies (bsAb) and bispecific antibody fragments (bsFab) according to at least some embodiments

of the invention have at least one arm that specifically binds to a B-cell antigen or epitope and at least one other arm that specifically binds a targetable conjugate.

[0479] According to at least some embodiments the invention encompasses also a fusion antibody protein, which is a recombinantly produced antigen-binding molecule in which two or more different single-chain antibody or antibody fragment segments with the same or different specificities are linked. A variety of bispecific fusion antibody proteins can be produced using molecular engineering. In one form, the bispecific fusion antibody protein is monovalent, consisting of, for example, a sent with a single binding site for one antigen and a Fab fragment with a single binding site for a second antigen. In another form, the bispecific fusion antibody protein is divalent, consisting of, for example, an IgG with two binding sites for one antigen and two scFv with two binding sites for a second antigen.

[0480] The invention further encompasses engineered antibodies with three or more functional antigen-binding sites, including "Octopus antibodies" (see, e.g. US 2006/0025576A1), and "Dual Acting FAb" or "DAF" antibodies comprising an antigen-binding site that binds to VISTA as well as another, different antigen (see e.g. US 2008/0069820). Accordingly, the present invention includes bispecific molecules comprising at least one first binding specificity for VISTA and a second binding specificity for a second target epitope. According to at least some embodiments of the invention, the second target epitope is an Fc receptor, e.g., human FcγRI (CD64) or a human FcαR receptor (CD89). Therefore, the invention includes bispecific molecules capable of binding both to FcγR, FcαR or FcsR expressing effector cells (e.g., monocytes, macrophages or polymorphonuclear cells (PMNs)), and to target cells expressing VISTA, respectively. These bispecific molecules target VISTA expressing cells to effector cell and trigger Fc receptor-mediated effector cell activities, such as phagocytosis of an VISTA expressing cells, antibody dependent cell-mediated cytotoxicity (ADCC), cytokine release, or generation of superoxide anion.

[0481] According to at least some embodiments of the invention in which the bispecific molecule is multispecific, the molecule can further include a third binding specificity, in addition to an anti-Fc binding specificity. In one embodiment, the third binding specificity is an anti-enhancement factor (EF) portion, e.g., a molecule which binds to a surface protein involved in cytotoxic activity and thereby increases the immune response against the target cell.

[0482] The "anti-enhancement factor portion" can be an antibody, functional antibody fragment or a ligand that binds to a given molecule, e.g., an antigen or a receptor, and thereby results in an enhancement of the effect of the binding determinants for the Fc receptor or target cell antigen. The "anti-enhancement factor portion" can bind an Fc receptor or a target cell antigen. Alternatively, the anti-enhancement factor portion can bind to an entity that is different from the entity to which the first and second binding specificities bind. For example, the anti-enhancement factor portion can bind a cytotoxic T-cell (e.g., via CD2, CD3, CD8, CD28, CD4, CD40, ICAM-1 or other immune cell that results in an increased immune response against the target cell).

[0483] According to at least some embodiments of the invention, the bispecific molecules comprise as a binding specificity at least one antibody, or an antibody fragment thereof, including, e.g., an Fab, Fab', F(ab')2, Fv, or a single chain Fv. The antibody may also be a light chain or heavy chain dimer, or any minimal fragment thereof such as a Fv or a single chain construct as described in Ladner et al. U.S. Pat. No. 4,946,778, the contents of which are expressly incorporated by reference.

[0484] In one embodiment, the binding specificity for an Fcγ receptor is provided by a monoclonal antibody, the binding of which is not blocked by human immunoglobulin G (IgG). As used herein, the term "IgG receptor" refers to any of the eight γ-chain genes located on chromosome 1. These genes encode a total of twelve transmembrane or soluble receptor isoforms which are grouped into three Fcγ receptor classes: FcγRI (CD64), FcγRII (CD32), and FcγRIII (CD16). In one preferred embodiment, the Fcγ receptor is a human high affinity FcγRI. The human FcγRI is a 72 kDa molecule, which shows high affinity for monomeric IgG. The production and characterization of certain preferred anti-Fcγ monoclonal antibodies are described by Fanger et al. in PCT Publication WO 88/00052 and in U.S. Pat. No. 4,954,617, the teachings of which are fully incorporated by reference herein. These antibodies bind to an epitope of FcγRI, FcγRII or FcγRIII at a site which is distinct from the Fey binding site of the receptor and, thus, their binding is not blocked substantially by physiological levels of IgG. Known anti-FcγRI antibodies include mAb 22, mAb 32, mAb 44, mAb 62 and mAb 197. The hybridoma producing mAb 32 is available from the American Type Culture Collection, ATCC Accession No. HB9469. In other embodiments, the anti-Fcγ receptor antibody is a humanized form of monoclonal antibody 22 (H22). The production and characterization of the H22 antibody is described in Graziano, R. F. et al. (1995) *J. Immunol.* 155 (10): 4996-5002 and PCT Publication WO 94/10332. The H22 antibody producing cell line is deposited at the American Type Culture Collection under the designation HA022CLI and has the accession no. CRL 11177.

[0485] In still other embodiments, the binding specificity for an Fc receptor is provided by an antibody that binds to a human IgA receptor, e.g., an Fc-α receptor (Fc αRI (CD89)), the binding of which is preferably not blocked by human immunoglobulin A (IgA). The term "IgA receptor" is intended to include the gene product of one a-gene (FcαRI) located on chromosome 19. This gene is known to encode several alternatively spliced transmembrane isoforms of 55 to 10 kDa. FcαRI (CD89) is constitutively expressed on monocytes/macrophages, eosinophilic and neutrophilic granulocytes, but not on non-effector cell populations. Fc αRI has medium affinity (Approximately 5×10^{-7} M^{-1}) for both IgA1 and IgA2, which is increased upon exposure to cytokines such as G-CSF or GM-CSF (Morton, H. C. et al. (1996) *Critical Reviews in Immunology* 16:423-440). Four FcαRI-specific monoclonal antibodies, identified as A3, A59, A62 and A77, which bind FcaRI outside the IgA ligand binding domain, have been described (Monteiro, R. C. et al. (1992) *J. Immunol.* 148: 1764).

[0486] While human monoclonal antibodies are preferred, other antibodies which can be employed in the bispecific molecules according to at least some embodiments of the invention are murine, chimeric and humanized monoclonal antibodies. The bispecific molecules of the present invention can be prepared by conjugating the constituent binding specificities, e.g., the anti-FcR and anti-VISTA binding specificities, using methods known in the art. For example, the binding specificity of each bispecific molecule can be

generated separately and then conjugated to one another. When the binding specificities are proteins or peptides, a variety of coupling or cross-linking agents can be used for covalent conjugation. Examples of cross-linking agents include protein A, carbodiimide, N-succinimidyl-S-acetyl-thioacetate (SATA), 5,5'-dithiobis(2-nitrobenzoic acid) (DTNB), o-phenylenedimaleimide (oPDM), N-succinimidyl-3-(2-pyridyld-dithio propionate (SPDP), and sulfosuccinimidyl 4-(N-maleimidomethyl) cyclohexane-I-carboxylate (sulfo-SMCC) (see e.g., Karpovsky et al. (1984) *J. Exp. Med.* 160: 1686; Liu, M A et al. (1985) *Proc. Natl. Acad. Sci. USA* 82:8648). Other methods include those described in Paulus (1985) Behring Ins. Mitt. No. 78, 118-132; Brennan et al. (1985) *Science* 229:81-83), and Glennie et al. (1987) *J. Immunol.* 139: 2367-2375). Preferred conjugating agents are SATA and sulfo-SMCC, both available from Pierce Chemical Co. (Rockford, Il.). When the binding moieties are antibodies, they can be conjugated via sulfhydryl bonding of the C-terminus hinge regions of the two heavy chains. In a particularly preferred embodiment, the hinge region is modified to contain an odd number of sulfhydryl residues, preferably one, prior to conjugation.

[0487] Alternatively, both binding specificities can be encoded in the same vector and expressed and assembled in the same host cell. This method is particularly useful where the bispecific molecule is a mAbXmAb, mAbXFab, FabXF (ab')2 or ligandXFab fusion protein. A bispecific molecule according to at least some embodiments of the invention can be a single chain molecule comprising one single chain antibody and a binding determinant, or a single chain bispecific molecule comprising two binding determinants. Bispecific molecules may comprise at least two single chain molecules. Methods for preparing bispecific molecules are described for example in U.S. Pat. Nos. 5,260,203; 5,455,030; 4,881,175; 5,132,405; 5,091,513; 5,476,786; 5,013,653; 5,258,498; and 5,482,858.

[0488] Techniques for making multispecific antibodies include, but are not limited to, recombinant co-expression of two immunoglobulin heavy chain-light chain pairs having different specificities (see Milstein and Cuello, *Nature* 305: 537 (1983)), WO 93/08829, and Traunecker et al., *EMBO J.* 10: 3655 (1991)), and "knob-in-hole" engineering (see, e.g., U.S. Pat. No. 5,731,168). Multi-specific antibodies may also be made by engineering electrostatic steering effects for making antibody Fc-heterodimeric molecules (WO 2009/089004A1); controlled Fab-arm exchange (see Labrijn et al., *Proc. Natl. Acad. Sci. USA* 110(13):5145-50 (2013)); cross-linking two or more antibodies or fragments (see, e.g., U.S. Pat. No. 4,676,980, and Brennan et al., *Science,* 229: 81 (1985)); using leucine zippers to produce bi-specific antibodies (see, e.g., Kostelny et al., *J. Immunol.,* 148(5): 1547-1553 (1992)); using "diabody" technology for making bispecific antibody fragments (see, e.g., Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993)); and using single-chain Fv (sFv) dimers (see, e.g. Gruber et al., *J. Immunol.,* 152:5368 (1994)); and preparing trispecific antibodies as described, e.g., in Tutt et al. *J. Immunol.* 147: 60 (1991).

[0489] Binding of the bispecific molecules to their specific targets can be confirmed by, for example, enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), FACS analysis, bioassay (e.g., growth inhibition), or Western Blot assay. Each of these assays generally detects the presence of protein-antibody complexes of particular interest by employing a labeled reagent (e.g., an antibody) specific for the complex of interest. For example, the FcR-antibody complexes can be detected using e.g., an enzyme-linked antibody or antibody fragment which recognizes and specifically binds to the antibody-FcR complexes. Alternatively, the complexes can be detected using any of a variety of other immunoassays. For example, the antibody can be radioactively labeled and used in a radioimmunoassay (RIA) (see, for example, Weintraub, B., *Principles of Radioimmunoassays*, Seventh Training Course on Radioligand Assay Techniques, The Endocrine Society, March, 1986, which is incorporated by reference herein). The radioactive isotope can be detected by such means as the use of a γ counter or a scintillation counter or by autoradiography.

Use of Agonistic Anti-Vista Antibodies and Pharmaceutical Compositions Containing for Treatment of Autoimmune Disease

[0490] According to at least some embodiments, anti-VISTA antibodies, fragments, conjugates thereof or a pharmaceutical composition comprising same, as described herein, which function as VISTA stimulating therapeutic agents, may optionally be used for treating an immune system related disease.

[0491] Optionally, the immune system related condition comprises an immune related condition, autoimmune diseases as recited herein, transplant rejection and graft versus host disease and/or for blocking or promoting immune stimulation mediated by VISTA, immune related diseases as recited herein and/or for immunotherapy (promoting or inhibiting immune stimulation).

[0492] Optionally the immune condition is selected from autoimmune disease, transplant rejection, inflammatory disease, allergic condition or graft versus host disease. Optionally the treatment is combined with another moiety useful for treating immune related condition.

[0493] Thus, treatment of multiple sclerosis using the agents according to at least some embodiments of the present invention may be combined with, for example, any known therapeutic agent or method for treating multiple sclerosis, optionally as described herein.

[0494] Thus, treatment of rheumatoid arthritis or other arthritic condition, using the subject agonist antibodies may be combined with, for example, any known therapeutic agent or method for treating rheumatoid arthritis, optionally as described herein.

[0495] Thus, treatment of IBD, using the using the subject agonist antibodies may be combined with, for example, any known therapeutic agent or method for treating IBD, optionally as described herein.

[0496] Thus, treatment of psoriasis, using the subject agonist antibodies may be combined with, for example, any known therapeutic agent or method for treating psoriasis, optionally as described herein.

[0497] Thus, treatment of type 1 diabetes using the subject agonist antibodies may be combined with, for example, any known therapeutic agent or method for treating type 1 diabetes, optionally as described herein.

[0498] Thus, treatment of uveitis, using the subject agonist antibodies may be combined with, for example, any known therapeutic agent or method for treating uveitis, optionally as described herein.

[0499] Thus, treatment of Sjögren's syndrome, using the subject agonist antibodies may be combined with, for

example, any known therapeutic agent or method for treating for Sjögren's syndrome, optionally as described herein.

[0500] Thus, treatment of systemic lupus erythematosus, using the subject agonist antibodies may be combined with, for example, any known therapeutic agent or method for treating for systemic lupus erythematosus, optionally as described herein.

[0501] Thus, treatment of GVHD, using the subject agonist antibodies may be combined with, for example, any known therapeutic agent or method for treating GVHD, optionally as described herein.

[0502] Thus, treatment of chronic or acute infection and/or hepatotoxicity associated therewith, e.g., hepatitis, using the subject agonist antibodies may be combined with, for example, any known therapeutic agent or method for treating for chronic or acute infection and/or hepatotoxicity associated therewith, optionally as described herein.

[0503] In the above-described therapies preferably a subject with one of the aforementioned or other autoimmune or inflammatory conditions will be administered an immmunoinhibitory anti-VISTA antibody disclosed herein or antigen-binding fragment according to the invention, which antibody mimics or agonizes at least one VISTA-mediated effect on immunity, e.g., it suppresses cytotoxic T cells, or NK activity and/or the production of proinflammatory cytokines which are involved in the disease pathology, thereby preventing or ameliorating the disease symptoms and potentially resulting in prolonged disease remission, e.g., because of the induction of Tregs which elicit T cell tolerance or prolonged immunosuppression.

[0504] The therapeutic agents and/or a pharmaceutical composition comprising same, as recited herein, according to at least some embodiments of the invention, may be administered as the sole active ingredient or together with other drugs in immunomodulating regimens or other anti-inflammatory agents e.g. for the treatment or prevention of allo- or xenograft acute or chronic rejection or inflammatory or autoimmune disorders, or to induce tolerance.

Use of Agonistic Anti-Vista Antibodies and Pharmaceutical Compositions Containing for Treatment of Sepsis

[0505] According to at least some embodiments, VISTA antibodies, fragments, conjugates thereof and/or pharmaceutical compositions as described herein, may be used for treating sepsis. Sepsis is a potentially life-threatening complication of an infection. Sepsis represents a complex clinical syndrome that develops when the initial host response against an infection becomes inappropriately amplified and dysregulated, becoming harmful to the host. The initial hyperinflammatory phase ('cytokine storm') in sepsis is followed by a state of immunosuppression (Hotchkiss et al 2013 *Lancet Infect*. Dis. 13:260-268). This latter phase of impaired immunity, also referred to as 'immunoparalysis', is manifested in failure to clear the primary infection, reactivation of viruses such as HSV and cytomegalovirus, and development of new, secondary infections, often with organisms that are not particularly virulent to the immunocompetent patient. The vast majority of septic patients today survive their initial hyperinflammatory insult only to end up in the intensive care unit with sepsis-induced multi-organ dysfunction over the ensuing days to weeks. Sepsis-induced immunosuppression is increasingly recognized as the overriding immune dysfunction in these vulnerable patients. The impaired pathogen clearance after primary infection and/or susceptibility to secondary infections contribute to the high rates of morbidity and mortality associated with sepsis.

[0506] According to at least some embodiments of the present invention, there is provided use of a combination of the therapeutic agents and/or a pharmaceutical composition comprising same, as recited herein, and a known therapeutic agent effective for treating sepsis.

[0507] According to at least some embodiments of the present invention, there is provided use of a combination of the therapeutic agents and/or a pharmaceutical composition comprising same, as recited herein, can be combined with standard of care or novel treatments for sepsis, with therapies that block the cytokine storm in the initial hyperinflammatory phase of sepsis, and/or with therapies that have immunostimulatory effect in order to overcome the sepsis-induced immunosuppression phase.

[0508] Combination with standard of care treatments for sepsis, as recommended by the "International Guidelines for Management of Severe Sepsis and Septic Shock" (Dellinger et al 2013 *Intensive Care Med* 39: 165-228), some of which are described below.

[0509] 1. Broad spectrum antibiotics having activity against all likely pathogens (bacterial and/or fungal—treatment starts when sepsis is diagnosed, but specific pathogen is not identified)—example Cefotaxime (Claforan®), Ticarcillin and clavulanate (Timentin®), Piperacillin and tazobactam (Zosyn®), Imipenem and cilastatin (Primaxin®), Meropenem (Merrem®), Clindamycin (Cleocin), Metronidazole (Flagyl®), Ceftriaxone (Rocephin®), Ciprofloxacin (Cipro®), Cefepime (Maxipime®), Levofloxacin (Levaquin®), Vancomycin or any combination of the listed drugs.

[0510] 2. Vasopressors: example Norepinephrine, Dopamine, Epinephrine, vasopressin

[0511] 3. Steroids: example: Hydrocortisone, Dexamethasone, or Fludrocortisone, intravenous or otherwise Inotropic therapy: example Dobutamine for sepsis patients with myocardial dysfunction

[0512] 4. Recombinant human activated protein C (rhAPC), such as drotrecogin alfa (activated) (DrotAA).

[0513] 5. β-blockers additionally reduce local and systemic inflammation.

[0514] 6. Metabolic interventions such as pyruvate, succinate or high dose insulin substitutions.

Use of Anti-Vista Antibodies and Pharmaceutical Compositions Containing for Reducing the Undesirable Immune Activation that Follows Gene or Cell Therapy or Transplant

[0515] As used herein the term "gene therapy" encompasses any type of gene therapy, vector-mediated gene therapy, gene transfer, virus-mediated gene transfer and further encompasses certain cell therapies, e.g., CAR T and CAR NK cell therapies. According to at least some embodiments of the present invention, agonist VISTA antibodies, a fragment, a conjugate thereof and/or a pharmaceutical compositions as described herein, which target VISTA and have inhibitory activity on immune responses, could be used as therapeutic agents for reducing the undesirable immune activation that follows gene or cell therapy used for treatment of various genetic diseases. Without wishing to be limited by a single hypothesis, such antibodies have VISTA-like inhibitory activity on immune responses and/or enhance VISTA immune inhibitory activity, optionally by inhibition of pathogenic T cells and/or NK cells.

[0516] Many gene therapy products for the treatment of genetic diseases are currently in clinical trials. Recent studies document therapeutic success for several genetic diseases using gene therapy vectors. Gene therapy strategies are characterized by 3 critical elements, the gene to be transferred, the target tissue into which the gene will be introduced, and the vector (gene delivery vehicle) used to facilitate entry of the gene to the target tissue. The vast majority of gene therapy clinical trials have exploited viral vectors as very efficient delivery vehicles, including retroviruses, lentiviruses, adenoviruses, adeno-associated viruses, pseudotype viruses and herpes simplex viruses. However, the interactions between the human immune system and all the components of gene therapy vectors seem to represent one of the major limitations to long-lasting therapeutic efficacy. Human studies have shown that the likelihood of a host immune response to the viral vector is high. Such immune responses to the virus or the transgene product itself, resulting in formation of neutralizing antibodies and/or destruction of transduced cells by cytotoxic cells, can greatly interfere with therapeutic efficacy (Seregin and Amalfitano 2010 *Viruses* 2:2013; Mingozzi and High 2013 Blood 122: 23; Masat et al 2013 *Discov Med.* 15:379). Therefore, developing strategies to circumvent immune responses and facilitate long-term expression of transgenic therapeutic proteins is one of the main challenges for the success of gene therapy in the clinic.

[0517] Factors influencing the immune response against transgenic proteins encoded by viral vectors include route of administration, vector dose, immunogenicity of the transgenic protein, inflammatory status of the host and capsid serotype. These factors are thought to influence immunogenicity by triggering innate immunity, cytokine production, APC maturation, antigen presentation and, ultimately, priming of naive T lymphocytes to functional effectors (Mingozzi and High 2013 *Blood* 122:23). Therefore, the idea to dampen immune activation by interfering with these very mechanisms has logically emerged with the aim to induce a short-term immunosuppression, avoid the early immune priming that follows vector administration and promote long-term tolerance.

[0518] As a strategy to inhibit the undesirable immune activation that follows gene therapy, particularly after multiple injections, immunomodulation treatment by targeting of two non-redundant checkpoints of the immune response at the time of vector delivery was tested in animal models. Studies of vector-mediated immune responses upon adenoviral vector instilled into the lung in mice or monkeys showed that transient treatment with an anti-CD40L antibody lead to suppression of adenovirus-induced immune responses; consequently, the animals could be re-administered with adenovirus vectors. Short treatment with this Ab resulted in long-term effects on immune functions and prolonged inhibition of the adenovirus-specific humoral response well beyond the time when the Ab effects were no longer significant, pointing to the therapeutic potential in blockade of this costimulatory pathway as an immunomodulatory regimen to enable administration of gene transfer vectors (Scaria et al. 1997 *Gene Ther.* 4: 611; Chirmule et al 2000 *J. Virol.* 74: 3345). Other studies showed that co-administration of CTLA4-Ig and an anti-CD40L Ab around the time of primary vector administration decreased immune responses to the vector, prolonged long term adenovirus-mediated gene expression and enabled secondary adenovirus-mediated gene transfer even after the immunosuppressive effects of these agents were no longer present, indicating that it may be possible to obtain persistence as well as secondary adenoviral-mediated gene transfer with transient immunosuppressive therapies (Kay et al 1997 *Proc. Natl. Acad. Sci. U.S.A* 94:4686). In another study, similar administration of CTLA4-Ig and an anti-CD40L Ab abrogated the formation of neutralizing Abs against the vector, and enabled gene transfer expression, provided the treatment was administered during each gene transfer injection (Lorain et al 2008 *Molecular Therapy* 16:541). Furthermore, administration of CTLA4-Ig to mice, even as single administration, resulted in suppression of immune responses and prolonged transgene expression at early time points (Adriouch et al 2011 *Front. Microbiol.* 2: 199). However, CTLA4-Ig alone was not sufficient to permanently wipe out the immune responses against the transgene product. Combined treatment targeting two immune checkpoints with CTLA4-Ig and PD-Li or PDL-2 resulted in synergistic improvement of transgene tolerance at later time points, by probably targeting two non-redundant mechanisms of immunomodulation, resulting in long term transgene persistence and expression (Adriouch et al 2011 *Front. Microbiol.* 2: 199).

[0519] According to at least some embodiments of the present invention, the subject agonists may be used to overcome the limitation of immune responses to gene therapy, could be used for reducing the undesirable immune activation that follows gene therapy alone or with other actives. Current approaches include exclusion of patients with antibodies to the delivery vector, administration of high vector doses, use of empty capsids to adsorb anti-vector antibodies allowing for subsequent vector transduction, repeated plasma exchange (plasmapheresis) cycles to adsorb immunoglobulins and reduce the anti-vector antibody titer.

[0520] Novel approaches attempting to overcome these limitations can be divided into two broad categories: selective modification of the Ad vector itself and pre-emptive immune modulation of the host (Seregin and Amalfitano 2010 *Viruses* 2:2013). The first category comprises several innovative strategies including: (1) Ad-capsid-display of specific inhibitors or ligands; (2) covalent modifications of the entire Ad vector capsid moiety; (3) the use of tissue specific promoters and local administration routes; (4) the use of genome modified Ads; and (5) the development of chimeric or alternative serotype Ads.

[0521] The second category of methods includes the use of immunosuppressive drugs or specific compounds to block important immune pathways, which are known to be induced by viral vectors. Immunosuppressive agents have been tested in preclinical studies and shown efficacy in prevention or eradication of immune responses to the transfer vector and transgene product. These include general immunosuppressive agents such as cyclosporine A; cyclophosphamide; FK506; glucocorticoids or steroids such as dexamethasone; TLR9 blockade such as the TLR9 antagonist oligonucleotide ODN-2088; TNF-a blockade with anti-TNF-a antibodies or TNFR-Ig antibody, Erk and other signaling inhibitors such as U0126. In the clinical setting, administration of glucocorticoids has been successfully used to blunt T cell responses directed against the viral capsid upon liver gene transfer of adenovirus-associated virus

(AAV) vector expressing human factor IX transgene to severe hemophilia B patients (Nathwani et al 2011 *N. Engl. J. Med.* 365:2357).

[0522] In contrast to the previous approaches that utilize drugs that tend to "globally" and non-specifically immunosuppress the host, more selective immunosuppressive approaches have been developed. These include the use of agents which provide blockade of positive co-stimulatory interactions, such as between CD40 and CD154, ICOS and ICOSL, CD28 and CD80 or CD86 (including CTLA4-Ig), NKG2D and NKG2D ligands, LFA-1 and ICAM, LFA-3 and CD2, 4-1BB and 4-1BBL, OX40 and OX40L, GITR and GITRL and agents that stimulate negative costimulatory receptors such as CTLA-4, PD-1, BTLA, LAG-3, TIM-1, TEVI-3, KIRs, and the receptors for B7-H4 and B7-H3. Some of these have been utilized in preclinical or clinical transplantation studies (Pilat et al 2011 *Sem. Immunol.* 23:293).

[0523] In the above-described gene or cell therapies or in treating transplant indications preferably a subject who has or is to receive cell or gene therapy or a transplanted tissue or organ will be administered an immmunoinhibitory anti-VISTA antibody disclosed herein or antigen-binding fragment according to the invention, which antibody enhances, agonizes or mimics at least one VISTA-mediated effect on immunity, e.g., its inhibitory effect on cytotoxic T cells or NK activity and/or its inhibitory effect on the production of proinflammatory cytokines, or its stimulatory effect on Tregs thereby preventing or reducing host immune responses against the cell or gene used in therapy or an undesired immune response against the transplanted cells, organ or tissue. Preferably the treatment will elicit prolonged immune tolerance against the transplanted or infused cells, tissue or organ. In some instances, e.g., in the case of transplanted cells, tissues or organs containing immune cells, the immmunoinhibitory anti-VISTA antibody disclosed herein or antigen-binding fragment may be contacted with the cells, tissue or organ prior to infusion or transplant, and/or potentially immune cells of the transplant recipient in order to tolerize the immune cells and potentially prevent an undesired immune response or GVHD immune reaction.

Pharmaceutical Compositions

[0524] In another aspect, the present invention provides a composition, e.g., a pharmaceutical composition, containing one or a combination of anti-human VISTA antibodies according to the invention and optionally another immunosuppressive or other active agent. Thus, the present invention features a pharmaceutical composition comprising a therapeutically effective amount of anti-human VISTA antibodies according to at least some embodiments of the present invention. In particular the present invention features a pharmaceutical composition comprising a therapeutically effective [immunosuppressive] amount of at least one agonist anti-human VISTA antibody or antibody fragment according to the present invention.

[0525] A pharmaceutical composition according to at least some embodiments of the present invention may be used for the treatment of immune related disorders, autoimmunity, allergy, GVHD, inflammation or hepatotoxicity associated with infectious disorder and/or sepsis. "Treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disorder as well as those in which the disorder is to be prevented. Hence, the mammal to be treated herein may have been diagnosed as having the disorder or may be predisposed or susceptible to the disorder. "Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, horses, cats, cows, etc. Preferably, the mammal is human.

[0526] The term "therapeutically effective amount" refers to an amount of agent according to the present invention that is effective to treat a disease or disorder in a mammal. The therapeutic agents of the present invention can be provided to the subject alone or as part of a pharmaceutical composition where they are mixed with a pharmaceutically acceptable carrier. In many instances agonist or antagonist anti-VISTA antibodies according to the invention will be used in combination with other immunotherapeutics or other therapeutic agents useful in treating a specific condition.

[0527] A composition is said to be a "pharmaceutically acceptable carrier" if its administration can be tolerated by a recipient patient. As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Preferably, the carrier is suitable for intravenous, intramuscular, subcutaneous, parenteral, spinal or epidermal administration (e.g., by injection or infusion).

[0528] Such compositions include sterile water, buffered saline (e.g., Tris-HCl, acetate, phosphate), pH and ionic strength and optionally additives such as detergents and solubilizing agents (e.g., Polysorbate 20, Polysorbate 80), antioxidants (e.g., ascorbic acid, sodium metabisulfite), preservatives (e.g., Thimersol, benzyl alcohol) and bulking substances (e.g., lactose, mannitol). Non-aqueous solvents or vehicles may also be used as detailed below.

[0529] Examples of suitable aqueous and nonaqueous carriers that may be employed in the pharmaceutical compositions according to at least some embodiments of the invention include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants. Depending on the route of administration, the active compound, i.e., monoclonal or polyclonal antibodies and antigen-binding fragments and conjugates containing same, and/or alternative scaffolds, that specifically bind any one of VISTA proteins, or bispecific molecule, may be coated in a material to protect the compound from the action of acids and other natural conditions that may inactivate the compound. The pharmaceutical compounds according to at least some embodiments of the invention may include one or more pharmaceutically acceptable salts. A "pharmaceutically acceptable salt" refers to a salt that retains the desired biological activity of the parent compound and does not impart any undesired toxicological effects (see e.g., Berge, S. M., et al. (1977) *J. Pharm. Sci.* 66: 1-19). Examples of such salts include acid addition salts and base addition salts. Acid addition salts include those derived from nontoxic inorganic acids, such as hydrochloric, nitric, phosphoric, sulfuric, hydrobromic, hydriodic, phosphorous and the like, as well as from nontoxic organic acids such as aliphatic mono- and dicarboxylic acids, phenyl-substituted

alkanoic acids, hydroxy alkanoic acids, aromatic acids, aliphatic and aromatic sulfonic acids and the like. Base addition salts include those derived from alkaline earth metals, such as sodium, potassium, magnesium, calcium and the like, as well as from nontoxic organic amines, such as N,N'-dibenzylethylenediamine, N-methylglucamine, chloroprocaine, choline, diethanolamine, ethylenediamine, procaine and the like.

[0530] A pharmaceutical composition according to at least some embodiments of the invention also may include a pharmaceutically acceptable anti-oxidant. Examples of pharmaceutically acceptable antioxidants include: (1) water soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, a-tocopherol, and the like; and (3) metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

[0531] These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of presence of microorganisms may be ensured both by sterilization procedures, supra, and by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the like. It may also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents which delay absorption such as aluminum monostearate and gelatin.

[0532] Pharmaceutically acceptable carriers include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. The use of such media and agents for pharmaceutically active substances is known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the pharmaceutical compositions according to at least some embodiments of the invention is contemplated. Supplementary active compounds can also be incorporated into the compositions.

[0533] Therapeutic compositions typically must be sterile and stable under the conditions of manufacture and storage. The composition can be formulated as a solution, microemulsion, liposome, or other ordered structure suitable to high drug concentration. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts and gelatin. Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by sterilization microfiltration. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying (lyophilization) that yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0534] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by sterilization microfiltration. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying (lyophilization) that yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0535] A composition of the present invention can be administered via one or more routes of administration using one or more of a variety of methods known in the art. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results. Preferred routes of administration for therapeutic agents according to at least some embodiments of the invention include intravascular delivery (e.g. injection or infusion), intravenous, intramuscular, intradermal, intraperitoneal, subcutaneous, spinal, oral, enteral, rectal, pulmonary (e.g. inhalation), nasal, topical (including transdermal, buccal and sublingual), intravesical, intravitreal, intraperitoneal, vaginal, brain delivery (e.g. intra-cerebroventricular, intracerebral, and convection enhanced diffusion), CNS delivery (e.g. intrathecal, perispinal, and intra-spinal) or parenteral (including subcutaneous, intramuscular, intravenous and intradermal), transmucosal (e.g., sublingual administration), administration or administration via an implant, or other parenteral routes of administration, for example by injection or infusion, or other delivery routes and/or forms of administration known in the art. The phrase "parenteral administration" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion. In a specific embodiment, a protein, a therapeutic agent or a pharmaceutical composition according to at least some embodiments of the present invention can be administered intraperitoneally or intravenously.

[0536] Alternatively, a VISTA specific antibody according to the invention can be administered via a non-parenteral route, such as a topical, epidermal or mucosal route of administration, for example, intranasally, orally, vaginally, rectally, sublingually or topically.

[0537] The active compounds can be prepared with carriers that will protect the compound against rapid release, such as a controlled release formulation, including implants, transdermal patches, and microencapsulated delivery sys-

tems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Many methods for the preparation of such formulations are patented or generally known to those skilled in the art. See, e.g., *Sustained and Controlled Release Drug Delivery Systems*, J. R. Robinson, ed., Marcel Dekker, Inc., New York, 1978.

[0538] Therapeutic compositions can be administered with medical devices known in the art. For example, in a preferred embodiment, a therapeutic composition according to at least some embodiments of the invention can be administered with a needles hypodermic injection device, such as the devices disclosed in U.S. Pat. Nos. 5,399,163; 5,383,851; 5,312,335; 5,064,413; 4,941,880; 4,790,824; or 4,596,556. Examples of well-known implants and modules useful in the present invention include: U.S. Pat. No. 4,487,603, which discloses an implantable micro-infusion pump for dispensing medication at a controlled rate; U.S. Pat. No. 4,486,194, which discloses a therapeutic device for administering medicaments through the skin; U.S. Pat. No. 4,447,233, which discloses a medication infusion pump for delivering medication at a precise infusion rate; U.S. Pat. No. 4,447,224, which discloses a variable flow implantable infusion apparatus for continuous drug delivery; U.S. Pat. No. 4,439,196, which discloses an osmotic drug delivery system having multi-chamber compartments; and U.S. Pat. No. 4,475,196, which discloses an osmotic drug delivery system. These patents are incorporated herein by reference. Many other such implants, delivery systems, and modules are known to those skilled in the art.

[0539] In certain embodiments, the anti-VISTA antibodies can be formulated to ensure proper distribution in vivo. For example, the blood-brain barrier (BBB) excludes many highly hydrophilic compounds. To ensure that the therapeutic compounds according to at least some embodiments of the invention cross the BBB (if desired), they can be formulated, for example, in liposomes. For methods of manufacturing liposomes, see, e.g., U.S. Pat. Nos. 4,522,811; 5,374,548; and 5,399,331. The liposomes may comprise one or more moieties which are selectively transported into specific cells or organs, thus enhance targeted drug delivery (see, e.g., V. V. Ranade (1989) *J. Clin. Pharmacol.* 29:685). Exemplary targeting moieties include folate or biotin (see, e.g., U.S. Pat. No. 5,416,016 to Low et al.); mannosides (Umezawa et al., (1988) *Biochem. Biophys. Res. Commun.* 153: 1038); antibodies (P. G. Bloeman et al. (1995) *FEBS Lett.* 357: 140; M. Owais et al. (1995) *Antimicrob. Agents Chemother.* 39: 180); surfactant protein A receptor (Briscoe et al. (1995) *Am. J Physiol.* 1233: 134); p120 (Schreier et al. (1994) *J. Biol. Chem.* 269:9090); see also K. Keinanen; M. L. Laukkanen (1994) *FEBS Lett.* 346: 123; J. J. Killion; and I. J. Fidler (1994) *Immunomethods* 4:273.

[0540] In yet another embodiment, immunoconjugates of the invention can be used to target compounds (e.g., therapeutic agents, labels, cytotoxins, radiotoxins immunosuppressants, etc.) to cells which have VISTA cell surface receptors by linking such compounds to the antibody disclosed herein. Thus, the invention also provides methods for localizing ex vivo or in vivo cells expressing VISTA (e.g., with a detectable label, such as a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor). Alternatively, the immunoconjugates can be used to kill cells which have VISTA cell surface receptors by targeting cytotoxins or radiotoxins to VISTA antigen.

[0541] As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Preferably, the carrier is suitable for intravenous, intramuscular, subcutaneous, parenteral, spinal or epidermal administration (e.g., by injection or infusion). Depending on the route of administration, the active compound, i.e., soluble polypeptide conjugate containing the ectodomain of the VISTA antigen, antibody, immunoconjugate, alternative scaffolds, and/or bispecific molecule, may be coated in a material to protect the compound from the action of acids and other natural conditions that may inactivate the compound. The pharmaceutical compounds according to at least some embodiments of the present invention may include one or more pharmaceutically acceptable salts. A "pharmaceutically acceptable salt" refers to a salt that retains the desired biological activity of the parent compound and does not impart any undesired toxicological effects (see e.g., Berge, S. M., et al. (1977) *J. Pharm. Sci.* 66: 1-19). Examples of such salts include acid addition salts and base addition salts. Acid addition salts include those derived from nontoxic inorganic acids, such as hydrochloric, nitric, phosphoric, sulfuric, hydrobromic, hydroiodic, phosphorous and the like, as well as from nontoxic organic acids such as aliphatic mono- and dicarboxylic acids, phenyl-substituted alkanoic acids, hydroxy alkanoic acids, aromatic acids, aliphatic and aromatic sulfonic acids and the like. Base addition salts include those derived from alkaline earth metals, such as sodium, potassium, magnesium, calcium and the like, as well as from nontoxic organic amines, such as N,N'-dibenzylethylenediamine, N-methylglucamine, chloroprocaine, choline, diethanolamine, ethylenediamine, procaine and the like.

[0542] A pharmaceutical composition according to at least some embodiments of the present invention also may include a pharmaceutically acceptable anti-oxidant. Examples of pharmaceutically acceptable antioxidants include: (1) water soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, a-tocopherol, and the like; and (3) metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like. Examples of suitable aqueous and nonaqueous carriers that may be employed in the pharmaceutical compositions according to at least some embodiments of the present invention include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants.

[0543] These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of presence of microorganisms may be ensured both by sterilization procedures, supra, and by the inclusion of various antibacterial and

antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the like. It may also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents which delay absorption such as aluminum monostearate and gelatin.

[0544] Pharmaceutically acceptable carriers include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. The use of such media and agents for pharmaceutically active substances is known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the pharmaceutical compositions according to at least some embodiments of the present invention is contemplated. Supplementary active compounds can also be incorporated into the compositions.

[0545] Therapeutic compositions typically must be sterile and stable under the conditions of manufacture and storage. The composition can be formulated as a solution, microemulsion, liposome, or other ordered structure suitable to high drug concentration. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts and gelatin. Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by sterilization microfiltration. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying (lyophilization) that yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0546] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by sterilization microfiltration. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying (lyophilization) that yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0547] The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will vary depending upon the subject being treated, and the particular mode of administration. The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will generally be that amount of the composition which produces a therapeutic effect. Generally, out of one hundred percent, this amount will range from about 0.01 percent to about ninety-nine percent of active ingredient, preferably from about 0.1 percent to about 70 percent, most preferably from about I percent to about 30 percent of active ingredient in combination with a pharmaceutically acceptable carrier.

[0548] Dosage regimens are adjusted to provide the optimum desired response (e.g., a therapeutic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms according to at least some embodiments of the present invention are dictated by and directly dependent on (a) the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

[0549] For administration of the VISTA antibody disclosed herein, the dosage ranges from about 0.0001 to 100 mg/kg, and more usually 0.01 to 5 mg/kg, of the host body weight. For example dosages can be 0.3 mg/kg body weight, 1 mg/kg body weight, 3 mg/kg body weight, 5 mg/kg body weight or 10 mg/kg body weight or within the range of 1-10 mg/kg. An exemplary treatment regime entails administration once per week, once every two weeks, once every three weeks, once every four weeks, once a month, once every 3 months or once every three to 6 months. Preferred dosage regimens for an antibody disclosed herein according to at least some embodiments of the present invention include 1 mg/kg body weight or 3 mg/kg body weight via intravenous administration, with the antibody disclosed herein being given using one of the following dosing schedules: (i) every four weeks for six dosages, then every three months; (ii) every three weeks; (iii) 3 mg/kg body weight once followed by 1 mg/kg body weight every three weeks.

[0550] In some methods, two or more monoclonal antibodies with different binding specificities are administered simultaneously; in which case the dosage of each antibody disclosed herein administered falls within the ranges indicated. Antibody disclosed herein is usually administered on multiple occasions. Intervals between single dosages can be, for example, daily, weekly, monthly, every three months or yearly. Intervals can also be irregular as indicated by measuring blood levels of antibody to the target antigen in the patient. In some methods, dosage is adjusted to achieve a plasma antibody concentration of about 1-1000 mug/ml and in some methods about 25-300 microgram/ml.

[0551] Alternatively, therapeutic agent can be administered as a sustained release formulation, in which case less frequent administration is required. Dosage and frequency

vary depending on the half-life of the therapeutic agent in the patient. In general, human antibodies show the longest half-life, followed by humanized antibodies, chimeric antibodies, and nonhuman antibodies. The half-life for fusion proteins may vary widely. The dosage and frequency of administration can vary depending on whether the treatment is prophylactic or therapeutic. In prophylactic applications, a relatively low dosage is administered at relatively infrequent intervals over a long period of time. Some patients continue to receive treatment for the rest of their lives. In therapeutic applications, a relatively high dosage at relatively short intervals is sometimes required until progression of the disease is reduced or terminated, and preferably until the patient shows partial or complete amelioration of symptoms of disease. Thereafter, the patient can be administered a prophylactic regime.

[0552] Actual dosage levels of the active ingredients in the pharmaceutical compositions of the present invention may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient. The selected dosage level will depend upon a variety of pharmacokinetic factors including the activity of the particular compositions of the present invention employed, or the ester, salt or amide thereof, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts.

Functional Screening Using In Vivo Animal Models

1. Testing of Vista Agonist Antibodies According to the Invention in Concanavalin A-Induced Hepatitis Animal Model.

[0553] Autoimmune hepatitis (AIH) is a chronic inflammatory disease of the liver, characterized by the loss of self-tolerance leading to B and T cell responses against the liver. The ConA model represents the best-characterized system for understanding the pathogenesis of AIH. ConA is a lectin that binds to specific sugar moieties, which are enriched in the liver. The modification of these sugar residues by ConA results in rapid $CD4^+$ T cell activation through interaction with modified MHC structures expressed by liver macrophages. An intense, but transient, cytokine production occurs with most canonical T cell cytokines (IL-2, IL-3, IFNγ and TNFα) reaching peak plasma levels within 4-6 hours. Notably, ConA induced inflammation can be blocked by depleting CD4+ T cells. The ConA model with hV-KI mice may be used to confirm suppressive activity of agonistic anti-VISTA mAbs according to the invention. Mice are weighed and treated with 10 mpk of anti-VISTA antibody or the appropriate isotype control 3 hours prior to injection with 15 mpk of ConA. The anti-VISTA mAbs are administered I.P. while ConA is injected via the tail-vein in these mice. At the 6-hour time-point post ConA administration, the mice are euthanized and blood is collected. The plasma fraction is then be analyzed for plasma cytokines by a multiplex assay for 32 cytokines. Each antibody is tested two times in independent experiments to confirm activity. For each cytokine in the 32-plex, a one-way ANOVA will be performed, with a Dunnett's post-test to compare each anti-VISTA antibody to the isotype control. The tested anti-VISTA mAb is ranked based upon efficacy of cytokine suppression (how much was the cytokine suppressed) and variability (how consistent is the suppression within each experiment and between experiments). Additional emphasis is placed on mAb that suppress cytokines that are canonically associated with T cell activation.

[0554] Numerous anti-human VISTA antibodies according to the invention have been screened in the ConA model and were efficacious (immunosuppressive) therein, i.e., they suppressed ConA-induced cytokine production and promoted survival and in particular suppressed the expression of cytokines involved in T cell activation including IL-2. Particularly, the inventors tested INX800, INX801, and INX903 as well as agonist anti-murine VISTA antibodies and all were efficacious (immunosuppressive) in the ConA hepatitis model. Therefore, agonist anti-human VISTA antibodies according to the invention should be useful in treating/preventing inflammation and hepatotoxicity associated with some chronic and acute infectious conditions such as hepatitis.

2. Testing of Vista Agonist Antibodies According to the Invention in Graft Versus Host Disease Animal Models

[0555] GVHD is a systemic disease mediated by adoptive transfer of allogeneic T cells into an irradiated host. There are five major steps that are critical in the pathogenesis of GVHD; 1) Damage to the host, most commonly in the form of the irradiation event that precedes the T cell transfer; 2) Activation of the allogeneic T cells by both host and donor APCs; 3) Expansion of the T cells in the lymph nodes and spleen; 4) Trafficking into peripheral sites such as the skin, gut, liver and lung; and 5) Damage to the host driven by T cells and also recruited myeloid cells. In certain models, such as F1→Parental strain, a chronic GVHD occurs that is a suitable model for lupus as the mice develop anti-nuclear mAb and immune complex mediated glomerular nephritis. Of note, genetic deletion of VISTA from the donor T cells results in a more aggressive form of GHVD than seen in mice receiving WT T cells.

[0556] This assay may be used to identify and rank agonism of agonistic anti-human VISTA candidates. Also this assay may be used to confirm that agonist antibodies according to the invention may be used to treat or prevent GVHD. In this model BALB/c mice are lethally irradiated and given allogeneic bone marrow and splenic T cells from hV-KI mice to induce GVHD; with one group not receiving T cells as a negative control. Mice receiving the allogeneic T cells are split into the control Ig group and the treatment groups. Up to four unique VISTA mAb will be used in a single experiment, with eight mice per group, and two replicate experiments will be conducted. 10 mpk or another dose of antibody is administered at the time of T cell transfer, as well as at days 2 and 4 post transfer. The body weight of each mouse will be tracked, and any mouse that loses more than 20% of its initial starting bodyweight will be sacrificed. Kaplan Meier curves are generated for each experiment with a log-rank statistical test comparing each anti-VISTA antibody to the control. Should all four VISTA mAb fully protect against GVHD, then dose response assays

will be run in the GVHD model with groups being treated with 10, 3, 1 and 0.3 mpk of antibody. LD50 values will be calculated for each antibody.

[0557] A number of agonist anti-human VISTA antibodies according to the invention were evaluated in this animal model. These tested antibodies all were efficacious (immunosuppressive) in this model, i.e., they reduced the symptoms of the disease, slowed disease progression, reduced disease-associated weight loss and promoted survival. Particularly, each of INX800, INX801, INX901, INX902, INX903 and INX904 were evaluated and were demonstrated to alleviated or prevent disease symptoms in this animal model. Also, it was determined using the A and B forms of INX901 that either the A or B form were equally effective in the GVHD animal model.

3. Testing of Vista Agonist Antibodies According to the Invention in an Animal Model of Inflammatory Bowel Disease.

[0558] Inflammatory bowel diseases (IBD), Crohn's disease and ulcerative colitis result from incompletely defined and complex interactions between host immune responses, genetic susceptibility, environmental factors, and the enteric luminal contents. Recent genome-wide association studies report associations between immune cell regulatory genes and IBD susceptibility. Both innate and adaptive immune cell intrinsic genes are represented in these studies, indicating a central role for these cell populations in IBD pathogenesis. There currently exist more than 50 animal models of human IBD. While no one model perfectly phenocopies human IBD, many are useful for studying various aspects of human disease, including disease onset and progression and the wound-healing response.

[0559] In one well established IBD model intestinal inflammation is initiated with syngeneic splenic $CD4^{+}$ $CD45RB^{hi}$ T cell adoptive transfer into T and B cell deficient recipient mice. The CD4+ $CD45RB^{hi}$ T cell population contains mainly naive T cells primed for activation that are capable of inducing chronic small bowel and colonic inflammation. This method allows the researcher to modify key experimental variables, including both innate and adaptive immune cell populations, to answer biologically relevant questions relating to disease pathogenesis. Additionally, this method provides precise initiation of disease onset and a well-characterized experimental time course permitting the kinetic study of clinical features of disease progression in mice. Intestinal inflammation induced by this method shares many features with human IBD, including chronic large and small bowel transmural inflammation, pathogenesis driven by cytokines such as TNF and IL-12, and systemic symptoms such as wasting. Thus, it is an ideal model system for studying the pathogenesis of human IBD.

[0560] An agonistic anti-human VISTA antibody according to the invention (INX901) was tested and shown to be efficacious in this IBD model. Particularly this agonist antibody was demonstrated to suppress cytokine levels and to effectively prevent or inhibit (i) colitis related weight loss, (ii) weight loss associated with colitis progression, (iii) colon shortening, (iv) the recruitment of inflammatory infiltrates to the colon and (v) the development of colitis. Therefore, agonist VISTA antibodies according to the invention may be used in the treatment of IBD and related inflammatory and intestinal conditions.

4. Testing of Vista Agonist Antibodies According to the Invention in Lupus Animal Models.

[0561] Lupus is an autoimmune or inflammatory condition with symptoms including kidney inflammation, increased proteinuria, and splenomegaly. There are 4 types of lupus of which Systemic Lupus Erythematosus or ("SLE") is the most common form. This disease can be mild or severe and can affect major organ systems. Lupus is an autoimmune condition of unknown cause that may result in inflammation of the kidneys—called lupus nephritis—which can affect the body's ability to filter waste from the blood, and or if severe may result in kidney damage requiring dialysis or kidney transplant. Also SLE may result in an increase in blood pressure in the lungs—called pulmonary hypertension—which can cause difficulty breathing. Further SLE may cause Inflammation of the nervous system and brain which can cause memory problems, confusion, headaches, and strokes. Further SLE may result in inflammation in the brain's blood vessels which can cause high fevers, seizures, and behavioral changes. Also SLE may result in hardening of the arteries or coronary artery disease—the buildup of deposits on coronary artery walls—can lead to a heart attack.

[0562] Agonistic anti-human VISTA antibodies according to the invention (INX903, INX901, INX901-A and INX901-B) and anti-murine VISTA antibodies were tested and shown to be efficacious in different lupus models including the MRL/lpr lupus model, the NZBWF-1 lupus model and the B6D2F model. The B6D2F model is a murine model wherein SLE is induced by the transfer of human VISTA knock-in DDE1 CD8 depleted splenocytes (donor) into a B6D2F1 host (recipient) In this model, donor CD4 T cell polyclonal activation drives cognate host B cell activation, expansion, and their production of autoantibodies leading to renal disease. Lupus-like features of B6 CD8 depleted transferred to B6D2F1 model include: (1) Immune complex glomerulonephritis; (2) anti-nuclear abs; (3) anti-dsDNA abs; and (4) anti-RBC abs (Coombs positivity). Additionally, this model meets sex-based differences in renal disease severity.

[0563] In these 3 different lupus models agonistic anti-human and murine VISTA antibodies were demonstrated to be efficacious and to reduce the incidence of lupus disease development, disease progression, reduce proteinuria levels, inhibit nephritis and kidney damage, reduce T cell activation and accumulation, reduce B cell activation and accumulation, and to inhibit autoantibody production. Particularly, INX903, INX901, INX901-A and INX901-B were shown to (i) reduce T cell proliferation and activation, (ii) reduce cognate B cell activation (MHCII expression) and accumulation, reduce splenomegaly, reduce anti-dsDNA IgG autoantibody production and to reduce type I interferon signature. Also these immunosuppressive effects were not impacted by whether the human IgG2 constant region of the antibody was in the A or B form. Therefore, agonist VISTA antibodies according to the invention may be used in the treatment of lupus and related inflammatory and autoimmune conditions.

5. Testing of Vista Agonist Antibodies in a Psoriasis Animal Model

Imiquimod (IMQD) Induced Psoriasis Model

[0564] The ability of anti-VISTA antibodies to treat psoriasis was evaluated using the Imiquimod (IMQD) induced

Psoriasis Model. Imiquimod (IMQD) is a commercially available cream containing TLR7/8 agonists that is widely used for dermatological conditions such as viral infections and melanoma. Application of IMQD to the skin over multiple days results in thickening of the epidermis via proliferation of the keratinocytes. Additionally, an immunological infiltration into the dermis layer occurs, with populations of both T cells and myeloid cells. Recurrent administration of IMQD creates a skin lesion similar to what is observed in patients with Psoriasis. IL-17 and IL-23 are thought to be the major cytokines involved in the immune response to IMQD.

[0565] An agonistic anti-murine VISTA antibody was tested and shown to be efficacious in this psoriasis model. Particularly, this antibody reduced the number of $CD3^+$ T cells infiltrating Imiquimod treated skin. Based on the observed results VISTA agonist antibodies may be used in the treatment or prevention of psoriasis and other T cell mediated autoimmune or inflammatory skin conditions.

6. Testing of Vista Agonist Antibodies in Arthritis Animal Model

[0566] The immunosuppressive effects of anti-VISTA antibodies to treat arthritis may be tested in different animal models. Agonistic anti-murine and anti-human VISTA antibodies were tested and shown to be efficacious in a well-accepted arthritis model, i.e., the Collagen induced arthritis or CIA Model. INX800, INX901, INX902 and INX903 as well as a hamster anti-murine anti-VISTA antibodies were all tested in this arthritis model. Disease development was assessed by measuring inflammation swelling in the affected joints over time. Clinical scoring was accomplished by awarding a score of 1 for each swollen digit, a score of 5 for a swollen footpad and a score of 5 for a swollen wrist or ankle (Charles River Labs scoring system), which added together give a maximal score of 60 for each animal.

[0567] As described infra each of these antibodies decreased the arthritis disease and INX901 and INX902 significantly decreased disease scope. Based on these results anti-human VISTA agonist antibodies may be used in the treatment or prevention of rheumatoid arthritis and other inflammatory or autoimmune conditions.

[0568] Having described the invention the following examples are provided to further illustrate the invention and its inherent advantages.

EXAMPLES

Example 1: Use of Assays to Screen for Immunosuppressive Anti-Mouse VISTA Abs

[0569] The present inventors developed various assays to screen for putative agonistic anti-mouse VISTA antibodies. As shown in FIG. **1** in vitro and in vivo screening assays were used to identify immunosuppressive anti-VISTA mAbs. In the experiments in FIG. **1**A purified T cells were plated on top of anti-CD3 in the presence of the indicated mAb for 72 hours. Proliferation was measured by H3 incorporation. In the experiments in FIG. **1**B purified DO11. 10 T cells were stimulated by ISQ pulsed APCs for 6 days in the presence of the indicated antibody. Proliferation was measured through use of CTV dilution dye. In the experiments in FIG. **1**C GVHD was induced by transfer of C57BL/6 cells into irradiated BALB/c recipients. Mice were injected I.P. with 200 μg of antibody on day 0, 2 and 4 post transfer and survival was analyzed. In the experiments in FIG. **1**D mice were treated with 10 mpk of the indicated antibody 3 hours prior to administration of ConA (15 mpk) and IL-2 was analyzed in plasma at 6 by Luminex.

[0570] More particularly, in the first assay, $CD4^+$ T cells were isolated and incubated with Ab1, Ab2 or Ab3 before being added to anti-CD3 coated plates. After 3 days in culture, the T cells were pulsed with tritiated thymidine, which is incorporated by proliferating cells. Notably, both Ab1 and Ab2 induced a significant reduction in the proliferative rate of the T cells, while Ab3 had no effect (FIG. **1**) In a similar assay where transgenic T cells were stimulated with antigen pulsed APCs instead, T cell activation was measured by proliferative dye dilution. Similar to the anti-CD3 assay, Ab1 suppressed antigen-specific T cell proliferation by ~50% (FIG. **1**B). These data indicate that the Ab3 mAb blocks mVISTA function (i.e., enhances immune responses) whereas Ab1 and Ab3 stimulate mVISTA function and down regulate key immune responses.

[0571] We also determined whether Ab3 and Ab1 could be distinguished using in vivo animal models, particularly in GVHD and ConA hepatitis models. Mice with GVHD which were treated with a control antibody (Ham Ig) had progressive disease and needed to be euthanized by 4 weeks post graft as expected (FIG. **1**C). Ab3 treated mice were also susceptible to GVHD, and in fact most mice died prior to the control treated group, indicating Ab3 may exacerbate disease. Conversely, all of the Ab1 treated mice showed no obvious symptoms of GVHD and almost all were healthy for at least 40 days. Specifically in these experiments mice with GVHD treated with a control antibody (Ham Ig) had progressive disease and needed to be euthanized by 4 weeks post graft as expected (FIG. **1**C). Ab3 treated mice were also susceptible to GVHD, and in fact most mice died prior to the control treated group, indicating Ab3 may exacerbate disease. Conversely, all of the Ab1 treated mice showed no obvious symptoms of GVHD and almost all were healthy for at least 40 days.

[0572] In the ConA model, the inventors tested whether each VISTA antibody would impact the well-characterized T cell cytokine response to ConA. Notably Ab1, but not Ab3, induced decreased plasma cytokine levels of IL-2 (FIG. **1**D). Specifically, in the ConA model, the inventors further tested whether each VISTA antibody would impact the well-characterized T cell cytokine response to ConA. Notably Ab1, but not Ab3, induced decreased plasma cytokine levels of IL-2 (FIG. **1**D).

[0573] Accordingly these results demonstrate that both anti-VISTA mAbs (Ab1 and Ab2) are immunosuppressive and it has also been shown that such immunosuppressive anti-mouse VISTA antibodies can be distinguished from inflammatory immunosuppressive anti-mouse VISTA antibodies (Ab3). As shown in FIG. **1** Ab1 is efficacious (immunosuppressive) in multiple inflammatory models including GVHD, NZB/W F1 lupus-like glomerulonephritis, concanavalin A (ConA)-induced hepatitis, collagen antibody induced arthritis (CAIA), and Imiquimod induced psoriasis. In each of these diseases, administration of Ab1 during the progression of disease greatly diminished pathology and/or mortality. Each model listed has a unique requirement on T cells for disease progression. GVHD and ConA are both driven by Th1 T cell responses.

Example 2: Identification of Anti-VISTA Abs which Suppresses Autoimmunity in Different Autoimmune Disease Models

[0574] In the experiments in FIG. **2**A-F the effects of different anti-mouse VISTA Abs were again compared in different disease models. In the experiments in FIG. **2**A NZB/W F1 mice were treated 3×/week with either Ab1 or Ham Ig (200 μg) starting at 25 weeks until the end of the experiment. "X" denotes time points where the control treated group had all been sacrificed. In the experiment in FIG. **2**B mice were treated with 200 μg of antibody 3 hours prior to administration of 15 mg/kg (mpk) of ConA and survival was followed for 80 hours. In the experiment in FIG. **2**C mice were treated sequentially with Collagen II mAb followed by LPS and arthritis was measured by measuring for paw swelling. In the experiments Ab1 and Ham-Ig were administered (200 μg) 3× every other day. In the experiment in FIG. **2**D Imiquimod was applied to the ear of mice daily. At day 14, Ab1 or Ham-Ig (200 μg) were administered every other day and ear thickness was measured with calipers. In the experiment in the same FIG. **2**E-F imiquimod was applied to the backs of mice daily. At day 9, mice were euthanized and skin was sectioned & stained for CD3 expression by IHC.

[0575] As shown in FIG. **2**A-F, in each of these experimental models, administration of Ab1 during the progression of the particular disease greatly diminished pathology and/or mortality. Each model listed has a unique requirement on T cells for disease progression. GVHD and ConA are both driven by Th1 T cell responses.

[0576] Imiquimod induced psoriasis is an IL-17/23 driven disease where T cells are recruited into the dermal layer of the skin. Ab1 drastically reduced the number of $CD3^+$ cells in the dermis (FIGS. **2**E and F), but had no impact on splenic T cell populations (data not shown), indicating that this anti-mouse VISTA Ab preferentially suppressed immunity at the inflammatory lesion.

[0577] NZB/W F1 lupus is a multifactorial disease with contributions from B cells, T cells and myeloid cells. In this model, therapeutic administration of Ab1 reduced proteinuria levels indicating decreased damage to the kidneys. Finally, CAIA does not involve adaptive immunity, instead being driven by macrophages and granulocytes. Suppression by anti-VISTA in this model indicates that the antibody may also impact upon the myeloid compartment. As such, suppressive VISTA mAb appear to mediate effects on both the T cell and innate immune compartments.

[0578] Therefore, as shown in FIG. **1** and FIG. **2** both monoclonal hamster anti-mouse VISTA Abs Ab1 and AB2 induced a significant reduction in the proliferative rate of the T cells, while Ab3 had no effect (FIG. **1**). In a similar assay where transgenic T cells were stimulated with antigen pulsed APCs, T cell activation was measured by proliferative dye dilution. Similar to the anti-CD3 assay, Ab1 suppressed antigen-specific T cell proliferation by ~50% (FIG. **1**B). These data suggest that Ab1 and Ab2 stimulate VISTA function and thereby down regulate key immune responses.

[0579] Particularly, Ab1, a hamster anti-mouse VISTA antibody was efficacious in multiple inflammatory models including GVHD, NZB/W F1 lupus-like glomerulonephritis, concanavalin A (ConA)-induced hepatitis, collagen antibody induced arthritis (CAIA), and Imiquimod induced psoriasis (FIGS. **1** and **2**). In each of these diseases, administration of Ab1 during the progression of disease greatly diminished pathology and/or mortality. Each model listed has a unique requirement on T cells for disease progression. GVHD and ConA are both driven by Th1 T cell responses. As noted above, Imiquimod induced psoriasis is an IL-17/23 driven disease where T cells are recruited into the dermal layer of the skin. Therefore, suppression by Ab1 in this particular autoimmune model indicates that this antibody may also be affecting the myeloid compartment. Therefore, these immunosuppressive anti-mouse VISTA mAb's appear to mediate effects on both the T cell and innate immune compartments.

Example 3: Development of Human VISTA Knock-In Mice for Use in Screening for Agonistic Anti-Human VISTA Abs

[0580] The previous examples relate to the isolation and characterization of agonistic anti-mouse VISTA Abs. Heretofore an agonistic anti-human VISTA Ab has never been reported in the literature. This is despite the fact that very many antagonistic anti-human VISTA antibodies have been identified by the present Assignee and other groups. Accordingly, prior to this invention it was uncertain whether agonistic anti-human VISTA antibodies would be identified.

[0581] Such antibodies would be highly beneficial as currently there is no approved human therapeutics that exploit the natural function of NCR's to suppress the immune response. Although Orencia (CTLA4-Ig) is effective, it only acts by blocking the CD28-B7 interaction and pathway and does not work by stimulating a downregulatory pathway. As illustrated by the potent immunosuppressive effects of 2 different agonistic anti-VISTA mAbs as shown in the examples which follow, the engagement of this pathway may prove to be a revolution in the management of different human autoimmune diseases. Moreover, the immunosuppressive impact of anti-VISTA on both adaptive and innate autoimmune effector mechanisms sets it apart from many other anti-inflammatory agents.

[0582] With respect to the foregoing, it was hypothesized that a desirable and necessary reagent in screening for agonistic anti-human VISTA Abs is a human VISTA knock-in mouse. A human VISTA knock-in mouse has been created by the present Assignee ("hV-KI Mouse"). These hV-KI mice express human VISTA in replacement of mouse VISTA. Particularly, as shown in FIG. **3** $CD4^+$ T cells, $CD8^+$ T cells, Tregs ($CD4^+$ $FoxP3^+$), and monocytes, $CD11b^+$, $Ly6C^+$, $Ly6G^-$ were isolated from the lymph nodes of WT and VISTA KI mice, and stained with aVISTA antibodies against mouse or human protein respectively. The expression pattern of the hV-KI is identical to what is seen in WT mice as $CD4^+$ and $CD8^+$ T cells, regulatory T cells and monocytes all express consistent amounts of surface protein between the two strains (see FIG. **3**).

[0583] Additionally, hV-KI mice do not develop any signs of inflammatory disease that are observed in VISTA KO mice, indicating that hVISTA is fully functional within the mouse immune system (data not shown). Accordingly, this mouse model may be used in different assays to screen for immunosuppressive mAbs.

Example 4: Synthesis of Putative Agonistic Anti-Human VISTA Antibodies

[0584] The sequences of different anti-human VISTA antibodies is contained in FIG. **4**. These antibodies specifically

bind to human VISTA, e.g., VSTB49-VSTB116, and possess VISTA antagonist properties, i.e., these antibodies inhibit the suppressive effects of VISTA on immunity when in the IgG1 format, e.g., when the antibody comprises an IgG1 Fc region which is wild-type, i.e., unmodified.

[0585] Among the antibodies identified in FIG. **4** is 1E8. This murine anti-human VISTA antibody comprises the variable heavy and light chain polypeptides set forth below and was converted by the inventors into two human chimeric forms. The first chimeric antibody referred to herein as INX800 was obtained by the attachment of human IgG2 heavy and light constant region polypeptides to the 1E8 variable heavy and light chain polypeptides. In this first chimeric antibody none of the amino acid residues within the IgG2 constant regions were modified.

[0586] The second chimeric antibody referred to herein as INX801 was similarly obtained by the attachment of human IgG2 heavy and light constant region polypeptides to the 1E8 variable heavy and light chain polypeptides. In this second chimeric antibody the cysteine residue at position 127 within the human IgG2 kappa chain was converted into a serine. Otherwise none of the amino acid residues within the IgG2 constant regions were modified.

1E8 V_H Polypeptide

(SEQ ID NO: 57)

EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIG
EVYPDSSTINYTPSLKDKFIISRDNAKNTLYLQMIKVRSEDTALYYCAR
GRGDYWGQGTSVTVSS

1E8 V_L Polypeptide

(SEQ ID NO: 58)

DIQMTQSPASLSASVGETVTITCRASGNIHNYLSWYHQKQGKSPCILLV
YNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQNFWSTPFT
FGSGTKLEIKR.

Example 5: Evaluation of Putative Agonistic Anti-Human VISTA Antibodies in ConA Animal Model

[0587] The effects of both chimeric IgG2 antibodies and control antibodies were compared in a Concavalin A Hepatitis model. In this in vivo model different animals were predosed with 10 mg/kg of either chimeric IgG2 antibody (INX800 or INX801) or with a control antibody 3 hours prior to Concavalin A administration. 3 hours after antibody administration the mice were then dosed with ConA at 12 mg/kg. These animals and the controls were then bled by cardiac puncture 6 hours after ConA dosing. All of the mice appeared fine, no obvious morbidity or mortality.

[0588] The blood was then analyzed for cytokine expression. Particularly, a 32-plex was run using plasma obtained from the collected blood samples using conventional methods and cytokine test kit conventionally used for cytokine analysis. As shown in FIG. **5** the expression of several proinflammatory cytokines was significantly suppressed in the animals administered INX800 or INX801 antibodies compared to the control animals. Particularly, GM-CSF, IL-2, IL-4, IL-6, IL-17 and TNF-α levels were all significantly lower in the INX800 or INX801 treated animals compared to the controls. [Reduced] expression of these cytokines was substantially identical in the INX800 or INX801 treated animals.

[0589] Also, the expression of certain chemokines (keratinocyte derived chemokine or "KC") and macrophage inflammatory protein 2 (MIP-2) were substantially increased in the INX800 or INX801 treated animals compared to the controls. Again, the [increased] expression of these proteins was substantially identical in the INX800 or INX801 treated animals. Based on these results both INX800 and INX801 appear to be potent VISTA agonists as they appear to elicit the analogous immunosuppressive effects that VISTA elicits ion the expression of various inflammatory cytokines.

Example 6: Evaluation of Putative Agonistic Anti-Human VISTA Antibodies in Graft Versus Host Disease (GVHD) Animal Model

[0590] The effects of the same putative agonistic anti-human VISTA antibodies, INX800 and INX801 were also compared in a graft versus host disease (GVHD) animal model compared to untreated animals or controls treated with irrelevant antibody. In this animal model T cells were adoptively transferred into irradiated hosts and body-weight was measured as a read out of disease. Based on GVHD disease progression all of the Control mice (8/8) had to be euthanized. The results of these animal studies are shown in FIG. **6**. As shown none of the INX800 or INX801 [0/8] treated mice needed to be euthanized as GVHD was considerably depressed as a result of treatment with INX800 or INX801 antibody. Based on these results both INX800 and INX801 appear to be potent VISTA agonists as they appear to potently suppress GVHD immune responses.

Example 7: Effects of Putative Agonistic Anti-Human VISTA Antibodies on CD3-Driven T Cell Immune Responses

[0591] The effects of the same agonistic anti-human VISTA antibodies, INX800 and INX801 were also compared as to their potential to suppress CD3-driven T cell immune response. In these experiments plates were coated with OKT3 (2.5 μg/ml). T cells were the preincubated with antibody for 30 minutes. The antibody treated T cells were then added to the OKT3 coated plates and the T cells cultured on these plates for 72 hours. As a readout of the possible effects of the antibodies on CD3-driven T cell immune responses T cell proliferation was determined using Tritium incorporation methods, a well-accepted method for detecting T cell proliferation. As shown in FIG. **7**, T cell proliferation was considerably reduced in the cultured T cells which were treated with INX800 or INX801 antibodies compared to the control T cell cultures.

Example 8: Effects of Putative Agonistic Anti-Human VISTA Antibodies on Specific T Cell Populations and Total T Cell Numbers

[0592] Experiments were also affected in order to compare the possible effects of the same anti-human VISTA antibodies, INX800 and INX801, on the numbers of specific T cells as well as on the total number of T cells. These experiments were conducted in order to assess whether the observed effects of the subject anti-human VISTA antibodies on cytokines and T cells could have been attributable to cell depletion (a non-specific effect) rather than thee antibodies eliciting an immunosuppressive effect based on their promoting specific VISTA-mediated immunosuppressive effects on immunity.

[0593] Both agonistic anti-human VISTA antibodies, INX800 and INX801, had no significant effect on the

number of specific T cell populations, or on the total number of T cells. Moreover, the results with both the INX800 and INX801 antibodies were substantially the same. The results of exemplary experiments are in FIG. **8**.

[0594] Based thereon, the observed agonistic effects of INX800 and INX801 do not appear to be attributable to cell depletion. Rather, both of these antibodies appear to elicit an immunosuppressive effect on T cell activation/proliferation, GVHD immune responses and the expression of proinflammatory cytokines based on their promoting specific VISTA-mediated immunosuppressive effects on immunity.

Example 9: Summary of Effects of Different Agonistic Anti-Human VISTA Abs in Different Immune Models

[0595] As shown in Table 1 and 2 below the agonistic or immunosuppressive effects of different anti-human VISTA antibodies was evaluated having the sequences are in FIG. **4**. To date 12 different chimeric anti-human VISTA antibodies have been demonstrated to be immunosuppressive. Some of the results obtained to date are summarized in the Tables. Antibodies in Bin 1 all compete for binding to human VISTA but do not compete for VISTA binding with antibodies in Bin 2. Conversely, the anti-human VISTA antibodies in Bin 2 all compete for binding to human VISTA with each other but not with antibodies in Bin 1.

[0596] The antibody in Table 2 which is marked "inconclusive" elicited different effects, including immunosuppressive effects in the same assay or elicited ambiguous results for other reasons. As shown in Table 1 and 2 a total of 12 anti-human VISTA antibodies have been isolated which are immunosuppressive in MLR assays or ConA assays and/or other in vitro and in vivo assays or autoimmune, inflammatory or GVHD disease models and which mimic or agonize the immunosuppressive effects of human VISTA. Based on these results it is expected that other anti-human VISTA antibodies may be obtained by analogous methods including those having the same or different VISTA epitopic specificity.

[0597] Also, the experiments in FIG. **9** compare the effects of different anti-human VISTA antibodies in ConA assays and on the expression of select proinflammatory cytokines and inflammation markers, i.e., IL-2 γ interferon and IL-12p70.

TABLE 1

(HUMAN OR HUMANIZED ANTI-HUMAN VISTA ANTIBODIES)

mAb ID	Epitope Group	Origin	1st Assay MLR Prolif as IgG1	Kd, M	Status	Suppression as IgG2 In MLR and/or ConA Hep Assay	2nd Assay MLR Prolif. as IgG1)
INX903|VSTB95	1	HFA Hybr (His)	++	1.26E−10	Tested For immunosuppression	+	
INX904|VSTB103	1	Phage, original	−	6.36E−10	Tested For immunosuppression	+/−	yes
INX905|VSTB53	1	HFA Hybr (Fc)	++	2.64E−11	Tested For immunosuppression	++	
INX908|VSTB92	1	HFA Hybr (Fc)	++	9.34E−11	**Tested For immunosuppression	++	
INX900|VSTB50	2	HFA Hybr (Fc)	++	6.32E−10	Tested For immunosuppression	+/−	
INX901|VSTB56	2	HFA Hybr (Fc)	+/−	2.35E−11	Tested For immunosuppression	++	yes
INX902|VSTB63	2	HFA Hybr (Fc)	+/−	8.30E−10	Tested For immunosuppression	++	yes
INX906|VSTB54	2	HFA Hybr (Fc)	+/−	2.53E−11	Tested For immunosuppression	++	
INX907|VSTB66	2	HFA Hybr (Fc)	+/−	8.06E−11	Tested For immunosuppression	+	yes
INX909|VSTB67	1	HFA Hybr (Fc)	+/−	6.29E−11	To be tested		
INX913|VSTB85	1	HFA Hybr (InterFAD)	++	3.78E−11	To be tested		
INX914|VSTB97	1	Phage, original	+/−	7.68E−10	To be tested		
INX915|VSTB106	1	Phage, ILM	+/−	1.67E−10	To be tested		
INX916|VSTB107	1	Phage, ILM	++	8.90E−11	To be tested		
INX917|VSTB110	1	Phage, ILM	+/−	2.02E−10	To be tested		
INX918|VSTB113	1	Phage, ILM	++	4.33E−11	To be tested		
INX919|VSTB115	1	Phage, ILM	+/−	1.45E−10	To be tested		yes
INX910|VSTB73	2	HFA Hybr (His)	+/−	2.26E−09	To be tested		yes
INX911|VSTB76	2	HFA Hybr (His)	+/−	1.31E−09	To be tested		
INX912|VSTB84	2	HFA Hybr (InterFAD)	+	2.03E−09	To be tested		
VSTB100	1	Phage, original	+/−	1.48E−09			
VSTB101	1	Phage, original	+/−	3.18E−09			
VSTB102	1	Phage, original	+/−	2.98E−09			
VSTB104	1	Phage, original	+	6.75E−10			
VSTB105	1	Phage, ILM	+	1.15E−10			
VSTB108	1	Phage, ILM	+	4.94E−10			
VSTB109	1	Phage, ILM	+/−	1.02E−10			
VSTB111	1	Phage, ILM	++	1.71E−10			
VSTB112	1	Phage, ILM	++	1.56E−10			
VSTB114	1	Phage, ILM	++	1.52E−10			
VSTB116	1	Phage, ILM	++	2.13E−10			
VSTB49	1	HFA Hybr (Fc)	+	5.07E−10			
VSTB51	1	HFA Hybr (Fc)	++	1.04E−10			

TABLE 1-continued

(HUMAN OR HUMANIZED ANTI-HUMAN VISTA ANTIBODIES)

mAb ID	Epitope Group	Origin	1st Assay MLR Prolif as IgG1	Kd, M	Status	Suppression as IgG2 In MLR and/or ConA Hep Assay	2nd Assay MLR Prolif. as IgG1)
VSTB59	1	HFA Hybr (Fc)	+	1.06E−10			
VSTB65	1	HFA Hybr (Fc)	++	1.08E−09			
VSTB70	1	HFA Hybr (His)	+/−	2.23E−09			
VSTB81	1	HFA Hybr (InterFAD)	+/−	3.12E−10			
VSTB98	1	Phage, original	+	2.28E−09			
VSTB99	1	Phage, original	+/−	1.54E−09			
VSTB60	2	HFA Hybr (Fc)	+	3.56E−10			
VSTB78	2	HFA Hybr (InterFAD)	++	1.13E−09			
VSTB74	4	HFA Hybr (His)	−	5.62E−10			

TABLE 2

(MURINE ANTI-HUMAN VISTA ANTIBODIES)

Antibody	Bin	Suppressive?	MLR Prolif.	Kd, M
1E8*	1	Yes	++	NT
GG8	1	Yes	++	NT
GA1	2	Inconclusive	−	NT

*Shown to be immunosuppressive in 2 different IgG2 forms.

Example 10: Determination of Epitopes of Anti-Human VISTA Antibodies By B Cell Epitope Mapping

[0598] The epitopic specificity of some putative agonistic anti-human VISTA antibodies was determined using custom peptide arrays using fragments of human VISTA, using proprietary methods [ProArray Ultra™] Essentially, the determination of peptide-antibody binding was performed by incubation of antibody samples with a ProArray Ultra™ peptide microarray, followed by incubation with a fluorescently labeled secondary antibody. After several washing steps the ProArray Ultra™ arrays were dried and scanned using a high-resolution fluorescence microarray scanning.

[0599] All peptides (listed below) are synthesized separately, and then bound to the ProArray Ultra™ slide surface using ProImmune's proprietary technology. This optimized process ensures that peptides are presented on the array in such a manner as to closely mimic the properties of the corresponding protein region, circumventing the inherent physiochemical variation of the free peptides themselves and making a compatible, combined peptide and protein array platform. The test analytes (peptides and proteins) are dispensed onto the ProArray Ultra™ slide in discrete spots and appropriate gal-files enable exact alignment of the resulting array features back to the analyte deposited.

[0600] Peptide-antibody binding is determined by incubation of antibody samples (provided by the customer) with the ProArray Ultra™ slides, followed by incubation with a fluorescently labeled secondary antibody. After the final incubation and washing steps the microarrays are dried and scanned in a high-resolution microarray scanning system.

[0601] After scanning the fluorescently labeled ProArray Ultra™ slides, the scanner records an image which is evaluated using image analysis software—enabling interpretation and quantification of the levels of fluorescent intensities associated with each fluorescent spot on the scanned microarray slide. The peptide microarray was based on an overlapping peptide library synthesized from the human VISTA polypeptide sequence. Based on the sequence 15-mer microarray peptides, overlapping by 12 amino acids, were generated using ProImmune's ProArray Ultra™ technology. Details of the peptides synthesized are listed in TABLE 3 (below). 'Position' refers to the start and end amino acid within the polypeptide sequence from which the peptide was derived. Synthesized peptides were immobilised onto ProArray Ultra™ slides in 24 identical sub-arrays, each comprising test-peptides and control features in sextuplicate spots. The peptides are shown in Table 3 below.

TABLE 3

ProArray Ultra ™ Peptide Details

Peptide ID	Position	Sequence
1	1-15	FKVATPYSLY VCPEG (SEQ ID NO: 7)
2	4-18	ATPYSLYVCP EGQNV (SEQ ID NO: 8)
3	7-21	YSLYVCPEGQ NVTLT (SEQ ID NO: 9)
4	10-24	YVCPEGQNV TLTCRL (SEQ ID NO: 10)
5	13-27	PEGQNVTLTC RLLGP (SEQ ID NO: 11)
6	16-30	QNVTLTCRLL GPVDK (SEQ ID NO: 12)
7	19-33	TLTCRLLGPV DKGHD (SEQ ID NO: 13)
8	22-36	CRLLGPVDKG HDVTF (SEQ ID NO: 14)
9	25-39	LGPVDKGHD VTFYKT (SEQ ID NO: 15)

TABLE 3-continued

ProArray Ultra ™ Peptide Details		
Peptide ID	Position	Sequence
10	28-42	VDKGHDVTF YKTWYR (SEQ ID NO: 16)
11	31-45	GHDVTFYKT WYRSSR (SEQ ID NO: 17)
12	34-48	VTFYKTWYRS SRGEV (SEQ ID NO: 18)
13	37-51	YKTWYRSSRG EVQTC (SEQ ID NO: 19)
14	40-54	WYRSSRGEV QTCSER (SEQ ID NO: 20)
15	43-57	SSRGEVQTCS ERRPI (SEQ ID NO: 21)
16	46-60	GEVQTCSERR PIRNL (SEQ ID NO: 22)
17	49-63	QTCSERRPIR NLTFQ (SEQ ID NO: 23)
18	52-66	SERRPIRNLTF QDLH (SEQ ID NO: 24)
19	55-69	RPIRNLTFQD LHLHH (SEQ ID NO: 25)
20	58-72	RNLTFQDLHL HHGGH (SEQ ID NO: 26)
21	61-75	TFQDLHLHH GGHQAA (SEQ ID NO: 27)
22	64-78	DLHLHHGGH QAANTS (SEQ ID NO: 28)
23	67-81	LHHGGHQAA NTSHDL (SEQ ID NO: 29)

TABLE 3-continued

ProArray Ultra ™ Peptide Details		
Peptide ID	Position	Sequence
24	70-84	GGHQAANTS HDLAQR (SEQ ID NO: 30)
25	73-87	QAANTSHDL AQRHGL (SEQ ID NO: 31)
26	76-90	NTSHDLAQR HGLESA (SEQ ID NO: 32)
27	79-93	HDLAQRHGL ESASDH (SEQ ID NO: 33)
28	82-96	AQRHGLESAS DHHGN (SEQ ID NO: 34)
29	85-99	HGLESASDH HGNFSI (SEQ ID NO: 35)
30	88-102	ESASDHHGN FSITMR (SEQ ID NO: 36)
31	91-105	SDHHGNFSIT MRNLT (SEQ ID NO: 37)
32	94-108	HGNFSITMR NLTLLD (SEQ ID NO: 38)
33	97-111	FSITMRNLTLL DSGL (SEQ ID NO: 39)
34	100-114	TMRNLTLLDS GLYCC (SEQ ID NO: 40)
35	103-117	NLTLLDSGLY CCLVV (SEQ ID NO: 41)
36	106-120	LLDSGLYCCLV VEIR (SEQ ID NO: 42)
37	109-123	SGLYCCLVVEI RHHH (SEQ ID NO: 43)

TABLE 3-continued

ProArray Ultra ™ Peptide Details		
Peptide ID	Position	Sequence
38	112-126	YCCLVVEIRH HHSEH (SEQ ID NO: 44)
39	115-129	LVVEIRHHHS EHRVH (SEQ ID NO: 45)
40	118-132	EIRHHHSEHR VHGAM (SEQ ID NO: 46)
41	121-135	HHHSEHRVH GAMELQ (SEQ ID NO: 47)
42	124-138	SEHRVHGAM ELQVQT (SEQ ID NO: 48)
43	127-141	RVHGAMELQ VQTGKD (SEQ ID NO: 49)
44	130-144	GAMELQVQT GKDAPS (SEQ ID NO: 50)
45	133-147	ELQVQTGKD APSNCV (SEQ ID NO: 51)
46	136-150	VQTGKDAPS NCVVYP (SEQ ID NO: 52)
47	139-153	GKDAPSNCV VYPSSS (SEQ ID NO: 53)
48	142-156	APSNCVVYPS SSQDS (SEQ ID NO: 54)
49	145-159	NCVVYPSSSQ DSENI (SEQ ID NO: 55)
50	148-162	VYPSSSQDSE NITAA (SEQ ID NO: 56)

[0602] The results of this epitope analysis with particular anti-human VISTA antibodies are summarized in FIG. **4** and in the examples below.

Example 11: Epitope Binning Assay

[0603] Additionally the epitopic binding properties of some anti-human VISTA antibodies having sequences shown in FIG. **4** were characterized by placing these antibodies into different epitope "bins" based on their binding characteristics as described below.

[0604] Methods: ProteOn XPR36 system (BioRad) was used to perform epitope binning. ProteOn GLC chips (Bio-Rad, Cat #176-5011) were coated with two sets of 6 monoclonal antibodies (mAbs) using the manufacturer instructions for amine-coupling chemistry (BioRad, cat #176-2410). Competing mAbs were pre-incubated in excess (250 nM final concentration) with human VISTA (25 nM final concentration) for 4 hours at room temperature and 6 at a time were run over the chip coated with the panels of coated mAbs with an association time of 4 minutes followed by dissociation for 5 minutes. Following each run, the chips were regenerated with 100 nM phosphoric acid.

[0605] The data analysis involved grouping all sensorgrams by ligand and applying an alignment wizard, which automatically performs an X and Y axis alignment, and artifact removal. An Interspot correction was then applied to the data.

[0606] A non-competing mAb was defined as having a binding signal the same or >AI signal (binding to human VISTA only). A competing mAb was defined as having binding signal AI signal {i.e., binding to human VISTA only). For example VSTB49 and VSTB51 complexed with VISTA did not bind to the VSTB85 coated on the chip and therefore were classified as competing for the same binding site on VISTA as VSTB85. The results of this binning analysis with particular anti-human VISTA antibodies are summarized in FIG. **4**.

Example 12: Epitope Mapping of Anti-VISTA Antibodies Using Hydrogen/Deuterium (H D) Exchange Studies

[0607] Antibody epitopes of anti-VISTA antibodies may be identified by various methods such as alanine scanning and Hydrogen/Deuterium (H D) Exchange and overlapping peptide arrays as described in the previous Example. Another exemplary means for identifying epitopes of putative agonistic anti-human VISTA antibodies is described below.

[0608] To identify the epitopes for VSTB50, 60, 95 and 112 on human VISTA, solution hydrogen/deuterium exchange-mass spectrometry (HDX-MS) was performed using the corresponding Fabs. For H/D exchange, the procedures used to analyze the Fab perturbation were similar to that described previously (Hamuro et al, *J. Biomol. Techniques* 14:171-182, 2003; Horn et al, Biochemistry 45:8488-8498, 2006) with some modifications. Fabs were prepared from the IgGs with papain digestion and Protein A capture using Pierce Fab Preparation Kit (Thermo Scientific, Cat #44985). The human VISTA protein sequence contains six N-linked glycosylation sites. To improve the sequence coverage, the protein was deglycosylated with PNGase F. The deglycosylated VISTA protein was incubated in a deuterated water solution for predetermined times resulting in deuterium incorporation at exchangeable hydrogen atoms. The deuterated VISTA protein was in complex with a Fab of VSTB50, VSTB60, VSTB95 or VSTB112 in 46 deuterium oxide (D20) at 4° C. for 30 sec, 2 min, 10 min and 60 min.

The exchange reaction was quenched by low pH and the proteins were digested with pepsin. The deuterium levels at the identified peptides were monitored from the mass shift on LC-MS. As a reference control, VISTA protein was processed similarly except that it was not in complex with the Fab molecules. Regions bound to the Fab were inferred to be those sites relatively protected from exchange and, thus, containing a higher fraction of deuterium than the reference VISTA protein. About 94% of the protein could be mapped to specific peptides.

[0609] The solution HDX-MS perturbation maps of VISTA with VSTB50/VSTB60, and VSTB95/VSTB112 were mapped and two epitope groups were identified. Anti-VISTA VSTB50 recognizes the same epitope as VSTB60 does; VSTB95 binds to another epitope region as VSTB112 does on VISTA. Anti-VISTA VSTB50 and 60 share the same epitope which comprises segments, 103 NLTLLDSGL111 (SEQ ID NO:59), and 136VQTGKDAPSNC146 (SEQ ID NO:60) Anti-VISTA VSTB95 and VSTB112 appear to target similar epitopes, comprising segments 27PVDKGHDVTF36 (SEQ ID NO:61), and 54RRPIRDLTFQDL65 (SEQ ID NO:62). These HDX-MS results provide the peptide level epitopes for exemplary anti-VISTA antibodies having the sequences identified in FIG. **4**. There were no overlapping epitope regions for these two epitope groups. These results are in agreement with the previous competition binning data in that they do not compete with each other. Again the epitope analysis results for various anti-human VISTA antibodies analyzed as described herein is summarized in FIG. **4**.

Example 13: Evaluation of the Role of the Human IgG2 Backbone on α-Human VISTA Antibody INX901 Agonist/Immune-Suppressive Activity in Different In Vitro and In Vivo Models

[0610] Antibodies on a native human IgG2 backbone exist as a mixture of isoforms caused by disulfide bond shuffling among cysteines present in the heavy chain hinge, CH1, and light chain (Zhang, A., (2015), "Conformational difference in human IgG2 disulfide isoforms revealed by hydrogen/deuterium exchange mass spectrometry", *Biochemistry,* 54(10), 1956-1962; FIG. **10**). These isoforms were assessed by RP-HPLC (FIG. **10**), based on methods developed by Dillon et al., "Optimization of a reversed-phase high-performance liquid chromatography/mass spectrometry method for characterizing recombinant antibody heterogeneity and stability", J Chromatography A, 1120(1), 112-120. The optimized method used a shallower and higher organic mobile phase B content relative to that in Dillon (id). Separate A and B forms enriched from INX901 were prepared closely following the conditions reported in Dillon (id) but combined with a buffer exchange back into DPBS and an endotoxin removal procedure employed subsequent to the enrichment reactions (FIG. **11**).

[0611] In the course of preparing these experiments it was observed that reversion of the A-enriched form occurs more quickly than expected, and at lower residual redox reagent concentrations than expected. Utilization of a fast-spin, size-exclusion based desalting procedure was therefore employed, which appeared to largely prevent this reversion. As shown in panel (A) in FIG. **10** disulfide shuffling leads to isoforms A and B, along with the transition for A/B (reproduced from Zhang, A. et al., 2015). (B) Isoforms are distinguishable by RP-HPLC (figure from Zhang, A. et al., 2015). (C) Observed RP-HPLC chromatogram for INX901.

[0612] The inventors optimized RP-HPLC Method for detecting IgG2 isoforms is described below. In FIG. **11**: (Black line, top) the chromatogram shows a dominant left-most peak defining the B-form. (Red line, bottom) Chromatogram shows a dominant right peak defining the A-form.

Optimized RP-HPLC Methods for Isoform Detection

Mobile Phase A Preparation (0.1% v/v TFA in Water):

[0613] 1. Measured 1.0 L Milli-Q water in a 1.0 L graduated cylinder

[0614] 2. Added 1.0 mL of TFA to the 1 L of water using a 1 mL glass Hamilton syringe

[0615] 3. Transferred the solution to a 1 L bottle, mixed well.

[0616] 4. Expiry is 2 weeks after preparation

Mobile Phase B Preparation (70% v/v IPA, 20% v/v ACN, 9.9% v/v Water, 0.1% v/v TFA):

[0617] 1. Measured 700 mL IPA into a 1.0 L graduated cylinder

[0618] 2. Measured 200 mL ACN into a 250 mL graduated cylinder and transferred to the 1.0 L graduated cylinder containing the 700 mL IPA

[0619] 3. Added Milli-Q water to the 1.0 L graduated cylinder containing the 700 mL IPA and 200 mL ACN until the liquid reached to 1.0 L mark

[0620] 4. Added 1.0 mL of TFA to the 1 L of water using a 1 mL glass Hamilton syringe

[0621] 5. Transferred the solution to a 1 L bottle, mixed well.

[0622] 6. Expiry is 2 weeks after preparation

RP-HPLC Chromatography Conditions

[0623] 1. Column A (large bore): Zorbax 300SB-C8, 5 μm, 2.1×150 mm, <<OR>>

[0624] 2. Column B (narrow bore): Zorbax 300SB-C8, 3.5 μm, 1×50 mm

[0625] 3. Mobile Phase A: 0.1% v/v TFA in water

[0626] 4. Mobile Phase B: 70% v/v IPA, 20% v/v ACN, 9.9% v/v water, 0.1% v/v TFA

[0627] 5. Flow rate: 0.5 mL/min for Column A or 0.25 mL/min for Column B

[0628] 6. Column compartment: 75.0±1.0° C.

[0629] 7. Detection: 214 nm

[0630] 8. RP-HPLC mobile phase gradient (Table below)

Time (min)	Mobile Phase B %
0	15
2	26
34	36
35	75
36	15
40	15

INX901 Disulfide Isoform Enrichment Methods

B-form Enrichment

[0631] 1. Into endotoxin free non-pyrogenic tube, add:

[0632] 2.1 mL of INX901 (5.66 mg/mL)

[0633] 792.6 μL 1 M Tris pH 8.0

[0634] 495.4 μL endo-free water

[0635] 396.3 additional endo-free water

[0636] 237.8 μL of 100 mM Cysteine

[0637] 39.6 μL of 100 mM Cystamine

[0638] 2. Finger vortex (lightly), then place capped at 2-8° C. for 24 hr

[0639] 3. Soaked Pall microsep spin-concentrator in 0.3M NaOH 2 hr at RT, then rinsed 3× with 10× DPBS, then 3× with endo-free water. Air dried in BSC before use

[0640] 4. Followed vendor's instructions for regenerating 0.5 mL endotoxin removal column, using the 0.2N NaOH/95% ethanol (2 hrs at RT) option for step 3; used 1×DPBS as final equilibration buffer

[0641] 5. Concentrated ~4,020 μL of reaction (from Step 2) in a separate PALL microsep (as prepared above).

[0642] 6. Concentrated at 2,500× G for 35 min to less 0.4 mL (≥10×) then re-diluted with 4 mL 1× DPBS, repeated 2 additional times

[0643] 7. Concentrated at 2,500×G for 15 min to below 2 mL, then added back 1×DPBS to 2 mL

[0644] 8. Added all 2 mL of buffer exchanged sample to the regenerated, spun dried, bottom capped endotoxin removal column, capped the top tightly, inverted, placed at room temp-inverted 3 more times every ~20 minutes, then spun out the sample into non-pyrogenic tube (1 min at 500×G, as per Vendor's instructions), placed at 2-8° C.

A-Form Enrichment

[0645] 1. Into endotoxin free non-pyrogenic tube, add:

[0646] 1750 μL INX901 (6.2 mg/mL)

[0647] 370 μL endo-free water

[0648] 700 μL 1M Tris pH8.0

[0649] 435 μL 8M GdCl

[0650] 210 μL 0.1 M Cysteine HCl (made fresh from 1 M stock)

[0651] 35 μL 0.1 M Cystamine −2HCl (made fresh from 1 M stock) (Final volume 3500 μL)

[0652] 2. Finger vortex (lightly), then place capped at 2-8° C. for 24 hr

[0653] 3. Prepared #7-2 mL Zeba spin columns (Thermo P/N 89890) as per vendor's instructions, equilibrating into 1×Dulbecco's Phosphate Buffered Saline (DPBS).

[0654] 4. Loaded 500 μL of the above reaction mixture onto each of the #7, and spun 2 minutes at 1000×G (also as per vendor's instructions), collecting into clean pyrogen free tubes.

[0655] 5. Placed in de-pyrogenated PALL microsep, spun total of 1 hour, 10 minutes, concentrated to approximately 1.7 mL at approximately 5 mg/mL

[0656] 6. Added all ~1.7 mL above to one 0.5 mL endotoxin removal spin column (Thermo P/N 88274) prepared as per Vendor's instructions (including overnight in 0.2 M NaOH at room tempo), equilibrated into 1×DPBS. Left at room temp approximately 1 hr, then placed at 4° C. for approximately another 1 hr, in both cases inverting the capped tube about every 15 minutes.

[0657] 7. Recovered prep by spinning 500×G for 1 minute (also as per vendor's instructions).

[0658] 8. Recovered volume: approximately 1.3 mL at 4.61 mg/mL (all concentrations based on the NanoDrop's built-in IgG extinction coefficient of 0.73)

IgG2 A- and B-Locked Variants

[0659] Specific substitutions to the amino acid sequence of IgG2 are capable of preventing disulfide shuffling, and depending on the mutation will result in a locked conformation that is either A-like or B-like (Martinez, et al., (2008). "Disulfide connectivity of human immunoglobulin G2 structural isoforms", *Biochemistry,* 47(28), 7496-7508; Allen, et al., (2009), "Interchain disulfide bonding in human IgG2 antibodies probed by site-directed mutagenesis", *Biochemistry,* 48(17), 3755-3766.

[0660] The inventors therefore designed INX901 and INX908 variants with either the C233S (A-locked) or C127S (B-locked) mutation (Eu numbering) to match the IgG2 variants used by White et al., (2015), "Conformation of the human immunoglobulin G2 hinge imparts superagonistic properties to immunostimulatory anticancer antibodies", *Cancer Cell,* 27(1), 138-148.

[0661] Constant heavy chain sequences are listed below.

```
IgG2 C233S (A-locked)
                                        (SEQ ID NO: 63)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG

VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV

ERKCSVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH

EDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK

EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT

CLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKS

RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

IgG2 C127S (B-locked)
                                        (SEQ ID NO: 64)
ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG

VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV

ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH

EDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK

EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT

CLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKS

RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
```

Silent Fc Variants

[0662] The inventors designed INX901 and INX908 variants with a silent Fc region by introducing the following point mutations on an IgG1 backbone: L234A/L235A/G237A/P238A/H268A/A330S/P331S (McCarthy et al., (2015) U.S. patent application Ser. No. 14/818,864. Washington, DC: U.S. In one type of variant (INX901Si and INX908Si), the CH1/hinge region of the heavy constant region is native IgG1, which does not support the disulfide

shuffling of a native IgG2 (FIG. **12**, middle). In a second type of variant (INX901HSi and INX908HSi), the CH1/hinge region is native IgG2, which does support disulfide shuffling (White, A. L. et al., 2015) (FIG. **12**, bottom). Constant heavy chain sequences for both types of variants are listed below.

```
IgG1 with silent Fc (INX901Si and INX908Si)
                                        (SEQ ID NO: 65)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG

VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV

EPKSCDKTHTCPPCPAPEAAGASSVFLFPPKPKDTLMISRTPEVTCVVV

DVSAEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW

LNGKEYKCKVSNKALPSSIEKTISKAKGQPREPQVYTLPPSREEMTKNQ

VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT

VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

IgG2 CH1/hinge + IgG1 silent Fc (INX901HSi and
INX908HSi)
                                        (SEQ ID NO: 66)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG

VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV

ERKCCVECPPCPAPEAAGASSVFLFPPKPKDTLMISRTPEVTCVVVDVS

AEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG

KEYKCKVSNKALPSSIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL

TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK

SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
```

[0663] The experiments in FIG. **12** compare the immune properties of INX901 Fc-silent variants with respect to disulfide shuffling. (Top) INX901 on an IgG2 backbone exhibits an expected mixture of A, A/B, and B isoforms. (Middle) INX901Si on a silent IgG1 backbone exists as a single isoform. (Bottom) INX901HSi possesses an IgG1 silent Fc region with a CH1/hinge from IgG2, which enables disulfide shuffling equivalent to native IgG2. These results indicate that FcR binding appears to affect the agonist properties of the inventive antibodies.

Example 14: Function of INX901 and INX908 in Various Ig Backbones to Determine Requirement of Hinge and Fc Regions

[0664] We conducted experiments to assess the functional requirements of the CH1/hinge and Fc regions of the heavy chain of the anti-human VISTA antibodies, INX901 and INX908. In their original state, both molecules are on native human IgG2 backbones, and are therefore mixtures of conformationally distinct isoforms resulting disulfide shuffling. The high cell density mixed lymphocyte reaction (MLR) was chosen for these studies as previous data indicates that this assay provides a robust read out of functionality for both INX901 and INX908. The following modifications of INX901 and/or INX908 were made to investigate whether specific isoforms are responsible for function: biochemical skewing to either the A or B isoform, genetic modifications to "lock" the conformation into the A or B form, and chimeric molecules where the Fc was silenced and the CH1/hinge region came from either IgG1, in which disulfide shuffling does not occur, or IgG2, which allows for native disulfide shuffling.

[0665] The results of the assay indicate that INX901 and INX908 retain function regardless of whether in the A form, B form, or the mixture of forms that characterizes a native IgG2. Additionally, both INX901 and INX908 require an active Fc region for functionality.

[0666] The MLR is a standard immunological assay that depends upon MHC class I and II mismatching to drive an allogeneic T cell response. Peripheral blood mononuclear cells are isolated from two mismatched individuals, incubated together and as a result of these mismatches, proliferation and cytokine production occurs. High cell density conditions (HCD), meaning cultures with $>1\times10^7$ cells/ml, have previously been reported to elucidate agonistic functions of antibodies in vitro. Our previous data indicates that both INX901 and INX908 can suppress the expression of TNFα under HCD conditions in the MLR.

[0667] The HCD MLR assay was used to assess the function of INX901 and INX908 following either genetic or biochemical modifications with respect to IgG2 disulfide isoforms and/or Fc silencing of each antibody. Prior to running the MLR, each antibody was confirmed to bind recombinant VISTA via ELISA. INX901 was sent to Elion, LLC (Louisville, CO) where it was modified by redox to either be predominantly A form (INX901 A skew) or B form (INX901 B skew). Skewing was confirmed by RP-HPLC as described in the prior example. (FIG. **11**). Each antibody, as well as the parental INX901, was diluted in a dose response in the HCD MLR and cytokine production was measured by Luminex. Previous data has indicated that TNFα and/or IL-2 are robust readouts for antibody function of the parental INX901 antibody. In two separate MLRs, both TNFα and IL-2 were reduced by INX901 parental, INX901 A skew and INX901 B skew compared to the IgG2 control (FIG. **13**).

[0668] To confirm the data from FIG. **13**, additional variants of INX901 were made with mutations to generate locked variants in either the A form or the B form. Additionally, chimeric versions of INX901 were made with fully silent Fc regions to test the function of the Fc domain. INX901 Si is a fully silent IgG1 antibody. INX901 HSi has a fully silent IgG1 Fc, but also possesses an IgG2 CH1/hinge region that enables disulfide shuffling that is indistinguishable from a native IgG2. Prior to running the MLR, each antibody was confirmed to bind recombinant VISTA via ELISA. Confirming the data from the biochemical skewing, both the A lock and B locked versions of INX901 were able to reduce the production of both IL-2 and TNFα (FIG. **14**). In contrast, both the Si and HSi versions of INX901 were unable to reduce production of IL-2 and TNFα (FIG. **14**).

[0669] To confirm the data from FIG. **14**, identical mutations were made to the INX908 antibody to generate locked variants in either the A form or the B form. Additionally, chimeric versions of INX908 were made with fully silent Fc regions to test the function of the Fc domain. INX908 Si is a fully silent IgG1 antibody. INX908 HSi has a fully silent IgG1 Fc but contains the IgG2 CH1/hinge region. Prior to running the MLR, each antibody was confirmed to bind recombinant VISTA via ELISA. Confirming the data with the INX901 variants, both the A lock and B locked versions of INX908 was able to reduce the production of both IL-2

and TNFα (FIG. **15**). In contrast, both the Si and HSi versions of INX908 were unable to reduce production of IL-2 and TNFα (FIG. **15**).

Example 15: Discontinuous Epitope Mapping of Agonist Antibodies Using PEPPSCAN Methods

[0670] Pepscan uses peptide arrays to determine both linear and discontinuous epitopes. This methodology is an accepted method used by many researchers and companies to ascertain antibody epitopes. FIG. **16** schematically describes the Pepscan® technology used to identify linear and discontinuous epitopes bound by various agonist anti-human VISTA antibodies according to the invention.

The Principles of Clips Technology

[0671] CLIPS technology structurally fixes peptides into defined three-dimensional structures. This results in functional mimics of even the most complex binding sites. CLIPS technology is now routinely used to shape peptide libraries into single, double or triple looped structures as well as sheet- and helix-like folds. The CLIPS reaction takes place between bromo groups of the CLIPS scaffold and thiol sidechains of cysteines. The reaction is fast and specific under mild conditions. Using this elegant chemistry, native protein sequences are transformed into CLIPS constructs with a range of structures.

Combinatorial Clips Library Screening in Detail

[0672] CLIPS library screening starts with the conversion of the target protein into a library of up to 10,000 overlapping peptide constructs, using a combinatorial matrix design. On a solid carrier, a matrix of linear peptides is synthesized, which are subsequently shaped into spatially defined CLIPS constructs. Constructs representing both parts of the discontinuous epitope in the correct conformation bind the antibody with high affinity, which is detected and quantified. Constructs presenting the incomplete epitope bind the antibody with lower affinity, whereas constructs not containing the epitope do not bind at all. Affinity information is used in iterative screens to define the sequence and conformation of epitopes in detail. The results of this epitope analysis are summarized below.

Antibodies INX901, INX902, INX904, INX906, INX907, INX908

[0673] When tested under moderate stringency conditions antibodies INX901, INX902, INX904, INX906, INX907, INX908 strongly bound linear and conformational epitope mimics. Bound peptides contain core sequences $_{48}$NVTLTCRLLGPV$_{60}$ (SEQ ID NO:67), $_{79}$EVQTCSERRPIR$_{90}$(SEQ ID NO:68), $_{123}$SDHHGNFS$_{130}$ (SEQ ID NO:69) and $_{153}$HHHSEH$_{158}$ (SEQ ID NO:70), where peptide stretch $_{79}$EVQTCSERRPIR$_{90}$ (SEQ ID NO:68) is the dominant part of the epitope.

[0674] Additional analysis of data recorded with linear epitope mimics allowed us to identify residues that are important for binding for INX904, INX906, INX907 and INX908, as double Ala mutants on certain positions notably decreased signal intensities. In particular, replacement of residues CR within $_{48}$NVTLTCRLLGPV$_{60}$ (SEQ ID NO:71) affects binding of INX906, INX907 and INX908. Also the replacement of residues TC within $_{79}$EVQTCSERRPIR$_{90}$ (SEQ ID NO:68) notably affects binding of INX904 and INX907.

Antibody INX800

[0675] When tested under moderate stringency conditions antibody INX800 did not detectably bind linear and simple constrained epitope mimics, but showed detectable binding with discontinuous epitope mimics. Analysis of data obtained with discontinuous epitope mimics suggest that antibody INX800 recognizes a discontinuous epitope with core sequences s$_3$TCRLLGPVDKG$_{63}$(SEQ ID NO:72), 101HGGHQAA$_{107}$(SEQ ID NO:73), $_{121}$SASDHHGNFS$_{130}$ (SEQ ID NO:74) and $_{153}$HHHSEHRVHGAM$_{164}$ (SEQ ID NO:75), where sequence $_{153}$HHHSEHRVHGAM$_{164}$ (SEQ ID NO:76) represents the dominant recognition site.

Antibodies INX803 AND INX804

[0676] When tested under high stringency conditions antibodies INX803 and INX804 did not bind any peptide present on the array. When tested under moderate stringency conditions both antibodies bound discontinuous epitope mimics. Cumulative analysis of binding profiles suggests that both antibodies similarly recognize peptide stretches $_{52}$LTCRLLGPV$_{60}$ (SEQ ID NO:77), $_{79}$EVQTCSERRPIR$_{90}$ (SEQ ID NO:78), $_{98}$HLHHGGHQAA$_{107}$ (SEQ ID NO:79), $_{123}$SDHHGNFS$_{130}$(SEQ ID NO:80), $_{153}$HHHSEHRVHGAM$_{164}$(SEQ ID NO:81), where region $_{52}$LTCRLLGPV$_{60}$ (SEQ ID NO:77) is the dominant recognition site.

Antibody INX900

[0677] When tested under high stringency conditions antibody INX900 very weakly bound linear epitope mimics with core sequence $_{79}$EVQTCSERRPIR$_{90}$ (SEQ ID NO:68). Notably higher binding was observed with discontinuous epitope mimics, which in addition to sequence $_{79}$EVQTCSERRPIR$_{90}$ (SEQ ID NO:68) contain core sequences $_{56}$LLGPVDKGHDVTFYK$_{70}$ (SEQ ID NO:82), $_{113}$LAQRHGLESASDHHG$_{127}$(SEQ ID NO:83), $_{153}$HHHSEHRVHGAM$_{164}$(SEQ ID NO:84).

Antibody INX903

[0678] When tested under high stringency conditions antibody INX903 did not bind linear epitope mimics, but weakly bound conformational epitope mimics. Analysis of recorded intensity profiles suggests that the antibody recognizes a discontinuous epitope composed of core sequences $_{79}$EVQTCSERR$_{87}$(SEQ ID NO:85), $_{93}$TFQDLHLHHGGHQAA$_{107}$(SEQ ID NO:86), $_{146}$CLVVEIRHHHSEH$_{158}$(SEQ ID NO:87), where sequence $_{79}$EVQTCSERR$_{87}$ (SEQ ID NO:85) is the core of the epitope.

Antibody INX905

[0679] When tested under high stringency conditions antibody INX905 bound linear peptides with core sequence $_{79}$EVQTCSERRP$_{88}$(SEQ ID NO:88). Data acquired with double Ala mutants indicate that motif RR within $_{79}$EVQTCSERRP$_{88}$ (SEQ ID NO:88) is critical for the recognition. Intensity profiles recorded with discontinuous epitope mimics suggest that addition of peptide sequences

$_{53}$TCRLLGPVDKG$_{63}$ (SEQ ID NO:89), $_{123}$SDHHG$_{127}$ (SEQ ID NO:90) and $_{153}$HHHSEHRVHGAM$_{114}$(SEQ ID NO:91) augments binding of the antibody. FIG. **17** shows that most agonist anti-human VISTA antibodies bind to the same core sequence. FIG. **18** also summarizes the epitope results. FIG. **19** shows the epitopes bound by agonist anti-human VISTA antibodies and identifies important residues involved in binding.

Example 16: Use of Agonist Anti-VISTA Antibodies in Treating Inflammatory Bowel Disease

[0680] Intestinal inflammation is initiated with syngeneic splenic CD4$^+$ CD45^{RBhu} T cell adoptive transfer into T and B cell deficient recipient mice. The CD4+ CD45^{RBhi} T cell population contains mainly naïve T cells primed for activation that are capable of inducing chronic small bowel and colonic inflammation. This method provides precise initiation of disease onset and a well-characterized experimental time course permitting the kinetic study of clinical features of disease progression in mice. Intestinal inflammation induced by this method shares many features with human IBD, including chronic large and small bowel transmural inflammation, pathogenesis driven by cytokines such as TNF and IL-12, and systemic symptoms such as wasting. Thus, it is an ideal model system for studying the pathogenesis of human IBD.

Materials & Methods

[0681] INX901 treatment was administered at days 0, 3, and 6 following DDE1 CD4$^+$ CD45RBhi spleen cell transfer. At day 14, peripheral blood was analyzed by flow cytometry. Mouse weight was recorded during the whole experiment. As soon as the mice started losing weight, at day 46 the experiment was terminated and cardiac blood and spleen cells were analyzed by flow cytometry; colons were dissected and processed for histology after being measured. There were two treatment groups: human IgG2 and INX901 (8 mice each), as well as a control group (8 mice) that received a whole CD4$^+$ cell iv injection and is a negative control for disease development.

Mice

[0682] Donor mice: Human VISTA knock-in (DDE1) mice have the human VISTA cDNA knocked-in in place of the mouse VISTA gene, and express only human VISTA both at RNA and protein level. The mice are bred at Sage Labs (Boyertown, PA). The mice, aged 8-12 weeks, first transited for 3 weeks in the quarantine facility, and then were transferred to our regular facility. 4-month old male DDE1 mice were used.

[0683] Recipient mice: 9 weeks old male Rag1 Knockout mice were purchased from the Jackson Lab (B6.129S7-Rag$^{1tm1Mom/J}$).

Spleen Cell Isolation and Transfer

[0684] CD4$^+$ T cells were isolated by negative selection using the StemCell EasySep™ Mouse Naïve CD4+ T cell isolation kit (#19765), skipping the memory T cell depletion step. One DDE1 spleen was mechanically dissociated between 2 glass slides and CD4 T cells were isolated following manufacturer instructions. Briefly spleen cells were resuspended in PBS 2% FBS, 1 mM EDTA. They were then incubated with rat serum and CD4 T cell isolation cocktail. After 7.5 min, magnetic beads were added and incubated for 2.5 min. The tubes containing spleen cells and beads are then placed onto a magnet and after 2.5 minutes, the unbound cells are transferred into a new tube. We obtained a total of 11.3×10^6 CD4 T cells. Each control mouse received intravenous (i.v.) injection of 0.5×10^6 cells in 200 μl.

[0685] Naïve CD4 T cell transfer: T cell isolation was conducted on 11 DDE1 spleens. Naïve CD4+ were isolated by negative selection using the StemCell EasySep™ Mouse Naïve CD4$^+$ T cell isolation kit (#19765) following manufacturer instructions as described above adding the memory T cell depletion step.

[0686] To select CD45RB+ cells, CD4$^+$ cells were resuspended at 100×10^6 cells/ml in PBS 2% FBS, 2 mM EDTA (binding buffer) and anti CD45RB PE antibody and incubated for 10 min at 4° C. After 2 washes in binding buffer, anti PE MicroBeads (Miltenyi #130-048-801) were added and incubated for 15 min at 4° C. After 2 washes in binding buffer, cells were resuspended in 1 ml of binding buffer and placed on 2 Miltenyi MS columns. Cells were eluted in twice 1 ml per column. A total of 5.6×10^6 CD4$^+$ CD45RB$^+$ cells were obtained. Mice received by i.v. injection 0.329×10^6 cells in 200 μl.

[0687] Cell purity was evaluated by flow cytometry using the following panel:

[0688] CD4 APC-Cy7 (BioLegend at 1:200)

[0689] CD45RB PE (BioLegend at 1:200)

[0690] Yellow Live/Dead (Invitrogen at 1:1000)

Anti-Human VISTA Antibodies and Dosage

[0691] INX901 and control human IgG2 were dosed at 3 mg/kg. At day 0, antibodies were injected i.p. 3 hours before i.v. cell transfer into recipient Rag1 KO mice. Mice were then dosed on day 3 and 6 via intraperitoneal (i.p.) injections. Control group received human IgG2 (Lot AB150073-4.7 mg/mL). Treated group received INX901 (Lot BP-021-016-14-5.46 mg/mL).

Evaluation of "Absolute" Immune Cell Change in Peripheral Blood

[0692] At day 14 after donor cell transfer, donor CD4 T cell accumulation and activation status were evaluated by flow cytometry on retro-orbital bleed. Briefly, blood was collected in Eppendorf tubes containing 10 μl of heparin. To obtain a close to absolute cell count, 100 μl of whole blood was stained by directly adding the antibody cocktail+mouse Fc block in 10 μl. After 30 min at 4° C., 760 μl ofACK lysis buffer is added to each sample. After 20 min incubation, samples are washed once in PBS. Samples were run on a MACSQuant flow cytometer and analyzed with the FlowJo program.

Antibody Cocktail

Fluorophore	FITC	PE	PerCP Cy5.5	PE-Cy7	APC	eFluor780	BV421	BV510
Antigen	CD62L	CD45RB	CD11b	CD25	PD1	CD44	CD4	CD45
Dilution	1:200	1:200	1:200	1:200	1:200	1:200	1:200	1:200

Tissue Collection for Histology

[0693] On day 46, mice were euthanized and the colon dissected. After length measurement, the colons were emptied, transferred in cassettes. After o/n in 10% formalin, the cassettes were transferred into 70% ethanol and processed by the Pathology department for paraffin embedded, sectioning and H&E staining.

Evaluation of Immune Cell Change in Spleen at Terminal Time Point

[0694] Briefly, spleens were collected and mechanically dissociated. Following ACK lysis, cells were washed and stained with the following antibody cocktail. Samples were run on a MACSQuant flow cytometer and analyzed with the FlowJo program.

Antibody Cocktail

Fluorophore	FITC	PE	PerCP Cy5.5	PE-Cy7	APC	eFluor780	BV421	BV510
Antigen	CD62L	CD45RB	CD11b	CD25	FoxP3	CD44	CD4	LD Yellow
Dilution	1:200	1:200	1:200	1:200	1:200	1:200	1:200	1:1000

INX901 Treatment Leads to Decreases in CD4 T Cell Numbers in Peripheral Blood

[0695] Analysis of immune cell changes in peripheral blood at day 14 showed decreases in CD4 T cells both as absolute count or as a fraction of $CD5^+$ cells and the CD4 T cells that remained were mainly $CD45RB^{hi}$ (FIG. **20**). As shown therein absolute numbers in 100 μl of blood (left graph); frequencies of $CD45^+$ cells (center graph); frequencies of $CD4^+$ cells (right graph) (n=8 per group, SEM, statistic unpaired T-test, no equal SD). The small population CD4 T cells that were present at day 14 post INX901 treatment appeared to be still naïve as shown by the statistically higher expression level of CD62L and CD45RB (FIG. **21**). The figure shows changes in CD4 T cell activation status in peripheral blood. (n=8 per group, SEM, statistic unpaired T-test, no equal SD) (MFI: median fluorescence intensity).

[0696] By day 30, the mice that received $CD45RB^{hi}$ naïve CD4 T cells started losing weight as colitis progressed while the control group that received whole T cell fraction did not develop any disease (FIG. **22**). INX901 treatment prevented the weight loss and mice appeared to gain weight instead when compared to control group. Mice were euthanized at day 46 and colon and spleen collected for histology and flow cytometry respectively.

[0697] Further, mice suffering from colitis showed a shortening of the colon when compared to the control (total CD4) group, no shortening occurred in the group treated with INX901. As shown in FIG. **23**, while mice suffering from colitis showed a shortening of the colon when compared to the control (total CD4) group, no shortening occurred in the group treated with INX901. As additionally shown in FIG. **24**, mice that were subjected to CD4 $CD45RB^{hi}$ cell transfer all developed colitis as shown by the presence of important inflammatory infiltrates between intestinal villi (arrows, middle pictures at low and high magnification) when compared to the control group that received total cell transfer and subsequently did not develop any colitis (upper pictures). INX901 treatment completely prevented the development of colitis as shown by the complete absence of inflammatory infiltrate in all the samples analyzed (8 mice per group).

[0698] As shown in the figure INX901 treatment prevented colitis development. Representative pictures of H&E stained sections of the colon for each mouse group. Magnification: pictures on the top are at 4×, on the bottom at 20×. Arrows indicate areas with abundant inflammatory infiltrates. Note their complete absence in the INX901-treated colon sample.

[0699] Immunohistochemistry staining of CD3 (FIG. **25**) and CD11b (FIG. **26**) expressing cells confirmed colitis development in the IgG2 treated animals. Similar numbers of $CD3^+$ and CD11b+ cells in control and INX901-treated samples again show the complete absence of disease following INX901 treatment. FIG. **25** shows that INX901 treatment prevented $CD3^+$ T cell recruitment to the colon. Representative pictures of CD3 stained sections of the colon for each mouse group. (Magnification: pictures on the top are at 4×, on the bottom at 20×).

[0700] FIG. **26** shows that INX901 treatment prevented myeloid (CD11b+) cell recruitment to the colon. Representative pictures of CD11b stained sections of the colon for each mouse group. Magnification: pictures on the top are at 4×, on the bottom at 20×. Yet additionally, INX901 treatment further was shown to induce long term CD4 T cell changes. Analysis by flow cytometry on spleen cells showed that 40 days post INX901 treatment, there was still highly significant decreases in CD4 T cell frequencies as compared to the IgG2 treated group, and 10 to 30% of the CD4 T cells were still CD45RB+ (FIG. **27**), left and right graphs)). No changes in regulatory T cells were observed following INX901 treatment (FIG. **27**, center graph). As shown in the figure spleens were collected at day 46 (40 days post last antibody dosage) and analyzed by flow cytometry (n=8 or 4 per group, SEM, statistic unpaired T-test, no equal SD).

[0701] Accordingly we have shown that anti-VISTA INX901 treatment prevents colitis development as shown by the absence of weight loss, change in colon length and inflammatory infiltrate present in the colon Additionally, we observed long-term decreases in CD4 T cells (at 14 and 40 days post treatment) that retained naïve T cell characteristics

such as CD45RB expression. Therefore, anti-VISTA agonist antibodies may be used to treat or prevent colitis.

Example 17: Use of Agonist Anti-VISTA Antibodies in Treating Psoriasis

Imiquimod (IMQD) Induced Psoriasis Model

[0702] Imiquimod (IMQD) is a commercially available cream containing TLR7/8 agonists that is widely used for dermatological conditions such as viral infections and melanoma. Application of IMQD to the skin over multiple days results in thickening of the epidermis via proliferation of the keratinocytes. Additionally, an immunological infiltration into the dermis layer occurs, with populations of both T cells and myeloid cells. Recurrent administration of IMQD creates a skin lesion similar to what is observed in patients with Psoriasis. IL-17 and IL-23 are thought to be the major cytokines involved in the immune response to IMQD.

[0703] In these experiments, we test the function of 8G8, a hamster α mouse VISTA antibody, on the IMQD induced Psoriasis. Mice were dosed every other day with 8G8, while IMQD was administered topically to the back of mice for 7 days. The skin was then isolated, fixed and embedded in paraffin blocks. Sections were then stained for H&E analysis and expression of several immunological populations by IHC. Notably, 8G8 drastically reduced the overall cellular infiltrate into the dermis, much of which appears to be a reduction in the $CD3^+$ population.

Materials and Methods

Mouse Treatment

1. 7-week old mice Balb/c mice were purchased from Jackson and stored in SPF conditions at the DHMC. The backs of the mice were shaved prior to the start of the experiment.
2. Imiquimod was purchased from the Dartmouth Hitchcock animal facility. 62.5 mg was applied to skin daily through the use of a Q-tip.
3. 8G8 was administered every other day at 200 ag/mouse.
4. Mice were sacrificed at day 7 and the skin was isolated by cutting a square from the shaved section. The skin was placed in Formalin for 24 hours before being delivered to the Dartmouth Pathology department for embedding in Paraffin.

Splenic Analysis

1. The spleen was isolated and ground into a single cell suspension.
2. After centrifugation, the red blood cells were lysed using ACK solution (5 minutes at RT).
3. Cells were centrifuged and resuspended in PBS before counting.
4. 1×10^5 cells from each spleen were labeled with CD4, CD8, CD19, CD11b, Ly6C and Ly6G in the presence of mouse Fc block, at 20 minutes on ice.
5. Labeled cells were run on the Miltenyi MACSquant and analyzed using FlowJo.
6. Statistics were performed in PRISM 6, with groups compared by one-way ANOVA followed by Sidak's multiple comparisons test. P-values are denoted as follows: $p<0.0001$****, $p<0.001$***, $p<0.01$**, $p<0.05$*.

H&E and IHC Analysis

1. Samples were put into cassettes and fixed O/N in 10% Formalin at room temperature, then briefly washed in PBS and transferred and kept into 70% Ethanol (Fisher Scientific) prior to being transferred to the Pathology Translational Research Core at the Geisel School of Medicine at Dartmouth where they were paraffin embedded, sectioned and then stained.
2. Paraffin embedded tissue sections (4 μm) were stained using a Leica BOND RX automated stainer. After dewaxing, the sections were subjected to antigen retrieval (Bond epitope retrieval solution 2, 100° C., 20 min) and incubated with the primary antibody (see dilution below) for 30-60 min, at room temperature in Leica diluent. Slides are then washed 3×5 min washes in PBS and incubated with secondary antibody (from Leica Bond Refine detection kit, DS9800). After 3 final washes in PBS the sections were incubated with DAB (Leica Bond polymer detection kit), rinsed, counterstained with hernatoxylin and mounted.
3. Statistics on CD3+ infiltration were performed in R statistical programming language. The chi-squared test for outlier (in the "outliers" package) was performed for each group, and if $p<0.05$ that data point was removed. Groups were then compared using Student's t-test with pooled variance, and $p<0.05$ denoted as *.

Specificity	Ig type	Clone/Format	Catalog #	Company	Retrieval	Dilution
mouse CD3	rabbit	Polyclonal	AB5690	Abcam	EDTA	0.25
mouse CD4	rabbit	clone 1	50134-R001	SinoBiologicals	EDTA	0.32
mouse MPO	rabbit	Polyclonal	A0398	Dako	EDTA	0.74
mouse CD11b	rabbit	Polyclonal	ab-75476	Abcam	EDTA	0.25
mouse F4/80	rabbit	clone SP115	NBP2-12506	Nevus	EDTA	0.11

Results

[0704] We determined whether an agonist anti-VISTA antibody would be effective in a psoriasis model, particularly we determined if an agonist anti-human antibody, 8G8, was capable of altering the immunological response to Imiquimod induced Psoriasis. IMQD cream was administered to the back skin of Balb/c mice every day for 7 days. Mice were given 200 μg of 8G8 or Hamster Ig at the time of initial IMQD treatment (day 0), and at day 2, day 4 and

day 6. The mice were sacrificed at day 7 and the skin was analyzed by H&E and IHC for several immune subset markers.

[0705] The H&E analysis indicated a reduced number of dense nucleated cells (lymphocyte characteristic) into the dermis of 8G8 treated mice compared to controls (see FIG. **28**). We therefore performed IHC analysis for several cell surface markers expressed by immunological cells. Of note, the number of $CD3^+$ cells was reduced in the 8G8 treated mice compared to the Hamster Ig control group (see FIG. **29**, **30**). IMQD Psoriasis is thought to be canonically driven by T cells, specifically IL-17 producing populations including Th17 and γδ T cells.

[0706] We also profiled the splenic populations to see whether 8G8 treatment reduced global T cell populations, or if they $CD3^+$ decreases were just observed in the skin. No changes to the T cell populations were observed, however small decreases in $CD11b^+$ $Ly6G^-$ (% of total) and CD19+ (total number) populations did occur with 8G8 (see FIG. **31**).

[0707] Therefore, these experiments revealed that an anti-human VISTA agonist antibody was effective in a psoriasis model as 8G8 was shown to reduce the number of $CD3^+$ T cells infiltrating Imiquimod treated skin. Based on these results VISTA agonist antibodies may be used in the treatment or prevention of psoriasis and other T cell mediated autoimmune or inflammatory skin conditions.

Example 18: Use of Agonist INX800 and INX801 Anti-VISTA Antibodies in Concanavalin A Induced Hepatitis Model

[0708] Concanavalin A (ConA) is a lectin that binds to specific sugars ultimately leading to the activation of the immune system, mainly in the liver. ConA induces rapid production of multiple cytokines, such as T cell derived IL-2, IL-3, Il-4, TNF-α and IFN-γ. The T cell activation and subsequent cytokine response induces acute hepatitis, and in high dose models, mortality. ImmuNext has created a human VISTA knock-in mouse where human VISTA is expressed in replacement of mouse VISTA. The mice are phenotypically normal, indicating that hVISTA functions appropriately in the mice. We have therefore tested two anti-human VISTA antibodies, called INX800 and INX801 in the ConA model of hepatitis in these mice.

Materials and Methods

[0709] 10-week old mice were purchased from Jackson and stored in SPF conditions at the DHMC.

[0710] Concanavalin A from *Canavalia ensiformis* (Sigma, cat #C2010-100MG) was reconstituted in 10 ml of fresh PBS and shaken for 30 minutes at RT. 300 μL aliquots were made for storage at −20 C.

[0711] 200 μL of α-hVISTA antibodies, or the Control Ig control (Crown Biosciences) were administered to mice 3 hours prior to ConA treatment by I.P injection in PBS. Antibodies were given at 10 mpk.

[0712] Animals were weighed and given either 15 mg/kg of ConA for the cytokine analysis experiments. Injections were performed through the tail vein. In all cases, mice were monitored every several hours for morbidity and sacrificed if cold to touch.

[0713] For the cytokine analysis, mice were bled by sacrifice using CO2 and then cardiac puncture. Blood was collected in plasma collection tubes and then centrifuged to remove the cellular component. Samples were stored for short periods of time at −80 C before being analyzed by multiplex per manufacturer's instructions.

[0714] Calibration curves from recombinant cytokine standards were prepared with threefold dilution steps in the same matrix as the samples.

[0715] High and low spikes (supernatants from stimulated human PBMCs and dendritic cells) were included to determine cytokine recovery.

[0716] Standards and quality controls were measured in technical triplicate, each triplicate test sample was measured once, and blank values were subtracted from all readings. All assays were carried out directly in a 96-well filtration plate (Millipore, Billerica, MA) at room temperature and protected from light.

[0717] Briefly, wells were pre-wet with 100 μl PBS containing 1% BSA, then beads together with a standard, sample, spikes, or blank was added in a final volume of 100 μl, and incubated together at room temperature for 30 min with continuous shaking.

[0718] Beads were washed three times with 100 μl PBS containing 1% BSA and 0.05% Tween 20.

[0719] A cocktail of biotinylated antibodies (50 μl/well) was added to beads for a 30-min incubation at room temperature with continuous shaking.

[0720] Beads were washed three times, then streptavidin-PE was added for 10 min. Beads were again washed three times and resuspended in 125 μl of PBS containing 1% BSA and 0.05% Tween 20.

[0721] The fluorescence intensity of the beads was measured using the Bio-Plex array reader. Bio-Plex Manager software with five parametric-curve fitting was used for data analysis.

[0722] Statistics for the cytokine analysis were carried out in R Statistical Computing Language or in Prism 6. Cytokine concentration values below detection (<OOR) were rescaled to the lowest detectable concentration, and values above accurate quantitation (>OOR) were rescaled to the maximum linearly quantifiable concentration. Pair-wise comparisons between the antibody-treated groups and an Ig-control were made using One-Way ANOVA with Tukey Honest Significant Differences. P-values less than 0.1 were deemed significant and denoted as follows: $p<0.0001$****, $p<0.001$***, $p<0.01$**, $p<0.05$*, $p<0.1$~.

Results

[0723] Two replicate experiments (#13 and #14) were designed to determine whether INX800 and/or INX801, both anti-hVISTA antibodies, were capable of altering the cytokine response to ConA. Mice were given 10 mpk of INX800, INX801 or Control Ig three hours prior to treatment with ConA (15 mg/kg) and then mice were sacrificed at the 6-hour time point and the cytokine response was determined by 32-plex. Most cytokines were unchanged, however IL-2 was consistently decreased by both INX800 and INX801 (FIGS. **32**, **33**). All cytokine profiles can be seen in the links found in the Appendix.

[0724] The naïve mice and mice from experiment 14 were also analyzed for changes in immune populations to determine whether the decrease in cytokines could be associated with any sign of T cell depletion. The flow gating strategy included markers for B220 (B cells); CD3, CD4, and CD8 (T cells); and CD11b and Gr1 (myeloid cells). No statisti-

cally significant association in the total number of cells with antibody treatment was observed for any population (See FIG. **34**). Therefore, INX801 and INX801 both are capable of suppressing a ConA induced IL-2 response. There is no obvious sign of cellular depletion caused by INX800 or INX801 either in naïve mice or during the ConA response. These experimental results suggest that VISTA agonist antibodies may be used to treat and prevent hepatitis infection and inflammation and cytokine responses elicited during acute infection. These experimental results suggest that VISTA agonist antibodies may be used to treat and prevent hepatotoxicity or liver damage associated with hepatitis and other infections and inflammatory diseases that affect the liver.

Example 19: Use of Agonist Anti-VISTA 8G8 and 13F3 Antibodies in Concanavalin A Induced Hepatitis Model

[0725] The ConA model is described in the prior example. In these experiments we examined the ability of two different α-mVISTA antibodies (8G8 and 13F3) on the cytokine responses induced by ConA. As 8G8 was able to decrease production of several T cell derived cytokines, we also examined whether it could protect against a lethal dose of ConA.

Materials & Methods

[0726] 7-week old mice were purchased from Jackson and stored in SPF conditions at the DHMC.

[0727] Concanavalin A from *Canavalia ensiformis* (Sigma, cat #C2010-100MG) was reconstituted in 10 ml of fresh PBS and shaken for 30 minutes at RT. 300 μL aliquots were made for storage at −20 C.

[0728] 200 μL of α-mVISTA antibodies 8G8 and 13F3, or the Hamster Ig control (BioXcell) were administered to mice 3 hours prior to ConA treatment by L.P injection in PBS.

[0729] Animals were weighed and given either 15 mg/kg of ConA for the cytokine analysis experiments or 30 mg/kg of ConA for the mortality experiments. Injections were performed through the tail vein. In all cases, mice were monitored every several hours for morbidity and sacrificed if cold to touch.

[0730] For the cytokine analysis, mice were bled either by cheek puncture or by sacrifice using CO2 and then cardiac puncture. Blood was collected in plasma collection tubes, incubated for 30 min at RT and then centrifuged to remove the cellular component. Samples were stored for short periods of time at −80 C before being analyzed by multiplex per manufacturer's instructions.

[0731] Calibration curves from recombinant cytokine standards were prepared with threefold dilution steps in the same matrix as the samples.

[0732] High and low spikes (supernatants from stimulated human PBMCs and dendritic cells) were included to determine cytokine recovery.

[0733] Standards and quality controls were measured in technical triplicate, each triplicate test sample was measured once, and blank values were subtracted from all readings. All assays were carried out directly in a 96-well filtration plate (Millipore, Billerica, MA) at room temperature and protected from light.

[0734] Briefly, wells were pre-wet with 100 μl PBS containing 1% BSA, then beads together with a standard, sample, spikes, or blank were added in a final volume of 100 μl, and incubated together at room temperature for 30 min with continuous shaking.

[0735] Beads were washed three times with 100 μl PBS containing 1% BSA and 0.05% Tween 20.

[0736] A cocktail of biotinylated antibodies (50 μl/well) was added to beads for a 30-min incubation at room temperature with continuous shaking.

[0737] Beads were washed three times, then streptavidin-PE was added for 10 min. Beads were again washed three times and resuspended in 125 μl of PBS containing 1% BSA and 0.05% Tween 20.

[0738] The fluorescence intensity of the beads was measured using the Bio-Plex array reader. Bio-Plex Manager software with five parametric-curve fitting was used for data analysis.

[0739] Statistics for the cytokine analysis were carried out in R Statistical Computing Language or in Prism 6. Cytokine concentration values below detection (<OOR) were rescaled to the lowest detectable concentration, and values above accurate quantitation (>OOR) were rescaled to the maximum linearly quantifiable concentration. Pair-wise comparisons between antibody-treated groups and the Ig-control were made using One-Way ANOVA with Tukey Honest Significant Differences. P-values less than 0.05 for all tests and comparisons were deemed significant.

Results

[0740] Our initial experiment was designed to determine whether 8G8 or 13F3, both anti-mVISTA antibodies, were capable of altering the cytokine response to ConA. Mice were given 200 μg of 8G8, 13F3 or Hamster Ig three hours prior to treatment with ConA (15 mg/kg) and then mice were sacrificed at the 6-hour time point and the cytokine response was determined by 32-plex (FIG. **35**). Most cytokines were unchanged, however IL-2 was decreased in the presence of 8G8 but not 13F3. We then wanted to determine if the reductions in IL-2 could be correlated with protection for ConA-induced mortality. To do so, mice were pre-treated with 8G8 or Hamster-Ig and then given ConA at 30 mg/kg and followed for survival (FIG. **36**). While all of the Hamster Ig treated mice had to be euthanized within 40 hours, 80% of the 8G8 treated mice survived past 72 hours and appeared healthy. Therefore, 8G8, the agonist antibody but not 13F3, can induce changes to IL-2 in the ConA induced hepatitis model. Further 8G8 protects against a lethal challenge of ConA (30 mg/kg). These experimental results suggest that VISTA agonist antibodies may be used to treat and prevent hepatitis infection and pathological inflammation and proinflammatory cytokine responses elicited during acute or chronic infection. These experimental results further suggest that VISTA agonist antibodies may be used to treat and prevent hepatotoxicity or liver damage associated with hepatitis and other infections and inflammatory diseases that affect the liver.

Example 20: Use of Agonist Anti-VISTA INX903 Antibody in Concanavalin A Induced Hepatitis Model

[0741] The ConA model is described in the prior example. In these experiments we have tested an additional anti-human VISTA antibody, INX903 in the ConA model of hepatitis, using INX800 as a control. In one experiment, we

also compared INX903 and INX800 to an antagonistic VISTA antibody, which has previously been shown to enhance cytokine production by immune cells.

Materials and Methods

[0742] 10-week old mice were purchased from Jackson and stored in SPF conditions at the DHMC.

[0743] Concanavalin A from *Canavalia ensiformis* (Sigma, cat #C2010-100MG) was reconstituted in 10 ml of fresh PBS and shaken for 30 minutes at RT. 300 μL aliquots were made for storage at −20 C.

[0744] 200 μL of α-hVISTA antibodies, or the Control Ig control (Crown Biosciences) were administered to mice 3 hours prior to ConA treatment by I.P injection in PBS. Antibodies were given at 10 mpk.

[0745] Animals were weighed and given either 15 mg/kg of ConA for the cytokine analysis experiments. Injections were performed through the tail vein. In all cases, mice were monitored every several hours for morbidity and sacrificed if cold to touch.

[0746] For the cytokine analysis, mice were bled by sacrifice using CO2 and then cardiac puncture. Blood was collected in plasma collection tubes and then centrifuged to remove the cellular component. Samples were stored for short periods of time at −80 C before being analyzed by Luminex or MSD multiplex per manufacturer's instructions.

[0747] Statistics for the cytokine analysis were carried out in R Statistical Computing Language. Cytokine concentration values below detection (<OOR) were rescaled to the lowest detectable concentration, and values above accurate quantitation (>OOR) were rescaled to the maximum linearly quantifiable concentration. Pair-wise comparisons between antibody-treated groups and the Ig-control were made using One-Way ANOVA with Tukey Honest Significant Differences. P-values less than 0.1 were deemed significant and denoted as follows: $p<0.000^{1}$****, $p<0.001$***, $p<0.01$**, $p<0.05$*, $p<0.1$~.

[0748] The results of these experiments are contained in FIG. **37** and FIG. **38**. In FIG. **37** IL-2 expression was detected in the plasma from the 6-hour time point of mice treated with Control-Ig, INX800 or INX903. Mice were pretreated at −3 hours with each of the indicated antibodies. At time 0, mice were dosed with 15 mg/kg of ConA, and then sacrificed and bled at the 6-hour time point. FIG. **38** shows IL-2 and MIP-1β expression in the plasma from the 6-hour time point of mice treated with Control-Ig, 2 agonist VISTA abs (INX800 and INX903) or a VISTA antagonist Ab. Mice were pretreated at −3 hours with each of the indicated antibodies. At time 0, mice were dosed with 15 mg/kg of ConA, and then sacrificed and bled at the 6-hour time point. These experiments show that INX800 and INX903 are capable of suppressing ConA induced cytokine responses.

[0749] These experimental results suggest that VISTA agonist antibodies may be used to treat and prevent hepatitis infection and pathological inflammation and proinflammatory cytokine responses elicited during acute or chronic infection. These experimental results further suggest that VISTA agonist antibodies may be used to treat and prevent hepatotoxicity or liver damage associated with hepatitis and other acute or chronic infections and inflammatory diseases that affect the liver.

Example 21: Use of Agonist 8G8 Anti-VISTA Antibody in Collagen Induced Arthritis or CIA Model

[0750] Immunization of rodents and primates with Collagen type II (CII) in adjuvant induces an autoimmune arthritis, the so-called Collagen induced arthritis or CIA that, in many ways, reproduces Rheumatoid Arthritis (RA) symptoms. CII is the major constituent protein of the cartilage of diarthrodial joints, the site of inflammation in RA, and immunity to CII can be detected in RA patients.

[0751] A cocktail of 5 monoclonal antibodies (Arthrogen-CIA® Arthritogenic 5-Monoclonal Antibody Cocktail) recognizing the conserved epitopes on various species of CII can induce arthritis in naïve mice. This model is called Collagen Antibody-induced Arthritis (CAIA). In vitro studies with the 5-Antibody cocktail showed that these antibodies could be pathogenic to chondrocytes even in the absence of inflammatory mediators, and impair cartilage formation; they also inhibit collagen synthesis, fibrillogenesis and cause disorganization of CII fibrils in the extracellular matrix with or without increased matrix synthesis. Furthermore, the 5-antibody cocktail also has deleterious effects on the preformed cartilage.

[0752] In the present experiments, we tested the impact of 8G8 (hamster anti-mouse VISTA monoclonal antibody) treatment on CAIA mouse model of RA. Mice were dosed with 8G8 every other day starting at day −2. They were administered the 5-antibody cocktail on day 0 and LPS on day 3. Disease development was assessed by measuring inflammation swelling in the affected joints over time. Clinical scoring was accomplished by awarding a score of 1 for each swollen digit, a score of 5 for a swollen footpad and a score of 5 for a swollen wrist or ankle (Charles River Labs scoring system), which added together give a maximal score of 60 for each animal.

Materials and Methods

Mouse Treatment

[0753] The DBA mice, 8-week old, were obtained from Jackson Labs. They were acclimated for 2 days prior to having their tails tattooed.

[0754] CAIA induction: On day 0, mice were injected intraperitoneally (ip) with the 5-antibody cocktail purchased from AMSBIO/Chondrex at a dosage of 1.5 mg per mouse. Then on day 3, they received ip 50 μg of LPS (from AMSBIO).

[0755] Anti-VISTA treatment: Mice were dosed every other day, starting at day −2, with anti-VISTA 8G8 or control hamster IgG at a dosage of 10 mg/Kg during the whole course of the experiment. (see FIG. **39**)

Statistical Analysis

[0756] CAIA scoring was analyzed using Excel for data management and GraphPad Prism for graphing. Statistical analysis was performed using a macro for R statistical computing software that measures divergence in tumor volume between two groups of differentially treated mice and is named 'mixed effect repeated measures'.

Results

[0757] The objective of the experiment was to determine if an agonist anti-VISTA antibody would be effective in an

arthritis model. In the experiments it was shown that the anti-VISTA agonist antibody 8G8 could affect disease progression in the CAIA experimental model of RA. The data in FIG. **40** show significant decreases in disease progression and scope in response to 8G8 (interaction term P<0.000005). As shown treatment was initiated at day −2 and subsequently mice were dosed every other day. (n=10 in each group). 8G8 treatment significantly reduced disease severity (interaction term P<0.000005).

Example 22: Use of Agonist (INX903) Anti-VISTA Antibody in Collagen Induced Arthritis or CIA Model

[0758] The CIA model is described in the prior example. In the present experiment, we tested the impact of INX903 (human anti-human VISTA-IgG2) treatment on CAIA mouse model of RA. Mice were dosed with INX903 every other day starting at day −2. They were administered the 5-antibody cocktail on day 0 and LPS on day 3. Disease development was assessed by measuring inflammation swelling in the affected joints over time. Clinical scoring was accomplished by awarding a score of 1 for each swollen digit, a score of 5 for a swollen footpad and a score of 5 for a swollen wrist or ankle (Charles River Labs scoring system), which added together give a maximal score of 60 for each animal.

Materials and Methods

Mouse Treatment

[0759] The experimental protocol is shown schematically in FIG. **41**.

[0760] The hVISTA knock-in (KI) mice are bred at Horizon Discovery (Sage) Labs (Boyertown, PA). The mice, aged 8-12 weeks, first transit for 3 weeks in the quarantine facility, and then are transferred to the regular facility. 4 month-old mice were used for this experiment. Mice got their tail tattooed 2 days before experiment start.

[0761] CAIA induction: On day 0, mice were injected intraperitoneally (ip) with the 5-antibody cocktail purchased from AMSBIO/Chondrex at a dosage of 5 mg per mouse. Then on day 3, they received ip 50 μg of LPS (from AMSBIO).

[0762] Anti-VISTA treatment: Mice were dosed every other day, starting at day −2, with anti-VISTA INX903 or control human IgG2 at a dosage of 10 mg/Kg during the whole course of the experiment.

[0763] As shown in FIG. **42** treatment was initiated at day −2 and subsequently mice were dosed every other day. (n=9 in control group and 8 in INX903 treated group; 1 mouse was removed from the control group as it never showed any signs of disease). INX903 treatment significantly reduced disease severity (interaction term P=0.0005). CAIA scoring was analyzed as in the prior example. The data shown in FIG. **42** indicate that there is significant decreases in disease progression and scope in response to INX903 (interaction term P=0.0005).

Example 23: Use of Agonist (INX903) Anti-VISTA Antibody in Collagen Induced Arthritis or CIA Model

[0764] In the present experiment, we again tested the impact of INX903 (human anti-human VISTA-IgG2) treatment on CAIA mouse model of RA. Mice were dosed with INX903 every other day starting at day −2. They were administered the 5-antibody cocktail on day 0 and LPS on day 3. Disease development was assessed by measuring inflammation swelling in the affected joints over time. Clinical scoring was accomplished by awarding a score of 1 for each swollen digit, a score of 5 for a swollen footpad and a score of 5 for a swollen wrist or ankle (Charles River Labs scoring system), which added together give a maximal score of 60 for each animal.

Materials and Methods

Mouse Treatment

[0765] The hVISTA knock-in (KI) mice are bred at Horizon Discovery (Sage) Labs (Boyertown, PA). The mice, aged 8-12 weeks, first transit for 3 weeks in the quarantine facility, and then are transferred to the regular facility. 4 month-old mice were used for this experiment. Mice got their tail tattooed 2 days before experiment start.

[0766] CAIA induction: On day 0, mice were injected intraperitoneally (ip) with the 5-antibody cocktail purchased from AMSBIO/Chondrex at a dosage of 5 mg per mouse. Then on day 3, they received ip 50 μg of LPS (from AMSBIO).

[0767] Anti-VISTA treatment: Mice were dosed every other day, starting at day −2, with anti-VISTA INX903 or control human IgG2 at a dosage of 10 mg/Kg during the whole course of the experiment as shown below.

[0768] CAIA scoring was analyzed as in the prior example.

[0769] The data shown in FIG. **43** show there to be significant decreases in disease progression and scope in response to INX903 (interaction term P=0.01).

Example 24: Use of Agonist (8G8) Anti-VISTA Antibody in Collagen Induced Arthritis or CIA Model

[0770] In the present experiments, we tested the impact of 8G8 (hamster anti-mouse VISTA monoclonal antibody) treatment on CAIA mouse model of RA. Mice were dosed with 8G8 (agonist anti-murine VISTA antibody) every other day starting at day −2. They were administered the 5-antibody cocktail on day 0 and LPS on day 3. Disease development was assessed by measuring inflammation swelling in the affected joints over time. Clinical scoring was accomplished by awarding a score of 1 for each swollen digit, a score of 5 for a swollen footpad and a score of 5 for a swollen wrist or ankle (Charles River Labs scoring system), which added together give a maximal score of 60 for each animal. As shown in FIG. **44** the 8G8 antibody resulted in significant decreases in disease progression and scope in response to 8G8 (interaction term P<0.0001.

Example 25: Use of Agonist Antibodies (INX800, 901 and 902) on Disease Progression in The Collagen Antibody Induced Rheumatoid Arthritis Mouse Model

[0771] We tested the impact of INX800 (chimeric mouse anti-human VISTA-IgG2), INX901, and INX902 (human anti human VISTA-IgG2) treatment on CAIA mouse model of RA. Mice were dosed with INX800, INX901, or INX902 every other day starting at day −2. They were administered

the 5-antibody cocktail on day 0 and LPS on day 3. Disease development was assessed by measuring inflammation swelling in the affected joints over time. Clinical scoring was accomplished by awarding a score of 1 for each swollen digit, a score of 5 for a swollen footpad and a score of 5 for a swollen wrist or ankle (Charles River Labs scoring system), which added together give a maximal score of 60 for each animal.

[0772] CAIA scoring was analyzed as previously described. As shown in FIG. **45** INX800 treatment qualitatively decreases disease progression, although not with statistical significance in this experiment (interaction P=0.46) By contrast, as shown in FIG. **46**, INX901 treatment fully prevented disease progression (interaction P<0.0001). As further shown in FIG. **47**, INX902 treatment fully prevented disease progression (interaction P<0.0001).

Example 26: Use of Agonist VISTA Antibody (8G8) in C57/B16 GVHD Model

[0773] The most commonly studied mouse model of MHC-mismatched acute GvHD is C57/B16 (H2b) →BALB/c (H2d) (transplantation of cellular isolates from C57/B16 (H2b) donors into BALB/c (H2d) recipients). Here we used C57/B16 mice as donor for spleen cells and bone marrow transferred in irradiated BALB/c recipient. We examined the immune-suppressive efficacy of Hamster α-mouse VISTA antibody 8G8 compared to Hamster α-mouse VISTA antibody 13F3 and Hamster IgG control.

Materials and Methods

[0774] 10-week old females BALB/c recipient mice and C57/B16 donor mice were purchased from Charles River Laboratories. All mice were housed in SPF conditions at the DHMC vivarium.

[0775] Recipient mice were subjected to total body irradiation (TBI) emanating from a cesium-137 source twice at 450 cGy at DO (9.30 am and 1.30 pm) prior transfer

[0776] Donor mice were euthanized and bone marrow was harvested by flushing femur and tibia with HBSS. Red blood cells were lysed using ACT solution. Single cell suspension prepared isolated from spleens and red blood cells were lysed using ACT solution.

[0777] Recipient mice received 10 million bone marrow cells and 10 million spleen cells along with 200 ug Hamster IgG (BioXcell, BE0091 lot #18206/1015) or 8G8 (lot #AB-130318) or 13F3-2E9 (lot #BP-075-014). Cells and antibodies were administered by tail vein intravenous injection.

[0778] Three additional doses of antibodies were injected IP at D2, 4 and 6.

[0779] Mice were weighed regularly to monitor disease progression. However, all mice lost a lot of weight due to irradiation sickness and were provided liquid recovery food for the duration of the experiment. Mice were euthanized when showing signs of morbidity.

Results

[0780] FIG. **48**A-B shows weights and survival of recipient mice treated with 8G8, 13F3, or control Hamster IgG antibodies in acute GvHD disease model. FIG. **48**A shows mice appearance at day 21 and FIG. **48**B shows survival. As shown the hamster α-mouse VISTA antibody 8G8 is immune-suppressive and strongly attenuates disease severity as illustrated by mice fur appearance at day 21 (FIG. **48***a*) and protects against GvHD induced lethality (FIG. **48***b*). In contrast, 13F3 did not show any such protection. Thus hamster 8G8 α-mouse VISTA is immune-suppressive and strongly attenuates acute GvHD severity promoting long-term survival. In contrast, 13F3 did not alter disease progression.

Example 27: Use of Agonist VISTA Antibodies (INX901, INX902, INX903 and INX904) in C57/B16 GVHD Disease Model

[0781] We examined the immune-suppressive efficacy of α-human VISTA antibodies, INX901, INX902, INX903 and INX904, compared to Human Ig control by measuring their ability to modulate disease progression/severity in a C57/B16 GvHD model. We also verified the presence of donor T-cells and complete chimerism in the surviving mice by flow cytometry of peripheral blood taken from the recipient mice at 41 days post-treatment.

Materials & Methods

[0782] 9-11-week old males BALB/c recipient mice were purchased from Jackson. 11-weeks old males Human-KI VISTA donor mice (DDE1) on C57/B16 background were purchased from Sage labs. All mice were housed in SPF conditions at the DHMC vivarium.

[0783] Recipient mice were subjected to total body irradiation (TBI) emanating from a cesium-137 source at 300 cGy at Day-1 and DO prior transfer.

[0784] Donor mice were euthanized and bone marrow was harvested by flushing femur and tibia with HBSS. Red blood cells were lysed using ACK solution. T cells were isolated from spleens by negative selection (Stemcell #19851).

[0785] Recipient mice received 10 million bone marrow cells and 2 million T cells along with 10 mg/kg human IgG2 (Crown Bioscience, lot #AB150073) or INX901 (lot #BP-021-016-2), INX902 (lot #BP-021-016-3), INX903 (lot #BP-021-016-4) or INX904 (lot #BP-021-016-5). Cells and antibodies were administered by tail vein intravenous injection.

[0786] Mice were weighed regularly to monitor disease progression and euthanized if their weight dropped lower than 75% of their initial weight.

Flow Cytometric Analysis of Peripheral Blood

[0787] Peripheral blood was isolated from mice by retro-orbital bleed at 41 days post-transfer.

[0788] Total blood was stained with Biolegend's fluorescently labelled antibodies to CD45, CD11b, CD3, H2Kd (recipient) and H2Kb (donor) then RBC were lysed using BD FACS Lysing solution (#349202). Cells were washed once with PBS after lysis.

[0789] Labeled cells were run on the Miltenyi MACSquant and analyzed using FlowJo.

Results

[0790] FIG. **49**A-C illustrates the mean (A and B) weight loss and survival (c) for each treated group during the course of the experiment. Immune-suppressive α-human VISTA antibodies can be ranked based on their impact at suppressing or attenuating GVHD disease severity (weight loss) at the peak of disease (FIG. **49**A).

[0791] INX904 (yellow) is poorly suppressive and only half the mice survive. INX901 (Green), INX902 (Red) and

INX903 (orange) are strongly suppressive and fully protective with INX901 completely inhibiting the disease and INX902 and INX903 strongly attenuating disease severity. As shown the α-human VISTA treated mice survive long term (FIGS. **49**B and C).

[0792] After 41 days, peripheral blood is harvested from surviving mice and tested for chimerism (donor derived hematopoietic system) by staining for donor (H2Kb) or recipient (H2Kd) MHC class I. Figure SOA illustrates one example of a surviving α-human VISTA treated mouse in which the vast majority of CD11b in the blood express donor type MHC class I compared to the blood of a BALB/c control. Of note, 4/8 mice that received bone marrow cells only and 3/8 mice treated with INX901 failed to reach chimerism due to "failure of engraftment" (Figure SOB) and was retrospectively removed from the analysis. This phenomenon could be explained by a suboptimal irradiation dose and the high potency of INX901 to suppress T cell activation. It is well established that T cells help engraftment especially at low doses of TBI ("The history and future of T-cell depletion as graft-versus-host disease prophylaxis for allogeneic hematopoietic stem cell transplantation", Vincent T. Ho, Robert J. Soiffer Blood 2001 98:3192-3204; doi:10.1182/blood.V98.12.3192). Complete chimerism was achieved in 100% of the mice treated with INX902, INX903 and INX904. Donor derived T cells were enumerated in the blood of all surviving chimeric mice. All α-human VISTA treated surviving chimeric mice present a 4 to 9 times higher number of T cells in the blood than mice that received bone marrow cells only (FIG. **50**C) arguing against a depleting effect of α-human VISTA antibodies.

[0793] Therefore, INX901, INX902, INX903 and INX904 α-human VISTA antibodies all showed immune suppressive activities and partially attenuated or completely suppressed acute GvHD.

Example 28: Effects of α-Human VISTA Antibody INX901 (10 mg/kg) on Xenogeneic GvHD in NSG Mice

[0794] Humanized mouse models of xenogeneic Graft-versus Host Disease (GvHD) allow the study of immunomodulatory compounds specific to human drug targets in vivo. These are based on immune-deficient strains of mice injected with peripheral blood mononuclear cells (PBMCs) from human. The NOD-SCID IL-2Rγnull (NSG) strain lack mature T cells, B cells, and natural killer cells and are amendable to xenogeneic GvHD studies. In the NSG model of xeno-GvHD, donor human T-cells expand robustly in recipient mice and effect anti-host cell reactivity leading to cutaneous tissue infiltration. The mice lose weight and if left untreated will succumb to GvHD. The timeframe of disease progression can range from 3 to 5 weeks. The time of disease occurrence and progression can be accelerated by irradiating the mice with 3Gy prior to transfer of the human PBMCs. In this case the disease initiates after approximately 1-2 weeks and mice will succumb by the 2-3-week mark.

[0795] Herein we describe the results of experiments wherein we examined the ability of human VISTA specific antibody INX901 to modulate disease progression in NSG GvHD. Briefly, we irradiated and injected the mice with 2.5 million human PBMCs along with a single dose of control immunoglobulin (Ig) or INX901. We confirmed the presence of human T-cells by flow cytometry of peripheral blood taken from the recipient mice at 10 days post-treatment. Disease progression was monitored by regularly weighing mice. It was seen that NX901 drastically reduced disease progress and increased mouse survival.

Materials and Methods

Mice and Disease Induction

[0796] 7-week old NSG mice were purchased from the laboratory of Steve Fiering at DHMC and housed in SPF conditions at the DHMC. Mice were tattooed prior to the initiation of the experiment.

[0797] Human peripheral blood was isolated from apheresis cones provided from a volunteer donor at the DHMC blood donor program.

[0798] PBMCs were isolated by Ficoll gradient centrifugation.

[0799] Mice were irradiated with 3Gy prior to cellular transfer (DHMC).

[0800] Six mice received 2.5 million PBMCs diluted in 10 mg/ml human IgG (Crown Bioscience, lot #AB150073) in 200 μl PBS. Six mice received 2.5 million PBMCs diluted in 10 mg/ml INX901 (lot #BP-021-016-2) in 200 μl PBS. All therapeutics were delivered via tail vein injection.

[0801] Mice were weighed regularly to monitor disease progression and euthanized if their weight dropped to lower than 80% of their starting weight.

Flow Cytometric Analysis of Peripheral Blood

[0802] Peripheral blood was isolated from mice by retro-orbital bleed at 10 days post-treatment.

[0803] Cells were subjected to RBC lysis, thoroughly rinsed and stained with Biolegend's fluorescently labelled antibodies, anti-mouse CD45 BrV421, anti-mouse CD3-APC-Cy7, anti-human CD45-PE, and anti-human CD3-PE-Cy7 using standard immunological flow cytometric protocols.

[0804] Labeled cells were run on the Miltenyi MACSquant and analyzed using FlowJo.

Results

[0805] The experiment in FIG. **51**A compares the mean weight of mice within the group during the course of the experiment. FIG. **51**B compares the weight of individual mice. FIG. **52** shows the results of the flow cytometry analysis of mouse peripheral blood at day 10 post-treatment. The experiment shows T-cell expansion in NSG mice treated with INX901 or control AB in xeno-GvHD disease model where the values indicate the % of total $CD45^+$ cells in the mouse peripheral circulation made up of human $CD3^+$ T-cells.

[0806] These results show that expansion of peripheral human T-cells is reduced in the INX901 treated group and that mice in the INX901-treated group do not lose weight as quickly or consistently as those in the control-treated group. These results provide further evidence that VISTA agonist antibodies may be used to treat and prevent GvHD disease.

Example 29: Efficacy of Hamster α-Mouse VISTA Antibody 8G8 at 8 mg/Kg on GvHD in Irradiated BALB/c Mice Injected with C57/B16 T Cells and Bone Marrow

[0807] We examined the immune-suppressive efficacy of Hamster α-mouse VISTA antibody 8G8 by its ability to modulate GVHD disease progression/severity compared to a hamster IgG control.

Materials and Methods

[0808] 10-week old males BALB/c recipient mice and C57/B16 donor mice were purchased from Jackson. All mice were housed in SPF conditions at the DHMC vivarium.

[0809] Recipient mice were subjected to total body irradiation (TBI) emanating from a cesium-137 source at 300 cGy at Day-1 and DO prior transfer.

[0810] Donor mice were euthanized and bone marrow was harvested by flushing femur and tibia with HBSS. Red blood cells were lysed using ACK solution. T cells were isolated from spleens by negative selection (Stemcell #19851).

[0811] Recipient mice received 10 million bone marrow cells and 2 million T cells along with 200 ug Hamster IgG (BioXcell, BE0091 lot #18206/1015) or 8G8 (lot #AB130318-1). Cells and antibodies were administered by tail vein intravenous injection.

[0812] Mice were weighed regularly to monitor disease progression and euthanized if their weight dropped lower than 75% of their initial weight.

Results

[0813] FIG. **53**A-C illustrates the mean (a) and individual (b) weight loss and survival (c) for each treatment group during the course of the experiment. Immune-suppressive Hamster α-mouse VISTA antibody 8G8 strongly attenuates disease severity at the peak of disease (D8-10) and promotes long-term survival in the majority of the mice. Specifically, FIG. **53**A shows mean weight loss by group (N=8 mice per group); FIG. **53**B shows individual weight loss by group (N=8 mice per group) and FIG. **53**C survival. These results show that 8G8 is immune-suppressive and strongly attenuates acute GvHD severity promoting long term survival. These results provide further evidence that VISTA agonist antibodies may be used to treat and prevent GvHD disease.

Example 30: Dose Efficacy of α-Human VISTA Antibodies INX902 (10, 2.5, and 1 mg/kg) on GvHD in Irradiated BALB/c Mice Injected with DDE1 T Cells and Bone Marrow

[0814] In these experiments fully C57/B16 Human-VISTA Knock in mice (DDE1) were used as donor for T cells and bone marrow transferred in irradiated BALB/c recipient. Disease progression was monitored by regularly weighting mice. We examined the immune-suppressive efficacy of the α-human VISTA antibody, INX902, at various doses compared to Human Ig control by measuring their ability to modulate disease progression/severity. We also verified the presence of donor T-cells and chimerism in the surviving mice by flow cytometry of peripheral blood taken from the recipient mice at 21 days post-treatment.

Materials and Methods

GvHD Model and Disease Severity Evaluation

[0815] 10-week old males BALB/c recipient mice were purchased from Jackson. 14-weeks old males Human-KI VISTA donor mice (DDE1) on C57/B16 background were purchased from Sage labs. All mice were housed in SPF conditions at the DHMC vivarium.

[0816] Recipient mice were subjected to total body irradiation (TBI) emanating from a cesium-137 source at 350 cGy at Day-1 and DO prior transfer.

[0817] Donor mice were euthanized and bone marrow was harvested by flushing femur and tibia with HBSS. Red blood cells were lysed using ACK solution. T cells were isolated from spleens by negative selection (Stemcell #19851).

[0818] Recipient mice received 10 million bone marrow cells and 2 million T cells along with 10 mg/kg human IgG2 (Crown Bioscience, lot #AB150073) or 10 mg/kg, 2.5 mg/kg or 1 mg/kg INX902 (lot #BP-021-016-3). Cells and antibodies were administered by tail vein intravenous injection.

[0819] Mice were weighed regularly to monitor disease progression and euthanized if their weight dropped lower than 75% of their initial weight.

Flow Cytometric Analysis of Peripheral Blood

[0820] Peripheral blood was isolated from mice by retro-orbital bleed at 21 days post-transfer.

[0821] Total blood was stained with Biolegend's fluorescently labelled antibodies to CD45, CD11b, CD3, H2Kd (recipient) and H2Kb (donor) then RBC were lysed using BD FACS Lysing solution (#349202). Cells were washed once with PBS after lysis.

[0822] Labeled cells were run on the Miltenyi MACSquant® and analyzed using FlowJo.

Results

[0823] Acute GvHD is induced in irradiated BALB/c recipient by transferring allogenic (C57/B16) bone marrow and splenic T cells isolated from human VISTA-KI mice. Disease severity is measured by following weight loss.

[0824] FIG. **54**A-B illustrates the mean weight loss (A) and survival (B) for INX902 treated mice. INX902 attenuates disease severity at all doses tested as assessed by the reduced weight loss compared to Control Ig treated mice (FIG. **54**A). INX902 appears more efficient at higher doses (10 m/kg) than at lower doses in preventing both weight loss (**54**A) and mortality (FIG. **54**B).

[0825] After 21 days, peripheral blood is harvested from surviving mice and tested for chimerism (donor derived hematopoietic system) by staining for donor (H2Kb) or recipient (H2Kd) MHC class 1. FIG. **55**A illustrates the percentage of chimerism in INX902 treated mice. With irradiation doses of 350 cGy, all mice reached complete chimerism including those that received bone marrow cells only. FIG. **55**B shows that T cell numbers are increased in INX902 treated mice compared to mice that received bone marrow cells only. Specifically, FIG. **55**A-B shows chimerism in surviving mice treated with various doses of INX902 or control Ig in acute GvHD disease model. FIG. **55**A shows the percentage of donor derived CD11b in the blood of

INX902 treated mice and FIG. **55**A the donor derived T cells number in 25 μL of blood in INX902 treated mice or in DDE1 control mice.

[0826] Therefore Acute GvHD is effectively treated in irradiated BALB/c recipient using the INX902 agonist antibody. These results provide further evidence that VISTA agonist antibodies may be used to treat and prevent GvHD disease.

Example 31: Dose Efficacy of α-Human VISTA Antibodies INX901 and INX903 (10, 2.5, and 1 Mg/Kg) on GvHD in Irradiated BALB/c Mice Injected with DDE1 T Cells and Bone Marrow

[0827] We examined the immune-suppressive efficacy of α-human VISTA antibodies, INX901 and INX903, at various doses compared to a human Ig control by measuring their ability to modulate GVHD disease progression/severity. We also verified chimerism in the surviving mice by flow cytometry of peripheral blood taken from the recipient mice at 27-34 days post-treatment.

Materials and Methods

GvHD Model and Disease Severity Evaluation

[0828] 9-week old males BALB/c recipient mice were purchased from Jackson. 12-weeks old males Human-KI VISTA donor mice (DDE1) on C57/B16 background were purchased from Sage labs. All mice were housed in SPF conditions at the DHMC vivarium.

[0829] Recipient mice were subjected to total body irradiation (TBI) emanating from a cesium-137 source at 300 cGy at Day-1 and DO prior transfer.

[0830] Donor mice were euthanized and bone marrow was harvested by flushing femur and tibia with HBSS. Red blood cells were lysed using ACK solution. T cells were isolated from spleens by negative selection (Stemcell #19851).

[0831] Recipient mice received 10 million bone marrow cells and 2 million T cells along with 10 mg/kg human IgG2 (Crown Bioscience, lot #AB150073) or 10 mg/kg, 2.5 mg/kg or 1 mg/kg of INX901 (lot #BP-021-016-2) or INX903 (lot #BP-021-016-4). Cells and antibodies were administered by tail vein intravenous injection.

[0832] Mice were weighed regularly to monitor disease progression and euthanized if their weight dropped lower than 75% of their initial weight.

Flow Cytometric Analysis of Peripheral Blood

[0833] Peripheral blood was isolated from mice by retro-orbital bleed at 27 days (INX901) or 34 days (INX903) post-transfer.

[0834] Total blood was stained with Biolegend's fluorescently labelled antibodies to CD45, CD11b, CD3, H2Kd (recipient) and H2Kb (donor) then RBC were lysed using BD FACS Lysing solution (#349202). Cells were washed once with PBS after lysis.

[0835] Labeled cells were run on the Miltenyi MACSquant and analyzed using FlowJo.

Results

[0836] Acute GvHD is induced in irradiated BALB/c recipient by transferring allogenic (C57/B16) bone marrow and splenicT cells isolated from human VISTA-KI mice. Disease severity is measured by following weight loss. FIG. **56**A-D illustrates the mean (FIG. **56**A and FIG. **56**C) weight loss and survival (b and d) for INX901 (FIG. **56**C and FIG. **56**D) and INX903 (FIG. **56**A and FIG. **56**B) treated mice during the course of the experiment.

[0837] INX903 attenuates disease severity at all doses tested as assessed by the reduced weight loss compared to Control Ig treated mice (FIG. **56**A). INX903 also increases survival at all dose tested with the lowest dose of 1 mg/kg appearing more protective than higher doses (FIG. **56**B).

[0838] INX901 completely inhibits disease at all doses tested as assessed by the absence of weight loss compared to Control Ig treated mice (FIG. **56**C). INX901 also increases survival at all doses tested with the lowest dose of 1 mg/kg appearing more protective than higher doses (FIG. **56**D).

[0839] After 27 to 34 days, peripheral blood is harvested from surviving mice and tested for chimerism (donor derived hematopoietic system) by staining for donor (H2Kb) or recipient (H2Kd) MHC class I.

[0840] FIG. **57**A illustrates the percentage of chimerism in INX903 treated mice and FIG. **57**B the percentage of chimerism in INX901 treated mice. All mice that received bone marrow cells only and nearly all mice that received T cells and were treated with INX901 failed to reach chimerism due to "failure of engraftment" (FIG. **57**A and FIG. **57**B). This phenomenon could be explained by a suboptimal irradiation dose and the high potency of INX901 to suppress T cell activation. As noted above it is well established that T cells help engraftment especially at low doses of TBI. As evidence thereof, complete chimerism was achieved in almost all the mice that received T cells and were treated with the less suppressive INX903 (FIG. **57**A).

[0841] Therefore, INX901 and INX903 respectively suppress or attenuate acute GvHD at doses as low as 1 mg/kg. Lower doses appear more effective than higher doses although mortality could also be due to engraftment failure in mice receiving strong immune suppressive antibodies in the context of low doses of TBI. These results provide further evidence that VISTA agonist antibodies may be used to treat and prevent GvHD disease.

Example 32: Compared Efficacy of α-Human VISTA Antibodies INX803, INX804 at 10 mg/Kg on GvHD in Irradiated BALB/c Mice Injected with DDE1 T Cells and Bone Marrow

[0842] In these experiments we used fully C57/B16 Human-VISTA Knock in mice (DDE1) as donor for T cells and bone marrow transferred in irradiated BALB/c recipient. Disease progression was monitored by regularly weighting mice. We examined the immune-suppressive efficacy of α-human VISTA antibodies INX803 and INX804 compared to Human Ig control by measuring their ability to modulate disease progression/severity.

Materials and Methods

GvHD Model and Disease Severity Evaluation

[0843] 9-week old males BALB/c recipient mice were purchased from Jackson. 10-weeks old males Human-KI VISTA donor mice (DDE1) on C57/B16 background were purchased from Sage labs. All mice were housed in SPF conditions at the DHMC vivarium.

[0844] Recipient mice were subjected to total body irradiation (TBI) emanating from a cesium-137 source at 350 cGy at Day-1 and DO prior transfer.

[0845] Donor mice were euthanized and bone marrow was harvested by flushing femur and tibia with HBSS. Red blood cells were lysed using ACK solution. T cells were isolated from spleens by negative selection (Stemcell #19851).

[0846] Recipient mice received 10 million bone marrow cells and 2 million T cells along with 10 mg/kg human IgG2 (Crown Bioscience, lot #AB150073) or INX803 (lot #BP-018-016), INX804 (lot #BP-019-016). Cells and antibodies were administered by tail vein intravenous injection.

[0847] Mice were weighed regularly to monitor disease progression and euthanized if their weight dropped lower than 75% of their initial weight.

Results

[0848] FIG. **58**A-C illustrates the mean (**58**A) and individual (**58**B) weight loss and survival (**58**C) for each treated group during the course of the experiment. INX803 (Green) is strongly suppressive, inhibits disease development and fully protects the mice. INX804 attenuates disease severity at the peak of disease but fails to provide complete protection to the mice long term, half of which eventually succumb to GvHD. Therefore, the tested α-human VISTA antibodies showed immune-suppressive activity in their ability to attenuate or completely suppress acute GvHD. These results provide further evidence that anti-human VISTA agonist antibodies may be used to treat and prevent GvHD disease.

Example 33: Efficacy of α-Human VISTA Antibodies INX800 and INX801 on GvHD in Irradiated BALB/c Mice Injected with DDE1 T Cells and Bone Marrow

[0849] In these experiments we again used fully C57/B16 Human-VISTA Knock in mice (DDE1) as donor for T cells and bone marrow transferred in irradiated BALB/c recipient. Disease progression was monitored by regularly weighing mice. We examined the immune-suppressive efficacy of α-human VISTA antibodies INX800 and INX801, at 10 mg/kg compared to Human Ig control by measuring the ability to modulate disease progression/severity.

Materials and Methods

GvHD Model and Disease Severity Evaluation

[0850] 9-week old males BALB/c recipient mice were purchased from Jackson. 12-weeks old males Human-KI VISTA donor mice (DDE1) on C57/B16 background were purchased from Sage labs. All mice were housed in SPF conditions at the DHMC vivarium.

[0851] Recipient mice were subjected to total body irradiation (TBI) emanating from a cesium-137 source at 300 cGy at Day-1 and DO prior transfer.

[0852] Donor mice were euthanized and bone marrow was harvested by flushing femur and tibia with HBSS. Red blood cells were lysed using ACK solution. T cells were isolated from spleens by negative selection (Stemcell #19851).

[0853] Recipient mice received 5 million bone marrow cells and 1.6 million T cells along with 10 mg/kg human IgG2 (Crown Bioscience, lot #AB150073) 10 mg/kg of INX800 or INX801. Cells and antibodies were administered by tail vein intravenous injection.

[0854] Mice were weighed regularly to monitor disease progression and euthanized if their weight dropped lower than 80% of their initial weight.

Results

[0855] Both INX800 and INX801 mice lost less weight than the control treated group (FIG. **59**). In fact, while all mice from the control group had to be sacrificed within 2 weeks, all of the mice treated with INX800 or INX801 survived for >32 days (FIG. **59**). In the experiment acute GvHD was induced bytransfer ofT cells and BM from hV-KI mice into irradiated Balb/c recipients. Mice were tracked for disease by weight loss, with mice being sacrificed if more than 20% of the initial starting weight was lost.

[0856] Therefore, both INX800 and INX801 attenuate acute GvHD at a dose of 10 mg/kg. These mice suffered less weight loss and showed increased survival over the Ig control group. These results provide further evidence that anti-human VISTA agonist antibodies may be used to treat and prevent GvHD disease, both acute and chronic forms.

Example 34: Effects of Anti-Murine Vista Antibodies in NZBWF-1 Lupus Model

NZBWF-1 Lupus Model

[0857] New Zealand black×New Zealand white (NZBWF-1) is a commercially available lupus prone strain available through The Jackson Laboratory. These mice spontaneous develop lupus similar to systemic lupus erythematosus (SLE) patients with prevalence in female mice. Hallmarks of disease include the onset of proteinuria, glomerulonephritis, elevated levels of self-reactive antibodies such as ds DNA antibodies, hemolytic anemia and immune complex deposition in the kidneys. At the cellular level, T cell, B cell and myeloid cell abnormalities have been reported.

[0858] In these experiments, we examined the function of 8G8, a hamster a mouse VISTA antibody in female NZBWF-1 mice. Mice were treated three times a week with control-Ig or 8G8. Mice were monitored weekly for proteinuria and body weight. Serum was collected every two weeks during the treatment. At the end of the experiment, serum, spleens and kidneys were harvested. Serum was stored at −80° C. until required for Luminex assay.

[0859] Spleens were processed for flow cytometric analysis, cell sorting or snap frozen in OCT for immunofluorescence staining and RNA isolation for gene profiling and nanoString analysis. One kidney was snap frozen in OCT for immunofluorescence staining and RNA isolation for gene profiling and nanoString analysis. The second kidney was fixed and paraffin embedded. Paraffin sections were H&E stained for clinical pathology.

Materials and Methods

Mouse Treatment

[0860] 8-week old female NZBWF-1 mice were purchased from Jackson and stored in SPF conditions at the DHMC.

[0861] Proteinuria and body weight were monitored weekly in the Dartmouth Hitchcock animal facility.

[0862] Control-IgG/Hamster Ig or 8G8 was administered three times a week at 300 ag/mouse by i.p injection.

[0863] Mice were sacrificed upon signs of poor health and reduced activity, and according to animal facility protocols.

Proteinuria

[0864] Chemstrips 10 were purchased from Roche. Urine was collected from mice and placed onto the chemstrip. To determine protein in the urine, the colorimetric scale was used: Omg/dL, trace (1 mg/dL), 30 mg/dL, 100 mg/dL and 500 mg/dL.

Serum Analysis

[0865] Serum was collected and stored at −80° C. until required. Chemokine and cytokine levels were determined using a 32 Milliplex Mouse Cytokine/Chemokine Magnetic Bead Panel (Millipore) and the assay run on a Bio-plex 200 System (Life Science Research, Bio Rad). Data was analyzed using the Bio-Plex Manager 6.0 software.

Clinical Pathology

[0866] Kidneys were placed into cassettes and fixed O/N in 10% Formalin at room temperature, then briefly washed in PBS and transferred and kept into 70% Ethanol (Fisher Scientific) prior to being transferred to the Pathology Translational Research Core at the Geisel School of Medicine at Dartmouth where they were paraffin embedded, sectioned and then stained.

[0867] Paraffin embedded tissue sections (4 μm) were stained using a Leica BOND RX automated stainer. After dewaxing, the sections were subjected to antigen retrieval (Bond epitope retrieval solution 2, 1002C, 20 min) and incubated with the primary antibody (see dilution below) for 30-60 min, at room temperature in Leica diluent. Slides are then washed 3×5 min washes in PBS and incubated with secondary antibody (from Leica Bond Refine detection kit, DS9800). After 3 final washes in PBS the sections were incubated with DAB (Leica Bond polymer detection kit), rinsed, counterstained with hematoxylin and mounted.

[0868] Clinical pathology will be assessed by a pathologist.

Results

[0869] This experiment was designed to examine whether 8G8 mediated an immunosuppressive role in female NZBWF-1 mice. Mice were monitored weekly from 16 weeks old for proteinuria development. At week 32, the week after proteinuria was detected, mice were treated with 300 μg of Hamster Ig or 8G8 by i.p injection three times a week. At week 33 all mice in the Hamster Ig group were sacrificed due to poor health, and spleens, kidneys and plasma were collected. AS shown in FIG. **60**, the mice in the 8G8 group displayed better health and reduced proteinuria.

[0870] To determine the effect of 8G8 on mediators in the plasma, a 32 Multiplex Mouse Cytokine/Chemokine Magnetic Luminex assay was run. A significant reduction in LIX/CXCL5 and an increase in IL-9 was detected (FIG. **61**). Specifically, as shown in FIG. **61** LIX/CXCL5 and IL-9 levels in the serum of Control-Ig and 8G8 treated NZBWF-1 mice were detected. Serum was collected at week 33 from Control-IgG (n=5) and 8G8 mice (n=5) and chemokines and cytokines were assessed on a 32 plex run using Bio-plex 200 Systems and analyzed by Bio Plex manager 6.0 software. Data is shown as the mean+/−SEM and statistical significance was determined by the unpaired Student t Test. In FIG. **61** **denotes significance ($p<0.01$) between groups.

[0871] The decrease in LIX/CXCL5 is of note as its expression is regulated by IL-17 and is a pathogenic cytokine in lupus. It is also associated with neutrophil recruitment and accelerated atherosclerosis in SLE (Nalbandian et al., "Interleukin-17 and systemic lupus erythematosus: current concepts", *Clinical and Experimental Immunology.* 2009; 157(2):209-15; Lopez-Pedrera et al., "Accelerated atherosclerosis in systemic lupus erythematosus: role of proinflammatory cytokines and therapeutic approaches", *Journal of Biomedicine & Biotechnology,* 2010 Article ID 607084). The increase of IL-9 suggests 8G8 promotes and anti-inflammatory environment, as IL-9 can play a role in reducing inflammation in SLE (Leng et al., "Potential roles of IL-9 in the pathogenesis of systemic lupus erythematosus", *American Journal of Clinical and Experimental Immunology* 2012; 1(1):28-32)

CONCLUSION

[0872] The agonistic anti-VISTA agonistic 8G8 improved survival, increased protective anti-inflammatory cytokines and reduced inflammatory cytokines and further reduced the development of proteinuria (FIG. **60**, **61**). These results indicate that agonistic anti-VISTA antibodies may be used in the treatment or prevention of lupus and for managing the pathological side effects of lupus such as its deleterious effects on kidney function and for enhancing survival.

Example 35: Effects of Anti-Mouse Vista Antibody in NZBWF-1 Lupus Model

NZBWF-1 Lupus Model

[0873] The NZBWF-1 lupus model is described supra. In this group of experiments using the NZBWF-1 lupus model, we again examined the function of 8G8, a hamster a mouse VISTA antibody in female NZBWF-1 mice. Mice were treated three times a week with control-Ig or 8G8. Mice were monitored weekly for proteinuria and body weight. Serum was collected every two weeks during the treatment. At the end of the experiment, serum, spleens and kidneys were harvested. Serum was stored at −80° C. until required for Luminex assay.

[0874] Spleens were processed for flow cytometric analysis, cell sorting or snap frozen in OCT for immunofluorescence staining and RNA isolation for gene profiling and nanoString analysis. One kidney was snap frozen in OCT for immunofluorescence staining and RNA isolation for gene profiling and nanoString analysis. The second kidney was fixed and paraffin embedded. Paraffin sections were H&E stained for clinical pathology.

Materials and Methods

Mouse Treatment

[0875] 8-week old female NZBWF-1 mice were purchased from Jackson and stored in SPF conditions at the DHMC.

[0876] Proteinuria and body weight were monitored weekly in the Dartmouth Hitchcock animal facility.

[0877] Control-IgG/Hamster Ig or 8G8 was administered three times a week at 300 ag/mouse by i.p injection

[0878] Mice were sacrificed upon signs of poor health and reduced activity, and according to animal facility protocols.

Proteinuria

[0879] Chemstrips 10 were purchased from Roche. Urine was collected from mice and placed onto the chemstrip. To determine protein in the urine, the colorimetric scale was used: Omg/dL, trace (1 mg/dL), 30 mg/dL, 100 mg/dL and 500 mg/dL.

Serum Analysis

[0880] Serum was collected and stored at −80° C. until required. Chemokine and cytokine levels were determined using a 32 Milliplex Mouse Cytokine/Chemokine Magnetic Bead Panel (Millipore) and the assay run on a Bio-plex 200 System (Life Science Research, Bio Rad). Data was analyzed using the Bio-Plex Manager 6.0 software.

Myeloid-Derived Suppressor Cell Isolation Kit

[0881] Myeloid-Derived Suppressor Cells (MDSCs) were isolated using the Myeloid-Derived Suppressor Cell Isolation Kit from Miltenyi Biotec according to the manufacturer's instructions. RNA Isolation and nanoString

[0882] RNA was isolated from MDSCs using Trizol (Life Technologies) and the PureLink RNA Mini Kit (Ambion). RNA was run on a mouse inflammatory nanoString 12 assay (nanoString Technologies) and the data was quantified using the nSolver Analysis Software.

Clinical Pathology

[0883] Kidneys were placed into cassettes and fixed O/N in 10% Formalin at room temperature, then briefly washed in PBS and transferred and kept into 70% Ethanol (Fisher Scientific) prior to being transferred to the Pathology Translational Research Core at the Geisel School of Medicine at Dartmouth where they were paraffin embedded, sectioned and then stained.

[0884] Paraffin embedded tissue sections (4 μm) were stained using a Leica BOND RX automated stainer. After dewaxing, the sections were subjected to antigen retrieval (Bond epitope retrieval solution 2, 1002C, 20 min) and incubated with the primary antibody (see dilution below) for 30-60 min, at room temperature in Leica diluent. Slides are then washed 3×5 min washes in PBS and incubated with secondary antibody (from Leica Bond Refine detection kit, DS9800). After 3 final washes in PBS the sections were incubated with DAB (Leica Bond polymer detection kit), rinsed, counterstained with hematoxylin and mounted.

[0885] Clinical pathology will be assessed by a pathologist.

Results

[0886] This experiment was designed to examine whether 8G8 mediated an immunosuppressive role in female NZBWF-1 mice. Mice were monitored weekly from 22 weeks old for proteinuria development. On week 28, the week after proteinuria was detected; mice were treated with 300 μg of Hamster Ig or 8G8 by i.p injection three times a week. Whereas disease severity in the control group continued to increase, the mice in the 8G8 group displayed reduced proteinuria levels (FIG. **62**).

[0887] As shown in the figure the agonistic anti-VISTA antibody 8G8 reduced the development of proteinuria (FIG. **62**).

Example 36: Evaluation of Anti-Vista Antibodies in I MRL/lpr Lupus Model

I MRL/lpr Lupus Animal Model

[0888] As noted, MRL/lpr is a commercially available lupus prone strain available through The Jackson Laboratory. These mice show signs of lymphoproliferation due to a spontaneous mutation in Fas (Faslpr). Hallmarks of disease include immune complex glomerulonephrosis and high levels of circulating immune complexes. Abnormalities in the T cell compartment have also been reported. In this experiment, we examined the function of 8G8, a hamster a mouse VISTA antibody in female MRL/lpr mice. Mice were treated three times a week with control-Ig/hamster-Ig or 8G8. Mice were monitored weekly for proteinuria and body weight. Serum was collected every two weeks during the treatment. At the end of the experiment, serum, spleens and kidneys were harvested. Serum was stored at −80° C. until required for Luminex assay. Spleens and lymph nodes were processed for cell sorting or snap frozen in OCT for immunofluorescence staining and RNA isolation for gene profiling and nanoString analysis. One kidney was snap frozen in OCT for immunofluorescence staining and RNA isolation for gene profiling and nanoString analysis. The second kidney was fixed and paraffin embedded. Paraffin sections were H&E stained for clinical pathology.

Materials and Methods

Mouse Treatment

[0889] 12-week old female NZBWF-1 mice were purchased from Jackson and stored in SPF conditions at the DHMC.

[0890] Proteinuria and body weight was monitored weekly in the Dartmouth Hitchcock animal facility.

[0891] Control-Ig/Hamster Ig or 8G8 was administered three times a week at 300 ag/mouse by i.p injection

[0892] Mice were sacrificed when proteinuria was 500 mg/dL.

Proteinuria

[0893] Chemstrips 10 were purchased from Roche. Urine was collected from mice and placed onto the chemstrip. To determine protein in the urine, the colorimetric scale was used: Omg/dL, trace (1 mg/dL), 30 mg/dL, 100 mg/dL and 500 mg/dL.

Serum Analysis

[0894] Serum was collected and stored at −80° C. until required. Chemokine and cytokine levels were determined using a 32 Milliplex Mouse Cytokine/Chemokine Magnetic Bead Panel (Millipore) and the assay run on a Bio-plex 200 System (Life Science Research, Bio Rad). Data was analyzed using the Bio-Plex Manager 6.0 software.

RNA Isolation and nanoString

[0895] RNA was isolated using Trizol (Life Technologies) and the PureLink RNA Mini Kit (Ambion). RNA was run on

a mouse inflammatory nanoString 12 assay (nanoString Technologies) and the data was quantified using the nSolver Analysis Software.

Clinical Pathology

[0896] Kidneys were placed into cassettes and fixed O/N in 10% Formalin at room temperature, then briefly washed in PBS and transferred and kept into 70% Ethanol (Fisher Scientific) prior to being transferred to the Pathology Translational Research Core at the Geisel School of Medicine at Dartmouth where they were paraffin embedded, sectioned and then stained.

[0897] Paraffin embedded tissue sections (4 μm) were stained using a Leica BOND RX automated stainer. After dewaxing, the sections were subjected to antigen retrieval (Bond epitope retrieval solution 2, 100° C., 20 min) and incubated with the primary antibody (see dilution below) for 30-60 min, at room temperature in Leica diluent. Slides are then washed 3×5 min washes in PBS and incubated with secondary antibody (from Leica Bond Refine detection kit, DS9800). After 3 final washes in PBS the sections were incubated with DAB (Leica Bond polymer detection kit), rinsed, counterstained with hematoxylin and mounted.

[0898] Clinical pathology will be assessed by a pathologist.

Results

[0899] This experiment was designed to examine whether 8G8 mediated an immunosuppressive role in female MRL/lpr mice. Mice were monitored weekly from 15 weeks old for proteinuria development. On week 16, mice were treated with 300 μg of Hamster Ig or 8G8 by i.p injection three times a week. To determine the effect of 8G8 on mediators in the plasma was collected and stored at −80° C. Spleens and lymph nodes were harvested and snap frozen for immunofluorescence staining and RNA isolation. The agonistic anti-VISTA antibody 8G8 reduced the incidence of disease development as characterized by high proteinuria levels (see FIG. **63**).

[0900] As shown in FIG. **63** the agonist anti-mouse VISTA antibody 8G8 reduces proteinuria development in MRL/lpr mice in an experiment wherein 15 week old female MRL/lpr mice were monitored weekly for proteinuria. Proteinuria values were recorded using chemstrips and quantified as mg/dL. On week 16, mice were treated with either 300 ug hamster-Ig (black line, n=8) or 300 ug 8G8 (red line, n=8) by i.p injection three times a week. Data at week 21 were discarded due to technical problems with the chemstrips. (FIG. **63** A) Average proteinuria is shown with standard error bars. (FIG. **63** B) Disease incidence at each time point was calculated as the percent of mice in each group that exhibited proteinuria at or greater than 100 mg/dL. Accordingly 8G8 reduced the incidence of disease development as characterized by high proteinuria levels.

[0901] As shown in FIG. **64** 8G8 also reduces splenomegaly in MRL/lpr mice in an experiments wherein spleens were harvested on week 23 from mice were treated with either 300 ug Control-Ig/hamster-Ig or 300 ug 8G8 by i.p injection three times a week. Splenomegaly was observed in Control-Ig treated mice compared to 8G8 treated mice. (representative spleens shown in the Figure).

[0902] As further shown in FIG. **65** 8G8 also reduces lymphoproliferation of cervical lymph nodes in MRL/lpr mice in experiments wherein cervical lymph nodes were harvested on week 23 from mice treated with either 300 ug Control-Ig/hamster-Ig or 300 ug 8G8 by i.p injection three times a week. Lymphoproliferation was observed in Control-Ig treated mice compared to 8G8 treated mice. Shown here are representative cervical lymph nodes.

[0903] These results further indicate that agonistic anti-VISTA antibodies may be used in the treatment or prevention of lupus and for managing the pathological side effects of lupus such as its deleterious effects on kidney function, and on the spleen and on pathological lymphoproliferation.

Example 37: Evaluation of Anti-Vista Antibodies in I MRL/lpr Lupus Model

I MRL/lpr Lupus Animal Model

[0904] The MRL/lpr lupus model is described supra. In this experiment, we again examined the effects of 8G8, a hamster a mouse VISTA antibody in female MRL/lpr mice. Mice were treated three times a week with PBS, control-Ig/hamster-Ig or 8G8. Mice were monitored weekly for proteinuria and body weight. Serum was collected every two weeks during the treatment. At the end of the experiment, serum, lymph nodes, spleens and kidneys were harvested. Serum was stored at −80° C. Organs were fixed and paraffin embedded. Paraffin sections were H&E stained for clinical pathology.

Materials and Methods

Mouse Treatment

[0905] 8-week old female MRL/lpr mice were purchased from Jackson and stored in SPF conditions at the DHMC.

[0906] Proteinuria and body weight was monitored weekly in the Dartmouth Hitchcock animal facility.

[0907] 10 mg/kg/mouse control-Ig/hamster Ig or 8G8 or 200 μL of PBS was administered three times a week by i.p injection starting at week 11.

[0908] Mice were sacrificed when proteinuria was 500 mg/dL.

Proteinuria

[0909] Chemstrips 10 were purchased from Roche. Urine was collected from mice and placed onto the chemstrip. To determine protein in the urine, the colorimetric scale was used: 0 mg/dL, trace (1 mg/dL), 30 mg/dL, 100 mg/dL and 500 mg/dL.

Serum Analysis

[0910] Serum was collected and stored at −80° C. until required.

Clinical Pathology

[0911] Kidneys were placed into cassettes and fixed O/N in 10% Formalin at room temperature, then briefly washed in PBS and transferred and kept into 70% Ethanol (Fisher Scientific) prior to being transferred to the Pathology Translational Research Core at the Geisel School of Medicine at Dartmouth where they were paraffin embedded, sectioned and then stained.

[0912] Paraffin embedded tissue sections (4 μm) were stained using a Leica BOND RX automated stainer. After dewaxing, the sections were subjected to antigen retrieval (Bond epitope retrieval solution 2, 1002C, 20 min) and incubated with the primary antibody (see dilution below) for 30-60 min, at room temperature in Leica diluent. Slides are

then washed 3×5 min washes in PBS and incubated with secondary antibody (from Leica Bond Refine detection kit, DS9800). After 3 final washes in PBS the sections were incubated with DAB (Leica Bond polymer detection kit), rinsed, counterstained with hematoxylin and mounted.

[0913] Clinical pathology will be assessed by a pathologist.

Results

[0914] This experiment was designed to examine whether 8G8 mediated an immunosuppressive role in female MRL/lpr mice. Mice were monitored weekly from 9 weeks old for proteinuria development. On week 11, mice were treated with 200 μL of PBS or 10 mg/kg of hamster Ig or 8G8 by i.p injection three times a week. To determine the effect of 8G8 on mediators in the plasma was collected and stored at −80° C.

[0915] Thus, the VISTA agonist 8G8 reduced the incidence of disease development as characterized by high proteinuria levels (see FIG. **66**). In the experiments 9 week old female MRL/lpr mice were monitored weekly for proteinuria. Proteinuria values were recorded using chemstrips and quantified as mg/dL. On week 11, mice were treated with either 200 uL PBS (dotted black line, n=8) or 10 mg/kg hamster-Ig (solid black line, n=8) or 10 mg/kg 8G8 (red line, n=8) by i.p injection three times a week. (FIG. **66**A) Average proteinuria is shown with standard error bars. (FIG. **66**B) Disease incidence at each time point was calculated as the percent of mice in each group that exhibited proteinuria at or greater than 100 mg/dL.

[0916] These results further indicate that agonistic anti-VISTA antibodies may be used in the treatment or prevention of lupus and for managing the pathological side effects of lupus such as its deleterious effects on kidney function.

Example 38: Effects of Anti-Human VISTA Agonist Antibody INX903 on Disease Induction in a Mouse Model of Systemic Lupus Erythematosus

[0917] In the present experiment, we tested the effects of an anti-human VISTA agonist antibody in an accepted lupus model. In this murine model SLE is induced by the transfer of human VISTA knock-in DDE1 CD8 depleted splenocytes (donor) into a B6D2F1 host (recipient) Further, in this model, donor CD4 T cell polyclonal activation drives cognate host B cell activation, expansion, and their production of autoantibodies leading to renal disease.

[0918] This lupus animal model meets 4 out of 11 American College of Rheumatology (ACR) criteria for lupus ("Systemic lupus erythematosus;" Tsokos G C. N Engl J Med. 2011 Dec. 1; 365(22):2110-21). Lupus-like features of B6 CD8 depleted transferred to B6D2F1 model include: (1) Immune complex glomerulonephritis; (2) anti-nuclear ab; (3) anti-dsDNA ab; and (4) anti-RBC ab (Coombs positivity). Additionally, this model meets sex-based differences in renal disease severity.

[0919] More particularly, we tested the effects of INX903 (human anti-human VISTA-IgG2 wherein treatment was effected in the early stages of SLE induction. It is accepted in the art that two-week phenotypes reliably predict the long-term clinical phenotypes and can serve as early surrogate markers for long-term disease ("Advances in lupus stemming from the parent-into-F1 model". Via CS. *Trends Immunol.,* 2010 June 31(6):236-45).

Materials and Methods

Study Design

[0920] A schematic summarizing the experimental parameters is contained in FIG. **67**. As shown therein INX903 (anti-human IgG2 agonist antibody containing variable regions of VSTB95 antibody) was administered at days 0, 2, and 6 following DDE1 transfer. At each time point, 4 mice per group were analyzed plus 1 naïve mouse. Spleens were processed for flow cytometry, and serum was recovered from cardiac blood for detection of anti-dsDNA IgG by ELISA.

Mice

[0921] Human VISTA KI (DDE1) mice have the human VISTA cDNA knocked-in in place of the mouse VISTA gene, and express only human VISTA both at RNA and protein level. The mice are bred at Sage Labs (Boyertown, PA). The mice, aged 8-12 weeks, first transited for 3 weeks in the quarantine facility, and then were transferred to our regular facility. 4-month old female DDE1 mice were used. 9 weeks old female B6D2F1 mice were purchased from the Jackson Lab.

Spleen Cell Isolation and Transfer

[0922] The equivalent of 1 DDE1 donor spleen was transferred per B6D2F1 mouse recipient.

[0923] Single cell suspensions were prepared from 36 DDE1 spleens by mechanical disruption. RBCs were lysed with ACK.

[0924] CD8 T cells were depleted using Dynabeads® Mouse CD8 (Lyt 2) (Thermofisher #11447D) according to manufacturer instruction.

[0925] To follow cell proliferation, spleen cells were stained with Cell Trace Violet (Cell Trace™ Violet Cell Proliferation Kit, for flow cytometry (Thermofisher #C34557) according to manufacturer instruction.

[0926] A total of $1{,}230\times10^6$ CD8 depleted spleen cells was obtained.

[0927] Each B6D2F1 mouse received 34×10^6 CD8 depleted spleen cells in a volume of 20011 per tail vein injection (iv).

Anti-Human VISTA Antibodies and Dosage

[0928] INX903 was dosed at 10 mg/kg.

[0929] At day 0, antibodies were directly added to the cell suspension just prior IV transfer into recipient B6D2F1 mice.

[0930] Mice were then dosed on day 2 and 6 via intraperitoneal (ip) injections.

[0931] Control group received human IgG2 (Lot AB150073—4.7 mg/mL).

[0932] Treated group received INX903 (Lot BP-021-016-4—6 mg/mL).

Analysis of Immune Cell by Flow

[0933] At day 1, 3, 7 and 14 after donor cell transfer, donor CD4 T cell activation, proliferation, accumulation, and host B cell activation and accumulation were evaluated by flow cytometry on the spleens. Four animals per group +1 naïve mouse were analyzed at each time point. Spleens were mechanically disrupted, RBCs were lysed using ACK buffer and total viable nucleated cell number was evaluated using a Cellometer automated cell counting system and AOPI. 2 million cells were stained with the following panels as shown below:

Day 1

B1 FITC	B2 PE	B3 PerCp Cy5.5	B4 PE-Cy7	R1 AF647	R2 APC-Cy7	V1 BV421	V2 BV510	
IAd 1/1000	H2Kd 1/200	B220 1/200	CD69 1/200	H2Kb 1/200	CD4 1/300	CTV NA	Yellow LD 1/1000	FcBlock 1/200

Following Days:

B1 FITC	B2 PE	B3 PerCp Cy5.5	B4 PE-Cy7	R1 AF647	R2 APC-Cy7	V1 BV421	V2 BV510	
IAd 1/1000	H2Kd 1/200	B220 1/200	CD25 1/200	H2Kb 1/200	CD4 1/300	CTV NA	Yellow LD 1/1000	FcBlock 1/200

[0934] Samples were run on a MacsQuant flow cytometer and analyzed with the FlowJo program.

[0935] Donor CD4 T cells were identified as Live, CD4+ B220− H2Kb+H2Kd− and analyzed for activation marker expression (CD69 or CD25) and proliferation (Cell Trace Violet dilution). Donor CD4 cell number per spleen were calculated by applying the percentage of donor CD4 T cells on total viable cell number in the spleens.

[0936] Recipient B cells were identified as Live, CD4-B220+ H2Kb+H2Kd+ and analyzed for MHC class II expression. At each time point a naïve B6D2F1 served for basal MHC class II expression comparison. Recipient B cell numbers per spleen were calculated by applying the percentage of Host B cells on total viable cell number in the spleens.

Anti-Double Stranded DNA Detection

[0937] Anti-dsDNA IgG in the serum at day 7 and 14 were quantified using an ELISA kit from Alpha Diagnostic (Cat. No. 5120) according to manufacturer instruction.

Identification of Recipient and Donor Cell Population

[0938] As shown in FIG. **68**, the SLE mice generated by transfer of DDE1 spleen cells (minus $CD8^+$ cells) show the presence of both donor and recipient B and CD4 T cells. Donor CD4 T cells were identified as Live, $CD4^+B220^-$ $H2Kb^+$ $H2Kd^-$. Recipient B cells were identified as Live, CD4-$B220^+$ H2Kb+ $H2Kd^+$. In the experiments in FIG. **68** donor and host cell populations are distinguished by their MHC class I alleles. The host B6D2F1 cells express both H-2Kb and H-2Kd, whereas the donor DDE1 cells express only H-2Kb.

INX903 Leads to Decreases in SLE Disease Progression

[0939] To determine if the anti-VISTA agonist antibody INX903 can affect early disease progression, we evaluated recipient B cell activation, production of dsDNA antibodies, CD4 T cell activation and proliferation. It was shown that INX903 administration leads to a decrease in recipient B cell activation and accumulation and resulting splenomegaly. B cell activation was demonstrated by the increased expression of MHC class II I^{Ad} over time following the transplantation in the human IgG2 (HuIgG2) treated group while no change in IAd was noted in the INX903 treated group which appear similar to naïve mice. These results are shown in FIG. **69**A. To note, this is an indirect effect as B cells from recipient mice do not express human VISTA and as such cannot respond directly to INX903.

[0940] B cell gradual expansion following the transplantation in the human IgG2 (HuIgG2) treated group reaching 200% of normal F1 values at D14 and resulting in mild splenomegaly is also prevented in the INX903 treated group (See FIGS. **69**B and C). The data in the figure further show that B cells activation during SLE progression is also prevented by INX903 treatment. FIG. **69**A contains histogram plots of MHCII IAd expression on recipient B cells. FIG. **69**B shows the total number of recipient B cells and spleen cells over the course of the experiment and MHC class II IAd MFI on recipient B cell over the course of the experiment (n=4, SEM). FIG. **69**C shows spleen size in the treated animal at D14.

[0941] The experimental data in FIG. **70** further demonstrates that INX903 administration leads to reduced anti-dsDNA autoantibodies production. In these experiments anti-dsDNA IgG titer in serum measured by ELISA in naïve (n=2), and HuIgG2 or INX903 treated mice at D7 and D14 (n=4, SEM). The experimental data in FIG. **71** additionally shows that INX903 administration leads to a decrease in T cell activation and proliferation. As shown therein CD69 expression is decreased at early time points. Specifically it can be seen that CD69 expression is decreased at Day 1 in INX903-treated CD4 T cells (n=4).

[0942] The experimental data in FIGS. **72** and **73** further shows that there is a sustained reduction in the accumulation of donor $CD4^+$ T cells following transfer. Despite dividing with the same frequency as the huIgG2-treated group CD4 T cells in INX903-treated mice are dramatically decreased over time (n=4). These experimental results show that administration of the exemplified anti-human VISTA agonist Ab resulted in the following: (i) reduced T cell proliferation and activation (this is the only model available where disease-initiating T cells can be tracked); (ii) reduced cognate B cell activation (MHCII expression) and accumulation; (iii) reduced splenomegaly and (iv) reduced anti-dsDNA IgG auto-antibodies production.

[0943] While observed after a relatively short duration, these results are significant because in this model, 2-week phenotypes are known to reliably predict the long-term clinical phenotypes and can serve as early surrogate markers for long-term disease.

Example 39: Effects of the α-Mouse VISTA Antibody 8G8 on Systemic Lupus Erythematosus—MRL/lpr-SCD8G8MRL1

[0944] In this experiment, we again examined the effects of 8G8, a hamster anti-mouse VISTA agonist antibody in female MRL/lpr mice. Mice were treated three times a week with control-Ig/hamster-Ig or 8G8. Mice were monitored weekly for proteinuria and body weight. Serum was collected every two weeks during the treatment. At the end of the experiment, serum, spleens and kidneys were harvested. Serum was stored at −80° C. until required for luminex assay. Spleens and lymph nodes were processed for cell sorting or snap frozen in OCT for immunofluorescence staining and RNA isolation for gene profiling and nanoString analysis. One kidney was snap frozen in OCT for immunofluorescence staining and RNA isolation for gene profiling and nanoString analysis. The second kidney was fixed and paraffin embedded. Paraffin sections were H&E stained for clinical pathology.

Materials and Methods

Mouse Treatment

[0945] 12-week old female NZBWF-1 mice were purchased from Jackson and stored in SPF conditions at the DHMC.

[0946] Proteinuria and body weight was monitored weekly in the Dartmouth Hitchcock animal facility.

[0947] Control-Ig/Hamster Ig or 8G8 was administered three times a week at 300 ag/mouse by i.p injection

[0948] Mice were sacrificed when proteinuria was 500 mg/dL.

Proteinuria

[0949] Chemstrips 10 were purchased from Roche. Urine was collected from mice and placed onto the chemstrip. To determine protein in the urine, the colorimetric scale was used: Omg/dL, trace (1 mg/dL), 30 mg/dL, 100 mg/dL and 500 mg/dL.

Serum Analysis

[0950] Serum was collected and stored at −80° C. until required. Chemokine and cytokine levels were determined using a 32 Milliplex Mouse Cytokine/Chemokine Magnetic Bead Panel (Millipore) and the assay run on a Bio-plex 200 System (Life Science Research, Bio Rad). Data was analyzed using the Bio-Plex Manager 6.0 software.

RNA Isolation and nanoString

[0951] RNA was isolated using Trizol (Life Technologies) and the PureLink RNA Mini Kit (Ambion). RNA was run on a mouse inflammatory nanoString 12 assay (nanoString Technologies) and the data was quantified using the nSolver Analysis Software.

Clinical Pathology

[0952] Kidneys were placed into cassettes and fixed O/N in 10% Formalin at room temperature, then briefly washed in PBS and transferred and kept into 70% Ethanol (Fisher Scientific) prior to being transferred to the Pathology Translational Research Core at the Geisel School of Medicine at Dartmouth where they were paraffin embedded, sectioned and then stained.

[0953] Paraffin embedded tissue sections (4 μm) were stained using a Leica BOND RX automated stainer. After dewaxing, the sections were subjected to antigen retrieval (Bond epitope retrieval solution 2, 100° C., 20 min) and incubated with the primary antibody (see dilution below) for 30-60 min, at room temperature in Leica diluent. Slides are then washed 3×5 min washes in PBS and incubated with secondary antibody (from Leica Bond Refine detection kit, DS9800). After 3 final washes in PBS the sections were incubated with DAB (Leica Bond polymer detection kit), rinsed, counterstained with hematoxylin and mounted.

[0954] Clinical pathology was assessed by a pathologist.

Results

[0955] Mice were monitored weekly from 15 weeks old for proteinuria development. On week 16, mice were treated with 300 μg of Hamster Ig or 8G8 by i.p injection three times a week. To determine the effect of 8G8 on mediators in the plasma was collected and stored at −80° C. Spleens and lymph nodes were harvested and snap frozen for immunofluorescence staining and RNA isolation. As shown in FIG. **74**A-B 8G8 reduces proteinuria development in MRL/lpr mice. In these experiments 15 week old female MRL/lpr mice were monitored weekly for proteinuria. Proteinuria values were recorded using chemstrips and quantified as mg/dL. On week 16, mice were treated with either 300 ug hamster-Ig (black line, n=8) or 300 ug 8G8 (red line, n=8) by i.p injection three times a week. Data at week 21 were discarded due to technical problems with the chemstrips. (FIG. **74**A) Average proteinuria is shown with standard error bars. (FIG. **74**B) Disease incidence at each time point was calculated as the percent of mice in each group that exhibited proteinuria at or greater than 100 mg/dL.

[0956] As further shown in FIG. **75** 8G8 administration also reduces splenomegaly in MRL/lpr mice. In these experiments spleens were harvested on week 23 from mice were treated with either 300 ug Control-Ig/hamster-Ig or 300 ug 8G8 by i.p injection three times a week. Splenomegaly was observed in Control-Ig treated mice compared to 8G8 treated mice. Shown here are representative spleens.

[0957] As further shown in FIG. **76** 8G8 administration also 8G8 reduces lymphoproliferation of cervical lymph nodes in MRL/lpr mice. In these experiments cervical lymph nodes were harvested on week 23 from mice treated with either 300 ug Control-Ig/hamster-Ig or 300 ug 8G8 by i.p injection three times a week. Lymphoproliferation was observed in Control-Ig treated mice compared to 8G8 treated mice.

Example 40: Effects of the α-Mouse VISTA Antibody 8G8 on Systemic Lupus Erythematosus—New Zealand Black×New Zealand White (NZBWF-1 Mice)

[0958] We examined the function of 8G8, a hamster a mouse VISTA antibody in female NZBWF-1 mice. Mice were treated three times a week with control-Ig or 8G8. Mice were monitored weekly for proteinuria and body weight. Serum was collected every two weeks during the treatment. At the end of the experiment, serum, spleens and kidneys were harvested. Serum was stored at −80° C. until required for luminex assay.

[0959] Spleens were processed for flow cytometric analysis, cell sorting or snap frozen in OCT for immunofluores-

cence staining and RNA isolation for gene profiling and nanoString analysis. One kidney was snap frozen in OCT for immunofluorescence staining and RNA isolation for gene profiling and nanoString analysis. The second kidney was fixed and paraffin embedded. Paraffin sections were H&E stained for clinical pathology.

Materials and Methods

Mouse Treatment

[0960] 8-week old female NZBWF-1 mice were purchased from Jackson and stored in SPF conditions at the DHMC.

[0961] Proteinuria and body weight were monitored weekly in the Dartmouth Hitchcock animal facility.

[0962] Control-IgG/Hamster Ig or 8G8 was administered three times a week at 300 ag/mouse by i.p injection

[0963] Mice were sacrificed upon signs of poor health and reduced activity, and according to animal facility protocols.

Proteinuria

[0964] Chemstrips 10 were purchased from Roche. Urine was collected from mice and placed onto the chemstrip. To determine protein in the urine, the colorimetric scale was used: Omg/dL, trace (1 mg/dL), 30 mg/dL, 100 mg/dL and 500 mg/dL.

Serum Analysis

[0965] Serum was collected and stored at −80° C. until required. Chemokine and cytokine levels were determined using a 32 Milliplex Mouse Cytokine/Chemokine Magnetic Bead Panel (Millipore) and the assays run on a Bio-plex 200 System (Life Science Research, Bio Rad). Data was analyzed using the Bio-Plex Manager 6.0 software.

Myeloid-Derived Suppressor Cell Isolation Kit

[0966] Myeloid-Derived Suppressor Cells (MDSCs) were isolated using the Myeloid-Derived Suppressor Cell Isolation Kit from Miltenyi Biotec according to the manufacturer's instructions.

RNA Isolation and nanoString

[0967] RNA was isolated from MDSCs using Trizol (Life Technologies) and the PureLink RNA Mini Kit (Ambion). RNA was run on a mouse inflammatory nanoString 12 assay (nanoString Technologies) and the data was quantified using the nSolver Analysis Software.

Immunofluorescence Staining

[0968] Kidneys were embedded in OCT and 9 μ[illegible] sections cut and stored at −80° C. Slides were placed at RT for 20 mins, fixed in pre-chilled acetone for 10 mins and removed to evaporate excess acetone, rehydrated in PBS for 5 mins and sections circled using an ImmEdge pen (Vector Labs). They were incubated with 10% goat serum (Jackson ImmunoResearch) for 1 hr at RT and washed. Sections were stained with directly conjugated antibodies to C3 and IgG diluted in PBS for 2 hr at RT and washed for 2 mins, then mounted in ProLong Gold Antifade Mountant with DAPI (Life Technologies) and stored at RT in the dark for 48 hr. Images were acquired on a Zeiss Confocal Microscope and analyzed with LSM 510 Meta software.

Clinical Pathology

[0969] Kidneys were placed into cassettes and fixed O/N in 10% Formalin at room temperature, then briefly washed in PBS and transferred and kept into 70% Ethanol (Fisher Scientific) prior to being transferred to the Pathology Translational Research Core at the Geisel School of Medicine at Dartmouth where they were paraffin embedded, sectioned and then stained.

[0970] Paraffin embedded tissue sections (4 μm) were stained using a Leica BOND RX automated stainer. After dewaxing, the sections were subjected to antigen retrieval (Bond epitope retrieval solution 2, 100° C., 20 min) and incubated with the primary antibody (see dilution below) for 30-60 min, at room temperature in Leica diluent. Slides are then washed 3×5 min washes in PBS and incubated with secondary antibody (from Leica Bond Refine detection kit, DS9800). After 3 final washes in PBS the sections were incubated with DAB (Leica Bond polymer detection kit), rinsed, counterstained with hematoxylin and mounted.

[0971] Clinical pathology was assessed by a pathologist.

Results

[0972] This experiment was designed to examine whether 8G8 mediated an immunosuppressive role in female NZBWF-1 mice. Mice were monitored weekly from 22 weeks old for proteinuria development. On week 28, the week after proteinuria was detected, mice were treated with 300 μg of Hamster Ig or 8G8 by i.p injection three times a week. Whereas disease severity in the control group continued to increase, the mice in the 8G8 group displayed reduced proteinuria levels

[0973] Particularly, as shown in FIG. **77** 8G8 antibody administration educes proteinuria development in NZBWF-1 mice. As shown therein these 22-week-old female NZBWF-1 mice were monitored weekly for proteinuria. Proteinuria values were recorded using chemstrips and quantified as mg/dL. On week 28, mice were treated with either 300 ug Ham-Ig (black line, n=6) or 300 ug 8G8 (red line, n=6) by i.p injection three times a week.

[0974] As shown in FIG. **78** 8G8 exerted no impact on immune complex deposition in NZBWF-1 mice. As shown therein the same 22-week-old female NZBWF-1 mice were monitored weekly for proteinuria. Mice were treated 3 times a week with 300 ug Ham-Ig (n=8) or 300 ug 8G8. To determine immune complex (ICs) deposition in B6, Ham-Ig and 8G8 mice, immunofluorescence staining was performed on frozen OCT kidney sections to detect C3 (red) and IgG (green) ICs by confocal microscopy at a magnification ×40 microscopy.

[0975] The results are further shown in the Table below. These values further corroborate that 8G8 reduces kidney damage in NZBWF-1 mice. In the experiments clinical pathology was examined using paraffin embedded kidneys from Ham-Ig or 8G8 treated NZBWF-1 and C57BL/6 (naïve controls) mice which were H&E stained and blindly clinically examined for interstitial inflammation and glomerular damage. *Denotes significance between groups.

TABLE 4

8G8 reduces kidney damage in NZBWF-1 mice

Strain	Interstitial inflammation score	Glomerular score
B6	0	0
Ham-Ig	1.5 ± 0.5	2.5 ± 0.8
8G8	0.8 ± 0.4*	0.8 ± 0.4**

CONCLUSIONS

[0976] The results of these animal assays and other experiments disclosed herein indicate that agonist or immunosuppressive anti-VISTA agonist antibodies may be used for the treatment and prevention of autoimmune, allergic, inflammatory conditions or other conditions where immunosuppression is therapeutically desired; and in particular provide compelling evidence that agonist anti-VISTA agonist antibodies may be used for treating and preventing lupus, GVHD, RA, IBD, chronic infection and hepatotoxicity, psoriasis and for preventing, reducing or managing the symptoms of other acute and chronic autoimmune, allergic, inflammatory conditions.

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[0977] The following references and other references cited in this application are incorporated by reference in their entireties.

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SEQUENCE LISTING

SEQUENCE LISTING

SEQ ID NO: 1: *Homo sapiens* VISTA (Alternate names: B7-H5; B7H5; DD1alpha; GI24; PP2135; SISP1) AMINO ACID SEQUENCE

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121      sasdhhgnfs itmrnltlld sglycclvve irhhhsehrv hgamelqvqt gkdapsncvv

181      ypsssqdsen itaaalatga civgilclpl illlvykqrq aasnrraqel vrmdsniqgi

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301      pvpdspnfev i
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 61      skghdvtiyk twylssrgev qmckehrpir nftlqhlqhh gshlkanash dqpqkhglel

121      asdhhgnfsi tlrnvtprds glycclviel knhhpeqrfy gsmelqvqag kgsgstcmas

181      neqdsdsita aalatgaciv gilclplill lvykqrqvas hrraqelvrm dsntqgienp

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SEQUENCE LISTING

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 121      asdhhgnfsi tlrnvtprds glycclviel knhhpeqrfy gsmelqvqag kgsgstcmas

 181      neqdsdsita aalatgaciv gilclplill lvykqrqvas hrraqelvrm dssntqgien

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4141      acagggggct gcaggggtcc tgccaccacc gagcaccaac ttggcccctg gggtcctgcc

4201      tcatgaatga ggccttcccc agggctggcc tgactgtgct gggggctggg ttaacgtttt

4261      ctcagggaac cacaatgcac gaaagaggaa ctggggttgc taaccaggat gctgggaaca

4321      aaggcctctt gaagcccagc cacagcccag ctgagcatga ggcccagccc atagacggca

4381      caggccacct ggcccattcc ctgggcattc cctgctttgc attgctgctt ctcttcaccc

4441      catggaggct atgtcaccct aactatcctg gaatgtgttg agagggattc tgaatgatca

4501      atatagcttg gtgagacagt gccgagatag atagccatgt ctgccttggg cacgggagag

4561      ggaagtggca gcatgcatgc tgtttcttgg ccttttctgt tagaatactt ggtgctttcc

4621      aacacacttt cacatgtgtt gtaacttgtt tgatccaccc ccttccctga aaatcctggg

4681      aggttttatt gctgccattt aacacagagg gcaatagagg ttctgaaagg tctgtgtctt

4741      gtcaaaacaa gtaaacggtg gaactacgac taaa

//
```

SEQ ID NO: 5: *Homo sapiens* VISTA (Alternate names: B7-H5; B7H5; DD1alpha; GI24; PP2135; SISP1) CODING NUCLEIC ACID SEQUENCE

```
   1      ctcgccgcgc tgagccgcct cgggacggag ccatgcggcg ctgggcctgg gccgcggtcg

  61      tggtccccct cgggccgcag ctcgtgctcc tcgggggcgt cggggcccgg cgggaggcac

 121      agaggacgca gcagcctggc cagcgcgcag atccccccaa cgccaccgcc agcgcgtcct

 181      cccgcgaggg gctgcccgag gcccccaagc catcccaggc ctcaggacct gagttctccg

 241      acgcccacat gacatggctg aactttgtcc ggcggccgga cgacggcgcc ttaaggaagc

 301      ggtgcggaag cagggacaag aagccgcggg atctcttcgg tcccccagga cctccaggtg

 361      cagaagtgac cgcggagact ctgcttcacg agtttcagga gctgctgaaa gaggccacgg

 421      agcgccggtt ctcagggctt ctggacccgc tgctgcccca gggggcgggc ctgcggctgg

 481      tgggcgaggc ctttcactgc cggctgcagg gtccccgccg ggtggacaag cggacgctgg

 541      tggagctgca tggtttccag gctcctgctg cccaaggtgc cttcctgcga ggctccggtc

 601      tgagcctggc ctcgggtcgg ttcacggccc ccgtgtccgg catcttccag ttctctgcca

 661      gtctgcacgt ggaccacagt gagctgcagg gcaaggcccg gctgcgggcc cgggacgtgg

 721      tgtgtgttct catctgtatt gagtccctgt gccagcgcca cacgtgcctg gaggccgtct

 781      caggcctgga gagcaacagc agggtcttca cgctacaggt gcaggggctg ctgcagctgc

 841      aggctggaca gtacgcttct gtgtttgtgg acaatggctc cggggccgtc ctcaccatcc

 901      aggcgggctc cagcttctcc gggctgctcc tgggcacgtg agggcgccca ggggggctgg

 961      cgaggagctg ccgccggatc ccggggaccc tcctactgat gcccgtggtc accacaataa

1021      agagccctcc accctcaaaa aaaaaaaaaa aaaaa

//
```

SEQ ID NO: 6: *Mus musculus* VISTA CODING NUCLEIC ACID SEQUENCE

```
   1      ctcgccgcgc tgagccgcct cgggacggag ccatgcggcg ctgggcctgg gccgcggtcg

  61      tggtccccct cgggccgcag ctcgtgctcc tcgggggcgt cggggcccgg cgggaggcac
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SEQUENCE LISTING

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 121      agaggacgca gcagcctggc cagcgcgcag atccccccaa cgccaccgcc agcgcgtcct

 181      cccgcgaggg gctgcccgag gcccccaagc catcccaggc ctcaggacct gagttctccg

 241      acgcccacat gacatggctg aactttgtcc ggcggccgga cgacggcgcc ttaaggaagc

 301      ggtgcggaag cagggacaag aagccgcggg atctcttcgg tcccccagga cctccaggtg

 361      cagaagtgac cgcggagact ctgcttcacg agtttcagga gctgctgaaa gaggccacgg

 421      agcgccggtt ctcagggctt ctggacccgc tgctgcccca gggggcgggc ctgcggctgg

 481      tgggcgaggc ctttcactgc cggctgcagg gtccccgccg ggtggacaag cggacgctgg

 541      tggagctgca tggtttccag gctcctgctg cccaaggtgc cttcctgcga ggctccggtc

 601      tgagcctggc ctcgggtcgg ttcacggccc ccgtgtccgg catcttccag ttctctgcca

 661      gtctgcacgt ggaccacagt gagctgcagg gcaaggcccg gctgcgggcc cgggacgtgg

 721      tgtgtgttct catctgtatt gagtccctgt gccagcgcca cacgtgcctg gaggccgtct

 781      caggcctgga gagcaacagc agggtcttca cgctacaggt gcaggggctg ctgcagctgc

 841      aggctggaca gtacgcttct gtgtttgtgg acaatggctc cggggccgtc ctcaccatcc

 901      aggcgggctc cagcttctcc gggctgctcc tgggcacgtg agggcgccca ggggggctgg

 961      cgaggagctg ccgccggatc ccggggaccc tcctactgat gcccgtggtc accacaataa

1021      agagccctcc accctcaaaa aaaaaaaaaa aaaaa

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SEQUENCE LISTING

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Sequence total quantity: 819
SEQ ID NO: 1            moltype = AA  length = 311
FEATURE                 Location/Qualifiers
source                  1..311
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1
MGVPTALEAG SWRWGSLLFA LFLAASLGPV AAFKVATPYS LYVCPEGQNV TLTCRLLGPV  60
DKGHDVTFYK TWYRSSRGEV QTCSERRPIR NLTFQDLHLH HGGHQAANTS HDLAQRHGLE  120
SASDHHGNFS ITMRNLTLLD SGLYCCLVVE IRHHHSEHRV HGAMELQVQT GKDAPSNCVV  180
YPSSSQDSEN ITAAALATGA CIVGILCLPL ILLLVYKQRQ AASNRRAQEL VRMDSNIQGI  240
ENPGFEASPP AQGIPEAKVR HPLSYVAQRQ PSESGRHLLS EPSTPLSPPG PGDVFFPSLD  300
PVPDSPNFEV I                                                       311

SEQ ID NO: 2            moltype = AA  length = 308
FEATURE                 Location/Qualifiers
source                  1..308
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 2
MGVPAVPEAS SPRWGTLLLA IFLAASRGLV AAFKVTTPYS LYVCPEGQNA TLTCRILGPV  60
SKGHDVTIYK TWYLSSRGEV QMCKEHRPIR NFTLQHLQHH GSHLKANASH DQPQKHGLEL  120
ASDHHGNFSI TLRNVTPRDS GLYCCLVIEL KNHHPEQRFY GSMELQVQAG KGSGSTCMAS  180
NEQDSDSITA AALATGACIV GILCLPLILL LVYKQRQVAS HRRAQELVRM DSNTQGIENP  240
GFETTPPFQG MPEAKTRPPL SYVAQRQPSE SGRYLLSDPS TPLSPPGPGD VFFPSLDPVP  300
DSPNSEAI                                                           308

SEQ ID NO: 3            moltype = AA  length = 309
FEATURE                 Location/Qualifiers
source                  1..309
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 3
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MGVPAVPEAS SPRWGTLLLA IFLAASRGLV AAFKVTTPYS LYVCPEGQNA TLTCRILGPV  60
SKGHDVTIYK TWYLSSRGEV QMCKEHRPIR NFTLQHLQHH GSHLKANASH DQPQKHGLEL  120
ASDHHGNFSI TLRNVTPRDS GLYCCLVIEL KNHHPEQRFY GSMELQVQAG KGSGSTCMAS  180
NEQDSDSITA AALATGACIV GILCLPLILL LVYKQRQVAS HRRAQELVRM DSSNTQGIEN  240
PGFETTPPFQ GMPEAKTRPP LSYVAQRQPS ESGRYLLSDP STPLSPPGPG DVFFPSLDPV  300
PDSPNSEAI                                                          309

SEQ ID NO: 4            moltype = DNA  length = 4774
FEATURE                 Location/Qualifiers
source                  1..4774
                        mol_type = unassigned DNA
                        organism = Homo sapiens
SEQUENCE: 4
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agtcgcggga ggcttccccg cgccggccgc gtcccgcccg ctccccggca ccagaagttc  120
ctctgcgcgt ccgacggcga catgggcgtc cccacggccc tggaggccgg cagctggcgc  180
tggggatccc tgctcttcgc tctcttcctg gctgcgtccc taggtccggt ggcagccttc  240
aaggtcgcca cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc  300
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cgcaacctga ccctgctgga tagcggcctc tactgctgcc tggtggtgga gatcaggcac  600
caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac aggcaaagat  660
gcaccatcca actgtgtggt gtacccatcc tcctcccagg atagtgaaaa catcacggct  720
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ggaagtggca gcatgcatgc tgtttcttgg ccttttctgt tagaatactt ggtgctttcc  4620
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aggttttatt gctgccattt aacacagagg gcaatagagg ttctgaaagg tctgtgtctt  4740
gtcaaaacaa gtaaacggtg gaactacgac taaa                              4774

SEQ ID NO: 5            moltype = DNA  length = 1055
FEATURE                 Location/Qualifiers
source                  1..1055
                        mol_type = unassigned DNA
                        organism = Homo sapiens
SEQUENCE: 5
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tggtcccccct cgggccgcag ctcgtgctcc tcgggggcgt cggggcccgg cgggaggcac  120
agaggacgca gcagcctggc cagcgcgcag atcccccaa cgccaccgcc agcgcgtcct  180
cccgcgaggg gctgcccgag gcccccaagc catcccaggc ctcaggacct gagttctccg  240
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tgagcctggc ctcgggtcgg ttcacggccc ccgtgtccgg catcttccag ttctctgcca  660
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aggctggaca gtacgcttct gtgtttgtgg acaatggctc cggggccgtc ctcaccatcc  900
aggcgggctc cagcttctcc gggctgctcc tgggcacgtg agggcgccca gggggggctgg  960
cgaggagctg ccgccggatc ccggggaccc tcctactgat gcccgtggtc accacaataa  1020
agagccctcc accctcaaaa aaaaaaaaaa aaaaa                             1055

SEQ ID NO: 6            moltype = DNA  length = 1055
FEATURE                 Location/Qualifiers
source                  1..1055
                        mol_type = unassigned DNA
                        organism = Mus musculus
SEQUENCE: 6
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tggtcccccct cgggccgcag ctcgtgctcc tcgggggcgt cggggcccgg cgggaggcac  120
agaggacgca gcagcctggc cagcgcgcag atcccccaa cgccaccgcc agcgcgtcct  180
cccgcgaggg gctgcccgag gcccccaagc catcccaggc ctcaggacct gagttctccg  240
acgcccacat gacatggctg aactttgtcc ggcggccgga cgacggcgcc ttaaggaagc  300
ggtgcggaag cagggacaag aagccgcggg atctcttcgg tcccccagga cctccaggtg  360
cagaagtgac cgcggagact ctgcttcacg agtttcagga gctgctgaaa gaggccacgg  420
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aggcgggctc cagcttctcc gggctgctcc tgggcacgtg agggcgccca gggggggctgg  960
cgaggagctg ccgccggatc ccggggaccc tcctactgat gcccgtggtc accacaataa  1020
agagccctcc accctcaaaa aaaaaaaaaa aaaaa                             1055

SEQ ID NO: 7            moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 7
FKVATPYSLY VCPEG                                                    15
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SEQ ID NO: 8            moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
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                        organism = Homo sapiens
SEQUENCE: 8
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SEQ ID NO: 9            moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 9
YSLYVCPEGQ NVTLT                                                15

SEQ ID NO: 10           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 10
YVCPEGQNVT LTCRL                                                15

SEQ ID NO: 11           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 11
PEGQNVTLTC RLLGP                                                15

SEQ ID NO: 12           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 12
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SEQ ID NO: 13           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 13
TLTCRLLGPV DKGHD                                                15

SEQ ID NO: 14           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 14
CRLLGPVDKG HDVTF                                                15

SEQ ID NO: 15           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 15
LGPVDKGHDV TFYKT                                                15

SEQ ID NO: 16           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 16
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SEQ ID NO: 17           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
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SEQUENCE: 17
GHDVTFYKTW YRSSR                                                15

SEQ ID NO: 18           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 18
VTFYKTWYRS SRGEV                                                15

SEQ ID NO: 19           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 19
YKTWYRSSRG EVQTC                                                15

SEQ ID NO: 20           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 20
WYRSSRGEVQ TCSER                                                15

SEQ ID NO: 21           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 21
SSRGEVQTCS ERRPI                                                15

SEQ ID NO: 22           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 22
GEVQTCSERR PIRNL                                                15

SEQ ID NO: 23           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 23
QTCSERRPIR NLTFQ                                                15

SEQ ID NO: 24           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 24
SERRPIRNLT FQDLH                                                15

SEQ ID NO: 25           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 25
RPIRNLTFQD LHLHH                                                15

SEQ ID NO: 26           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 26
RNLTFQDLHL HHGGH                                                15
```

-continued

```
SEQ ID NO: 27          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 27
TFQDLHLHHG GHQAA                                                15

SEQ ID NO: 28          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 28
DLHLHHGGHQ AANTS                                                15

SEQ ID NO: 29          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 29
LHHGGHQAAN TSHDL                                                15

SEQ ID NO: 30          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 30
GGHQAANTSH DLAQR                                                15

SEQ ID NO: 31          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 31
QAANTSHDLA QRHGL                                                15

SEQ ID NO: 32          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 32
NTSHDLAQRH GLESA                                                15

SEQ ID NO: 33          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 33
HDLAQRHGLE SASDH                                                15

SEQ ID NO: 34          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 34
AQRHGLESAS DHHGN                                                15

SEQ ID NO: 35          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 35
HGLESASDHH GNFSI                                                15

SEQ ID NO: 36          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
```

-continued

```
                        organism = Homo sapiens
SEQUENCE: 36
ESASDHHGNF SITMR                                                15

SEQ ID NO: 37           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 37
SDHHGNFSIT MRNLT                                                15

SEQ ID NO: 38           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 38
HGNFSITMRN LTLLD                                                15

SEQ ID NO: 39           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 39
FSITMRNLTL LDSGL                                                15

SEQ ID NO: 40           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 40
TMRNLTLLDS GLYCC                                                15

SEQ ID NO: 41           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 41
NLTLLDSGLY CCLVV                                                15

SEQ ID NO: 42           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 42
LLDSGLYCCL VVEIR                                                15

SEQ ID NO: 43           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 43
SGLYCCLVVE IRHHH                                                15

SEQ ID NO: 44           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 44
YCCLVVEIRH HHSEH                                                15

SEQ ID NO: 45           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 45
LVVEIRHHHS EHRVH                                                15
```

-continued

```
SEQ ID NO: 46          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 46
EIRHHHSEHR VHGAM                                                15

SEQ ID NO: 47          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 47
HHHSEHRVHG AMELQ                                                15

SEQ ID NO: 48          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 48
SEHRVHGAME LQVQT                                                15

SEQ ID NO: 49          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 49
RVHGAMELQV QTGKD                                                15

SEQ ID NO: 50          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 50
GAMELQVQTG KDAPS                                                15

SEQ ID NO: 51          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 51
ELQVQTGKDA PSNCV                                                15

SEQ ID NO: 52          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 52
VQTGKDAPSN CVVYP                                                15

SEQ ID NO: 53          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 53
GKDAPSNCVV YPSSS                                                15

SEQ ID NO: 54          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 54
APSNCVVYPS SSQDS                                                15

SEQ ID NO: 55          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
```

-continued

```
                        organism = Homo sapiens
SEQUENCE: 55
NCVVYPSSSQ DSENI                                                15

SEQ ID NO: 56           moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 56
VYPSSSQDSE NITAA                                                15

SEQ ID NO: 57           moltype = AA  length = 114
FEATURE                 Location/Qualifiers
REGION                  1..114
                        note = IE8 VH Polypeptide
source                  1..114
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 57
EVKLLESGGG LVQPGGSLKL SCAASGFDFS RYWMSWVRQA PGKGLEWIGE VYPDSSTINY  60
TPSLKDKFII SRDNAKNTLY LQMIKVRSED TALYYCARGR GDYWGQGTSV TVSS        114

SEQ ID NO: 58           moltype = AA  length = 108
FEATURE                 Location/Qualifiers
REGION                  1..108
                        note = IE8 VL Polypeptide
source                  1..108
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 58
DIQMTQSPAS LSASVGETVT ITCRASGNIH NYLSWYHQKQ GKSPQLLVYN AKTLADGVPS  60
RFSGSGSGTQ YSLKINSLQP EDFGSYYCQN FWSTPFTFGS GTKLEIKR               108

SEQ ID NO: 59           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 59
NLTLLDSGL                                                       9

SEQ ID NO: 60           moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 60
VQTGKDAPSN C                                                    11

SEQ ID NO: 61           moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 61
PVDKGHDVTF                                                      10

SEQ ID NO: 62           moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 62
RRPIRDLTFQ DL                                                   12

SEQ ID NO: 63           moltype = AA  length = 326
FEATURE                 Location/Qualifiers
REGION                  1..326
                        note = IgG2 C233S (A-locked)
source                  1..326
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 63
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTVER KCSVECPPCP APPVAGPSVF  120
```

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```
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTFR  180
VVSVLTVVHQ DWLNGKEYKC KVSNKGLPAP IEKTISKTKG QPREPQVYTL PPSREEMTKN  240
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPMLDSD GSFFLYSKLT VDKSRWQQGN  300
VFSCSVMHEA LHNHYTQKSL SLSPGK                                       326

SEQ ID NO: 64          moltype = AA  length = 326
FEATURE                Location/Qualifiers
REGION                 1..326
                       note = IgG2 C127S (B-blocked)
source                 1..326
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 64
ASTKGPSVFP LAPSSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTVER KCCVECPPCP APPVAGPSVF  120
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTFR  180
VVSVLTVVHQ DWLNGKEYKC KVSNKGLPAP IEKTISKTKG QPREPQVYTL PPSREEMTKN  240
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPMLDSD GSFFLYSKLT VDKSRWQQGN  300
VFSCSVMHEA LHNHYTQKSL SLSPGK                                       326

SEQ ID NO: 65          moltype = AA  length = 330
FEATURE                Location/Qualifiers
REGION                 1..330
                       note = IgG1 with silent Fc (INX901Si and INX908Si)
source                 1..330
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 65
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPEAAGA  120
SSVFLFPPKP KDTLMISRTP EVTCVVVDVS AEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPSSIEKTIS KAKGQPREPQ VYTLPPSREE  240
MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 66          moltype = AA  length = 327
FEATURE                Location/Qualifiers
REGION                 1..327
                       note = IgG2 CH1/hinge and IgG1 silent Fc (INX901HSi and
                        INX908HSi)
source                 1..327
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 66
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTVER KCCVECPPCP APEAAGASSV  120
FLFPPKPKDT LMISRTPEVT CVVVDVSAED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  180
RVVSVLTVLH QDWLNGKEYK CKVSNKALPS SIEKTISKAK GQPREPQVYT LPPSREEMTK  240
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  300
NVFSCSVMHE ALHNHYTQKS LSLSPGK                                      327

SEQ ID NO: 67          moltype = AA  length = 12
FEATURE                Location/Qualifiers
source                 1..12
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 67
NVTLTCRLLG PV                                                      12

SEQ ID NO: 68          moltype = AA  length = 12
FEATURE                Location/Qualifiers
source                 1..12
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 68
EVQTCSERRP IR                                                      12

SEQ ID NO: 69          moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 69
SDHHGNFS                                                           8

SEQ ID NO: 70          moltype = AA  length = 6
```

-continued

```
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 70
HHHSEH                                                          6

SEQ ID NO: 71           moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 71
NVTLTCRLLG PV                                                   12

SEQ ID NO: 72           moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 72
TCRLLGPVDK G                                                    11

SEQ ID NO: 73           moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 73
HGGHQAA                                                         7

SEQ ID NO: 74           moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 74
SASDHHGNFS                                                      10

SEQ ID NO: 75           moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 75
HHHSEHRVHG AM                                                   12

SEQ ID NO: 76           moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 76
HHHSEHRVHG AM                                                   12

SEQ ID NO: 77           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 77
LTCRLLGPV                                                       9

SEQ ID NO: 78           moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 78
EVQTCSERRP IR                                                   12

SEQ ID NO: 79           moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
```

-continued

```
SEQUENCE: 79
HLHHGGHQAA                                                          10

SEQ ID NO: 80          moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 80
SDHHGNFS                                                            8

SEQ ID NO: 81          moltype = AA  length = 12
FEATURE                Location/Qualifiers
source                 1..12
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 81
HHHSEHRVHG AM                                                       12

SEQ ID NO: 82          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 82
LLGPVDKGHD VTFYK                                                    15

SEQ ID NO: 83          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 83
LAQRHGLESA SDHHG                                                    15

SEQ ID NO: 84          moltype = AA  length = 12
FEATURE                Location/Qualifiers
source                 1..12
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 84
HHHSEHRVHG AM                                                       12

SEQ ID NO: 85          moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 85
EVQTCSERR                                                           9

SEQ ID NO: 86          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 86
TFQDLHLHHG GHQAA                                                    15

SEQ ID NO: 87          moltype = AA  length = 13
FEATURE                Location/Qualifiers
source                 1..13
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 87
CLVVEIRHHH SEH                                                      13

SEQ ID NO: 88          moltype = AA  length = 10
FEATURE                Location/Qualifiers
source                 1..10
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 88
EVQTCSERRP                                                          10

SEQ ID NO: 89          moltype = AA  length = 11
```

-continued

```
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 89
TCRLLGPVDK G                                                    11

SEQ ID NO: 90           moltype = AA  length = 5
FEATURE                 Location/Qualifiers
source                  1..5
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 90
SDHHG                                                           5

SEQ ID NO: 91           moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 91
HHHSEHRVHG AM                                                   12

SEQ ID NO: 92           moltype =   length =
SEQUENCE: 92
000

SEQ ID NO: 93           moltype =   length =
SEQUENCE: 93
000

SEQ ID NO: 94           moltype =   length =
SEQUENCE: 94
000

SEQ ID NO: 95           moltype =   length =
SEQUENCE: 95
000

SEQ ID NO: 96           moltype =   length =
SEQUENCE: 96
000

SEQ ID NO: 97           moltype =   length =
SEQUENCE: 97
000

SEQ ID NO: 98           moltype =   length =
SEQUENCE: 98
000

SEQ ID NO: 99           moltype =   length =
SEQUENCE: 99
000

SEQ ID NO: 100          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 100
GYTLTDYN                                                        8

SEQ ID NO: 101          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 101
INLNYAIT                                                        8

SEQ ID NO: 102          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
source                  1..14
                        mol_type = protein
                        organism = Mus musculus
```

-continued

```
SEQUENCE: 102
ARGGYRYTYY AMDY                                                    14

SEQ ID NO: 103          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 103
ENIYSN                                                             6

SEQ ID NO: 104          moltype =   length =
SEQUENCE: 104
000

SEQ ID NO: 105          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 105
QHFWGTPRT                                                          9

SEQ ID NO: 106          moltype = AA  length = 121
FEATURE                 Location/Qualifiers
source                  1..121
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 106
EVQLQQFGAE LVKPGASVKI SCKASGYTLT DYNMDWVKQS HGKSLEWIGH INLNYAITTY  60
NQKFKGKATL TVDKSSSTAY MELRSLTSED TAVYYCARGG YRYTYYAMDY WGQGTSVTVS  120
S                                                                  121

SEQ ID NO: 107          moltype = AA  length = 222
FEATURE                 Location/Qualifiers
source                  1..222
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 107
AKTTPPSVYP LAPGSAAQTN SMVTLGCLVK GYFPEPVTVT WNSGSLSSGV HTFPAVLQSD  60
LYTLSSSVTV PSSTWPSETV TCNVAHPASS TKVDKKIVPR DCGCKPCICT VPEVSSVFIF  120
PPKPKDVLTI TLTPKVTCVV VDISKDDPEV QFSWFVDDVE VHTAQTQPRE EQFNSTFRSV  180
SELPIMHQDW LNGKEFKCRV NSAAFPAPIE KTISKTKLNP KS                     222

SEQ ID NO: 108          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 108
DIQMTQSPAS LSVSVGETVT ITCRASENIY SNLAWYQQKQ GKSPQLLVYA ATNLADGVPS  60
RFSGSGSGTQ YSLKINSLQS EDFGSYYCQH FWGTPRTFGG GTKLEIK                107

SEQ ID NO: 109          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 109
RADAAPTVSI FPPSSEQLTS GGASVVCFLN NFYPKDINVK WKIDGSERQN GVLNSWTDQD  60
SKDSTYSMSS TLTLTKDEYE RHNSYTCEAT HKTSTSPIVK SFNRNEC                107

SEQ ID NO: 110          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 110
GYTLTDYN                                                           8

SEQ ID NO: 111          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 111
```

-continued

```
INLNYAIT                                                            8

SEQ ID NO: 112          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
source                  1..14
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 112
ARGGYRYTYY AMDY                                                     14

SEQ ID NO: 113          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 113
ENIYSN                                                              6

SEQ ID NO: 114          moltype =   length =
SEQUENCE: 114
000

SEQ ID NO: 115          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 115
QHFWGTPRT                                                           9

SEQ ID NO: 116          moltype = AA  length = 121
FEATURE                 Location/Qualifiers
source                  1..121
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 116
EVQLQQFGAE LVKPGASVKI SCKASGYTLT DYNMDWVKQS HGKSLEWIGH INLNYAITTY  60
NQKFKGKATL TVDKSSSTAY MELRSLTSED TAVYYCARGG YRYTYYAMDY WGQGTSVTVS  120
S                                                                   121

SEQ ID NO: 117          moltype = AA  length = 326
FEATURE                 Location/Qualifiers
source                  1..326
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 117
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTVER KCCVECPPCP APPVAGPSVF  120
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTFR  180
VVSVLTVVHQ DWLNGKEYKC KVSNKGLPAP IEKTISKTKG QPREPQVYTL PPSREEMTKN  240
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPMLDSD GSFFLYSKLT VDKSRWQQGN  300
VFSCSVMHEA LHNHYTQKSL SLSPGK                                        326

SEQ ID NO: 118          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 118
DIQMTQSPAS LSVSVGETVT ITCRASENIY SNLAWYQQKQ GKSPQLLVYA ATNLADGVPS  60
RFSGSGSGTQ YSLKINSLQS EDFGSYYCQH FWGTPRTFGG GTKLEIK                 107

SEQ ID NO: 119          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 119
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                 107

SEQ ID NO: 120          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Mus musculus
```

-continued

```
SEQUENCE: 120
GYSFTGYT                                                            8

SEQ ID NO: 121          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 121
INPYNGGI                                                            8

SEQ ID NO: 122          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 122
ARRTLLRPYF FDY                                                      13

SEQ ID NO: 123          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 123
QSVSTSTFSY                                                          10

SEQ ID NO: 124          moltype =   length =
SEQUENCE: 124
000

SEQ ID NO: 125          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 125
QHSWEIPYT                                                           9

SEQ ID NO: 126          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 126
EVQLQQSGPE LVKPGTSMKI SCKASGYSFT GYTMNWVRQS HGKNLEWIGL INPYNGGINY  60
NQKFKARATL TVDKSSSTAY MELLSLTSED SAVYYCARRT LLRPYFFDYW GQGTTLTVSS  120

SEQ ID NO: 127          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 127
EVQLQQSGPE LVKPGTSMKI SCKASGYSFT GYTMNWVRQS HGKNLEWIGL INPYNGGINY  60
NQKFKARATL TVDKSSSTAY MELLSLTSED SAVYYCARRT LLRPYFFDYW GQGTTLTVSS  120

SEQ ID NO: 128          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 128
DIVLTQSPAS LAVSLGQRAT ISCRASQSVS TSTFSYMHWY QQKPGQPPKL LIKYASNLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDTATY YCQHSWEIPY TFGGGTKLEI K           111

SEQ ID NO: 129          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 129
DIVLTQSPAS LAVSLGQRAT ISCRASQSVS TSTFSYMHWY QQKPGQPPKL LIKYASNLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDTATY YCQHSWEIPY TFGGGTKLEI K           111

SEQ ID NO: 130          moltype = AA  length = 8
```

-continued

```
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 130
GYSFTGYT                                                            8

SEQ ID NO: 131          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 131
INPYNGGI                                                            8

SEQ ID NO: 132          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 132
ARRTLLRPYF FDY                                                      13

SEQ ID NO: 133          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 133
QSVSTSTFSY                                                          10

SEQ ID NO: 134          moltype =   length =
SEQUENCE: 134
000

SEQ ID NO: 135          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 135
QHSWEIPYT                                                           9

SEQ ID NO: 136          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 136
EVQLQQSGPE LVKPGTSMKI SCKASGYSFT GYTMNWVRQS HGKNLEWIGL INPYNGGINY  60
NQKFKARATL TVDKSSSTAY MELLSLTSED SAVYYCARRT LLRPYFFDYW GQGTTLTVSS  120

SEQ ID NO: 137          moltype = AA  length = 326
FEATURE                 Location/Qualifiers
source                  1..326
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 137
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTVER KCCVECPPCP APPVAGPSVF  120
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTFR  180
VVSVLTVVHQ DWLNGKEYKC KVSNKGLPAP IEKTISKTKG QPREPQVYTL PPSREEMTKN  240
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPMLDSD GSFFLYSKLT VDKSRWQQGN  300
VFSCSVMHEA LHNHYTQKSL SLSPGK                                       326

SEQ ID NO: 138          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 138
DIVLTQSPAS LAVSLGQRAT ISCRASQSVS TSTFSYMHWY QQKPGQPPKL LIKYASNLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDTATY YCQHSWEIPY TFGGGTKLEI K           111

SEQ ID NO: 139          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
```

-continued

```
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 139
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 140          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 140
GFDFSRYW                                                           8

SEQ ID NO: 141          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 141
VYPDSSTI                                                           8

SEQ ID NO: 142          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 142
ARGRGDY                                                            7

SEQ ID NO: 143          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 143
GNIHNY                                                             6

SEQ ID NO: 144          moltype =   length =
SEQUENCE: 144
000

SEQ ID NO: 145          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 145
QNFWSTPFT                                                          9

SEQ ID NO: 146          moltype = AA  length = 114
FEATURE                 Location/Qualifiers
source                  1..114
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 146
EVKLLESGGG LVQPGGSLKL SCAASGFDFS RYWMSWVRQA PGKGLEWIGE VYPDSSTINY  60
TPSLKDKFII SRDNAKNTLY LQMIKVRSED TALYYCARGR GDYWGQGTSV TVSS        114

SEQ ID NO: 147          moltype = AA  length = 326
FEATURE                 Location/Qualifiers
source                  1..326
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 147
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTVER KCCVECPPCP APPVAGPSVF  120
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTFR  180
VVSVLTVVHQ DWLNGKEYKC KVSNKGLPAP IEKTISKTKG QPREPQVYTL PPSREEMTKN  240
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPMLDSD GSFFLYSKLT VDKSRWQQGN  300
VFSCSVMHEA LHNHYTQKSL SLSPGK                                       326

SEQ ID NO: 148          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
```

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```
                      mol_type = protein
                      organism = Mus musculus
SEQUENCE: 148
DIQMTQSPAS LSASVGETVT ITCRASGNIH NYLSWYHQKQ GKSPQLLVYN AKTLADGVPS  60
RFSGSGSGTQ YSLKINSLQP EDFGSYYCQN FWSTPFTFGS GTKLEIK                107

SEQ ID NO: 149        moltype = AA  length = 107
FEATURE               Location/Qualifiers
source                1..107
                      mol_type = protein
                      organism = Mus musculus
SEQUENCE: 149
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 150        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 150
GFDFSRYW                                                           8

SEQ ID NO: 151        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 151
VYPDSSTI                                                           8

SEQ ID NO: 152        moltype = AA  length = 7
FEATURE               Location/Qualifiers
source                1..7
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 152
ARGRGDY                                                            7

SEQ ID NO: 153        moltype = AA  length = 6
FEATURE               Location/Qualifiers
source                1..6
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 153
GNIHNY                                                             6

SEQ ID NO: 154        moltype =   length =
SEQUENCE: 154
000

SEQ ID NO: 155        moltype = AA  length = 9
FEATURE               Location/Qualifiers
source                1..9
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 155
QNFWSTPFT                                                          9

SEQ ID NO: 156        moltype = AA  length = 114
FEATURE               Location/Qualifiers
source                1..114
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 156
EVKLLESGGG LVQPGGSLKL SCAASGFDFS RYWMSWVRQA PGKGLEWIGE VYPDSSTINY  60
TPSLKDKFII SRDNAKNTLY LQMIKVRSED TALYYCARGR GDYWGQGTSV TVSS        114

SEQ ID NO: 157        moltype = AA  length = 326
FEATURE               Location/Qualifiers
source                1..326
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 157
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTVER KCCVECPPCP APPVAGPSVF  120
```

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```
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTFR  180
VVSVLTVVHQ DWLNGKEYKC KVSNKGLPAP IEKTISKTKG QPREPQVYTL PPSREEMTKN  240
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPMLDSD GSFFLYSKLT VDKSRWQQGN  300
VFSCSVMHEA LHNHYTQKSL SLSPGK                                       326

SEQ ID NO: 158         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 158
DIQMTQSPAS LSASVGETVT ITCRASGNIH NYLSWYHQKQ GKSPQLLVYN AKTLADGVPS  60
RFSGSGSGTQ YSLKINSLQP EDFGSYYCQN FWSTPFTFGS GTKLEIK                107

SEQ ID NO: 159         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 159
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 160         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 160
GFDFSRYW                                                           8

SEQ ID NO: 161         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 161
VYPDSSTI                                                           8

SEQ ID NO: 162         moltype = AA  length = 7
FEATURE                Location/Qualifiers
source                 1..7
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 162
ARGRGDY                                                            7

SEQ ID NO: 163         moltype = AA  length = 6
FEATURE                Location/Qualifiers
source                 1..6
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 163
GNIHNY                                                             6

SEQ ID NO: 164         moltype =   length =
SEQUENCE: 164
000

SEQ ID NO: 165         moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 165
QNFWSTPFT                                                          9

SEQ ID NO: 166         moltype = AA  length = 114
FEATURE                Location/Qualifiers
source                 1..114
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 166
EVKLLESGGG LVQPGGSLKL SCAASGFDFS RYWMSWVRQA PGKGLEWIGE VYPDSSTINY  60
TPSLKDKFII SRDNAKNTLY LQMIKVRSED TALYYCARGR GDYWGQGTSV TVSS        114
```

-continued

```
SEQ ID NO: 167          moltype = AA  length = 326
FEATURE                 Location/Qualifiers
source                  1..326
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 167
ASTKGPSVFP LAPSSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTVER KCCVECPPCP APPVAGPSVF  120
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTFR  180
VVSVLTVVHQ DWLNGKEYKC KVSNKGLPAP IEKTISKTKG QPREPQVYTL PPSREEMTKN  240
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPMLDSD GSFFLYSKLT VDKSRWQQGN  300
VFSCSVMHEA LHNHYTQKSL SLSPGK                                       326

SEQ ID NO: 168          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 168
DIQMTQSPAS LSASVGETVT ITCRASGNIH NYLSWYHQKQ GKSPQLLVYN AKTLADGVPS  60
RFSGSGSGTQ YSLKINSLQP EDFGSYYCQN FWSTPFTFGS GTKLEIK                107

SEQ ID NO: 169          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 169
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 170          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 170
GYSFTSYW                                                           8

SEQ ID NO: 171          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 171
IYPGDSDT                                                           8

SEQ ID NO: 172          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
source                  1..16
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 172
ARDVSSFYGY SPMFDY                                                  16

SEQ ID NO: 173          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 173
QSVSSY                                                             6

SEQ ID NO: 174          moltype =   length =
SEQUENCE: 174
000

SEQ ID NO: 175          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 175
QQRSNWPLT                                                          9

SEQ ID NO: 176          moltype = AA  length = 123
```

-continued

```
FEATURE                 Location/Qualifiers
source                  1..123
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 176
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT SYWIGWVRQM PGKGLEWMGI IYPGDSDTRY  60
SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCARDV SSFYGYSPMF DYWGQGTLVT  120
VSS                                                                123

SEQ ID NO: 177          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 177
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 178          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 178
EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA  60
RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RSNWPLTFGQ GTKVEIK                107

SEQ ID NO: 179          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 179
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 180          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 180
GYSFTSYW                                                           8

SEQ ID NO: 181          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 181
IYPGDSDT                                                           8

SEQ ID NO: 182          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
source                  1..16
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 182
ARDAHSFYGY SALLDY                                                  16

SEQ ID NO: 183          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 183
QSVSSSY                                                            7

SEQ ID NO: 184          moltype =   length =
SEQUENCE: 184
000
```

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```
SEQ ID NO: 185          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 185
QQYGSSPLT                                                           9

SEQ ID NO: 186          moltype = AA  length = 123
FEATURE                 Location/Qualifiers
source                  1..123
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 186
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT SYWIGWVRQM PGKGLEWMGI IYPGDSDTRY  60
SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCARDA HSFYGYSALL DYWGQGTLVT  120
VSS                                                                 123

SEQ ID NO: 187          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 187
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 188          moltype = AA  length = 108
FEATURE                 Location/Qualifiers
source                  1..108
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 188
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY GASSRATGIP  60
DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPLTFG QGTKVEIK               108

SEQ ID NO: 189          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 189
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 190          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 190
GYSFTSYW                                                            8

SEQ ID NO: 191          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 191
IYPGDSDT                                                            8

SEQ ID NO: 192          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
source                  1..16
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 192
ARDSYSFYGH TPVLDY                                                   16

SEQ ID NO: 193          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
```

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```
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 193
QSVSSSY                                                           7

SEQ ID NO: 194        moltype =   length =
SEQUENCE: 194
000

SEQ ID NO: 195        moltype = AA  length = 9
FEATURE               Location/Qualifiers
source                1..9
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 195
QQYGSSPLT                                                         9

SEQ ID NO: 196        moltype = AA  length = 123
FEATURE               Location/Qualifiers
source                1..123
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 196
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT SYWIGWVRQM PGKGLEWMGI IYPGDSDTRY  60
SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCARDS YSFYGHTPVL DYWGQGTLVT  120
VSS                                                               123

SEQ ID NO: 197        moltype = AA  length = 330
FEATURE               Location/Qualifiers
source                1..330
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 197
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 198        moltype = AA  length = 108
FEATURE               Location/Qualifiers
source                1..108
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 198
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY GASSRATGIP  60
DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPLTFG QGTKVEIK              108

SEQ ID NO: 199        moltype = AA  length = 107
FEATURE               Location/Qualifiers
source                1..107
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 199
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC               107

SEQ ID NO: 200        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 200
GYSFTSYW                                                          8

SEQ ID NO: 201        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 201
IYPGDSDT                                                          8

SEQ ID NO: 202        moltype = AA  length = 14
FEATURE               Location/Qualifiers
```

-continued

```
source                  1..14
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 202
ARDDALYGGY YLDY                                                  14

SEQ ID NO: 203          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 203
QSVLYSSNNK NY                                                    12

SEQ ID NO: 204          moltype =   length =
SEQUENCE: 204
000

SEQ ID NO: 205          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 205
QQYYSTPLT                                                        9

SEQ ID NO: 206          moltype = AA  length = 121
FEATURE                 Location/Qualifiers
source                  1..121
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 206
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT SYWIGWVRQM PGKGLEWMGI IYPGDSDTRY  60
SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCARDD ALYGGYYLDY WGQGTLVTVS  120
S                                                                  121

SEQ ID NO: 207          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 207
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 208          moltype = AA  length = 113
FEATURE                 Location/Qualifiers
source                  1..113
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 208
DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR  60
ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQQYYST PLTFGQGTKV EIK         113

SEQ ID NO: 209          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 209
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 210          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 210
GYSFTSYW                                                         8

SEQ ID NO: 211          moltype = AA  length = 8
```

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```
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 211
IYPGDSDT                                                            8

SEQ ID NO: 212          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
source                  1..16
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 212
ARDANSFYSA ASIFDY                                                   16

SEQ ID NO: 213          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 213
QSVLYSSNNK NY                                                       12

SEQ ID NO: 214          moltype =   length =
SEQUENCE: 214
000

SEQ ID NO: 215          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 215
QQYYSTPLT                                                           9

SEQ ID NO: 216          moltype = AA  length = 123
FEATURE                 Location/Qualifiers
source                  1..123
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 216
EVQLVQSGAE VKKPGESLKI SCKGSGYSFT SYWIGWVRQM PGKGLEWMGI IYPGDSDTRY  60
SPSFQGQVTI SADKSISTAY LQWSSLKASD TAMYYCARDA NSFYSAASIF DYWGQGTLVT  120
VSS                                                                 123

SEQ ID NO: 217          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 217
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 218          moltype = AA  length = 113
FEATURE                 Location/Qualifiers
source                  1..113
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 218
DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR  60
ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQQYYST PLTFGQGTKV EIK         113

SEQ ID NO: 219          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 219
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107
```

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```
SEQ ID NO: 220          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 220
GGTFSSYA                                                        8

SEQ ID NO: 221          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 221
IIPIFGTA                                                        8

SEQ ID NO: 222          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 222
ARSSYGWSYE FDY                                                  13

SEQ ID NO: 223          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 223
QSIATN                                                          6

SEQ ID NO: 224          moltype =   length =
SEQUENCE: 224
000

SEQ ID NO: 225          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 225
QQNDDRPIT                                                       9

SEQ ID NO: 226          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 226
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSS YGWSYEFDYW GQGTLVTVSS  120

SEQ ID NO: 227          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 227
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 228          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 228
DIQMTQSPSS LSASVGDRVT ITCRASQSIA TNLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ NDDRPITFGQ GTKVEIK               107

SEQ ID NO: 229          moltype = AA  length = 107
```

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```
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 229
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 230          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 230
GGTFSSYA                                                           8

SEQ ID NO: 231          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 231
IIPIFGTA                                                           8

SEQ ID NO: 232          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 232
ARSSYGWSYE FDY                                                     13

SEQ ID NO: 233          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 233
QSIRTD                                                             6

SEQ ID NO: 234          moltype =   length =
SEQUENCE: 234
000

SEQ ID NO: 235          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 235
QQNERTPIT                                                          9

SEQ ID NO: 236          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 236
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSS YGWSYEFDYW GQGTLVTVSS  120

SEQ ID NO: 237          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 237
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 238          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
```

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```
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 238
DIQMTQSPSS LSASVGDRVT ITCRASQSIR TDLNWYQQKP GKAPKLLIYS ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ NERTPITFGQ GTKVEIK                107

SEQ ID NO: 239          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 239
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 240          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 240
GGTFSSYA                                                           8

SEQ ID NO: 241          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 241
IIPIFGTA                                                           8

SEQ ID NO: 242          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 242
ARSSYGWSYE FDY                                                     13

SEQ ID NO: 243          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 243
QSINND                                                             6

SEQ ID NO: 244          moltype =   length =
SEQUENCE: 244
000

SEQ ID NO: 245          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 245
QQNRATPIT                                                          9

SEQ ID NO: 246          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 246
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSS YGWSYEFDYW GQGTLVTVSS  120

SEQ ID NO: 247          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 247
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
```

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```
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 248         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 248
DIQMTQSPSS LSASVGDRVT ITCRASQSIN NDLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ NRATPITFGQ GTKVEIK                107

SEQ ID NO: 249         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 249
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 250         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 250
GGTFSSYA                                                           8

SEQ ID NO: 251         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 251
IIPIFGTA                                                           8

SEQ ID NO: 252         moltype = AA  length = 13
FEATURE                Location/Qualifiers
source                 1..13
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 252
ARNTFGWSGE LDY                                                     13

SEQ ID NO: 253         moltype = AA  length = 6
FEATURE                Location/Qualifiers
source                 1..6
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 253
QSISNR                                                             6

SEQ ID NO: 254         moltype =   length =
SEQUENCE: 254
000

SEQ ID NO: 255         moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 255
QQNHDNPIT                                                          9

SEQ ID NO: 256         moltype = AA  length = 120
FEATURE                Location/Qualifiers
source                 1..120
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 256
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARNT FGWSGELDYW GQGTLVTVSS  120
```

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```
SEQ ID NO: 257          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 257
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 258          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 258
DIQMTQSPSS LSASVGDRVT ITCRASQSIS NRLNWYQQKP GKAPKLLIYS ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ NHDNPITFGQ GTKVEIK                107

SEQ ID NO: 259          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 259
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 260          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 260
GGTFSSYA                                                           8

SEQ ID NO: 261          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 261
IIPIFGTA                                                           8

SEQ ID NO: 262          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 262
ARSSYGWSYE FDY                                                     13

SEQ ID NO: 263          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 263
QSIATY                                                             6

SEQ ID NO: 264          moltype =   length =
SEQUENCE: 264
000

SEQ ID NO: 265          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 265
QQNHNRPIT                                                          9
```

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```
SEQ ID NO: 266          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 266
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSS YGWSYEFDYW GQGTLVTVSS  120

SEQ ID NO: 267          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 267
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 268          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 268
DIQMTQSPSS LSASVGDRVT ITCRASQSIA TYLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ NHNRPITFGQ GTKVEIK                107

SEQ ID NO: 269          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 269
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 270          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 270
GGTFSSYA                                                           8

SEQ ID NO: 271          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 271
IIPIFGTA                                                           8

SEQ ID NO: 272          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 272
ARHSIGWVAE LDY                                                     13

SEQ ID NO: 273          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 273
QSINTD                                                             6

SEQ ID NO: 274          moltype =   length =
SEQUENCE: 274
000
```

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```
SEQ ID NO: 275          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 275
QQGASDPIT                                                           9

SEQ ID NO: 276          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 276
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARHS IGWVAELDYW GQGTLVTVSS  120

SEQ ID NO: 277          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 277
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 278          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 278
DIQMTQSPSS LSASVGDRVT ITCRASQSIN TDLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ GASDPITFGQ GTKVEIK                107

SEQ ID NO: 279          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 279
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 280          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 280
GGTFSSYA                                                            8

SEQ ID NO: 281          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 281
IIPIFGTA                                                            8

SEQ ID NO: 282          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 282
ARSSYGWSYE FDY                                                      13

SEQ ID NO: 283          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
```

-continued

```
                        organism = Homo sapiens
SEQUENCE: 283
QSINTD                                                          6

SEQ ID NO: 284          moltype =   length =
SEQUENCE: 284
000

SEQ ID NO: 285          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 285
QQNRGSPIT                                                       9

SEQ ID NO: 286          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 286
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSS YGWSYEFDYW GQGTLVTVSS  120

SEQ ID NO: 287          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 287
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 288          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 288
DIQMTQSPSS LSASVGDRVT ITCRASQSIN TDLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ NRGSPITFGQ GTKVEIK               107

SEQ ID NO: 289          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 289
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC               107

SEQ ID NO: 290          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 290
GGTFSSYA                                                        8

SEQ ID NO: 291          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 291
IIPIFGTA                                                        8

SEQ ID NO: 292          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
```

-continued

```
                        organism = Homo sapiens
SEQUENCE: 292
ARHSIGWVAE LDY                                                  13

SEQ ID NO: 293          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 293
QSIATD                                                          6

SEQ ID NO: 294          moltype =   length =
SEQUENCE: 294
000

SEQ ID NO: 295          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 295
QQAHWYPLT                                                       9

SEQ ID NO: 296          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 296
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARHS IGWVAELDYW GQGTLVTVSS  120

SEQ ID NO: 297          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 297
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 298          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 298
DIQMTQSPSS LSASVGDRVT ITCRASQSIA TDLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ AHWYPLTFGQ GTKVEIK               107

SEQ ID NO: 299          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 299
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC               107

SEQ ID NO: 300          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 300
GGTFSSYA                                                        8

SEQ ID NO: 301          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
```

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```
                        organism = Homo sapiens
SEQUENCE: 301
IIPIFGTA                                                        8

SEQ ID NO: 302          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 302
ARHSIGWVAE LDY                                                  13

SEQ ID NO: 303          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 303
QSIATS                                                          6

SEQ ID NO: 304          moltype =   length =
SEQUENCE: 304
000

SEQ ID NO: 305          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 305
QQGAYYPLT                                                       9

SEQ ID NO: 306          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 306
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARHS IGWVAELDYW GQGTLVTVSS  120

SEQ ID NO: 307          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 307
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 308          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 308
DIQMTQSPSS LSASVGDRVT ITCRASQSIA TSLNWYQQKP GKAPKLLIYY ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ GAYYPLTFGQ GTKVEIK               107

SEQ ID NO: 309          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 309
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC               107

SEQ ID NO: 310          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
```

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```
                        organism = Homo sapiens
SEQUENCE: 310
GGTFSSYA                                                        8

SEQ ID NO: 311          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 311
IIPIFGTA                                                        8

SEQ ID NO: 312          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 312
ARSSYGWSYE FDY                                                  13

SEQ ID NO: 313          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 313
QSIRTY                                                          6

SEQ ID NO: 314          moltype =   length =
SEQUENCE: 314
000

SEQ ID NO: 315          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 315
QQAYSNPIT                                                       9

SEQ ID NO: 316          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 316
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSS YGWSYEFDYW GQGTLVTVSS  120

SEQ ID NO: 317          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 317
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 318          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 318
DIQMTQSPSS LSASVGDRVT ITCRASQSIR TYLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ AYSNPITFGQ GTKVEIK               107

SEQ ID NO: 319          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
```

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```
SEQUENCE: 319
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 320          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 320
GGTFSSYA                                                           8

SEQ ID NO: 321          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 321
IIPIFGTA                                                           8

SEQ ID NO: 322          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 322
ARSSYGWSYE FDY                                                     13

SEQ ID NO: 323          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 323
QSINTN                                                             6

SEQ ID NO: 324          moltype =   length =
SEQUENCE: 324
000

SEQ ID NO: 325          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 325
QQARDTPIT                                                          9

SEQ ID NO: 326          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 326
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSS YGWSYEFDYW GQGTLVTVSS  120

SEQ ID NO: 327          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 327
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 328          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 328
```

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```
DIQMTQSPSS LSASVGDRVT ITCRASQSIN TNLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ ARDTPITFGQ GTKVEIK                107

SEQ ID NO: 329          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 329
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 330          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 330
GYTFPSHT                                                           8

SEQ ID NO: 331          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 331
IYPFIDST                                                           8

SEQ ID NO: 332          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 332
ARGIRGYTMD Y                                                       11

SEQ ID NO: 333          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 333
ESVDNYGLSF                                                         10

SEQ ID NO: 334          moltype =   length =
SEQUENCE: 334
000

SEQ ID NO: 335          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 335
QQSKEVPYT                                                          9

SEQ ID NO: 336          moltype = AA  length = 118
FEATURE                 Location/Qualifiers
source                  1..118
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 336
QVQLVQSGAE VKKPGASVKV SCKASGYTFP SHTIHWVRQA PGQRLEWMGS IYPFIDSTIY  60
NQKFKDRVTI TRDTSASTAY MELSSLRSED TAVYYCARGI RGYTMDYWGQ GTLVTVSS    118

SEQ ID NO: 337          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 337
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
```

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QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                    330

SEQ ID NO: 338          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 338
DVVMTQSPLS LPVTLGQPAS ISCRASESVD NYGLSFMNWF QQRPGQSPRR LIYGASNQGS  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQSKEVPY TFGQGTKLEI K           111

SEQ ID NO: 339          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 339
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 340          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 340
GYTFTNYG                                                            8

SEQ ID NO: 341          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 341
INPYTGEP                                                            8

SEQ ID NO: 342          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 342
AREGYGNYIF PY                                                       12

SEQ ID NO: 343          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 343
ESVDTYANSL                                                          10

SEQ ID NO: 344          moltype =   length =
SEQUENCE: 344
000

SEQ ID NO: 345          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 345
QQTNEDPRT                                                           9

SEQ ID NO: 346          moltype = AA  length = 119
FEATURE                 Location/Qualifiers
source                  1..119
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 346
QVQLVQSGSE LKKPGASVKV SCKASGYTFT NYGLNWVRQA PGQGLEWMGW INPYTGEPTY  60
ADDFKGRFVF SLDTSVSTAY LQICSLKAED TAVYYCAREG YGNYIFPYWG QGTLVTVSS   119

SEQ ID NO: 347          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
```

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```
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 347
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 348        moltype = AA  length = 111
FEATURE               Location/Qualifiers
source                1..111
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 348
DIVMTQTPLS LSVTPGQPAS ISCRASESVD TYANSLMHWY LQKPGQPPQL LIYRASNLES  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQTNEDPR TFGQGTKLEI K           111

SEQ ID NO: 349        moltype = AA  length = 107
FEATURE               Location/Qualifiers
source                1..107
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 349
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 350        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 350
GFTFSSYT                                                           8

SEQ ID NO: 351        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 351
ISNSGSYT                                                           8

SEQ ID NO: 352        moltype = AA  length = 11
FEATURE               Location/Qualifiers
source                1..11
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 352
ARDTVLSPFD Y                                                       11

SEQ ID NO: 353        moltype = AA  length = 5
FEATURE               Location/Qualifiers
source                1..5
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 353
SSISY                                                              5

SEQ ID NO: 354        moltype =   length =
SEQUENCE: 354
000

SEQ ID NO: 355        moltype = AA  length = 7
FEATURE               Location/Qualifiers
source                1..7
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 355
HQRSSFT                                                            7

SEQ ID NO: 356        moltype = AA  length = 118
FEATURE               Location/Qualifiers
source                1..118
                      mol_type = protein
```

-continued

```
                        organism = Homo sapiens
SEQUENCE: 356
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYTMSWVRQA PGKGLEWVAT ISNSGSYTYY  60
LDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARDT VLSPFDYWGQ GTTVTVSS    118

SEQ ID NO: 357          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 357
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 358          moltype = AA  length = 104
FEATURE                 Location/Qualifiers
source                  1..104
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 358
EIVLTQSPDF QSVTPKEKVT ITCSATSSIS YMHWYQQKPD QSPKLLIKDT SELASGVPSR  60
FSGSGSGTDF TLTINSLEAE DAATYYCHQR SSFTFGQGTK LEIK                   104

SEQ ID NO: 359          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 359
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 360          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 360
GGTFSNYW                                                           8

SEQ ID NO: 361          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 361
IYPGGGFT                                                           8

SEQ ID NO: 362          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
source                  1..14
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 362
ARYYRSDEDY SMDF                                                    14

SEQ ID NO: 363          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 363
QSLLYSNGKT Y                                                       11

SEQ ID NO: 364          moltype =   length =
SEQUENCE: 364
000

SEQ ID NO: 365          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
```

-continued

```
                        organism = Homo sapiens
SEQUENCE: 365
VQATHFPQT                                                          9

SEQ ID NO: 366          moltype = AA  length = 121
FEATURE                 Location/Qualifiers
source                  1..121
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 366
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS NYWIGWVRQA PGQGLEWMGE IYPGGGFTHY  60
NEKFKGRVTI TADESTSTAY MELSSLRSED TAVYYCARYY RSDEDYSMDF WGQGTLVTVS  120
S                                                                  121

SEQ ID NO: 367          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 367
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 368          moltype = AA  length = 112
FEATURE                 Location/Qualifiers
source                  1..112
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 368
DVVMTQSPLS LPVTLGQPAS ISCKSSQSLL YSNGKTYLNW FQQRPGQSPR RLIYLVSKLD  60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCVQATHFP QTFGQGTKLE IK          112

SEQ ID NO: 369          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 369
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 370          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 370
GYTFTHYT                                                           8

SEQ ID NO: 371          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 371
IIPSSGYS                                                           8

SEQ ID NO: 372          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
source                  1..16
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 372
ARGAYDDYYD YYAMDY                                                  16

SEQ ID NO: 373          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 373
QTIVHSNGNT Y                                                       11
```

-continued

```
SEQ ID NO: 374          moltype =   length =
SEQUENCE: 374
000

SEQ ID NO: 375          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 375
FQASHVPWT                                                           9

SEQ ID NO: 376          moltype = AA  length = 123
FEATURE                 Location/Qualifiers
source                  1..123
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 376
QVQLVQSGAE VKKPGASVKV SCKASGYTFT HYTIHWVRQA PGQGLEWMGY IIPSSGYSEY  60
NQKFKDRVTM TRDTSTSTVY MELSSLRSED TAVYYCARGA YDDYYDYYAM DYWGQGTLVT  120
VSS                                                                 123

SEQ ID NO: 377          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 377
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 378          moltype = AA  length = 112
FEATURE                 Location/Qualifiers
source                  1..112
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 378
DIVMTQSPLS LPVTPGEPAS ISCRSSQTIV HSNGNTYLEW YLQKPGQSPQ LLIYKVSNRF  60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQASHVP WTFGQGTKLE IK          112

SEQ ID NO: 379          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 379
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 380          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 380
GYNIKDTY                                                            8

SEQ ID NO: 381          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 381
IDPTHGYV                                                            8

SEQ ID NO: 382          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 382
```

-continued

```
ARDRFDPYWF LDV                                                    13

SEQ ID NO: 383          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 383
ESVEYYGTSL                                                        10

SEQ ID NO: 384          moltype =   length =
SEQUENCE: 384
000

SEQ ID NO: 385          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 385
QQSRKVPWT                                                         9

SEQ ID NO: 386          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 386
QVQLVQSGAE VKKPGASVKV SCKASGYNIK DTYMHWVRQA PGQGLEWMGR IDPTHGYVIY  60
DPKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARDR FDPYWFLDVW GQGTLVTVSS  120

SEQ ID NO: 387          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 387
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 388          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 388
DIVMTQTPLS LSVTPGQPAS ISCRASESVE YYGTSLMQWY LQKPGQSPQL LIYDAFNVES  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQSRKVPW TFGQGTKLEI K          111

SEQ ID NO: 389          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 389
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC               107

SEQ ID NO: 390          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 390
GYSIASDYV                                                         9

SEQ ID NO: 391          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 391
```

-continued

```
ISYSGST                                                             7

SEQ ID NO: 392          moltype = AA  length = 17
FEATURE                 Location/Qualifiers
source                  1..17
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 392
ARITTVVPTG SYYGVDF                                                  17

SEQ ID NO: 393          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
source                  1..5
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 393
SSVNF                                                               5

SEQ ID NO: 394          moltype =   length =
SEQUENCE: 394
000

SEQ ID NO: 395          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 395
QQWSNYPFT                                                           9

SEQ ID NO: 396          moltype = AA  length = 124
FEATURE                 Location/Qualifiers
source                  1..124
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 396
QVQLQESGPG LVKPSETLSL TCAVSGYSIA SDYVWNWIRQ PPGKGLEWIG YISYSGSTSN  60
NPSLNSRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCARIT TVVPTGSYYG VDFWGQGTTV  120
TVSS                                                                124

SEQ ID NO: 397          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 397
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 398          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
source                  1..106
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 398
EIVLTQSPDF QSVTPKEKVT ITCSGSSSVN FMYWYQQKPD QSPKLLIKDT SNLASGVPSR  60
FSGSGSGTDF TLTINSLEAE DAATYYCQQW SNYPFTFGQG TKLEIK                 106

SEQ ID NO: 399          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 399
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 400          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
```

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```
SEQUENCE: 400
GYTFTSYW                                                            8

SEQ ID NO: 401          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 401
IIPNTLHT                                                            8

SEQ ID NO: 402          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 402
ARLDGDYDYA LDY                                                      13

SEQ ID NO: 403          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 403
ESVEYYGTSF                                                          10

SEQ ID NO: 404          moltype =   length =
SEQUENCE: 404
000

SEQ ID NO: 405          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 405
QQSRKVPYT                                                           9

SEQ ID NO: 406          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 406
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYWLHWVRQA PGQGLEWMGY IIPNTLHTDY  60
NQKFKDRVTM TRDTSTSTVY MELSSLRSED TAVYYCARLD GDYDYALDYW GQGTLVTVSS  120

SEQ ID NO: 407          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 407
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 408          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 408
DIVMTQTPLS LSVTPGQPAS ISCRASESVE YYGTSFMQWY LQKPGQPPQL LIYTASNVES  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQSRKVPY TFGQGTKLEI K           111

SEQ ID NO: 409          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 409
```

-continued

```
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 410          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 410
GFTFSTYA                                                           8

SEQ ID NO: 411          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 411
ISSGGSDT                                                           8

SEQ ID NO: 412          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
source                  1..14
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 412
ARPTYYGIFS YFDY                                                    14

SEQ ID NO: 413          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
source                  1..5
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 413
SSVSY                                                              5

SEQ ID NO: 414          moltype =   length =
SEQUENCE: 414
000

SEQ ID NO: 415          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 415
HQWRTYPT                                                           8

SEQ ID NO: 416          moltype = AA  length = 121
FEATURE                 Location/Qualifiers
source                  1..121
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 416
EVQLVESGGG LVQPGGSLRL SCAASGFTFS TYAMSWVRQA PGKGLEWVAT ISSGGSDTYY  60
PDTVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARPT YYGIFSYFDY WGQGTLVTVS  120
S                                                                  121

SEQ ID NO: 417          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 417
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 418          moltype = AA  length = 105
FEATURE                 Location/Qualifiers
source                  1..105
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 418
```

-continued

```
DIQLTQSPSF LSASVGDRVT ITCSASSSVS YMHWYQQKPG KAPKLLIYST SNLASGVPSR  60
FSGSGSGTEF TLTISSLQPE DFATYYCHQW RTYPTFGQGT KLEIK                  105

SEQ ID NO: 419          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 419
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 420          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 420
GFSLTNYG                                                           8

SEQ ID NO: 421          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 421
IWRGGNT                                                            7

SEQ ID NO: 422          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 422
ARSMVSYTVD Y                                                       11

SEQ ID NO: 423          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
source                  1..5
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 423
SSVSY                                                              5

SEQ ID NO: 424          moltype =   length =
SEQUENCE: 424
000

SEQ ID NO: 425          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 425
QQWSSYPPT                                                          9

SEQ ID NO: 426          moltype = AA  length = 117
FEATURE                 Location/Qualifiers
source                  1..117
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 426
QVQLQESGPG LVKPSETLSL TCTVSGFSLT NYGVHWIRQP PGKGLEWIGV IWRGGNTDYN  60
AAFMSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCARSMV SYTVDYWGQG TLVTVSS     117

SEQ ID NO: 427          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 427
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
```

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```
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                    330

SEQ ID NO: 428          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
source                  1..106
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 428
EIVLTQSPDF QSVTPKEKVT ITCSASSSVS YMHWYQQKPD QSPKLLIKDT SNLASGVPSR  60
FSGSGSGTDF TLTINSLEAE DAATYYCQQW SSYPPTFGQG TKLEIK                 106

SEQ ID NO: 429          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 429
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 430          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 430
GYTFTDYW                                                            8

SEQ ID NO: 431          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 431
IETSLNYP                                                            8

SEQ ID NO: 432          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 432
ARWGIYGNPW FAY                                                      13

SEQ ID NO: 433          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 433
ESVDSYVNSF                                                          10

SEQ ID NO: 434          moltype =   length =
SEQUENCE: 434
000

SEQ ID NO: 435          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 435
QQSNEDPYT                                                           9

SEQ ID NO: 436          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 436
QVQLVQSGAE VKKPGASVKV SCKASGYTFT DYWMHWVRQA PGQGLEWMGA IETSLNYPSY  60
NQKFKGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARWG IYGNPWFAYW GRGTLVTVSS  120

SEQ ID NO: 437          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
```

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```
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 437
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 438        moltype = AA  length = 111
FEATURE               Location/Qualifiers
source                1..111
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 438
DIVMTQTPLS LSVTPGQPAS ISCRASESVD SYVNSFVHWY LQKPGQPPQL LIYRASNLES  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQSNEDPY TFGQGTKLEI K          111

SEQ ID NO: 439        moltype = AA  length = 107
FEATURE               Location/Qualifiers
source                1..107
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 439
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC               107

SEQ ID NO: 440        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 440
GYTFTNYG                                                          8

SEQ ID NO: 441        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 441
INTYTGES                                                          8

SEQ ID NO: 442        moltype = AA  length = 12
FEATURE               Location/Qualifiers
source                1..12
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 442
ARDYYGIYVS AY                                                     12

SEQ ID NO: 443        moltype = AA  length = 10
FEATURE               Location/Qualifiers
source                1..10
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 443
ESVDNYANSF                                                        10

SEQ ID NO: 444        moltype =   length =
SEQUENCE: 444
000

SEQ ID NO: 445        moltype = AA  length = 9
FEATURE               Location/Qualifiers
source                1..9
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 445
QQSHEDPYT                                                         9

SEQ ID NO: 446        moltype = AA  length = 119
FEATURE               Location/Qualifiers
source                1..119
                      mol_type = protein
```

-continued

```
                        organism = Homo sapiens
SEQUENCE: 446
QVQLVQSGSE LKKPGASVKV SCKASGYTFT NYGMTWVRQA PGQGLEWMGW INTYTGESTY  60
ADDFKGRFVF SLDTSVSTAY LQICSLKAED TAVYYCARDY YGIYVSAYWG QGTLVTVSS   119

SEQ ID NO: 447          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 447
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 448          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 448
DIVMTQTPLS LSVTPGQPAS ISCRASESVD NYANSFMHWY LQKPGQSPQL LIYRASNLES  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQSHEDPY TFGQGTKLEI K           111

SEQ ID NO: 449          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 449
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 450          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 450
GYTFTSHW                                                           8

SEQ ID NO: 451          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 451
INPRDGRT                                                           8

SEQ ID NO: 452          moltype = AA  length = 16
FEATURE                 Location/Qualifiers
source                  1..16
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 452
ARGDFHYGDY FWYFDV                                                  16

SEQ ID NO: 453          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 453
QNVHGA                                                             6

SEQ ID NO: 454          moltype =   length =
SEQUENCE: 454
000

SEQ ID NO: 455          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
```

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```
                        organism = Homo sapiens
SEQUENCE: 455
LQHWNYLT                                                          8

SEQ ID NO: 456          moltype = AA  length = 123
FEATURE                 Location/Qualifiers
source                  1..123
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 456
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SHWMHWVRQA PGQGLEWMGE INPRDGRTNY  60
NEKFKTRVTM TRDTSTSTVY MELSSLRSED TAVYYCARGD FHYGDYFWYF DVWGQGTLVT  120
VSS                                                               123

SEQ ID NO: 457          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 457
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 458          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
source                  1..106
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 458
DIQMTQSPSS LSASVGDRVT ITCKASQNVH GAVAWYQQKP GKVPKLLIYM ASNRPTGVPS  60
RFSGSGSGTD FTLTISSLQP EDVATYYCLQ HWNYLTFGQG TKLEIK                106

SEQ ID NO: 459          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 459
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC               107

SEQ ID NO: 460          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 460
GYTFTHYW                                                          8

SEQ ID NO: 461          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 461
IYPGDGDT                                                          8

SEQ ID NO: 462          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 462
ARRDYDYGDY                                                        10

SEQ ID NO: 463          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
source                  1..5
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 463
SSVSH                                                             5
```

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```
SEQ ID NO: 464          moltype =   length =
SEQUENCE: 464
000

SEQ ID NO: 465          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 465
QQYQTYPPT                                                           9

SEQ ID NO: 466          moltype = AA  length = 117
FEATURE                 Location/Qualifiers
source                  1..117
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 466
QVQLVQSGAE VKKPGASVKV SCKASGYTFT HYWIQWVRQA PGQGLEWMGA IYPGDGDTRY  60
TQKFKGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARRD YDYGDYWGQG TTVTVSS     117

SEQ ID NO: 467          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 467
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 468          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
source                  1..106
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 468
EIVLTQSPDF QSVTPKEKVT ITCSASSSVS HMYWYQQKPD QSPKLLIKLT SNLASGVPSR  60
FSGSGSGTDF TLTINSLEAE DAATYYCQQY QTYPPTFGQG TRLEIK                 106

SEQ ID NO: 469          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 469
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 470          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 470
GFSITSDFA                                                           9

SEQ ID NO: 471          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 471
ITYSGFT                                                             7

SEQ ID NO: 472          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
source                  1..14
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 472
ARQEYGNYVW YFDV                                                     14
```

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```
SEQ ID NO: 473          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 473
ESVEYYGTSL                                                          10

SEQ ID NO: 474          moltype =   length =
SEQUENCE: 474
000

SEQ ID NO: 475          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 475
QQSRKVPWT                                                           9

SEQ ID NO: 476          moltype = AA  length = 121
FEATURE                 Location/Qualifiers
source                  1..121
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 476
QVQLQESGPG LVKPSETLSL TCAVSGFSIT SDFAWNWIRQ PPGKGLEWIG YITYSGFTNY  60
NPSLESRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCARQE YGNYVWYFDV WGQGTLVTVS  120
S                                                                  121

SEQ ID NO: 477          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 477
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 478          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 478
DIVMTQTPLS LSVTPGQPAS ISCRASESVE YYGTSLLQWY LQKPGQPPQL LIYAASNVES  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQSRKVPW TFGQGTKLEI K           111

SEQ ID NO: 479          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 479
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 480          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 480
GYSITSGYF                                                           9

SEQ ID NO: 481          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 481
```

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MGYDGRI                                                          7

SEQ ID NO: 482          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
source                  1..14
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 482
AREGDYYGSG FAYW                                                  14

SEQ ID NO: 483          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 483
QNVNTN                                                           6

SEQ ID NO: 484          moltype =   length =
SEQUENCE: 484
000

SEQ ID NO: 485          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 485
QVQLQESGPG LVKPSETLSL TCAVSGYSIT SGYFWNWIRQ PPGKGLEWIG YMGYDGRIFY  60
SPSLKNRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCAREG DYYGSGFAYW GQGTLVTVSS  120

SEQ ID NO: 486          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 486
QVQLQESGPG LVKPSETLSL TCAVSGYSIT SGYFWNWIRQ PPGKGLEWIG YMGYDGRIFY  60
SPSLKNRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCAREG DYYGSGFAYW GQGTLVTVSS  120

SEQ ID NO: 487          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 487
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 488          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 488
DIQMTQSPSS LSASVGDRVT ITCKASQNVN TNLAWYQQKP GKVPKLLIYS ASYRYSGVPS  60
RFSGSGSGTD FTLTISSLQP EDVATYYCQQ YNNYPLTFGQ GTKLEIK               107

SEQ ID NO: 489          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 489
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC               107

SEQ ID NO: 490          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
```

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```
SEQUENCE: 490
GYTFTSYW                                                            8

SEQ ID NO: 491          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 491
INPSNGLT                                                            8

SEQ ID NO: 492          moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 492
ARSYDYDGDY YAMDY                                                    15

SEQ ID NO: 493          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 493
QSIVHSNGNT Y                                                        11

SEQ ID NO: 494          moltype =   length =
SEQUENCE: 494
000

SEQ ID NO: 495          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 495
FQASHVPWT                                                           9

SEQ ID NO: 496          moltype = AA  length = 122
FEATURE                 Location/Qualifiers
source                  1..122
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 496
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYWIHWVRQA PGQGLEWMGE INPSNGLTNY  60
NEKFRNRVTM TRDTSTSTVY MELSSLRSED TAVYYCARSY DYDGDYYAMD YWGQGTLVTV  120
SS                                                                  122

SEQ ID NO: 497          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 497
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 498          moltype = AA  length = 112
FEATURE                 Location/Qualifiers
source                  1..112
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 498
DIVMTQSPLS LPVTPGEPAS ISCRSTQSIV HSNGNTYLEW YLQKPGQSPQ LLIYKVSNRF  60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQASHVP WTFGQGTKLE IK          112

SEQ ID NO: 499          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
```

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```
SEQUENCE: 499
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 500          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 500
GYPFTGYF                                                           8

SEQ ID NO: 501          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 501
INPYNGGT                                                           8

SEQ ID NO: 502          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 502
ARWTFDGLFM DY                                                      12

SEQ ID NO: 503          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 503
ENVDKYGISF                                                         10

SEQ ID NO: 504          moltype =   length =
SEQUENCE: 504
000

SEQ ID NO: 505          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 505
QQSKEDPYT                                                          9

SEQ ID NO: 506          moltype = AA  length = 119
FEATURE                 Location/Qualifiers
source                  1..119
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 506
QVQLVQSGAE VKKPGASVKV SCKASGYPFT GYFMHWVRQA PGQGLEWMGR INPYNGGTVY  60
NQNFNDRVTM TRDTSTSTVY MELSSLRSED TAVYYCARWT FDGLFMDYWG QGTTVTVSS   119

SEQ ID NO: 507          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 507
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 508          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 508
```

-continued

```
DVVMTQSPLS LPVTLGQPAS ISCRASENVD KYGISFMNWF QQRPGQSPRR LIYATSNQGS  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQSKEDPY TFGQGTKLEI K          111

SEQ ID NO: 509         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 509
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC               107

SEQ ID NO: 510         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 510
DYIFSSYW                                                           8

SEQ ID NO: 511         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 511
IFPGSGGT                                                           8

SEQ ID NO: 512         moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 512
ARAIYYDYDM YYFDS                                                   15

SEQ ID NO: 513         moltype = AA  length = 6
FEATURE                Location/Qualifiers
source                 1..6
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 513
QDISSY                                                             6

SEQ ID NO: 514         moltype =   length =
SEQUENCE: 514
000

SEQ ID NO: 515         moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 515
QHVNTLPWT                                                          9

SEQ ID NO: 516         moltype = AA  length = 122
FEATURE                Location/Qualifiers
source                 1..122
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 516
QVQLVQSGAE VKKPGASVKV SCKASDYIFS SYWIQWVRQA PGQGLEWMGE IFPGSGGTNY  60
NEKFKGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARAI YYDYDMYYFD SWGQGTTVTV  120
SS                                                                 122

SEQ ID NO: 517         moltype = AA  length = 330
FEATURE                Location/Qualifiers
source                 1..330
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 517
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
```

-continued

```
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 518         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 518
DIQMTQSPSS LSASVGDRVT ITCRASQDIS SYLNWYQQKP GKVPKLLIYY TSRLHSGVPS  60
RFSGSGSGTD FTLTISSLQP EDVATYYCQH VNTLPWTFGQ GTKLEIK                107

SEQ ID NO: 519         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 519
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 520         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 520
GYTFTDYT                                                           8

SEQ ID NO: 521         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 521
INPYNGGT                                                           8

SEQ ID NO: 522         moltype = AA  length = 13
FEATURE                Location/Qualifiers
source                 1..13
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 522
ARHYGNYNWY FDV                                                     13

SEQ ID NO: 523         moltype = AA  length = 6
FEATURE                Location/Qualifiers
source                 1..6
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 523
QYVNTA                                                             6

SEQ ID NO: 524         moltype =   length =
SEQUENCE: 524
000

SEQ ID NO: 525         moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 525
QQHFTTPIT                                                          9

SEQ ID NO: 526         moltype = AA  length = 120
FEATURE                Location/Qualifiers
source                 1..120
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 526
QVQLVQSGAE VKKPGASVKV SCKASGYTFT DYTMNWVRQA PGQRLEWMGL INPYNGGTTY  60
NQKFKGRVTI TRDTSASTAY MELSSLRSED TAVYYCARHY GNYNWYFDVW GQGTTVTVSS  120

SEQ ID NO: 527         moltype = AA  length = 330
FEATURE                Location/Qualifiers
```

-continued

```
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 527
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 528          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 528
DIQLTQSPSF LSASVGDRVT ITCKASQYVN TAVAWYQQKP GKAPKLLIYS ASYRYTGVPS  60
RFSGSGSGTE FTLTISSLQP EDFATYYCQQ HFTTPITFGQ GTKLEIK                107

SEQ ID NO: 529          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 529
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 530          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 530
GYTFTNYG                                                           8

SEQ ID NO: 531          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 531
INTYTGEP                                                           8

SEQ ID NO: 532          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 532
ARNYGNYVAY                                                         10

SEQ ID NO: 533          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 533
QDINSY                                                             6

SEQ ID NO: 534          moltype =   length =
SEQUENCE: 534
000

SEQ ID NO: 535          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 535
LQYDEFPLT                                                          9

SEQ ID NO: 536          moltype = AA  length = 117
FEATURE                 Location/Qualifiers
source                  1..117
```

-continued

```
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 536
QVQLVQSGSE LKKPGASVKV SCKASGYTFT NYGMNWVRQA PGQGLEWMGW INTYTGEPTY  60
ADDFKGRFVF SLDTSVSTAY LQICSLKAED TAVYYCARNY GNYVAYWGQG TTVTVSS     117

SEQ ID NO: 537        moltype = AA  length = 330
FEATURE               Location/Qualifiers
source                1..330
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 537
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 538        moltype = AA  length = 107
FEATURE               Location/Qualifiers
source                1..107
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 538
DIQMTQSPSS LSASVGDRVT ITCKASQDIN SYLSWFQQKP GKAPKSLIYR ANRLVDGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCLQ YDEFPLTFGQ GTRLEIK                107

SEQ ID NO: 539        moltype = AA  length = 107
FEATURE               Location/Qualifiers
source                1..107
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 539
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 540        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 540
GYTFSNYW                                                           8

SEQ ID NO: 541        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 541
ILPGSGNV                                                           8

SEQ ID NO: 542        moltype = AA  length = 16
FEATURE               Location/Qualifiers
source                1..16
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 542
ATPPHYYGYD YYDVNY                                                  16

SEQ ID NO: 543        moltype = AA  length = 11
FEATURE               Location/Qualifiers
source                1..11
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 543
QSLLDSDGKT Y                                                       11

SEQ ID NO: 544        moltype =   length =
SEQUENCE: 544
000

SEQ ID NO: 545        moltype = AA  length = 9
FEATURE               Location/Qualifiers
source                1..9
```

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```
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 545
WQGTHFPQT                                                          9

SEQ ID NO: 546        moltype = AA  length = 123
FEATURE               Location/Qualifiers
source                1..123
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 546
EVQLVQSGAE VKKPGATVKI SCKVSGYTFS NYWIEWVQQA PGKGLEWMGE ILPGSGNVHY  60
NEKFKGRVTI TADTSTDTAY MELSSLRSED TAVYYCATPP HYYGYDYYDV NYWGQGTLVT  120
VSS                                                                123

SEQ ID NO: 547        moltype = AA  length = 330
FEATURE               Location/Qualifiers
source                1..330
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 547
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 548        moltype = AA  length = 112
FEATURE               Location/Qualifiers
source                1..112
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 548
DVVMTQSPLS LPVTLGQPAS ISCKSSQSLL DSDGKTYLNW FQQRPGQSPR RLIYLVSELD  60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCWQGTHFP QTFGQGTKLE IK          112

SEQ ID NO: 549        moltype = AA  length = 107
FEATURE               Location/Qualifiers
source                1..107
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 549
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 550        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 550
GYVFSRSW                                                           8

SEQ ID NO: 551        moltype = AA  length = 8
FEATURE               Location/Qualifiers
source                1..8
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 551
IYPGDGDT                                                           8

SEQ ID NO: 552        moltype = AA  length = 6
FEATURE               Location/Qualifiers
source                1..6
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 552
AARWFL                                                             6

SEQ ID NO: 553        moltype = AA  length = 12
FEATURE               Location/Qualifiers
source                1..12
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 553
```

-continued

```
QSLLNSGDQK SY                                                    12

SEQ ID NO: 554          moltype =   length =
SEQUENCE: 554
000

SEQ ID NO: 555          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 555
QNDHSYPLT                                                        9

SEQ ID NO: 556          moltype = AA  length = 113
FEATURE                 Location/Qualifiers
source                  1..113
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 556
QVQLVQSGAE VKKPGSSVKV SCKASGYVFS RSWINWVRQA PGQGLEWMGR IYPGDGDTNY  60
NGKFKGRVTI TADESTSTAY MELSSLRSED TAVYYCARRW FLWGQGTLVT VSS         113

SEQ ID NO: 557          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 557
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 558          moltype = AA  length = 113
FEATURE                 Location/Qualifiers
source                  1..113
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 558
DIVMTQSPDS LAVSLGERAT INCKSSQSLL NSGDQKSYLA WYQQKPGQPP KLLIYGASTR  60
ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNDHSY PLTFGQGTKL EIK         113

SEQ ID NO: 559          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 559
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 560          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 560
GFTFSSYA                                                         8

SEQ ID NO: 561          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 561
ISSGGSHT                                                         8

SEQ ID NO: 562          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 562
```

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```
ARRGNLYDGP Y                                                        11

SEQ ID NO: 563          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
source                  1..5
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 563
SSVSH                                                               5

SEQ ID NO: 564          moltype =   length =
SEQUENCE: 564
000

SEQ ID NO: 565          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 565
QQWNFYPFT                                                           9

SEQ ID NO: 566          moltype = AA  length = 118
FEATURE                 Location/Qualifiers
source                  1..118
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 566
EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVAE ISSGGSHTYY  60
PDTVTGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARRG NLYDGPYWGQ GTLVTVSS    118

SEQ ID NO: 567          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 567
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 568          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
source                  1..106
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 568
EIVLTQSPAT LSLSPGERAT LSCSASSSVS HMYWYQQKPG QAPRLLIYDT SKLASGIPAR  60
FSGSGSGTDF TLTISSLEPE DFAVYYCQQW NFYPFTFGQG TKLEIK                 106

SEQ ID NO: 569          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 569
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 570          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 570
GYTFTDYV                                                            8

SEQ ID NO: 571          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 571
```

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```
IYPGSGNT                                                            8

SEQ ID NO: 572          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 572
ARVLVSVMDY                                                          10

SEQ ID NO: 573          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
source                  1..5
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 573
SSINY                                                               5

SEQ ID NO: 574          moltype =   length =
SEQUENCE: 574
000

SEQ ID NO: 575          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 575
HQRSSYPWT                                                           9

SEQ ID NO: 576          moltype = AA  length = 117
FEATURE                 Location/Qualifiers
source                  1..117
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 576
QVQLVQSGAE VKKPGASVKV SCKASGYTFT DYVISWVRQA PGQGLEWMGE IYPGSGNTYY  60
YEKFKGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARVL VSVMDYWGQG TLVTVSS     117

SEQ ID NO: 577          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 577
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 578          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
source                  1..106
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 578
EIVLTQSPDF QSVTPKEKVT ITCSASSSIN YITWYQQKPD QSPKLLIKDT SKLASGVPSR  60
FSGSGSGTDF TLTINSLEAE DAATYYCHQR SSYPWTFGQG TRLEIK                 106

SEQ ID NO: 579          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 579
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 580          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 580
```

-continued

```
GYIFTDYN                                                            8

SEQ ID NO: 581          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 581
INPKYDST                                                            8

SEQ ID NO: 582          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 582
AADGSSAMDY                                                          10

SEQ ID NO: 583          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 583
QSLLNSGHQK NY                                                       12

SEQ ID NO: 584          moltype =   length =
SEQUENCE: 584
000

SEQ ID NO: 585          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 585
QNDHRYPLT                                                           9

SEQ ID NO: 586          moltype = AA  length = 117
FEATURE                 Location/Qualifiers
source                  1..117
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 586
QMQLVQSGPE VKKPGTSVKV SCKASGYIFT DYNIDWVRQA RGQRLEWIGD INPKYDSTRY  60
NQKFKGRVTI TRDMSTSTAY MELSSLRSED TAVYYCAADG SSAMDYWGQG TTVTVSS     117

SEQ ID NO: 587          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 587
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 588          moltype = AA  length = 113
FEATURE                 Location/Qualifiers
source                  1..113
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 588
DIVMTQSPDS LAVSLGERAT INCKSSQSLL NSGHQKNYLA WYQQKPGQPP KLLIYGASTR  60
ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNDHRY PLTFGQGTKL EIK         113

SEQ ID NO: 589          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 589
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
```

-continued

```
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 590          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 590
GFNIKDYY                                                           8

SEQ ID NO: 591          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 591
IDPENGNT                                                           8

SEQ ID NO: 592          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 592
ARDYGYFDYW                                                         10

SEQ ID NO: 593          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
source                  1..5
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 593
SSVIY                                                              5

SEQ ID NO: 594          moltype =   length =
SEQUENCE: 594
000

SEQ ID NO: 595          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 595
QQRSSYPHT                                                          9

SEQ ID NO: 596          moltype = AA  length = 116
FEATURE                 Location/Qualifiers
source                  1..116
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 596
QVQLVQSGAE VKKPGSSVKV SCKASGFNIK DYYIHWVRQA PGQGLEWMGW IDPENGNTIY  60
DPKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARDY GYFDYWGQGT LVTVSS      116

SEQ ID NO: 597          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 597
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 598          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
source                  1..106
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 598
DVVMTQSPAF LSVTPGEKVT ITCSAGSSVI YMYWYQQKPD QAPKLLIKST SNLASGVPSR  60
FSGSGSGTDF TFTISSLEAE DAATYYCQQR SSYPHTFGQG TKLEIK                 106
```

-continued

```
SEQ ID NO: 599          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 599
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 600          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 600
GYTFTDYW                                                           8

SEQ ID NO: 601          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 601
IYPSHSYT                                                           8

SEQ ID NO: 602          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
source                  1..14
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 602
ARGGYRYPYY AMDY                                                    14

SEQ ID NO: 603          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 603
ENIYGA                                                             6

SEQ ID NO: 604          moltype =   length =
SEQUENCE: 604
000

SEQ ID NO: 605          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 605
QNVLSTPYT                                                          9

SEQ ID NO: 606          moltype = AA  length = 121
FEATURE                 Location/Qualifiers
source                  1..121
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 606
QVQLVQSGAE VKKPGASVKV SCKASGYTFT DYWINWVRQA PGQGLEWMGN IYPSHSYTNY  60
NQEFKDRVTM TRDTSTSTVY MELSSLRSED TAVYYCARGG YRYPYYAMDY WGQGTTVTVS  120
S                                                                  121

SEQ ID NO: 607          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 607
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330
```

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```
SEQ ID NO: 608          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 608
AIQLTQSPSS LSASVGDRVT ITCGASENIY GALNWYQQKP GKAPKLLIYG ATNLADGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQN VLSTPYTFGQ GTKLEIK                107

SEQ ID NO: 609          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 609
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 610          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 610
GYTFTNYW                                                           8

SEQ ID NO: 611          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 611
INPSSGYT                                                           8

SEQ ID NO: 612          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 612
ARDGGSVLFG Y                                                       11

SEQ ID NO: 613          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 613
QSLLNSGIRK NY                                                      12

SEQ ID NO: 614          moltype =   length =
SEQUENCE: 614
000

SEQ ID NO: 615          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 615
KQSYNLYT                                                           8

SEQ ID NO: 616          moltype = AA  length = 118
FEATURE                 Location/Qualifiers
source                  1..118
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 616
QVQLVQSGAE VKKPGASVKV SCKASGYTFT NYWMHWVRQA PGQGLEWMGY INPSSGYTEY  60
NQKFKDRVTM TRDTSTSTVY MELSSLRSED TAVYYCARDG GSVLFGYWGQ GTTVTVSS    118

SEQ ID NO: 617          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
```

-continued

```
                        organism = Homo sapiens
SEQUENCE: 617
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 618         moltype = AA  length = 112
FEATURE                Location/Qualifiers
source                 1..112
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 618
DIVMTQSPDS LAVSLGERAT INCKSSQSLL NSGIRKNYLA WYQQKPGQPP KLLIYSASTR  60
ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCKQSYNL YTFGQGTKLE IK          112

SEQ ID NO: 619         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 619
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 620         moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 620
AYSITSDYA                                                          9

SEQ ID NO: 621         moltype = AA  length = 7
FEATURE                Location/Qualifiers
source                 1..7
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 621
ITYSGST                                                            7

SEQ ID NO: 622         moltype = AA  length = 6
FEATURE                Location/Qualifiers
source                 1..6
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 622
ARSFGY                                                             6

SEQ ID NO: 623         moltype = AA  length = 6
FEATURE                Location/Qualifiers
source                 1..6
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 623
QSIGTS                                                             6

SEQ ID NO: 624         moltype =   length =
SEQUENCE: 624
000

SEQ ID NO: 625         moltype = AA  length = 7
FEATURE                Location/Qualifiers
source                 1..7
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 625
QQINSWP                                                            7

SEQ ID NO: 626         moltype = AA  length = 113
FEATURE                Location/Qualifiers
source                 1..113
                       mol_type = protein
                       organism = Homo sapiens
```

-continued

```
SEQUENCE: 626
QVQLQESGPG LVKPSETLSL TCAVSAYSIT SDYAWNWIRQ PPGKGLEWIG YITYSGSTRY  60
NPSLKSRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCARSF GYWGQGTTVT VSS         113

SEQ ID NO: 627         moltype = AA  length = 330
FEATURE                Location/Qualifiers
source                 1..330
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 627
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 628         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 628
EIVMTQSPAT LSVSPGERAT LSCRASQSIG TSIHWYQQKP GQAPRLLIYY ASESISGIPA  60
RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ INSWPTTFGQ GTKLEIK                107

SEQ ID NO: 629         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 629
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 630         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 630
GFNIKDYY                                                           8

SEQ ID NO: 631         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 631
IDPENGDT                                                           8

SEQ ID NO: 632         moltype = AA  length = 10
FEATURE                Location/Qualifiers
source                 1..10
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 632
ARDMGSSYVY                                                         10

SEQ ID NO: 633         moltype = AA  length = 5
FEATURE                Location/Qualifiers
source                 1..5
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 633
SSVIY                                                              5

SEQ ID NO: 634         moltype =   length =
SEQUENCE: 634
000

SEQ ID NO: 635         moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Homo sapiens
```

-continued

```
SEQUENCE: 635
QQRSSYPFT                                                          9

SEQ ID NO: 636          moltype = AA  length = 117
FEATURE                 Location/Qualifiers
source                  1..117
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 636
QVQLVQSGAE VKKPGASVKV SCKASGFNIK DYYMHWVRQA PGQGLEWMGW IDPENGDTEY  60
APKFQDRVTM TRDTSTSTVY MELSSLRSED TAVYYCARDM GSSYVYWGRG TLVTVSS     117

SEQ ID NO: 637          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 637
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 638          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
source                  1..106
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 638
DVVMTQSPAF LSVTPGEKVT ITCSASSSVI YMHWYQQKPD QAPKLLIKST SNLASGVPSR  60
FSGSGSGTDF TFTISSLEAE DAATYYCQQR SSYPFTFGQG TKLEIK                 106

SEQ ID NO: 639          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 639
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 640          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 640
GFSLSTSGMG                                                         10

SEQ ID NO: 641          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 641
IYWDDDK                                                            7

SEQ ID NO: 642          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 642
ARRPDYFGSS YVD                                                     13

SEQ ID NO: 643          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 643
ESVDTYGNSF                                                         10

SEQ ID NO: 644          moltype =   length =
```

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```
SEQUENCE: 644
000

SEQ ID NO: 645          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 645
QQNNEDPWT                                                           9

SEQ ID NO: 646          moltype = AA  length = 121
FEATURE                 Location/Qualifiers
source                  1..121
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 646
QVTLKESGPA LVKPTQTLTL TCTFSGFSLS TSGMGVSWIR QPPGKALEWL AHIYWDDDKR  60
YNPSLKSRLT ISKDTSKNQV VLTMTNMDPV DTATYYCARR PDYFGSSYVD WGQGTTVTVS  120
S                                                                   121

SEQ ID NO: 647          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 647
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 648          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 648
DIVMTQTPLS LSVTPGQPAS ISCRASESVD TYGNSFMHWY LQKPGQPPQL LIYLASNLDF  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQNNEDPW TFGQGTKLEI K           111

SEQ ID NO: 649          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 649
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 650          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 650
GYSITSDYA                                                           9

SEQ ID NO: 651          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 651
ITYSGST                                                             7

SEQ ID NO: 652          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
source                  1..14
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 652
ARSHYGSTYW YFDV                                                     14
```

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```
SEQ ID NO: 653          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 653
ESVEYYGTSL                                                          10

SEQ ID NO: 654          moltype =   length =
SEQUENCE: 654
000

SEQ ID NO: 655          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 655
QQTRKVPWT                                                           9

SEQ ID NO: 656          moltype = AA  length = 121
FEATURE                 Location/Qualifiers
source                  1..121
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 656
QVQLQESGPG LVKPSETLSL TCAVSGYSIT SDYAWNWIRQ PPGKGLEWIG FITYSGSTNY  60
NPSLKSRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCARSH YGSTYWYFDV WGQGTTVTVS  120
S                                                                   121

SEQ ID NO: 657          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 657
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 658          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 658
DIVMTQTPLS LSVTPGQPAS ISCRASESVE YYGTSLMQWY LQKPGQSPQL LIYAASNVES  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQTRKVPW TFGQGTRLEI K           111

SEQ ID NO: 659          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 659
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 660          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 660
GYTFTSYD                                                            8

SEQ ID NO: 661          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 661
IYPGDGYT                                                            8
```

-continued

```
SEQ ID NO: 662          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 662
ARWGYGSYAM DY                                                       12

SEQ ID NO: 663          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 663
QSLVHSNGNT Y                                                        11

SEQ ID NO: 664          moltype =   length =
SEQUENCE: 664
000

SEQ ID NO: 665          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 665
SQSTHVPPT                                                           9

SEQ ID NO: 666          moltype = AA  length = 119
FEATURE                 Location/Qualifiers
source                  1..119
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 666
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYDINWVRQA PGQGLEWMGW IYPGDGYTEY  60
NEKFRGRVTM TRDTSTSTVY MELSSLRSED TAVYYCARWG YGSYAMDYWG QGTLVTVSS   119

SEQ ID NO: 667          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 667
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 668          moltype = AA  length = 112
FEATURE                 Location/Qualifiers
source                  1..112
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 668
DIVMTQSPLS LPVTPGEPAS ISCRSSQSLV HSNGNTYLHW YLQKPGQSPQ LLIYKVSNRF  60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCSQSTHVP PTFGQGTKLE IK         112

SEQ ID NO: 669          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 669
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 670          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 670
GYTFTSYW                                                            8
```

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```
SEQ ID NO: 671          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 671
INPSTGYP                                                          8

SEQ ID NO: 672          moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 672
ARSYYDYDGG AWFAY                                                  15

SEQ ID NO: 673          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 673
ESVEYYGTSL                                                        10

SEQ ID NO: 674          moltype =   length =
SEQUENCE: 674
000

SEQ ID NO: 675          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 675
QQSRKVPST                                                         9

SEQ ID NO: 676          moltype = AA  length = 122
FEATURE                 Location/Qualifiers
source                  1..122
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 676
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYWMHWVRQA PGQGLEWMGY INPSTGYPGY  60
NQKFKDRVTM TRDTSTSTVY MELSSLRSED TAVYYCARSY YDYDGGAWFA YWGQGTTVTV  120
SS                                                                122

SEQ ID NO: 677          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 677
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                  330

SEQ ID NO: 678          moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 678
DIVMTQTPLS LSVTPGQPAS ISCRASESVE YYGTSLMQWY LQKPGQPPQL LIYAASNVES  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQSRKVPS TFGQGTKLEI K          111

SEQ ID NO: 679          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 679
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
```

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SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 680          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 680
GYTFTDYA                                                           8

SEQ ID NO: 681          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 681
IDTYYGNT                                                           8

SEQ ID NO: 682          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 682
ARGGGDALDY                                                         10

SEQ ID NO: 683          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 683
QSVSND                                                             6

SEQ ID NO: 684          moltype =   length =
SEQUENCE: 684
000

SEQ ID NO: 685          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 685
QQGYTSLRT                                                          9

SEQ ID NO: 686          moltype = AA  length = 117
FEATURE                 Location/Qualifiers
source                  1..117
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 686
QVQLVQSGAE VKKPGASVKV SCKASGYTFT DYAMHWVRQA PGQGLEWMGV IDTYYGNTNY  60
NQKFKGRVTM TRDTSISTAY MELSRLRSDD TAVYYCARGG GDALDYWGQG TTVTVSS     117

SEQ ID NO: 687          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 687
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 688          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 688
DIQMTQSPSS LSASVGDRVT ITCKASQSVS NDVVWYQQKP GKAPKLLIYY ASNRYIGVPS  60
RFSGSGSGTD FTFTISSLQP EDIATYYCQQ GYTSLRTFGQ GTKLEIK                107
```

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SEQ ID NO: 689          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 689
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 690          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 690
GYSITSGYS                                                          9

SEQ ID NO: 691          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 691
IHYIGIT                                                            7

SEQ ID NO: 692          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 692
AREDYDYDGV FAY                                                     13

SEQ ID NO: 693          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 693
QSISNN                                                             6

SEQ ID NO: 694          moltype =   length =
SEQUENCE: 694
000

SEQ ID NO: 695          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 695
QQSNSWPHT                                                          9

SEQ ID NO: 696          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 696
QVQLQESGPG LVKPSETLSL TCAVSGYSIT SGYSWHWIRQ PPGKGLEWIG YIHYIGITNN  60
NPSLKSRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCARED YDYDGVFAYW GQGTLVTVSS  120

SEQ ID NO: 697          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 697
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330
```

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SEQ ID NO: 698          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 698
EIVLTQSPAT LSLSPGERAT LSCRASQSIS NNLHWYQQKP GQAPRLLIYY ASQSISGIPA  60
RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ SNSWPHTFGQ GTKLEIK                107

SEQ ID NO: 699          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 699
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 700          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 700
GFSLTNYD                                                            8

SEQ ID NO: 701          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 701
IWTGGGT                                                             7

SEQ ID NO: 702          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 702
AREGLLLPLY                                                          10

SEQ ID NO: 703          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 703
QNVGTN                                                              6

SEQ ID NO: 704          moltype =   length =
SEQUENCE: 704
000

SEQ ID NO: 705          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 705
QQYNSYPLT                                                           9

SEQ ID NO: 706          moltype = AA  length = 116
FEATURE                 Location/Qualifiers
source                  1..116
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 706
QVQLQESGPG LVKPSETLSL TCTVSGFSLT NYDISWIRQP PGKGLEWIGV IWTGGGTNYN  60
SAFMSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCAREGL LLPLYWGQGT LVTVSS      116

SEQ ID NO: 707          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
```

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```
SEQUENCE: 707
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 708         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 708
DIQMTQSPSS LSASVGDRVT ITCKASQNVG TNVAWYQQKP GKVPKLLIYS ASYRYSGVPS  60
RFSGSGSGTD FTLTISSLQP EDVATYYCQQ YNSYPLTFGQ GTKLEIK                107

SEQ ID NO: 709         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 709
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 710         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 710
GYTFTNFG                                                           8

SEQ ID NO: 711         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 711
INTYTGEP                                                           8

SEQ ID NO: 712         moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 712
ARGAYYYGSR VWFAY                                                   15

SEQ ID NO: 713         moltype = AA  length = 11
FEATURE                Location/Qualifiers
source                 1..11
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 713
QNLVHSNGNT Y                                                       11

SEQ ID NO: 714         moltype =   length =
SEQUENCE: 714
000

SEQ ID NO: 715         moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 715
SQSSHVPYT                                                          9

SEQ ID NO: 716         moltype = AA  length = 122
FEATURE                Location/Qualifiers
source                 1..122
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 716
```

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```
QVQLVQSGSE LKKPGASVKV SCKASGYTFT NFGMNWVRQA PGQGLEWMGW INTYTGEPTY  60
ADDFKGRFVF SLDTSVSTAY LQICSLKAED TAVYYCARGA YYYGSRVWFA YWGQGTLVTV  120
SS                                                                 122

SEQ ID NO: 717         moltype = AA  length = 330
FEATURE                Location/Qualifiers
source                 1..330
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 717
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 718         moltype = AA  length = 112
FEATURE                Location/Qualifiers
source                 1..112
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 718
DIVMTQSPLS LPVTPGEPAS ISCTSSQNLV HSNGNTYLHW YLQKPGQSPQ LLIYKVSNRF  60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCSQSSHVP YTFGQGTKLE IK          112

SEQ ID NO: 719         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 719
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 720         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 720
GFSLTSSG                                                           8

SEQ ID NO: 721         moltype = AA  length = 7
FEATURE                Location/Qualifiers
source                 1..7
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 721
IWSGGNT                                                            7

SEQ ID NO: 722         moltype = AA  length = 13
FEATURE                Location/Qualifiers
source                 1..13
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 722
AREDYDYDWY FDV                                                     13

SEQ ID NO: 723         moltype = AA  length = 10
FEATURE                Location/Qualifiers
source                 1..10
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 723
ESVEYYGTSL                                                         10

SEQ ID NO: 724         moltype =   length =
SEQUENCE: 724
000

SEQ ID NO: 725         moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Homo sapiens
```

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```
SEQUENCE: 725
QQSRKVPWT                                                          9

SEQ ID NO: 726         moltype = AA  length = 119
FEATURE                Location/Qualifiers
source                 1..119
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 726
QVQLQESGPG LVKPSETLSL TCTVSGFSLT SSGVHWIRQP PGKGLEWIGV IWSGGNTDYN  60
AAFISRVTIS VDTSKNQFSL KLSSVTAADT AVYYCAREDY DYDWYFDVWG QGTTVTVSS   119

SEQ ID NO: 727         moltype = AA  length = 330
FEATURE                Location/Qualifiers
source                 1..330
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 727
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 728         moltype = AA  length = 111
FEATURE                Location/Qualifiers
source                 1..111
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 728
DIVMTQTPLS LSVTPGQPAS ISCRASESVE YYGTSLMQWY LQKPGQPPQL LIYAASNVKS  60
GVPDRFSGSG SGTDFTLKIS RVEAEDVGVY YCQQSRKVPW TFGQGTKLEI K           111

SEQ ID NO: 729         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 729
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 730         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 730
GYTFANFW                                                           8

SEQ ID NO: 731         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 731
IFPGNSDT                                                           8

SEQ ID NO: 732         moltype = AA  length = 12
FEATURE                Location/Qualifiers
source                 1..12
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 732
ARELTGTYYF DY                                                      12

SEQ ID NO: 733         moltype = AA  length = 5
FEATURE                Location/Qualifiers
source                 1..5
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 733
SSVSY                                                              5

SEQ ID NO: 734         moltype =   length =
```

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```
SEQUENCE: 734
000

SEQ ID NO: 735          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 735
HQWSGHFT                                                            8

SEQ ID NO: 736          moltype = AA  length = 119
FEATURE                 Location/Qualifiers
source                  1..119
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 736
QVQLVQSGAE VKKPGASVKV SCKASGYTFA NFWMHWVRQA PGQGLEWMGA IFPGNSDTGY  60
NQKFKGRVTM TRDTSTSTVY MELSSLRSED TAVYYCAREL TGTYYFDYWG QGTLVTVSS   119

SEQ ID NO: 737          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 737
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 738          moltype = AA  length = 105
FEATURE                 Location/Qualifiers
source                  1..105
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 738
EIVLTQSPAT LSLSPGERAT LSCSATSSVS YMHWYQQKPG QAPRLLIYSS SNLASGIPAR  60
FSGSGSGTDF TLTISSLEPE DFAVYYCHQW SGHFTFGQGT KLEIK                  105

SEQ ID NO: 739          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 739
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 740          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 740
GYTFANYL                                                            8

SEQ ID NO: 741          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 741
IYPGGGFI                                                            8

SEQ ID NO: 742          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 742
ARRFDYGGYF FDY                                                      13

SEQ ID NO: 743          moltype = AA  length = 11
```

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```
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 743
QSIVHSNGNI Y                                                            11

SEQ ID NO: 744          moltype =   length =
SEQUENCE: 744
000

SEQ ID NO: 745          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 745
FQGSHVPWT                                                               9

SEQ ID NO: 746          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 746
QVQLVQSGAE VKKPGASVKV SCKASGYTFA NYLIGWVRQA PGQRLEWMGD IYPGGGFISY  60
NEKFKGRVTI TRDTSASTAY MELSSLRSED TAVYYCARRF DYGGYFFDYW GQGTLVTVSS  120

SEQ ID NO: 747          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 747
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 748          moltype = AA  length = 112
FEATURE                 Location/Qualifiers
source                  1..112
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 748
DIVMTQSPLS LPVTPGEPAS ISCRSSQSIV HSNGNIYLEW YLQKPGQSPQ LLIYKVSNRF  60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHVP WTFGQGTKLE IK         112

SEQ ID NO: 749          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 749
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 750          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 750
GFSITNYD                                                                8

SEQ ID NO: 751          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 751
IWTGGGT                                                                 7

SEQ ID NO: 752          moltype = AA  length = 12
```

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```
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 752
ARDRSPYFGY DY                                                       12

SEQ ID NO: 753          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 753
QSLVHSNGNT Y                                                        11

SEQ ID NO: 754          moltype =   length =
SEQUENCE: 754
000

SEQ ID NO: 755          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 755
SQSTHVPWT                                                           9

SEQ ID NO: 756          moltype = AA  length = 118
FEATURE                 Location/Qualifiers
source                  1..118
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 756
QVQLQESGPG LVKPSETLSL TCTVSGFSIT NYDISWIRQP PGKGLEWIGV IWTGGGTNYN  60
SAFMSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCARDRS PYFGYDYWGQ GTTVTVSS    118

SEQ ID NO: 757          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 757
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 758          moltype = AA  length = 112
FEATURE                 Location/Qualifiers
source                  1..112
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 758
DIVMTQTPLS LSVTPGQPAS ISCRSSQSLV HSNGNTYLHW YLQKPGQSPQ LLIYKVSNRF  60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCSQSTHVP WTFGQGTKLE IK          112

SEQ ID NO: 759          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 759
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 760          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 760
GYSITSDYA                                                           9

SEQ ID NO: 761          moltype = AA  length = 7
```

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```
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 761
MMYSGSA                                                             7

SEQ ID NO: 762          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 762
ARFDHYYGRF DY                                                       12

SEQ ID NO: 763          moltype = AA  length = 5
FEATURE                 Location/Qualifiers
source                  1..5
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 763
SSVSY                                                               5

SEQ ID NO: 764          moltype =   length =
SEQUENCE: 764
000

SEQ ID NO: 765          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 765
QQWNYPLFT                                                           9

SEQ ID NO: 766          moltype = AA  length = 119
FEATURE                 Location/Qualifiers
source                  1..119
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 766
QVQLQESGPG LVKPSETLSL TCAVSGYSIT SDYAWTWIRQ PPGKGLEWIG YMMYSGSASY  60
NPSLKGRVTI SVDTSKNQFS LKLSSVTAAD TAVYYCARFD HYYGRFDYWG QGTTVTVSS   119

SEQ ID NO: 767          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 767
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 768          moltype = AA  length = 106
FEATURE                 Location/Qualifiers
source                  1..106
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 768
AIQLTQSPSS LSASVGDRVT ITCSASSSVS YIHWYQQKPG KAPKLLIYEI SKLASGVPSR  60
FSGSGSGTDF TLTISSLQPE DFATYYCQQW NYPLFTFGQG TKLEIK                 106

SEQ ID NO: 769          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 769
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 770          moltype = AA  length = 8
```

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```
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 770
GFTFRNYG                                                            8

SEQ ID NO: 771          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 771
IISGGSYT                                                            8

SEQ ID NO: 772          moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 772
ARIYDHDGDY YAMDY                                                    15

SEQ ID NO: 773          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 773
QSIVHSNGNT Y                                                        11

SEQ ID NO: 774          moltype =   length =
SEQUENCE: 774
000

SEQ ID NO: 775          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 775
FQGSHVPWT                                                           9

SEQ ID NO: 776          moltype = AA  length = 122
FEATURE                 Location/Qualifiers
source                  1..122
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 776
EVQLVESGGG LVQPGGSLRL SCAASGFTFR NYGMSWVRQA PGKGLEWVAS IISGGSYTYY  60
PDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARIY DHDGDYYAMD YWGQGTTVTV  120
SS                                                                  122

SEQ ID NO: 777          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 777
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 778          moltype = AA  length = 112
FEATURE                 Location/Qualifiers
source                  1..112
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 778
DIVMTQSPLS LPVTPGEPAS ISCRSSQSIV HSNGNTYLEW YLQKPGQSPQ LLIYKVSNRF  60
SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCFQGSHVP WTFGQGTKLE IK          112

SEQ ID NO: 779          moltype = AA  length = 107
```

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```
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 779
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 780          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 780
GYTFTSYD                                                           8

SEQ ID NO: 781          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 781
IYPGDGST                                                           8

SEQ ID NO: 782          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 782
AREGITPFAY                                                         10

SEQ ID NO: 783          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 783
KSISKY                                                             6

SEQ ID NO: 784          moltype =   length =
SEQUENCE: 784
000

SEQ ID NO: 785          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 785
QQHNEYPWT                                                          9

SEQ ID NO: 786          moltype = AA  length = 117
FEATURE                 Location/Qualifiers
source                  1..117
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 786
QVQLVQSGAE VKKPGSSVKV SCKASGYTFT SYDINWVRQA PGQGLEWMGR IYPGDGSTKY  60
NEKFKGRVTI TADKSTSTAY MELSSLRSED TAVYYCAREG ITPFAYWGQG TTVTVSS     117

SEQ ID NO: 787          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 787
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 788          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
```

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```
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 788
AIQLTQSPSS LSASVGDRVT ITCRASKSIS KYLAWYQQKP GKAPKLLIYS GSTLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ HNEYPWTFGQ GTKLEIK                107

SEQ ID NO: 789          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 789
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 790          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 790
GGTFSSYA                                                           8

SEQ ID NO: 791          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 791
IIPIFGTA                                                           8

SEQ ID NO: 792          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 792
ARSSYGWSYE FDY                                                     13

SEQ ID NO: 793          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 793
QSISSY                                                             6

SEQ ID NO: 794          moltype =   length =
SEQUENCE: 794
000

SEQ ID NO: 795          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 795
QQSYSTPLT                                                          9

SEQ ID NO: 796          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 796
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSS YGWSYEFDYW GQGTLVTVSS  120

SEQ ID NO: 797          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 797
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
```

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GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 798         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 798
DIQMTQSPSS LSASVGDRVT ITCRASQSIS SYLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPLTFGQ GTKVEIK                107

SEQ ID NO: 799         moltype = AA  length = 107
FEATURE                Location/Qualifiers
source                 1..107
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 799
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 800         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 800
GGTFSSYA                                                           8

SEQ ID NO: 801         moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 801
IIPIFGTA                                                           8

SEQ ID NO: 802         moltype = AA  length = 13
FEATURE                Location/Qualifiers
source                 1..13
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 802
ARSTVGWSYE FDY                                                     13

SEQ ID NO: 803         moltype = AA  length = 6
FEATURE                Location/Qualifiers
source                 1..6
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 803
QSISSY                                                             6

SEQ ID NO: 804         moltype =   length =
SEQUENCE: 804
000

SEQ ID NO: 805         moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 805
QQSYSTPLT                                                          9

SEQ ID NO: 806         moltype = AA  length = 120
FEATURE                Location/Qualifiers
source                 1..120
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 806
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARST VGWSYEFDYW GQGTLVTVSS  120
```

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SEQ ID NO: 807          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 807
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 808          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 808
DIQMTQSPSS LSASVGDRVT ITCRASQSIS SYLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPLTFGQ GTKVEIK                107

SEQ ID NO: 809          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 809
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 810          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 810
GGTFSSYA                                                           8

SEQ ID NO: 811          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 811
IIPIFGTA                                                           8

SEQ ID NO: 812          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 812
ARHVLGWVLE LDY                                                     13

SEQ ID NO: 813          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 813
QSISSY                                                             6

SEQ ID NO: 814          moltype =   length =
SEQUENCE: 814
000

SEQ ID NO: 815          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 815
QQSYSTPLT                                                          9
```

-continued

```
SEQ ID NO: 816          moltype = AA  length = 120
FEATURE                 Location/Qualifiers
source                  1..120
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 816
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG IIPIFGTANY  60
AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARHV LGWVLELDYW GQGTLVTVSS  120

SEQ ID NO: 817          moltype = AA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 817
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 818          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 818
DIQMTQSPSS LSASVGDRVT ITCRASQSIS SYLNWYQQKP GKAPKLLIYA ASSLQSGVPS  60
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPLTFGQ GTKVEIK                107

SEQ ID NO: 819          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
source                  1..107
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 819
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107
```

1. A method of treating or preventing an autoimmune, allergic or inflammatory condition comprising administering to a patient in need thereof a therapeutically or prophylactically effective amount of an isolated antibody or antibody fragment thereof comprising an antigen binding region that specifically binds to human V-domain Ig Suppressor of T cell Activation (human VISTA), wherein the antibody or antibody fragment agonizes or promotes one or more of the effects of VISTA on immunity.

2-119. (canceled)

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