

Release of CCL17 from peripheral blood PBMCs induced by IL-4, IL-13, and TSLP

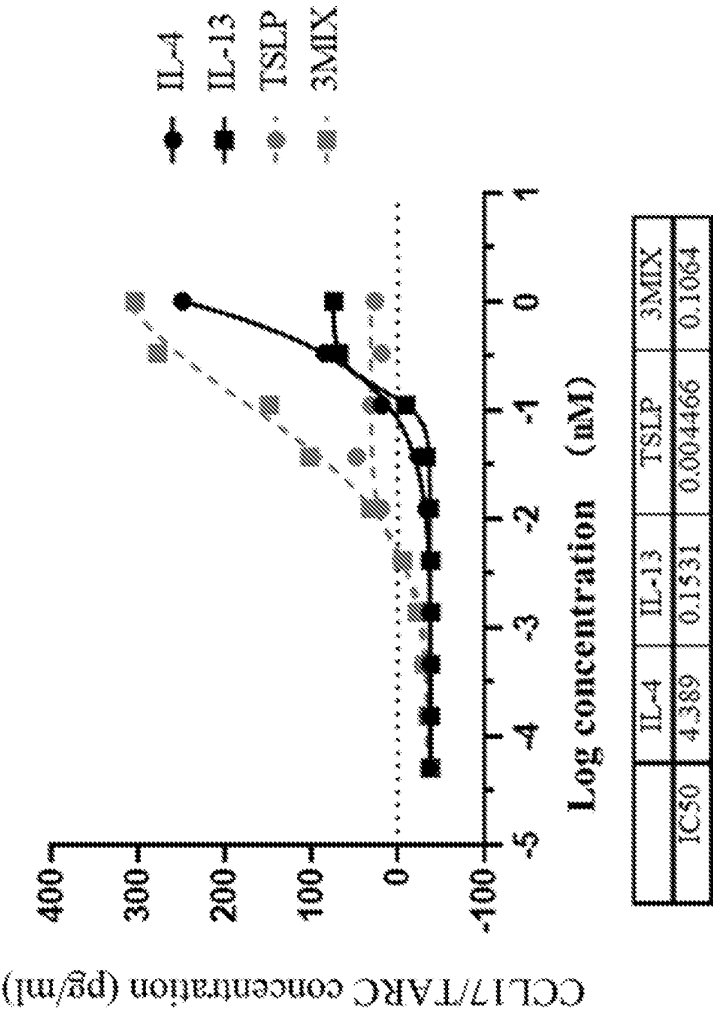


FIG. 1A

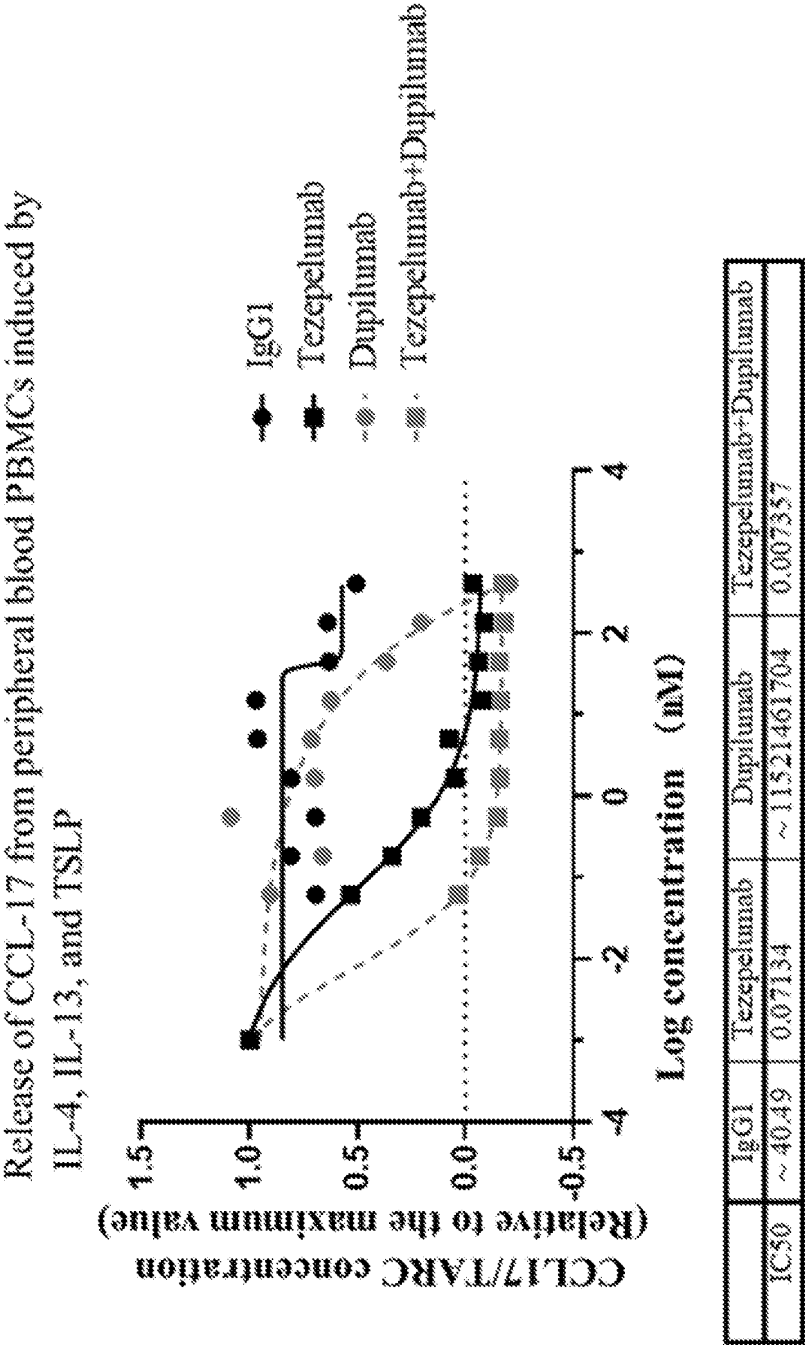


FIG. 1B

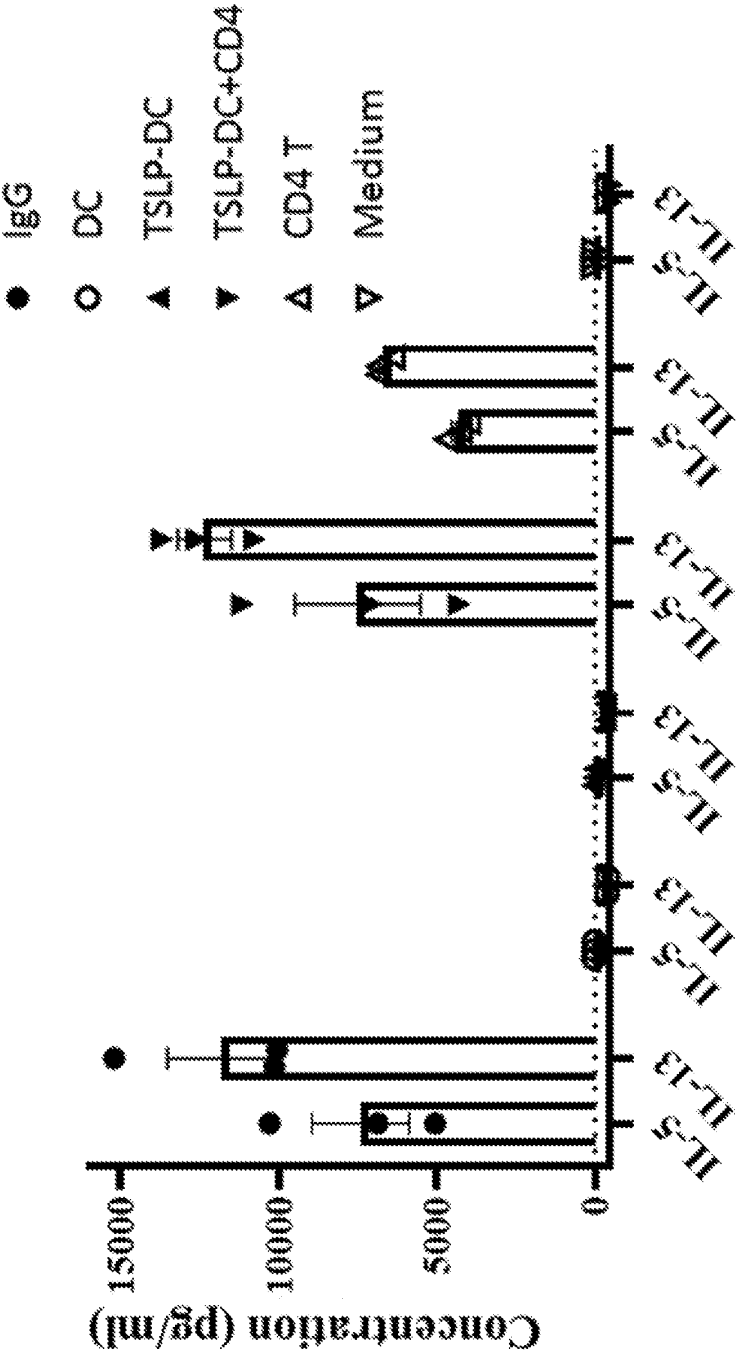


FIG. 2B

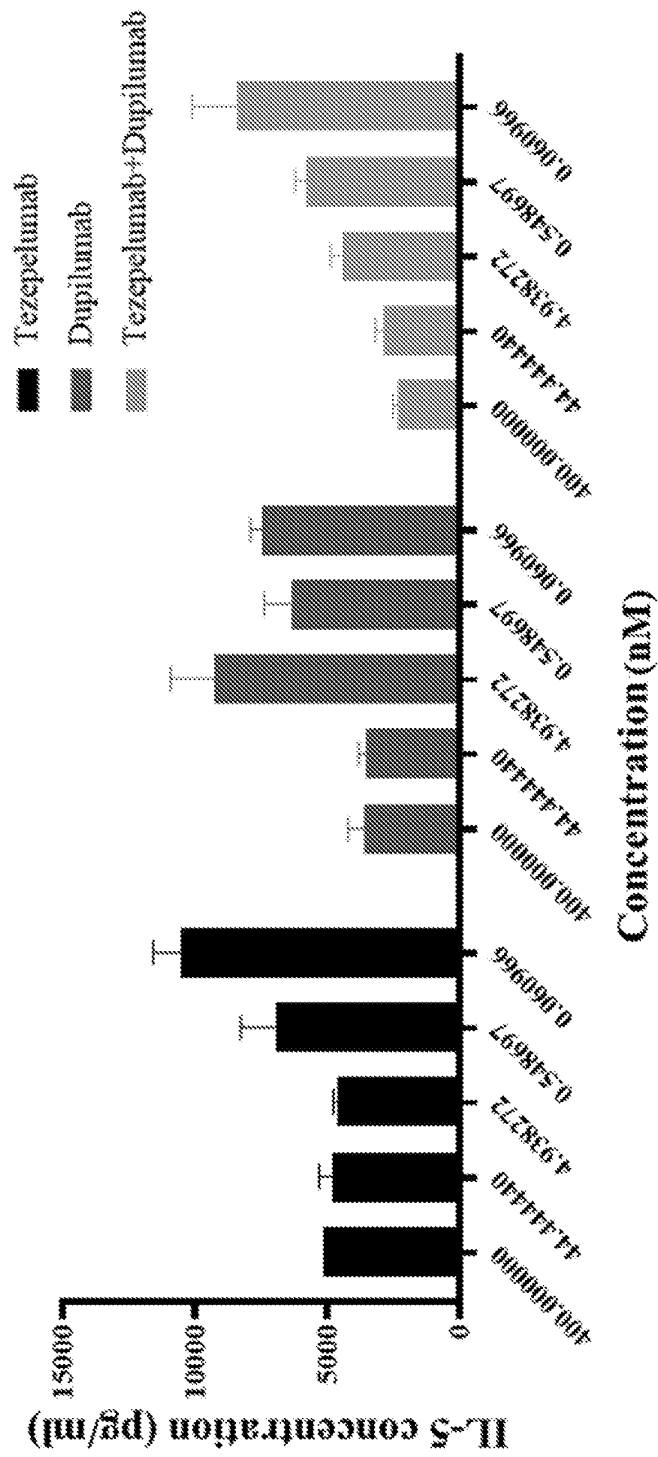


FIG. 2C

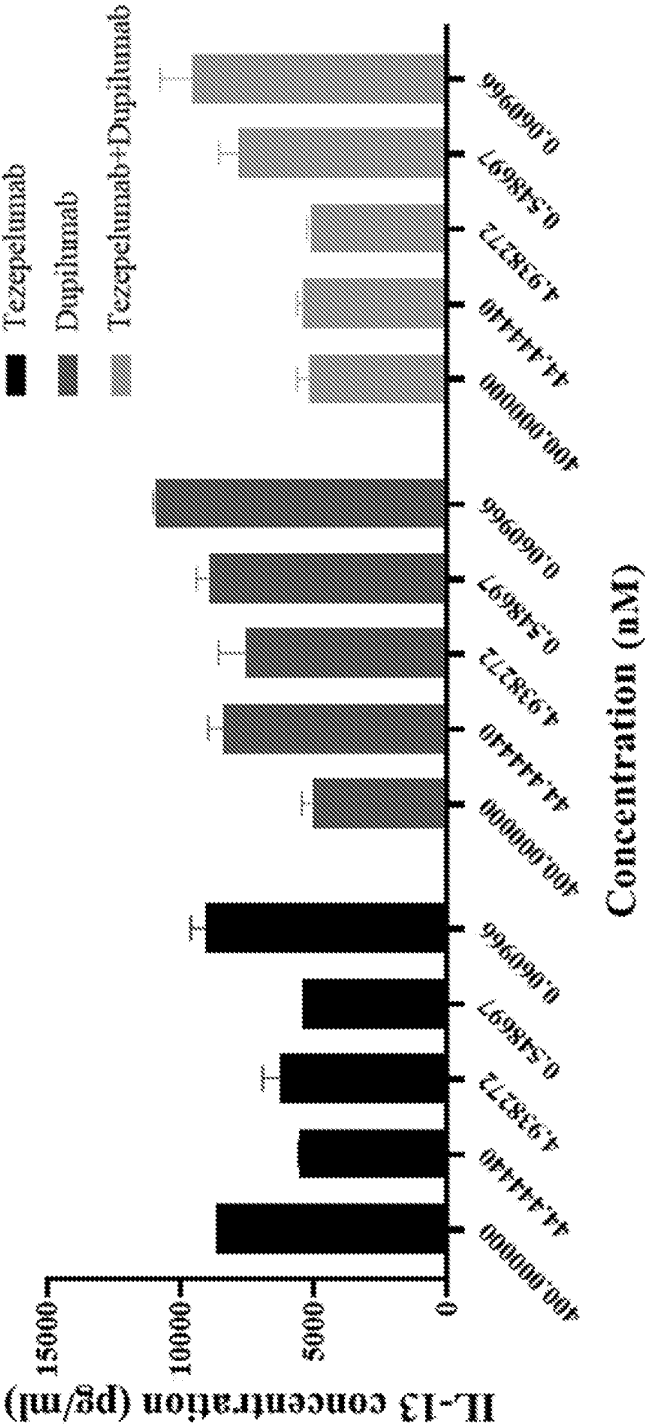


FIG. 2D

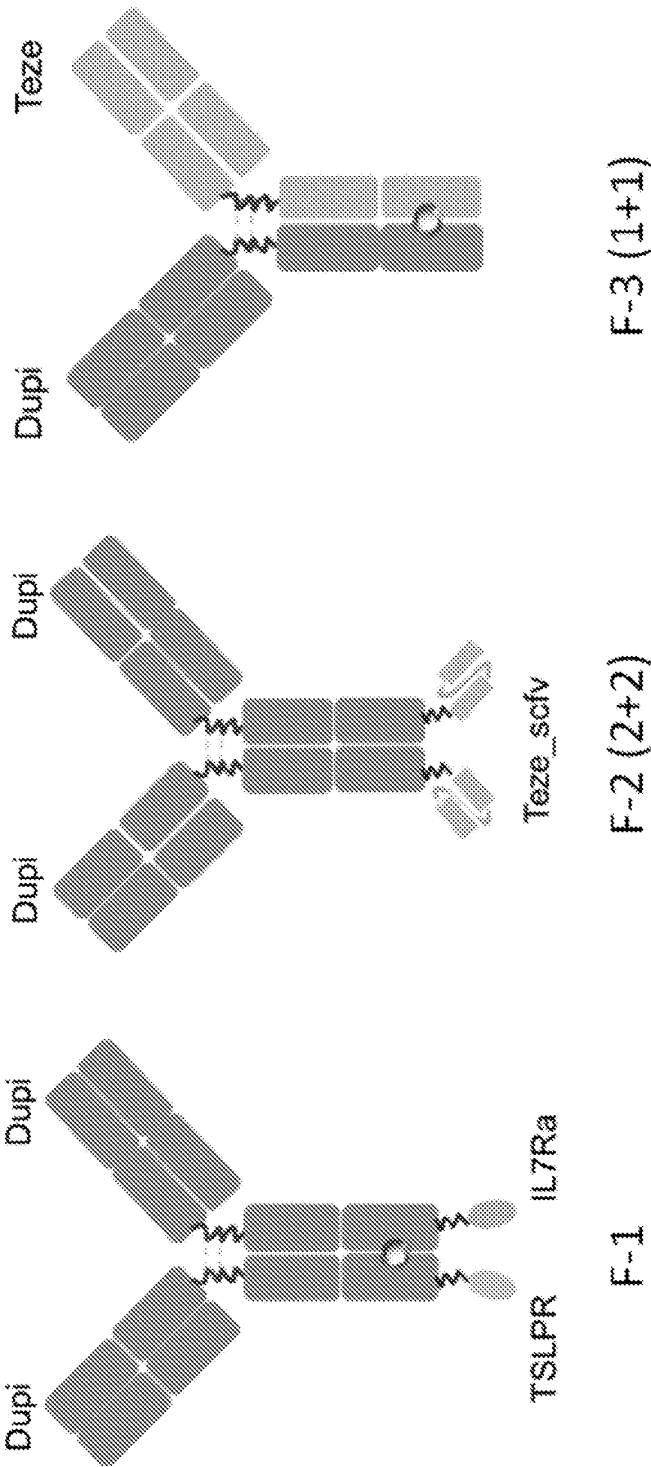


FIG. 3

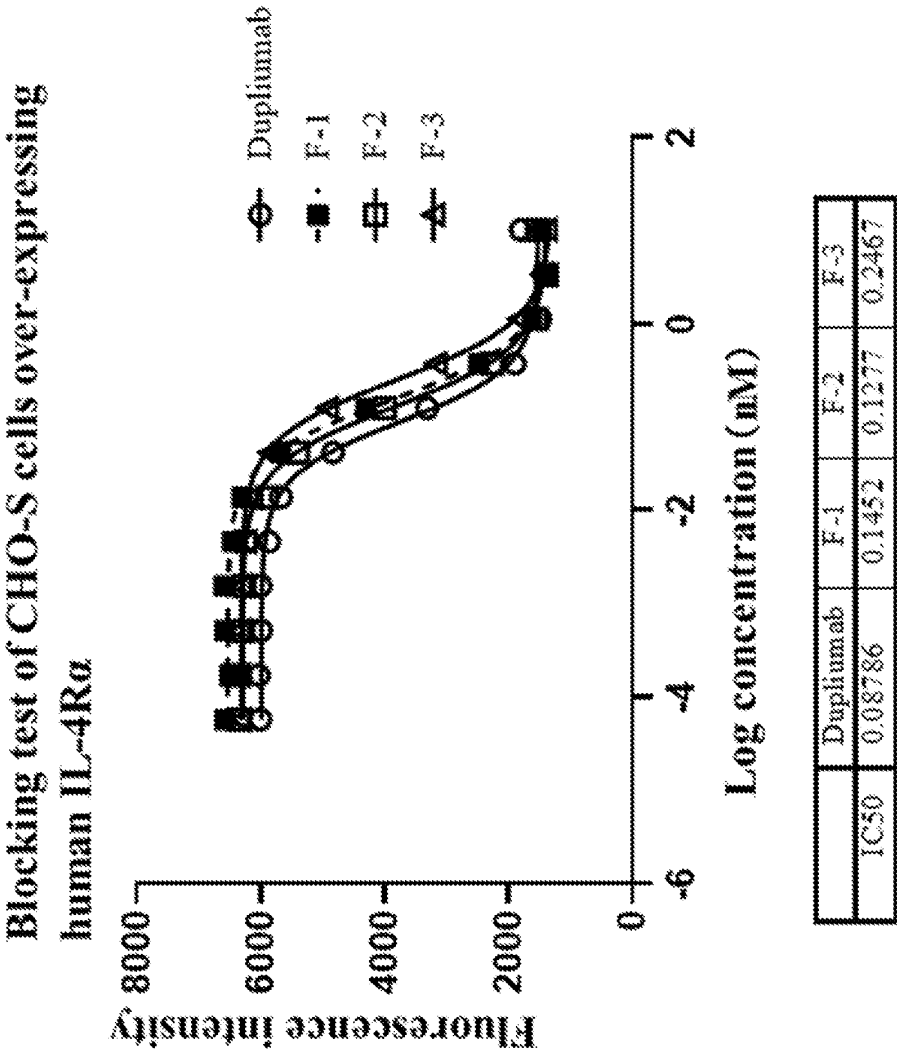


FIG. 4A

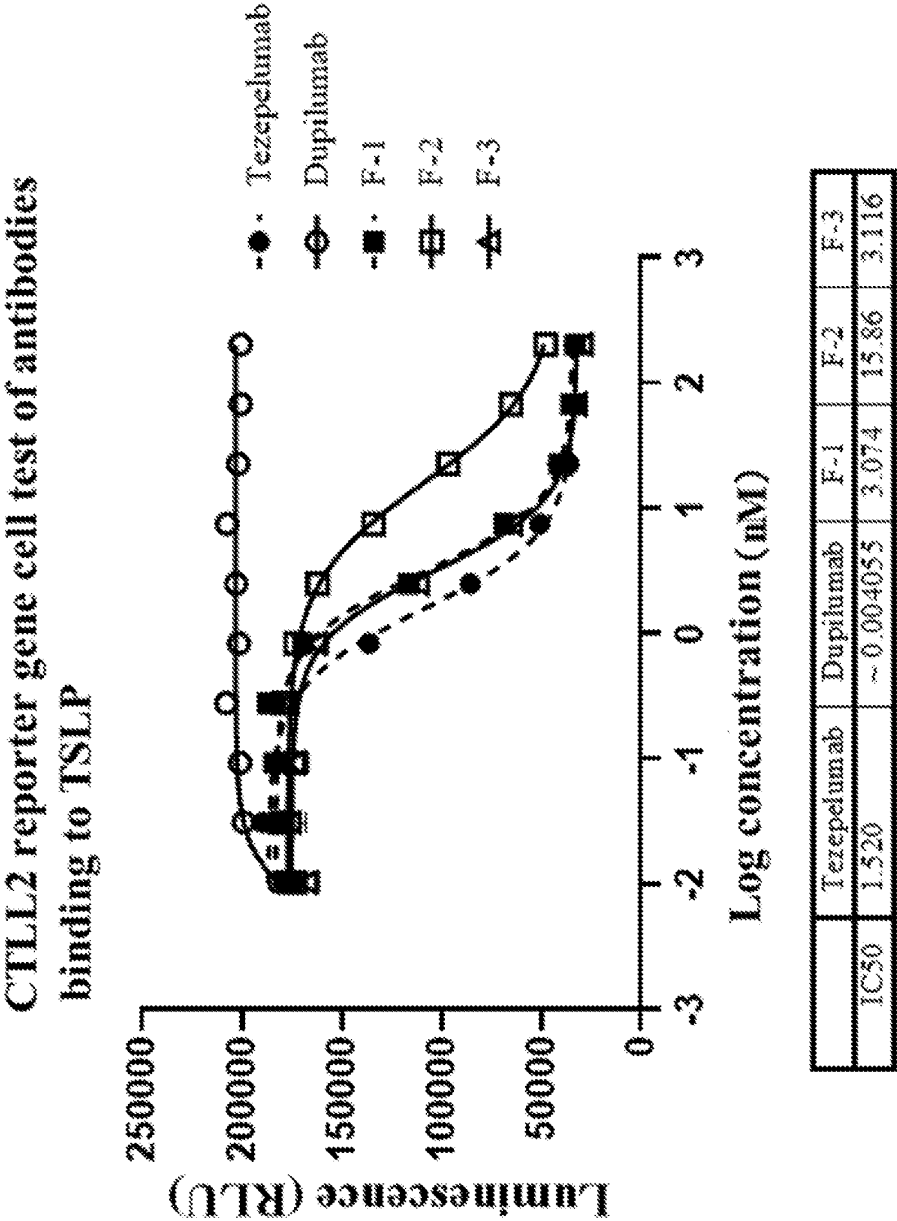


FIG. 4B

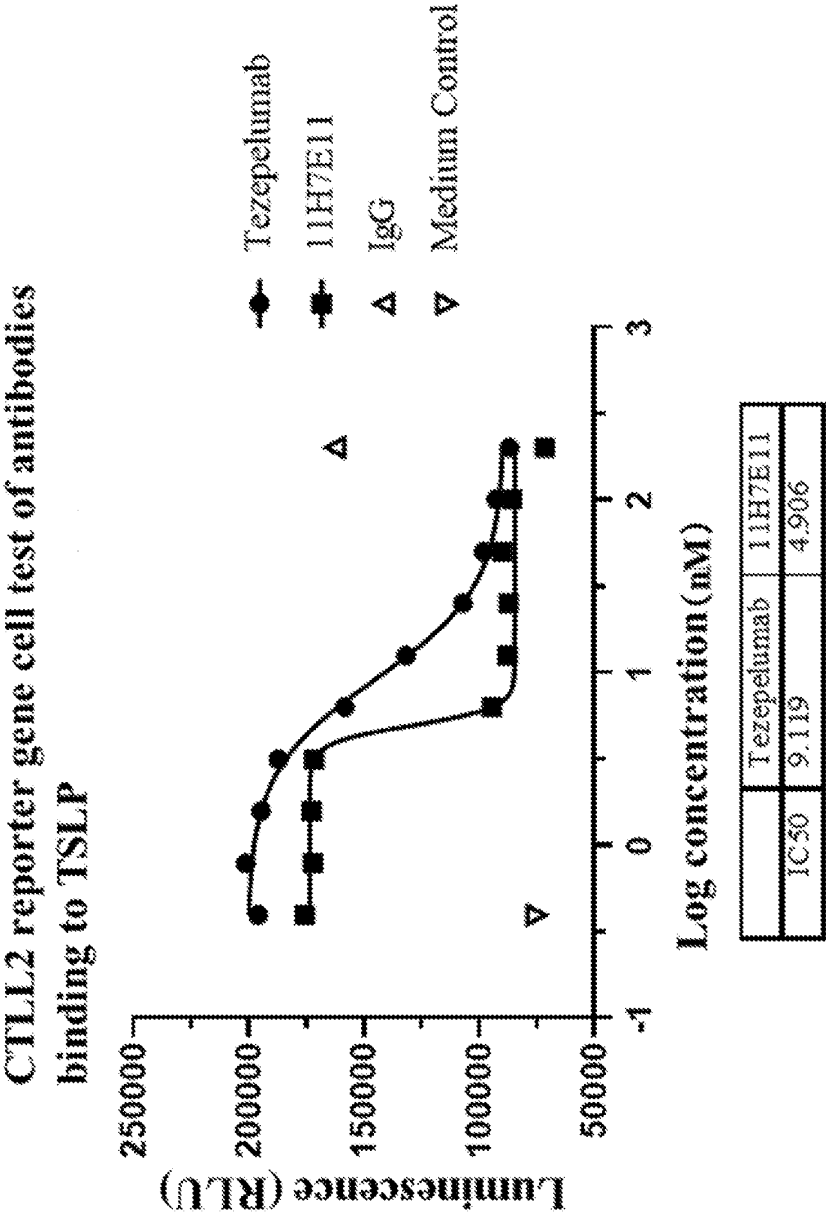


FIG. 5A

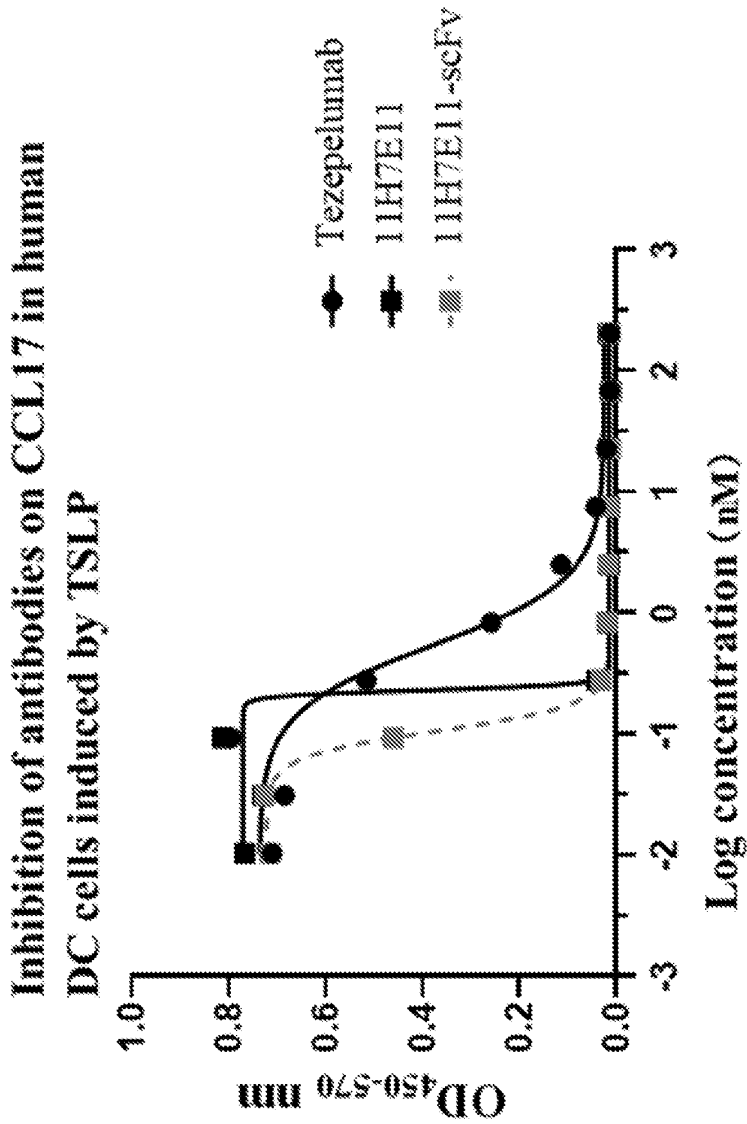


FIG. 5B

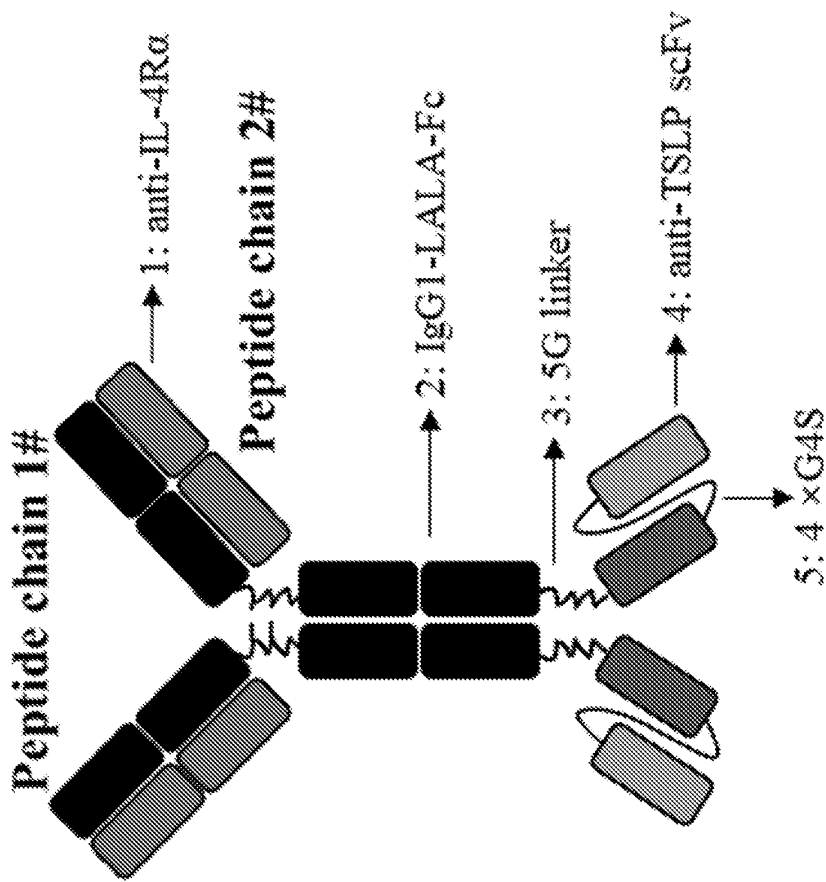


FIG. 6A

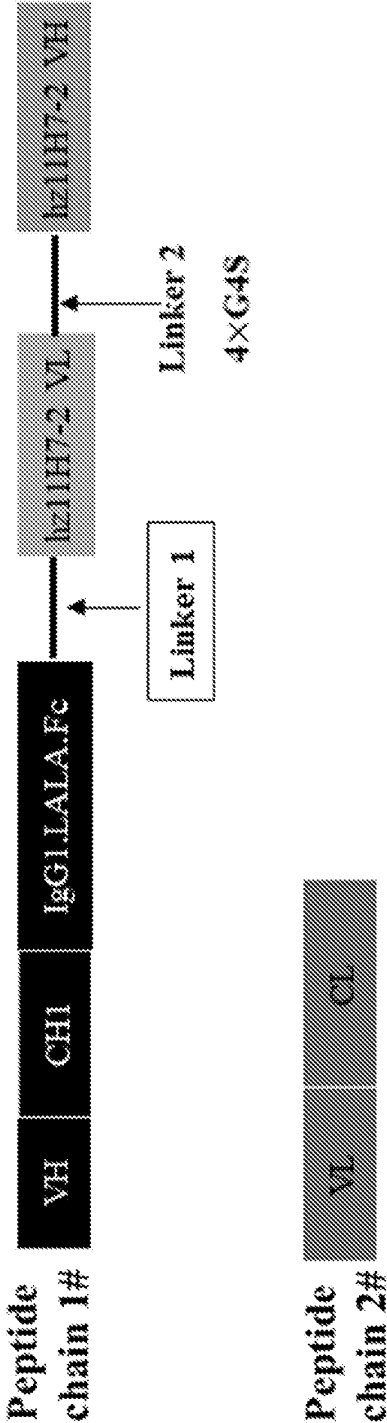


FIG. 6B

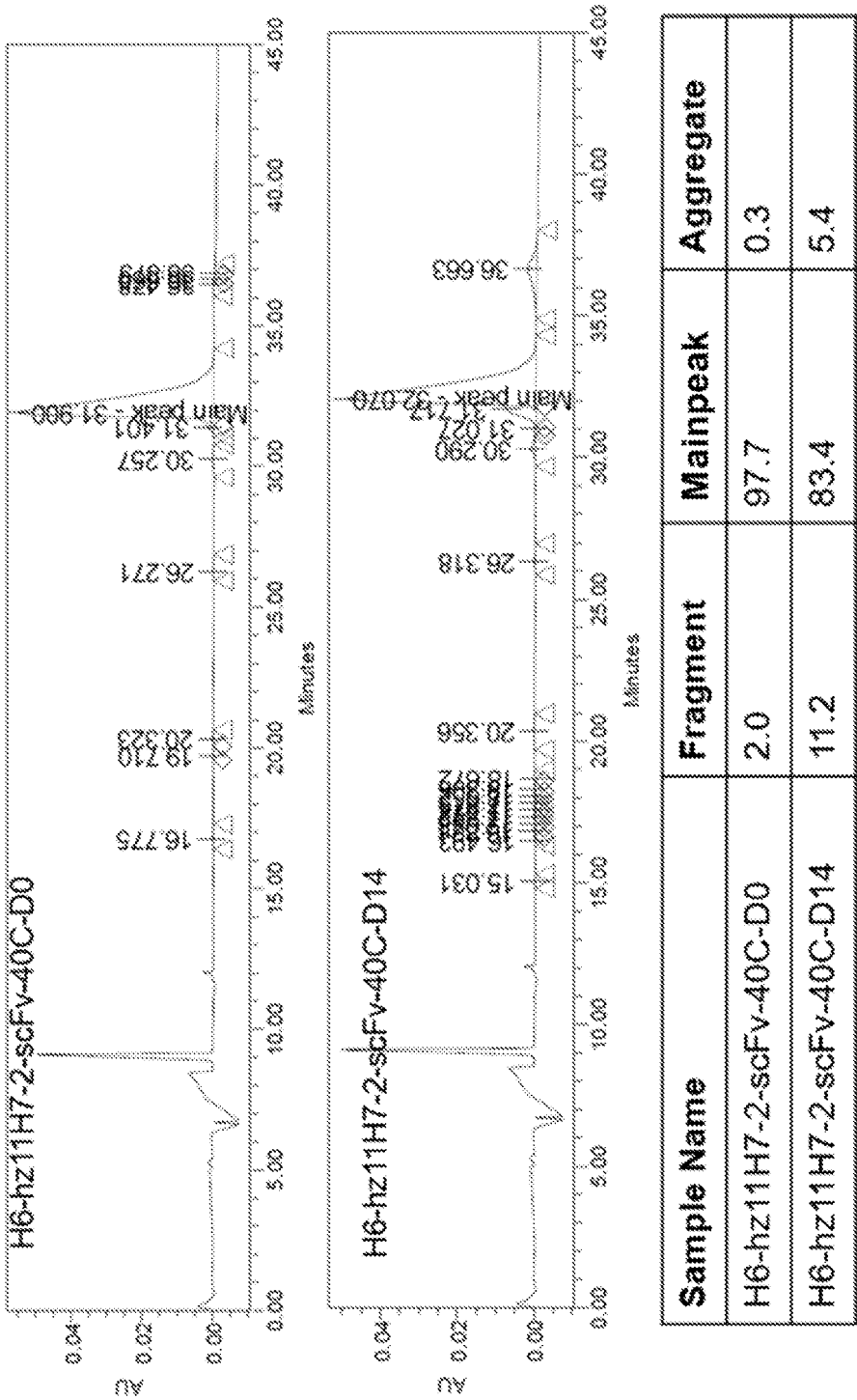


FIG. 7A

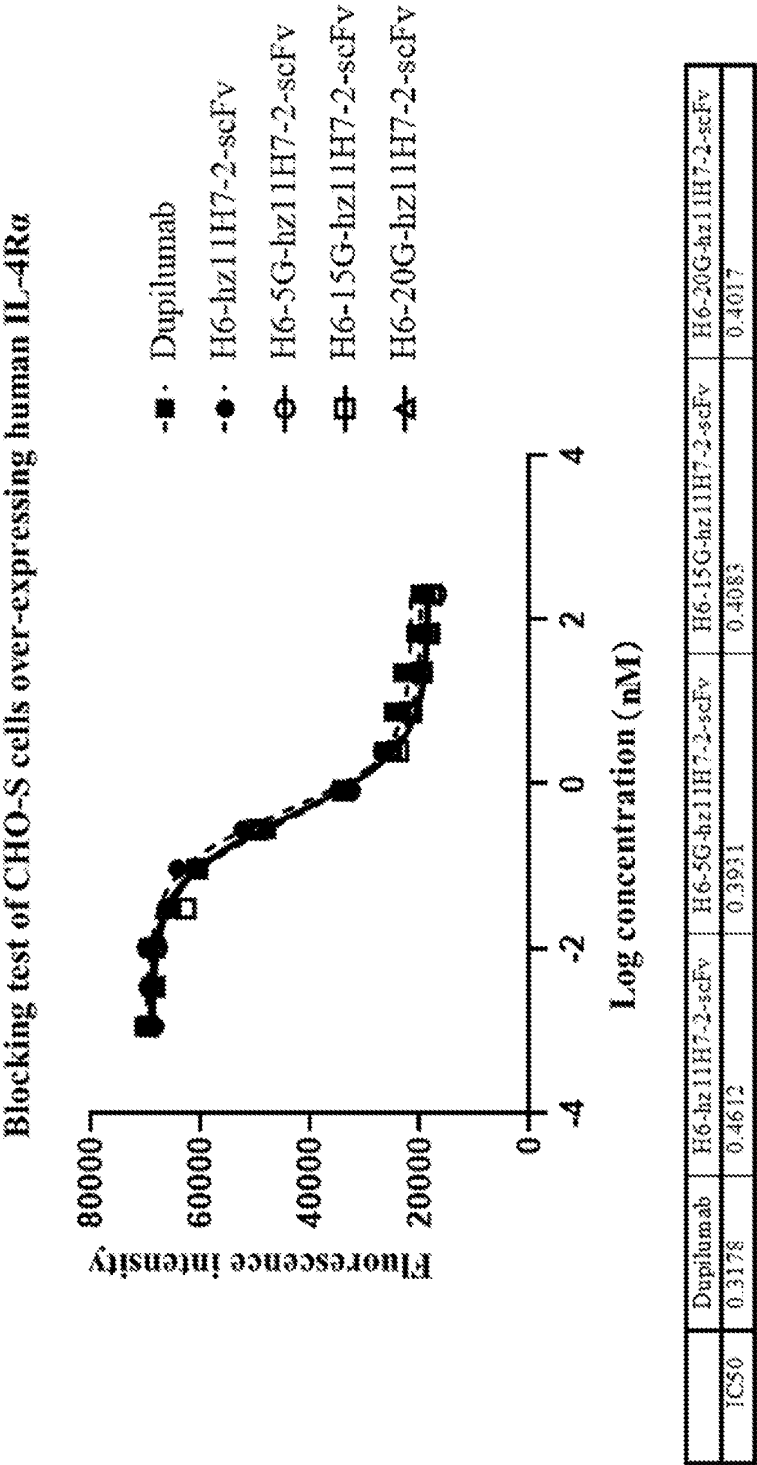


FIG. 8A

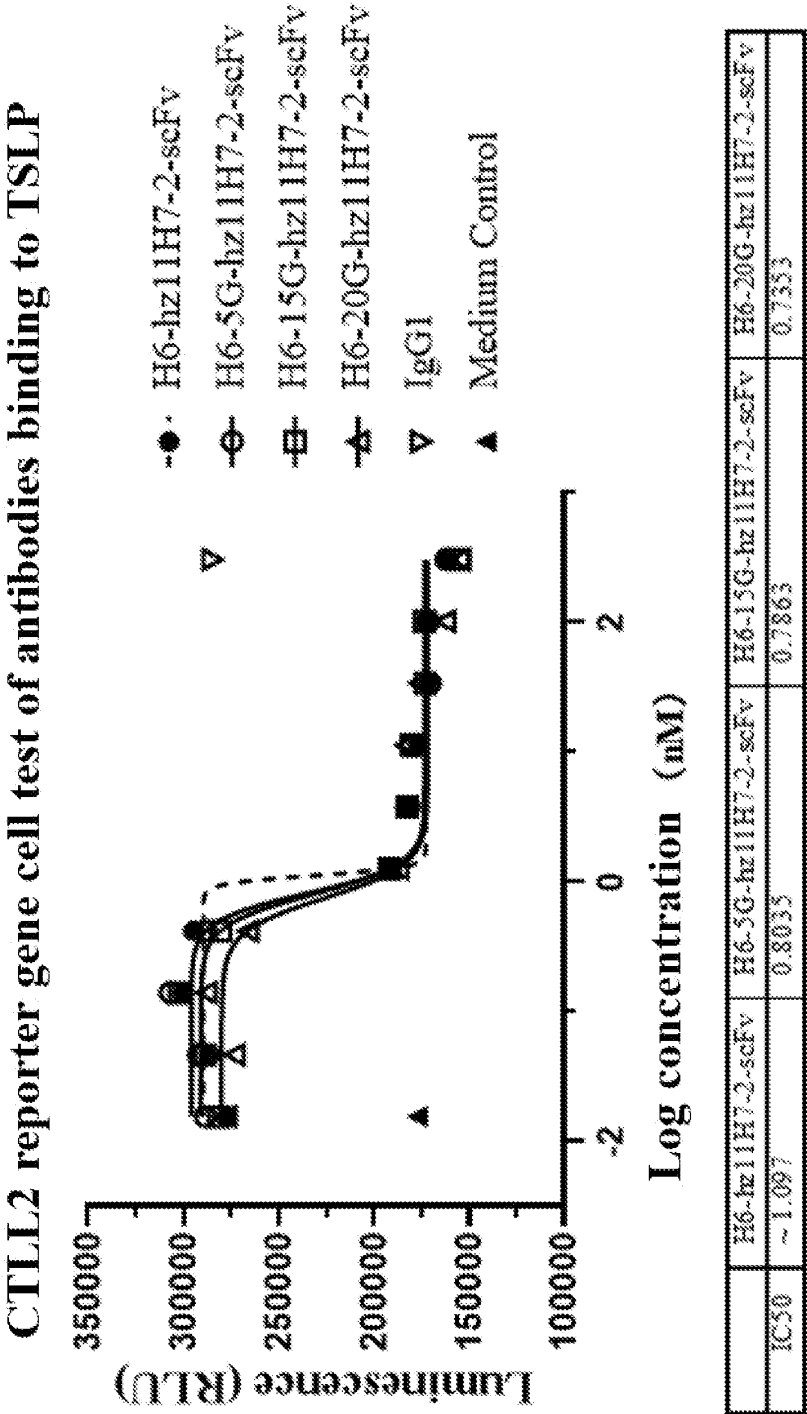


FIG. 8B

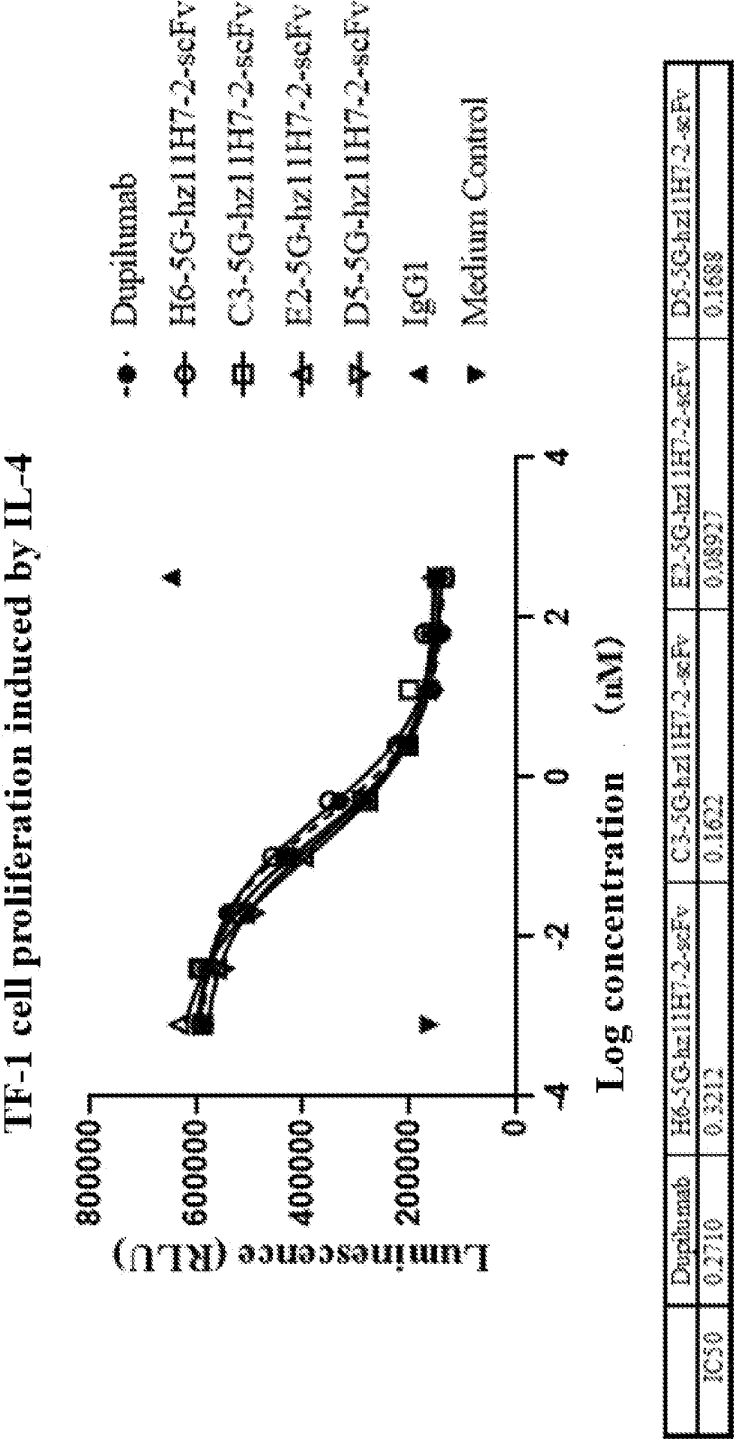


FIG. 9A

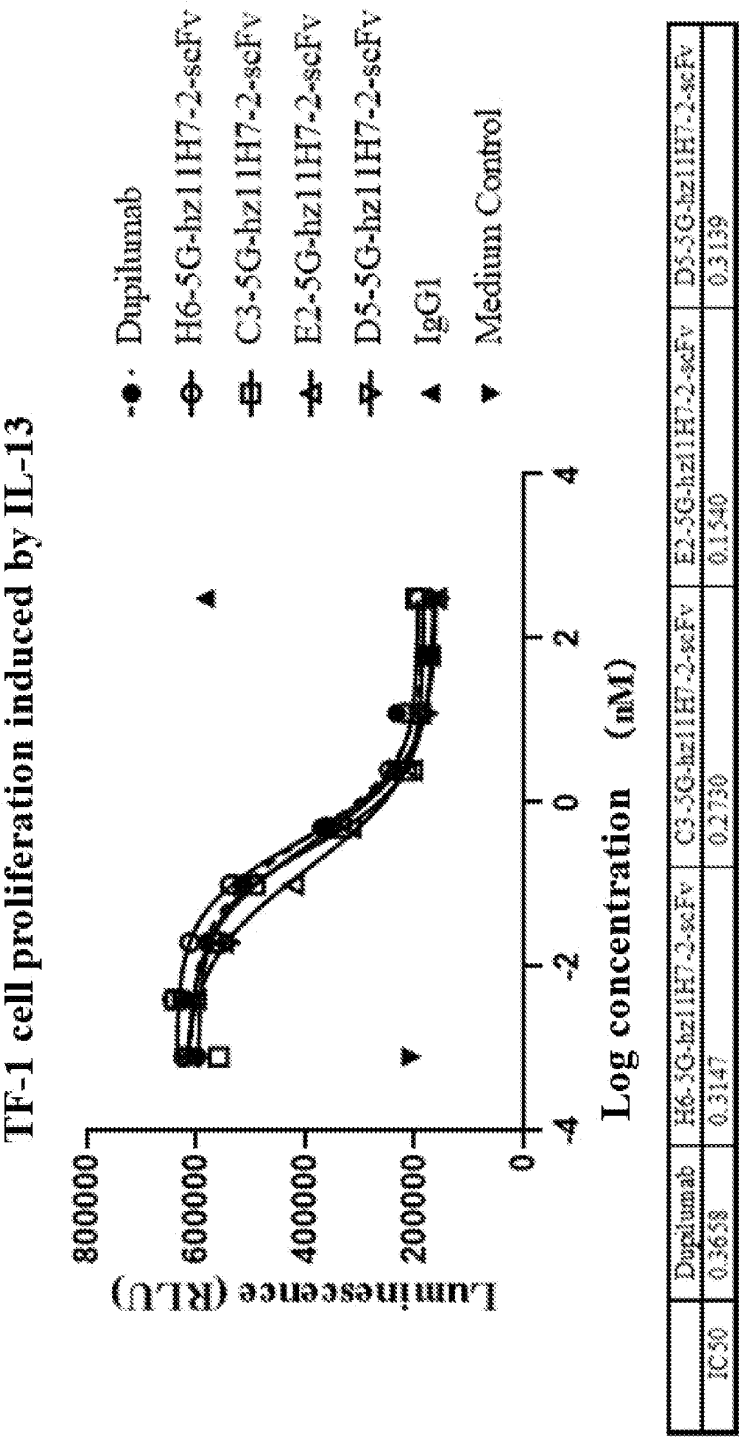


FIG. 9B

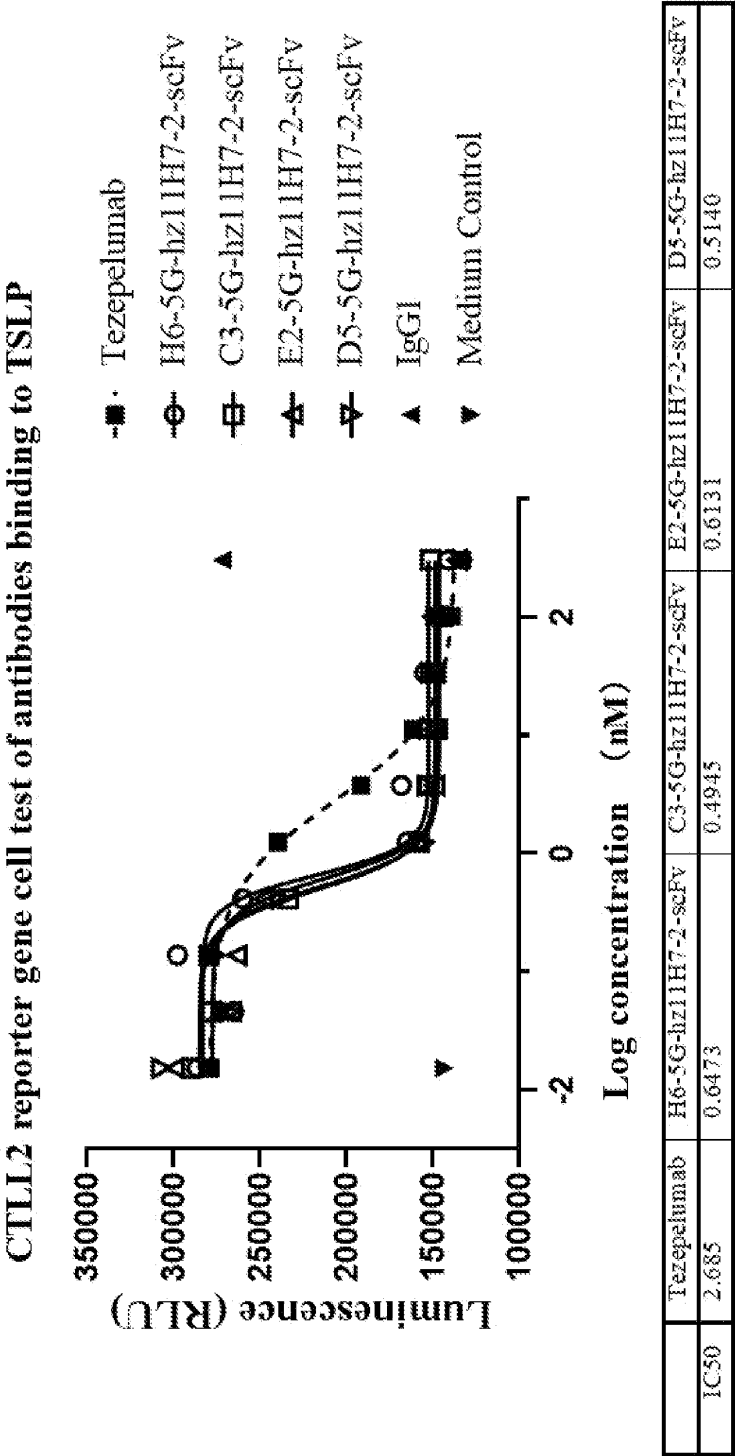


FIG. 10

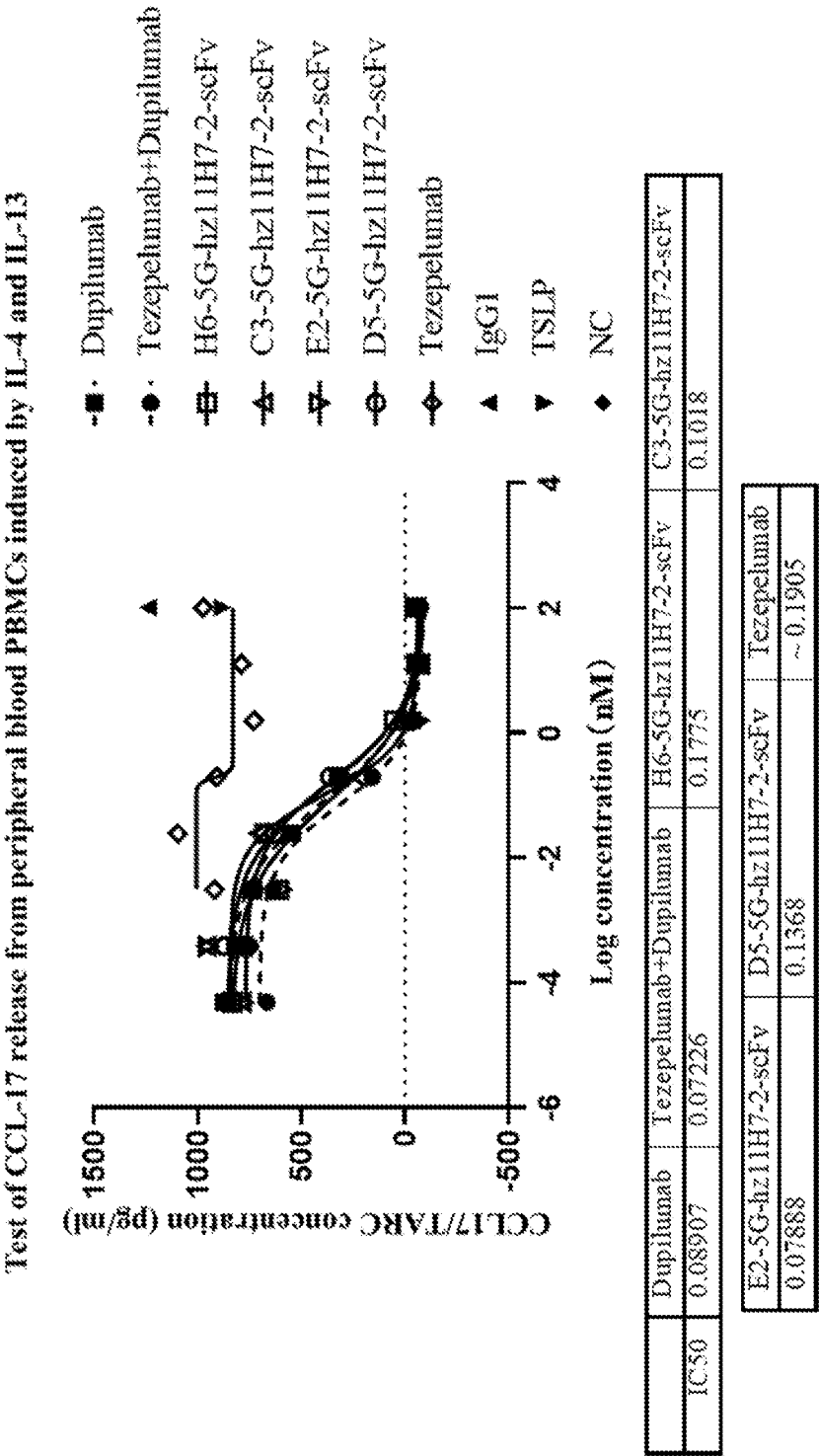


FIG. 11A

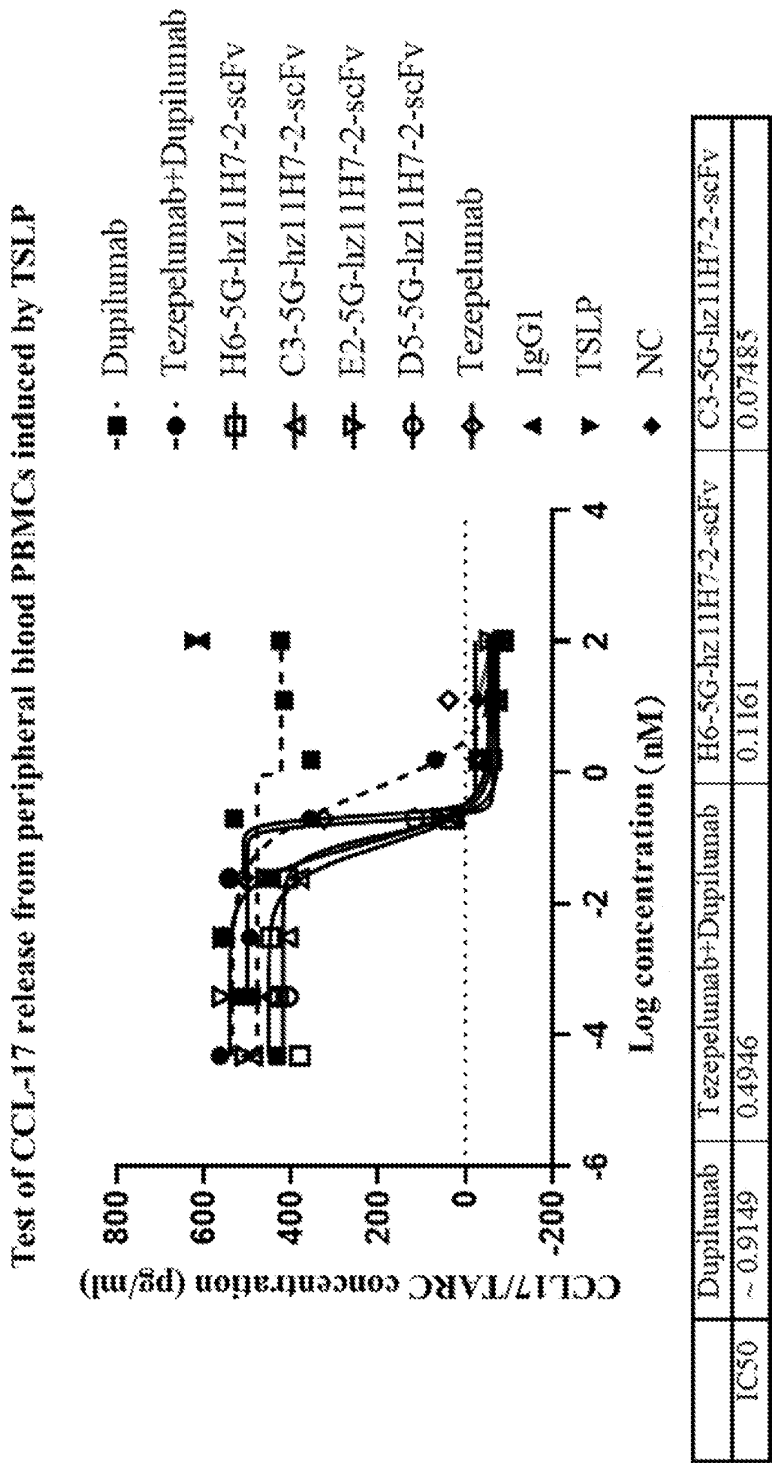
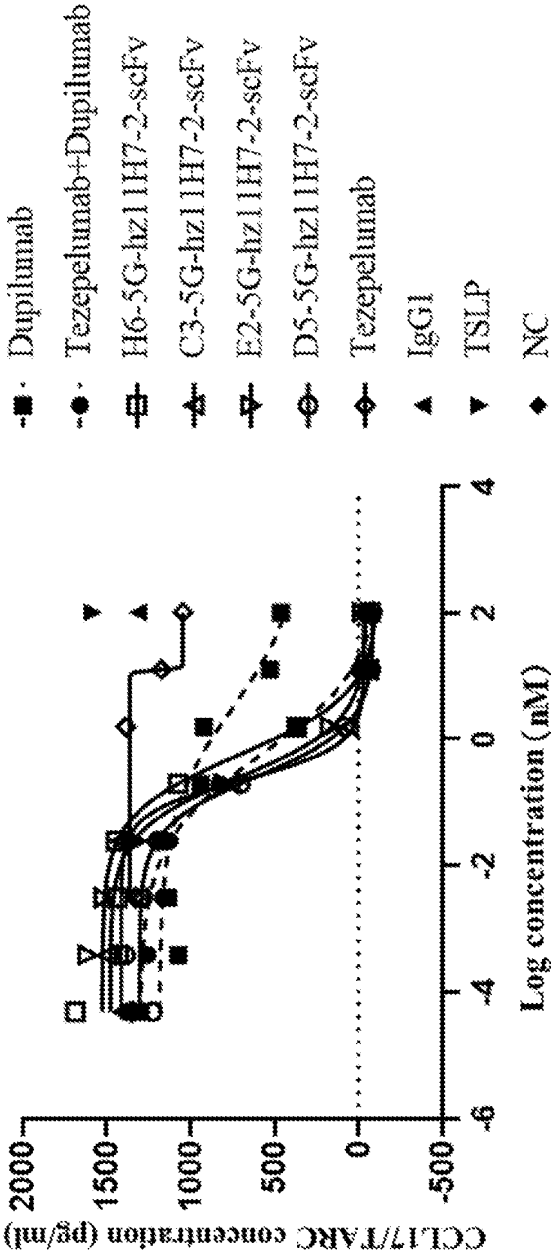


FIG. 11B

Test of CCL17 release from peripheral blood PBMCs induced by IL-4, IL-13, and TSLP



	Dupilumab	Tezepelumab+Dupilumab	H6-5G-hz11H7-2-scFv	C3-5G-hz11H7-2-scFv
IC50	3.071	0.5789	0.5720	0.2243

	E2-5G-hz11H7-2-scFv	D5-5G-hz11H7-2-scFv	Tezepelumab
	0.2455	0.2516	~12.32

FIG. 11C

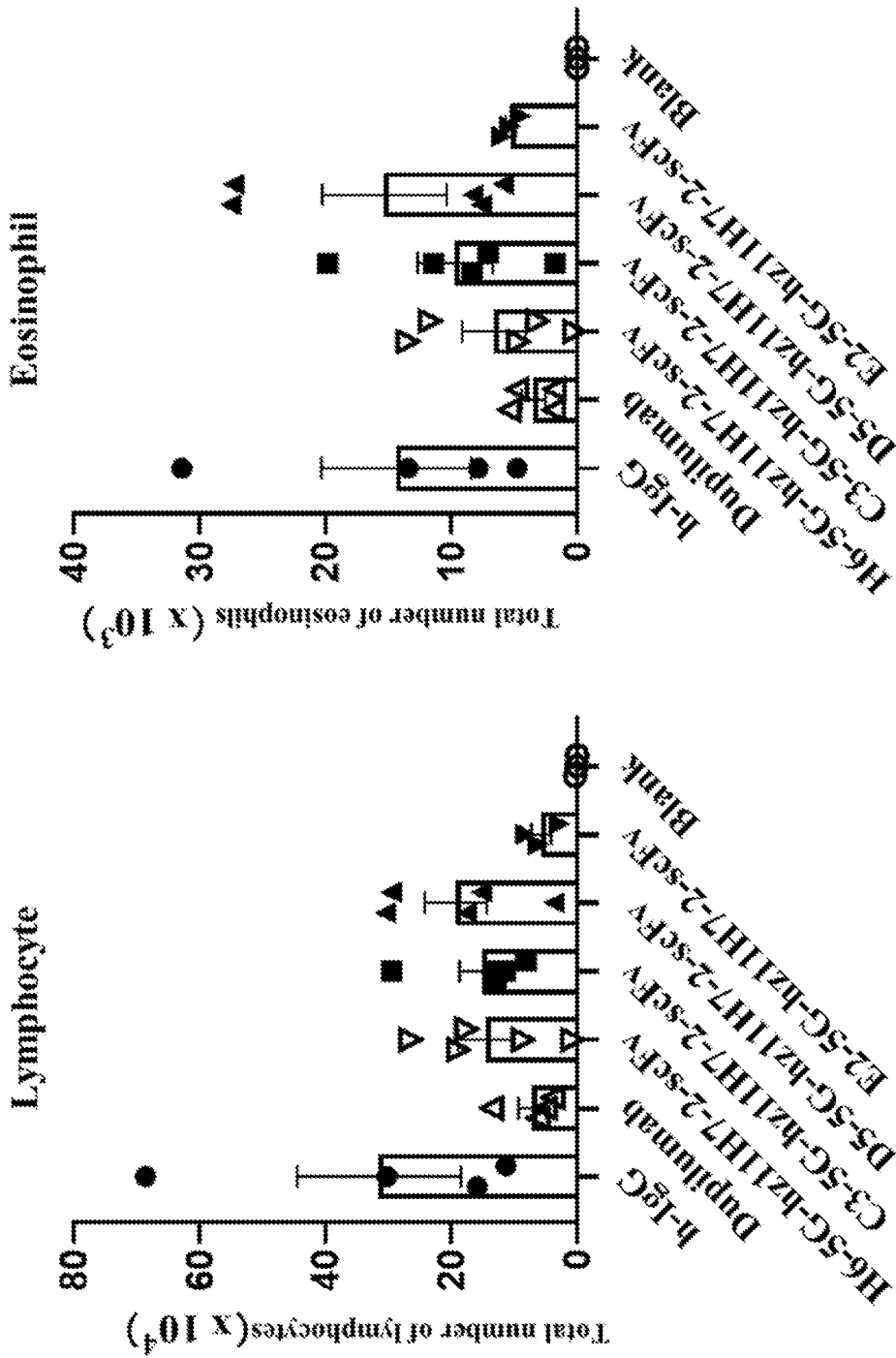


FIG. 12A

FIG. 12B

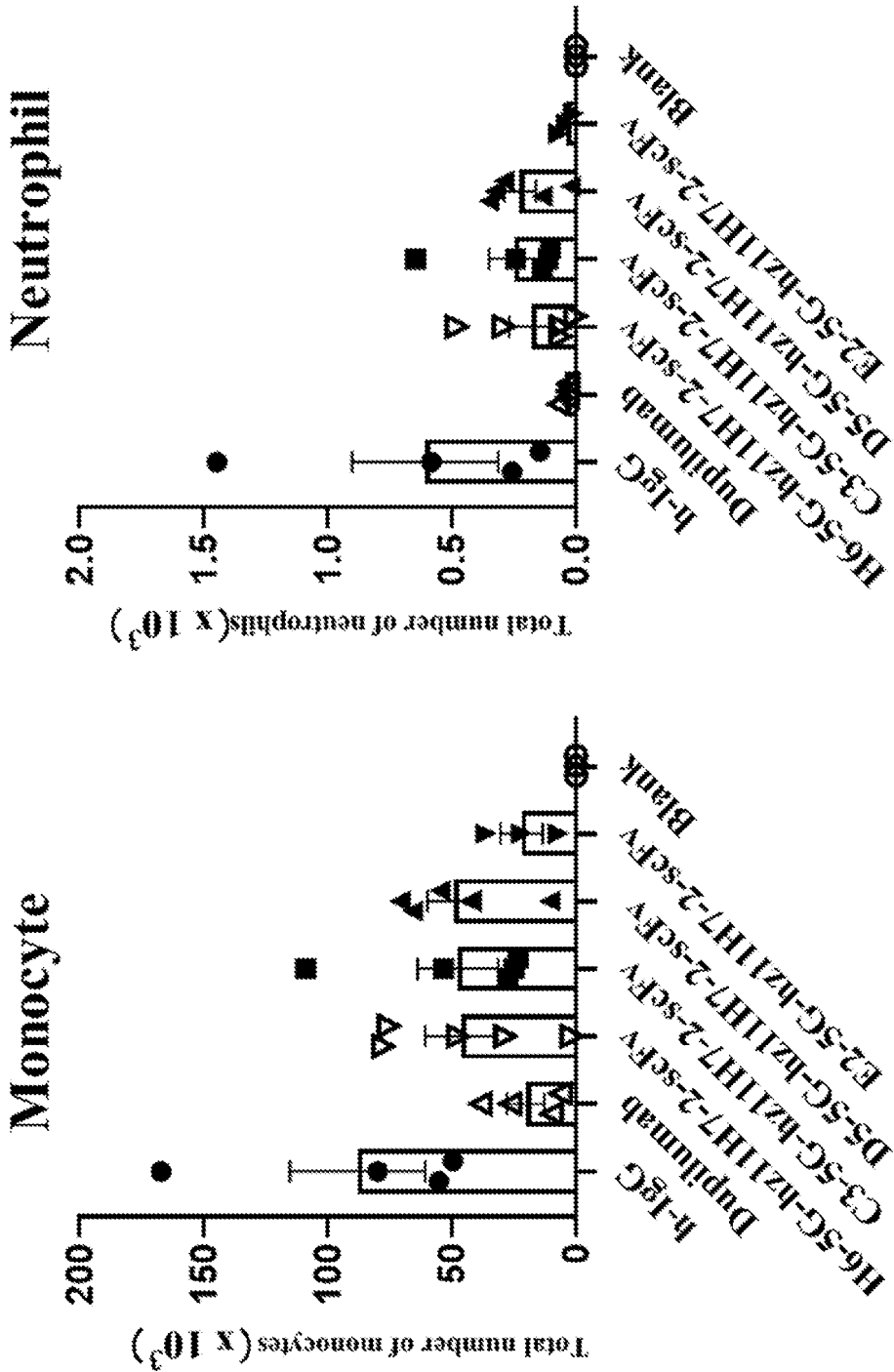


FIG. 12D

FIG. 12C

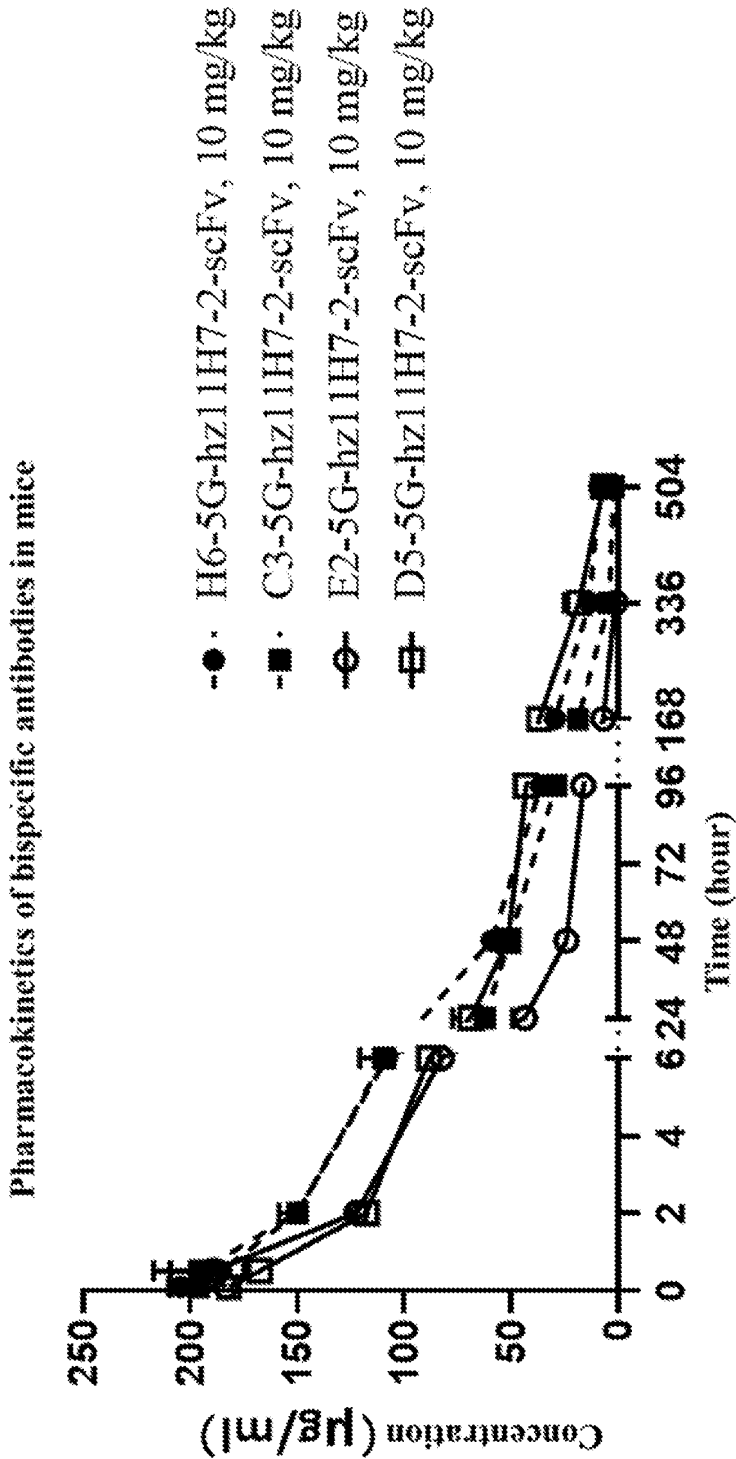


FIG. 13

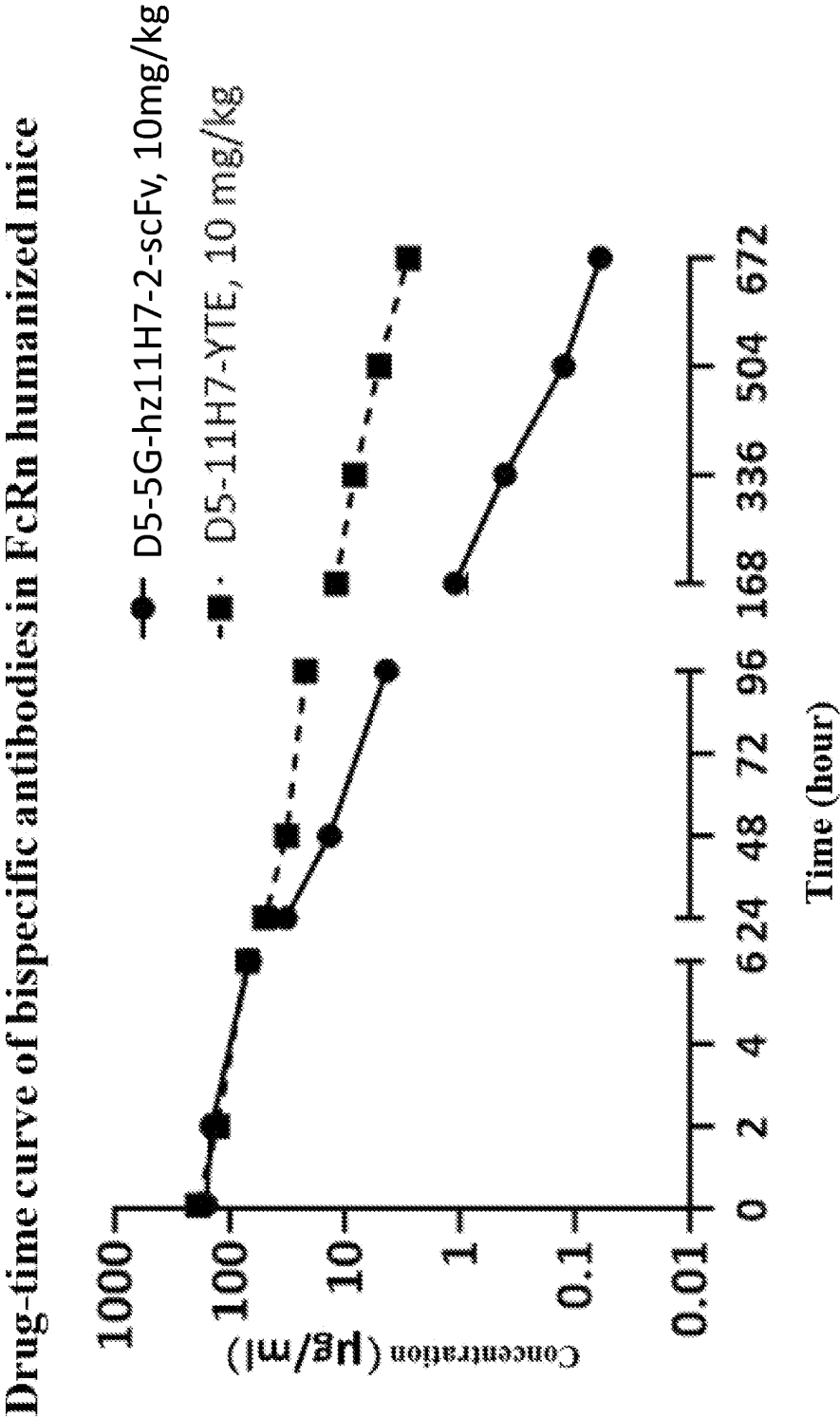


FIG. 14

Combined AbM/Kabat CDR

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
Anti-IL-4Rα 10H4.6	GTFNINA MN	1	RIRTKSNNYA TYHADSVKD	2	DVGRGFAY	3	RASKSVSTSG YSYM	4	LASNLQS	5	QHSRELPL T	6
Anti-IL-4Rα H6	GTFEMNA MN	11	RIRTKGNKYA TYHADSVKD	12	DVGRGFAY	3	RASKSVSFGG FSYM	13	LGTYLQS	14	QHSREIPLT	15
Anti-IL-4Rα D5	GFTFKMNA MN	18	RIRTKSADYA TYHADSVKD	19	DVGRGFAY	3	RASKSVSFSE YSYM	20	LGRFLQS	21	QHSRELPI T	22
Anti-IL-4Rα E2	GFTFDMN AMN	25	RIRTKTSNYA TYHADSVKD	26	DVGRGFAY	3	RASKSVSHRG YSYLH	27	LARHLQS	28	QHSTEIPLT	29
Anti-IL-4Rα C3	GFTFDMN AMN	32	RIRTKSADYA TYHADSVKD	19	DVGRGFAY	3	RASKSVSYHG YSYLH	33	LARHLQS	34	QHSRELPL T	6
Anti-TSLP 11H7E11	GSSITSDDYA W N	37	YITYSGSTNY NPSLKS	38	EDNSGVSPFT H	39	KASQSVGNDV A	40	YTSNRYT	41	LQDYSSP WT	42

FIG. 15A

Kabat CDR

FIG. 15B

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
Anti-IL-4Rα 10H4.6	INAMN	84	RIRTKSNNYA TYHADSVKD	2	DVGRGFAY	3	RASKSVSTSG YSYMH	4	LASNLQS	5	QHSRELPL T	6
Anti-IL-4Rα H6	MNAMN	85	RIRTKGNKYA TYHADSVKD	12	DVGRGFAY	3	RASKSVSFGG FSYMH	13	LGTYLQS	14	QHSREIPLT	15
Anti-IL-4Rα D5	MNAMN	85	RIRTKSADYA TYHADSVKD	19	DVGRGFAY	3	RASKSVSFSE YSYMH	20	LGRFLQS	21	QHSRELPI T	22
Anti-IL-4Rα E2	MNAMN	85	RIRTKTSNYA TYHADSVKD	26	DVGRGFAY	3	RASKSVSHRG YSYLH	27	LARHLQS	28	QHSTEIPLT	29
Anti-IL-4Rα C3	MNAMN	85	RIRTKSADYA TYHADSVKD	19	DVGRGFAY	3	RASKSVSYHG YSYLH	33	LARHLQS	34	QHSRELPL T	6
Anti-TSLP 11H7E11	SDYAWN	86	YITYSGSTNY NP SLKS	38	EDNSGYSPFT H	39	KASQSVGNDV A	40	YTSNRYT	41	LQDYSSP WT	42

Chothia CDR

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
Anti-IL-4Rα 10H4.6	GTFNI N	87	RTKSNIVA	88	DVGRGFAY	89	RASKSVSTSGYSY MH	90	LASNLS	91	QHSRELPL T	92
Anti-IL-4Rα H6	GTFE MN	93	RTKGNKYA	94	DVGRGFAY	95	RASKSVSFGGFS YMH	96	LGTYLQS	97	QHSREIPLT	98
Anti-IL-4Rα D5	GTFK MN	99	RTKSADYA	100	DVGRGFAY	101	RASKSVSFEYSY MH	102	LGRFLQS	103	QHSRELPI T	104
Anti-IL-4Rα E2	GTFD MN	105	RTKTSNVA	106	DVGRGFAY	107	RASKSVSHRGYS YLH	108	LARHLQS	109	QHSTEIPLT	110
Anti-IL-4Rα C3	GTFD MN	111	RTKSADYA	112	DVGRGFAY	113	RASKSVSVHGYS YLH	114	LARHLQS	115	QHSRELPL T	116
Anti-TSLP 11H7E11	GSSIIS D	117	TVSGS	118	EDNSGYSPFT H	119	KASQSVGNDVA	120	YTSNRYT	121	LQDYSSP WT	122

FIG. 15C

Ab VH or VL	SEQ ID NO	VH or VL Sequence
Anti-IL-4Rα 10H4.6 VH	7	EVQLLETGGG LVQPKGSLKL SCAASGFTFN INAMNWVRQA PGKGLEWVAR IRTKSNNYAT YHADSVKDRF TISRDDSQSM LYQMNNLKT EDTAMYCYVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα 10H4.6 VL	8	DIVLTQSPAS LAVSLGQRAT ISCRASKSVS TSGYSYMHWY QQKPGQPPLK LIYLASNLOS GVPARFSGSG SGTDFLTNIH PVEEDAATY YCQHSRELP LTFGAGTKLEI K
Anti-IL-4Rα Hz10H4.6 VH	9	EVQLVESGGG LVQPGGSLRL SCAASGFTFN INAMNWVRQA PGKGLEWVAR IRTKSNNYAT YHADSVKDRF TISRDDSKSS LYQMNSLKT EDTAVYCYVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα Hz10H4.6 VL	10	DIQMTQSPSS LSASVGDRVT ITCRASKSVS TSGYSYMHWY QQKPGKAPKL LIYLASNLOS GVPSPRFSGSG SGTDFLTIS SLOPEDFATY YCQHSRELP LTFGGGTKVEI
Anti-IL-4Rα H6 VH	16	EVQLVESGGG LVQPGGSLRL SCAASGTFTE MNAMNWVRQA PGKGLEWVAR IRTKGNKYAT YHADSVKDRF TISRDDSKSS LYQMNSLKT EDTAVYCYVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα H6 VL	17	DIQMTQSPSS LSASVGDRVT ITCRASKSVS FGGFSYMHWY QQKPGKAPKL LIYLGTYLQS GVPSPRFSGSG SGTDFLTIS SLOPEDFATY YCQHSRELP LTFGGGTKVEI K
Anti-IL-4Rα D5 VH	23	EVQLVESGGG LVQPGGSLRL SCAASGTFTE MNAMNWVRQA PGKGLEWVAR IRTKSADYAT YHADSVKDRF TISRDDSKSS LYQMNSLKT EDTAVYCYVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα D5 VL	24	DIQMTQSPSS LSASVGDRVT ITCRASKSVS FSEYSYMHWY QQKPGKAPKL LIYLGRLQS GVPSPRFSGSG SGTDFLTIS SLOPEDFATY YCQHSRELP LTFGGGTKVEI K
Anti-IL-4Rα E2 VH	30	EVQLVESGGG LVQPGGSLRL SCAASGTFD MNAMNWVRQA PGKGLEWVAR IRTKTSNVA YHADSVKDRF TISRDDSKSS LYQMNSLKT EDTAVYCYVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα E2 VL	31	DIQMTQSPSS LSASVGDRVT ITCRASKSVS HRGYSYLHWY QQKPGKAPKL LIYLARHLQS GVPSPRFSGSG SGTDFLTIS SLOPEDFATY YCQHSRELP LTFGGGTKVEI K
Anti-IL-4Rα C3 VH	35	EVQLVESGGG LVQPGGSLRL SCAASGTFD MNAMNWVRQA PGKGLEWVAR IRTKSADYAT YHADSVKDRF TISRDDSKSS LYQMNSLKT EDTAVYCYVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα C3 VL	36	DIQMTQSPSS LSASVGDRVT ITCRASKSVS YHGYSYLHWY QQKPGKAPKL LIYLARHLQS GVPSPRFSGSG SGTDFLTIS SLOPEDFATY YCQHSRELP LTFGGGTKVEI K
Anti-TSLP mouse 11H7E1 VH	43	DVQLQESGPG LVKPSQSLSL TCTVTGSSIT SDYAWNWIQR FPGNKLEWMG YITYSGSTNY NPSLKSRSFI TRDTSKNQOFF LQVNSATTED TATYCCARED NSGYSPTFW GLGLTVTVA
Anti-TSLP mouse 11H7E11 VL	44	NIVMTQTQPRF LLVSPGDRIT ITCASQSVG NDVAWYQQKP GRSPKLIYY TSNRYTGVPD HFTGSGYGTD FTFTISTVQT EDLAVYFCLQ DYSSPWTFGG GTKLEIK
Anti-TSLP Hz11H7 VH	45	QVQLQESGPG LVKPSLTL TCTVSGSSIT SDYAWNWIQR PPGKGLEWIG YITYSGSTNY NPSLKSRTVI SRDTSKNQFS LKLSVTAAD TAVYCCARED NSGYSPTFW GQGLTVTVSS
Anti-TSLP Hz11H7 VL	46	DIQMTQSPSS LSASVGDRVT ITCASQSVG NDVAWYQQKP GKAPKLIYY TSNRYTGVPSP RFSGSGSGTD FTFTISSLQP EDIATYYCLQ DYSSPWTFGQ GTKVEIK

FIG. 16

Combined AbM/Kabat CDR

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
Anti-IL-4Rα Common sequence -1	GFTFX ₁ X ₂ N AMN; X ₁ =N, E, K or D, X ₂ =I or M	57	RIRTKX ₃ X ₄ X ₅ Y ATYHADSVKD ; X ₃ =S, G or T, X ₄ =N, A or S, X ₅ =N, K or D	59	DVGRGFAY	3	RASKSVSX ₆ X ₇ X ₈ X ₉ SVX ₁₀ H; X ₆ =T, F, H or Y, X ₇ =S, G, R or H, X ₈ =G or E, X ₉ =Y or F, X ₁₀ =M or L	60	LX ₁₁ X ₁₂ X ₁₃ L QS; X ₁₁ =A or G, X ₁₂ =S, T or R, X ₁₃ =N, Y, F or H	61	QHSX ₁₄ EX ₁₅ PX ₁₆ T; X ₁₄ =R or T, X ₁₅ =L or I, X ₁₆ =L or I	62
Anti-IL-4Rα Common sequence-2	GFTFX ₁ MIN AMN; X ₁ =E, K or D	58	RIRTKX ₃ X ₄ X ₅ Y ATYHADSVKD ; X ₃ =S, G or T, X ₄ =N, A or S, X ₅ =N, K or D	59	DVGRGFAY	3	RASKSVSX ₆ X ₇ X ₈ X ₉ SVX ₁₀ H; X ₆ =T, F, H or Y, X ₇ =S, G, R or H, X ₈ =G or E, X ₉ =Y or F, X ₁₀ =M or L	60	LX ₁₁ X ₁₂ X ₁₃ L QS; X ₁₁ =A or G, X ₁₂ =S, T or R, X ₁₃ =N, Y, F or H	61	QHSX ₁₄ EX ₁₅ PX ₁₆ T; X ₁₄ =R or T, X ₁₅ =L or I, X ₁₆ =L or I	62

FIG. 17A

Kabat CDR

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
Anti-IL-4Rα Common sequence -3	X ₂ NAMN; X ₂ =I or M	123	RIRTKX ₃ X ₄ X ₅ Y ATYHADSVKD ; X ₃ =S, G or T, X ₄ =N, A or S, X ₅ =N, K or D	59	DVGRGFAY	3	RASKSVSX ₆ X ₇ X ₈ X ₉ SVX ₁₀ H; X ₆ =T, F, H or Y, X ₇ =S, G, R or H, X ₈ =G or E, X ₉ =Y or F, X ₁₀ =M or L	60	LX ₁₁ X ₁₂ X ₁₃ L QS; X ₁₁ =A or G, X ₁₂ =S, T or R, X ₁₃ =N, Y, F or H	61	QHSX ₁₄ EX ₁₅ PX ₁₆ T; X ₁₄ =R or T, X ₁₅ =L or I, X ₁₆ =L or I	62
Anti-IL-4Rα Common sequence-4	MINAMN	85	RIRTKX ₃ X ₄ X ₅ Y ATYHADSVKD ; X ₃ =S, G or T, X ₄ =N, A or S, X ₅ =N, K or D	59	DVGRGFAY	3	RASKSVSX ₆ X ₇ X ₈ X ₉ SVX ₁₀ H; X ₆ =T, F, H or Y, X ₇ =S, G, R or H, X ₈ =G or E, X ₉ =Y or F, X ₁₀ =M or L	60	LX ₁₁ X ₁₂ X ₁₃ L QS; X ₁₁ =A or G, X ₁₂ =S, T or R, X ₁₃ =N, Y, F or H	61	QHSX ₁₄ EX ₁₅ PX ₁₆ T; X ₁₄ =R or T, X ₁₅ =L or I, X ₁₆ =L or I	62

FIG. 17B

Chothia CDR

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
Anti-IL-4Rα Common sequence -5	GFTFX ₁ X ₂ N; X ₁ =N, E, K or D, X ₂ =I or M	124	RTKX ₃ X ₄ X ₅ YA; X ₃ =S, G or T, X ₄ =N, A or S, X ₅ =N, K or D	125	DVGRGFAY	3	RASKSVSX ₆ X ₇ X ₈ X ₉ SYX ₁₀ H; X ₆ =T, F, H or Y, X ₇ =S, G, R or H, X ₈ =G or E, X ₉ =Y or F, X ₁₀ =M or L	60	LX ₁₁ X ₁₂ X ₁₃ L QS; X ₁₁ =A or G, X ₁₂ =S, T or R, X ₁₃ =N, Y, F or H	61	QHSX ₁₄ EX ₁₅ PX ₁₆ T; X ₁₄ =R or T, X ₁₅ =L or I, X ₁₆ =L or I	62
Anti-IL-4Rα Common sequence-6	GFTFX ₁ MN; X ₁ =E, K or D	126	RTKX ₃ X ₄ X ₅ YA; X ₃ =S, G or T, X ₄ =N, A or S, X ₅ =N, K or D	125	DVGRGFAY	3	RASKSVSX ₆ X ₇ X ₈ X ₉ SYX ₁₀ H; X ₆ =T, F, H or Y, X ₇ =S, G, R or H, X ₈ =G or E, X ₉ =Y or F, X ₁₀ =M or L	60	LX ₁₁ X ₁₂ X ₁₃ L QS; X ₁₁ =A or G, X ₁₂ =S, T or R, X ₁₃ =N, Y, F or H	61	QHSX ₁₄ EX ₁₅ PX ₁₆ T; X ₁₄ =R or T, X ₁₅ =L or I, X ₁₆ =L or I	62

FIG. 17C

FIG. 18

heavy chain constant region (SEQ ID NO: 47)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVKDKKVEPKSCDKTH
TCPPCPAPEAAAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
IEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFNCSVMHEALHNHYTQ
KSLSLSPGK

light chain constant region (SEQ ID NO: 48)
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC

peptide chain #1 of H6-5G-hz11H7-2-scFv (SEQ ID NO: 49)
EVQLVESGGGLVQPGGSLRLSCAASGFTFEMNANMWVRQAPGKGLEWVARIRTKGNKYATYHADSVKDRFTISRDDSKSSLYLQMNLSLKTEDTAVYVCVKDVGRGFA
YWQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHTCPPCPAPEAAAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFNCS
VMHEALHNHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTVITCKASQSVGNDVAWYQQKPKGAPKLLIYYTSNRYTGVPSPRFSGSGSGTDFTFTISSIQPED
IATYYCLQDYSYPWTFCGTKVEIKGGGGSGGGGGGQVQLQESGGGLVQPKSETLSLTCTVSGSSITSDYAMNWIROPKPKCLEWIGYITYSGSTNYP
SLKSRVTISRDTSKNQFSLKLSVTAADTAVYYCAREDNISYSPFTHWGQGTIVTVSS

peptide chain #2 of H6-5G-hz11H7-2-scFv (SEQ ID NO: 50)
DIQMTQSPSSLSASVGDRTVITCRASKSVFSGFSYMHWYQQKPKGAPKLLIYLGTYLQSGVPSRFSGSGSGTDFTLTISSIQPEDFATYYCQHSREIPLTIFGGGTK
VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFN
RGEK

peptide chain #1 of D5-5G-hz11H7-2-scFv(SEQ ID NO: 51)
EVQLVESGGGLVQPGGSLRLSCAASGFTFKMANMWVRQAPGKGLEWVARIRTKSADYATYHADSVKDRFTISRDDSKSSLYLQMNLSLKTEDTAVYVCVKDVGRGFA
YWQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHTCPPCPAPEAAAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFNCS
VMHEALHNHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTVITCKASQSVGNDVAWYQQKPKGAPKLLIYYTSNRYTGVPSPRFSGSGSGTDFTFTISSIQPED
IATYYCLQDYSYPWTFCGTKVEIKGGGGSGGGGGGQVQLQESGGGLVQPKSETLSLTCTVSGSSITSDYAMNWIROPKPKCLEWIGYITYSGSTNYP
SLKSRVTISRDTSKNQFSLKLSVTAADTAVYYCAREDNISYSPFTHWGQGTIVTVSS

peptide chain #2 of D5-5G-hz11H7-2-scFv(SEQ ID NO: 52)
DIQMTQSPSSLSASVGDRTVITCRASKSVFSEYSYMHWYQQKPKGAPKLLIYLGFRFLQSGVPSRFSGSGSGTDFTLTISSIQPEDFATYYCQHSRELPITIFGGGTK
VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFN
RGEK

light chain of the antibody Tezepelumab (SEQ ID NO: 66)
SYVLTPPSVSVAPGQTARITCGGNNLGSKSVHWYQQKPGQAPLVVYDDSDRPSWI PERFGSGNSGNTATLTISRGEAGDEADYYCQVWDSSSDHVVFGGTFKLTIV
LGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQMKSHRSYSCQVTHEGSTVEKTVAPTECS

amino acid sequence of Teze_scFv (SEQ ID NO: 67)
SYVLTPPSVSVAPGQTARITCGGNNLGSKSVHWYQQKPGQAPLVVYDDSDRPSWI PERFGSGNSGNTATLTISRGEAGDEADYYCQVWDSSSDHVVFGGTFKLTIV
LGGGGGGGGGGGGGGGQQMLVSGGGVQPGRSRLRSCAASGTFRTYGMHWVRQAPGKCLEWVAVIWDGSKNHKHYADSVKGRFTITRDNSKNTLNLMQNSL
RAEDTAVYYCARAPQWELVHEAFDIWGQGTMTVYSS

heavy chain of the antibody Dupilumab (SEQ ID NO: 68)
EVQLVESGGGLEQPGGSLRLSCAGSGFTFRDYAMTWVRQAPGKGLEWVSSISGSGNTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDRLSITIRP
RYYGLDVWGQGTITVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGKTYTCNVDDHKP
SNTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPPKPKDTLIMISRTPEVTCVVVDVSDQDEPEVQFNWYVDGVEVHNAKTRPREEQFNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKRGFYPYSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSRLTVDKSRWQEGNVEF
SCSVMEALHNHYTQKSLSLIGK

light chain of the antibody Dupilumab (SEQ ID NO: 69)
DIVMTQSPFLSLPVTTPGEPASISCRSSQSLYSIGYNYLDWYIQKSGQSPQLLIYLGNSRASGVPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQALQTPYTFGQGT
KLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSSLTITLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC

TSLPR (SEQ ID NO: 70)
MGRVLLWGAAVFLLGGWMALGQGGAAEGVQIQIILYFNLETVQVTWNASKYSRTNLTfHYRFPNGDEAYDQCTNYLLQEGHTSGCLLDAEQRDDILYFSIRNGTHPVF
TASRMVYYLKPSSPKHVRFESWHQDAVTVCSDLSYGDLLYEYQYRSPDTEWQSKQENTCNVTIEGLDAEKCYFWVRVAMEDVYGPDTYPSDWSEVTCWQGEI
RDACAETPTPPKPKLSKFILISSLAILLMVSLLLSLWKLWRVKKFLIPSVDPKSIFFGLFEIHQGNFQEWITDTQNVAHLHKMAGAEQESGPEEPLVVQLAKTEA
ESPRMLDPQTEEREASGGSILQLPHQPLQGGDVVTIGGFTFVMNDRSYVAL

IL7Ra (SEQ ID NO: 71)
MTILGTTFGMVFSLLQVVSGESGYAQNGDLEDAELDDYSFSCYSQLEVNGSQHSILTCAFEDPDVNI TNLEFEICGALVEVKCINFRKLQEIYFIETKKFLLIGKSN
CVKVGESLTKCKIDLTITIVKPEAPFDLSVYREGANDFVVTFTNSHLQKKYKVKVIMHDVAYRQEKDENKWTNVNLSSTKLTLQRLQPAAMYELKVRSI PDHYFK
GFWSEWSPSYFFRTPETINNSSGEMDPILLTISILSFFSVALLVILACVLWKKRIKPIVWPSLPDHKKTLLEHLCKKPRKNLNVSNFNPESLDCQIHRVDDI QARDEVE
GFLQDTPPQQLEESEKQRLGGDVQSPNCPSEDVVTTPESFGRDSSLTCLAGNVSACDAPILSSRSRLDCRESGKNRPHVYQDILLLSLGTNTSTLPPPFSLQSGILTL
NPVAGQGPILTSLSGNSNQEEAYVTMSsfYQNQ

heavy chain of the negative control IgG1 (SEQ ID NO: 72)
QVQLVQSGAEVKKPGASVKVSQASGYRFSNFVIHWVRQAPGQRFEMGWINPYNGNKEFSAKFQDRVTFADTASNTAYMELRSLRSADTAVYYCARVGPYSWDDS
PQDNYMDVWGKGTIVIVSSASTKGPSVFPEPLAPSSTSGTGAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTRPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFFLYSKLTVDKSRWQ
QGNVFCSVMHEALHNHYTQKSLSLSPG

heavy chain constant region with LS mutation (SEQ ID NO: 83)
ASTKGFSPVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTH
TCPFPCPAPEAAGGFSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
IEKTIISKAKGQPREPQVYTTLPSSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQQGNVVFSCSVLHEALHSHYTYQ
KSLSLSPGK

Linker (SEQ ID NO: 127)
GGGS