

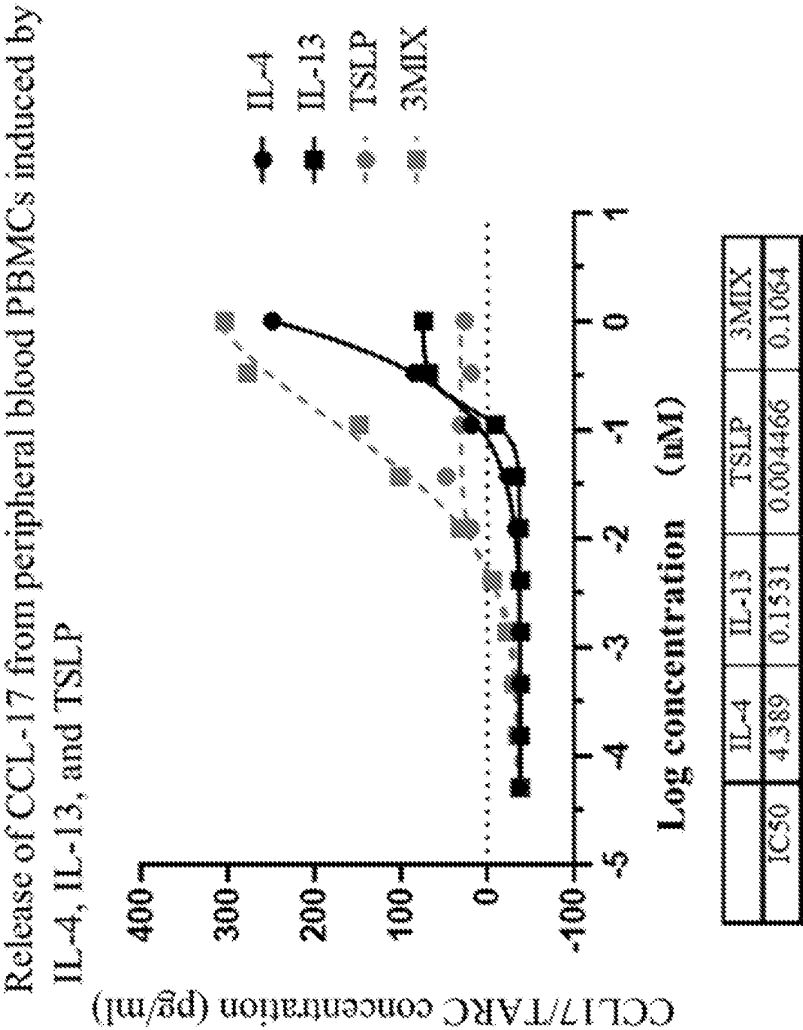


FIG. 1A

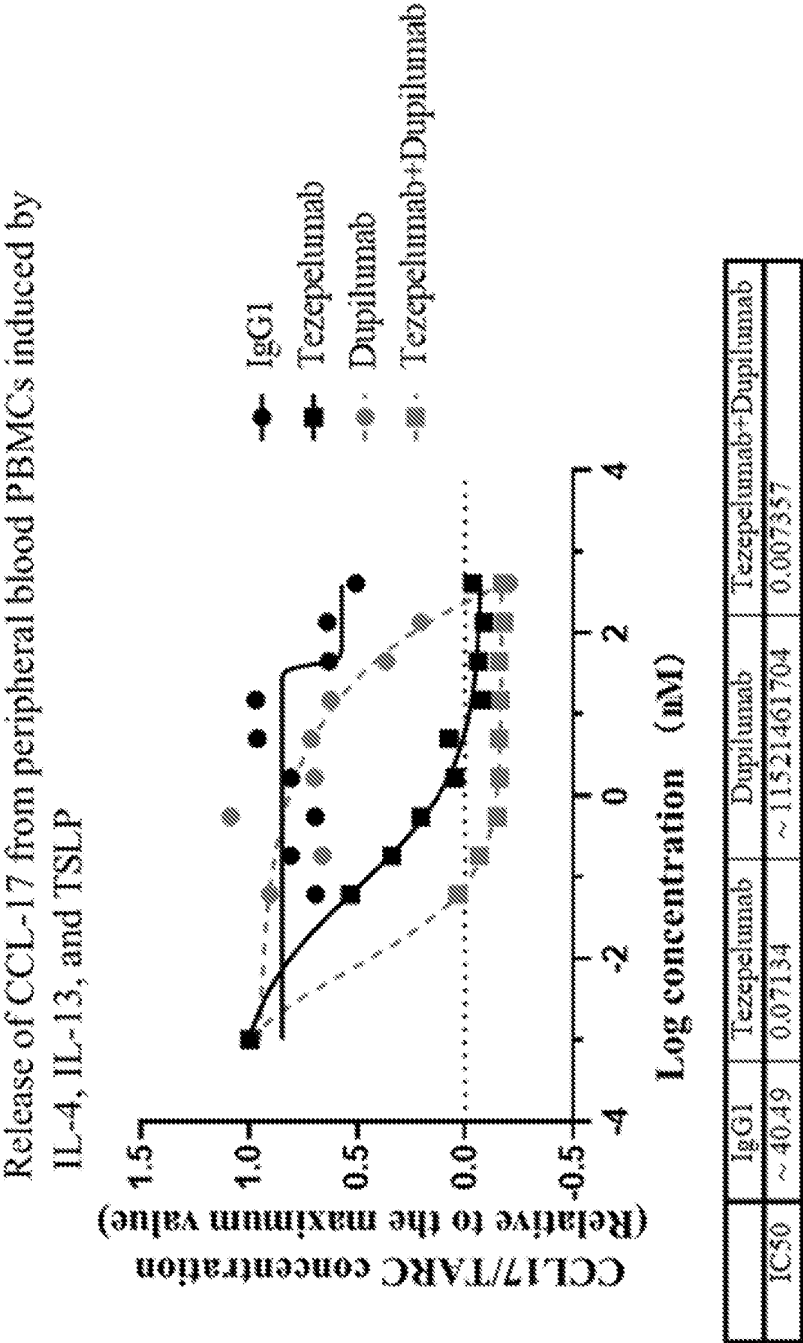


FIG. 1B

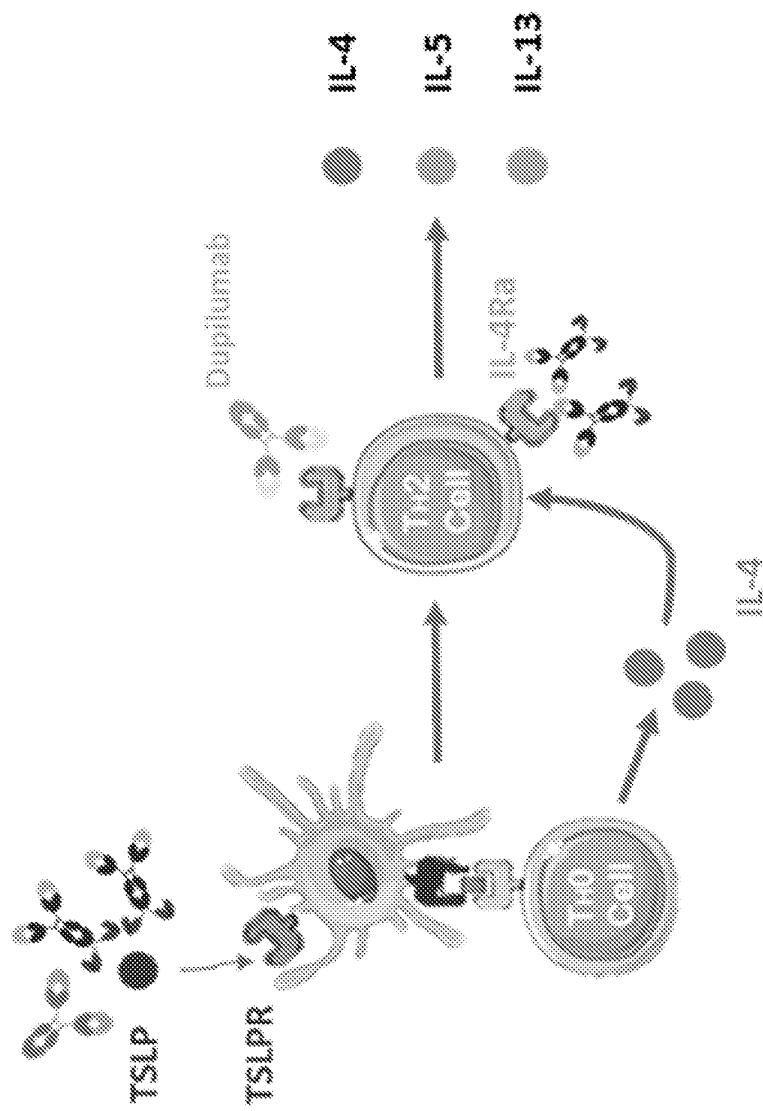


FIG. 2A

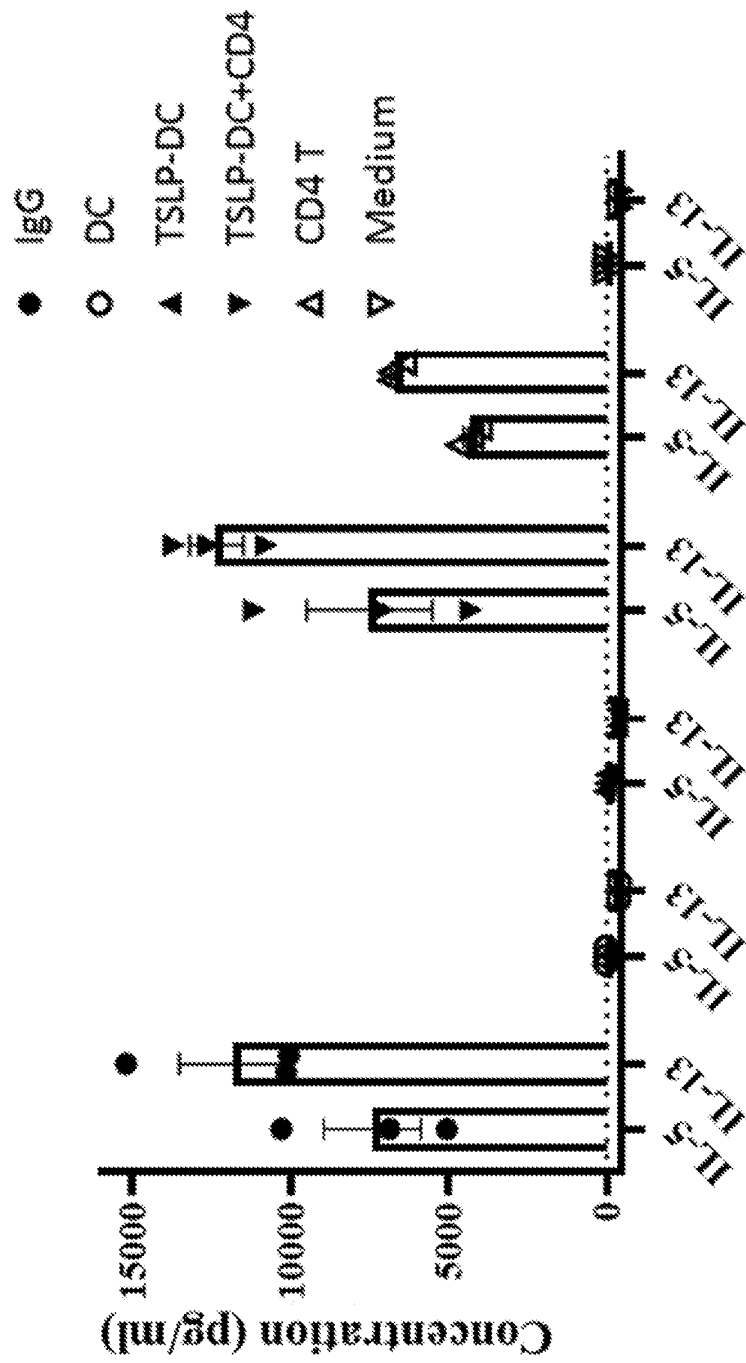


FIG. 2B

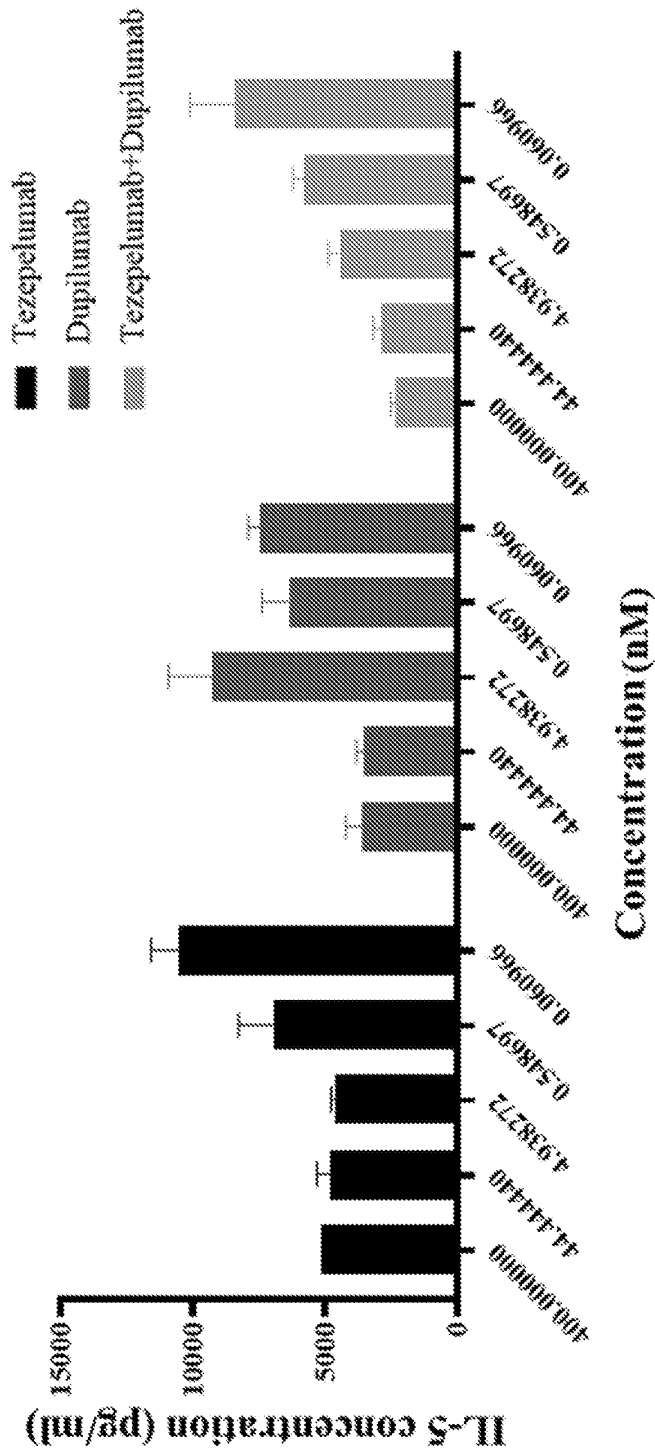


FIG. 2C

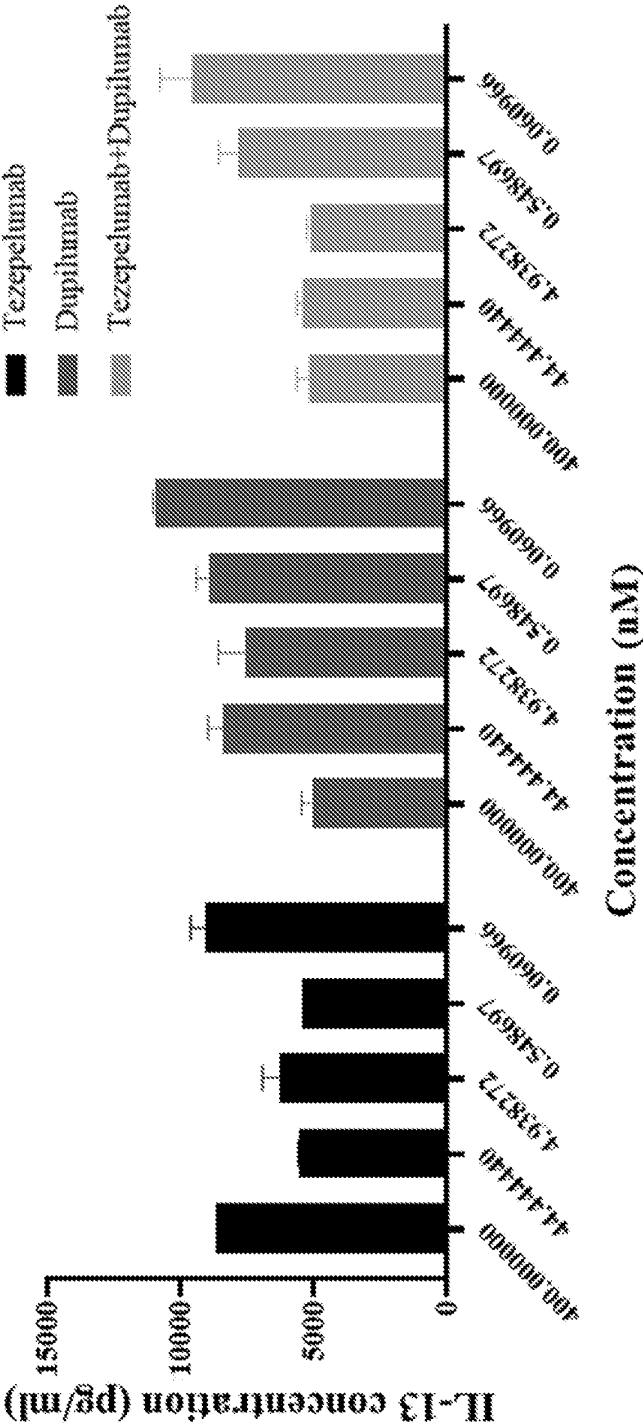


FIG. 2D

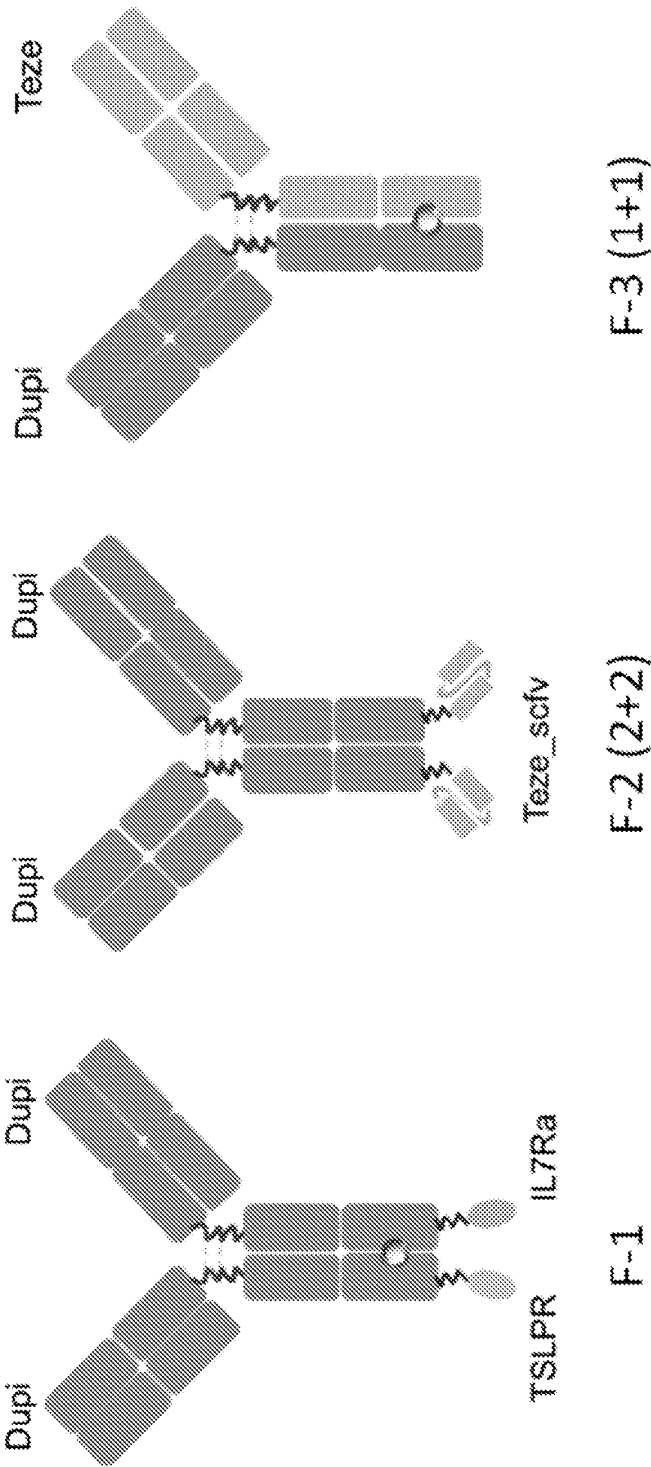


FIG. 3

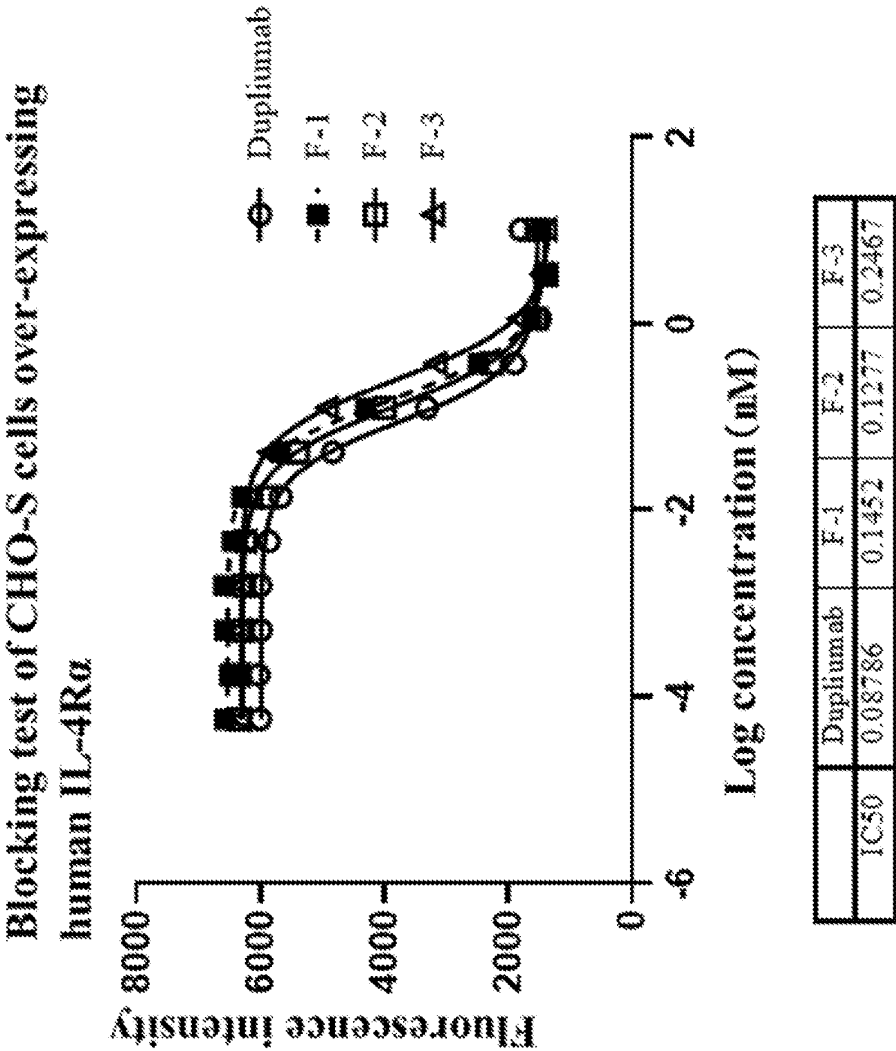


FIG. 4A

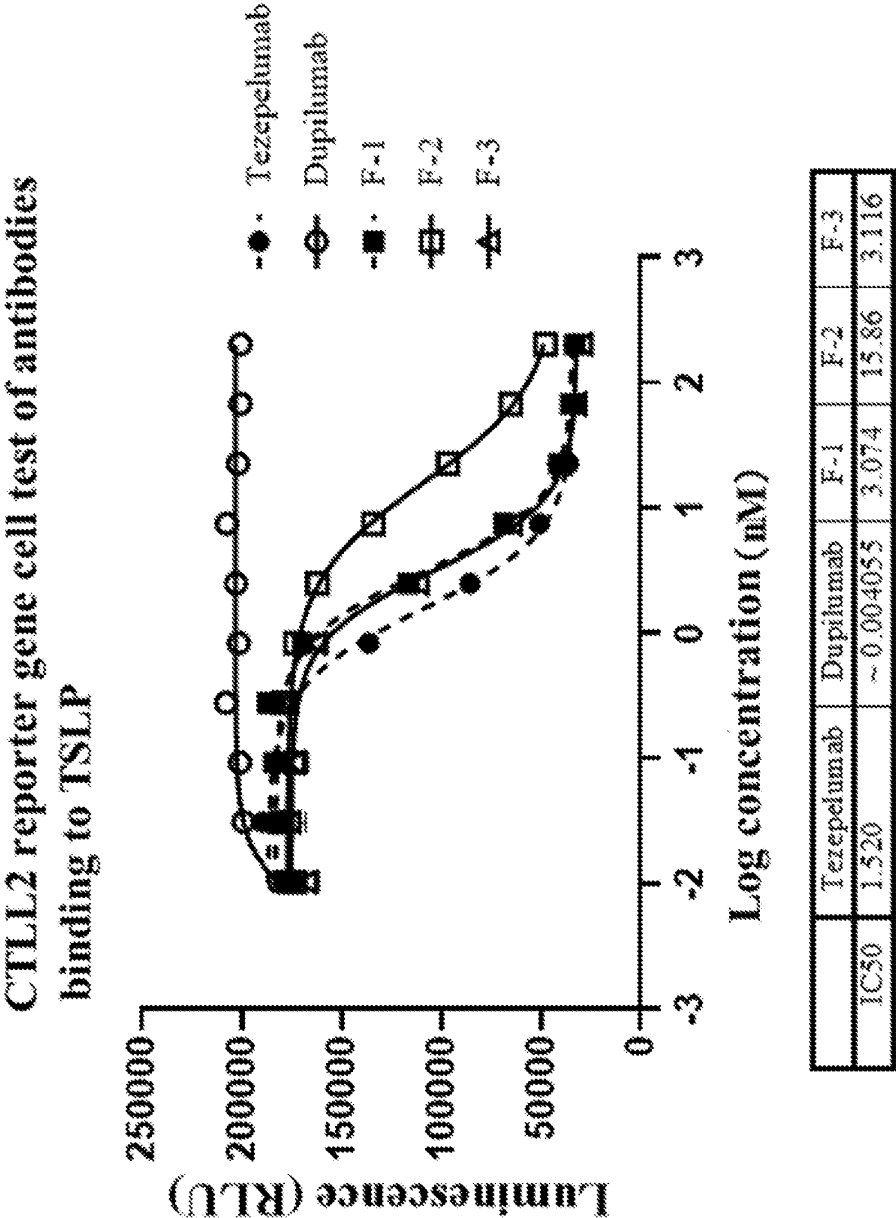


FIG. 4B

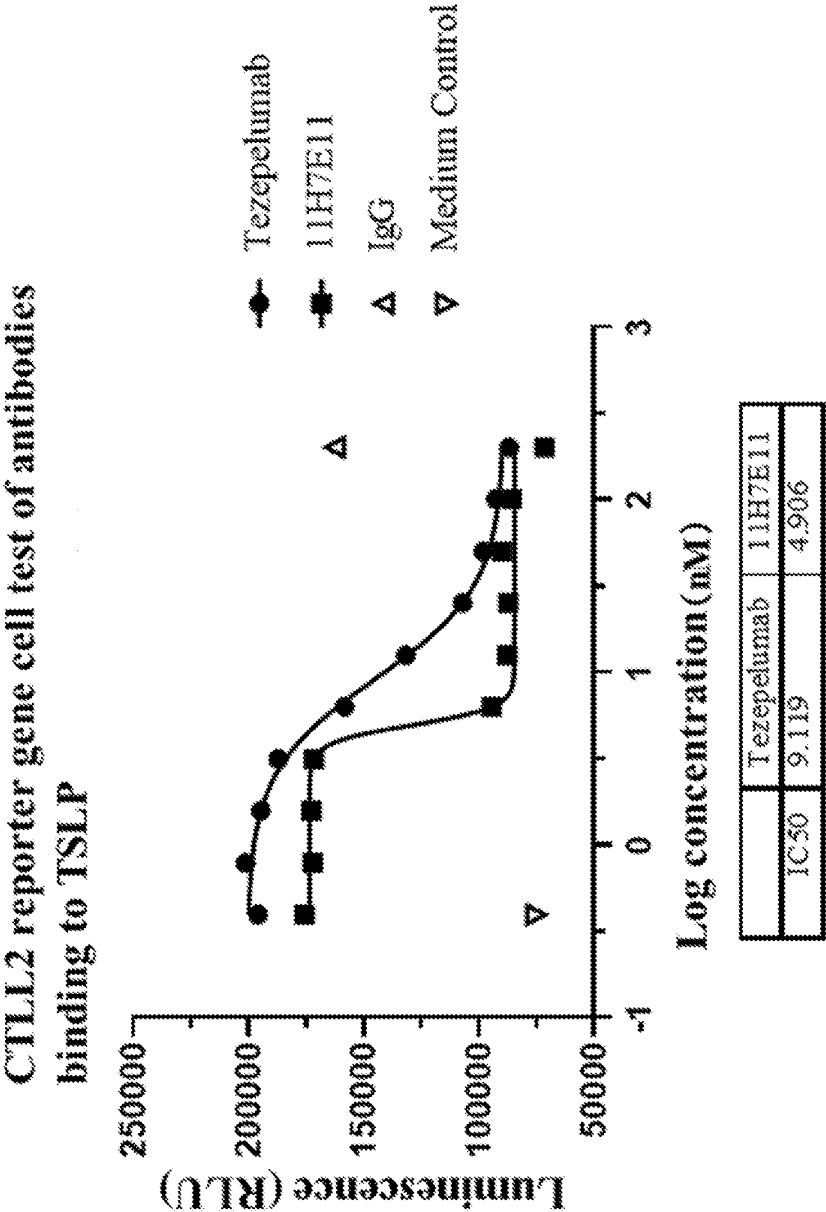
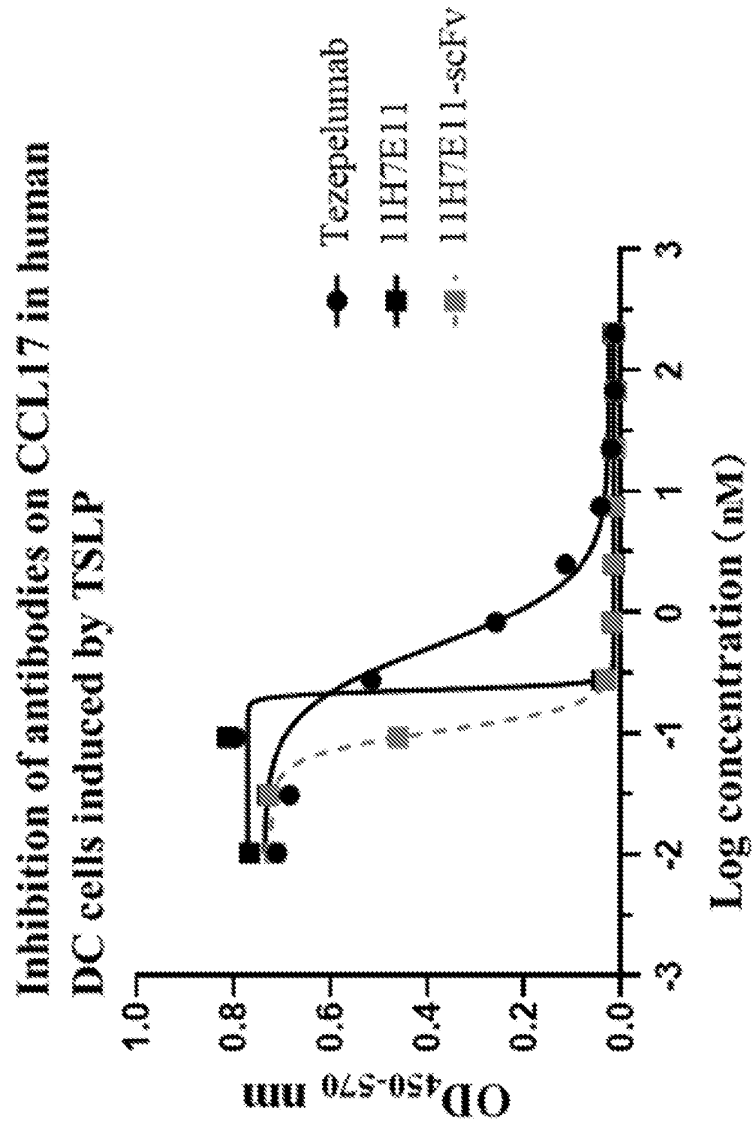


FIG. 5A



Donor: All cells #PCH20210600027

FIG. 5B

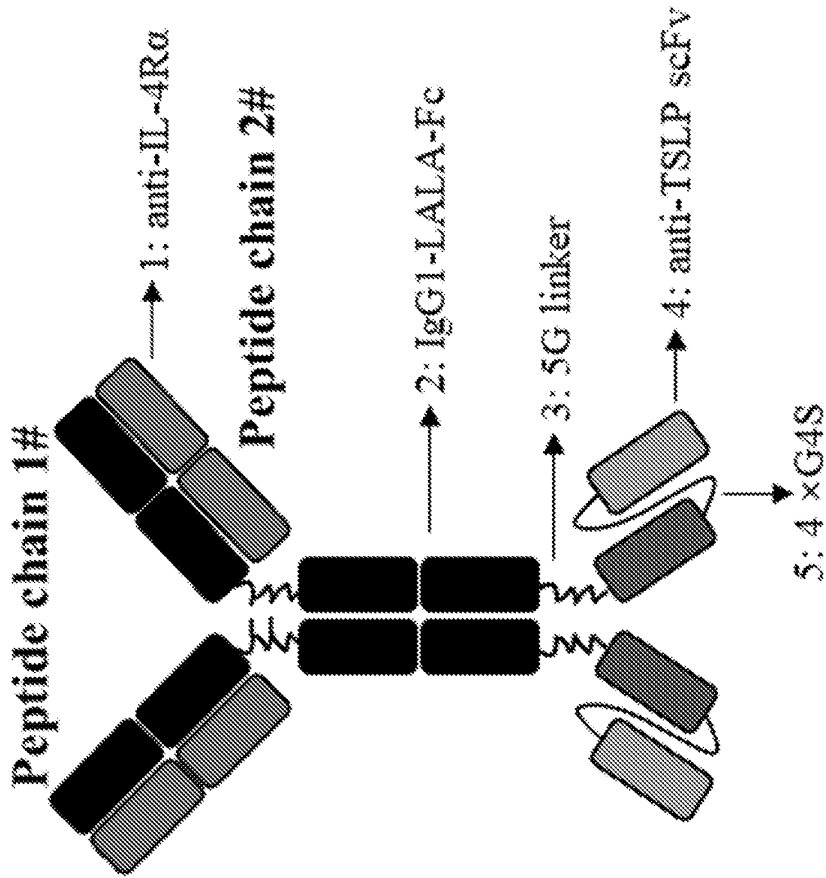


FIG. 6A

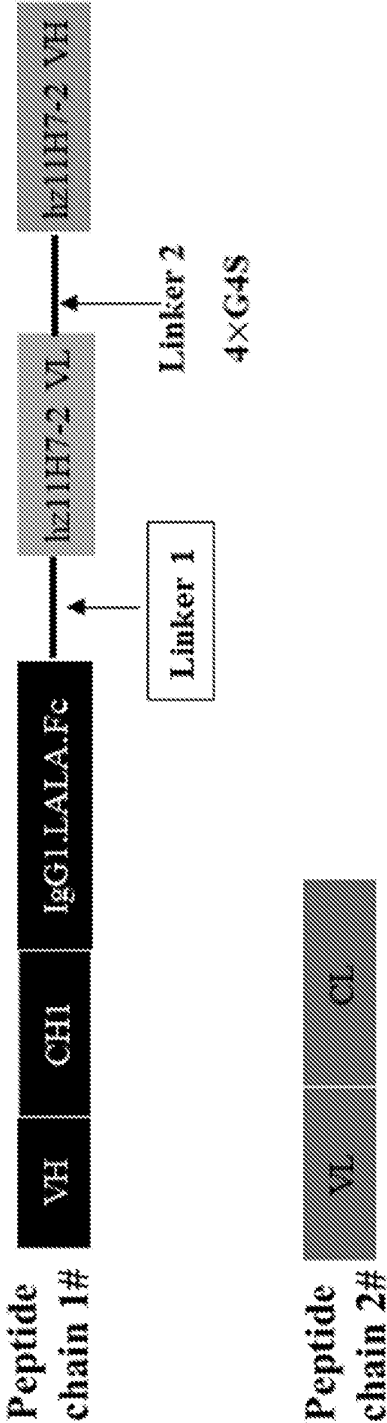


FIG. 6B

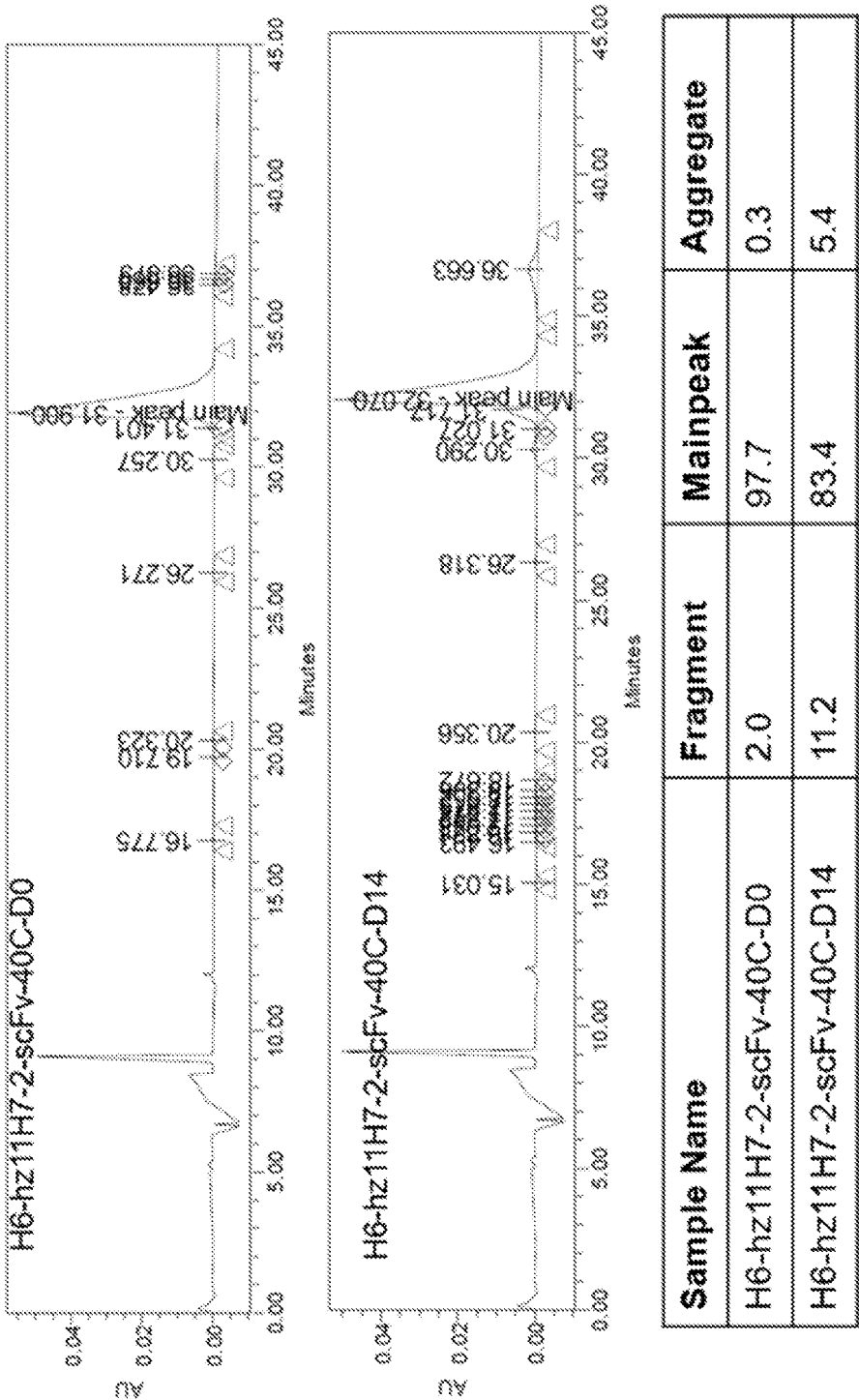
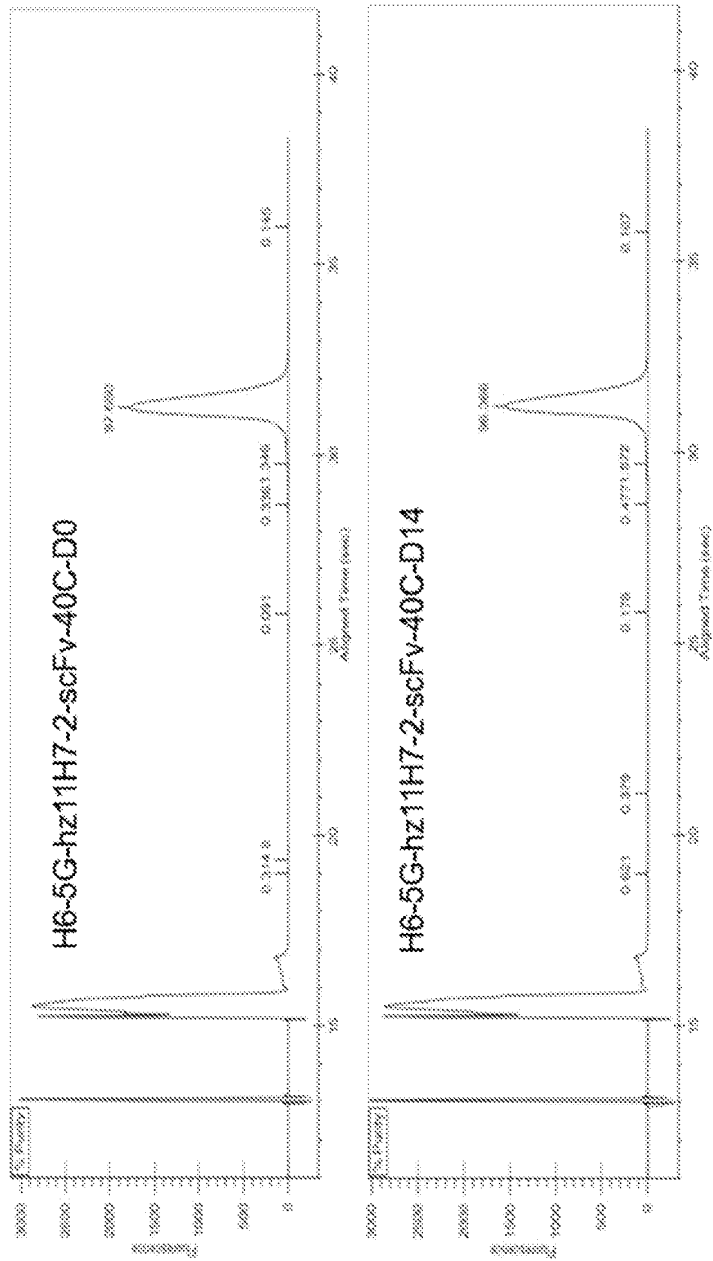


FIG. 7A



Sample Name	Fragment	Mainpeak	Aggregate
H6-5G-hz11H7-2-scFv-40C-D0	2.2	97.7	0.1
H6-5G-hz11H7-2-scFv-40C-D14	3.5	96.4	0.1

FIG. 7B

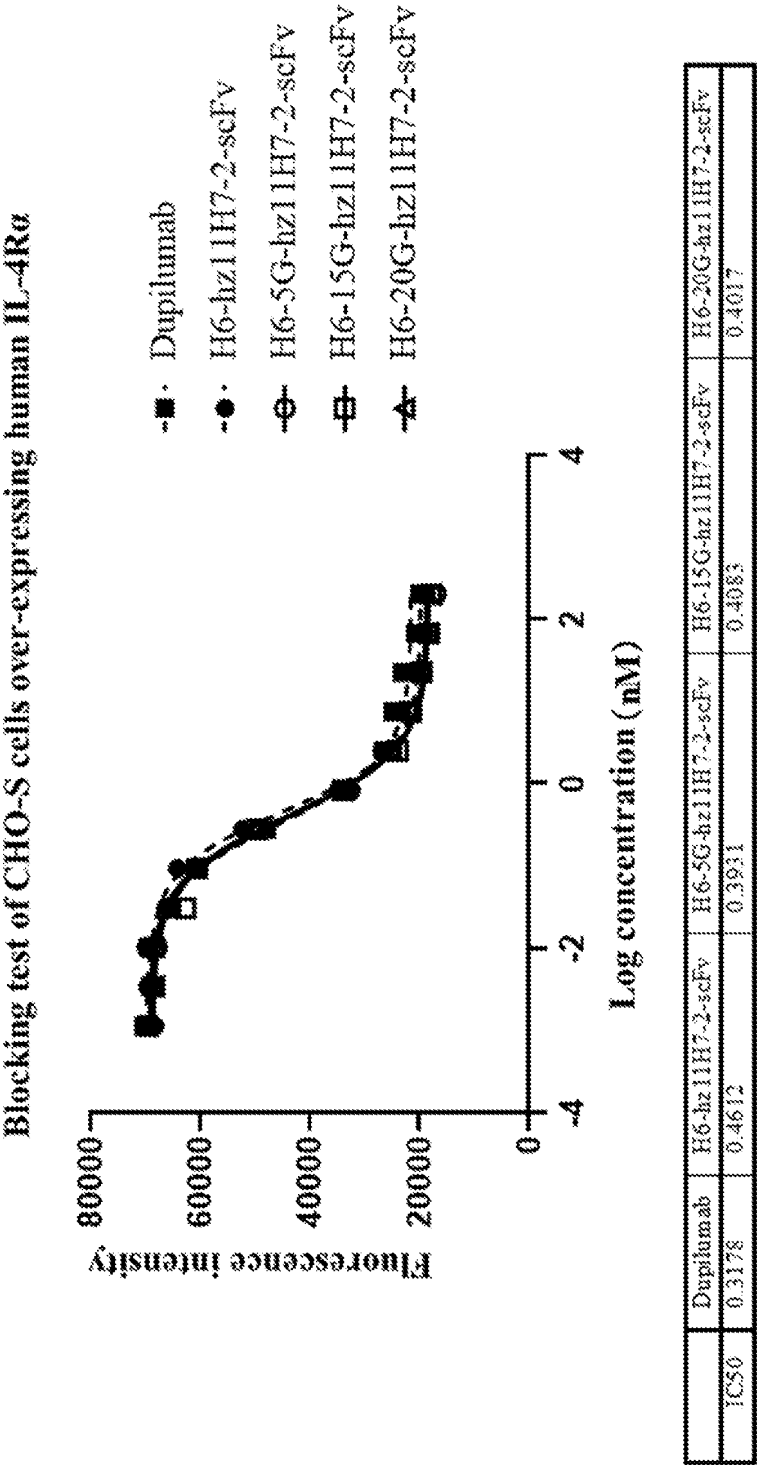


FIG. 8A

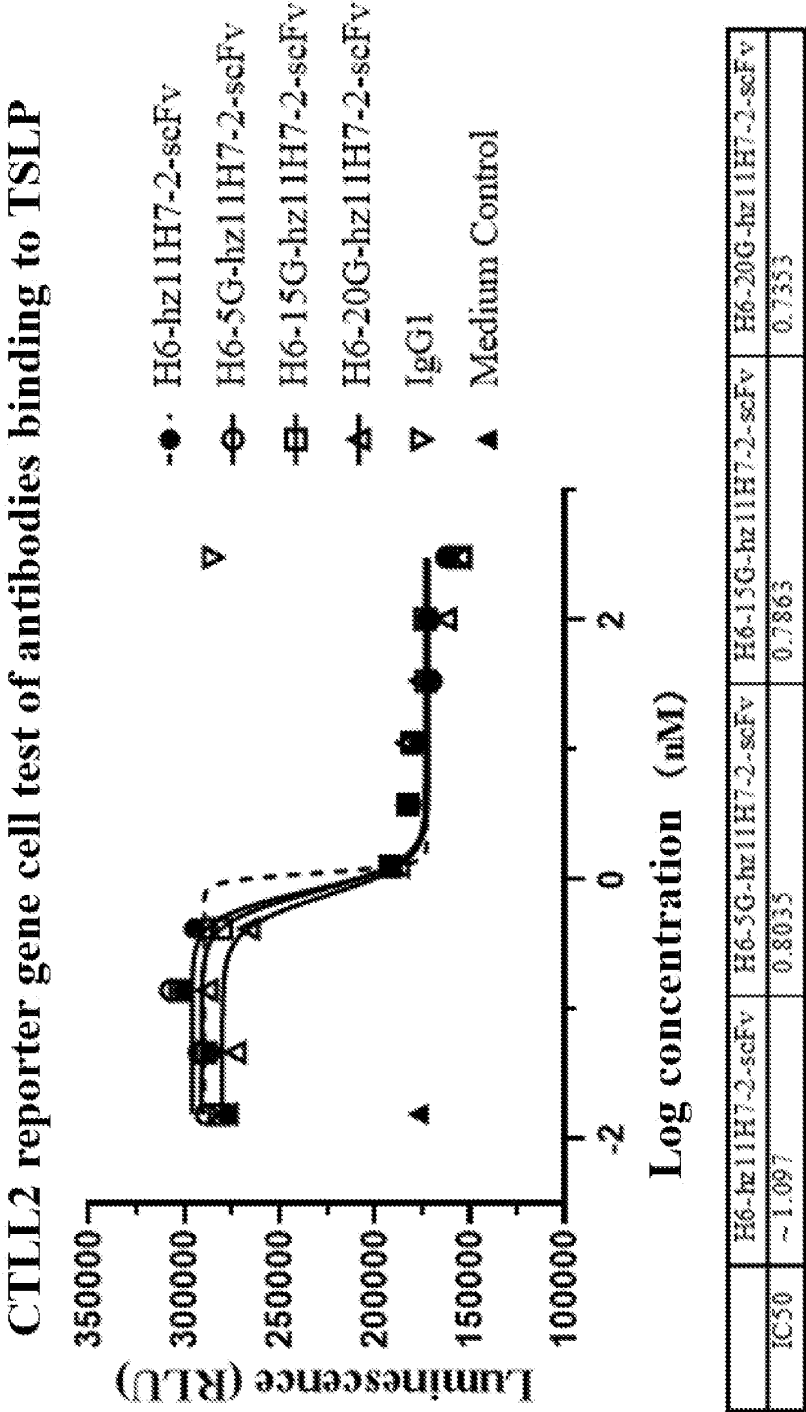


FIG. 8B

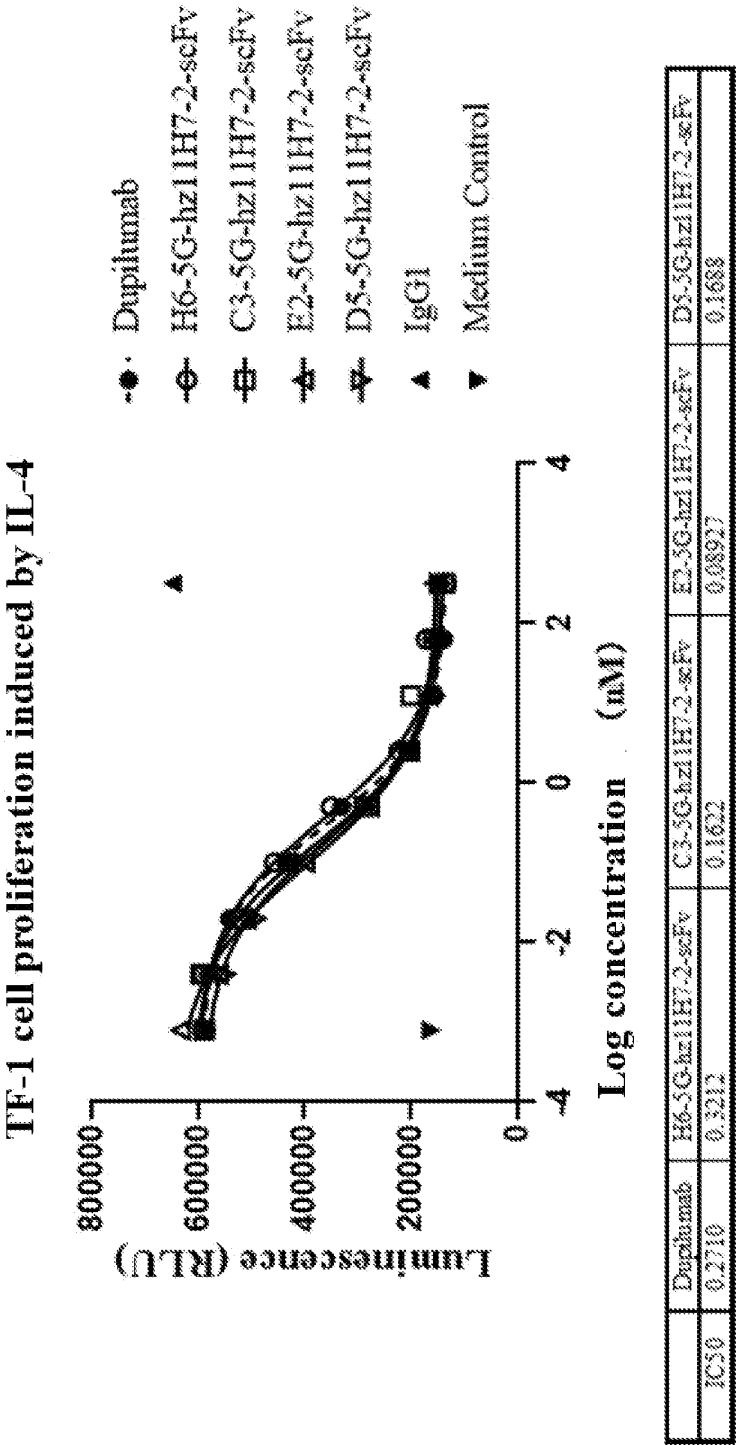


FIG. 9A

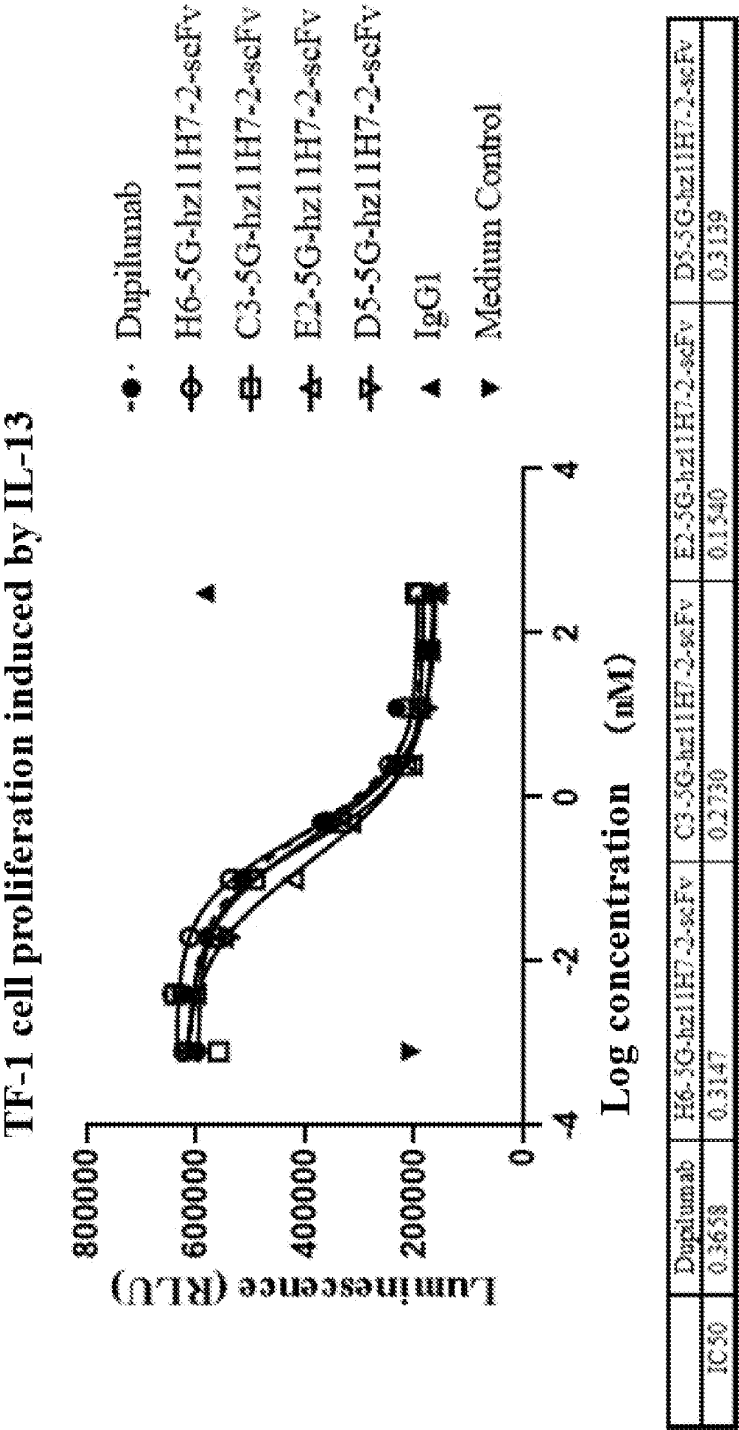


FIG. 9B

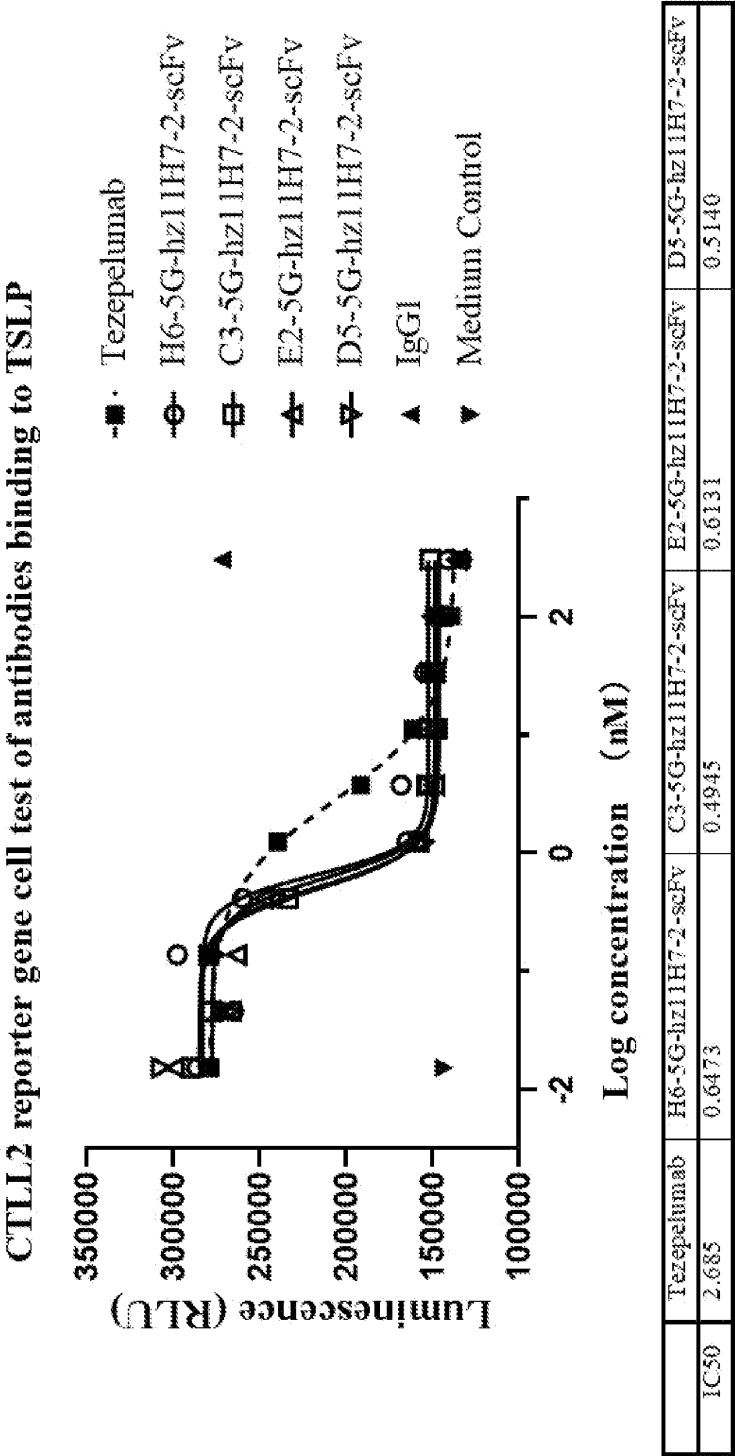


FIG. 10

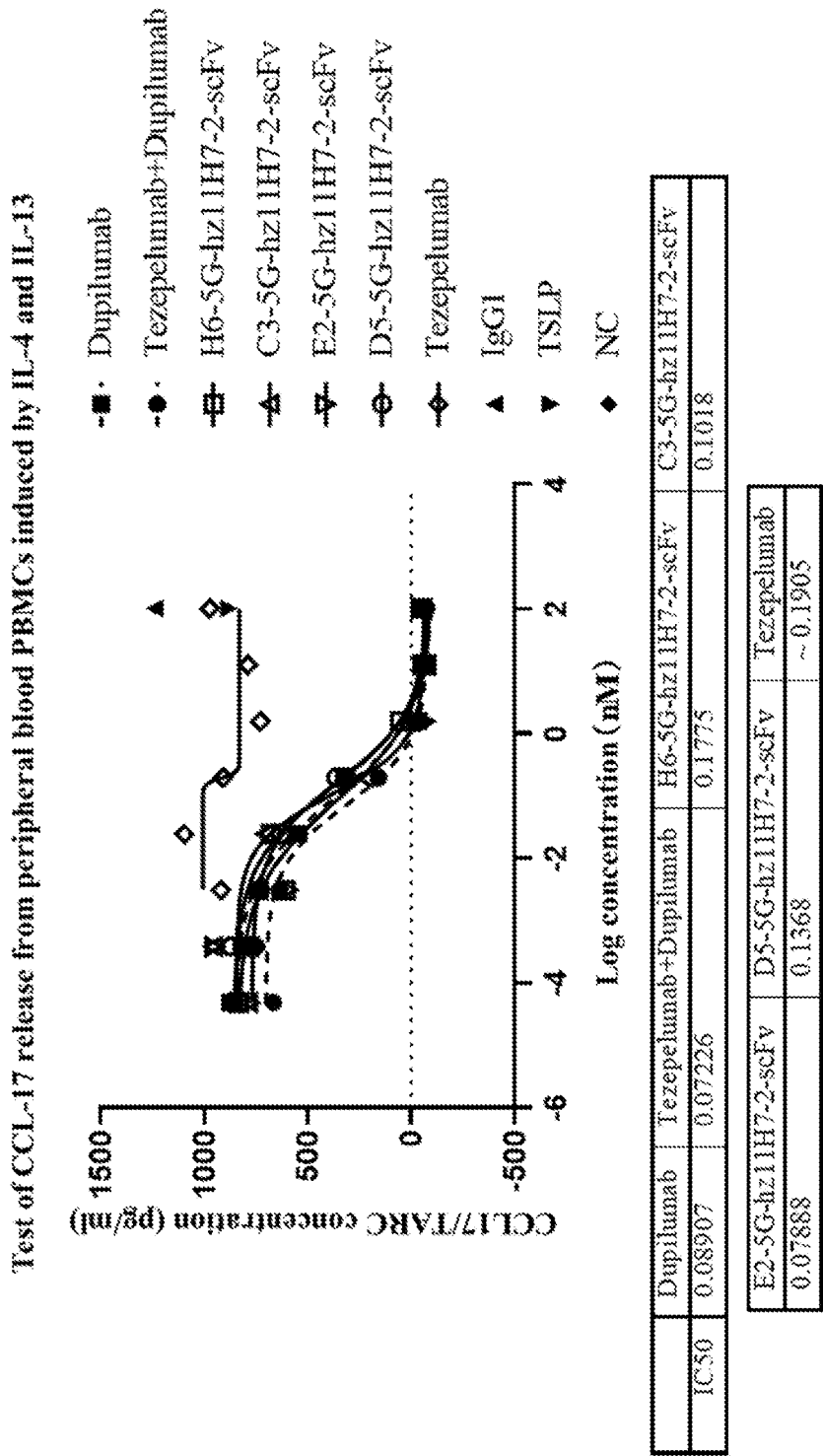


FIG. 11A

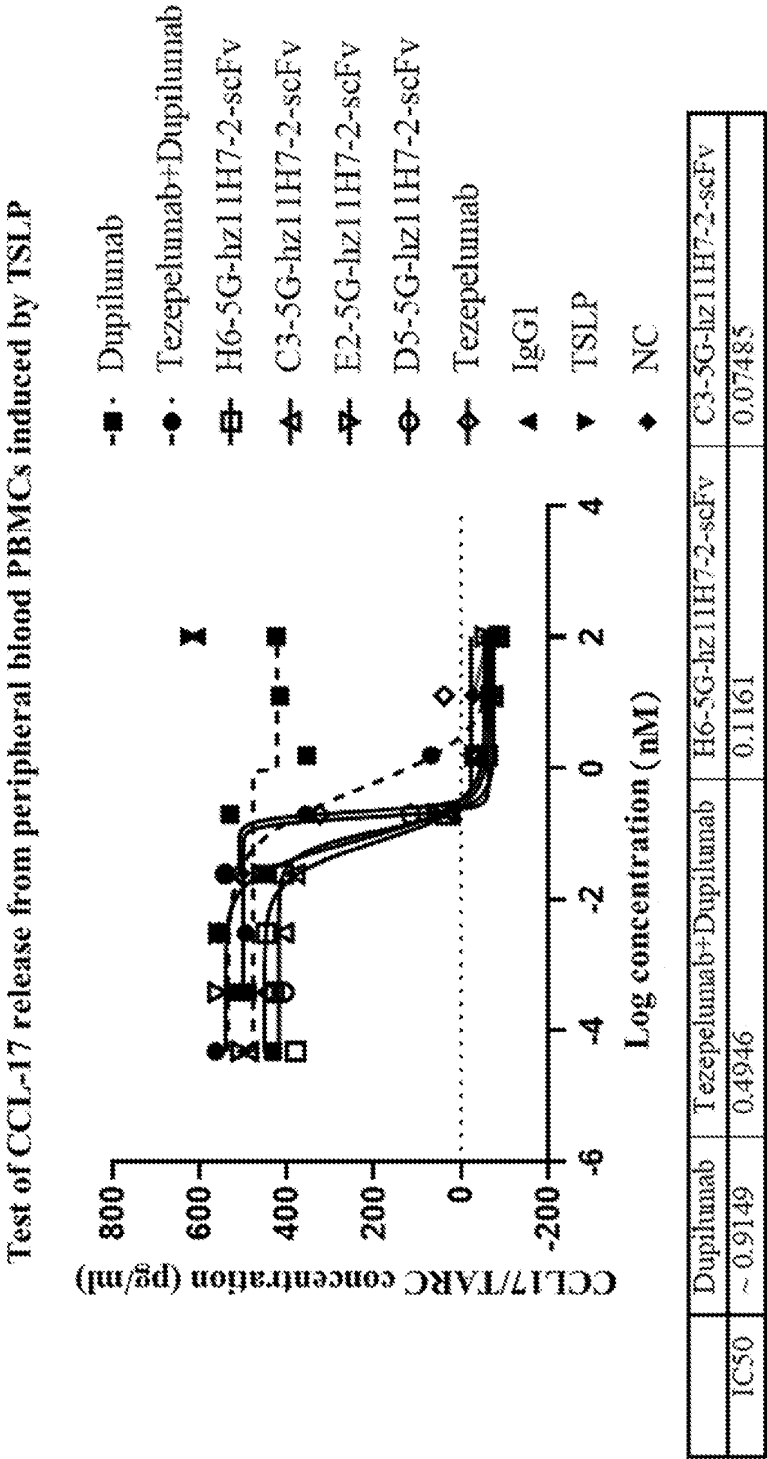


FIG. 11B

Test of CCL-17 release from peripheral blood PBMCs induced by IL-4, IL-13, and TSLP

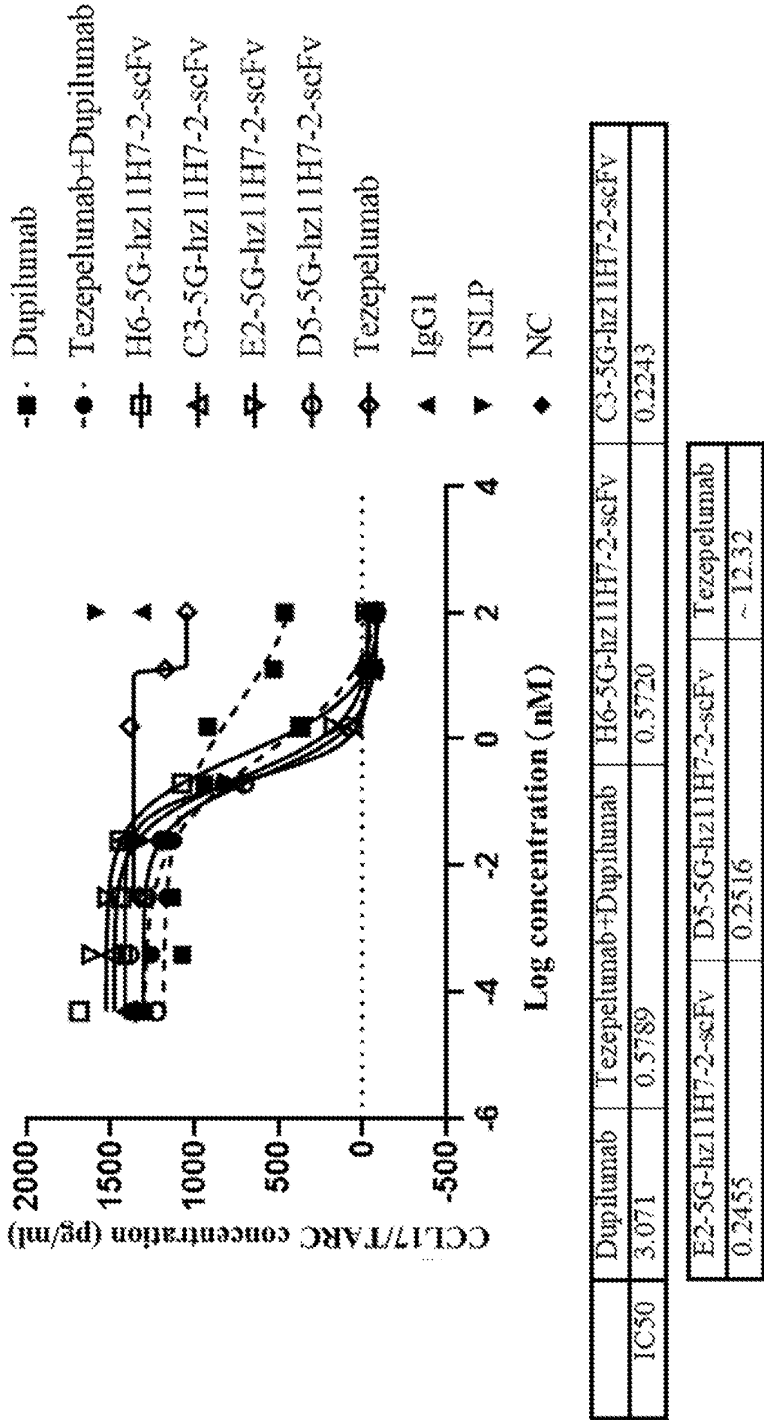


FIG. 11C

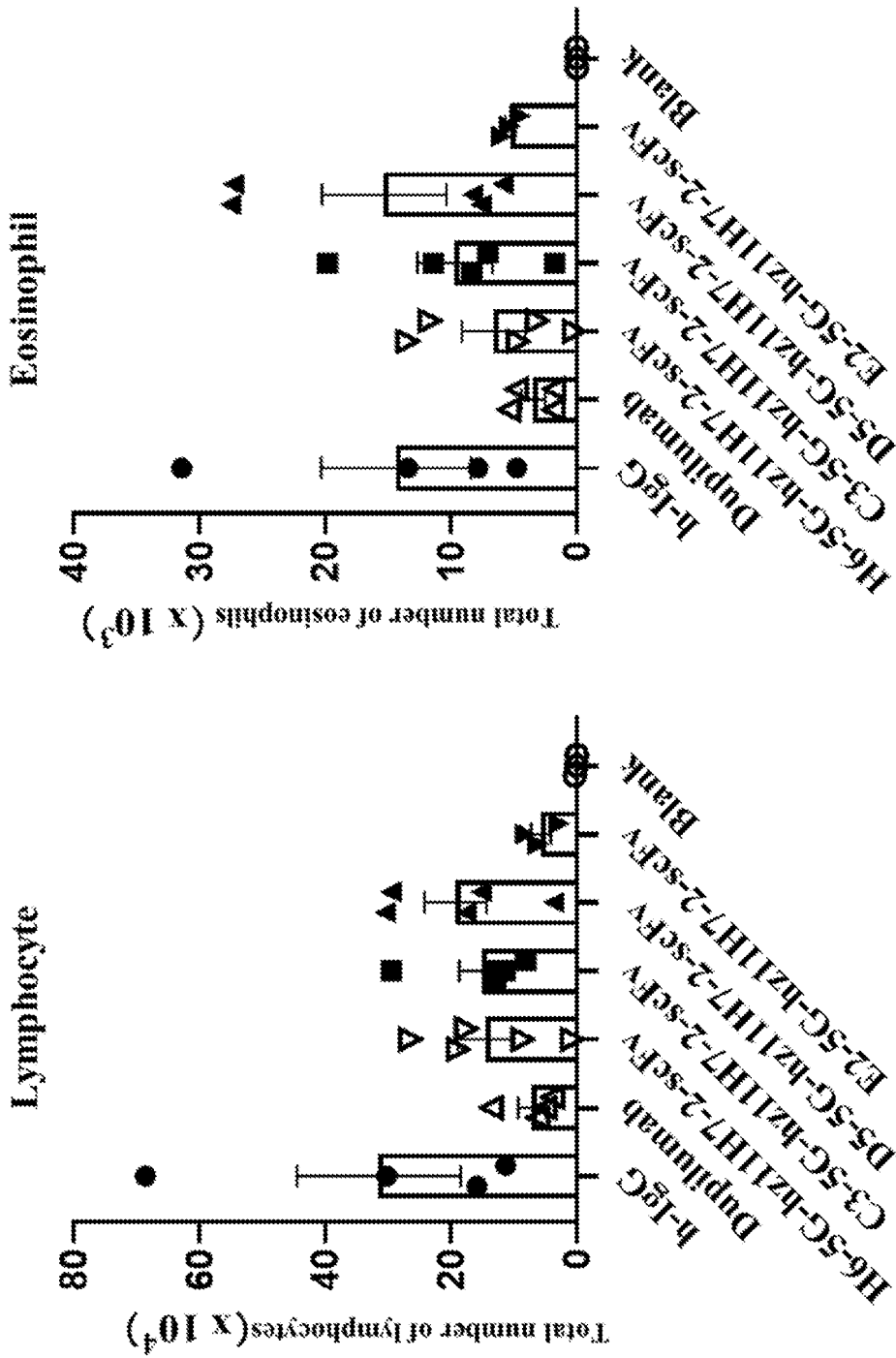


FIG. 12A

FIG. 12B

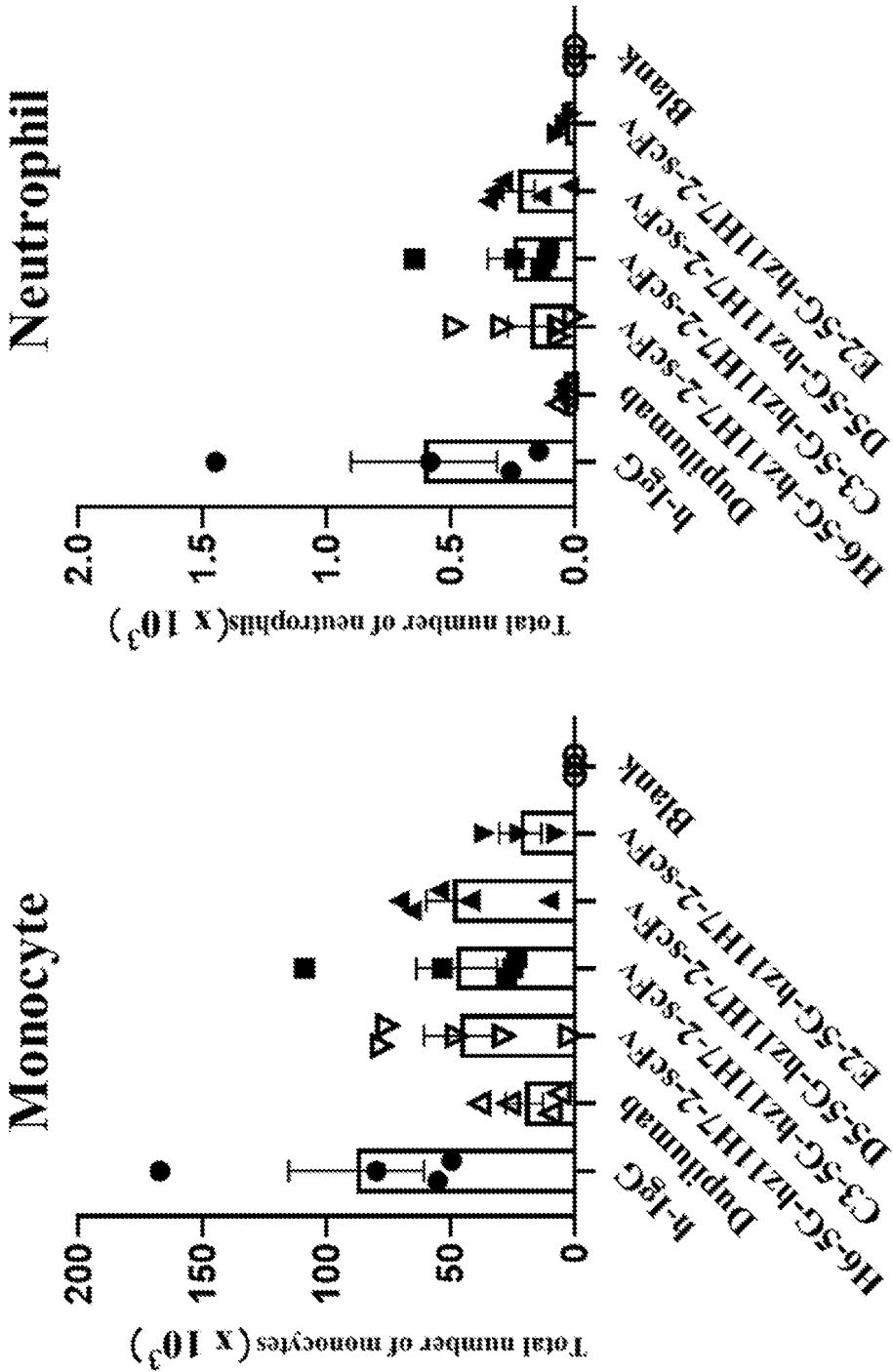


FIG. 12C

FIG. 12D

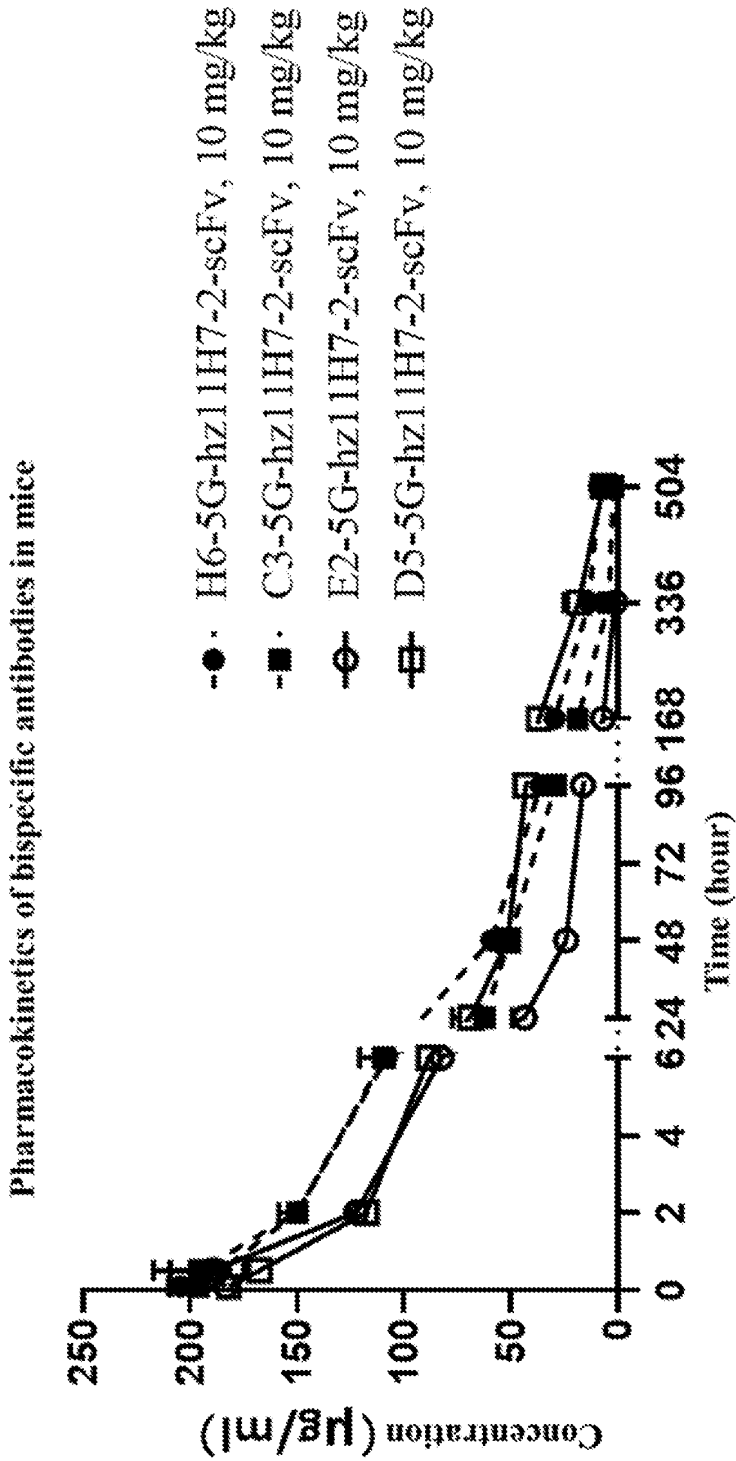


FIG. 13

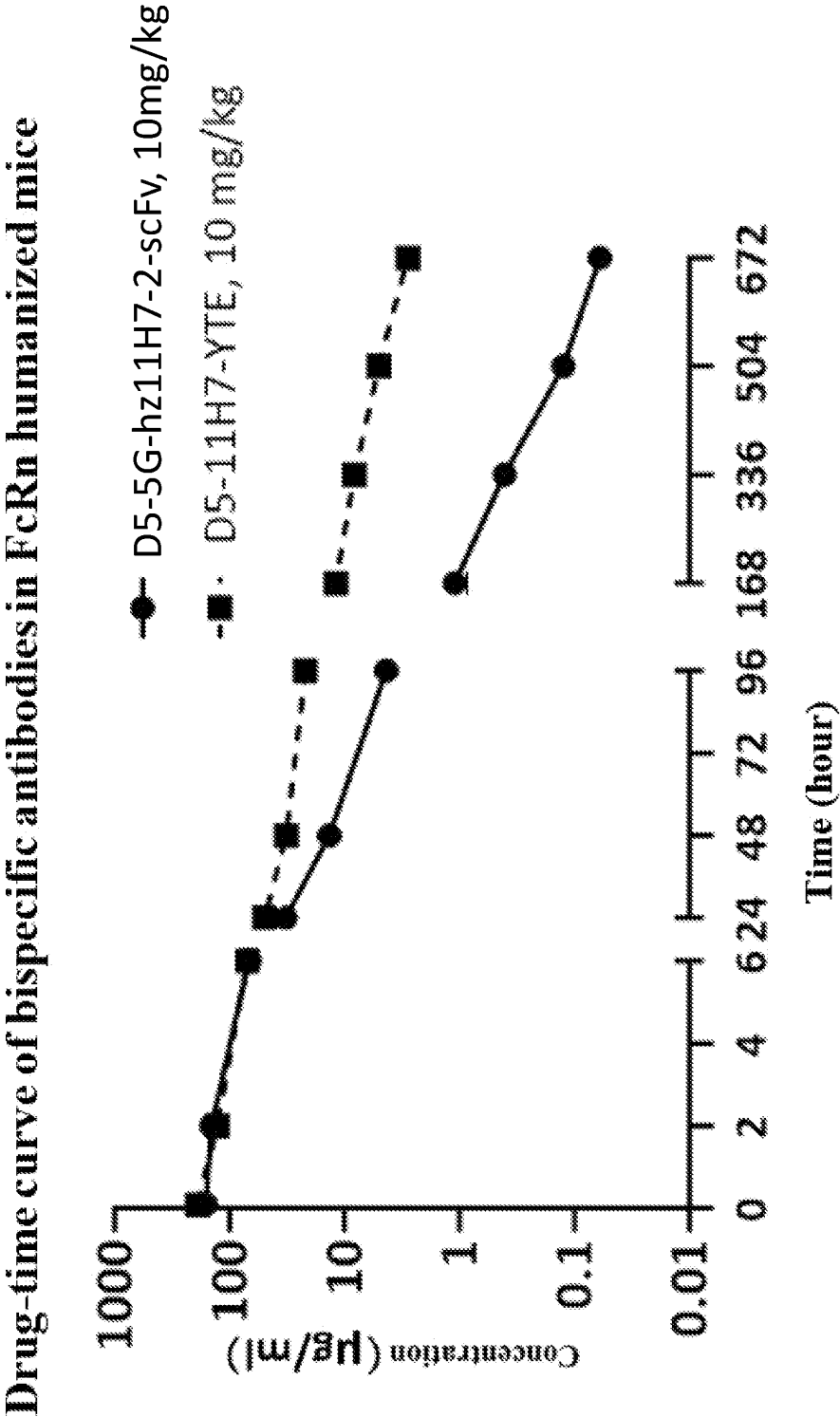


FIG. 14

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	GFTFNINA MN	1	RIRTKSNNYA TYHADSVKD	2	DVGRGFAY	3	RASKSVSTSG YSYMH	4	LASNLQS	5	QHSRELPL T	6
Anti-IL-4Rα H6	GFTFEMNA MN	11	RIRTKGNKYA TYHADSVKD	12	DVGRGFAY	3	RASKSVSFGG FSYMH	13	LGTYLQS	14	QHSREIPLT	15
Anti-IL-4Rα D5	GFTFKMNA MN	18	RIRTKSADYA TYHADSVKD	19	DVGRGFAY	3	RASKSVSFSE YSYMH	20	LGRFLQS	21	QHSRELPI T	22
Anti-IL-4Rα E2	GFTFDMIN AMN	25	RIRTKTSNYA TYHADSVKD	26	DVGRGFAY	3	RASKSVSHRG YSYLH	27	LARHLQS	28	QHSTEIPLT	29
Anti-IL-4Rα C3	GFTFDMIN AMN	32	RIRTKSADYA TYHADSVKD	19	DVGRGFAY	3	RASKSVSVHG YSYLH	33	LARHLQS	34	QHSRELPL T	6
Anti-TSLP 11H7E11	GSSIITSDYA W N	37	YITYSGSTNY NP SLKS	38	EDNSGYSPFT 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	RTKSNNYA	88	DVGRGFAY	89	RASKSVSTSGYSY MH	90	LASNLQS	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	RASKSVSFSEYSY MH	102	LGRFLQS	103	QHSRELPI T	104
Anti-IL-4Rα E2	GTFD MN	105	RTKTSNYA	106	DVGRGFAY	107	RASKSVSHRGYS YLH	108	LARHLQS	109	QHSTEIPLT	110
Anti-IL-4Rα C3	GTFD MN	111	RTKSADYA	112	DVGRGFAY	113	RASKSVSVHGYYS 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	EVQLLETTGGG LVQPKGSLKL SCAASGFTFN INAMNWVRQA PGKGLEWVAR IRTKSNNNYAT YHADSVKDRF TISRDDSQSM LYLQMNNLKT EDTAMYYCVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα 10H4.6 VL	8	DIVLTQSPAS LAVSLGQRAT ISCRASKSVS TSGYSYMHWY QQKPGQPPLK LIYLASNILQS GVPARFSGSG SGTDFLTNIH PVEEDAATY YCQHSRELP LTFGAGTKLEI K
Anti-IL-4Rα Hz10H4.6 VH	9	EVQLVESGGG LVQPGGSLRL SCAASGFTFN INAMNWVRQA PGKGLEWVAR IRTKSNNNYAT YHADSVKDRF TISRDDSKSS LYLQMNLSLKT EDTAVYYCVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα Hz10H4.6 VL	10	DIQMTQSPSS LSASVGDRVT ITCRASKSVS TSGYSYMHWY QQKPGKAPKL LIYLASNILQS GVPSRFSGSG SGTDFLTIS SLOPEDFATY YCQHSRELP LTFGGGTKVEI
Anti-IL-4Rα H6 VH	16	EVQLVESGGG LVQPGGSLRL SCAASGFTFE MNAMNWVRQA PGKGLEWVAR IRTKGNKYAT YHADSVKDRF TISRDDSKSS LYLQMNLSLKT EDTAVYYCVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα H6 VL	17	DIQMTQSPSS LSASVGDRVT ITCRASKSVS FGGFSYMHWY QQKPGKAPKL LIYLGTYLQS GVPSRFSGSG SGTDFLTIS SLOPEDFATY YCQHSRELP LTFGGGTKVEI K
Anti-IL-4Rα D5 VH	23	EVQLVESGGG LVQPGGSLRL SCAASGFTFK MNAMNWVRQA PGKGLEWVAR IRTKSADYAT YHADSVKDRF TISRDDSKSS LYLQMNLSLKT EDTAVYYCVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα D5 VL	24	DIQMTQSPSS LSASVGDRVT ITCRASKSVS FSEYSYMHWY QQKPGKAPKL LIYLGRELQS GVPSRFSGSG SGTDFLTIS SLOPEDFATY YCQHSRELP LTFGGGTKVEI K
Anti-IL-4Rα E2 VH	30	EVQLVESGGG LVQPGGSLRL SCAASGFTFD MNAMNWVRQA PGKGLEWVAR IRTKTSNVAT YHADSVKDRF TISRDDSKSS LYLQMNLSLKT EDTAVYYCVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα E2 VL	31	DIQMTQSPSS LSASVGDRVT ITCRASKSVS HRGYSYLHWY QQKPGKAPKL LIYLARHLQS GVPSRFSGSG SGTDFLTIS SLOPEDFATY YCQHSRELP LTFGGGTKVEI K
Anti-IL-4Rα C3 VH	35	EVQLVESGGG LVQPGGSLRL SCAASGFTED MNAMNWVRQA PGKGLEWVAR IRTKSADYAT YHADSVKDRF TISRDDSKSS LYLQMNLSLKT EDTAVYYCVK DVGRGFAYWG QGTLTVSS
Anti-IL-4Rα C3 VL	36	DIQMTQSPSS LSASVGDRVT ITCRASKSVS YHGYSYLHWY QQKPGKAPKL LIYLARHLQS GVPSRFSGSG SGTDFLTIS SLOPEDFATY YCQHSRELP LTFGGGTKVEI K
Anti-TSLP mouse 11H7E1 VH	43	DVQLQESGPG LVKPSQSLSL TCTVTGSSIT SDYAWNWIQR FPGNKLEWMG YITYSGSTNY NPSLKSRSFI TRDTSKNQFF LQVNSATTED TATYYCARED NSGYSPFTHW GLGLTLTVSA
Anti-TSLP mouse 11H7E11 VL	44	NIVMTQTPIRF LLVSPGDRIT ITCKASQSVG NDVAWYQQKP GRSPKLLIYY TSNRYTGVDP HFTGSGYGTD FTFTISTVQT EDLAVYFCLQ DYSSPWTFGG GTKLEIK
Anti-TSLP Hz11H7 VH	45	QVQLQESGPG LVKPSLTL TCTVSGSSIT SDYAWNWIQR PPGKGLEWIG YITYSGSTNY NPSLKSRTVI SRDTSKNQFS LKLSVTAAD TAVYYCARED NSGYSPFTHW GQGTLTVSS
Anti-TSLP Hz11H7 VL	46	DIQMTQSPSS LSASVGDRVT ITCASQSVG NDVAWYQQKP GKAPKLLIYY TSNRYTGVPS 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 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-2	GFTFX ₁ MN 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 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. 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 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-4	MNAMN	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 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. 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 MIN; 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)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVKDKKVEPKSCDKTH
TCPPCPAPEAAAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
IEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFNCSVMHEALHNHYTQ
KSLSLSPGK

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

peptide chain #1 of H6-5G-hz11H7-2-scFv (SEQ ID NO: 49)
EVQLVESGGGLVQPGGSLRLSCAASGFTFEMNANMWVRQAPGKGLEWVARIRTKGNKYATYHADSVKDRFTISRDDSKSLLYQMNSLKTEDTAVYVCVKDVGRGFA
YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHTCPPCPAPEAAAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFNCS
VMHEALHNHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTITCKASQSVGNDVAVYQKPKAPKLLIYYTSNRYTGVPSPRFSGSGSGTDFTFTISSLQPED
IATYYCLQDYSSPMTFGCGTKVEIKGGGGSGGGGGGQVQLQESGGGLVQPGGSLRLSCAASGFTFEMNANMWVRQAPGKGLEWVARIRTKGNKYATYHADSVKDRFTISRDDSKSLLYQMNSLKTEDTAVYVCVKDVGRGFA
SLKSRVTISRDTSKNQFSLKLSSTVAADTAVYYCAREDNISGYSPTFWGQGTIVTVSS

peptide chain #2 of H6-5G-hz11H7-2-scFv (SEQ ID NO: 50)
DIQMTQSPSSLSASVGDRTITCRASKSVFSGFSYMHVYQKPKAPKLLIYLGTYLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQHSREIPLTFGGGT
VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLTLSKADYEHKHVYACEVTHQGLSSPVTKSFN
RGE

peptide chain #1 of D5-5G-hz11H7-2-scFv (SEQ ID NO: 51)
EVQLVESGGGLVQPGGSLRLSCAASGFTFKMANMWVRQAPGKGLEWVARIRTKSADYATYHADSVKDRFTISRDDSKSLLYQMNSLKTEDTAVYVCVKDVGRGFA
YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHTCPPCPAPEAAAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFNCS
VMHEALHNHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTITCKASQSVGNDVAVYQKPKAPKLLIYYTSNRYTGVPSPRFSGSGSGTDFTFTISSLQPED
IATYYCLQDYSSPMTFGCGTKVEIKGGGGSGGGGGGQVQLQESGGGLVQPGGSLRLSCAASGFTFEMNANMWVRQAPGKGLEWVARIRTKSADYATYHADSVKDRFTISRDDSKSLLYQMNSLKTEDTAVYVCVKDVGRGFA
SLKSRVTISRDTSKNQFSLKLSSTVAADTAVYYCAREDNISGYSPTFWGQGTIVTVSS

peptide chain #2 of D5-5G-hz11H7-2-scFv (SEQ ID NO: 52)
DIQMTQSPSSLSASVGDRTITCRASKSVFSEYSYMHVYQKPKAPKLLIYLGFRFLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQHSRELPITIFGGGT
VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSSTLTLSKADYEHKHVYACEVTHQGLSSPVTKSFN
RGE

peptide chain #1 of C3-5G-hz11H7-2-scFv (SEQ ID NO: 53)
EVQLVESGGGLVQPGGSLRLSCAASGFTFDNMAMNWVRQAPGKGLWVARIRTKSADYATYHADSVKDRFTISRDDSKSSLYLQMNSLKTEDTAVYYCVKDVGRGFA
YWGQGTILVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVD
KKVEPKSCDKTHTCPCPAPEAAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLIVKGFPSDIAEVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGSGGGGDIQMTQSPSSLSASVGDRTVITTCASQSVGNDVAWYQQKPKGAPKLLIYYTASNRYTGVPFSRFGSGSGTDFTFTISLQPED
IATYYCLQDYSSPMTFGCGTKVEIKGGGGSGGGGGGQVQLQESGGPGILVKPSETLSLTCTVSGSSITSDYAMNWIRQPPGKCLEWIGYITYSGSTNYNP
SLKSRVTISRDTSKNQFSLKLSSTVAADTAVYYCAREDNISGSPFTHWGQGTLVTVSS

peptide chain #2 of C3-5G-hz11H7-2-scFv (SEQ ID NO: 54)
DIQMTQSPSSLSASVGDRTVITCRASKSVSYHGYSYLHWYQQKPGKAPKLLIYLARHLQSGVPSRFSGSGSGTDFTLTITSSLQPEDFATYYCQHSRELPLTTFGGGTK
VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTISLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGE

peptide chain #1 of E2-5G-hz11H7-2-scFv (SEQ ID NO: 55)
EVQLVESGGGLVQPGGSLRLSCAASGFTFDNMAMNWVRQAPGKGLWVARIRTKTSNATYHADSVKDRFTISRDDSKSSLYLQMNSLKTEDTAVYYCVKDVGRGFA
YWGQGTILVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVD
KKVEPKSCDKTHTCPCPAPEAAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLIVKGFPSDIAEVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGSGGGGDIQMTQSPSSLSASVGDRTVITTCASQSVGNDVAWYQQKPKGAPKLLIYYTASNRYTGVPFSRFGSGSGTDFTFTISLQPED
IATYYCLQDYSSPMTFGCGTKVEIKGGGGSGGGGGGQVQLQESGGPGILVKPSETLSLTCTVSGSSITSDYAMNWIRQPPGKCLEWIGYITYSGSTNYNP
SLKSRVTISRDTSKNQFSLKLSSTVAADTAVYYCAREDNISGSPFTHWGQGTLVTVSS

peptide chain #2 of E2-5G-hz11H7-2-scFv (SEQ ID NO: 56)
DIQMTQSPSSLSASVGDRTVITCRASKSVSHRGYSYLHWYQQKPGKAPKLLIYLARHLQSGVPSRFSGSGSGTDFTLTITSSLQPEDFATYYCQHSRELPLTTFGGGTK
VEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTISLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGE

linker 2 4 x G4S (SEQ ID NO: 63)
GGGGSGGGSGGGSGGGG

Linker 1 (SEQ ID NO: 64)
GGGG

heavy chain of the antibody Tezepelumab (SEQ ID NO: 65)
QMQLVESGGGVVQPGSRSLRLSCAASGFTFRTYGMHWVRQAPGKGLWVAVIWDGSKNKHVADSVKGRFTITRDNSKNTLNLMNSLRAEDTAVYYCARAPQWELVHE
AFDIWGQGTMTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSKVHTTTPAVLQSSGLYSLSSVTVPSNFGTQTYTCNVDHKPSNT
KVDKTVRKCCVECPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYK
CKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLIVKGFPYSDIAEVESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

light chain of the antibody Tezepelumab (SEQ ID NO: 66)
SYVLTPPSVSVAPGQTARITCGGNILGSKSVHWYQQKPGQAPLVVYDDSDRPSWI PERFGSGNSGNTATLTISRGEAGDEADYYCQVWDSSSDHVVFGGTFKLTIV
LGQKAPASVTLPFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQMKSHRSYSCQVTHEGSTVEKTVAPTECS

amino acid sequence of Teze scFv (SEQ ID NO: 67)
SYVLTPPSVSVAPGQTARITCGGNILGSKSVHWYQQKPGQAPLVVYDDSDRPSWI PERFGSGNSGNTATLTISRGEAGDEADYYCQVWDSSSDHVVFGGTFKLTIV
LGGGGGGGGGGGGGGGQQMLVSESGGVVQPGRSRLRSCAASGTFRTYGMHWVRQAPGKCLEWVAVIWDGSKNKHADSVKGRFTITRDNSKNTLNLQMNSL
RAEDTAVYYCARAPQEWELVHEAFDIWGQGTMTVTVSS

heavy chain of the antibody Dupilumab (SEQ ID NO: 68)
EVQLVESGGGLEQPGGSLRLSCAGSGFTFRDYAMTWVRQAPGKGLEWVSSISGSGNTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDRLSITIRP
RYYGLDVWGQGTITVTVSSASTKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGKTYTCNVDDHKP
SNTKVKRVEKSGPPCPCPAPEFLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSDQDEPEVQFNWYVDGVEVHNAKTRPEEQFNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKGLPSSIEKTTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKRGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSRLTVDKSRWQEGNVSF
SCSVMEALHNHYTQKSLSLGLK

light chain of the antibody Dupilumab (SEQ ID NO: 69)
DIVMTQSPFLSLPVTTPGEPASISCRSSQSLLYSIGVNYLDWYLQKSGQSPQLLIYLGNSRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGFYYCMQALQTPYTFGQGT
KLEIKRTVAAPSVFIFPPSDEQLKSGTASVWCCLLNLFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSSDTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC

TSLPR (SEQ ID NO: 70)
MGRVLVWGAAVFLGGWMALGQGGAAEGVQIQIIFYFNLETVQVTWNASKYSRTNLT FHYRFPNGDEAYDQCTNYLLQEGHTSGCLLDAEQRDDILYFISIRNGTHPVF
TASRMVYVYLPKSSPKHVRFSWHQDAVTVTCSDLSYGDLLYEVQYRSPFDTEWQSKQENTCNVTIEGLDAEKCYSFWRVRKAMEDVYGPDTYPSDWSEVTCWQGEI
RDACAETPTPPKPKLSKFILISSLAILLMVSLLLSLWKLWRVKKFLIPSPVDPKRSIFPGLFEIHQGNFQEWITDTQNVAHLHKMAGAEQESGPEEPLVVQLAKTEA
ESPRMLDPQTEEREASGGSLLQPHQPLQGGDVVTIGGFTFVMNDRSYVAL

IL7Ra (SEQ ID NO: 71)
MTILGTTFGMVFSLLQVVSGESGYAQNGDLEDAELDDYSFCYSQLEVNGSQHSILTCAFEDPDVNI TNLEFEICGALVEVKCINFRKLQEIYFIETKKFLLIGKSN I
CVKVGESLTCKKIDLTITIVKPEAPFDLSVYVREGANDFVVTFTNTSHLQKKYVKVIMHDVAYRQEKDENKWT HVNLSSTKLTLQRLQPAAMYELKVRSI PDHYFK
GFWSEWSPSYFFRTP EINNSSGEMDPILLTISILSFFSVALLVILACVLWKKRKPIVWPSLPDHKKTL EHLCKKPRKNLNVSNFNPESLDCQIHRVDDI QARDEVE
GFLQDTFPQOLESEKQRLGGDVQSPNCPSEDVVITPESFGRDSSLTCLAGNVSACDAPILSSSRSLDCRESGKNPHVYQDILLLSLGTNTSTLPPPFSLQSGILTL
NPVAQQGPILTSLGNSQEEAYVTMTSSFYQNQ

heavy chain of the negative control IgG1 (SEQ ID NO: 72)
QVQLVQSGAEVKKPGASVKVSCQASGYRFSNFVTHWVRQAPGQRFEFWMGWINPYNGNKEFSAKFQDRVTF TADTSANTAYMELRSLRSADTAVYYCARVGPYSWDDS
PQDNYNDVWGKGTIVIVSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTRPREEQINSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELITKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQ
QGNVFCSVMHEALHNHYTQKSLSLSPG

light chain of the negative control IgG1 (SEQ ID NO: 73)
EIVLTQSPGTLSPGERATFSCRSHSIRSRVAVYQHKGQAPRLVIHGVSNRASGISDRFSGSGSDTFTLTITRVEPEDFALYYCQVYGASSYTFGQGTKLER
KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQMWKDNALQSGNSQESVTEQDSKDSITYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGE
C

peptide chain #1 of H6-11H7-YTE (SEQ ID NO: 74)
EVQLVESGGGLVQPGGSLRLSCAASGFTFEMNANMWVRQAPGKGLWEVARIRTKGNKYATYHADSVKDRFTISRDDSKSSLYLQMNLSLKTEDTAVYYCVKDVGRGFA
YWGQGTLLTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSSGLYSLSVTVPPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHHTCCPPCPAPEAAGGPSVFLFPPKPKDTLITREPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTVITCKASQSVGNDVAVYQQKPGKAPKLLIYYTASNRYTGVPSRFSGSGSDTFTTISSLQPED
IATYYCLQDYSSPWTFCGKTKVEIKGGGGSGGGSGGGGGGQVQLQESGPGLVKPKSETLSLTCTVSGSSITSDYAMNWIROPKPKCLEWIGYITYSGSTNYP
SLKSRVTISRDTSKNQFSLKLSSTVAADTAVYYCAREDNISGYSPTTHWGQGTLLTVTSS

peptide chain #1 of D5-11H7-YTE (SEQ ID NO: 75)
EVQLVESGGGLVQPGGSLRLSCAASGFTFKMNANMWVRQAPGKGLWEVARIRTKSADYATYHADSVKDRFTISRDDSKSSLYLQMNLSLKTEDTAVYYCVKDVGRGFA
YWGQGTLLTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSSGLYSLSVTVPPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHHTCCPPCPAPEAAGGPSVFLFPPKPKDTLITREPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTVITCKASQSVGNDVAVYQQKPGKAPKLLIYYTASNRYTGVPSRFSGSGSDTFTTISSLQPED
IATYYCLQDYSSPWTFCGKTKVEIKGGGGSGGGSGGGGGGQVQLQESGPGLVKPKSETLSLTCTVSGSSITSDYAMNWIROPKPKCLEWIGYITYSGSTNYP
SLKSRVTISRDTSKNQFSLKLSSTVAADTAVYYCAREDNISGYSPTTHWGQGTLLTVTSS

peptide chain #1 of C3-11H7-YTE (SEQ ID NO: 76)
EVQLVESGGGLVQPGGSLRLSCAASGFTFDMNANMWVRQAPGKGLWEVARIRTKSADYATYHADSVKDRFTISRDDSKSSLYLQMNLSLKTEDTAVYYCVKDVGRGFA
YWGQGTLLTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSSGLYSLSVTVPPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHHTCCPPCPAPEAAGGPSVFLFPPKPKDTLITREPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTVITCKASQSVGNDVAVYQQKPGKAPKLLIYYTASNRYTGVPSRFSGSGSDTFTTISSLQPED
IATYYCLQDYSSPWTFCGKTKVEIKGGGGSGGGSGGGGGGQVQLQESGPGLVKPKSETLSLTCTVSGSSITSDYAMNWIROPKPKCLEWIGYITYSGSTNYP
SLKSRVTISRDTSKNQFSLKLSSTVAADTAVYYCAREDNISGYSPTTHWGQGTLLTVTSS

peptide chain #1 of E2-11H7-YTE (SEQ ID NO: 77)
EVQLVESGGGLVQPGGSLRLSCAASGFTFDMNANMWVRQAPGKGLWEVARIRTKTSNATYHADSVKDRFTISRDDSKSSLYLQMNLSLKTEDTAVYYCVKDVGRGFA
YWGQGTLLTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSSGLYSLSVTVPPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCDKTHHTCCPPCPAPEAAGGPSVFLFPPKPKDTLITREPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTVITCKASQSVGNDVAVYQQKPGKAPKLLIYYTASNRYTGVPSRFSGSGSDTFTTISSLQPED
IATYYCLQDYSSPWTFCGKTKVEIKGGGGSGGGSGGGGGGQVQLQESGPGLVKPKSETLSLTCTVSGSSITSDYAMNWIROPKPKCLEWIGYITYSGSTNYP
SLKSRVTISRDTSKNQFSLKLSSTVAADTAVYYCAREDNISGYSPTTHWGQGTLLTVTSS

peptide chain #1 of H6-11H7-LS (SEQ ID NO: 78)
EVQLVESGGGLVQPGGSLRLSCAASGFTFDMNMMWVRQAPGKGLEWVARIRTKGNKYATYHADSVKDRFTISRDDSKSSLYLQMNLSLKTEDTAVYVCVKDVGRGFA
YWGQGTILVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYYICNVNHPKNTKVD
KKVEPKSCDKTHHTCPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VLHEALHSHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTVITCKASQSVGNDVAWYQQKPKGAPKLLIYYTASNRYTGVPSRFSGSGSDFTFTTISLQPED
IATYYCLQDYSSPMTFGCGTKVEIKGGGGSGGGGGGQVQLQESGPGILVKPSETLSLTCTVSGSSITSDYAMNWIRQPPGKCLEWIGYITYSGSTNYP
SLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCAREDNNGYSPTFTHWGQGTILVTVSS

peptide chain #1 of D5-11H7-LS (SEQ ID NO: 79)
EVQLVESGGGLVQPGGSLRLSCAASGFTFKMNMWVRQAPGKGLEWVARIRTKSADYATYHADSVKDRFTISRDDSKSSLYLQMNLSLKTEDTAVYVCVKDVGRGFA
YWGQGTILVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYYICNVNHPKNTKVD
KKVEPKSCDKTHHTCPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VLHEALHSHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTVITCKASQSVGNDVAWYQQKPKGAPKLLIYYTASNRYTGVPSRFSGSGSDFTFTTISLQPED
IATYYCLQDYSSPMTFGCGTKVEIKGGGGSGGGGGGQVQLQESGPGILVKPSETLSLTCTVSGSSITSDYAMNWIRQPPGKCLEWIGYITYSGSTNYP
SLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCAREDNNGYSPTFTHWGQGTILVTVSS

peptide chain #1 of C3-11H7-LS (SEQ ID NO: 80)
EVQLVESGGGLVQPGGSLRLSCAASGFTFDMNMMWVRQAPGKGLEWVARIRTKSADYATYHADSVKDRFTISRDDSKSSLYLQMNLSLKTEDTAVYVCVKDVGRGFA
YWGQGTILVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYYICNVNHPKNTKVD
KKVEPKSCDKTHHTCPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VLHEALHSHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTVITCKASQSVGNDVAWYQQKPKGAPKLLIYYTASNRYTGVPSRFSGSGSDFTFTTISLQPED
IATYYCLQDYSSPMTFGCGTKVEIKGGGGSGGGGGGQVQLQESGPGILVKPSETLSLTCTVSGSSITSDYAMNWIRQPPGKCLEWIGYITYSGSTNYP
SLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCAREDNNGYSPTFTHWGQGTILVTVSS

peptide chain #1 of E2-11H7-LS (SEQ ID NO: 81)
EVQLVESGGGLVQPGGSLRLSCAASGFTFDMNMMWVRQAPGKGLEWVARIRTKTSNYATYHADSVKDRFTISRDDSKSSLYLQMNLSLKTEDTAVYVCVKDVGRGFA
YWGQGTILVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYYICNVNHPKNTKVD
KKVEPKSCDKTHHTCPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VLHEALHSHYTQKSLSLSPGGGGGDIQMTQSPSSLSASVGDRTVITCKASQSVGNDVAWYQQKPKGAPKLLIYYTASNRYTGVPSRFSGSGSDFTFTTISLQPED
IATYYCLQDYSSPMTFGCGTKVEIKGGGGSGGGGGGQVQLQESGPGILVKPSETLSLTCTVSGSSITSDYAMNWIRQPPGKCLEWIGYITYSGSTNYP
SLKSRVTISRDTSKNQFSLKLSSTAAADTAVYYCAREDNNGYSPTFTHWGQGTILVTVSS

heavy chain constant region with YTE mutation (SEQ ID NO: 82)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYYICNVNHPKNTKVDKKVEPKSCDKTH
TCPPCPAPEAAGGPSVFLFPPKPKDTLIYITREPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP
IEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHSHYTQ
KSLSLSPGK

heavy chain constant region with LS mutation (SEQ ID NO: 83)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
TCPGPCAPEAAGGFSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQQGNVVFSCSVLHEALHSHYTQ
KSLSLSPGK

Linker (SEQ ID NO: 127)
GGGS