

FIG. 1A

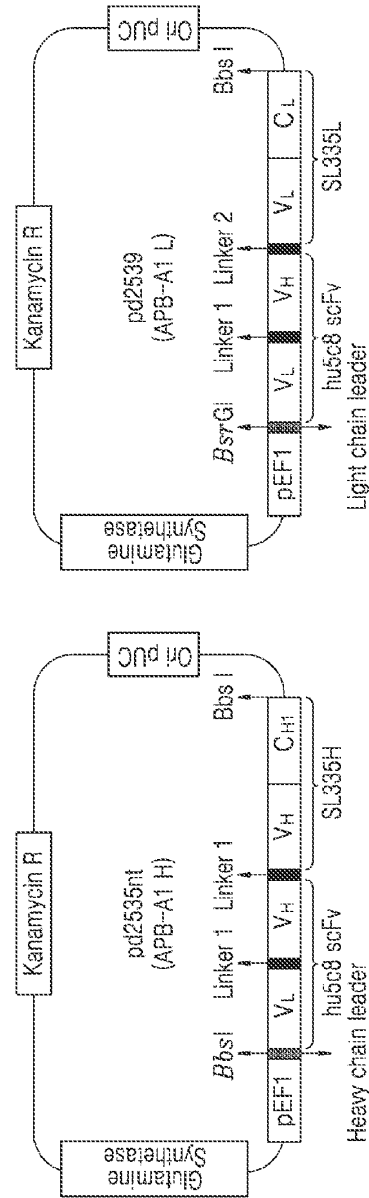


FIG. 1B

APB-A1 H amino acid sequence

10	20	30	40	50	60	70	80
DIVLTQSPAT	LSVSPGERAT	ISCRASQKRV	SSTYSIMHWY	QOKPGQPPKL	LIKYASNLES	GVPAEFGSG	SGTDFTLTIS
90	100	110	120	130	140	150	160
SVEPEDFATY	YQHSWEIIPP	TFGGGKLEI	KRGGGSGGG	GSGGGGSQVQ	LVQSGAEVVK	PGASVKLSCK	ASGYIFTSY
170	180	190	200	210	220	230	240
MYWVKQAPGQ	GLEWIGEINP	SNGDTNFNEK	FKSKATLTVD	KSASTAYMEL	SSLRSEDYAV	YYCTRSQDGRN	DMDSWGQGTIL
250	260	270	280	290	300	310	320
VTVSSGGGGS	GGGSGGGGS	QVQLVQSGGG	PVAPGCSLRL	SCAASGFMFR	AYSMNNWVQA	PKKCLEWVSS	ISSSCRYIHY
330	340	350	360	370	380	390	400
ADSVKGRFTI	SRDIAKNSLY	LQMSLRAED	TAVYYCARET	VMAGKALDYW	GGTLVTVSS	ASTKGPSVFP	LAPSSKSTSE
410	420	430	440	450	460	470	480
GTAALGCLVK	DYFPEPVTVS	WNSGALTSGV	HTFPAVLQSS	GLYSLSSVVT	VFSSSLGTQT	YICNVNHNKPS	NTKVDKKVER

KSS

APB-A1 L amino acid sequence

10	20	30	40	50	60	70	80
DIVLTQSPAT	LSVSPGERAT	ISCRASQKRV	SSTYSIMHWY	QOKPGQPPKL	LIKYASNLES	GVPAEFGSG	SGTDFTLTIS
90	100	110	120	130	140	150	160
SVEPEDFATY	YQHSWEIIPP	TFGGGKLEI	KRGGGSGGG	GSGGGGSQVQ	LVQSGAEVVK	PGASVKLSCK	ASGYIFTSY
170	180	190	200	210	220	230	240
MYWVKQAPGQ	GLEWIGEINP	SNGDTNFNEK	FKSKATLTVD	KSASTAYMEL	SSLRSEDYAV	YYCTRSQDGRN	DMDSWGQGTIL
250	260	270	280	290	300	310	320
VTVSSGSGSG	SGKPSGSGSG	TKGDIVLTQS	PGTSLSPGE	TATLSCRASQ	SVGSNLAWEY	QKPGQAPRLL	IYGASTGATG
330	340	350	360	370	380	390	400
VPAEFGSRS	GTDFTLTIS	LQEDFATY	CCQYYSFLAK	TFQGGTQLEI	KRTVAAPSVF	IEPPSDEQLK	SGTASVVCLL
410	420	430	440	450	460	470	
NNFYPREAKV	QWKVDNALQS	GNSQESVTEQ	DSKSDSTYSL	NTLTLSKADY	EKKHYACEV	THQGLSSPVT	KSFNRGES

FIG. 2A

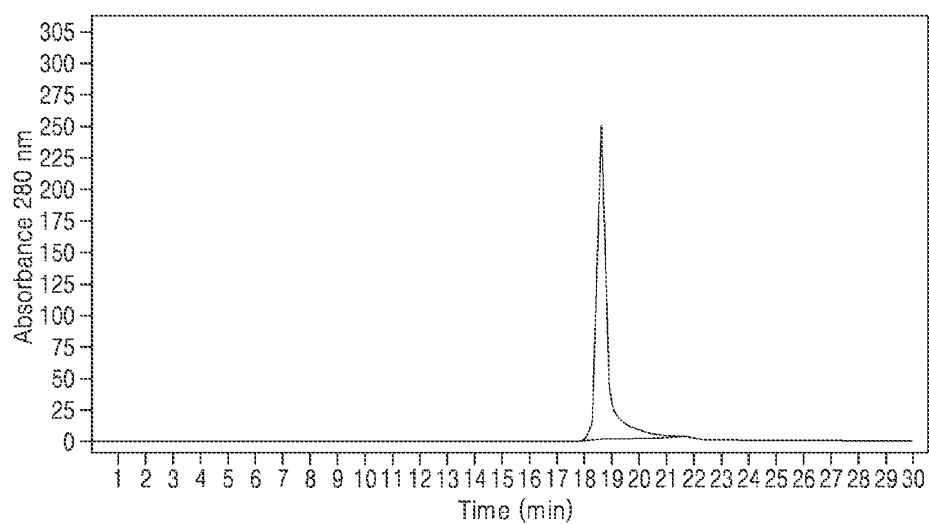


FIG. 2B

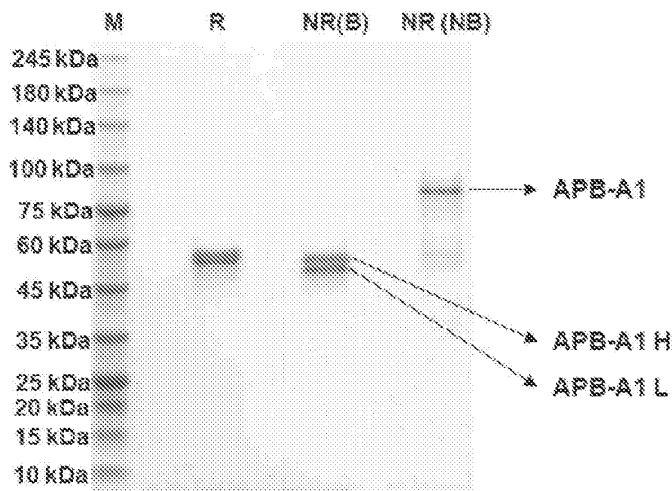


FIG. 3

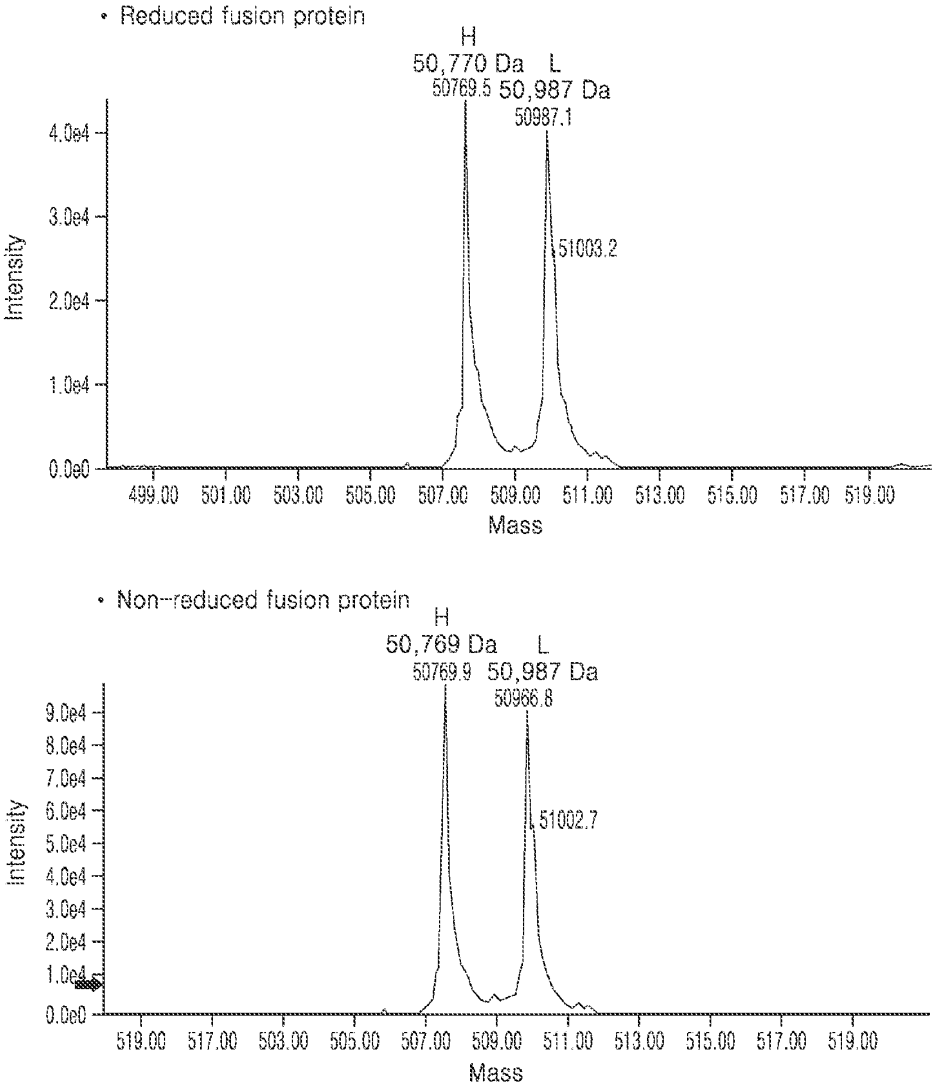


FIG. 4A

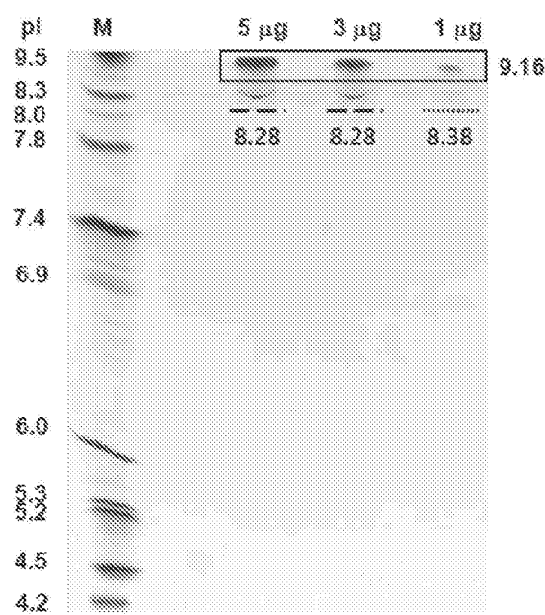


FIG. 4B

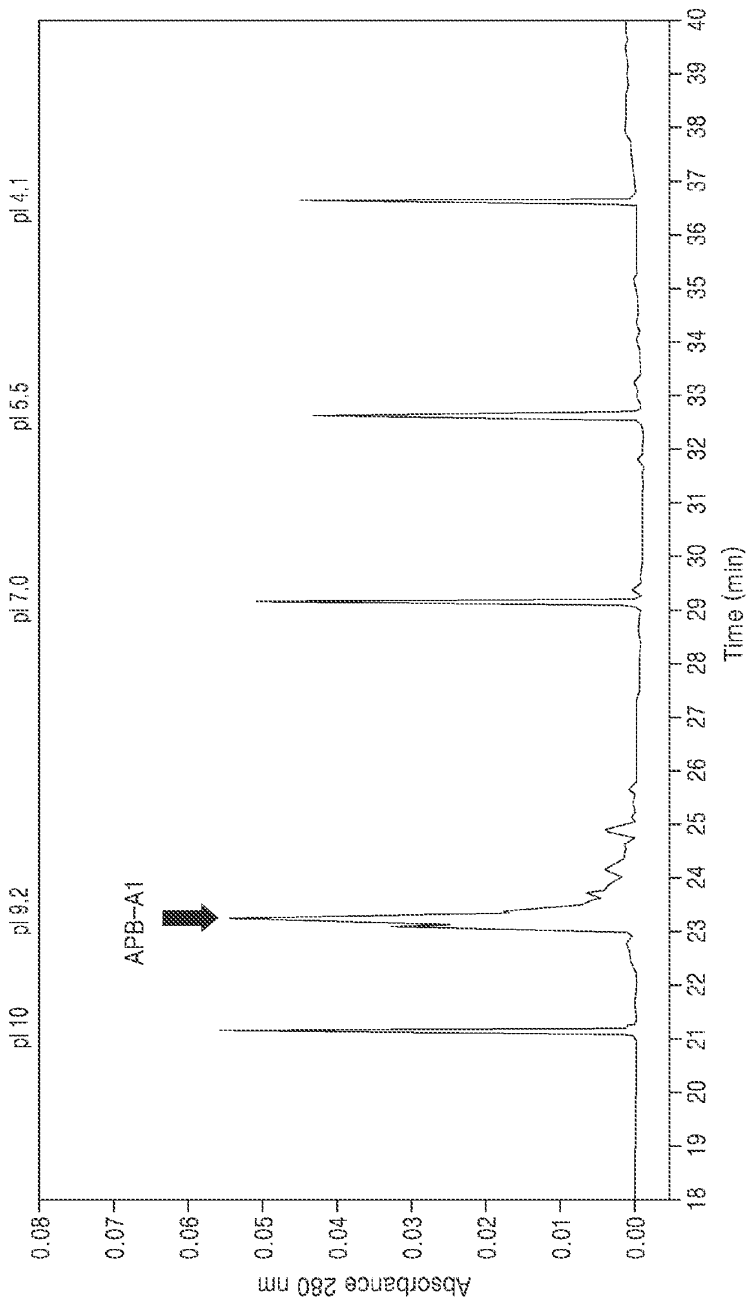


FIG. 5

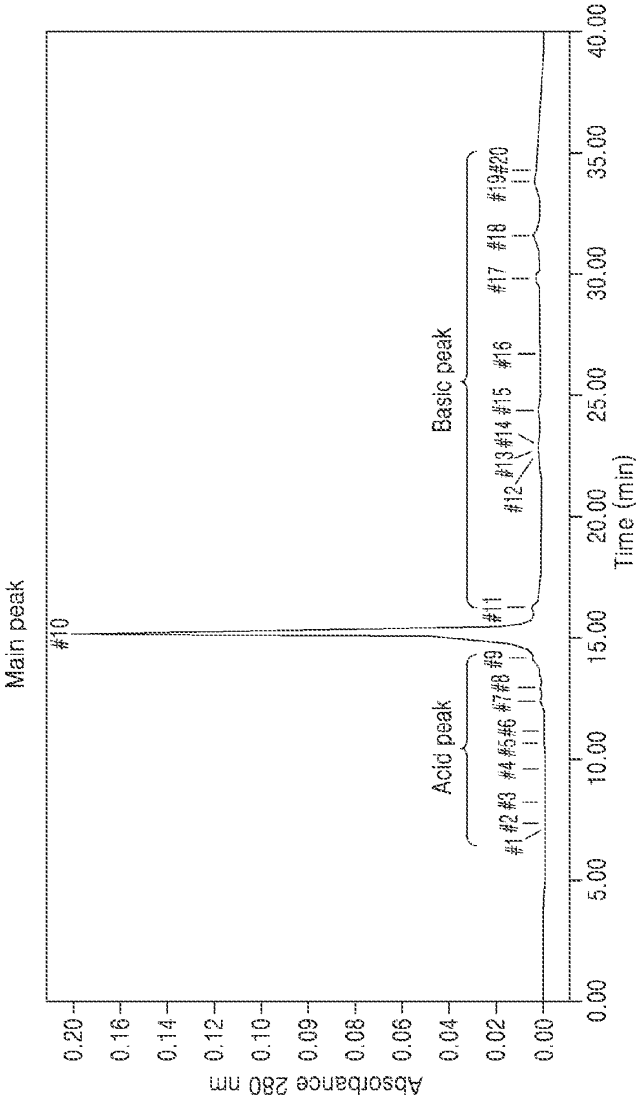


FIG. 6

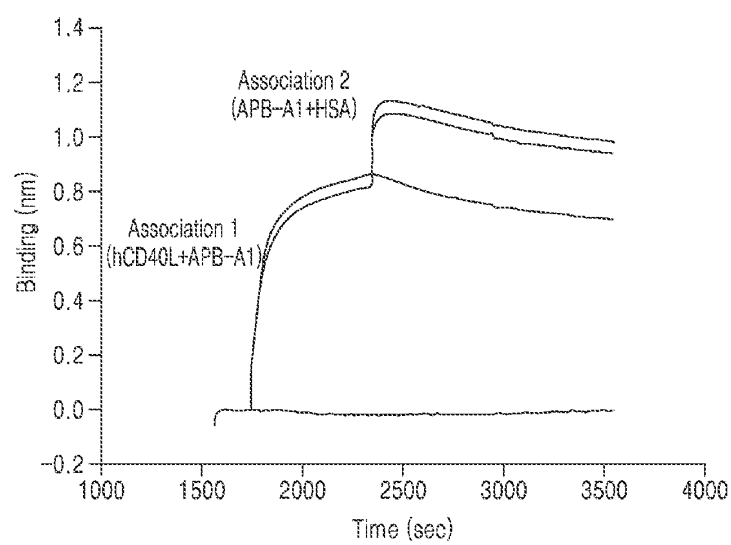


FIG. 7

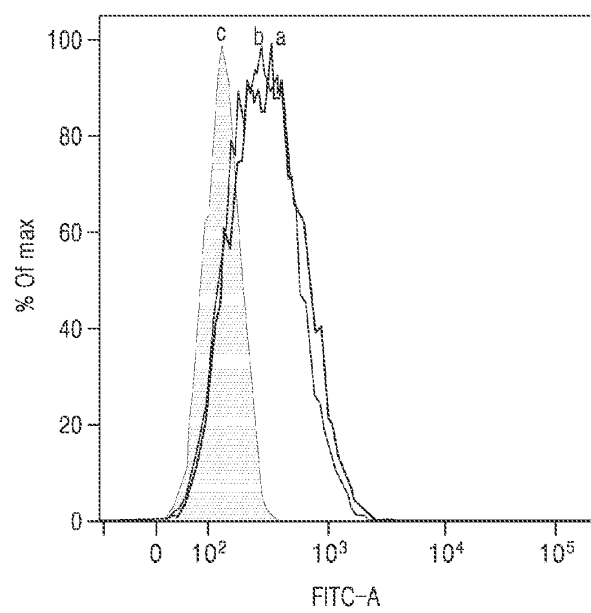


FIG. 8A

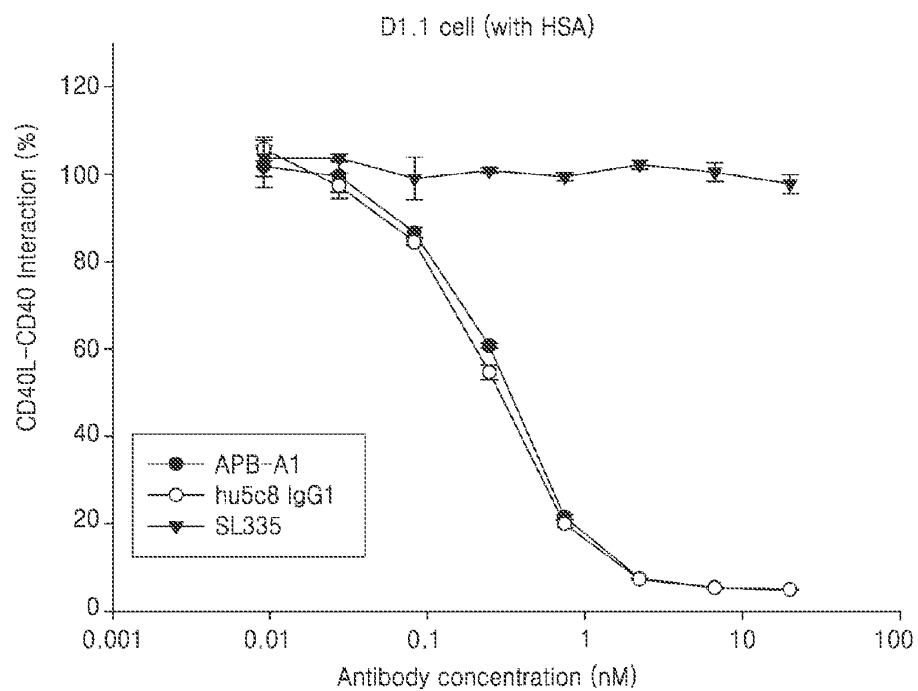


FIG. 8B

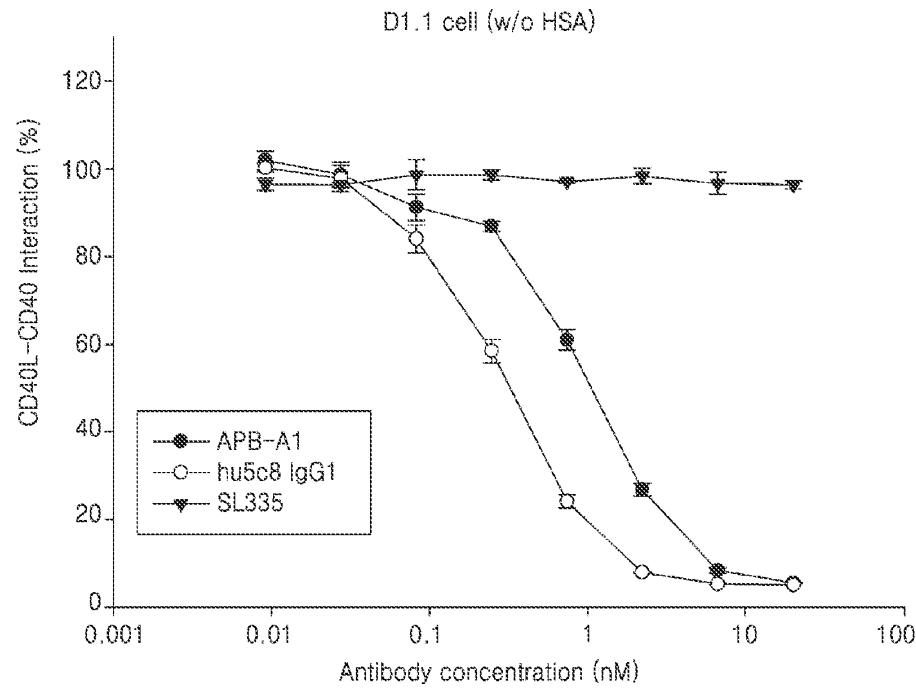


FIG. 8C

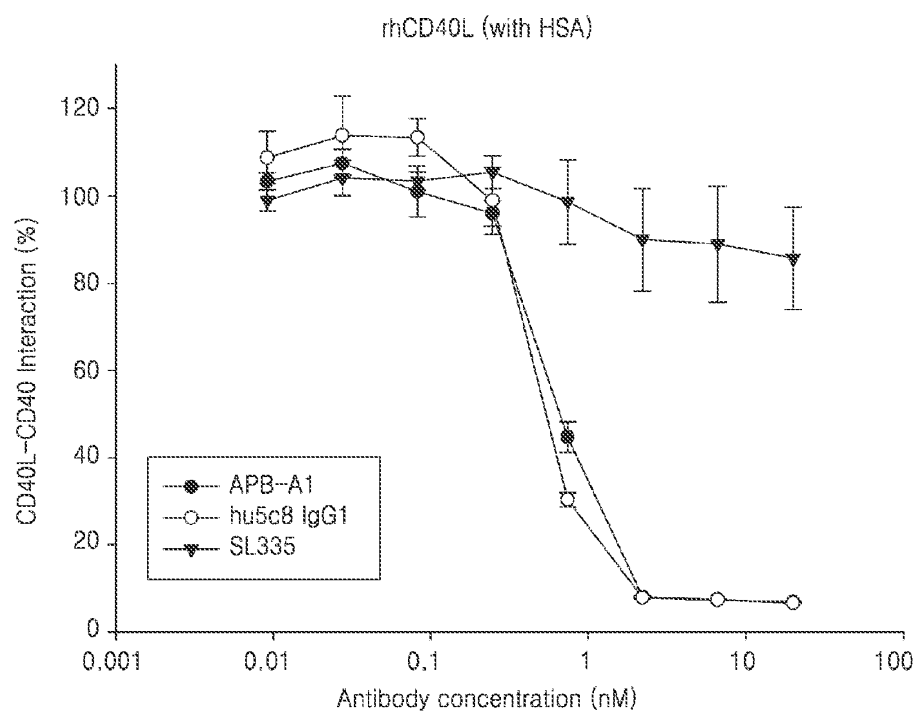


FIG. 8D

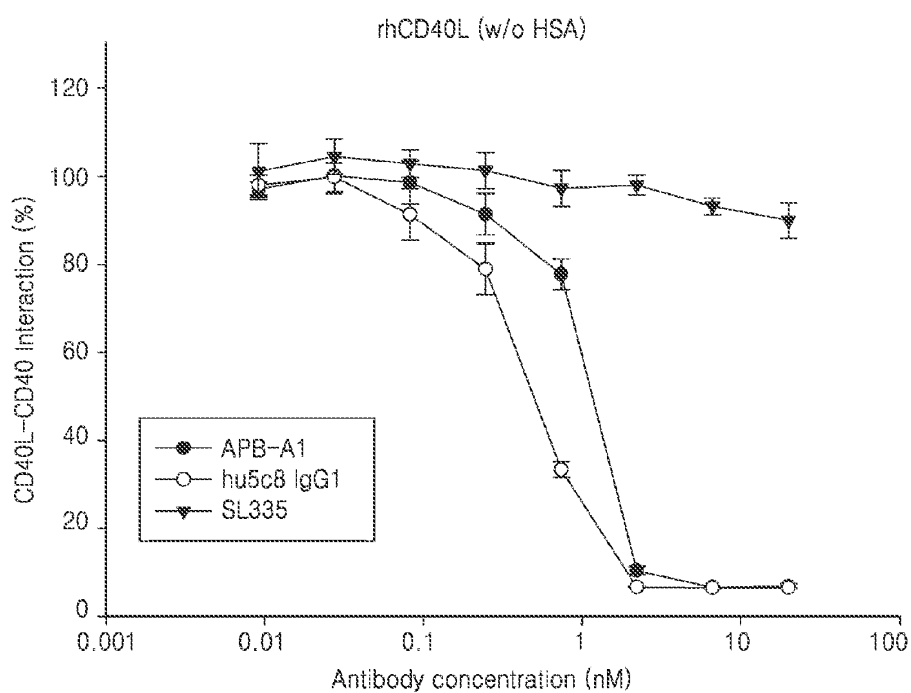


FIG. 9A

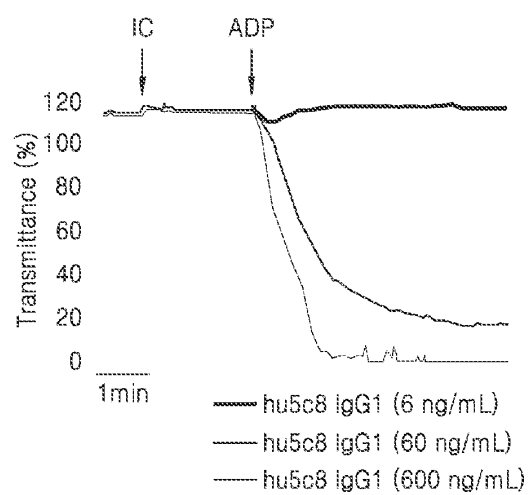


FIG. 9B

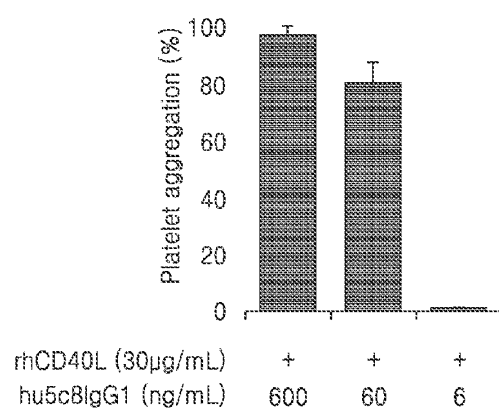


FIG. 9C

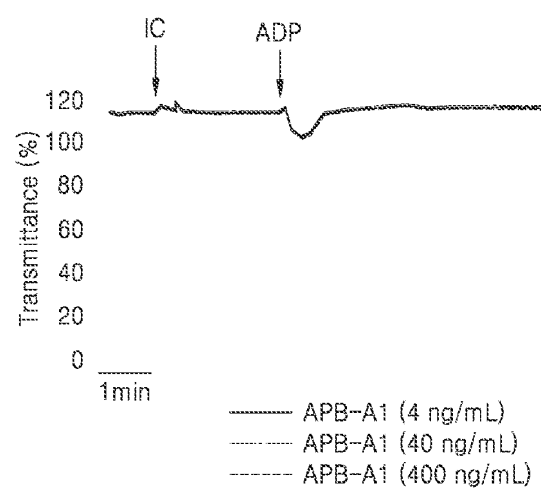


FIG. 9D

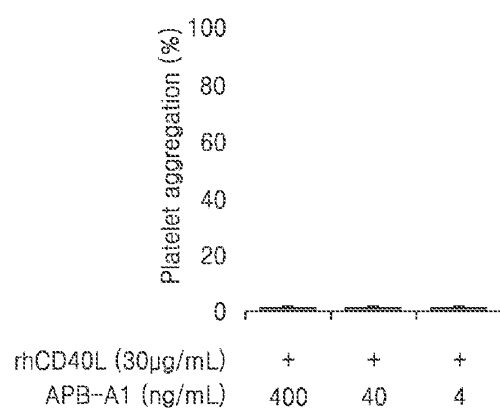


FIG. 10

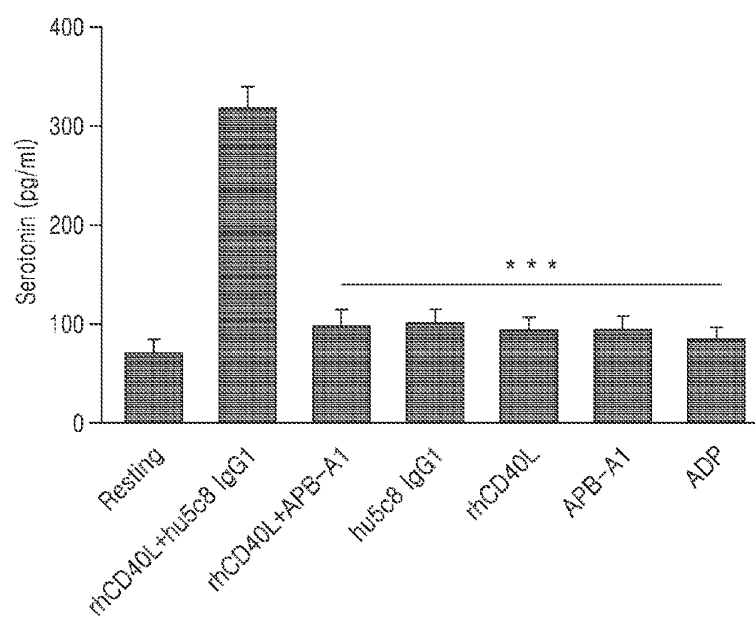


FIG. 11

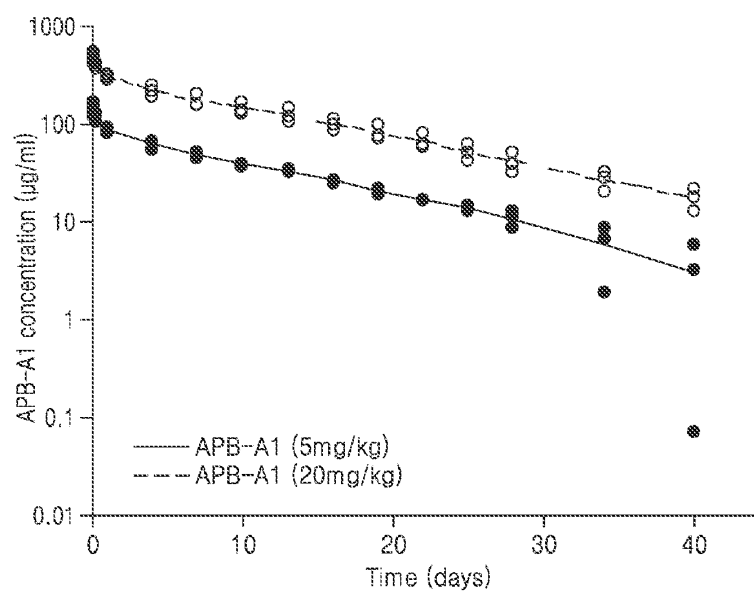


FIG. 12A

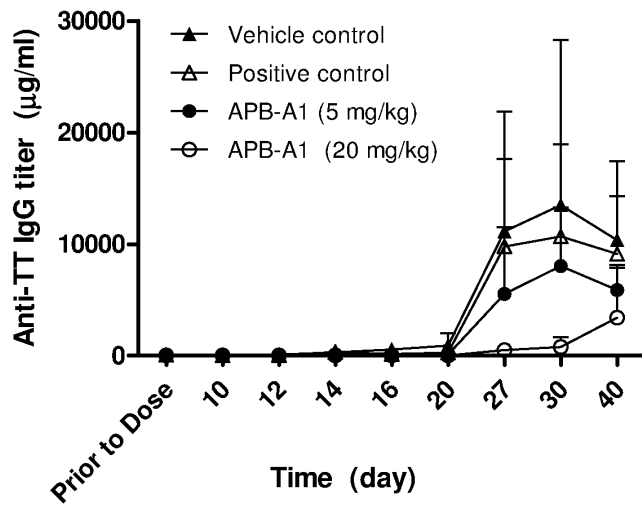


FIG. 12B

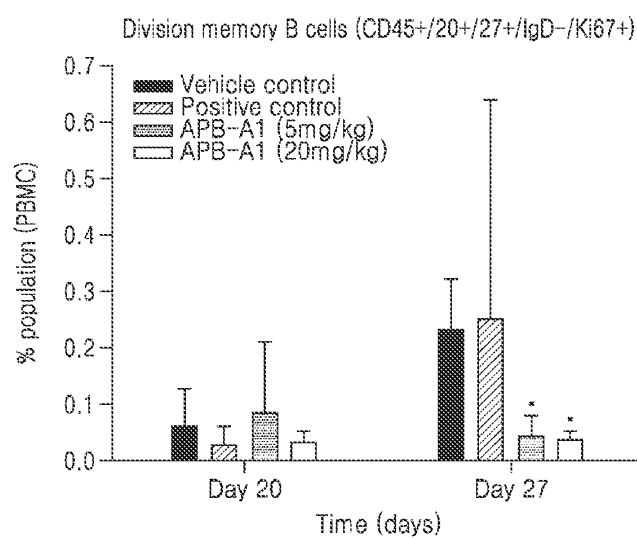


FIG. 13A

APB-B1a

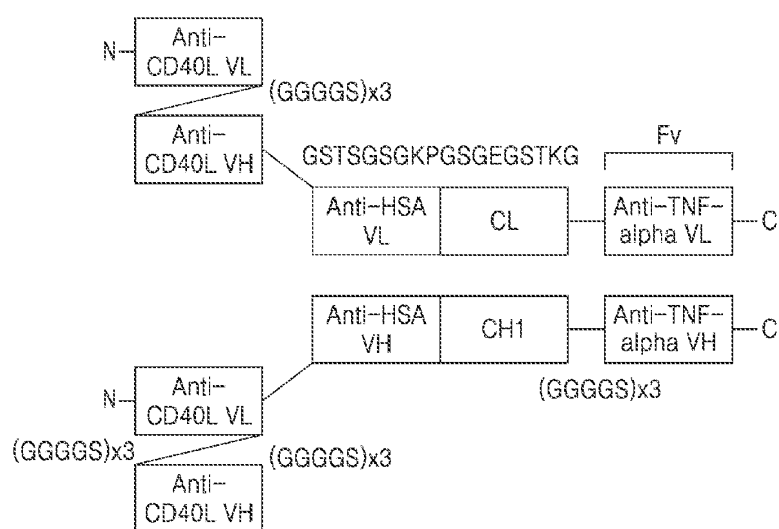


FIG. 13B

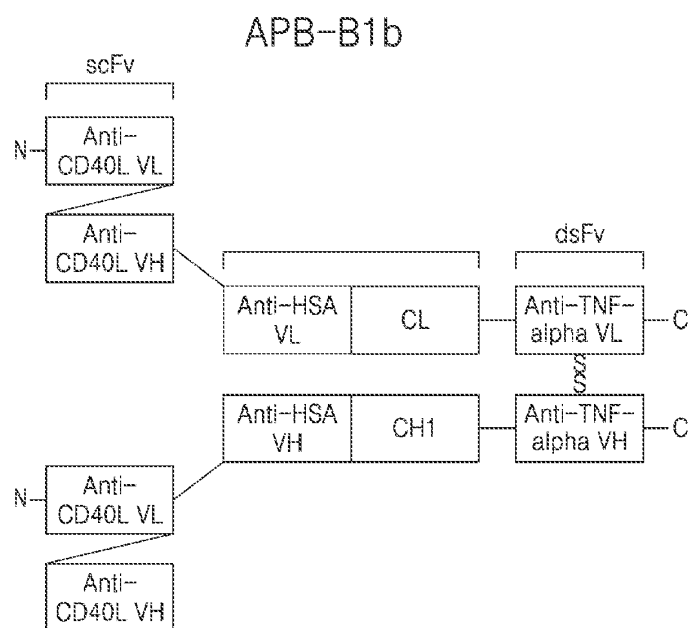


FIG. 13C

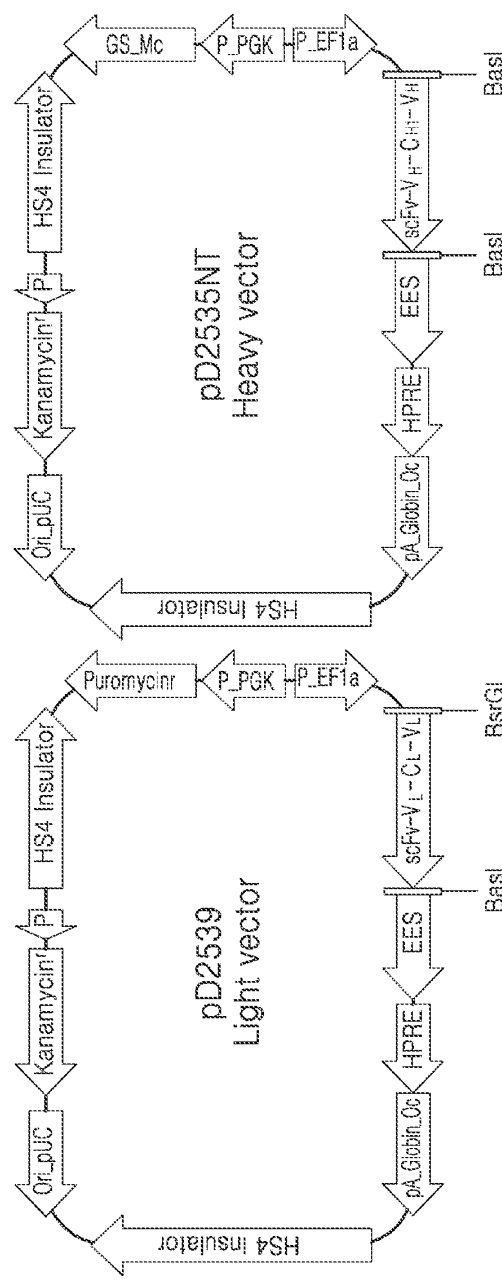


FIG. 14

APB-B1 heavy chain

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10      20      30      40      50      60      70      80
DIVLTQSPAT LSVSPGERAT ISCRASQRVS SSTYSYMHVY QOKPGQPPKL LIKYASNLES GVPARFSGSG SGTDFTLTIS

90      100     110     120     130     140     150     160
SVEPEDFATY YQHSWEIIP TFGQGTKLEI KPGGGSGGGG GSGGGGQVQ LVQSGAEVVK PGASVKLSCK ASGYIFTSYY

170     180     190     200     210     220     230     240
MYWVKQAPGQ GLEWIGEINP SNGDTFNEK FSKATLTVD KSASTAYMEL SSLRSEDVAV YYCTRSDGRN DMDSWGQGITL

250     260     270     280     290     300     310     320
VTVSSGGGGS GGGGSGGGGS QVQLVQSGGS PVKPGGSLRL SCAASGFMFR AYEMNWRQA PGXGLEWVSS ISSSGRIHY

330     340     350     360     370     380     390     400
ADSVKGRFTI SRDAKNSLY LQMSLRAD TAVYYCARET VMAGKALDYV GQGLTVTVSS ASTKGPSVFP LAPSSKSTSE

410     420     430     440     450     460     470     480
GTAALGCLVK DYFPEPVTS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VESSLGQTQ YICNVNHRPS NTKVDKVDSP

490     500     510     520     530     540     550     560
KSSGGGGSGG GGGGSGGGSV QLVESGGGIV QPGGSLRLSC AASGYVPTDY GMNWRQAPS KSLRWMCWIN TYIGEPYAD
C

570     580     590     600     610
SVKGRFTESL DTSKSTAYLQ ENSLRADTA VYFCARGYS YAMDIWGQGT LVIVSS

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APB-B1 light chain

```

10      20      30      40      50      60      70      80
DIVLTQSPAT LSVSPGERAT ISCRASQRVS SSTYSYMHVY QOKPGQPPKL LIKYASNLES GVPARFSGSG SGTDFTLTIS

90      100     110     120     130     140     150     160
SVEPEDFATY YQHSWEIIP TFGQGTKLEI KRGGGSGGGG GSGGGGQVQ LVQSGAEVVK PGASVKLSCK ASGYIFTSYY

170     180     190     200     210     220     230     240
MYWVKQAPGQ GLEWIGEINP SNGDTFNEK FSKATLTVD KSASTAYMEL SSLRSEDVAV YYCTRSDGRN DMDSWGQGITL

250     260     270     280     290     300     310     320
VTVSSGSTSQ SCKPGSGGGS TEGDIVLTQS PGTLSLSPGE TATLSRASQ SVGSNLAWYQ QKPGQAPRIL IYGASTGATG

330     340     350     360     370     380     390     400
VPAFEGSRK GTDFTLTIS LQPEDFATY CQYYSEFLAK TFGQGTQLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL

410     420     430     440     450     460     470     480
KNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSL NTLTSLKADY EKHKVYACEV THQGLSSPVT KSFNPGESGG

490     500     510     520     530     540     550     560
GGSGGGSGGG GGSIDIQMTQS PSSLSASVGD RVTITCKASQ NVGTNVAWYQ QKPGKAPKAL IYSASFLEYG VPIRFSGSGS

570     580     590     600
GTDFTLTIS LQPEDFATY CQYNIYPLT FGGGTKVEIK R
C

```

FIG. 15A

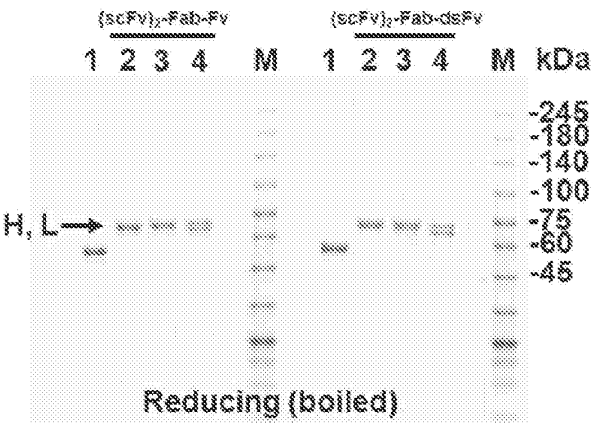


FIG. 15B

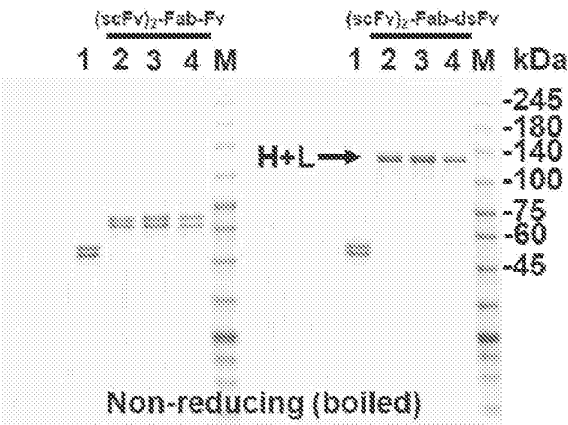


FIG. 15C

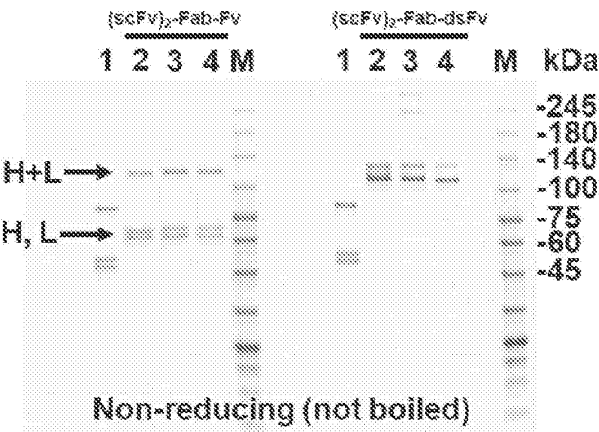


FIG. 15D

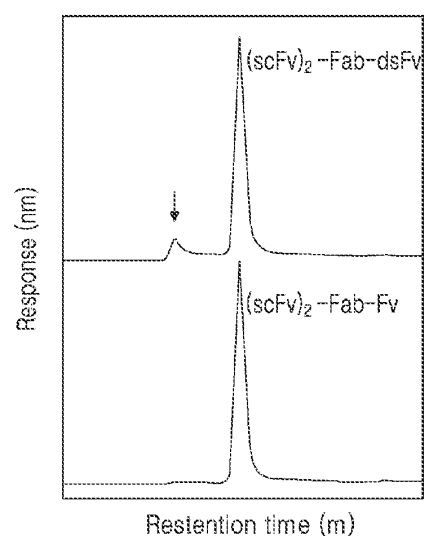


FIG. 16A

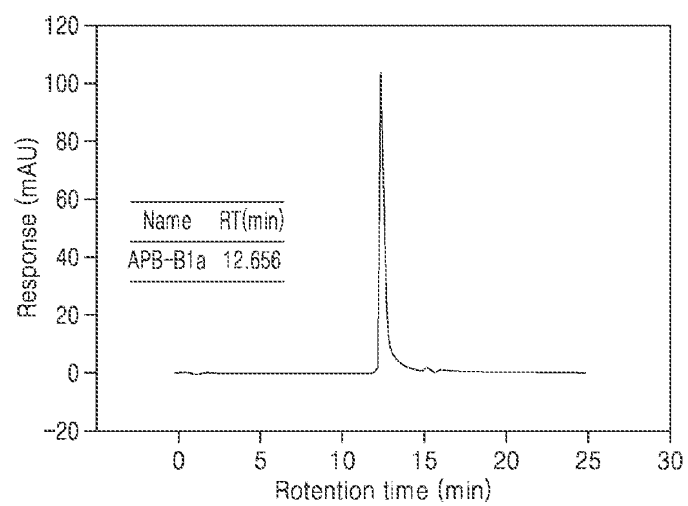


FIG. 16B

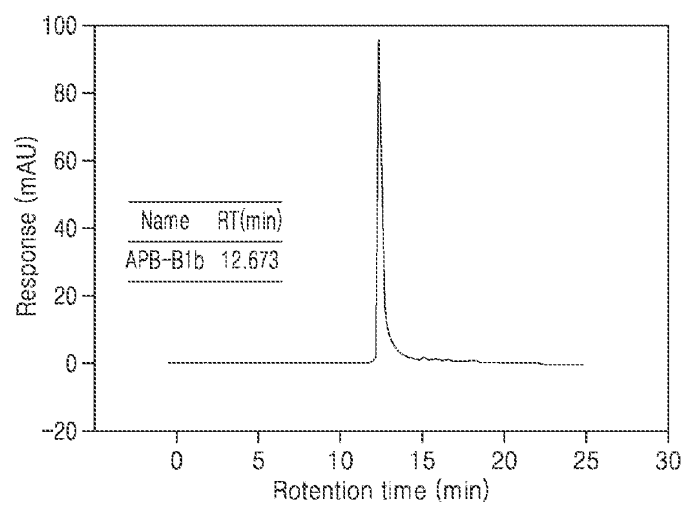


FIG. 17

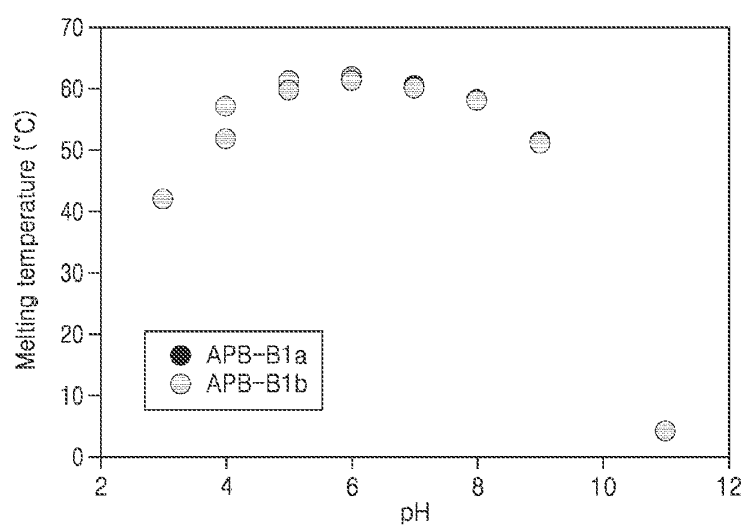


FIG. 18A

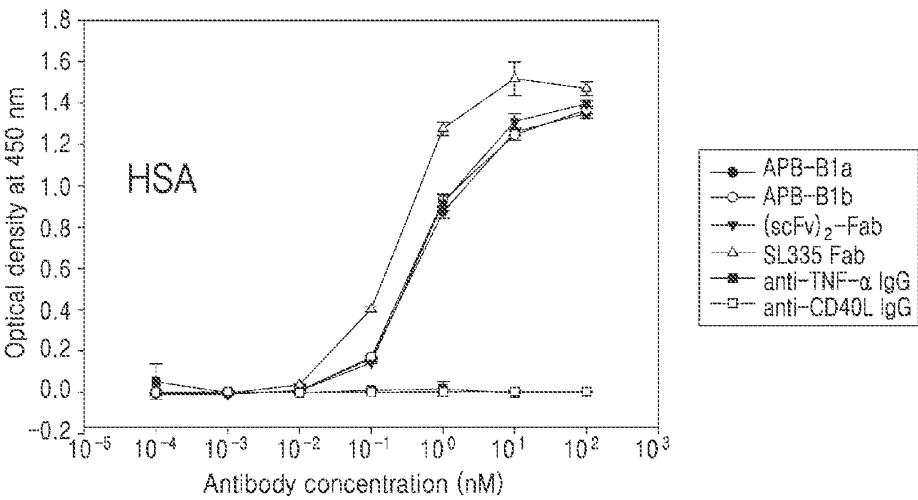


FIG. 18B

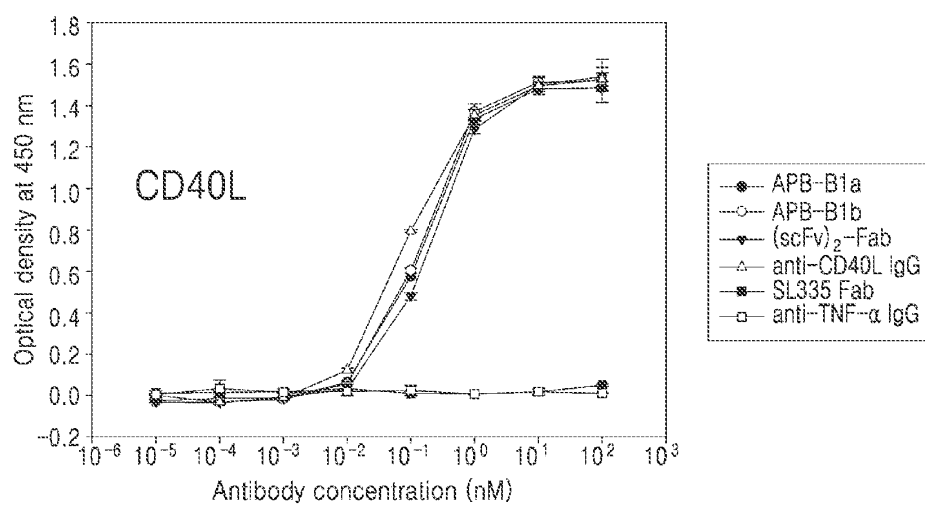


FIG. 18C

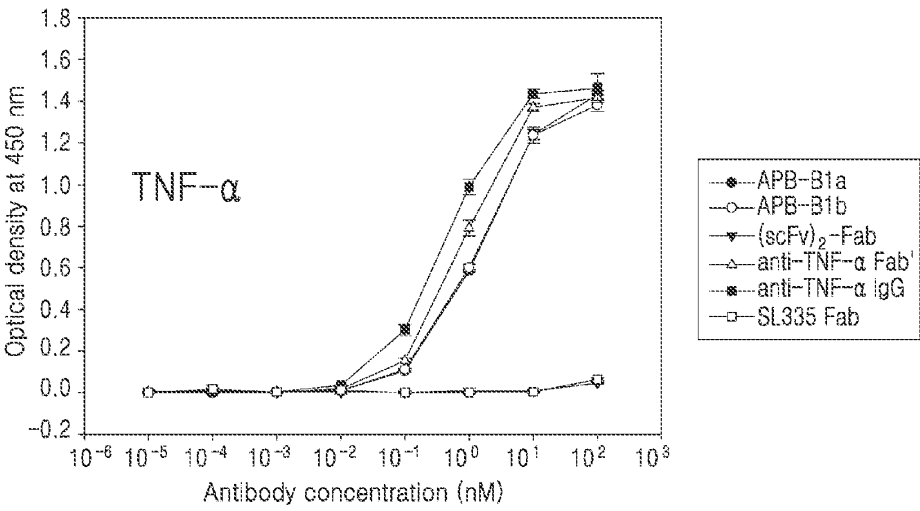


FIG. 19

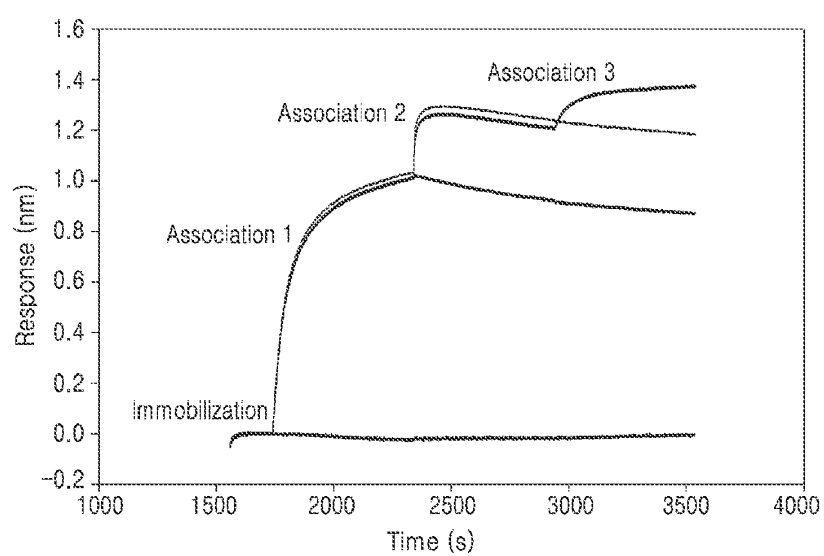


FIG. 20

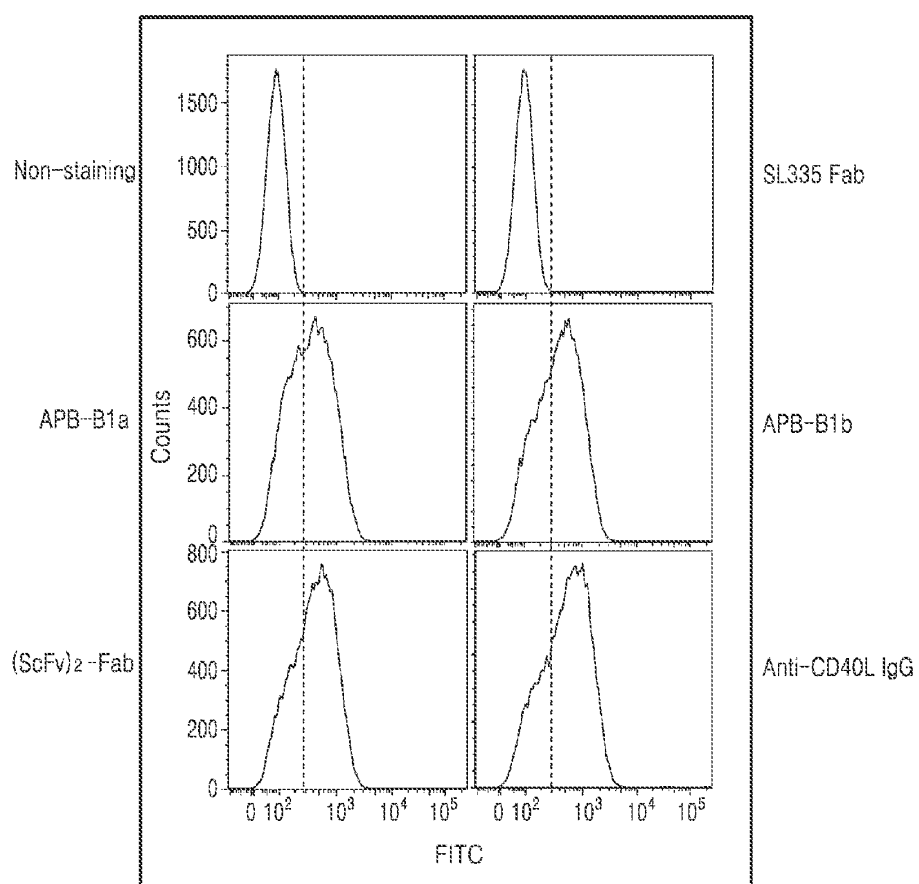


FIG. 21

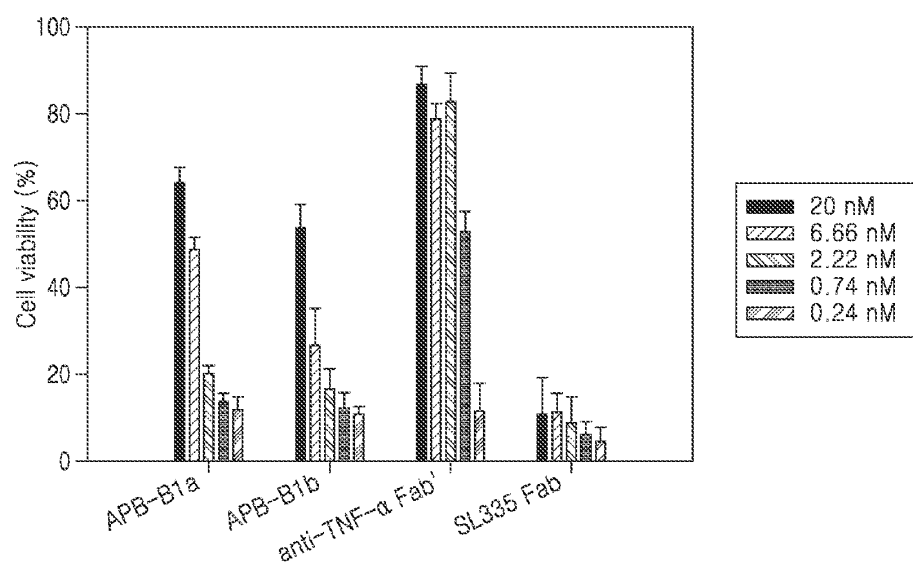


FIG. 22A

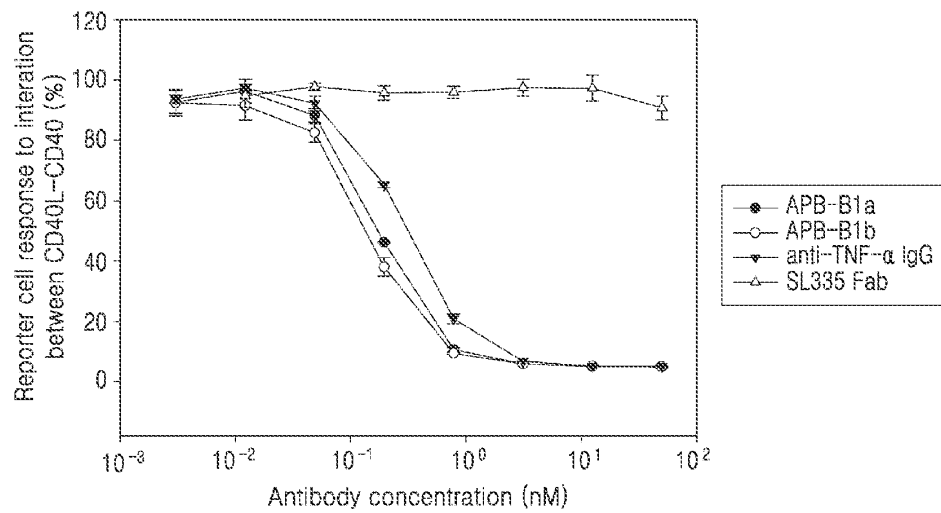


FIG. 22B

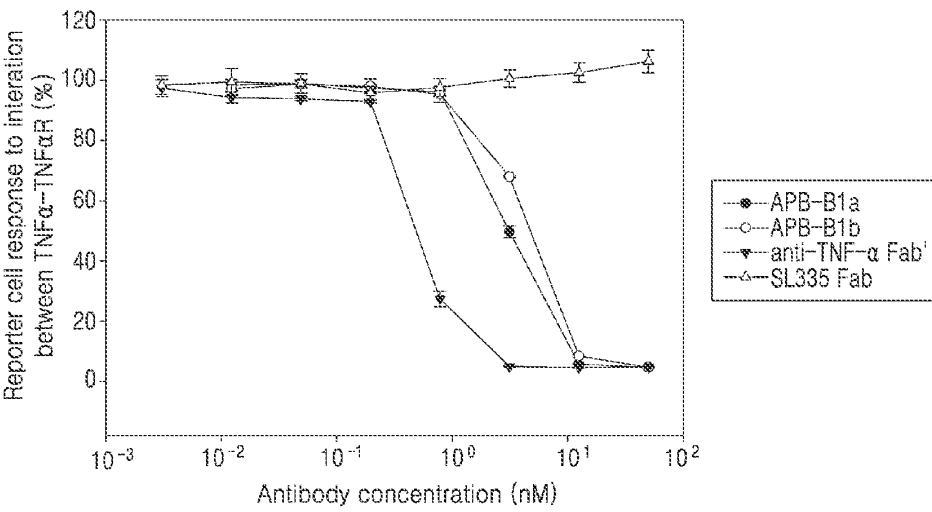


FIG. 22C

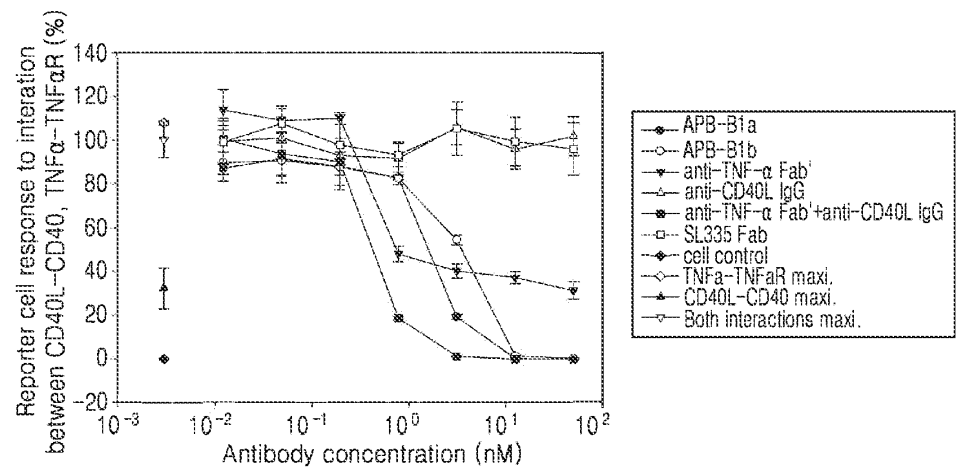


FIG. 23

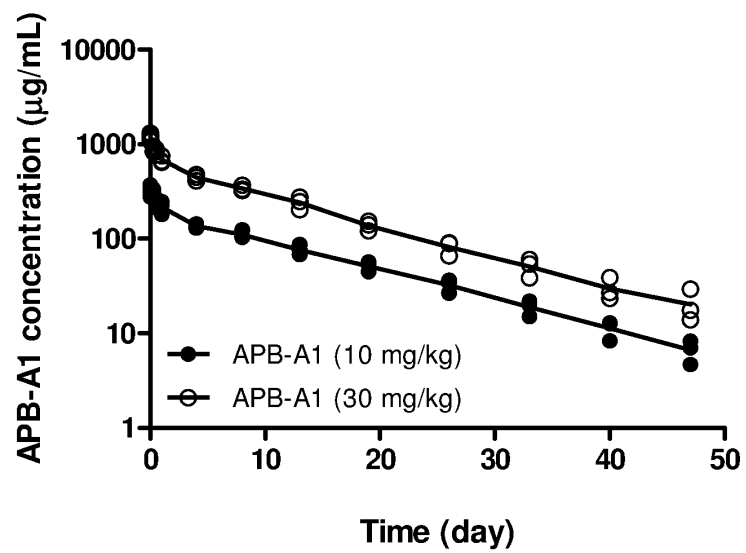


FIG. 24A

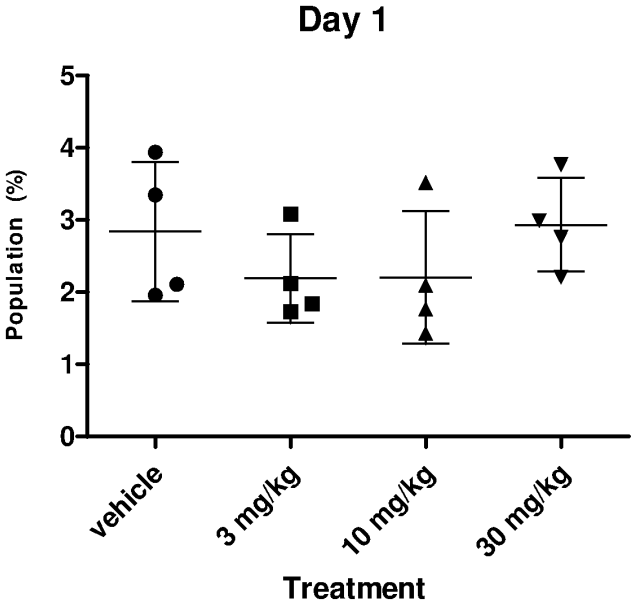


FIG. 24B

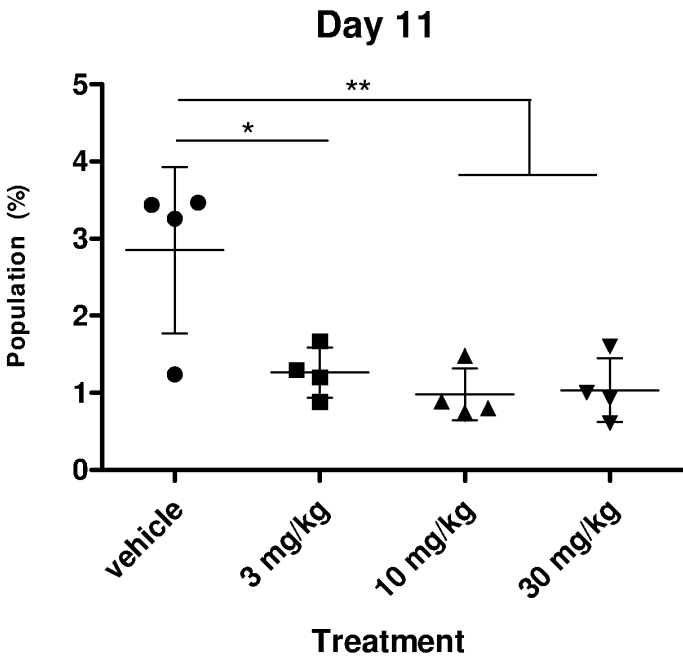


FIG. 25

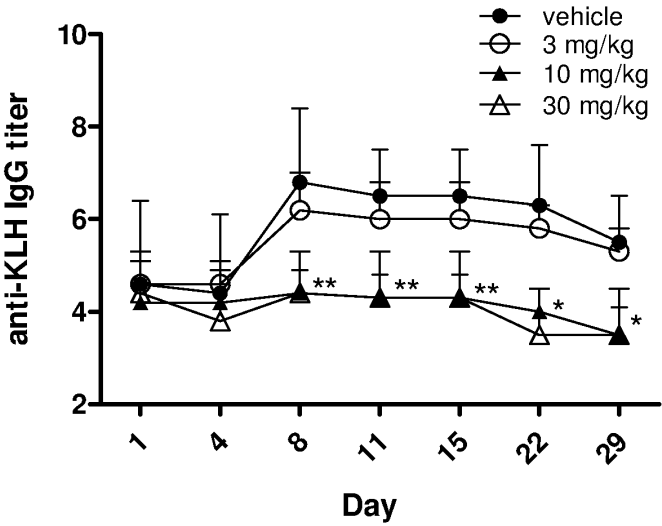


FIG. 26

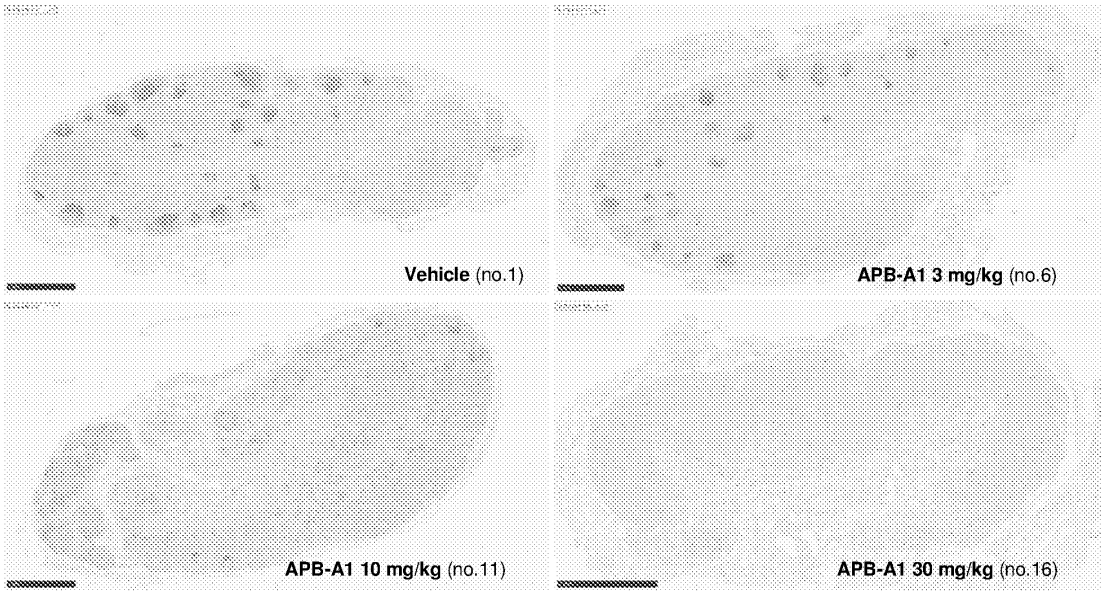


FIG. 27

