

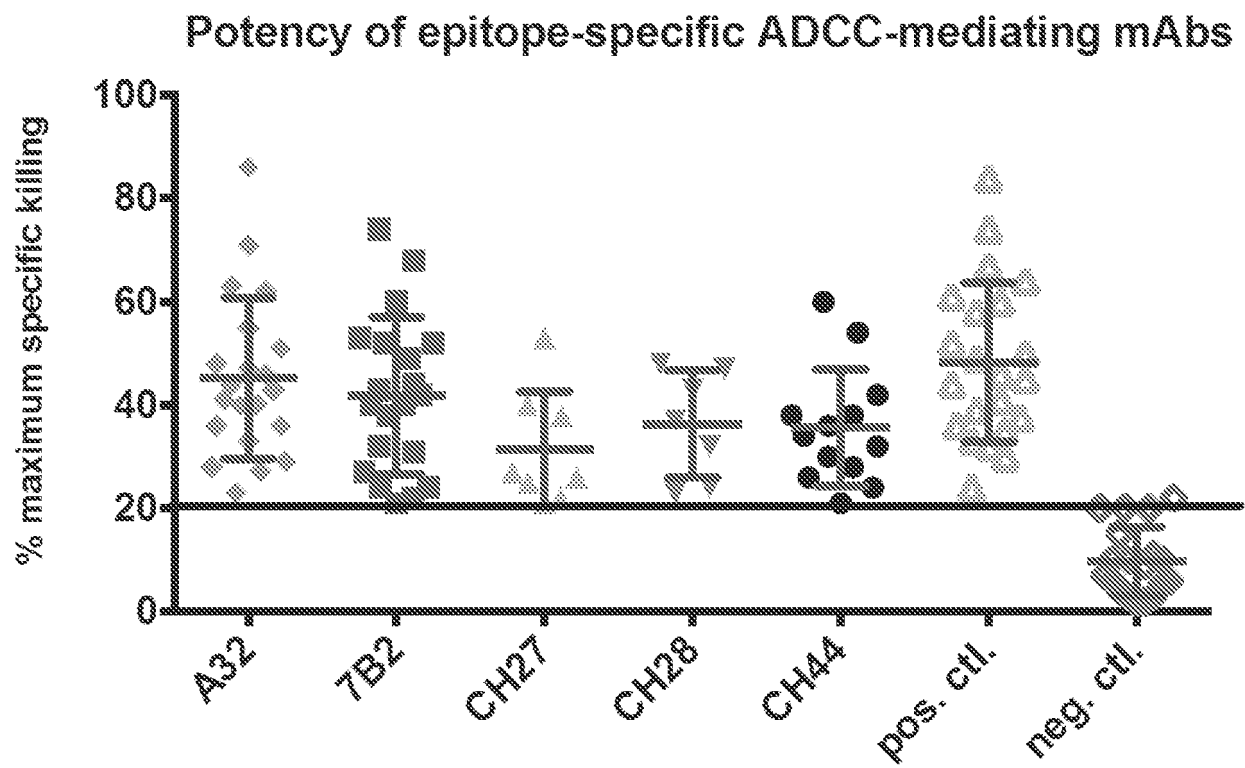


Figure 1

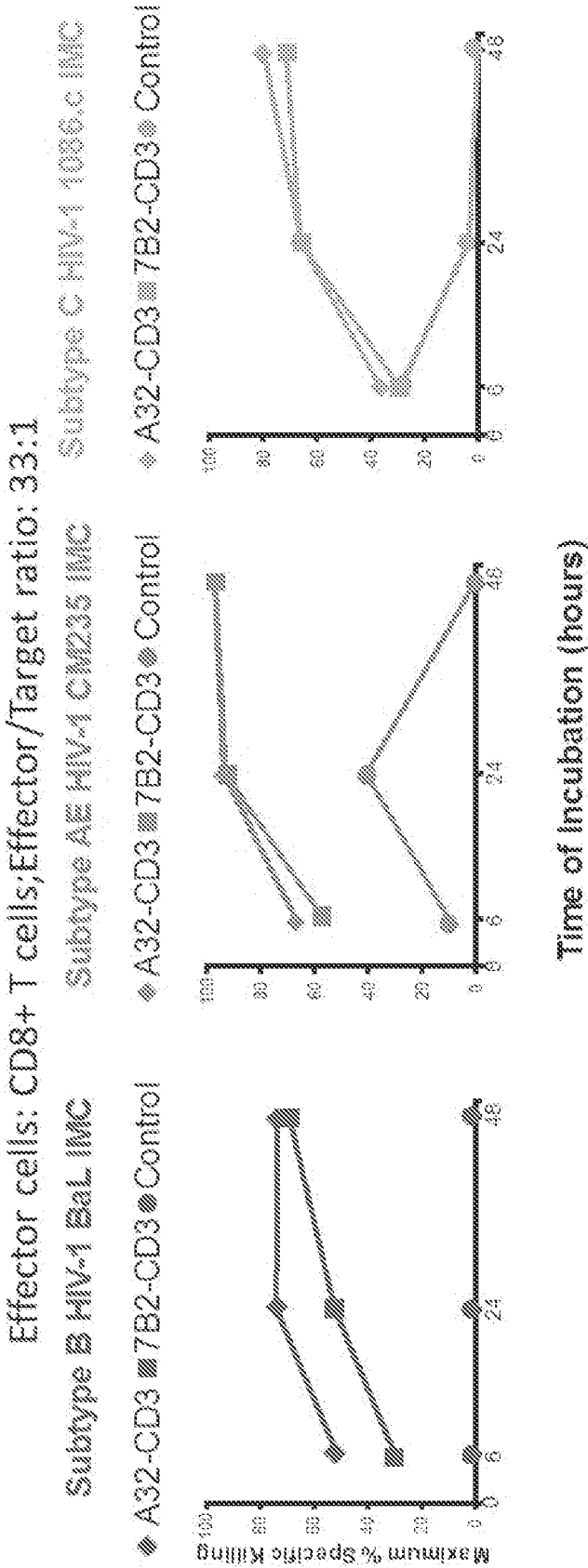


Figure 2

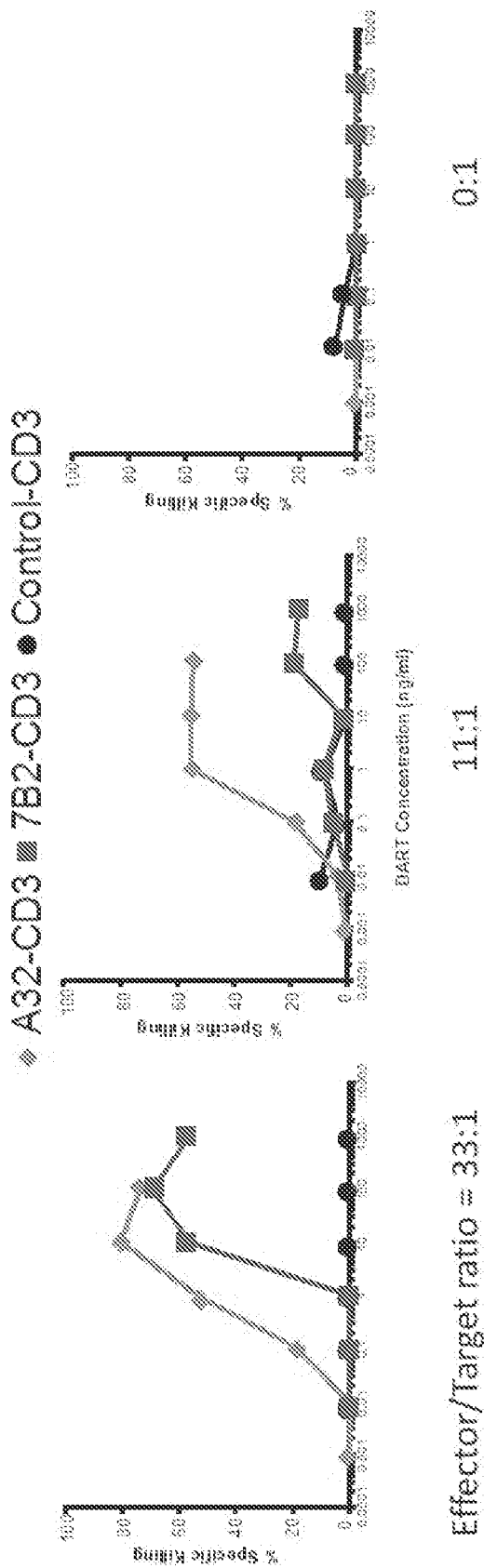


Figure 3

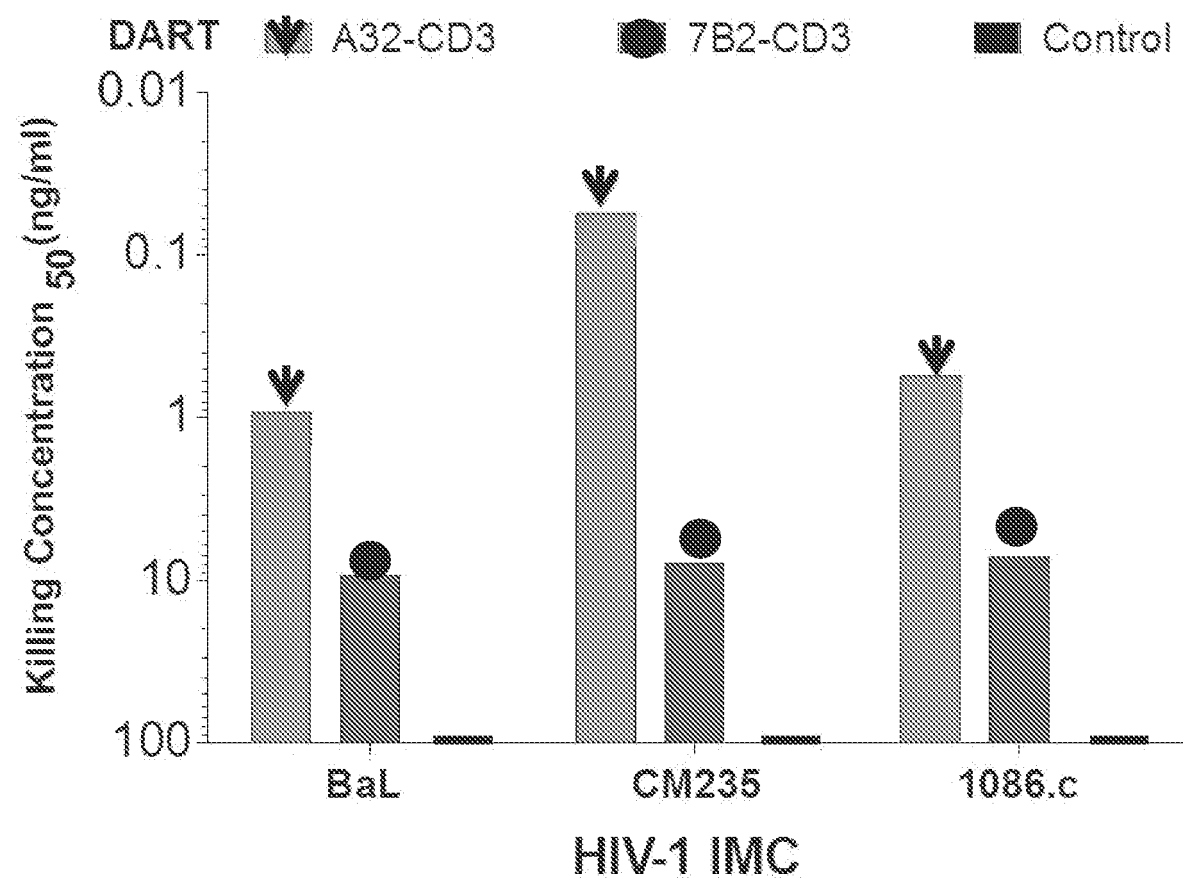


Figure 4

CDR1 is bold.CDR2 is bold green/underlined.CDR3 is bold red/italicized.

mAb CH27: original cDNA sequences

>H004021_CH27_HC SEQ ID NO: 57

GAGGTKCAGCTGGTGGAGTCTGGGGGTGGCTTGGTCCAGCCGGGGGGGTCCCTGAGACTCTCTTGTGC
AGCCTCTGGATTTCAGCGTCAGCTACGACTATATGGCCTGGGTCCGCCAGGCTCCAGGGAAGGGACTGG
AGTGGGTCTCTATTATTTATGGTGGTGGTAGTCCATATTACGCAGACTCTGTGAAGGGCCGATTCCGC
ATCTCCAGAGACACCTCCAGGAATACACTGGATCTTCAAATGAGCAGCCTGAGACGTGACGACAGCGG
TGTTTACTTCTGTGCGAGGGGACTCGCCTCGCTCTTCGATCTCTGGGGCCGAGGCACCCTGGTCACTG
TCTCGTCAGCATCCCCGACCAGCCCCAAGGTCTTCCCGCTGAGCCTCGACAGCACCAGC

>K003061_CH27_KC SEQ ID NO: 58

GAAATTGTGTTGACRCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGAGAAACAGCCACCCTCTCCTG
CAGGGCCAGTCGGCGTGTAAACGTCAACTACCTAGCCTGGTATCAACACAGACCTGGCCAGAGTCCCA
GGCTCCTCATGTACGGTCCTTACAACAGGCCCCACTGGCATCCCGGGCAGGTTCTGGGGCGAGTGGTCT
GGGCCACTCTTCACTCTCAACATCGACAGACTGGAGCCTGTTGATCGAGCAGTCTATTACTGTCTACA
CTTTGACTCTGATACTTCTTCGTGGGCGTTCGGCCGAGGGACCAAGGTGGAGGTCAAACGAACGTGGG
CTGCACCATCTTCTTCACTCTTCCAAAAACATCTGAAGCAGTTTTAATCTCAACTTCTCTCATCAAAC
CCGGGGGGGGGAGATCAAGACCGATGGGGCCAGCCACGGTTGGTTGGACCGGCACGGGGGGCCGGCCCCA
GCGAAAAAAGGGGGAGACCCAGAGTGTGAGGGCACTAGAGGGGTGGGGACAGACCCTTCTGGGGACT
TGAAGGGGGAGAGTCGCCCCACATGCCCAACCGGGGGCCACCACCGGGCGGTTTCACGGACGTTAT
TAACGGGCCCGGAATTTTTTCCCCCGTGTTCATACAAGCCCCCCCCCTGGAGGGGGGAAACAAACCCCGC
CAAAAAGGGGCCTTTATTCTCAAACCAACAACGCGCGCCCCCAAACCCTCCAAAATTTTTCCCCCAA
ACCAAACACAAACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

Figure 5

mAb CH27: cleaned DNA sequences

>H004021_CH27_HC_clean SEQ ID NO: 59

GAGGTKCAGCTGGTGGAGTCTGGGGGTGGCTTGGTCCAGCCGGGGGGGTCCCTGAGACTCTCTTGTGC
 AGCCTCTGGATTCAGCGTC**AGCTACGACTATATGGCCT**TGGGTCCGCCAGGCTCCAGGGAAGGGACTGG
 AGTGGGTCTCTA**TTA**TTT**ATGGTGGTGGTAGTCCATATTACGCAGACTCTGTGAAGGGCCGATTTCGCC**
 ATCTCCAGAGACACCTCCAGGAATACACTGGATCTTCAAATGAGCAGCCTGAGACGTGACGACAGCGG
 TGTTTACTTCTGTGCGAGGGGACTCGCCTCGCTCTTCGATCTCTGGGGCCGAGGCACCCTGGTCACTG
 TCTCGTCAGCA

>K003061_CH27_KC_clean SEQ ID NO: 60

GAAATTGTGTTGACRCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGAGAAACAGCCACCCTCTCCTG
 CAGGGCCAGTCGGCGTGT**TAAACGTCAACTACCTAGCCT**TGGTATCAACACAGACCTGGCCAGAGTCCCA
 GGCTCCTCATG**TA**CG**GTCC**TT**ACAACAGGCC**CC**ACTGGC**ATCCCGGGC**CAGGTTCTGGGGCGAGTGGTCT**
 GGGCCACTCTTCACTCTCAACATCGACAGACTGGAGCCTGTTGATCGAGCAGTCTATTACTGTCTACA
 CTTT**GA**CT**CTGA**FA**CTTCTTC**GTGGGCG**CTTCGGCCGAGGGACCAAGGTGGAGGTCAAACGA**

mAb CH27: amino acid sequences

>H004021_CH27_HC_AA SEQ ID NO: 61

EVQLVESGGGLVQPGGSLRLSCAASGFSV**SYDYMA**WVRQAPGKLEWVS**IIYGGGSFY**YADSVKGRFA
 ISRDTSRNTLDLQMS**SLR**RDDSGVYFC**ARGLASL**FDLWGRGTLTVSSA

>K003061_CH27_KC_AA SEQ ID NO: 62

EIVLTQSPGTLSLSPGETATLSCRASRRV**NVNYLA**WYQHRPGQSPRLLMYGFY**NRFTGI**PGRFWGEWS
 GPLFTLNIDRLEPVDRVYYC**LNFDSDTSSNA**FGRGTKVEVKR

Figure 5 cont.

mAb CH28: original cDNA sequences

>H004367__CH28__HC SEQ ID NO: 63

CAGGTGCAGCTGGTRCAGTCTGGGACTTAATCCTCTACACACACCCATATCTCCTACGCTCCATAACG
GACCTACTTTGCACTAATCCTTAGGACACGCCGACTCCTCCTCGGGGTAAACTCTATAAAGATGACAA
AAGATAGTAACCTAGGAATAGAACAATGCAATATACTAAAGAACTGATCCTTGACACTGCTACCGCCT
AGGTATTCGCAATATAACAAATATCATCATCCGACCCAAGTATATGCTGGATTTGTTAAAATAGTCAG
AGAACTATATCTATCTGCAATGGCTTACAGCTAAGCCAGAATCTACAATAAAAAACAACAAGCGGGAAC
GCTTCCAAAGAAAAAAACCATATACTCAGGTCTGTTCAACCATCTCAATCACCGACTTTTCACACATTTT
TTCCCAGGCTTACAAAGATATTCAGGGTTTTTTTTTTCCTTTTCCATTCCAGAGGAACCAAGTGCAGC
GTGTCAGTAGGGGGGTAAGGAAAATAAGCCTGGTTTCCTCAGTGTGTCTCTCTGGCAAGTCTTGGGGCG
CCTCCTTTAGAAATAATCTCACCCCAGCCCCCGCCACCTCCAGGGAATGGACGAGTAGTCGAGACAA
ATCTTCCCCCTTATGTTAGAAGAAACAACCAACCCAGATAAAATGCCGCGGAAGCGTCACATTTCTCC
CAAACCTCAACCTATATCGCATCTAACAGGGGGATAAAGCAGCTCAAAAAAAGACACGGCGGCCTGTATG
TGGGAGAGATCGGTTTCTCTCCTTACAGAACGGAGACCCCCGCGAATTAAAAATGGGGCCAAGAGAAA
AGAGTTAATTTTTCTTCTGGGTATGTGATGGGGGGGGAGAATAATCTGCGCACCAGACCACAGGGTAG
CTGCGTACGTCTCGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACAGCGTCAGGAACGACC
AGATGGCCTGGGTCCGCCAGGCTCCAGGGAAGCGACTGGAGTGGGTCT

>K003331__CH28__KC SEQ ID NO: 64

GAAATTGTGTTGACRCAGTCTCCAGGCACCCTGTCTTGTCTCCAGGGGAGAGAGCCACCCTCTCCTG
CAGGGCCAATCGGCGGATTGACATGAACGCCCTTGGCCTGGTACCAGCACCGATCTGGCCAGGCTCCCA
GGCTCCTCACCCATGGTGTCTATAACAGGGGCCACTGGCATCCCAGACAGGTTCAAGTGGCTATTGGTCT
GGGCCAGAGTTCACCCTCGTCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTCTATTACTGTGTACA
CTTTCTCTACGAAAATCCAGCGTGGGCGTTTCGGCCGAGGGACCAAGATAGAGGTCAAGCGAACTGTGG
CTGCACCATCTGCTCACATCTTCCAACCATATGATGAGCACTTGAAATCTGAAACTGCCTCATCACCC
CTGGCGGGGAAAAACAAGAACGGTGGGGGGCGCCACAGGTGCCAAAAACTTTATGTGCTCCGGGCAAA
AGCCCCCGTGGAATTTTCATGAAAAAGGGGTACCCATTAGTAGACCGCAAAATGCCGGGGCCAAATCTCC
TAAATAACAGAGGTAGAATTAACCAAACAGATGTCCAAAGAACTTTGCTGGAACACCGTAAGCGGTAT
CAAAGAGGAGGGGGGAGAGAACCAGGGGGGGCCCTGCCGGATATATATCTGTAAACAGCCGGGCCAATG
GATTTCTCCCCCTGTGGGCCCTAAAAAAGGGGGTGTCTTAAACCCACAAAAAAGGGAAAAACGG
TGTCCTCGGGAACACACCTTTCTCCCAATATTATTTGCGCGGGGAAAAAAGAAAAACAAAAA
AACCC

Figure 5 cont.

mAb CH28: cleaned DNA sequences

>H004367__CH28__HC__clean SEQ ID NO: 65

GAGGTGCAGCTGGTGGAGTCTGGGGGTAGCTGCGTACGTCTCGGGGGGTCCCTGAGACTCTCCTGTGC
 AGCCTCTGGATTTCAGCGTC**AGGAACGACCAGATGGCCT**GGGTCCGCCAGGCTCCAGGGAAGCGACTGG
 AGTGGGTCTCTATTATTAAAGATGGTGGCTAGTCCATACTACGCAGACTCTGTGAAGGGCCGCTTCGCC
 ATGTCCAGAGACACCTCCAAGAATACAGTGTTTCTTCAGATGAACAGCCTGAGACGTGACGACACAGC
 TGTTTATTTCTGTSCGAGGGGGATCGCCTCAFTCTTCGATGTCTGGGGCCGTGGCACGCTGGTCGCTG
 TCTCGTCAGCA

>K003331__CH28__KC__clean SEQ ID NO: 66

GAAATTGTGTTGACRCAGTCTCCAGGCACCCTGTCTTGTCTCCAGGGGAGAGAGCCACCCTCTCCTG
 CAGGGCCAATCGGCGGATT**GACATGAACGCCCTTGGCCT**TGGTACCAGCACCGATCTGGCCAGGCTCCCA
 GGCTCCTCACCCATGGTGTCTATAACAGGGGCCACTGGCATCCAGACAGGTTTCAGTGGCTATTGGTCT
 GGGCCAGAGTTTACCCTCGTCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTCTATTACTGTGTACA
 CTTTCTCTACGAAAATCCAGCGTGGGCGTTTCGGCCGAGGGACCAAGATAGAGGTCAAGCGA

mAb CH28: amino acid sequences

>H004367__CH28__HC__AA SEQ ID NO: 67

EVQLVESGGSCVRLGGSLRLSCAASGFSV**RNDQMA**WVFPQAPGKRLEWVSI**INDGASFPYADSVKGRFA**
 MSRDTSKNTVFLQMNSLRDDTAVYFC**ARGIASFFD**VWGRGTLVAVSSA

>K003331__CH28__KC__AA SEQ ID NO: 68

EIVLTQSPGTLISLSPGERATLSCRANRR**DMNALAWYQ**HRSGQAPRL**LTNGVYN**EA**ATGIF**DRFSGYWS
 GPEFTLVISRLEPEDFAVYYCV**NHFLYENP**AWAFGRGTKIEVKR

Figure 5 cont.

mAb CH44: original cDNA sequences

>H004016__CH44__HC SEQ ID NO: 69

GAGGTKCAGCTGGTGGAGTCTGGGGGTGGCGTGGTCCACCCTGGGGGGTCCCTGAGACTCTCCTGTGC
AGCCTCTGGATTCAGCGTCAGTCACGACTTCATGGCCTGGATCCGCCAGGCTCCAGGAAAGGGACTGG
AGTGGATCTCTATCATATATAACACTGGTTCTCGATACTACTACGCAGACTCTGTGAAGGGCCGCTTC
GCCCTCTCCAGAGATACGTCCAACAACACACTGATTCTTCACATGAGCGGCCTGAGACGTGACGACAC
GGCTATTTATTTCTGTGCCAGGGGAGTCGCCTCGTTCTTCGAATTGTGGGGCCGTGGCACCCCTGGTCA
CTGTCTCGTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGC

>K003056__CH44__KC SEQ ID NO: 70

GAAACGACACTCAGCAGTCTCCAGCCATCCTGTCTGTGTCTCCAGGGGAAACCGCCACCCTCTCCTG
CAGGGCCAGTCGCCGTGTTGACATGAACGGCCTCGCCTGGTACCAACACAGGCCTGGCCAGGCTCCCA
GGCTCCTCATGCATGGTGTTTATAATAGGGCCGCCGGCATCTCAGGCAGGTTCACTGGCAGTTGGTCT
GGGCCAGTCTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGGAGTCTATTACTGTCAACA
CTTTTACTATGAGACTTCAGCGTGGGCGTTCGGCCGAGGGACCAGGGTGGAGGGCAAACGAACTGTGG
CTGCACCATCTTCTCCTATCTTCCAAAAAACAACCTCCCAATGACAGCTGTAAATGTAAACATAACTG
TGGCACAATCCATCAGCATCCGCCGCGGAAGGGCGAGCAAAGGGCCCCCGCCGCCCGCCCGGGGGGG
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CCCCCCCCCCCCCCCCCCCCCCCC

Figure 5 cont.

mAb CH44: cleaned DNA sequences

>H004016__CH44__HC__clean SEQ ID NO: 71

GAGGTKCAGCTGGTGGAGTCTGGGGGTGGCGTGGTCCACCCTGGGGGGTCCCTGAGACTCTCCTGTGC
 AGCCTCTGGATTTCAGCGTC**AGTCACGACTTCATGGCCT**TGGATCCGCCAGGCTCCAGGAAAGGGACTGG
 AGTGGATCTCTATCATATATAACACTGGTTCTCGATACTACTACGCAGACTCTGTGAAGGGCCGCTTC
 GCCCTCTCCAGAGATACGTCCAACAACACACTGATTCTTCACATGAGCGGCCTGAGACGTGACGACAC
 GGCTATTTATTTCTGTGCCAGGGGAGTCGCCTCGTTCTTCGAATTGTGGGGCCGTGGCACCCCTGGTCA
 CTGTCTCGTCAGCC

>K003056__CH44__KC__clean SEQ ID NO: 72

GAAACGACACTCACGCAGTCTCCAGCCATCCTGTCTGTGTCTCCAGGGGAAACCGCCACCCTCTCCTG
 CAGGGCCAGTCGCCGTGTT**GACATGAACGGCCTCGCCT**TGGTACCAACACAGGCCTGGCCAGGCTCCCA
 GGCTCCTCATGCATGGTGTFFATAATAGGGCCCGCCGGCATCTCAGGCAGGTTCACTGGCAGTTGGTCT
 GGGCCAGTCTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGGAGTCTATTACTGTCAACA
 CTTTCTACTATGAGACTTCAGCGTGGGCGTTTCGGCCGAGGGACCAGGGTGGAGGGCAAACGA

mAb CH44: amino acid sequences

>H004016__CH44__HC__AA SEQ ID NO: 73

EVQLVESGGGVVHPGSLRLSCAASGFSV**SHDFMA**WIPQAPGKGLEWIS**IIYNFGSKYYYADSVKGRF**
 ALSRDTSNNTLILHMSGLRRDDTAIFYC**ASGVASFFEL**WGRGTLVTVSSA

>K003056__CH44__KC__AA SEQ ID NO: 74

ETTLTQSPAILSVPGETATLSCRASRRV**DMNGLAWY**QHRPGQAPRL**LMHGVYNRAAGISGRFTGSWS**
 GPVFTLTISRLEPEDFGVYYC**QNFYYETS**AWAFGRGTRVEGKR

Figure 5 cont.

>A32VH

CAGGTGCAGCTGTGTGCGGAGTCCGGCCAGGACTGTTGAAGCCCTTCACAGACCTTGTCCCTTCAGTTCGCACTGTCT
TCTGGTGGCTCCAGCAGTAGTGGCTGCTCACTACTGGAGTTGGATCCGCCAGTACCCAGGGAAGGGCCTGGAG
TGGATTGGTTACATCCATTACACTGGGAACACTTACTACAACCCGTCCCTCAAGAGTCCGAATTACCATATCA
CAACACACGCTCTGAGAACCAGTTCTCCCTGAAGCTCAACTCTGTGACTGTTGCAGACACGGCCGCTCATTTAC
TGTGCGAGAGGGACCCGCTCTCCGGACACTACGGAATGCTTTTGATATTTGGGGCCAGGGGACCAAGGGTCACC
GTCTCTTCA (SEQ ID NO:75)

>A32VL

CAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGGSTCTCCTGGACACTCAGTCACCATCTCTCTGCACTGGA
ACCAGCAGTGACCTTGGTGGTTATAACTATGTTTCTGTGATCCAACACACCACCCAGGCCAAAGCCCCCAAACTC
ATAATTTCTGAGGTCAATAACCGGCCCTCAGGGSTCCCTGATCGTTTCTCTGGCTCCAAGTCTGGCAACACG
GCCTCCCTGACCGTCTCTGGGCTCCAGGCTGAGGATGAGGCTGAATATTACTGCAGCTCATACACAGACATC
CACAATTTCTCTTCCGGCCGAGGGACCAAGCTGACCGTCTTA (SEQ ID NO:76)

>A32VE

QVQLCGVGPGLVKPSQTLSELSCTVSGGSSSGAHYNSWIRQYPGKGLEWIGYIHYSGNTYYNPSLKSRLTIS
QHTSENQPSLKLNSVTIVADTAVYYCARGTRLETLRNAPDIWQQGTRVTVSS (SEQ ID NO:77)

>A32VL

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLIISEVNNPSPGVPPDRFSGSKSGNT
ASLTVSGLQAEDEAEYYCESYTDIHNPFVFGGTELTVL (SEQ ID NO:78)

Figure 6

>7B2VH

CAGTTCAGCTGCTGTCAGTCTGGGGGAGGCGTTTCAAGCCTGGAGGGTCCCTGAGACTCTCTCTG
TGAAGCCTCTGGAATTCACATTTACTGAATATTACATGACTTGGGTCCGCCAGGCTCCTGGGAAGG
GGCTGGAGTGGCTTGGGTATATTAGTAAGAATGGTGAATATTCAAAATATTACCGTCTCTCAAAC
GGCGGGTTTCAACCATCTCCAGAGACAACGCCAAGAACTCAGTGTCTTCTGCAATTGGACAGACTGAG
CGCCGACGACACGGGCGGTCTATTACTGTGCGAGAGCGGACCGATTACATACTTCTCTGAATTAC
TCCAATACATTTTGGACCTCTGGGGCCAGGAGAGCCCGGGTCACCGTCTCTCTCG (SEQ ID NO:79)

>7B2VH

METDTLLLLWVLLLLWVPGSTGQVQLVQSGGVSFKPGGSLRLSCEASGFTFTEYYMTWVRQAPGKG
LEWLAYLSKNGEYSKYSPSSNGRPTISRDNAKNSVFLQDRLSADDTAVYYCARADGLTYFSELL
QYIFDLWGQGARVTVSS (SEQ ID NO:80)

>7B2VK

METDTLLLLWVLLLLWVPGSTGDETTLTQSPDSLAVSPGERATINCKSSQTLLYSSNNEHSIAWYQQ
RPGQPPKLLLLYWAMRLSGVDFRPSGSGSGTDEFTLTINNLAEDVAIYYCHQVSSHPPTFGHGR
VELR (SEQ ID NO:81)

>7B2VK

GAAACGACACTCACCGAGTCTCCAGACTCCCTGGCTGTGTCTCCGGGCGAGAGGGCCACCATCCA
CTGCAAGTCCAGCCAGACTCTTTTGTACAGCTCCAACAATAGACACTCCATTGCTTGGTAACCAAC
AGAGACCAGGACAGCCTCCTAAATTACTCCTTTATTGGGCATCTATGCGGCTTTCCGGGGTCCCT
GACCGATTCASTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAACAACCTGCGAGGCTGA
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GGGTGAGCTCASA (SEQ ID NO:82)

Figure 7

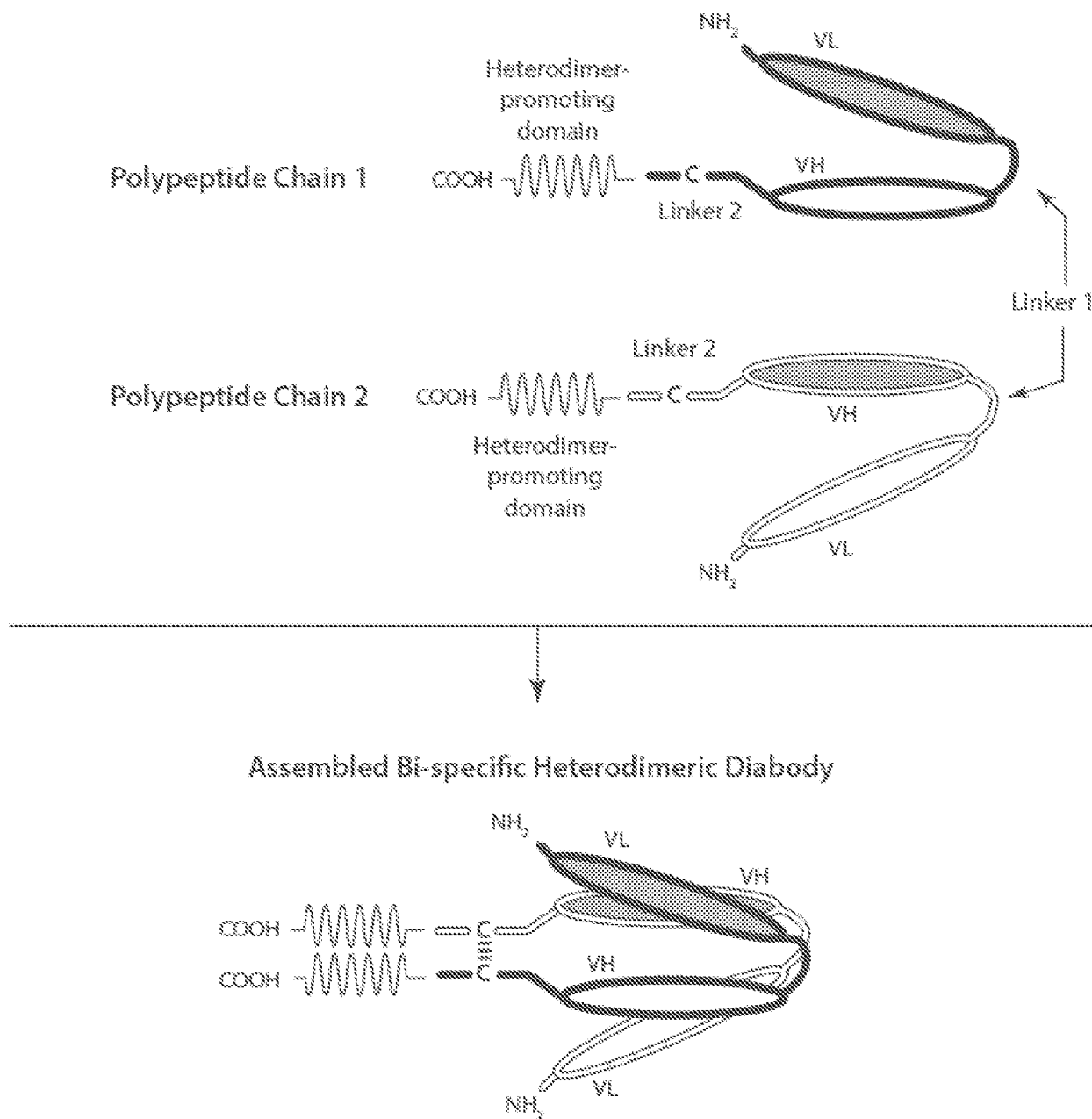


Figure 8A

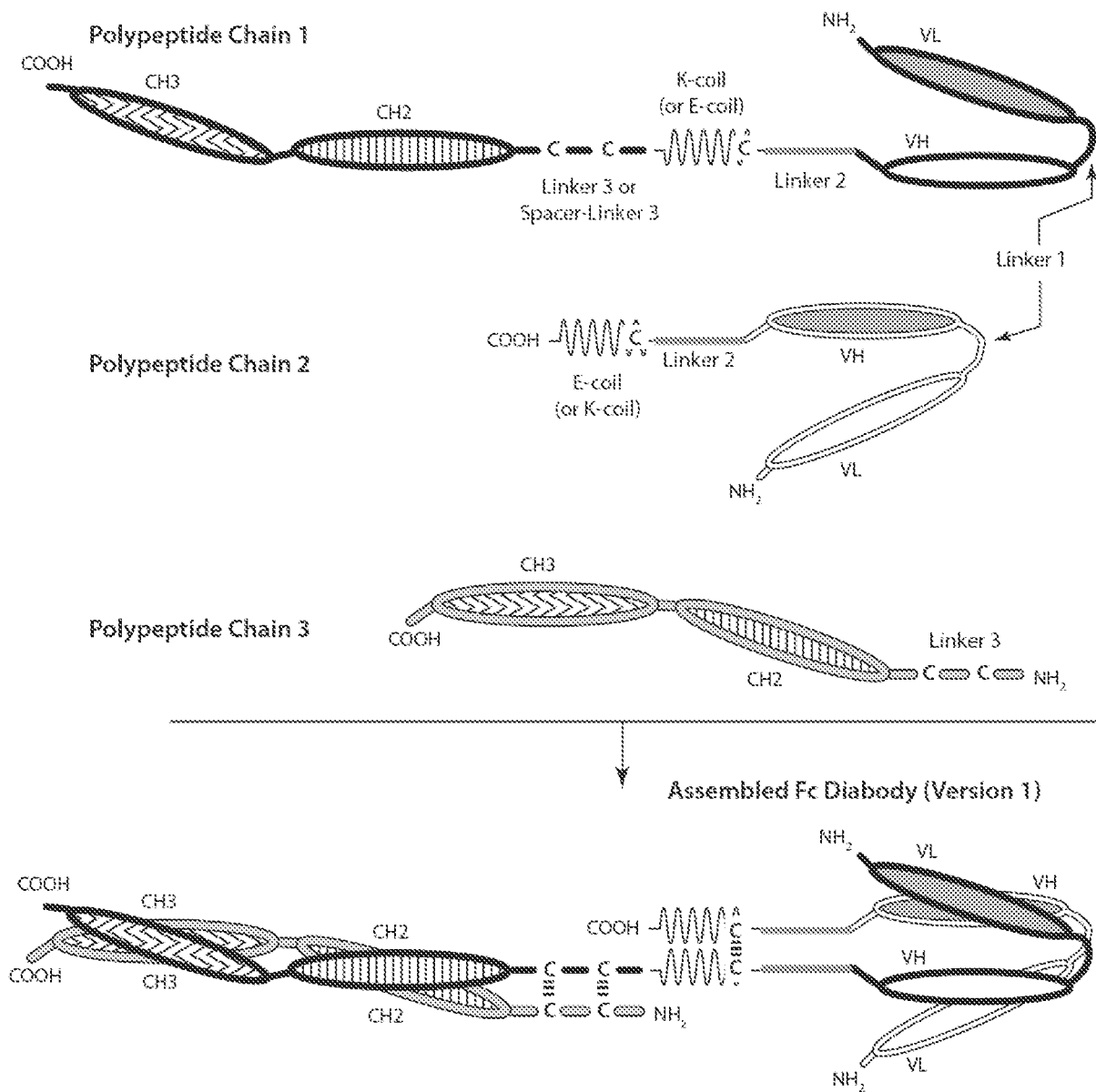


Figure 8B

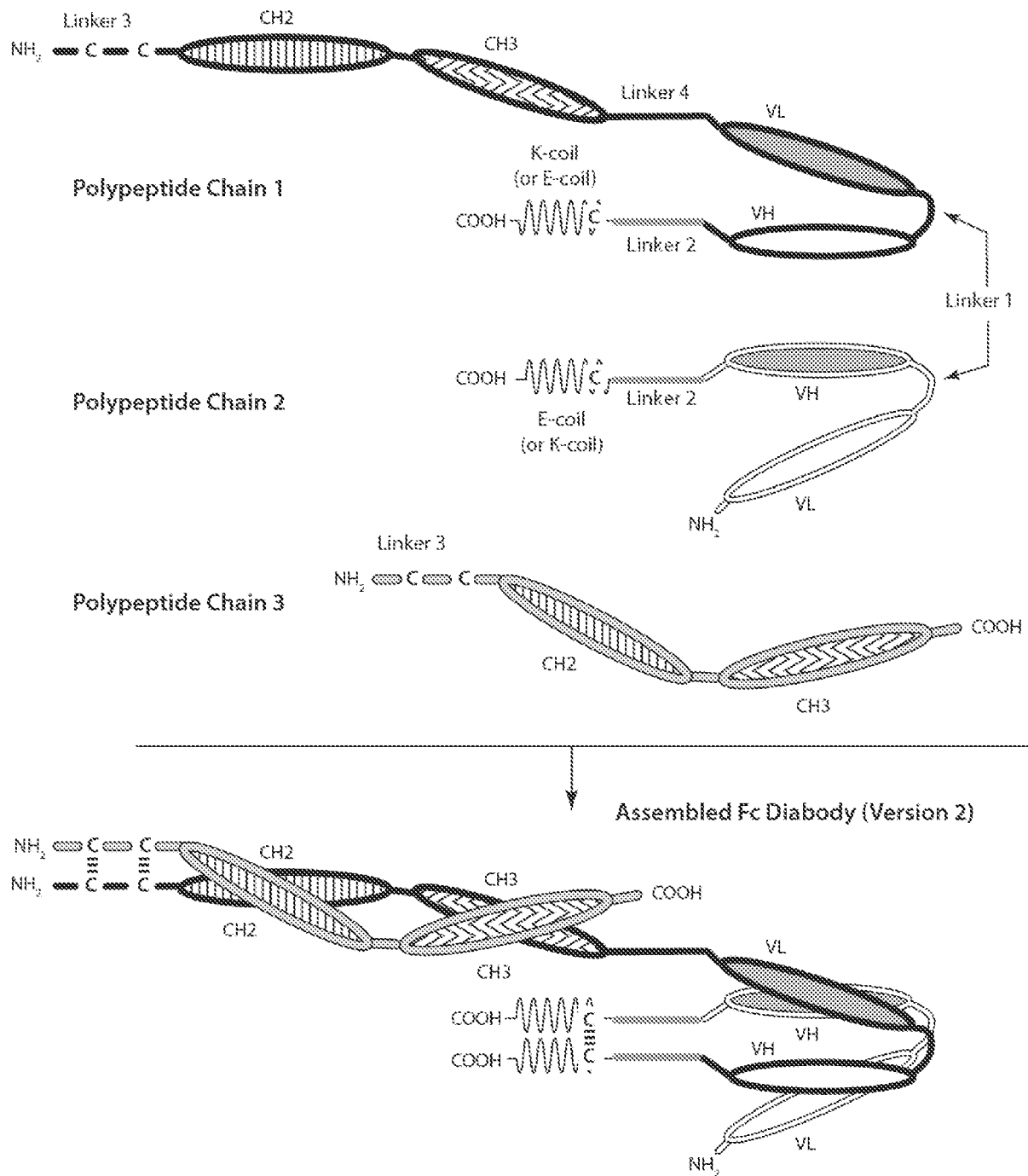


Figure 8C

Sequences

SEQ ID NO: 1

GGGSGGGG

SEQ ID NO: 2

GGCGGG

SEQ ID NO: 3

GVEPKSC

SEQ ID NO: 4

VEPKSC

SEQ ID NO: 5

GFNRGEC

SEQ ID NO: 6

FNRGEC

SEQ ID NO: 7

EVAALEKEVA ALEKEVAALE KEVAALEK

SEQ ID NO: 8

KVAALKEKVA ALKEKVAALK EKVAALKE

Figure 9

SEQ ID NO: 9

QSALTQPPSA SGSPGQSVTI SCTGTSSDVG GYNYVSWYQH HPGKAPKLII
 SEVNNRPSGV PDRFSGSKSG NTASLTVSGL QAEDEAEYYC SSYTDIHNHV
 FGGGTKLTVL GGGSGGGGEV QLVESSGGGLV QPGGSLRLSC AASGFTFSTY
 AMNWVRQAPG KGLEWVGRIK SKYNNYATYY ADSVKGRETI SRDDSKNSLY
 LQMNSLKTED TAVYYCVRHG NFGNSYVSWF AYWGQGTLLV VSSGGCGGGE
 VAALEKEVAA LEKEVAALEK EVAALEK

SEQ ID NO: 10

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 tcatgcaact ggacttcaag cgatgtgggc gggtacaact atgtgagttg gtaccagcac
 catcccgga aggcacctaa actgatcatt agcgaagtga acaatcgacc aagcggcgtc
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 gcagcctctg gattcacctt cagcacatac gctatgaatt gggtcgccca ggctccaggg
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SEQ ID NO: 11

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 FARFSGSLLG GKAALTITGA QAEDEADYYC ALWYSNLWVF GGGTKLTVLG GGGSGGGGQV
 QLQESGPGLV KPSQTLRLSC TVSGGSSSSG AHYWSWIRQY PGKGLEWIGY IHYSGNTIYN
 PSLKSRITIS QHTSENQFSL KLNSVTVADT AVYYCARGTR LRTLRNAFDI WGQGTLLTVS
 SGGCGGGKVA ALKEKVAALK EKVAALKEKV AALKE

Figure 9 cont.

SEQ ID NO: 12

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 gagaaggteg ccgcacttaa ggaaaaggtc gcagccctga aagag

SEQ ID NO: 13

DIVMTQSPDS LAVSPGERAT IHCKSSQTLL YSSNNRHSIA WYQQRPGQPP KLLLYWASMR
 LSGVPDRFSG SGSGTDFTLT INNLQAEDVA IYYCHQYSSH PPTFGHGTRV EIKGGGSGGG
 GEVQLVESGG GLVQPGGSLR LSCAASGFTF STYAMNWVRQ APGKGLEWVG RIRSKYNNYA
 TYYADSVKGR FTISRDDSKN SLYLQMNSLK TEDTAVYYCV RHGNFGNSIV SWFAYWGQGT
 LVTVSSGGCG GGEVAALEKE VAALEKEVAA LEKEVAALEK

SEQ ID NO: 14

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Figure 9 cont.

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SEQ ID NO: 15

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 PARFSGSLLG GKAALTITGA QAEDEADYYC ALWYSNLWVF GGGTKLTVLG GGGSGGGGQV
 QLVQSGGGVF KPGGSLRLSC EASGFTFTEY YMTWVRQAPG KGLEWLAYIS KNGEYSKYSP
 SSNGRFTISR DNAKNSVFLQ LDRLSADDTA VYYCARADGL TYFSELLQYI FDLWGQGARV
 TVSSGGCGGG KVAALKEKVA ALKEKVAALK EKVAALKE

SEQ ID NO: 16

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 acatgcagat ccagcacagg cgcagtgacc acatotaact acgccaattg ggtgcagcag
 aagccaggac aggcaccaag gggcctgacg gggggtacaa acaaaagggc tccctggacc
 cctgcacggg tttctggaag tctgctgggc ggaaaggccg ctctgactat taccggggca
 caggccgagg acgaagccga ttactattgt gctctgtggt atagcaatct gtgggtgttc
 gggggtggca caaaactgac tgtgctggga gggggtggat ccggcggagg tggacaggtg
 cagctggtgc agtctggggg aggcgttttc aagcctggag ggtccctgag actctcctgt
 gaagcctctg gattcacatt tactgaatat tacatgactt gggtcgcga ggctcctggg
 aaggggctgg agtggcttgc gtatattagt aagaatggtg aatattcaaa atattcacg
 tcctcaaacg gccggttcac catctccaga gacaacgcca agaactcagt gtttctgcaa
 ttggacagac tgagcgccga cgacaaggcc gtctattact gtgcgagagc ggacggatta
 acatacttct ctgaattact ccaatacatt ttgacctct ggggccaggg agcccgggtc
 accgtctcct ccggaggatg tggcgggtgga aaagtggccg cactgaagga gaaagttgct
 gctttgaaag agaaggctgc cgcacttaag gaaaaggctc cagccctgaa agag

Figure 9 cont.

SEQ ID NO: 17

EIVLTQSPGT LSLSPGERAT LSCRANRRID MNALAWYQHR SGQAPRLLTH GVYNRATGIP
 DRFSGYWSGP EFTLVISRLE PEDFAVYYCV HFLYENPAWA FGQGTKLEIK GGGSGGGGEV
 QLVESGGGLV QPGGSLRLSC AASGFTFSTY AMNWVRQAPG KGLEWVGRIR SKYNNYATYY
 ADSVKGRFTI SRDSKNSLY LQMNSLKTED TAVYYCVRHG NFGNSYVSWF AYWGQGTLVT
 VSSASTKGEV AACEKEVAAL EKEVAALEKE VAALEK

SEQ ID NO: 18

gaaatttgtgt tgacgcagtc tccaggcacc ctgtccttgt ctccagggga gagagccacc
 ctctcctgca gggccaatcg gcggattgac atgaacgcct tggcctggta ccagcaccca
 tctggccagg ctcccaggct cctcaccat ggtgtctata acagggccac tggcatcca
 gacaggttca gtggctattg gtctgggcca gagttcacc cgtcatcag cagactggag
 cctgaagatt ttgcagtcta ttactgtgta cactttctct acgaaaatcc agcgtgggag
 ttggccagg ggaccaagct ggagatcaag ggtggaggat ccggcggcgg aggcgaggtg
 cagctggtgg agtctggggg aggccttggtc cagcctggag ggtccctgag actctcctgt
 gcagcctctg gattcacctt cagcacatac gctatgaatt gggtcggcca ggctccaggg
 aaggggctgg agtgggttgg aaggatcagg tccaagtaca acaattatgc aacctactat
 gcgactctg tgaagggtag attcaccatc tcaagagatg attcaaagaa ctactgtat
 ctgcaaatga acagcctgaa aaccgaggac acggccgtgt attactgtgt gagacacggg
 aacttcggca attcttacgt gtcttggttt gcttattggg gacaggggac actggtgact
 gtgtcttcgg cctccaccaa gggcgaagtg gccgcagtgt agaaagaggt tgctgctttg
 gagaaggagg tcgctgcact tgaaaaggag gtcgcagccc tggagaaa

SEQ ID NO: 19

QAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KFGQAPRGLI GGTNKRAPWT
 PARFSGSLLG GKAALTITGA QAEDEADYYC ALWYSNLWVF GGGTKLTVLG GGGSGGGGEV
 QLVESGGGVV HPGGSLRLSC AASGFSVRND QMAWVRQAPG KRLEWVSIIN DGASPPYADS
 VKGRFAMSRD TSKNTVFLQM NSLRDDTAV YFCARGIASF FDVWGRGTLV TVSSASTKGK
 VAACKEKVAA LKEKVAALKE KVAALKE

Figure 9 cont.

SEQ ID NO: 20

caggctgtgg tgactcagga gccctcactg accgtgtccc caggcggaaac tgtgacctg
 acatgcagat ccagcacagg cgcagtgacc acatctaact acgccaattg ggtgcagcag
 aagccaggac aggcaccaag gggcctgac gggggtacaa acaaaagggc tccctggacc
 cotgcacggc tttctggaag tctgctgggc ggaaaggccg ctctgactat taccggggca
 caggccgagg acgaagccga ttactattgt gctctgtggt atagcaatct gtgggtgttc
 gggggtggca caaaactgac tgtgctggga gggggtggat ccggcggagg tggagagggtg
 cagctggtgg agtctggagg tggcgtggtc caccctggag gaagcctgag actctcctgt
 gcagcctctg gattcagcgt caggaaacgac cagatggcct gggtcggcca ggctccaggg
 aagcgactgg agtgggtctc tattattaac gatggtgcta gtccatacta cgcagactct
 gtgaagggcc gcttcgccat gtccagagac acctccaaga atacagtgtt tcttcagatg
 aacagcctga gacgtgacga cacagctgtt tatttctgtg cgagggggat cgccctattc
 ttcgatgtct ggggccgtgg cagcgtggtc actgtctcgt cagcctccac caagggcaaa
 gtggccgcat gtaaggagaa agttgctgct ttgaaagaga aggtcgccgc acttaaggaa
 aaggtcgag cctgaaaga

g

SEQ ID NO: 21

EIVLTQSPAI LSVSPGETAT LSCRASPRVD MNGLAWYQHR FGQAPRLMH GVYNRAAGIS
 GRFTGSWSGP VFTLTISRLE PEDFGVYYCQ HFYYETSAWA FGQGTRLEIK GGGSGGGGEV
 QLVESGGGLV QPGGSLRLSC AASGFTFSTY AMNWVRQAPG KGLEWVGRIR SKYNNYATYY
 ADSVKGRFTI SRDDSKNSLY LQMNSLKTED TAVYYCVRHG NFGNSYVSWF AYWQGQTLVT
 VSSASTKGEV AACEKEVAAL EKEVAALEKE VAALEK

SEQ ID NO: 22

gaaattgtgt tgacgcagtc tccagccatc ctgtctgtgt ctccagggga aaccgccacc
 ctctcctgca gggccagtcg ccgtgttgac atgaacggcc tcgcctggta ccaacacagg
 cctggccagg ctcccaggct cctcatgcat ggtgtttata atagggccgc cggcatctca
 ggcaggttca ctggcagttg gtctgggcca gtcttcactc tcaccatcag cagactggag
 cctgaagatt ttggagtcta ttactgtcaa cacttttact atgagacttc agcgtgggag
 ttcggccagg ggaccaggct ggagatcaaa ggtggaggat ccggcggcgg aggcgagggtg
 cagctggtgg agtctggggg aggcctggtc cagcctggag ggtccctgag actctcctgt

Figure 9 cont.

gcagcctctg gattcacctt cagcacatac gctatgaatt gggtcgcgca ggctccaggg
aaggggctgg agtgggttgg aaggatcagg tccaagtaca acaattatgc aacctactat
gccgactctg tgaagggtag attcaccatc tcaagagatg attcaaagaa ctactgtat
ctgcaaatga acagcctgaa aaccgaggac acggccgtgt attactgtgt gagacacggg
aacttcggca attcttacgt gtcttggttt gcttattggg gacaggggac actgggtgact
gtgtcttcgc cctccaccaa gggcgaagtg gcgcgatgtg agaaagaggt tgctgctttg
gagaaggagg tcgctgcact tgaaaaggag gtcgcagccc tggagaaa

SEQ ID NO: 23

QAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KPGQAPRGLI GGTNKRAPWT
PARFSGSLLG GKAALTITGA QAEDEADYYC ALWYSNLWVF GGGTKLTVLG GGGSGGGGEV
QLVESGGGVV HPGGSLRLSC AASGFSVSHD FMAWIRQAPG KGLEWISIIY NTGSRIYYAD
SVKGRFALS RDTSNNTLILH MSGLRDDTA IYFCARGVAS FFELWGRGTL VTVSSASTKG
KVAACKEKVA ALKEKVAALK EKVAALKE

SEQ ID NO: 24

caggctgtgg tgactcagga gccttcactg accgtgtccc caggcgggaa tgtgacctg
acatgcagat ccagcacagg cgcagtgaac acatotaact acgccaattg ggtgcagcag
aagccaggac aggcaccaag gggcctgac ggggggtacaa acaaaagggc tccctggacc
cctgcacggg tttctggaag tctgctgggc ggaaaggccg ctctgactat tacgggggca
caggccgagg acgaagccga ttactattgt gctctgtggg atagcaatct gtgggtgttc
gggggtggca caaaactgac tgtgctggga ggggtggat ccggcggagg tggagaggtg
cagctggtgg agtctggagg tggcgtgggc caccctggag gaagcctgag actctcctgt
gcagcctctg gattcagcgt cagtcacgac ttcattggcct ggatcaggca ggctccagga
aagggactgg agtggatctc tatcatatat aacactggtt ctcgatacta ctacgcagac
tctgtgaagg gccgcttcgc cctctccaga gatactcca acaacacact gattcttcac
atgagcggcc tgagacgtga cgacacggct atttatttct gtgccagggg agtcgcctcg
ttctttgaat tgtggggccg tggcaccctg gtcactgtct cgtcagcctc caccaagggc
aaagtggccg catgtaagga gaaagttgct gctttgaaag agaaggtcgc cgcacttaag
gaaaaggteg cagcctgaa
agag

Figure 9 cont.

SEQ ID NO: 25

DIVMTQSPDS LAVSPGERAT IHCKSSQTLL YSSNNRHSIA WYQQRPGQPP KLLLYWASMR
 LSGVPDRFSG SGSGTDFTLT INNLAEDVA IYYCHQYSSH PPTFGHGTRV EIKGGGSGGG
 GQVTLRESGP ALVKPTQTLT LTCTFSGFSL STSGMGVGIW RQPPGKALEW LAHIWDDDK
 RYNPALKSRL TISKDTSKNQ VVLTMTNMDP VDTATYYCAQ INPAWFAYWG QGTLVTVSSG
 GCGGGEVAAL EKEVALEKE VAALLEKEVAA LEK

SEQ ID NO: 26

gacatcgtga tgaccagtc tccagaactcc ctggetgtgt ctccggggoga gagggccacc
 atccactgca agtccagcca gactcttttg tacagctcca acaatagaca ctccattgct
 tggtagcaac agagaccagg acagcctcct aaattactcc tttattgggc atctatgagg
 ctttccgggg tcctgacog attcagtggc agcgggtctg ggacagattt cactctcacc
 atcaacaacc tgcaggctga ggatgtggcc atctattact gtcaccaata ttccagtcac
 cccccgacgt tcggccacgg gaccaggggtg gagatcaaag gtggaggatc cggcggcgga
 ggccagggtta cctgagaga gtctggccct gcgctgggtga agccacaca gacctcaca
 ctgacttgta ccttctctgg gttttcaactg agcacttctg gtatgggtgt aggctggatt
 cgtcagcctc cgggaaggc tctagagtgg ctggcacaca tttgggtggga tgatgacaag
 cgtataatac cagccctgaa gagccgactg acaatctcca aggatacctc caaaaaccag
 gtagtcctca caatgaccaa catggacct gtggatactg ccacatacta ctgtgctcaa
 ataaaccccg cctggtttgc ttactggggc caagggactc tggtcactgt gagctccgga
 ggatgtggcg gtggagaagt ggccgcactg gagaaagagg ttgctgcttt ggagaaggag
 gtcgctgcac ttgaaaagga ggtcgcagcc ctggagaaa

SEQ ID NO: 27

DIVMTQSPDS LAVSLGERAT INCKASQSVD FDGDSFMNWX QQKPGQPPKL LIYTTSNLES
 GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQSQNEDPY TFGQGTKLEI KGGGSGGGGQ
 VQLVQSGGGV FKPGGSLRLS CEASGFTFTE YYMTWVRQAP GKGLEWLAYI SKNGEYSKYS
 PSSNGRFTIS RDNKNSVFL QLDRLSADDT AVYYCARADG LTYFSELLQY IFDLWGQGAR
 VTVSSGGCGG GKVAALKEKV AALKEKVAAL KEKVAALKE

Figure 9 cont.

SEQ ID NO: 28

gacatcgtga tgacccaatc tccagaactct ttggctgtgt ctctagggga gagggccacc
 atcaactgca aggccagcca aagtgttgat ttgatggtg atagtittat gaactggtac
 caacagaaac caggacagcc acccaaaactc ctcatctata ctacatccaa tctagaatct
 ggggtcccag acaggtttag tggcagtggg tctgggacag acttcaccct caccatcagc
 agcctgcagg ctgaggatgt ggcagtttat tactgtcagc aaagtaatga agatccgtac
 acgttcggac aggggaccaa gcttgagatc aaaggaggcg gatccggcgg aggtggacag
 gtgcagctgg tgcagtctgg gggaggcgtt ttcaagcctg gagggtcctt gagactctcc
 tgtgaagcct ctggattcac atttactgaa tattacatga cttgggtccg ccaggctcct
 gggaaggggc tggagtggct tgcgtatatt agtaagaatg gtgaatattc aaaatattca
 ccgtcctcaa acggccgggt caccatctcc agagacaacg ccaagaactc agtgtttctg
 caattggaca gactgagcgc cgacgacacg gccgtctatt actgtgcgag agcggacgga
 ttaacatact tctctgaatt actccaatac atttttgacc tctggggcca gggagcccgg
 gtcaccgtct cctccggagg atgtggcggg ggaaaagtgg ccgcactgaa ggagaaagtt
 gctgctttga aagagaaggt cgcgcactt aaggaaaagg tcgcagccct gaaagag

SEQ ID NO: 29

QAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KPGQAPRGLI GGTNKRAPWT
 PARFSGSLLG GKAALTITGA QAEDEADYYC ALWYSNLWVF GGGTKLTVLG GGGSGGGGEV
 KLDETGGGLV QPGRPMKLSC VASGFTFSDY WMNWVRQSPE KGLEWVAQIR NKPYNYETYY
 SDSVKGRFTI SRDDSKSSVY LQMNNLRVED MGIYYCTGSY YGMDYWQGT SVTVSSGGCG
 GGEVAALEKE VAALEKEVAA LEKEVAALEK

SEQ ID NO: 30

DVVMTQTPFS LPVSLGDQAS ISCRSSQSLV HSNGNTYLRW YLQKPGQSPK VLIYKVSNRF
 SGVPDRFSGS GSGTDFTLKI SRVEAEDLGV YFCSQSTHVP WTFGGGTKLE IKGGS GGSGG
 QVQLQESGPG LVKPSQTLNL SCTVSGGSSS SGAHYWSWIR QYPGKGLEWI GYIHYSNTY
 YNPSLKSRLT ISQHTSENQF SLKLNSVTVA DTAVYYCARG TRLRTLRLNAF DIWGQGTILV
 VSSGGCGGGK VAALKEKVAA LKEKVAALE KVAALKE

Figure 9 cont.

SEQ ID NO: 31

DVVMTQTPFS LPVSLGDQAS ISCRSSQSLV HSNNGNTYLRW YLQKPGQSPK VLIYKVS NRF
 SGVPDRFSGS GSGTDFTLKI SRVEAEDLGV YFCSQSTHVP WTFGGG TKLE IKGGGSGGGG
 QVTLRSGPA LVKPTQTLTL TCTFSGFSL S TSGMGVGVIR QPPGKALEWL AHIWDDDKR
 YNPALKSRLT ISKDTSKNQV VLTMTNMDPV DTATYYCAQI NPAWFAYWGQ GTLTVVSSGG
 CGGGEVAAL E KEVAALKEV AALEKEVAAL EK

SEQ ID NO: 32

DIVMTQSPDS LAVSLGERAT INCKASQSVD FDGDSFMN WY QQKPGQPPKL LIYTTSNLES
 GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQOSNEDPY TFGQGT KLEI KGGGSGGGGE
 VKLDETGGGL VQPGRP MKLS CVASGFTFSD YWMNWVRQSP EKGLEWVAQI RNKPYNYETY
 YSDSVKGRFT ISRDDSKSSV YLQMN NLRVE DMGIYYCTGS YYGMDYWGQG TSVTVSSGGC
 GGGKVAALKE KVAALKEKVA ALKEKVAALK E

SEQ ID NO: 33

DIVMTQSPDS LAVSPGERAT IHCKSSQTLL YSSNNRHSIA WYQQRPGQPP KLLLYWASMR
 LSGVPDRFSG SSGTDFTLT INNLOAEDVA IYYCHQYSSH PPTFGH GTRV EIKGGGSGGG
 GEVKLDETGG GLVQPGRP MK LSCVASGFTF SDYWMNWVRQ SPEKLEWVA QIRNKP NYE
 TYYSDSVKGR FTISRDDSKS SVYLQMN NLR VEDMGIYYCT GSYYGMDYWG QGTSVTVSSG
 GCGGGEVAAL EKEVAALKE VAALKEKVAA LEK

SEQ ID NO: 34

DVVMTQTPFS LPVSLGDQAS ISCRSSQSLV HSNNGNTYLRW YLQKPGQSPK VLIYKVS NRF
 SGVPDRFSGS GSGTDFTLKI SRVEAEDLGV YFCSQSTHVP WTFGGG TKLE IKGGGSGGGG
 QVQLVQSGGG VFKPGGSLRL SCEASGFTFT EYYMTWVRQA PGKLEWLA Y ISKNGEYSKY
 SPSSNGRFTI SRDNAKNSVF LQLDRLSADD TAVYYCARAD GLTYFSELLQ YIFDLWGQGA
 RVTVSSGGCG GKGVAALKEK VAALKEKVAA LKEKVAALKE

SEQ ID NO: 35

QSALTQPPSA SGSPGQSVTI SCTGTSSDVG GYNYVSWYQH HPGKAPKLII SEVNNRPSGV
 PDRFSGSKSG NTASLTVSGL QAEDA EYYC SSYTDIHN FV FGGGTKLTVL GGGSGGGGEV
 KLDETGGGLV QPGRPMK LSC VASGFTFSDY WMNWVRQSPE KGLEWVAQIR NKP NYETYY
 SDSVKGRFTI SRDDSKSSVY LQMN NLRVED MGIYYCTGS YGMDYWGQGT SVTVSSGGCG
 GGEVAALKE VAALKEKVAA LEKEVAALKE

SEQ ID NO: 36

DVVMTQTPFS LPVSLGDQAS ISCRSSQSLV HSNNGNTYLRW YLQKPGQSPK VLIYKVS NRF
 SGVPDRFSGS GSGTDFTLKI SRVEAEDLGV YFCSQSTHVP WTFGGG TKLE IKGGGSGGGG
 QVQLQESGPG LVKPSQTL SL SCTVSGGSSS SGAHYWSWIR QYPGKGLEWI GYIHYSNTY
 YNPSLKSRLT ISQHTSENQF SLKLNSVTVA DTAVYYCARG TRLR TL RNAF DIWGQGT LVT
 VSSGGCGGGK VAALKEKVAA LKEKVAALKE KVAALKE

Figure 9 cont.

SEQ ID NO: 37

QAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KPGQAPRGLI GGTNKRAPWT
 PARFSGSLLG GKAALTITGA QAEDEADYYC ALWYSNLWVF GGGTKLTVLG GGGSGGGGQV
 TLRESGPALV KPTQTLTLTC TFSGFSLSSTS GMSVGWIRQP PGKALEWLAD IWWDDKKDYN
 PSLKSRLTIS KDTSKNQVVL KVTNMDPADT ATYYCARSMI TNWYFDVWGA GTTVTVSSGG
 CGGGEVAALE KEVAALEKEV AALEKEVAAL EK

SEQ ID NO 38

DIQMTQSPST LSASVGDRVT ITCRASQSVG YMHWYQQKPG KAPKLLIYDT SKLASGVPSR
 FSGSGSGTEF TLTISSLQPD DFATYYCFQG SGYPFTFEGG TKLEIKGGGS GGGGEVQLVE
 SGGGLVQPGG SRLSCAASG FTFSTYAMNW VRQAPGKGLE WVGRIIRSKYN NYATYYADSV
 KGRFTISRDD SKNSLYLQMN SLKTEDTAVY YCVRHGNFGN SYVSWFAYWG QGTLVTVSSG
 GCGGKVAAL KEKVAALKEK VAALKEKVAA LKE

SEQ ID NO: 39

APSSS

SEQ ID NO: 40

APSSSPME

SEQ ID NO: 41

APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK
 PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
 LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL
 TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK

SEQ ID NO:42

APEAAGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK
 PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
 LPPSREEMTK NQVSLWCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL
 TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK

SEQ ID NO: 43

APEAAGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK
 PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
 LPPSREEMTK NQVSLSCAVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL
 TVDKSRWQQG NVFSCSVME ALHNRYTQKS LSLSPGK

Figure 9 cont.

SEQ ID NO: 44

SQSALTQPPS ASGSPGQSVT ISCTGTSSDV GGYNYVSWYQ HHPGKAPKLI ISEVNNRPSG
 VPDREFSGSKS GNTASLTVSG LQAEDAEYY CSSYTDIHNH VFGGGTKLTV LGGSGGGGQ
 VTLRESGPAL VKPTQTLTCT CTFSGFSLST SGMGVGWIRQ PPGKALEWLA HIWDDDKRY
 NPALKSRLTI SKDTSKNQVV LTMTNMDPVD TATYYCAQIN PAWFAYWGQG TLVTVSSGGC
 GGGEVAALEK EVAALEKEVA ALEKEVAALE K

SEQ ID NO: 45

DIVMTQSPDS LAVSLGERAT INCKASQSVD FDGDSFMNWX QOKPGQPPKL LIYTTSNLES
 GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQOSNEDPY TFGQGTKLEI KGGSGGGGQ
 VQLQESGPGL VKPSQTLTSL CTVSGGSSSS GAHYWSWIRQ YPGKGLEWIG YIHYSNTYY
 NPSLKSRLTI SQHTSENQFS LKLNSVTVAD TAVYYCARGT RLRTLNAFD IWGQGTLLTV
 SSGGCGGGKV AALKEKVAAL KEKVAALKE VAALKE

SEQ ID NO: 46

DIVMTQSPDS LAVSPGERAT IHCKSSQTLL YSSNNRHSIA WYQQRPGQPP KLLLYWASMR
 LSGVPDRFSG SSGTDFTLT INNLAEDVA IYYCHQYSSH PPTFGHGTRV EIKGGSGGGG
 GEVQLVESGG GLVQPGGSLR LSQAASGFTF STYAMNWRQ APGKGLEWVG RIRSKYNNYA
 TYYADSVKGR FTISRDDSKN SLYLQMNLSK TEDTAVYYCV RHGNEFGNSYV SWFAYWGQGT
 LVTVSSGGCG GGEVAALEKE VALEKEVAA LEKEVAALEK GGGDKHTTCP PCPAPEAAGG
 PSVFLFPPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNA KTKPREEQYN
 STYRVSVLT VLHQDWLNK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE
 MTKNQVSLWCLVKGFYPSDI AVEWESNGQP ENNYKTTTPV LDSDGSFFLY SKLTVDKSRW
 QQGNVFSCSV MHEALHNHYT QKSLSLSPGK

SEQ ID NO: 47

QAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KPGQAPRGLI GGTNKRAPWT
 PARFSGSLLG GKAALTITGA QAEDAEYYC ALWYSNLWVF GGGTKLTVLG GGGSGGGGQV
 QLVQSGGGVF KPGGSLRLSC EASGFTFTEY YMTWVRQAPG KGLEWLAIS KNGEYSKYSP
 SSNGRFTISR DAKNSVFLQ LDRLSADDTA VYYCARADGL TYFSELLQYI FDLWGQGARV
 TVSSGGCGGG KVAALKEKVA ALKEKVAALK EKVAALKE

SEQ ID NO: 48

APEAAGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK
 PREEQYNSTY RVVSVLTVLH QDWLNKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
 LPPSREEMTK NQVSLSCAVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL
 TVDKSRWQQG NVFSCSVMHE ALHNRYTQKS LSLSPGK

Figure 9 cont.

SEQ ID NO: 49 (Linker 3)

DKTHTCPPCP

SEQ ID NO: 50 (Spacer Linker 3)

GGGDKTHTCPPCP

SEQ ID NO: 51 (VH CD3)

EVQLVESGGG LVQPGGSLRL SCAASGFTFS TYAMNWVRQA PGKGLEWVGR IRSKYNNYAT
YYADSVKGRF TISRDDSKNS LYLQMNSLKT EDTAVYYCVR HGNFGNSYVS WFAYWGQGT
LVTVSS

SEQ ID NO: 52 (VL CD3)

QAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KPGQAPRGLI GGTNKRAPWT
PARFSGSLLG GKAALTITGA QAEDEADYYC ALWYSNLWVF GGGTKLTVLG

SEQ ID NO: 53 (VH CD16)

QVTLRESGP ALVKPTQTLT LTCTESGFSL STSGMGVGWI RQPPGKALEW LAHIWWDDDK
RYNPALKSRL TISKDTSKNQ VVLTMTNMDP VDTATYYCAQ INPAWFAYWG QGTLVTVSS

SEQ ID NO: 54 (VL CD16)

DIVMTQSPDS LAVSLGERAT INCKASQSVD FDGDSEFMNWX QOKPGQPPKL LIYTTSNLES
GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQQSNEDPY TFGQGTKLEI K

SEQ ID NO: 55 (VL 7B2 GenBank: AFQ31503.1) DIVMTQSPDS LAVSPGERAT

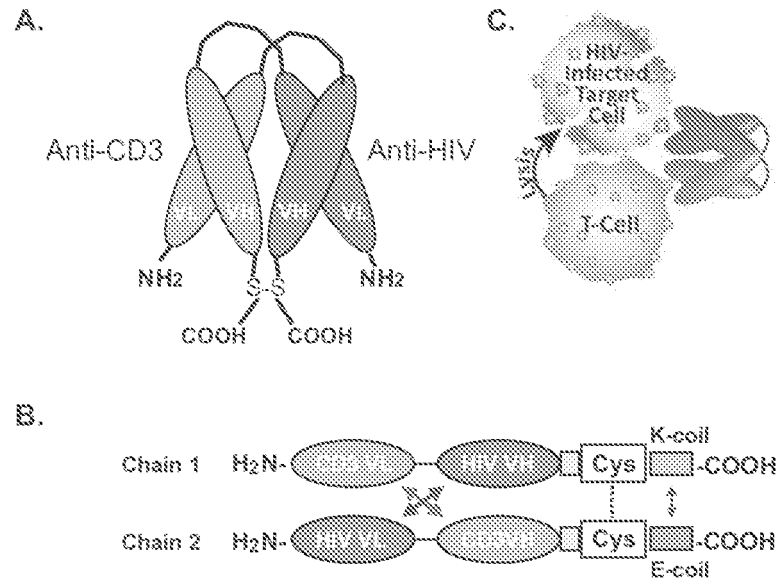
IHCKSSQTLL YSSNNRHSIA WYQQRPGQPP KLLLYWASMR

LSGVPDRFSG SSGTDFTLT INNLQAEDVA IYYCHQYSSH PPTFGHGTRV

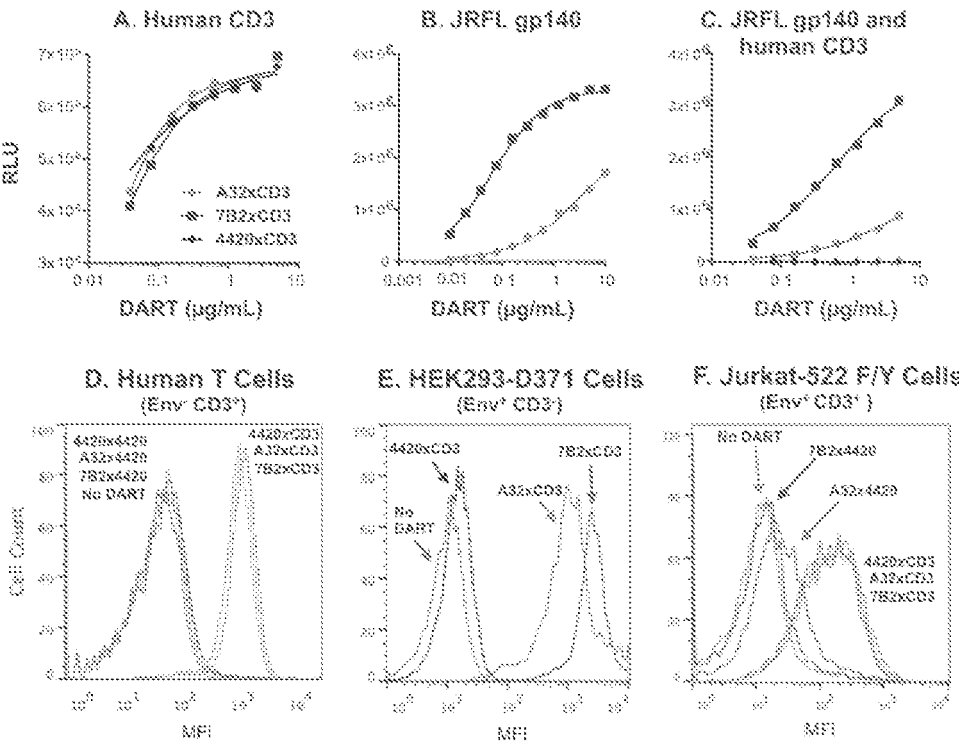
SEQ ID NO: 56 (VH 7B2 GenBank: AFQ31502.1)

QVQLVQSGGG VFKPGGSLRL SCEASGFTFT EYYMTWVRQA PGKGLEWLAY ISKNGEYSKY
SPSSNGRFTI SRONAKNSVF LQLDRLSADD TAVYYCARAD GLTYFSELLQ YIFDLWGQGA
RVTVSS

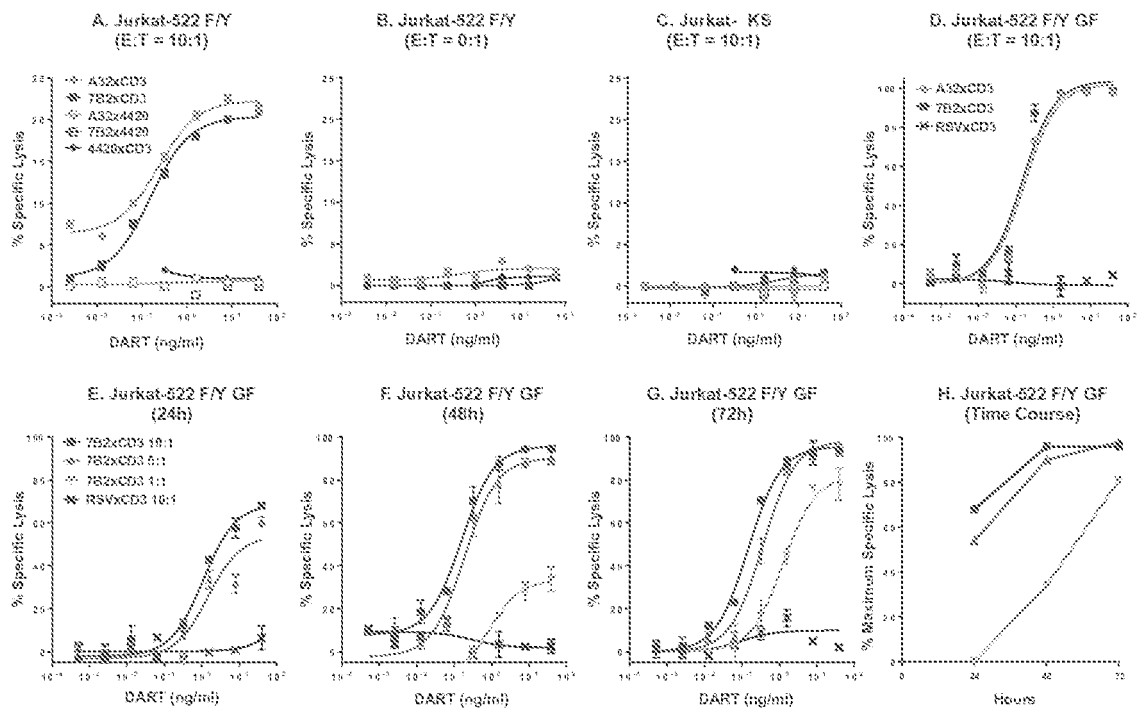
Figure 9 cont.



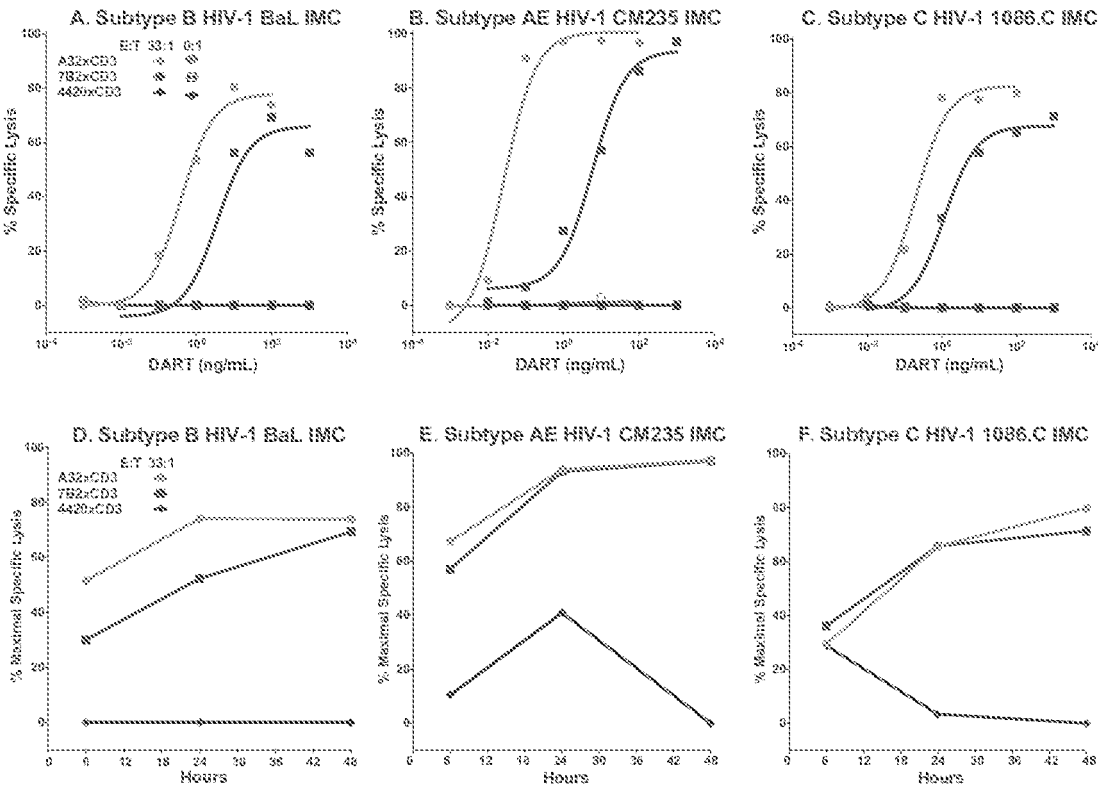
Figures 10A-10C



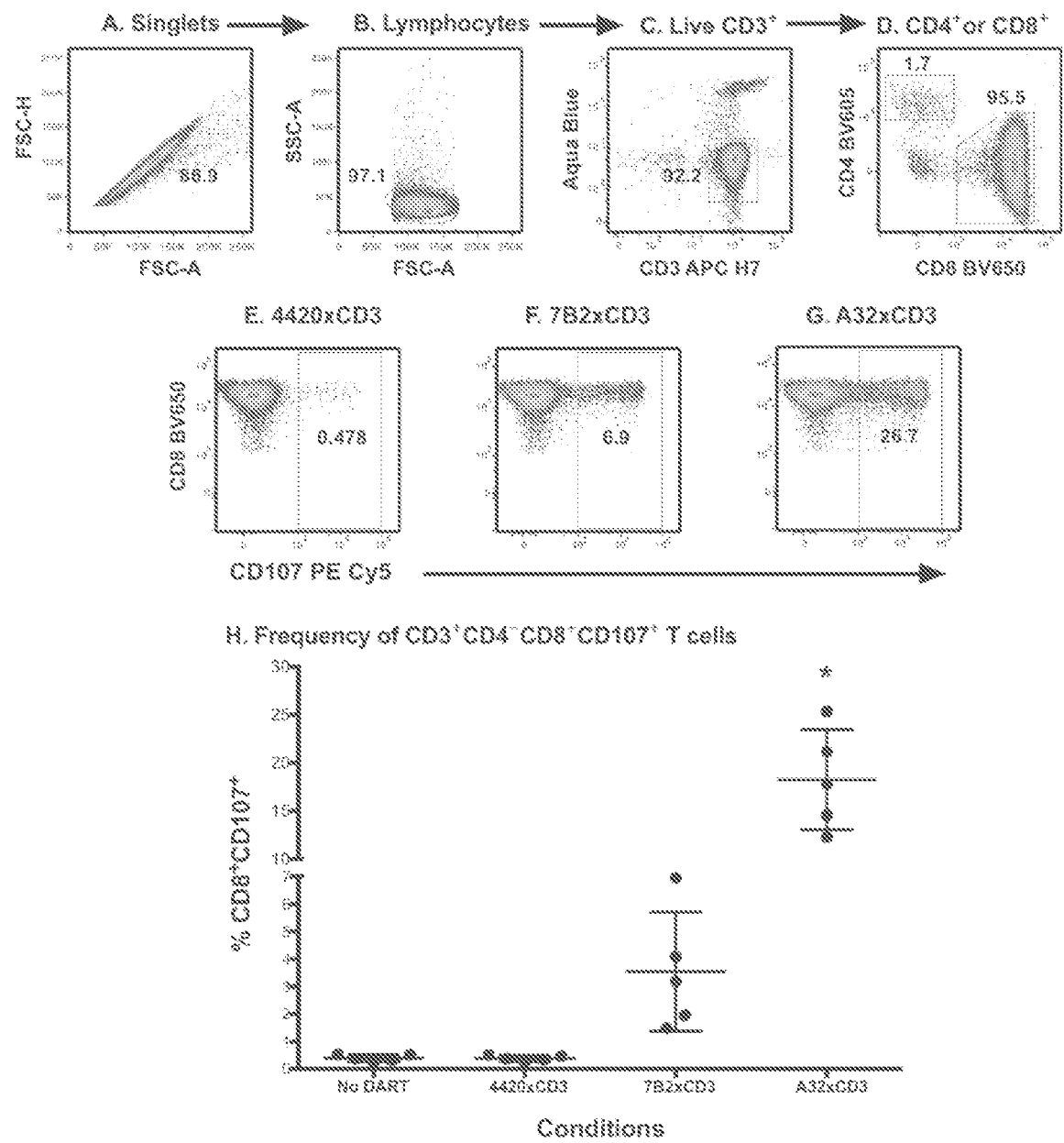
Figures 11A-11F



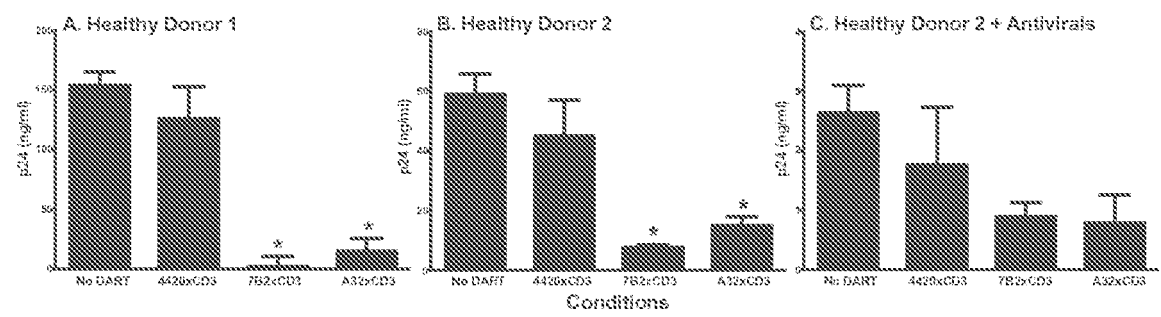
Figures 12A-12H



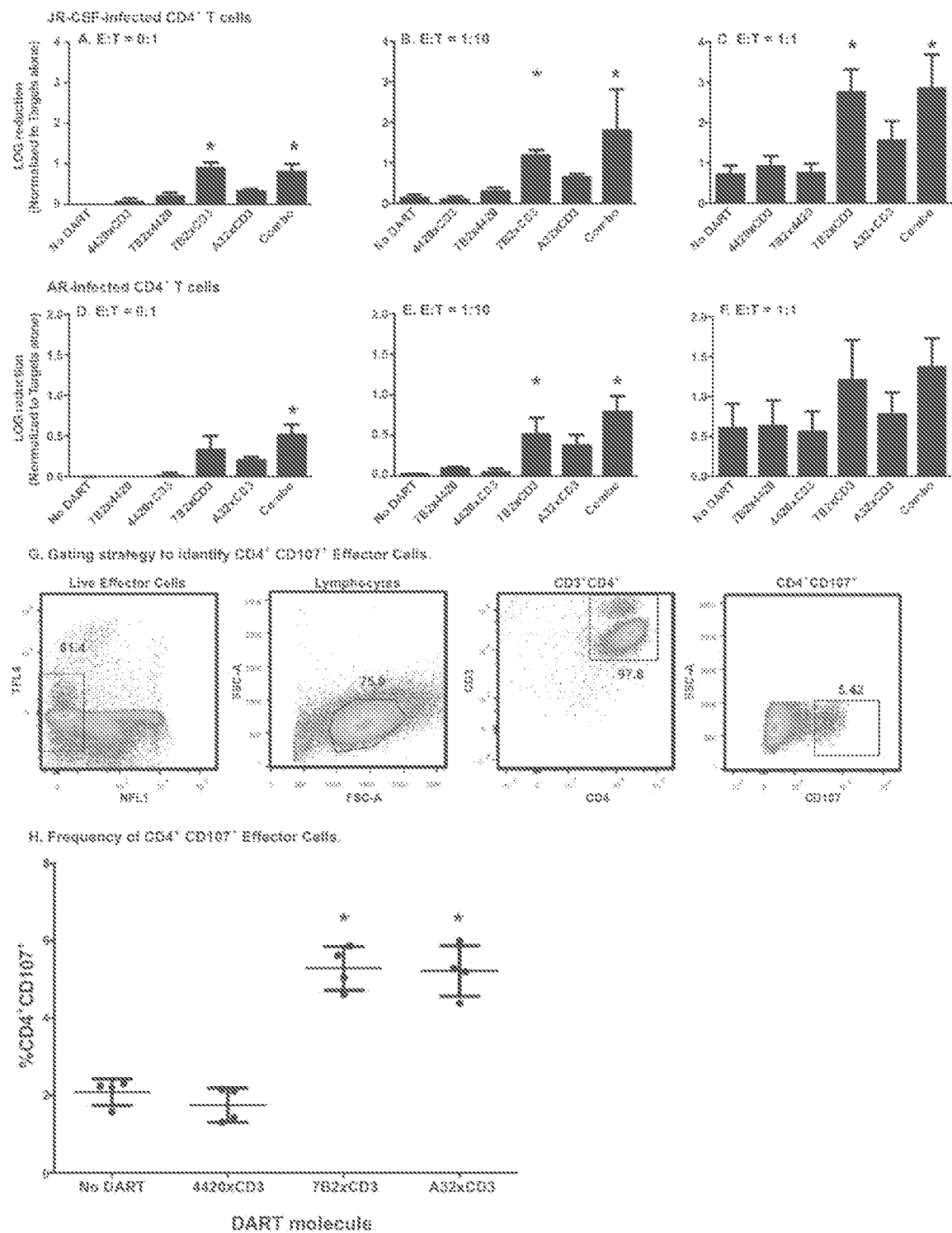
Figures 13A-13F



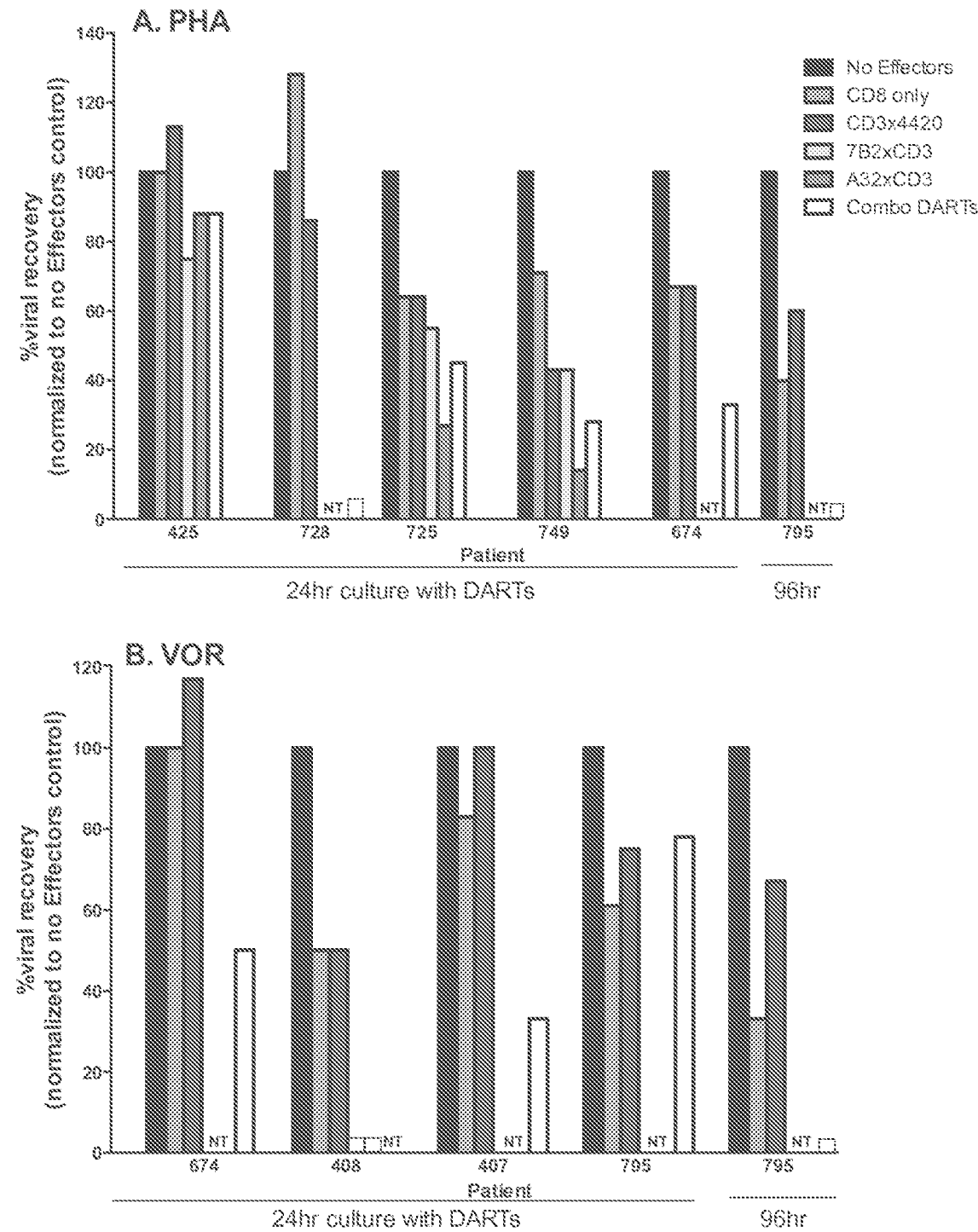
Figures 14A-14H



Figures 15A-15C



Figures 16A-16H



Figures 17A-17B

	Subtype A	Subtype AE	Subtype B	Subtype C
Tier 1	Q32.17	92TH023	BaL SF162	MW96.5
Tier 2		CM235 CM244 C1080.C03 427299 816763	CH040 CH058 SUMA WITO YU2	CAP45 CH505 DU151 DU422 TV1 1086.C 246-F3.C10

Figure 18

Antigen	DART	$k_a (\pm SD), M^{-1} s^{-1}$	$k_d (\pm SD), s^{-1}$	$K_D (\pm SD), nM$
Human CD3 ϵ/δ	A32xCD3	$6.8 (\pm 0.1) \times 10^5$	$2.4 (\pm 0.0) \times 10^{-3}$	$3.6 (\pm 0.1)$
	7B2xCD3	$4.1 (\pm 0.0) \times 10^4$	$2.5 (\pm 0.0) \times 10^{-4}$	$6.1 (\pm 0.0)$
M.ConS gp140	A32xCD3	$1.7 (\pm 0.0) \times 10^4$	$8.1 (\pm 1.8) \times 10^{-4}$	$47.7 (\pm 10.8)$
JR-FL gp140	7B2xCD3	$2.0 (\pm 0.1) \times 10^4$	$3.1 (\pm 0.9) \times 10^{-4}$	$15.1 (\pm 3.5)$

Figure 19

Patient	Virus used for infection in VCA*	Pre-ART Viral Load (copies/ml)	Nadir CD4	Current CD4 count	Duration of suppression (years)
493	JR-CSF	78,115	257	637	2.5
532	JR-CSF	unknown	130	623	14
673	JR-CSF	Unknown	unknown	707	7
527	JR-CSF, AR	184,781	600	718	4.5
728	JR-CSF, AR	45,000	354	456	4
749	JR-CSF, AR	unknown	404	402	1.5
725	JR-CSF, AR	234,048	475	789	3
720	JR-CSF, AR	586,930	166	446	3
425	Autologous	750,001	604	783	8
407	Autologous	1,042,734 (AHI)	499	706	2
408	Autologous	6095 (AHI)	830	1168	2
795	Autologous	175,718	526	850	2.5
674	Autologous	185,042	338	1045	4.5

* Virus Clearance Assay

AR = autologous reservoir virus

Autologous indicates patient cells used in latency clearance assay, no superinfection used.

AHI = Acute HIV Infection

Figure 20

Patient	E:T Ratio	HIV-1 gag p24 concentration (ng/ml) (SEM)					
		No DART	CD3x4420	7B2x4420	7B2xCD3	A32xCD3	Combo
493	No CD8s	10.6(2)	12.6(4)	NT	1.44(1.0)	10.8(2.2)	NT
	1:10	4.7(1.0)	7.35(2.1)	NT	1.05(0.6)	3.5(1.3)	NT
	1:1	.92(0.2)	1.29(.03)	NT	.04(.02)	.343(.01)	NT
532	No CD8s	12.9(2.7)	12.6(3.9)	NT	1.44(1.0)	10.8(4.1)	NT
	1:10	8.9(1.7)	7.35(2.1)	NT	1.05(.629)	3.5(1.3)	NT
	1:1	0.92(0.2)	1.5(0.16)	NT	0.04(0.02)	0.16(0.03)	NT
673	No CD8s	345(6.4)	194(25)	253(17)	213(28)	139(4.6)	NT
	1:10	329(1.2)	137(5.2)	184(12)	73(4.6)	57(5.2)	NT
	1:1	94(6.9)	8.8(0.2)	13.5(0.5)	4.4(0.5)	11.4(1.0)	NT
527	No CD8s	154(5.2)	185(22)	106(9.4)	27.3(12.3)	54.2(29.3)	62.9(3.4)
	1:10	164(16)	210(11)	78(6.6)	12.1(2.1)	21(2.8)	68(5.9)
	1:1	116(53)	139(10.8)	80(21)	13(6)	8.4(0.9)	34.9(5.6)
728	No CD8s	103(25)	111(10)	92(24)	19(10)	122(51)	30(11)
	1:10	114(18)	117(13)	90(2.2)	3.7(2.6)	54(11)	15.9(5.4)
	1:1	178(14)	121(32)	60(23)	1.9(1.1)	44(9.5)	0.9(0.4)
749	No CD8s	27.9(11)	7.3(6.8)	13.8(2.9)	0.9(0.5)	19.3(7.7)	16.5(12.2)
	1:1	11.4(0.5)	6.8(3.3)	5.5(3)	ND	ND	ND
725	No CD8s	191(3.7)	177(37)	189(24)	29(21)	134(16)	45(13)
	1:10	234(53)	187(14)	163(22)	6.5(5.5)	122(17)	ND
	1:1	60(22)	71(5)	53(17)	ND	4.5(3.3)	ND
720	No CD8s	15(4.8)	26.3(4.8)	22(2.3)	0.7(0.2)	5.9(2.6)	0.6(0.2)
	1:10	5.7(2.5)	17(2.3)	16(4.6)	0.4(0.1)	2.5(0.5)	1.0(0.6)
	1:1	1.1(0.1)	0.4(0.3)	1.1(0.3)	ND	1.3(0.4)	0.2(0.02)

SEM=standard error of the mean of 3 replicates

ND = not detected

NT = not tested due to cell availability

Figure 21

LRA	Patient	#wells plated	#positive wells after addition of DART MOLECULE					
			No Effectors	No DART	4420 xCD3	7B2 xCD3	A32 xCD3	Combo
PHA	425	12	8	8	9	6	7	7
	728	12	7	9	6	NT	NT	0
	725	12	11	7	7	6	3	5
	749	12	7	5	3	3	1	2
	674	12	6	4	4	NT	NT	2
	795*	12	10	4	6	NT	NT	0
VOR	674	12	6	6	7	NT	NT	3
	408	12	2	1	1	0	0	NT
	407	24	6	5	6	NT	NT	2
	795	36	28	17	21	NT	NT	22
	795*	12	3	1	2	NT	NT	0

LRA=latency reversing agent

NT=not tested due to cell availability

combo= Addition of 50ng/ml of 7B2xCD3 DART and 50ng/ml of A32xCD3 DART

* evaluated using 96 hours co-culture

VOR=vorinostat

Figure 22

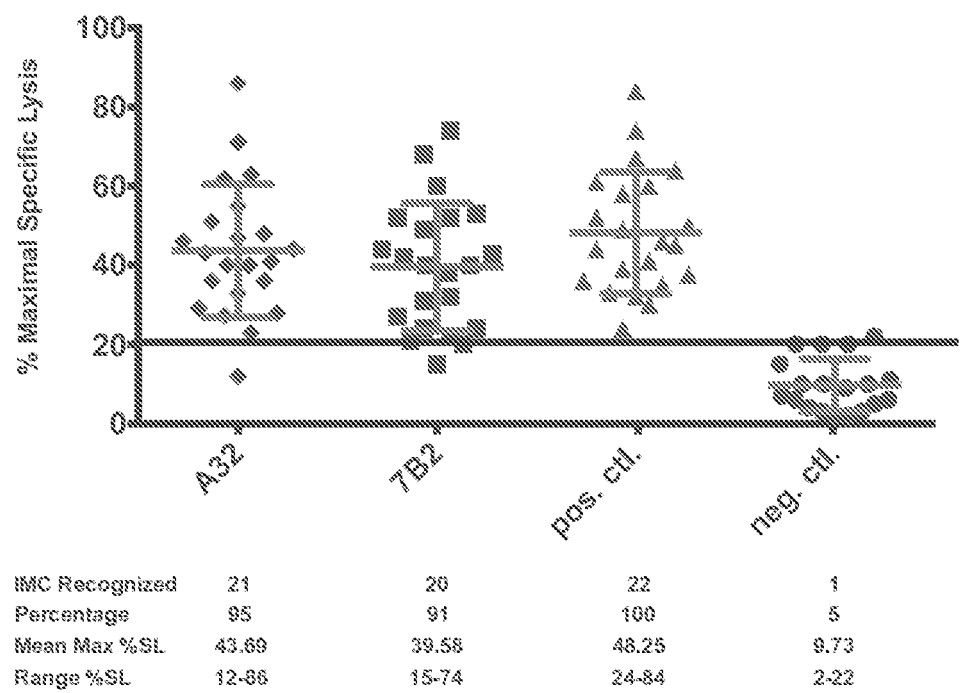


Figure 23

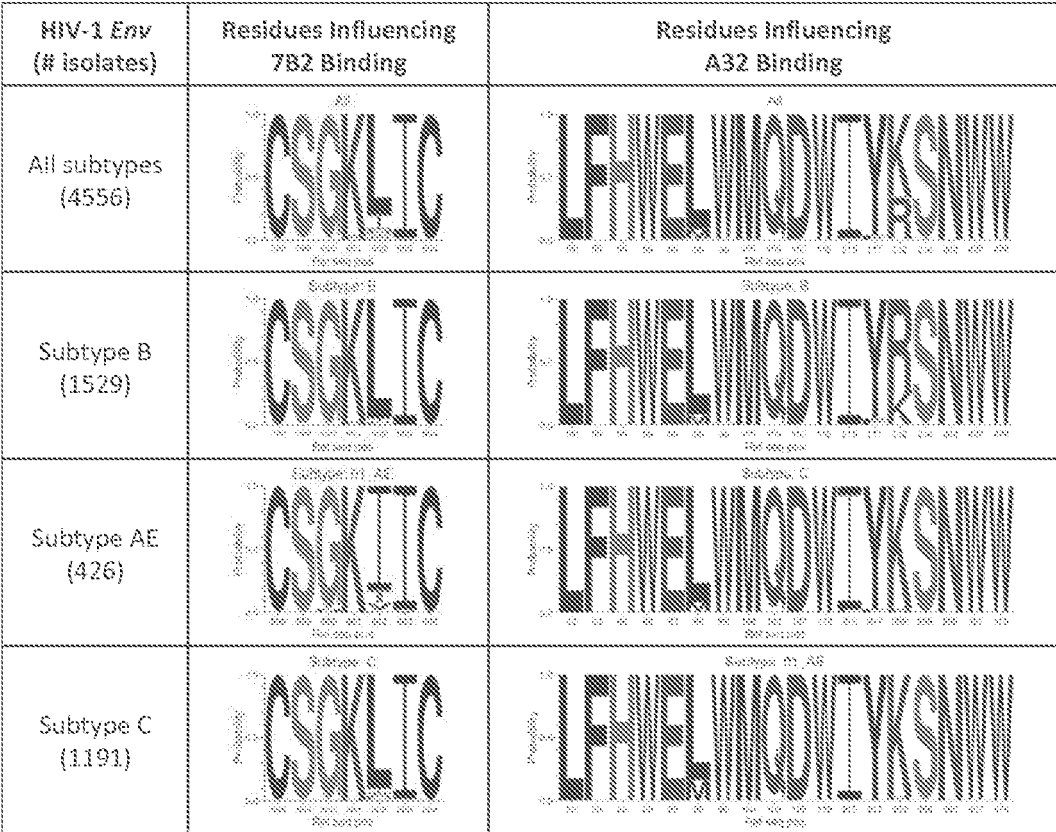


Figure 24

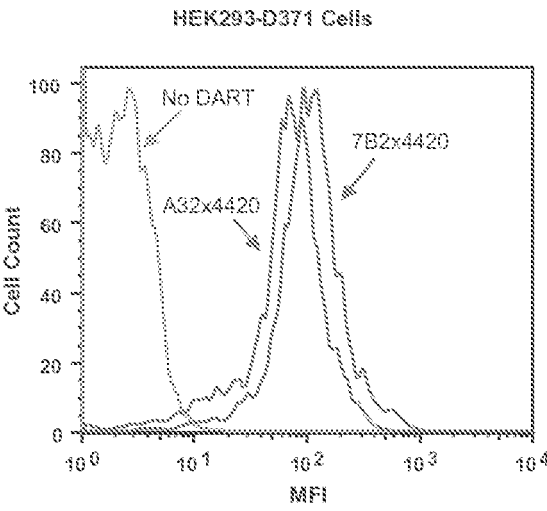
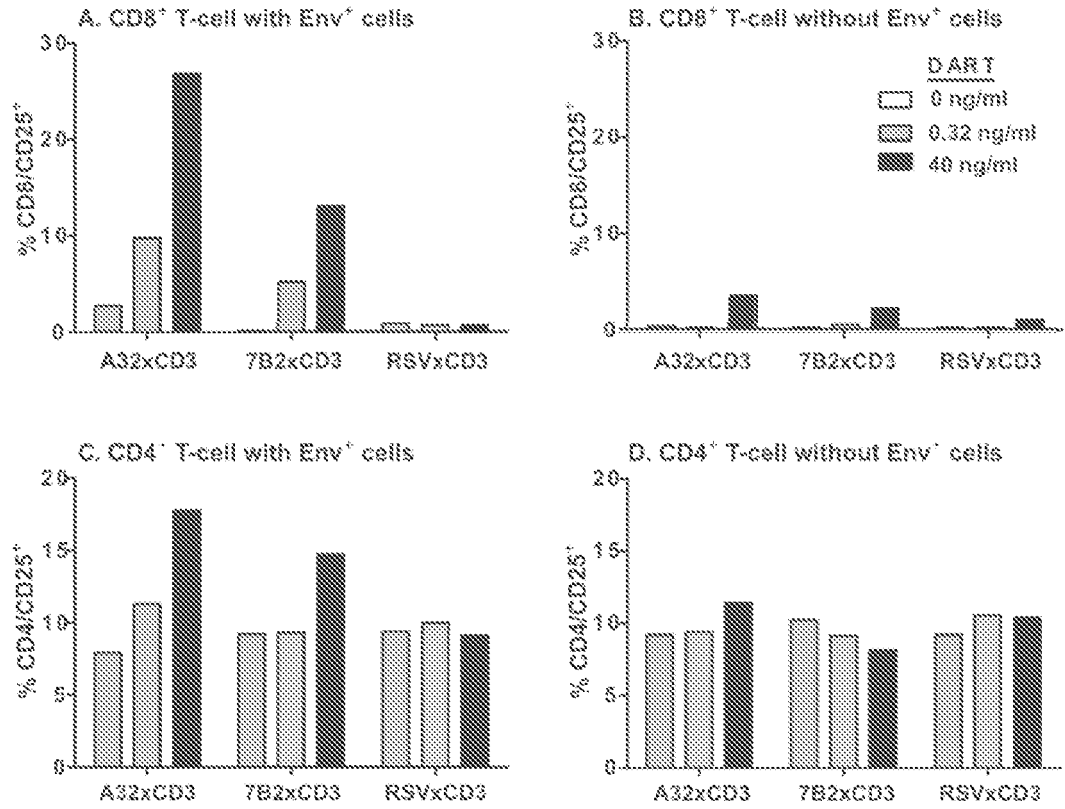


Figure 25



Figures 26A-26D

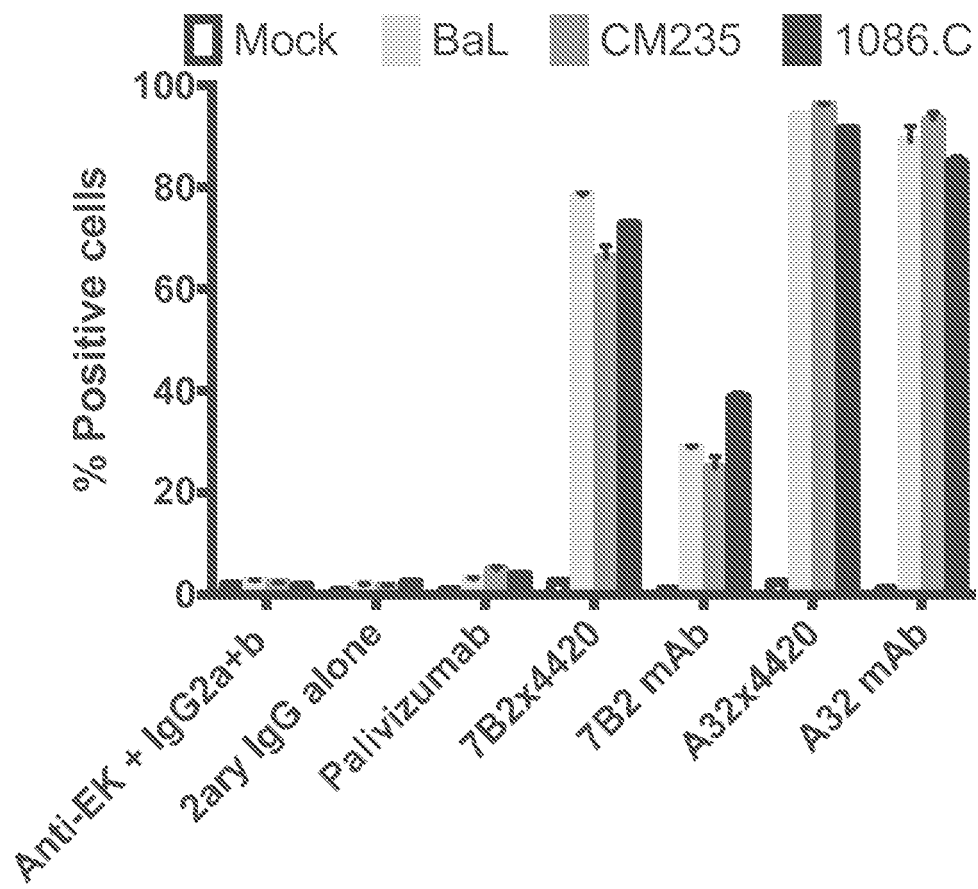
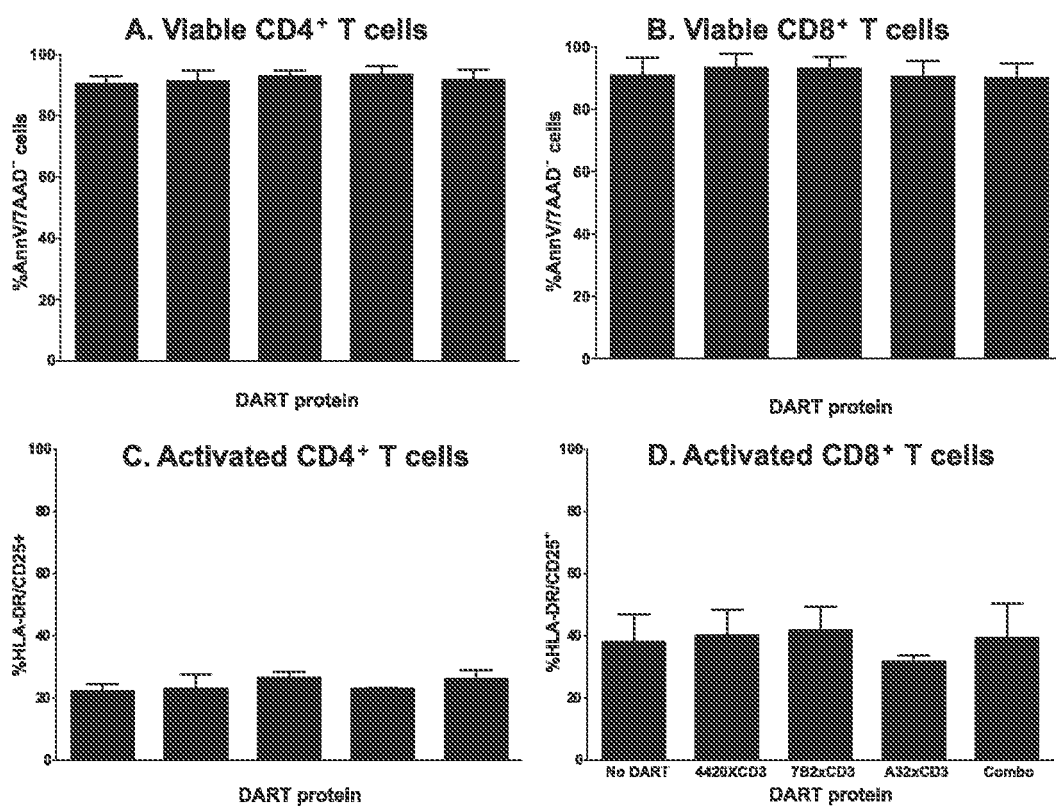


Figure 27



Figures 28A-28D