

FIG. 1A

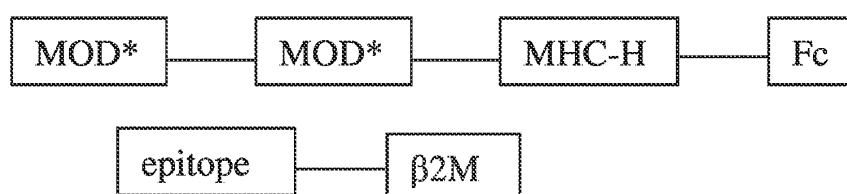


FIG. 1B

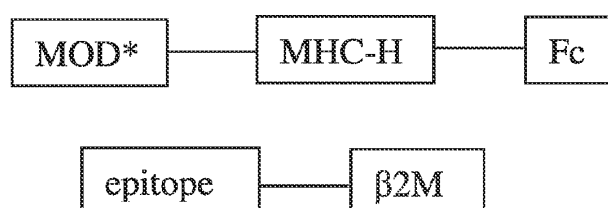


FIG. 1C

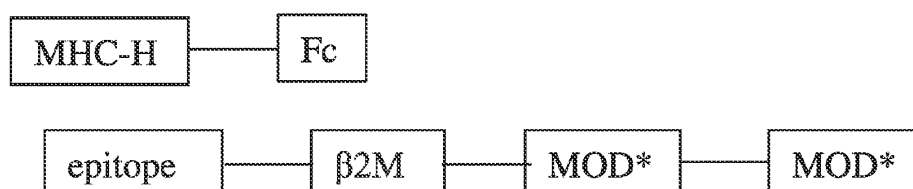


FIG. 1D

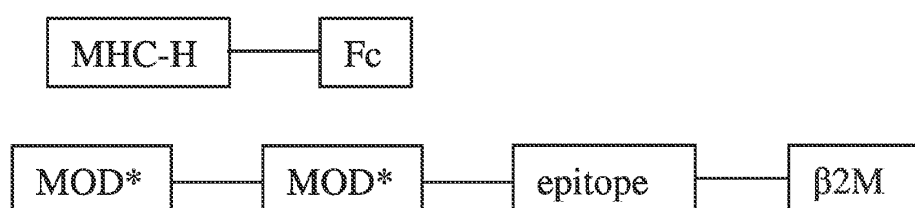


FIG. 1E

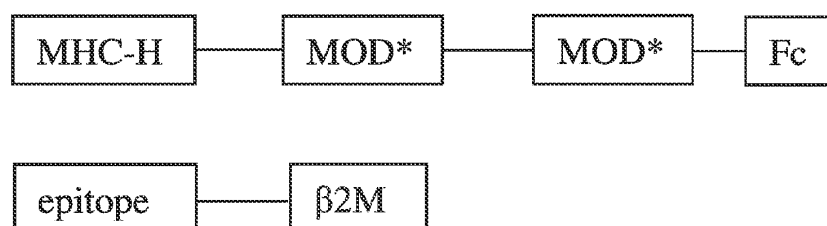


FIG. 1F

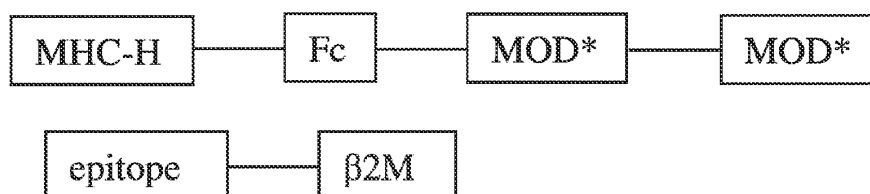


FIG. 2A

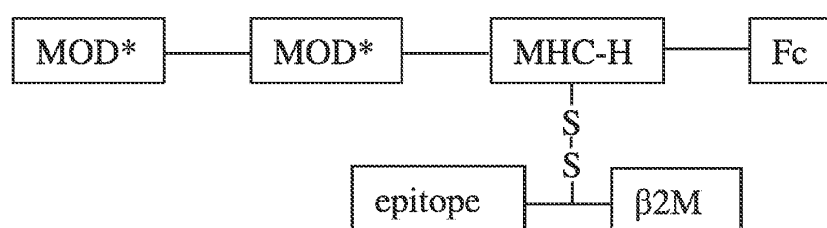


FIG. 2B

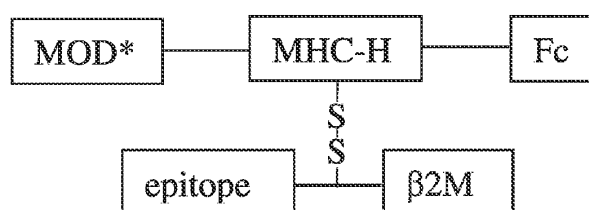


FIG. 2C

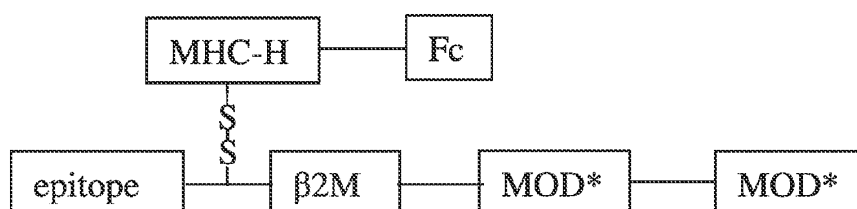


FIG. 2D

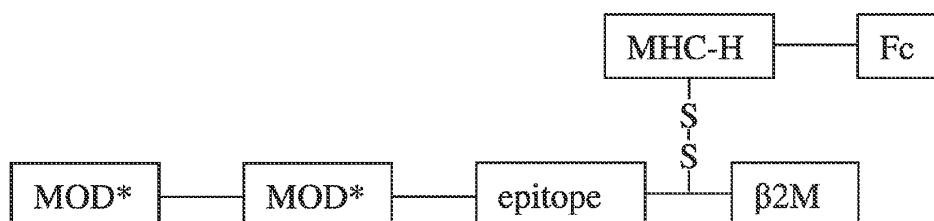


FIG. 2E

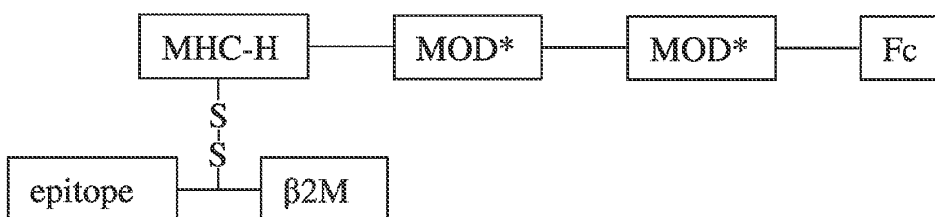


FIG. 2F

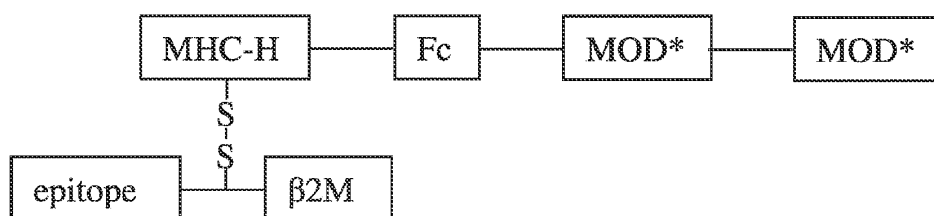


FIG. 3A

WT-1 isoform A

1 MDFLLLQDPA STCVPEPASQ HTLRSGPGCL QQPEQQGVRD PGGIWAKLGA AEASAERLQG
61 RRRSGASGSE PQQMGSDVRD LNALLPAVPS LGGGGGCALP VSGAAQWAPV LDFAPPGASA
121 YGSLGGPAPP PAPPPPPPPP PHSFIKQEPS WGAEPHEEQ CLSAFTVHFS GQFTGTAGAC
181 RYGPFGPAPP SQASSGQARM FPNAPYLPSC LESQPAIRNQ GYSTVTFDGT PSYGHTPSHH
241 AAQFPNHSFK HEDPMGQQGS LGEQQYSVPP PVYGCHTPTD SCTGSQALLL RTPYSSDNLY
301 QMTSQLECMT WNQMNLGATL KGHSTGYESD NHTTPILCGA QYRIHGHVF RGIQDVRRVP
361 GVAPTLVRS A SETSEKRPFM CAYPGCNKRY FKLSHLQMHS RKHTGEKPYQ CDFKDCERRF
421 SRSDQLKRHQ RRHTGVKPFQ CKTCQRKFSR SDHLKTHTRT HTGEKPFSCR WPSCQKKFAR
481 SDELVRHHNM HQRNMTKLQL AL

FIG. 3B

WT-1 isoform B

1 MDFLLLQDPA STCVPEPASQ HTLRSGPGCL QQPEQQGVRD PGGIWAKLGA AEASAERLQG
61 RRRSGASGSE PQQMGSDVRD LNALLPAVPS LGGGGGCALP VSGAAQWAPV LDFAPPGASA
121 YGSLGGPAPP PAPPPPPPPP PHSFIKQEPS WGAEPHEEQ CLSAFTVHFS GQFTGTAGAC
181 RYGPFGPAPP SQASSGQARM FPNAPYLPSC LESQPAIRNQ GYSTVTFDGT PSYGHTPSHH
241 AAQFPNHSFK HEDPMGQQGS LGEQQYSVPP PVYGCHTPTD SCTGSQALLL RTPYSSDNLY
301 QMTSQLECMT WNQMNLGATL KGVAAGSSSS VKWTEGQSNH STGYESDNHT TPILCGAQYR
361 IHTHGVFRGI QDVRRVPGVA PTLVRSASET SEKRPFM CAY PGCNKRYFKL SHLQMHSRKH
421 TGEKPYQCDF KDCERRFSRS DQLKRHQRRH TGVKPFQCKT CQRKFSRSDH LKTHTRHTG
481 EKPFSCRWPS CQKKFARSDE LVRHHNMHQR NMTKLQLAL

FIG. 3C

WT-1 isoform D

1 MDFLLLQDPA STCVPEPASQ HTLRSGPGCL QQPEQQGVRD PGGIWAKLGA AEASAERLQG
61 RRSRGASGSE PQQMGSQDVRD LNALLPAVPS LGGGGGICALP VSGAAQWAPV LDFAPPGASA
121 YGSLGGPAPP PAPPPPPPPP PHSFIKQEPS WGAEPHEEQ CLSAFTVHFS GQFTGTAGAC
181 RYGPFGPPPP SQASSGQARM FPNAPYLPSC LESQPAIRNQ GYSTVTFDGT PSYGHTPSHH
241 AAQFPNHSEK HEDPMGQQGS LGEQQYSVPP PVYGCHTPTD SCTGSQALLL RTPYSSDNLY
301 QMTSQLECMT WNQMNLGATL KGVAAGSSSS VKWTEGQSNH STGYESDNHT TPILCGAQYR
361 IHTHGVRFGI QDVRRVPGVA PTLVRSASET SEKRPFMCAY PGCNKRYFKL SHLQMHSRKH
421 TGEKPYQCDF KDCERRFSRS DQLKRHQRRH TGVKPFQCKT CQRKFERSDH LKTHTRHTIG
481 KTSEKPFSCR WPSCQKKFAR SDELVRHHNM HQNMTKLQL AL

FIG. 3D

WT-1 isoform E

1 MEKGYSTVTF DGTPSYGHTP SHHAAQFPNH SEKHEDPMGQ QGSLGEQQYS VPPPVYGCHT
61 PTDSCTGSQA LLLRTPYSSD NLYQMTSLE CMTWNQMNLG ATLKGVAAGS SSSVKWTEGQ
121 SNHSTGYESD NHTTPILCGA QYRIHTGVF RGIQDVRRVP GVAPTLVRS SETSEKRPFM
181 CAYPGCNKRY FKLSHLQMS RKHTGEKPYQ CDFKDCERRF SRSDQLKRHQ RRHTGVKPFQ
241 CKTCQRKFSR SDHLKTHTRT HTGEKPFSCR WPSCQKKFAR SDELVRHHNM HQNMTKLQL
301 AL

FIG. 3E

WT-1 isoform F

1 MEKGYSTVTF DGTPSYGHTP SHHAAQFPNH SEKHEDPMGQ QGSLGEQQYS VPPPVYGCHT
61 PTDSCTGSQA LLLRTPYSSD NLYQMTSLE CMTWNQMNLG ATLKGHSTGY ESDNHTTPIL
121 CGAQYRIHTH GVFRGIQDVR RVPGVAPTLV RASETSEKR PFMCAYPGCN KRYFKLSHLQ
181 MHSRKHTGEK PYQCDFKDCE RRFSDQLK RHQRRHTGVK PFQCKTCQRK FSRSDHLKTH
241 TRHTGTGTSE KPFSCRWPSC QKKFARSDEL VRHHNMHQRN MTKLQLAL

FIG. 4A

Construct 3158

GSHSMRYFSTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASORMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRALRAYNQSEAGSHTLQMMFGCDVGS DGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWORDGEDQTQDTELVETRPCGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWEGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQ MILNGIN
NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQ MILNGINNYKN
PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG GGGGS
GGGSGGGSGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQK
SLSLSPG (SEQ ID NO:405)

HLA-A*24:02 – double underlined

(G4S)₃ and (G4S)₄ – underlined (SEQ ID NOs:379-380)

IL-2 (H16A; F42A) – bold

Human IgG1 Fc (LALA) – italicized

FIG. 4B

Construct 2750

APTSSSTKKTQLQLEALLLDLQMI^{IL2(H16A; F42A)}LNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCL
 EEELKPLEEVNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL
 NRWITFCQSIISTLTGGGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMI
 L^{(G4S)4 linker}NGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVNLAQSKNFHLRPR
 DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGG
 SGGGGSGGGSGSGSHSMRYFSTSVSRPGRGEPRFI^{HLA-A*2402 (Y84A; A236C)}AVGYVDDTQFVRFSDAASQRM^{AAAGG linker}EP
 APWIEQEGPEYWDEETGKVK^{hlgG1 Fc (L234A; L235A)}SAHSQTDRENLR^{IL2(H16A; F42A)}IALRAYNQSEAGSHTLQMMFGCDVGS
 SDG RFLRGYHQYAYDGKDYLKEDLRSWTAADMAAQITKRKWEAAHVAEQRAYLEGTCVD
 GLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWORDGEDQT
 QDELVETRPCGDGTFQKWA^{AAAGG linker}AVVVP SGEEQRYTCHVQHEGLPKPLTLRWE**AAAGGDKTH**
TCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
 VHN^{IL2(H16A; F42A)}AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
 PREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD
 GSFFLYSKLTVDKSRWQQGNV^{AAAGG linker}FS^{hlgG1 Fc (L234A; L235A)}CSVMHEALHNHYTQKSLSLSPGK** (SEQ ID NO:406)

IL2(H16A; F42A) – bold

(G4S)4 linker – italicized (SEQ ID NO:380)

HLA-A*2402 (Y84A; A236C) – double underlined

AAAGG linker – bold and italicized (SEQ ID NO:283)

hlgG1 Fc (L234A; L235A) – bold and underlined

FIG. 4C

Construct 3159

GSHSMRYFSTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRIALRAYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWQRDGEDQTQDELVETRPCGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWEAAAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
HYTQKSLSLSPGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILN
GINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSK
NFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSHS
TLTGGGGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSHISTLT
 (SEQ ID NO:407)

HLA-A*24:02 – double underlined

Human IgG1 Fc (LALA) – italicized

(G4S)₃ and (G4S)₄ – underlined (SEQ ID NOs:379-380)

IL-2 (H16A; F42A) – bold

FIG. 4D

Construct 2752

CMTWNQMNLGGGGSGGGSGGGGS*IQRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDI*
EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVK
WDRDM (SEQ ID NO:408)

epitope: CMTWNQMNL – WT1 (235-243) (SEQ ID NO:266)
(G4S)₃ – underlined (SEQ ID NO:379)
 β 2M (R12C) – italicized

FIG. 4E

Construct 2753

CYTWNQMNLGGGGSGGGSGGGGS*IQRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDIE*
VDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVKW
DRDM (SEQ ID NO:409)

epitope: CYTWNQMNL – WT1 (235-243) (SEQ ID NO:267)
(G4S)₃ – underlined (SEQ ID NO:379)
 β 2M (R12C) – italicized

FIG. 5A

GenBank 3S7G_A

Homo sapiens IgG1 Fc

227 aa

```
1 dkthtcppcp apellggpsv flfppkpkdt lmisrtpevt cvvvdvshed pevknwyvd
61 gvevhnaktk preeqynsty rvsvltvlh qdwlngkeyk ckvsnkappa piektiskak
121 gqprepvyt lpsrdeltk nqvsltclvk gfypsdiave wesngqpenn ykttppvlds
181 dgsfflyskl tvdksrwqqg nvfscsvmhe alhnhytqks lslspgk
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GenBank AAN76044

Homo sapiens IgG2 Fc (amino acids 99-325)

227 aa

```
1 stkgpsvfpl apcsrsts taalgclvkd yfpepvtvsw nsgaltsgvh tfpavlqssg
61 lyslssvvtv pssnfgtqty tcnvdhkpsn tkvdkterk cvecppcpa ppvagpsvfl
121 fppkpkdtlm isrtpevtcv vvdvshedpe vqfnwyvdgv evhnaktkpr eeqfnstfrv
181 vsvltvvhqdw lngkeykck vsnkglpapi ektisktkgq prepqvytlp psreemtknq
241 vsltclvkgf ypsdiavewe sngqpennyk ttpmldsdg sfflyskltv dksrwqqgnv
301 fscsvmheal hnhytqksls lspgk
```

GenBank AAW65947

Homo sapiens IgG3 Fc (amino acids 19-246)

238 aa

```
1 hkpsntkvdk rvelktpkgd tthtcppcpa pellggpsvf lfppkpkdtl misrtpevtc
61 vvvvdvshedp evknwyvdg vevhnaktk preeqynstyr vvsvltvlhq dwlngkeykc
121 kvsnkappa iektiskakg qprepvytl ppsrdeltkn qvsltclvkg fypsdiavew
181 esngqpenny kttppvlds dgsfflyskl tvdksrwqqg nvfscsvmhea lhnhytqksl
241 slspgk
```

FIG. 5B

GenBank AAA52770

Homo sapiens IgD Fc (amino acids 162-383)

222 aa

```
1 ptkapdvfpi isgcrhpkdn spvvlacit gyhptsvtvt wymgtqsqqp rtfpeiqrdd
61 syymtssqls tplqqwrqge ykcvvqhtas kskkeifrwp espkaqassv ptaqpqaegs
121 lakattapat trntgrggee kkkekekeeq eeretktpec pshtqplgvy lltpavqdlw
181 lrdkatftcf vvgSDLkdah ltwevagkvp tggveeglle rhsngsqsqh sriltprslw
241 nagtsvtctl nhpslppqrl malrepaaqa pvklslnlla ssdppeaasw llcevsgfsp
301 pnillmwled qrevntsgfa parpppqprs ttfwawsvlr vpappspqpa tytcvvshed
361 srtilnasrs levsvtldhg pmk
```

GenBank 0308221A

Homo sapiens IgM Fc

276 aa

```
1 vtstltikzs dwlgesmftc rvdhrgltfq qnassmcvpd qdtairvfai ppsfasiflt
61 kstkltclvt dltybsvti swtreengav kthtnisesh pnatfsavge asicedbdws
121 gerftctvth tdlpsplkqt isrpkgvalh rpbvylppa rzzlnlresa titclvtgfs
181 padvfvevmq rgeplspqky vtsapmpepq apgryfahsi ltvseeewnt ggtytcvvah
241 ealpnrvter tvdkstgkpt lynvslvmsd tagtcy
```

FIG. 5C

GenBank P01876

Homo sapiens IgA Fc (amino acids 120-353)

234 aa

```
1 asptspkvfp lsicstqpdg nvviacivqg ffpqeplsvt wsesggqvta rnfppsqqdas
61 gdlyttssql tlpatqclag ksvtchvkhy tnpsqdvtp cpvpstpptp spstpptpsp
121 scchprlslh rpaledlllg seanltctlt glrdasgvtf twtpssgksa vggppperdlc
181 gcysvssvlp gcaepwnhgw tftctaaype sktpltatls ksgntfrpev hllpppseel
241 alnelvtltc largfspkdv lvrwlqgsqe lprekyltwa srqepsqgtt tfavtsilrv
301 aaedwkkgt fscmvghcal plaftqktid rlagkpthvn vsvvmaevdg tcy
```

GenBank 1F6A_B

Homo sapiens IgE Fc (amino acids 6-222)

212 aa

```
1 adpcdsnprg vsaylsrpsp fdlfirksp itclvvdlap skgtvnltws rasgkpvnhs
61 trkeekqrng tltvtstlpv gtrdwieget yqcrvthphl pralmrsttk tsgpraapev
121 yafatpewpg srdkrtlacl iqnfmpedis vqwlhnevql pdarhsttqp rktkgsgffv
181 fsrlevtrae weqkdeficr avheaaspsq tvqravsvnp gk
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GenBank P01861

Homo sapiens IgG4 Fc (amino acids 100-327)

228 aa

```
1 astkgpsvfp lapcsrstse staalgclvk dyfpepvtvs wnsqaltsgv htfpavllqss
61 glyslssvvt vpssslgktk ytcnvdhkps ntkvdkrves kygppcpscp apeflggpsv
121 flfppkpkdt lmsrtpevt cvvvdvsqed pevqfnwyvd gvevhnatk preeqfnsty
181 rvsvltvlh qdwlngkeyk ckvsnkglps siektiskak gqprepvyt lppsqeemtk
241 nqvsltclvk gfypsdiave wesngqpenn ykttppvlds dgsfflysrl tvdksrwqeg
301 nvfscsvmhe alhnhytqks lsllslgk
```

FIG. 5D

WT Human IgG1 Fc Sequence: -
DKHTCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

FIG. 5E

Human IgG1 Fc Mutant: L234F/L235E/P331S (Triple Mutant "TM")
DKHTCPCPCAPPEEAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

FIG. 5F

Human IgG1 Fc Mutant: N297A
DKHTCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

FIG. 5G

Human IgG1 Fc Mutant: L234A/L235A ("LALA")
DKHTCPCPCAPAEAAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Residue numbered according to EU index (Kabat Numbering)

FIG. 5H

Human IgG1 Fc Mutant: L234A/L235A ("LALA") without C-terminal Lys

DKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPG

FIG. 6

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NP_004039.1  msrvalavlallslsgleaiqrtpkiqvysrhrpaengksnflncyvsgfhpsdievdll 60
NP_001009066.1 msrvalavlallslsgleaiqrtpkiqvysrhrpaengksnflncyvsgfhpsdievdll 60
NP_001040602.1 msrvalavlallslsgleaiqrtpkiqvysrhrpaengksnflncyvsgfhpsdievdll 60
NP_776318.1   marfvalvllgllslsgldaiqrppkiqvysrhrppedgkpnynlncyvvygfhppqieidl 60
NP_033865.2   marsvtlvflvsltglyaiqktpqiqvysrhrppengkpnlncyvtqfhhphieiqml 60
               *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *:
NP_004039.1  kngeriekvehsdlsfskdwsfylllytteftptekdeyacrnhvltlsqpkivkwdrdm 119
NP_001009066.1 kngeriekvehsdlsfskdwsfylllytteftptekdeyacrnhvltlsqpkivkwdrdm 119
NP_001040602.1 kngekngkvehsdlsfskdwsfylllytteftptekdeyacrnhvltlsqprtivkwdrdm 119
NP_776318.1   kngekik-seqsdlsfskdwsfyllshaftpnkskdqyscrvkhtlegprivkwdrdl 118
NP033865      kngkkipkvemsdmsfskdwsfyllahtftptetdyacrkvkhasmaepktvywdrdm 119
               ***::: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *: * *:

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FIG. 7A

Homo sapiens HLA-A**5A.1 HLA-A*01:01:01:01 NCBI (National Center for Biotechnology Information)**

Accession NP_001229687.1

(SEQ ID NO: //)

1 MAVMAPRTLL LLLSGALALT QTWAGSHSMR YFFTSVSRPG RGEPRFIAVG YVDDTQFVRF
 61 DSDAASQKME PRAPWIEQEG PEYWDQETRN MKAHSQTDRA NLGTLRGYNN QSEDGSHTIQ
 121 IMYGCDVGPD GRFLRGYRQD AYDGKDYIAL NEDLRSWTAA DMAAQITKRK WEAVHAAEQR
 181 RYVLEGRCDV GLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT
 241 WORDGEDQTQ DTELVEPTRPA GDGTFQKWAA VVPSGEEQR YTCHVQHEGL PKPLTLRWEL
 301 SSQPTIPIVG IIAGLVLLGA VITGAVVAHV MWRKSSDRK GGSYTQAASS DSAQGSQVSL
 361 TACKV (SEQ ID NO: 23)

5A.2 HLA-A*1101 NCBI Accession P13746.1

1 MAVMAPRTLL LLLSGALALT QTWAGSHSMR YFYTSVSRPG RGEPRFIAVG YVDDTQFVRF
 61 DSDAASQKME PRAPWIEQEG PEYWDQETRN VKAQSQTDRV DLGTLRGYNN QSEDGSHTIQ
 121 IMYGCDVGPD GRFLRGYRQD AYDGKDYIAL NEDLRSWTAA DMAAQITKRK WEAAHAAEQQ
 181 RAYLEGRCDV GLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT
 241 WORDGEDQTQ DTELVEPTRPA GDGTFQKWAA VVPSGEEQR YTCHVQHEGL PKPLTLRWEL
 301 SSQPTIPIVG IIAGLVLLGA VITGAVVAHV MWRKSSDRK GGSYTQAASS DSAQGSQVSL
 361 TACKV (SEQ ID NO: 24)

5A.3 HLA-A*2402 NCBI Accession P05534.2

1 MAVMAPRTL V LLLSGALALT QTWAGSHSMR YFSTSVSRPG RGEPRFIAVG YVDDTQFVRF
 61 DSDAASQKME PRAPWIEQEG PEYWDEETGK VKAHSQTDRE NLRIALRYNN QSEAGSHTIQ
 121 MMFGCDVGS D GRFLRGYHQY AYDGKDYIAL KEDLRSWTAA DMAAQITKRK WEAAHVAEQQ
 181 RAYLEGTCVD GLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT
 241 WORDGEDQTQ DTELVEPTRPA GDGTFQKWAA VVPSGEEQR YTCHVQHEGL PKPLTLRWEF
 301 SSQPTVPIVG IIAGLVLLGA VITGAVVAHV MWRNSSDRK GGSYSQAASS DSAQGSQVSL
 361 TACKV (SEQ ID NO: 25)

5A.4 HLA-A*3303 NCBI Accession AAA79865.1

1 MAVMAPRTLL LLLL GALALT QTWAGSHSMR YFTTSVSRPG RGEPRFIAVG YVDDTQFVRF
 61 DSDAASQKME PRAPWIEQEG PEYWDRNTRN VKAHSQIDRV DLGTLRGYNN QSEAGSHTIQ
 121 MMYGCDVGS D GRFLRGYQQD AYDGKDYIAL NEDLRSWTAA DMAAQITQRK WEAAHVAEQL
 181 RAYLEGTCVE GLRRYLENGK ETLQRTDPPK THMTHHAVSD HEATLRCWAL SFYPAEITLT
 241 WORDGEDQTQ DTELVEPTRPA GDGTFQKWA S VVPSGQEQY YTCHVQHEGL PKPLTLRWEF
 301 SSQPTIPIVG IIAGLVLFGA VFAGAVVAHV RWRKSSDRK GGSYSQAASS DSAQGSQVSL
 361 TACKV (SEQ ID NO: 26)

SUBSTITUTE SHEET (RULE 26)

FIG. 7B

Homo sapiens HLA-B*07:02:01 HLA-B GenBank Accession NP_005505.2

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1 mlvmaprtvl lllsaalalt etwagshsmr yfytsvsrpg rgeprfisvg yvddtqfvrf
61 dsdaaspree prapwiegeg peywdrentqi ykaqaqtdre slrnrlgyyn qseagshtlq
121 smygcdvgpd grllrghdqy aydgkdyial nedlrswwta dtaaqitqrk weaareaeqr
181 raylegecve wlrrylengk dkleradppk thvthhpisd heatlrcwal gfypaeitlt
241 wqrdgedqtq dtelvetrpa gdrtfqkwaa vvvpsgeeqr ytchvqhegl pkpltlrwep
301 ssqstvpiwg ivaglavlav vvigavvaav mcrckssggk ggsysqaacs dsaggsdvsf
361 ta (SEQ ID NO: 27)
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FIG. 7C

Homo sapiens HLA-C

HLA-C GenBank Accession NP_001229971.1,

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1 mrvmaprall lllsgglalt etwacshsmr yfdtavsrbg rgeprfisvg yvddtqfvrf
61 dsdaasprge prapwvegeg peywdretqn ykrqaqadv slrnrlgyyn qsedgshtlq
121 rmygcdlgpd grllrgyds aydgkdyial nedlrswwta dtaaqitqrk leaaraaeql
181 raylegtcve wlrrylengk etlqraepk thvthhplsd heatlrcwal gfypaeitlt
241 wqrdgedqtq dtelvetrpa gdgtfqkwaa vvvpsgqeqr ytchmqhegl qepltlswep
301 ssqptipimg ivaglavlvv lavlgavva mmcrckssgg kggscsqaac snsaggsdes
361 litck (SEQ ID NO: 28)
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FIG. 8 (Cont.)

236

HLA-A	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPA	GDGTF
HLA-B	RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPA	GDRTF
HLA-C	RAEPPKTHVTHHPLSDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPA	GDGTF
HLA-A*0201	RTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL	VETRPA	GDGTF
MOUSE H2K	RTDSPKAHVITYHPRSQVDVTLRCWALGFYPADITLTWQLNGEDLTQDMEL	VETRPA	GDGTF
HLA_A(var. 2)	RTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL	VETRPA	GDGTF
HLA_A(var. 2C)	RTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL	VETRPA	GDGTF
HLA-A(var. 2CP)	RTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL	VETRPA	GDGTF
HLA-A*1101	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPA	GDGTF
HLA-A*2402	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPA	GDGTF
HLA-A*3303	RTDPPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL	VETRPA	GDGTF
	*.: *.*:.*: * :.*****.****.***** :*** ** *****.** **		
		aac5	aac6

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HLA-A      QKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-B      QKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-C      QKWAADVVPSSGEEQRYTCHMQHEGLQEPPLTSWE (SEQ ID NO://)
HLA-A*0201 QKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
MOUSE H2K   QKWAADVVPPLGKEQNYTCHVHHKGLPEPLTLRW (SEQ ID NO://)
HLA_A(var. 2) QKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA_A(var. 2C) QKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A(var. 2CP) QKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A*1101  QKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRWEL (SEQ ID NO://)
HLA-A*2402  QKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A*3303  QKWAADVVPSSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
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FIG. 9A

A*0101	GSHSMRYFFTSVSRPGRGEPREFIAVGYVDDTQFVRFSDAASQKMEPRAPWIEQEGPEYW	60
A*0201	GSHSMRYFFTSVSRPGRGEPREFIAVGYVDDTQFVRFSDAASQKMEPRAPWIEQEGPEYW	60
A*0301	GSHSMRYFFTSVSRPGRGEPREFIAVGYVDDTQFVRFSDAASQKMEPRAPWIEQEGPEYW	60
A*1101	GSHSMRYFFTSVSRPGRGEPREFIAVGYVDDTQFVRFSDAASQKMEPRAPWIEQEGPEYW	60
A*2301	GSHSMRYFFTSVSRPGRGEPREFIAVGYVDDTQFVRFSDAASQKMEPRAPWIEQEGPEYW	60
A*2402	GSHSMRYFFTSVSRPGRGEPREFIAVGYVDDTQFVRFSDAASQKMEPRAPWIEQEGPEYW	60
A*2407	GSHSMRYFFTSVSRPGRGEPREFIAVGYVDDTQFVRFSDAASQKMEPRAPWIEQEGPEYW	60
A*3303	GSHSMRYFFTSVSRPGRGEPREFIAVGYVDDTQFVRFSDAASQKMEPRAPWIEQEGPEYW	60
A*3401	GSHSMRYFFTSVSRPGRGEPREFIAVGYVDDTQFVRFSDAASQKMEPRAPWIEQEGPEYW	60

	84	
A*0101	DQETRNKKAHSQTDRANLGTLRGYYNQSEAGSHTIQIMYGCDVGPDGRFLRGYRQDAYDG	120
A*0201	DGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSQDWRLRGYHQYAYDG	120
A*0301	DQETRNKKAHSQTDRVDLGTLRGYYNQSEAGSHTIQIMYGCDVGSQDGRFLRGYRQDAYDG	120
A*1101	DQETRNKKAHSQTDRVDLGTLRGYYNQSEAGSHTIQIMYGCDVGPDGRFLRGYRQDAYDG	120
A*2301	DEETGKVKKAHSQTDRENLRALRYYNQSEAGSHTLQMMFGCDVGSQDGRFLRGYHQYAYDG	120
A*2402	DEETGKVKKAHSQTDRENLRALRYYNQSEAGSHTLQMMFGCDVGSQDGRFLRGYHQYAYDG	120
A*2407	DEETGKVKKAHSQTDRENLRALRYYNQSEAGSHTLQMMFGCDVGSQDGRFLRGYHQYAYDG	120
A*3303	DRNTRNVKAHSQIDRVDLGTLRGYYNQSEAGSHTIQMMYGCDVGSQDGRFLRGYQQDAYDG	120
A*3401	DRNTRNVKAHSQIDRVDLGTLRGYYNQSEAGSHTIQRMYGCDVGPDGRFLRGYQQDAYDG	120
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	aac1 aac2	
	139	
A*0101	KDYIALNEDLRSWTAADMAAQITKRKWEAAHVAEQQRRVYLEGRCVDGLRRYLENGKETLQ	180
A*0201	KDYIALKEDLRSWTAADMAAQITKHKWEAAHVAEQLRAYLEGTCVEWLRRYLENGKETLQ	180
A*0301	KDYIALNEDLRSWTAADMAAQITKRKWEAAHVAEQLRAYLDGTCVEWLRRYLENGKETLQ	180
A*1101	KDYIALNEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYLEGRCVEWLRRYLENGKETLQ	180
A*2301	KDYIALKEDLRSWTAADMAAQITQRKWEAAHVAEQLRAYLEGTCVDGLRRYLENGKETLQ	180
A*2402	KDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYLEGTCVDGLRRYLENGKETLQ	180
A*2407	KDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYLEGTCVDGLRRYLENGKETLQ	180
A*3303	KDYIALNEDLRSWTAADMAAQITQRKWEAAHVAEQLRAYLEGTCVEWLRRYLENGKETLQ	180
A*301	KDYIALNEDLRSWTAADMAAQITQRKWEAAHVAEQQRAYLEGTCVEWLRRYLENGKETLQ	180

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FIG. 9A (Cont.)

FIG. 9A (Cont.)

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A*0101	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTQWRDGEDQTQDTEIVETRPAGDGTG	241
A*0201	RTDAPKTHMTHHAUSDHEATLRCWALSFPYAEITLTQWRDGEDQTQDTEIVETRPAGDGTG	241
A*0301	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTQWRDGEDQTQDTEIVETRPAGDGTG	241
A*1101	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTQWRDGEDQTQDTEIVETRPAGDGTG	241
A*2301	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTQWRDGEDQTQDTEIVETRPAGDGTG	241
A*2402	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTQWRDGEDQTQDTEIVETRPAGDGTG	241
A*2407	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTQWRDGEDQTQDTEIVETRPAGDGTG	241
A*3303	RTDPPKTHMTHHAUSDHEATLRCWALSFPYAEITLTQWRDGEDQTQDTEIVETRPAGDGTG	241
A*3401	RTDAPKTHMTHHAUSDHEATLRCWALSFPYAEITLTQWRDGEDQTQDTEIVETRPAGDGTG	241
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A*0101	QKWAAVVVPSPGEEQRYTCHVQH EGLPKPLTLRWEL	276 (SEQ ID NO: 198)
A*0201	QKWAAVVVPSPQEQR Y TCHVQH EGLPKPLTLR WEP	276 (SEQ ID NO: 44)
A*0301	QKWAAVVVPSPGEEQRYTCHVQH EGLPKPLTLRWEL	276 (SEQ ID NO: 200)
A*1101	QKWAAVVVPSPGEEQRYTCHVQH EGLPKPLTLRWEL	276 (SEQ ID NO: 49)
A*2301	QKWAAVVVPSPGEEQRYTCHVQH EGLPKPLTLR WEP	276 (SEQ ID NO: 202)
A*2402	QKWAAVVVPSPGEEQRYTCHVQH EGLPKPLTLR WEP	276 (SEQ ID NO: 50)
A*2407	QKWAAVVVPSPGEEQRYTCHVQH EGLPKPLTLR WEP	276 (SEQ ID NO: 204)
A*3303	QKWASVVVPSPQEQR Y TCHVQH EGLPKPLTLR WEP	276 (SEQ ID NO: 51)
A*3401	QKWASVVVPSPQEQR Y TCHVQH EGLPKPLTLR WEP	276 (SEQ ID NO: 206)
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FIG. 9B

GSHSMRYFX1TSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQX2MEPRAPWIEQEGPEYWDX
3X4TX5X6X7KAX8SQX9X10RX11X12LX13X14X15X16X17YNOSEX18GSHTX19QX20
 MX21GCDVGX22DX23RFLRGYX24QX25AYDGKDYIALX26EDLRSWTAADMAAQX27TX28
29KWEX30X31X32EAEQX33RX34YLY35GX36CVX37X38LRRYLENGKETLQRTDX39PK
 THMTHHX40X41SDHEATLRCWALX42FYPAEITLTWQDGEDQTQDTELVETRAPAGDGTFOKW
 AX43VVVP SGX44EORYTCHVOHEGLPKPLTLRWEX45

X1 is F, Y, S, or T; X2 is K or R; X3 is Q, G, E, or R; X4 is N or E; X5 is R or G; X6 is N or K; X7 is M or V; X8 is H or Q; X9 is T or I; X10 is D or H; X11 is A, V, or E; X12 is N or D; X13 is G or R; X14 is T or I; X15 is L or A; X16 is R or L; X17 is G or R; X18 is A or D; X19 is I, L, or V; X20 is I, R or M; X21 is F or Y; X22 is S or P; X23 is W or G; X24 is R, H, or Q; X25 is D or Y; X26 is N or K; X27 is T or I; X28 is K or Q; X29 is R or H; X30 is A or T; X31 is A or V; X32 is H or R; X33 is R, L, Q, or W; X34 is V or A; X35 is D or E; X36 is R or T; X37 is D or E; X38 is W or G; X39 is P or A; X40 is P or A; X41 is V or I; X42 is S or G; X43 is A or S; X44 is Q or E; and X45 is P or L.

FIG. 10A

B*0702	GSHSMRYFYTSVSRPGRGEPFRFISVGIVDDTQFVRFSDAASPREEPRAPWIEQEGPEYW	60
B*0801	GSHSMRYFDTAMSRPGRGEPFRFISVGIVDDTQFVRFSDAASPREEPRAPWIEQEGPEYW	60
B*1502	GSHSMRYFYTAMSRPGRGEPFRFIAVGIVDDTQFVRFSDAASPRMAPRAPWIEQEGPEYW	60
B*3802	GSHSMRYFYTSVSRPGRGEPFRFISVGIVDDTQFVRFSDAASPREEPRAPWIEQEGPEYW	60
B*4001	GSHSMRYFHTAMSRPGRGEPFRFITVGIVDDTQFVRFSDATSPRKEPRAPWIEQEGPEYW	60
B*4601	GSHSMRYFYTAMSRPGRGEPFRFIAVGIVDDTQFVRFSDAASPRMAPRAPWIEQEGPEYW	60
B*5301	GSHSMRYFYTAMSRPGRGEPFRFIAVGIVDDTQFVRFSDAASPRTEPRAPWIEQEGPEYW	60

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		89	
B*0702	DRNTQIYKAQAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPGRLLRGHDQYAYDG	120	
B*0801	DRNTQIFKTNTQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPGRLLRGHNQYAYDG	120	
B*1502	DRNTQISKNTNTQTYRESLRNLRGYYNQSEAGSHIIQRMYGCDVGPGRLLRGYDQSAIDG	120	
B*3802	DRNTQICKNTNTQTYRESLRNLRGYYNQSEAGSHTLQRMYGCDVGPGRLLRGHNQFAYDG	120	
B*4001	DRETQISKNTNTQTYRESLRNLRGYYNQSEAGSHTLQRMYGCDVGPGRLLRGHNQYAYDG	120	
B*4601	DRETQYKQRQAQTDREVSLRNLRGYYNQSEAGSHTLQRMYGCDVGPGRLLRGHDQSAIDG	120	
B*5301	DRNTQIFKTNTQTYRENLRALRYNQSEAGSHIIQRMYGCDLGPGRLLRGHDQSAIDG	120	

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		139	
B*0702	KDYIALNEDLRSWTAADTAAQITQKWEAAREAEQRRAYLEGECEVWLRRLYLENGKDKLE	180	
B*0801	KKYIALNEDLRSWTAADTAAQITQKWEAARVAEQDRAYLEGTCEVWLRRLYLENGKDTLE	180	
B*1502	KDYIALNEDLSSWTAADTAAQITQKWEAAREAEQLRAYLEGLCEVWLRRLYLENGKETLQ	180	
B*3802	KKYIALNEDLSSWTAADTAAQITQKWEAARVAEQLRTYLEGTCEVWLRRLYLENGKETLQ	180	
B*4001	KDYIALNEDLRSWTAADTAAQISQKLEAARVAEQLRAYLEGECEVWLRRLYLENGKDKLE	180	
B*4601	KDYIALNEDLSSWTAADTAAQITQKWEAAREAEQWRAYLEGLCEVWLRRLYLENGKETLQ	180	
B*5301	KDYIALNEDLSSWTAADTAAQITQKWEAARVAEQLRAYLEGLCEVWLRRLYLENGKETLQ	180	

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FIG. 10A (Cont.)

B*0702	RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQTQDTEL	VETRPAGDRTF	241
B*0801	RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQTQDTEL	VETRPAGDRTF	241
B*1502	RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQTQDTEL	VETRPAGDRTF	241
B*3802	RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQTQDTEL	VETRPAGDRTF	241
B*4001	RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQTQDTEL	VETRPAGDRTF	241
B*4601	RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQTQDTEL	VETRPAGDRTF	241
B*5301	RADPPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQDGEDQTQDTEL	VETRPAGDRTF	241
*****:*****			
			236
			aac5 aac6

B*0702 QKWAAVVPSGEEQRYTCHVQHEGLPKPLTLRWE 276
 B*0801 QKWAAVVPSGEEQRYTCHVQHEGLPKPLTLRWE 276
 B*1502 QKWAAVVPSGEEQRYTCHVQHEGLPKPLTLRWE 276
 B*3802 QKWAAVVPSGEEQRYTCHVQHEGLPKPLTLRWE 276
 B*4001 QKWAAVVPSGEEQRYTCHVQHEGLPKPLTLRWE 276
 B*4601 QKWAAVVPSGEEQRYTCHVQHEGLPKPLTLRWE 276
 B*5301 QKWAAVVPSGEEQRYTCHVQHEGLPKPLTLRWE 276

FIG. 10B

GSHSMRYFX1TX2X3SRPGRGEPFIX4VGYVDDTX5FVRFDSAX6SPRX7X8PRAPWIEQEG
 PEYWDRX9TX10X11KTX12X13TX14YX15X16NLX17X18X19X20YYNQSEAGSHX21X
 22QX23MYGCDLGPDRLLRGHDQSAYDGKDYLALNEDLX24SWTAADTAAQIX25QRKX26EA
 ARX27AEQX28RX29YLEGX30CWEWLRRYLENGKX31X32LX33RADPPKTHVTHHPX34SDH
 EATLRCWALGFYPAEITLTWQDGEDQTQDTEL VETRPAGDRTFQKWAAVVPSGEEQRYTCHV
 QHEGLPKPLTLRWE

X1 is H, Y, or D; X2 is A or S; X3 is M or V; X4 is A, S, or T;
 X5 is Q or L; X6 is A or T; X7 is E, M K, or T; X8 is A or T; X9
 is E or N; X10 is I or K; X11 is Y, F, S, or C; X12 is N or Q;
 X13 is A or T; X14 is D or Y; X15 is E or V; X16 is S or N; X17
 is T, N, or I; X18 is A or L; X19 is L, or R; X20 is R or G; X21
 is T or I; X22 is L or I; X23 is R or S; X24 is R or S; X25 is S
 or T; X26 is L or W; X27 is E OR V; X28 is R, D, L or W; X29 is
 A or T; X30 is L, E or T; X31 is E or D; X32 is K or T; X33 is E
 or Q; and X34 is I or V.

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FIG. 11A

C*0102	CSHSMKYFFTSVSRPGRGEPFRFISVGYYDDTQFVRFSDAASPRGEPRAPWVEQEGPEYW	60
C*0303	GSHSMRYFYTA VSRPGRGEPHFIAVGYYDDTQFVRFSDAASPRGEPRAPWVEQEGPEYW	60
C*0304	GSHSMRYFYTA VSRPGRGEPHFIAVGYYDDTQFVRFSDAASPRGEPRAPWVEQEGPEYW	60
C*0401	GSHSMRYFSTSVSWPGRGEPFRFIAVGYYDDTQFVRFSDAASPRGEPREP WVEQEGPEYW	60
C*0602	CSHSMRYFDTAVSRPGRGEPFRFISVGYYDDTQFVRFSDAASPRGEPRAPWVEQEGPEYW	60
C*0701	CSHSMRYFDTAVSRPGRGEPFRFISVGYYDDTQFVRFSDAASPRGEPRAPWVEQEGPEYW	60
C*0702	CSHSMRYFDTAVSRPGRGEPFRFISVGYYDDTQFVRFSDAASPRGEPRAPWVEQEGPEYW	60
C*0801	CSHSMRYFYTA VSRPGRGEPFRFIAVGYYDDTQFVRFSDAASPRGEPRAPWVEQEGPEYW	60
C*1502	CSHSMRYFYTA VSRPGRGEPHFIAVGYYDDTQFVRFSDAASPRGEPRAPWVEQEGPEYW	60

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84

C*0102	DRETQKYKRAQTDRVSLRNLRGYNQSEAGSHTLQWMCGLGPDGRLLRGYDQYAYDG	120
C*0303	DRETQKYKRAQTDRVSLRNLRGYNQSEARSHIIQRMYGCDVGPDGRLLRGYDQYAYDG	120
C*0304	DRETQKYKRAQTDRVSLRNLRGYNQSEAGSHIIQRMYGCDVGPDGRLLRGYDQYAYDG	120
C*0401	DRETQKYKRAQADRVNLRKLRGYNQSEDCSHTLQRMFGCDLGPDGRLLRGYNQFAYDG	120
C*0602	DRETQKYKRAQADRVNLRKLRGYNQSEDCSHTLQWMYGCDLGPDGRLLRGYDQYAYDG	120
C*0701	DRETQNYKRAQADRVSLRNLRGYNQSEDCSHTLQRMYGCDLGPDGRLLRGYDQYAYDG	120
C*0702	DRETQKYKRAQADRVSLRNLRGYNQSEDCSHTLQRMSCDLPDGRLLRGYDQYAYDG	120
C*0801	DRETQKYKRAQTDRVSLRNLRGYNQSEAGSHTLQRMYGCDLGPDGRLLRGYNQFAYDG	120
C*1502	DRETQNYKRAQTDRVSLRNLRGYNQSEAGSHIIQRMYGCDLGPDGRLLRGHDQYAYDG	120

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139

C*0102	KDYIALNEDLRSWTAADTAAQITQKWEAAREAEQRRAYLEGTCVEWLRRYLENGKETLQ	180
C*0303	KDYIALNEDLRSWTAADTAAQITQKWEAAREAEQLRAYLEGTCVEWLRRYLENGKETLQ	180
C*0304	KDYIALNEDLRSWTAADTAAQITQKWEAAREAEQLRAYLEGTCVEWLRRYLENGKETLQ	180
C*0401	KDYIALNEDLRSWTAADTAAQITQKWEAAREAEQRRAYLEGTCVEWLRRYLENGKETLQ	180
C*0602	KDYIALNEDLRSWTAADTAAQITQKWEAAREAEQWRAYLEGTCVEWLRRYLENGKETLQ	180
C*0701	KDYIALNEDLRSWTAADTAAQITQKLEAARAAEQRAYLEGTCVEWLRRYLENGKETLQ	180
C*0702	KDYIALNEDLRSWTAADTAAQITQKLEAARAAEQRAYLEGTCVEWLRRYLENGKETLQ	180
C*0801	KDYIALNEDLRSWTAADTAAQITQKWEAARTAEQLRAYLEGTCVEWLRRYLENGKETLQ	180
C*1502	KDYIALNEDLRSWTAADTAAQITQKWEAAREAEQLRAYLEGTCVEWLRRYLENGKETLQ	180

*****:*****:***** ***** ***** *****:*****:*****

aac3 aac4

FIG. 11A (Cont.)

		236	
C*0102	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTEL	VETRPAGDGT	241
C*0303	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTEL	VETRPAGDGT	241
C*0304	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTEL	VETRPAGDGT	241
C*0401	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTEL	VETRPAGDGT	241
C*0602	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTEL	VETRPAGDGT	241
C*0701	RAEPPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTEL	VETRPAGDGT	241
C*0702	RAEPPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTEL	VETRPAGDGT	241
C*0801	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTEL	VETRPAGDGT	241
C*1502	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTEL	VETRPAGDGT	241
	*** *****:*****:***** *****	*****	*****
		aac5 aac6	
C*0102	QKWAAMVPSGEEQRYTCHVQHEGLPEPLTLRWE	P 276	
C*0303	QKWAAMVPSGEEQRYTCHVQHEGLPEPLTLRWE	P 276	
C*0304	QKWAAMVPSGEEQRYTCHVQHEGLPEPLTLRWE	P 276	
C*0401	QKWAAMVPSGEEQRYTCHVQHEGLPEPLTLRWE	P 276	
C*0602	QKWAAMVPSGEEQRYTCHVQHEGLPEPLTLRWE	P 276	
C*0701	QKWAAMVPSGEEQRYTCHVQHEGLPEPLTLRWE	P 276	
C*0702	QKWAAMVPSGEEQRYTCHVQHEGLPEPLTLRWE	P 276	
C*0801	QKWAAMVPSGEEQRYTCHVQHEGLPEPLTLRWE	P 276	
C*1502	QKWAAMVPSGEEQRYTCHVQHEGLPEPLTLRWE	P 276	
	*****:*****:***** ***** *		

FIG. 11B

X1SHSMX2YFX3TAVSX4PGRGEPX5FIX6VGYYDDTQFVX7FDSDAASPRGEPRX8PWVEQEG
 PEYWDRETQX9YKRQAQX10DRVX11LRX12LRGYYNQSEX13X14SHX15X16QX17MXX18GC
 DX19GPDGRLLRGX20X21QX22AYDGKDYLALNEDLRSWTAADTAQAQITQRKX23EAARX24A
 EQX25RAYLEGX26CVEWLRRLYLX27NGKX28TLQRAEX29PKTHVTHHPX30SDHEATLRCWA
 LGFYPAEITLTWQX31DGEDQTQDTELVETRPAGDGTX32VPSX33EQRYTCHX34
 QHEGLX35EPPLTLX36WX37P

X1 is C or G; X2 is R or K; X3 is F, Y, S, or D; X4 is R or W;
 X5 is H or R; X6 is A or S; X7 is Q or R; X8 is A or E; X9 is N
 or K; X10 is T or A; X11 is S or N; X12 is N or K; X13 is A or D;
 X14 is G or R; X15 is T or I; X16 is L or I; X17 is W or R; X18
 is C, Y, F, or S; X19 is L, or V; X20 is Y or H; X21 is D or N;
 X22 is Y, F, S, or L; X23 is L or W; X24 is E, A, or T; X25 is
 R, L, or W; X26 is L or T; X27 is E or K; X28 is E or K; X29 is
 H or P; X30 is R or V; X31 is W or R; X32 is V or M; X33 is E or
 Q; X34 is M or V; X35 is P or Q; X36 is R or S; and X37 is P or
 G.

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FIG. 12

HLA-E				
GSHSLKYFHT	SVSRPGRGEP	RFISVGYVDD	TQFVRFNDNA	ASPRMVPRAP
WMEQEGSEYW	DRETRSARDT	AQIFRVNLRT	LRG <u>Y</u> YNQ <u>SX1A</u>	GSHTLQWMHG
CELGPD <u>X2</u> RFL	RGYEQFAYDG	KDYLTILNEDL	RSWTAVDT <u>AA</u>	QISEQKSND
SEAEHQ <u>X3X4</u> YL	EDTCVEWLHK	YLEKGKETLL	HLEPPKTHVT	HHPISDHEAT
LRCWALGFYP	AEITLTWQOD	GEGHTQDTEL	VETRP <u>A</u> GDGT	FQKWAAVVVP
SGEE <u>X5</u> RYTCH	VQHEGL <u>X6</u> EPV	TLRWKPASQP	TIP	
X1= K or E; X2= R or G; X3= R or G; X4= A or V; X5= Q or P; and X6= P or S				
Encompasses: HLA-E*0101 (HLA-E*01:01:01:01); HLA-E*01:03 (HLA-E*01:03:01:01); HLA-E*01:04; HLA-E*01:05; HLA-E*01:06; HLA-E*01:07; HLA-E*01:09; HLA-E*01:10				
HLA-F				
GSHSLR <u>X1</u> FST	AVSRPGRGEP	RYIAVEYVDD	TQFLRFDSDA	AIPRMEPRE <u>X2</u>
WVEQEGPQYW	EWTGYAKAN	AQTDRVALRN	LLR <u>R</u> YNQSEA	GSHTLQGMNG
CDMGPDGRLL	RGYHQHAYDG	KDYISLNEDL	RSWTAADT <u>VA</u>	QITQRFYBAE
EYAEFEFRYL	EGECLELLRR	YLENGKETLQ	RADPPKAHVA	HHPISDHEAT
LRCWALGFYP	AEITLTWQOD	GEEQTQDTEL	VETRP <u>A</u> GDGT	FQKWAAVVVP
<u>X3</u> GEEQRYTCH	VQHEGLPQPL	ILRWEQ <u>SX4</u> QP	TIP	
X1= Y or F; X2= P or Q; X3= S or P; and X4= P or L				
Encompasses: HLA-F*0101 (HLA-F*01:01:01:01); HLA-F*01:02; HLA-F*01:03 (HLA-F*01:03:01:01); HLA-F*01:04; HLA-F*01:05; HLA-F*01:06;				
HLA-G				
GSHSMRYFSA	AV <u>X1</u> RPGRGEP	RFIAMG <u>X2</u> VDD	<u>X3</u> QF <u>X4</u> RFDSDS	ACPRMEPRAP
WVE <u>X5</u> EGPEYW	EEETRNTKAH	AQTRMNLQT	<u>X6</u> RG <u>Y</u> YNQSEA	SSHTLQWM <u>X7</u>
CDL <u>X8X9</u> DGRL <u>X10</u>	RGYEQYAYDG	KDYLA LNEDL	RSWTAADT <u>AA</u>	QISKRKCEAA
NVAEQRRAX <u>X11</u> L	EGTCVEWL <u>X12</u> R	<u>X13</u> LENGKE <u>X14</u> LQ	RADP <u>X15</u> KTHVT	HHPVFDYEAT
LRCWALGFYP	AEIILTWO <u>X16</u> D	GEDQTQDVEL	VETRP <u>A</u> GDGT	FQKWAAVVVP
SGEEQRY <u>X17</u> CH	VQHEGLPEPL	MLRW <u>X18</u> QSSLP	TIP	
X1= S or F; X2= Y or H; X3= T, S, or M; X4= L or V; X5= Q or R; X6= P or L; X7= G or D; X8= G or V; X9= S or C; X10= L or I; X11= Y or H; X12= H or R; X13= Y or H; X14= M or T; X15= P or A; X16= R, W, or Q; X17= T or M; X18= K or E;				
Encompasses: HLA-G*0101 (HLA-G*01:01:01:01); HLA-G*01:02; HLA-G*01:03 (HLA-G*01:03:01:01); HLA-G*01:04 (HLA-G*01:04:01:01); HLA-G*01:06; HLA-G*01:07; HLA-G*01:08; HLA-G*01:09; HLA-G*01:10; HLA-G*01:10; HLA-G*01:11; HLA-G*01:12; HLA-G*01:14; HLA-G*01:15; HLA-G*01:16; HLA-G*01:17; HLA-G*01:18; HLA-G*01:19; HLA-G*01:20; HLA-G*01:22				

FIG. 13

HLA-A	GSHSMRYFXTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQXMEPRAPWIEQEGPEYW	60
HLA-B	GSHSMRYFXTXSRPGRGEPRIAVGYVDDTQFVRFDSDAASPRXXPRAPWIEQEGPEYW	60
HLA-C	XSHSMRYFXTAVSXPRGEPFIIXVGYVDDTQFVRFDSDAASPRGEPXPWVEQEGPEYW	60
HLA-E	GSHSLRYFHTSVSRPGRGEPRIISVGYVDDTQFVRFDSDAASPRMVPRAPWMEQEGSEYW	60
HLA-F	GSHSLRXFSTAVSRPGRGEPRIIAVEYVDDTQFLRFDSDAIPRMEPREXWVEQEGPQYW	60
HLA-G	GSHSMRYFSAAVXRPGRGEPRIAMGXVDDXQFXRFDSDSACPRMEPRAPWVEXEGPEYW	60
	: * : ** : * : *** * **.*: ** *.* ** : **	
		84
HLA-A	DXXTXXXKAXSQXXRXIXXXXXYINQSEKGSHTXQXMXGCDVGXDXRFLRGYXQXAYDG	120
HLA-B	DRXTQXXKTXXTQXYXXIXXXXXYINQSEAGSHXXQXMYGCDLGPDGRLLRGHDQSAIDG	120
HLA-C	DRETQXYKROAQXDRVXIXRLRGYINQSEKXSHXXQXMXGCDXGPDGRLLRGXXQXAYDG	120
HLA-E	DRETRSARDTAQIFRVNIRTLRGYINQSEKXSHXXQXMXGCDXGPDGRLLRGYEQFAYDG	120
HLA-F	EWTTGYAKANAQTDRAVIRNLLIRYINQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG	120
HLA-G	EEETRNTKAHAQTDRMNLOTXRGYINQSEASSHTLQWMIXCDLXXDGRLLRGYEQYAYDG	120
	: * : ***** ** * * * : * : * * * * *	
	aac1 aac2	
		139
HLA-A	KDYIALXEDLRSTAAADMAAQXTXKKWEXXXEAEQXRXYLXGXCXVXXLRRLYLENGKETLQ	180
HLA-B	KDYIALNEDLRSTAAADTAQIXQRKXEAARXAEQXRXYLEGXCVEWLRRLYLENGKXXLX	180
HLA-C	KDYIALNEDLRSTAAADTAQITQRKXEAARXAEQXRAYLEGXCVEWLRRLYLXNGKXTLQ	180
HLA-E	KDYLTINEDLRSTAVDTAAQISEKSNDAASEAEHQXXYLEDTCEWLHLKYLEKGETLL	180
HLA-F	KDYISLNEDLRSTAAADTAQITQRFYEAEEYAEFFRTYLEGECLELLRRLYLENGKETLQ	180
HLA-G	KDYIALNEDLRSTAAADTAQISKRKCEANVAEQRRAXLEGTCVEWLRLXLENGKEXLQ	180
	***: * * * * * : * : * : * : * : * : * : *	
	aac3 aac4	
		236
HLA-A	RTDXPKTHMTHHXXSDHEATLRCWALXFYPAEITLTWQRDGEDQTQDTEIVETRPAGDGTF	241
HLA-B	RADPPKTHVTHHPXSDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEIVETRPAGDRTF	241
HLA-C	RAEXPKTHVTHHPXSDHEATLRCWALGFYPAEITLTWQXDGEDQTQDTEIVETRPAGDGTF	241
HLA-E	HLEPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDGTQDTEIVETRPAGDGTF	241
HLA-F	RADPPKAHVHHPISDHEATLRCWALGFYPAEITLTWQRDGEETQDTEIVETRPAGDGTF	241
HLA-G	RADPXKTHVTHHPVFDYEATLRCWALGFYPAEITLTWQXDGEDQTQDTEIVETRPAGDGTF	241
	: : *.*:*** *.*:***** ***** ***** * : * : * : * : * : *	
	ac5 ac6	
HLA-A	QKWAXVVVPSGXEQRYTCHVQHEGLPKPLTLRWEX-----	276
HLA-B	QKWAADVVPSEGEQRYTCHVQHEGLPKPLTLRWEP-----	276
HLA-C	QKWAADVVPSEGEQRYTCHVQHEGLPEPLTLXWXP-----	276
HLA-E	QKWAADVVPSEGEQRYTCHVQHEGLPEPLTLRWKSPQPTIPI	284
HLA-F	QKWAADVVPSEGEQRYTCHVQHEGLPEPLTLRWKSPQPTIPI	284
HLA-G	QKWAADVVPSEGEQRYTCHVQHEGLPEPLTLRWKSPQPTIPI	284
	**** * * * * * * * * * : * : *	

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FIG. 14A

1715

APTSSSTKKKTQLQLEALLLDLQMLNGINNYKNPKLTRMLTAKFYMPKKATELKHLCLEEEELKP
 LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIS
 TLTGGGGSGGGSGGGSGGGSGGGSAPTSSSTKKKTQLQLEALLLDLQMLNGINNYKNPKLTRMLTA
 KFYMPKKATELKHLCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
 ADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGGGSGSHSMRYFFTSVSRPGRGE
 PRFIAVGYVDDTQFVRFDSDAASQRMERAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRGC
 YNQSEAGSHTVQRMYGCDVGS DWRF LRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEA
 AHVAEQLRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFP AEIT
 LTWQRDGEDQTQDTELVETRECGDGTFOKWA AVVVP SGQEQR YTCHVQHEGLPKPLTLRWEAAAG
 GDKTHTCPPCPAPEAAGGPSVFLFPKPKDTLMI SRTP E VTCVVVDVSHEDPEVKFNWYVDGVEV
 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK
 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:422)

hIL2 (H16A; F42A) -- underlined
(G4S)_n – bold (SEQ ID NO:380)
HLA A0202 (Y84C; A236C) – double underlined
AAAGG – bold (SEQ ID NO:283)
IgG1 Fc (LALA) -- italicized

FIG. 14B

2380

VLDFAPPGAG**C**GGSGGGGSGGGGSIQRTPKIQVYS**C**HPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWRDM (SEQ ID NO:423)

WT1(37-45) epitope: VLDFAPPGA (SEQ ID NO:259)

G2C linker – bold

β 2M (R12C) – underlined

FIG. 14C

2381

RMFPNAPYL**C**GGSGGGGSGGGGSIQRTPKIQVYS**C**HPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWRDM (SEQ ID NO:424)

WT1(126-134) epitope: RMFPNAPYL (SEQ ID NO:260)

G2C linker -- bold

β 2M (R12C) – underlined

FIG. 14D

2405

APTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIS
TLT**GGGSGGGSGGGSGGGSGGGSG**APTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTA
KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLT**GGGSGGGSGGGSGGGSGGGSG**GSHSMRYFFTSVSRPGRGE
PRFIAVGYYDDTQFVRFSDAASQRMEPRAWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRG**C**
YNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEA
AHVAEQLRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFPAEIT
LTWQRDGEDQTQDELVETRP**AG**DGTFQKWAAVVPSGQEQRYTCHVQHEGLPKPLTLRWE**AAAG**
GDKTHTCPCPAPEAAGGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:425)

hIL2 (H16A; F42A) -- underlined
 (G4S)_n – bold (SEQ ID NO:380)
 HLA A0202 (Y84C) – double underlined
 AAAGG – bold (SEQ ID NO:283)
 IgG1 Fc (LALA) – italicized

FIG. 14E

1380

APTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIS
TLTGGGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTA
KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLTGGGSGGGSGGGSGGGSGSHSMRYFFTTSVSRPGRGE
PRFIAVGYYDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRGA
YNQSEAGSHTVQRMYGCDVGS DWRF LRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKEA
AHVAEQLRAYLEGTCEWLRRLRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEIT
LTWQRDGEDQTQDTEL VETRCGDGTFQKWA AVVVP SGQEQRYTCHVQHEGLPKPLTLRWEAAAG
GDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:426)

hIL2 (H16A; F42A) -- underlined
 (G4S)_n -- bold (SEQ ID NO:380)
 HLA A0202 (A236C) -- double underlined
 AAAGG -- bold (SEQ ID NO:283)
 IgG1 Fc (LALA) -- italicized

FIG. 14F

2762

VLDFAPPGAGCGGSGGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM (SEQ ID NO:427)

WT1(37-45) epitope: VLDFAPPGA (SEQ ID NO:259)

G2C linker – bold

β 2M – underlined

FIG. 14G

2763

RMFPNAPYLGCGGSGGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM (SEQ ID NO:428)

WT1 (126-134) epitope: RMFPNAPYL (SEQ ID NO:260)

G2C linker – bold

β 2M – underlined

FIG. 14H

3625

YMFPNAPYLGCGGSGGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM (SEQ ID NO:429)

WT1 (126-134; R126Y) epitope: YMFPNAPYL (SEQ ID NO:264)

G2C linker – bold

β 2M (R12C) – underlined

FIG. 14I

3626

YMFPNAPYL**GCGGSGGGGSGGGG**SIQRTPKIQVYSRHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM (SEQ ID NO:430)

WT1 (126-134; R126Y) epitope: YMFPNAPYL (SEQ ID NO:264)

G2C linker – bold

β 2M – underlined

FIG. 14J

1715 without C-terminal Lys

APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIS
TLT**GGGGSGGGSGGGSGGGGS**APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTA
KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLT**GGGGSGGGSGGGSGGGGS**GSHSMRYFFTSVSRPGRGE
PRFIAVGIVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRG**C**
YNQSEAGSHTVQRMYGCDVGS DWRF LRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKKHWEA
AHVAEQLRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFP AEIT
LTWQRDGEDQTQDTEL VETRE**C**GDGTFQKWA AVVVP SGQE QRYTCHVQHEGLPKPLTLRWE**AAAG**
GDKTHTCPPCPAPEAAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:486)

hIL2 (H16A; F42A) -- underlined

(G4S)_n – bold (SEQ ID NO:380)

HLA A0202 (Y84C; A236C) – double underlined

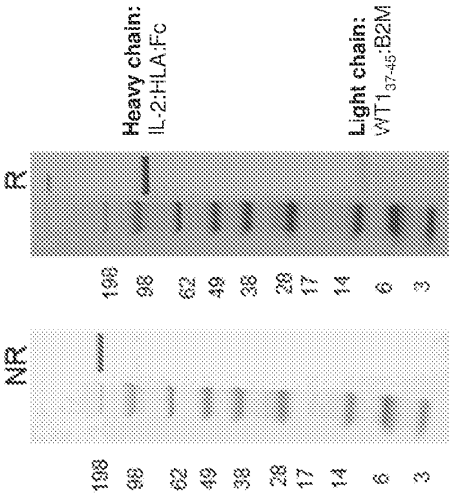
AAAGG – bold (SEQ ID NO:283)

IgG1 Fc (LALA) -- italicized

FIG. 15

	1715-2380
Serotype	A02:01
Peptide	WT1 (37-45)
MOD	2 x IL-2 (H16A, F42A)
Engineered Disulfide	R12C-A236C; G2C-Y84C
Titer (mg/L)	309
% monomer (post ProtA)	80
% monomer (post SEC)	98
Stability (25d @ 37°C / 42°C)*	51/2
Freeze-thaw (3x)	Stable, No Change
Tm** (°C)	52 (pHLA)
	67 (IL2)
	82 (Fc)
T _{agg} ** (°C)	47
Intact mass (LC-MS)	Confirmed

* % monomer after one month incubation at 37°C or 42°C, respectively
** buffer = unfractionated, PBS + 365 mM NaCl, pH 7.4



Non-reduced (NR) and Reduced (R)
Coomassie-stained SDS-PAGE
2.0 µg/lane

FIG. 16

	1715-2381
Serotype	A02:01
Peptide	WT1 (126-134)
MOD	2 x IL-2 (H16A, F42A)
Engineered Disulfide	R12C-A236C; G2C-Y84C
Titer (mg/L)	680
% monomer (post ProtA)	79
% monomer (post SEC)	97
Stability (28d @ 37°C / 42°C)*	37/3
Freeze-thaw (3x)	Stable, No Change
T _m (°C)	51 (pHLA)
	68 (IL2)
	82 (Fc)
T _{agg} (°C)	47
Intact mass (LC-MS)	Confirmed

* % monomer after one month incubation at 37°C or 42°C, respectively
** buffer = unfractionated, PBS + 365 mM NaCl, pH 7.4

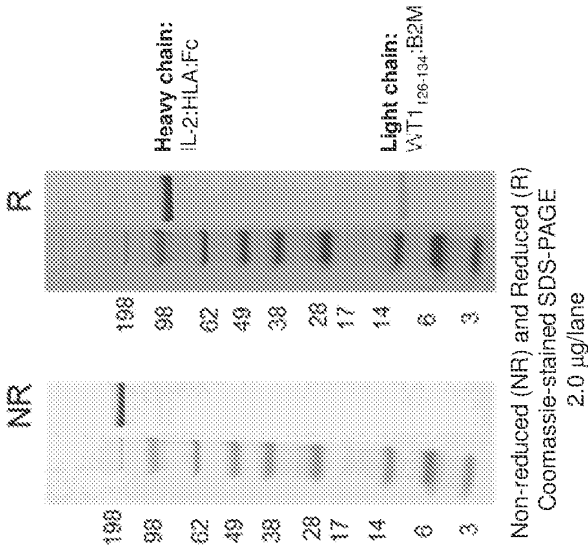


FIG. 17A

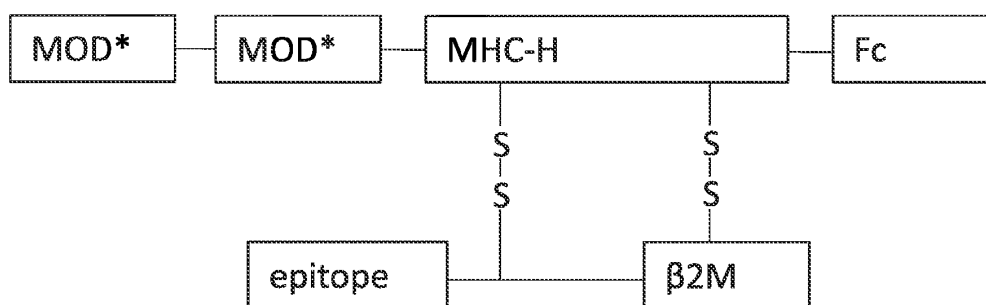


FIG. 17B

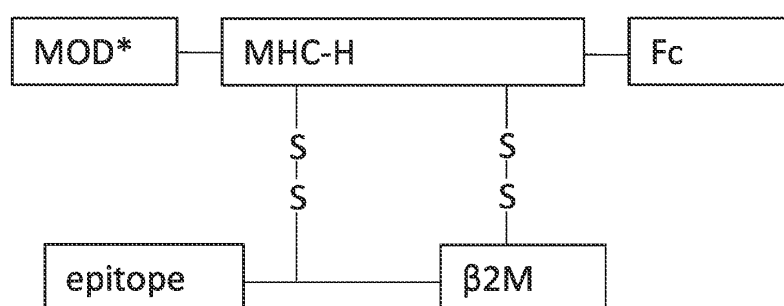


FIG. 17C

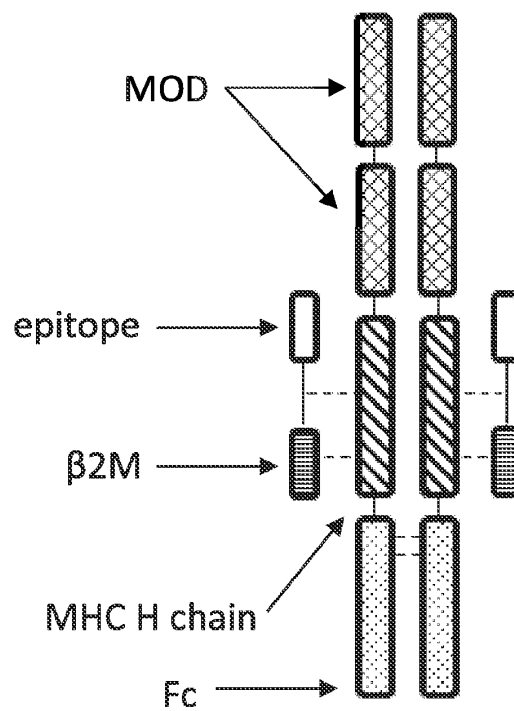


FIG. 17D

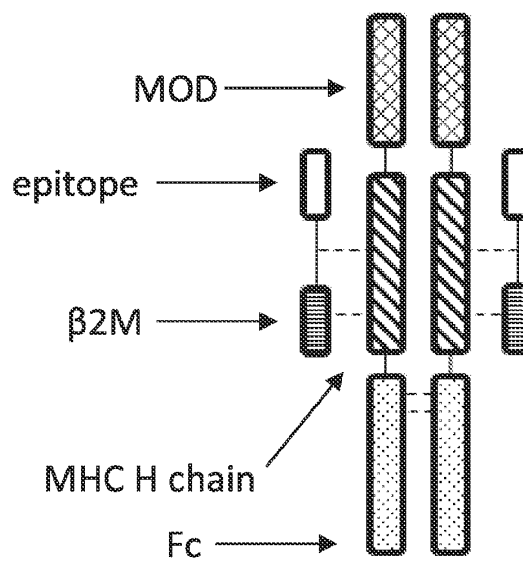


FIG. 18A

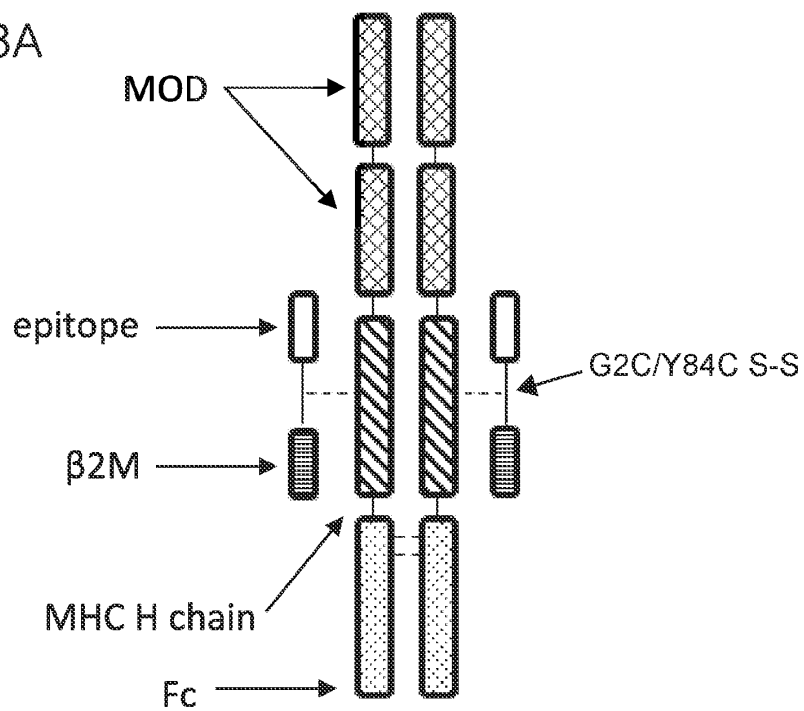


FIG. 18B

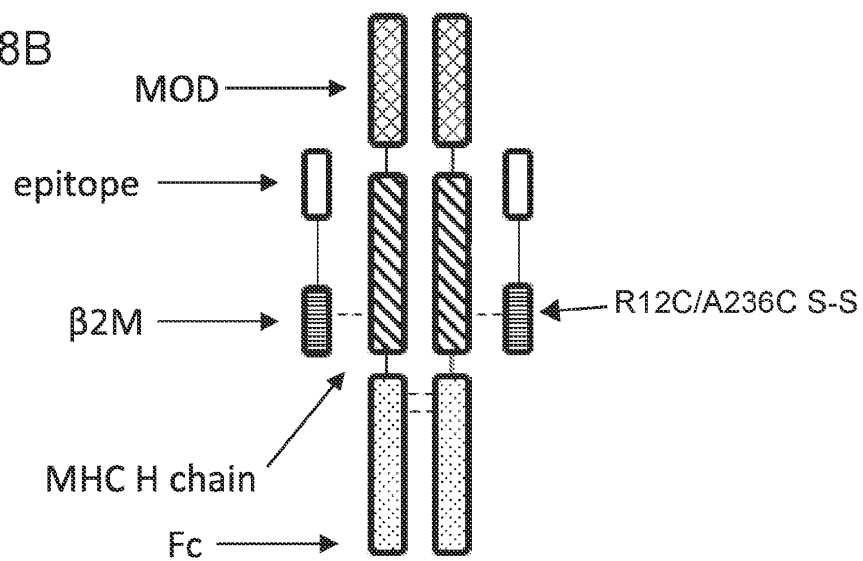
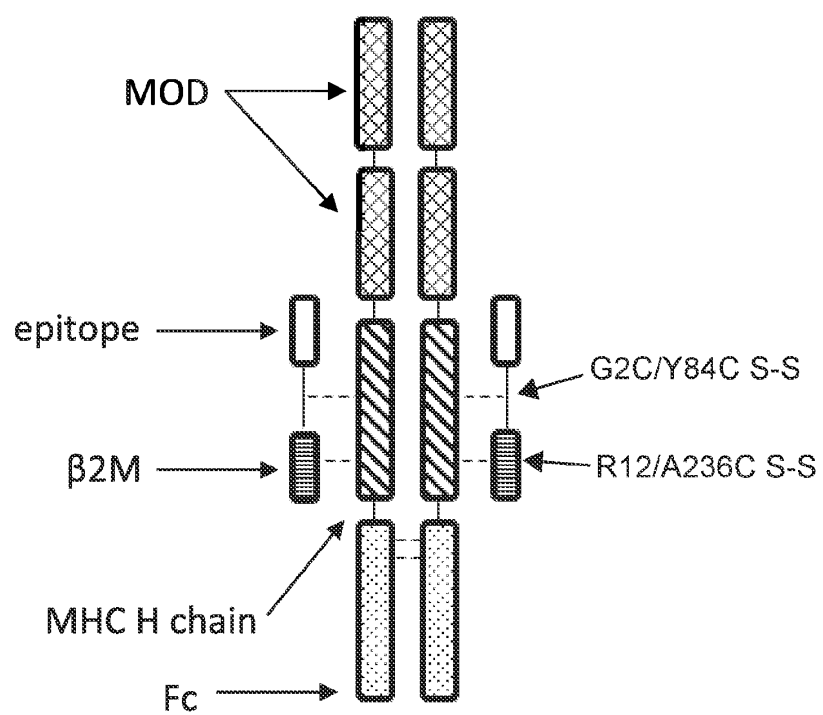


FIG. 18C



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FIG. 19

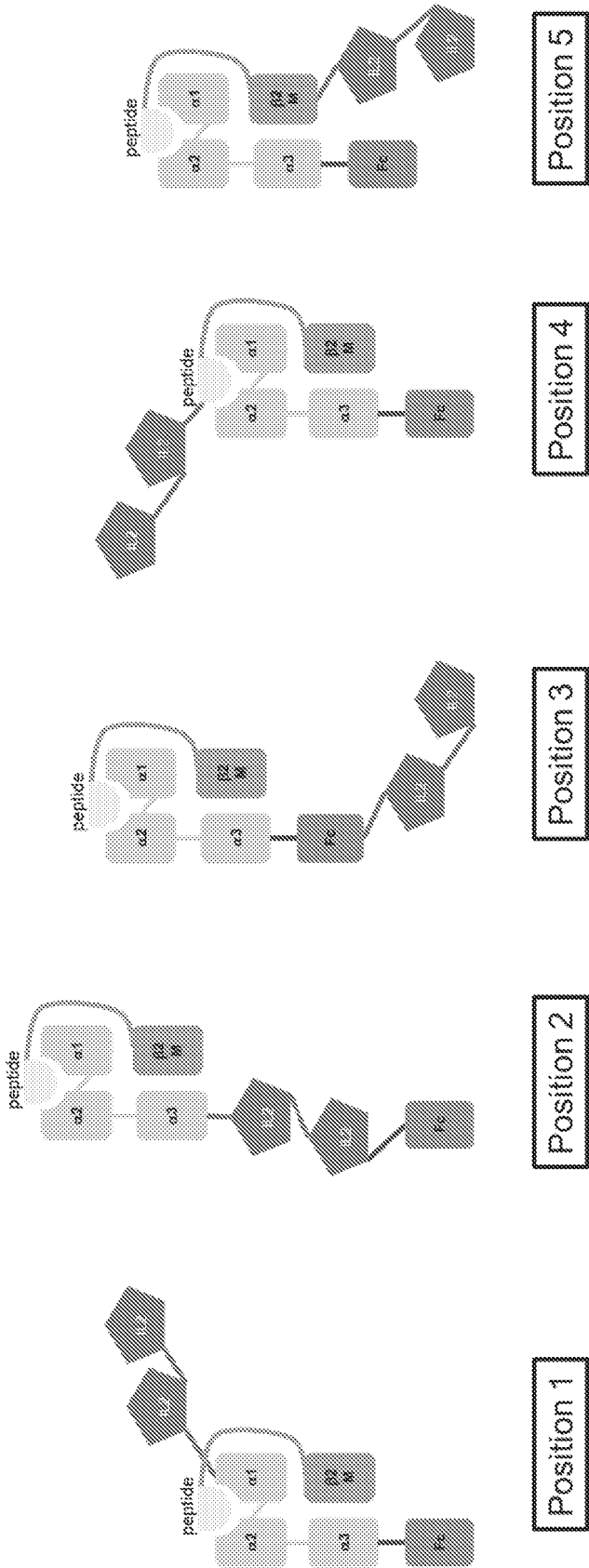


FIG. 20A

3592

APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKAT
ELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFM
CEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGGSAPTSS
STKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKH
LQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYA
DETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGSGSHSMRYFS
TSVSRPGRGEPREFIAVG YVDDTQFVREDSDAASORMEPRAPWIEQEGPEYWDEE
TGKVKAHSOTDRENLRALRCYNQSEAGSHTLOMMFGCDVGSDGRFLRGYHOY
AYDGKDYLKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYLEGTCVDGL
RRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWORDGE
DQTQDTELVETRFCDGDTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE
AAAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCL
VKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:431)

IL-2 (H16A; F42A) – bold

(G4S)₄ – underlined (SEQ ID NO:380)

HLA-A*24:02 (Y84C; A236C) – double underlined

AAAGG linker – bold and italicized (SEQ ID NO:283)

hlgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20B

3425

GSHSMRYESTSVSRPGRGEPREIAVG YVDDTQFVREDSDAASORMEPRAPWIEQE
GPEYWDEETGK VKAHSQTDRENLRIALRCYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKD YIALKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWORDGEDOTQDTELVETRPCGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWEAAAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGGGGGSGGGGSGGGGSAPT
SSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELK
HLQCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAPTSSSTK
KTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQC
LEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
ATIVEFLNRWITFCQSIISTLT (SEQ ID NO:432)

HLA-A*24:02 (Y84C; A236C) – double underlined
 AAAGG linker – bold and italicized (SEQ ID NO:283)
 hlgG1 Fc (L234A; L235A) – bold and underlined
 (G4S)₃ and (G4S)₄ – underlined (SEQ ID NOs:379-380)
 IL-2 (H16A; F42A) – bold

FIG. 20C

3196

GSHSMRYFSTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQORMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRALRCYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWORDGEDQTQDTELVETRPCGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWE***AAAGGDK***THTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:433)

HLA-A*24:02 (Y84C; A236C) – double underlined

AAAGG linker – bold and italicized (SEQ ID NO:283)

hIgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20D

2764

GSHSMRYFSTSVSRPGRGEPREIAVGYVDDTQFVRFDSDAASORMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRAYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWORDGEDQTQDTELVETRPCGDGTFOKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWE***AAAGGDK***THTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQOQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:434)

HLA-A*24:02 (Y84A; A236C) – double underlined

AAAGG linker – bold and italicized (SEQ ID NO:283)

hlgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20E

3593

APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKAT
 ELKHLQCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFM
 CEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGGGGSAPTSS
 STKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKH
 LQCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYA
 DETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGGGSGSHSMRYES
 TSVSRPGRGEPRIAUGYVDDTQFVRFDSDAASORMEPRAPWIEQEGPEYWDEE
 TGKVKAHSQTDRENLRALRCYNOSEAGSHTLOMMFGCDVGS DGRFLRGYHOY
 AYDGKDYLKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYLEGTCVDGL
 RRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWORDGE
 DQTQDTEL VETRPAGDGTFOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE
 AAAGGDKTHTCPPCPAPEAAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
 KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL
 VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWOO
 GNVFSCSVMHEALHNHYTOKSLSLSPG (SEQ ID NO:435)

IL-2 (H16A; F42A) – bold

(G4S)₄ – underlined (SEQ ID NO:380)

HLA-A*24:02 (Y84C; A236) – double underlined

AAAGG linker – bold and italicized (SEQ ID NO:283)

hIgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20F

3426

GSHSMRYFSTSVSRPGRGEPREFIAVGYVDDTQFVRFDSDAASORMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRIALRCCYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHOYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWORDGEDOTQDTELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVQHEGLP
KPLTLRWE***AAAGGDK***THTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGGGGSAPT
SSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELK
HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAPTSSSTK
KTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQC
LEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
ATIVEFLNRWITFCQSIISTLT (SEQ ID NO:436)

HLA-A*24:02 (Y84C; A236) – double underlined

AAAGG linker – bold and italicized (SEQ ID NO:283)

hIgG1 Fc (L234A; L235A) – bold and underlined

(G4S)₃ and (G4S)₄ – underlined (SEQ ID NOs:379-380)

IL-2 (H16A; F42A) – bold

FIG. 20G

3197

GSHSMRYFSTSVSRPGRGEPREIAVGYYDDTQFVRFDSDAASORMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRALRCYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHOYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYL
EGTCVDGLRRYLENGKETLORTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWORDGEDQTQDTELVETRPAGDGTFOKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWEAAAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:437)

HLA-A*24:02 (Y84C; A236) – double underlined

AAAGG linker – bold and italicized (SEQ ID NO:283)

hIgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20H

3188

CYTWNQMNLGCGGSGGGGSGGGGSI*QRTPKIQVYS***C**HPAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDM (SEQ ID NO:438)

epitope: CYTWNQMNL – WT1 (235-243; M236Y) (SEQ ID NO:262)
 (GCGGS)(G4S)₂ – underlined (SEQ ID NO:317)
 β2M (R12C) – italicized

FIG. 20I

3604

CYTWNQMNLGCGGSGGGGSGGGGSI*QRTPKIQVYS***C**HPAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDMGGGGSGGGGSGGGGSAPTSSSTKKTQLQLE**A**LLLDLQMILNGIN
 NYKNPKLTRMLT**A**KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
 LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSHSTLT**G**
GGGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLE**A**LLLDLQMILNGINNYKN
 PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
 DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSHSTLT

(SEQ ID NO:439)

epitope: CYTWNQMNL – WT1 (235-243; M236Y) (SEQ ID NO:262)
 (GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)
 β2M (R12C) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 20J

3603

CYTWNQMNLGGGGSGGGSGGGG*SIQRTPKIQVYS***CH**PAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDMGGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
 NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
 LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSHISTLTG
GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKN
 PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
 DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSHISTLT
 (SEQ ID NO:440)

epitope: CYTWNQMNL – WT1 (235-243; M236Y) (SEQ ID NO:262)
 (G4S)₃ and (G4S)₄ – underlined (SEQ ID NOs:379-380)
 β2M (R12C) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 20K

3192

CYTWNQMNLGCGGSGGGSGGGG*SIQRTPKIQVYS***R**HPAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDM (SEQ ID NO:441)

epitope: CYTWNQMNL – WT1 (235-243; M236Y) (SEQ ID NO:262)
 (GCGG)(G4S)₂ – underlined (SEQ ID NO:317)
 β2M (R12) – italicized

FIG. 20L

3605

CYTWNQMNLGCGGSGGGGSGGGGSIQRTPKIQVYS**R**HPAENGKSNFLNCYVSGFH
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
KIVKWDRDMGCGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
NYKNPKLTRMLT**A**KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
GCGGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYK
NPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRP
RDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
(SEQ ID NO:442)

epitope: CYTWNQMNL – WT1 (235-243; M236Y) (SEQ ID NO:262)
(GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)
β2M (R12) – italicized
IL-2 (H16A; F42A) – bold

FIG. 20M

3529

NYMNLGATLGCGGSGGGGSGGGGSIQRTPKIQVYS**R**HPAENGKSNFLNCYVSGFH
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
KIVKWDRDM (SEQ ID NO:443)

epitope: NYMNLGATL – WT1 (239-247; Q240Y) (SEQ ID NO:263)
(GCGGS)(G4S)₂ – underlined (SEQ ID NO:317)
β2M (R12C) – italicized

FIG. 20N

3709

NYMNLGATLGCGGSGGGGSGGGGSIQRTPKIQVYS**CH**PAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDMGCGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
 NYKNPKLTRMLT**AK**FYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
 LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT**G**
GCGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKN
 PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
 DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
 (SEQ ID NO:444)

epitope: NYMNLGATL – WT1 (239-247; Q240Y) (SEQ ID NO:263)
 (GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)
 β2M (R12C) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 20O

3528

NYMNLGATLGCGGSGGGGSGGGGSIQRTPKIQVYS**CH**PAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDM (SEQ ID NO:445)

epitope: NYMNLGATL – WT1 (239-247; Q240Y) (SEQ ID NO:263)
 (G4S)₃ – underlined (SEQ ID NO:379)
 β2M (R12C) – italicized

FIG. 20P

3708

NYMNLGATLGCGGSGGGGSGGGGSIQRTPKIQVYS**CH**PAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDMGCGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
 NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
 LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GCGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPK
 LTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN
 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT (SEQ ID NO:446)

epitope: NYMNLGATL (SEQ ID NO:263) – WT1 (239-247; Q240Y)
 (G4S)₃ and (G4S)₄ – underlined (SEQ ID NOs:379-380)
 β2M (R12C) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 20Q

3530

NYMNLGATLGCGGSGGGGSGGGGSIQRTPKIQVYS**CH**PAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDM (SEQ ID NO:447)

epitope: NYMNLGATL – WT1 (239-247; Q240Y) (SEQ ID NO:263)
 (GCGGS)(G4S)₂ – underlined (SEQ ID NO:317)
 β2M (R12) – italicized

FIG. 20R

3710

NYMNLGATLGCGGSGGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNCYVSGFH
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
KIVKWDRDMGCGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGIN
NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GCGGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGINNYKN
PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
(SEQ ID NO:448)

epitope: NYMNLGATL – WT1 (239-247; Q240Y) (SEQ ID NO:263)

(GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)

β2M (R12) – italicized

IL-2 (H16A; F42A) – bold

FIG. 21

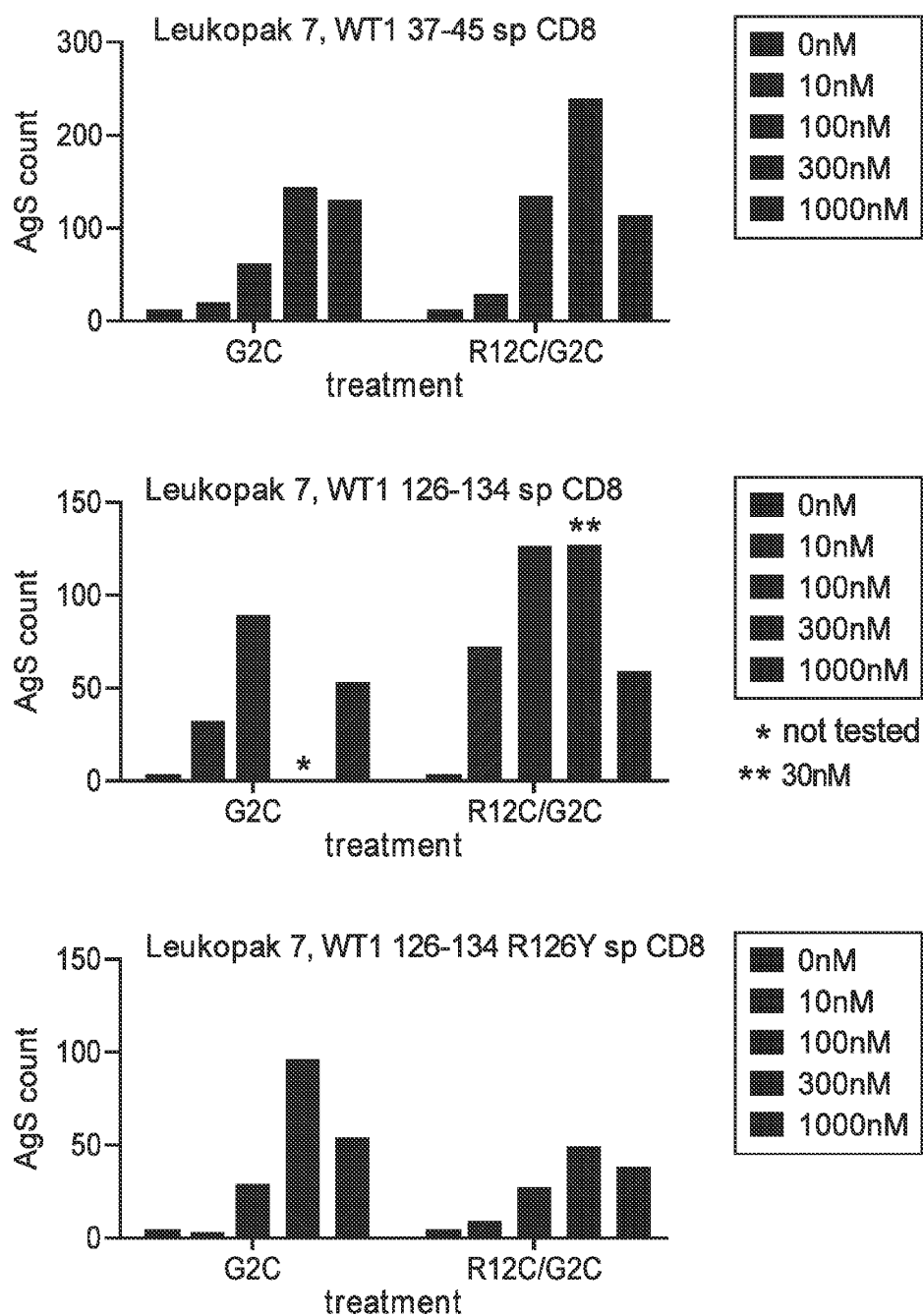


FIG. 21 (Cont.)

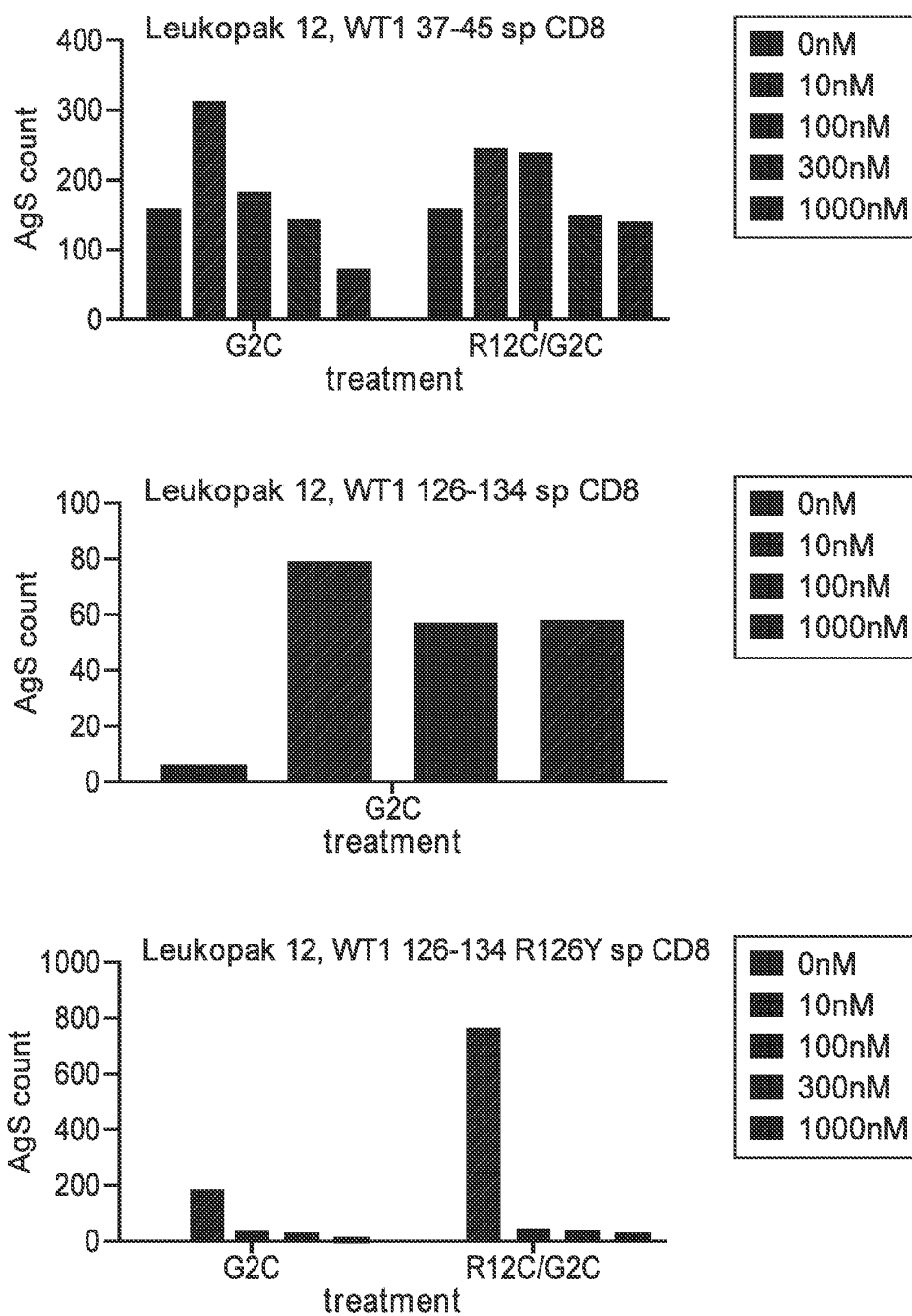


FIG. 22

WT1 37-45

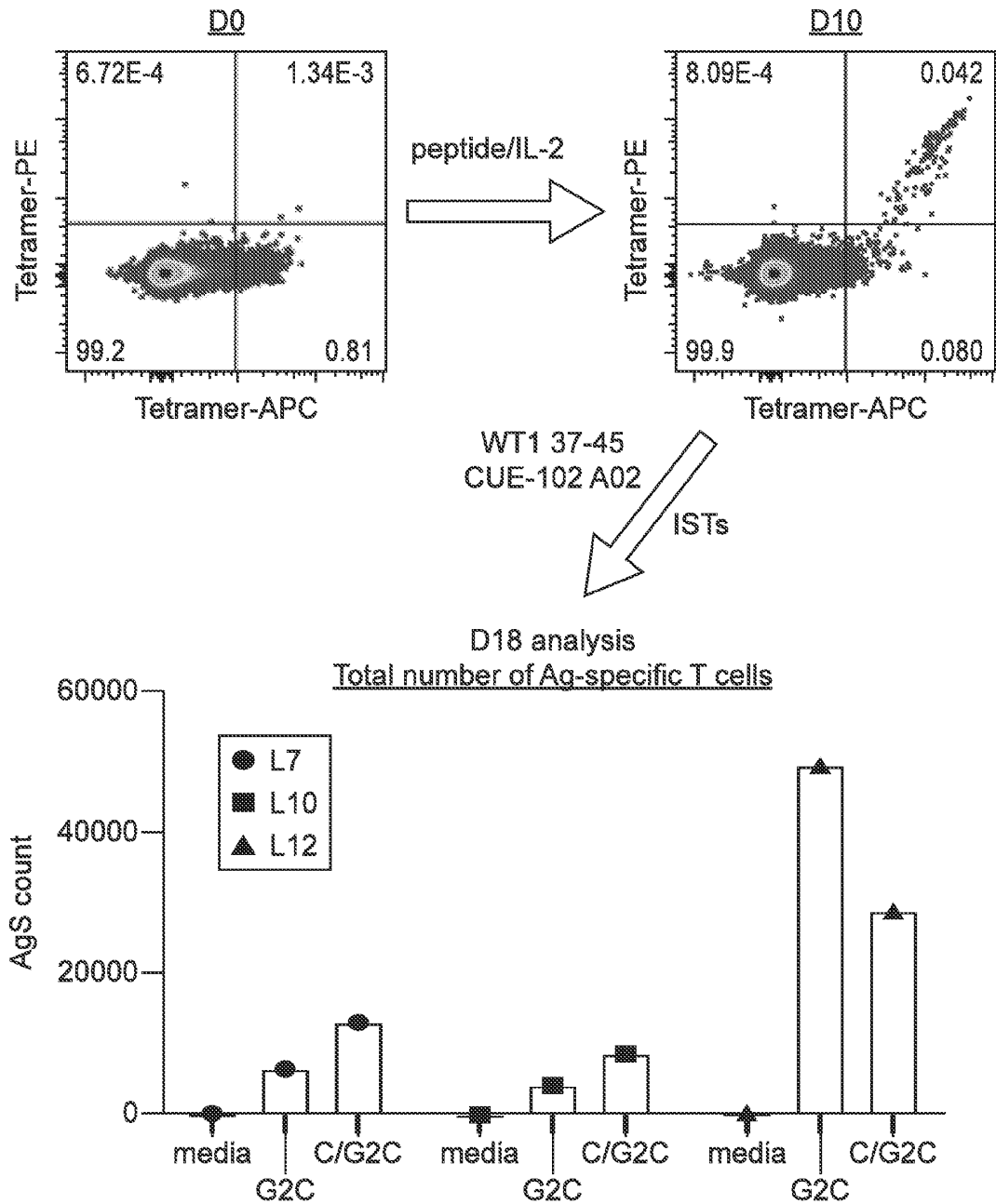


FIG. 22 (Cont.)

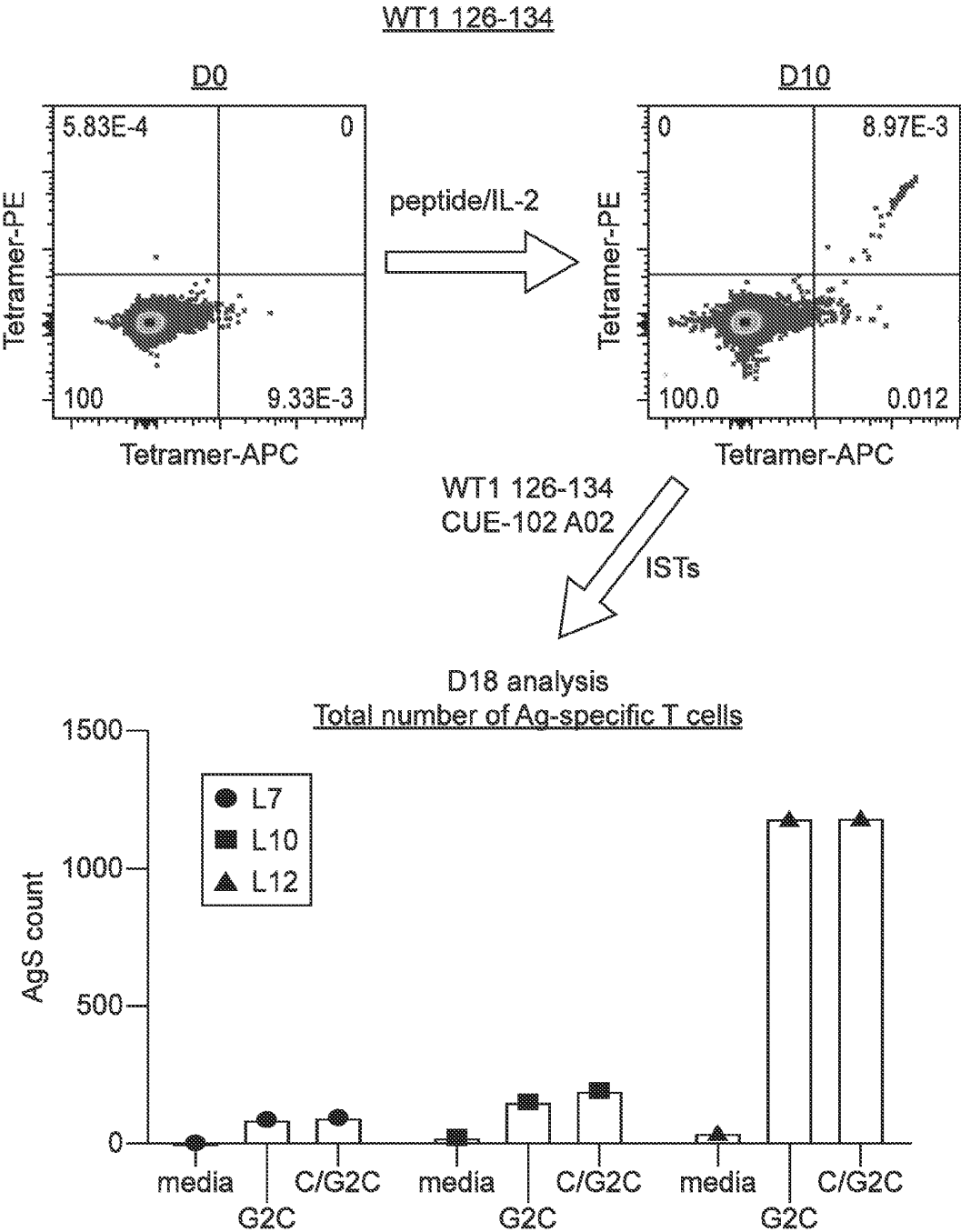
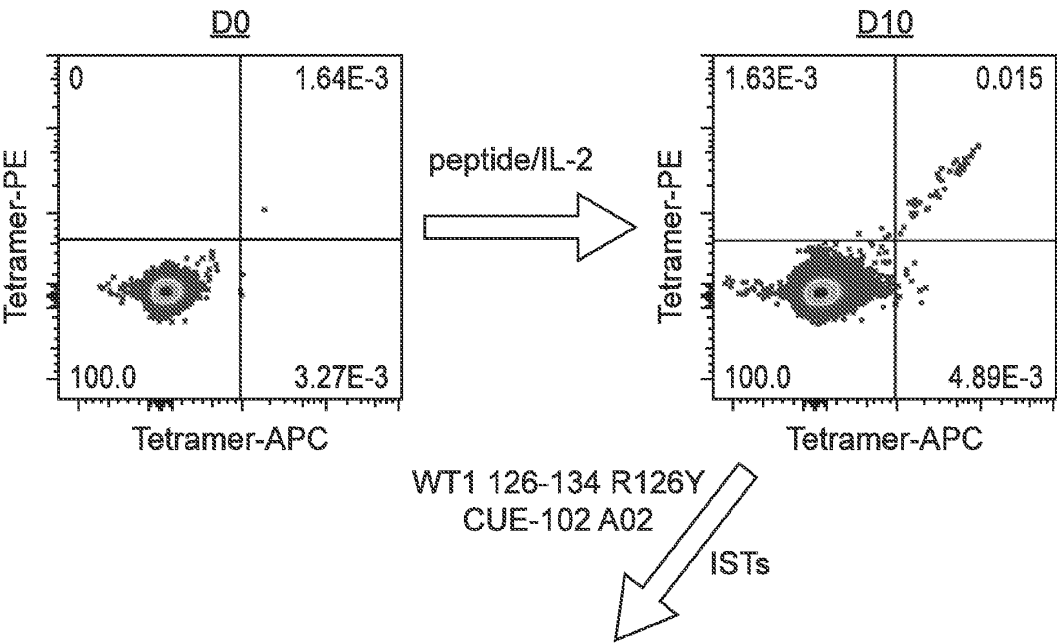


FIG. 22 (Cont.)

WT1 126-134 R126Y



WT1 126-134 R126Y
CUE-102 A02

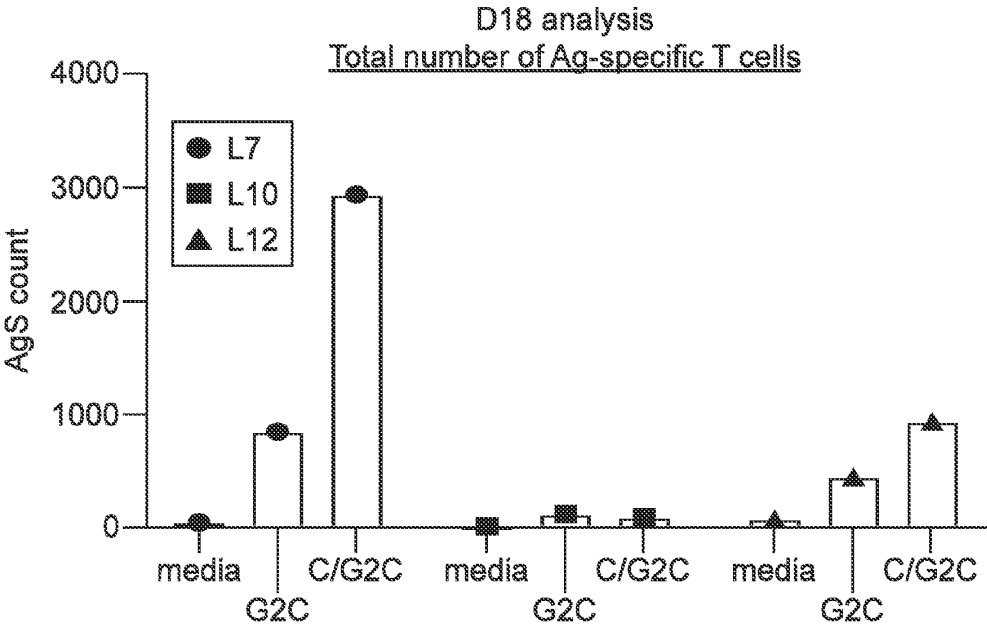


FIG. 23

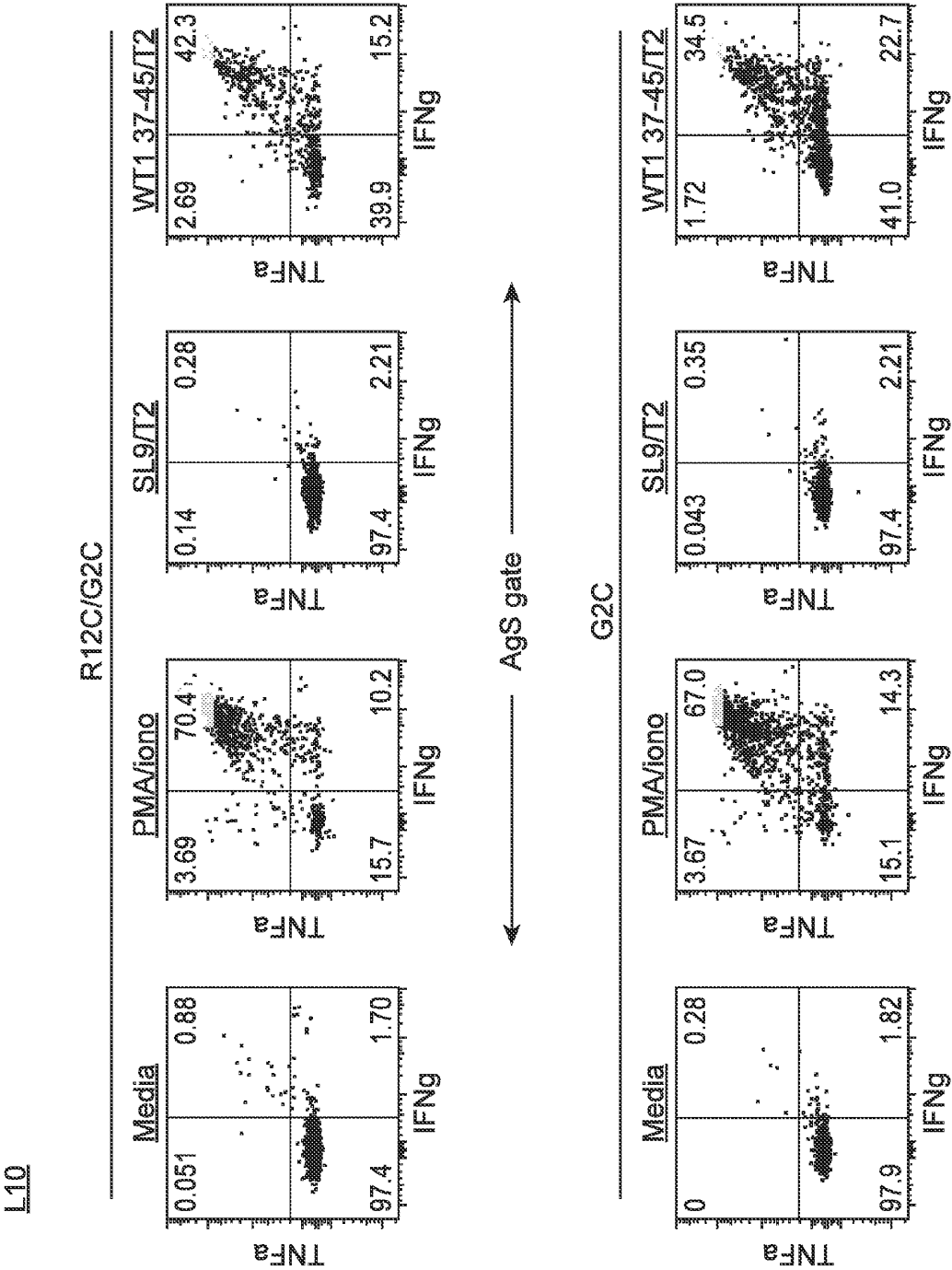


FIG. 24

L10

AgS gate

R12C/G2C

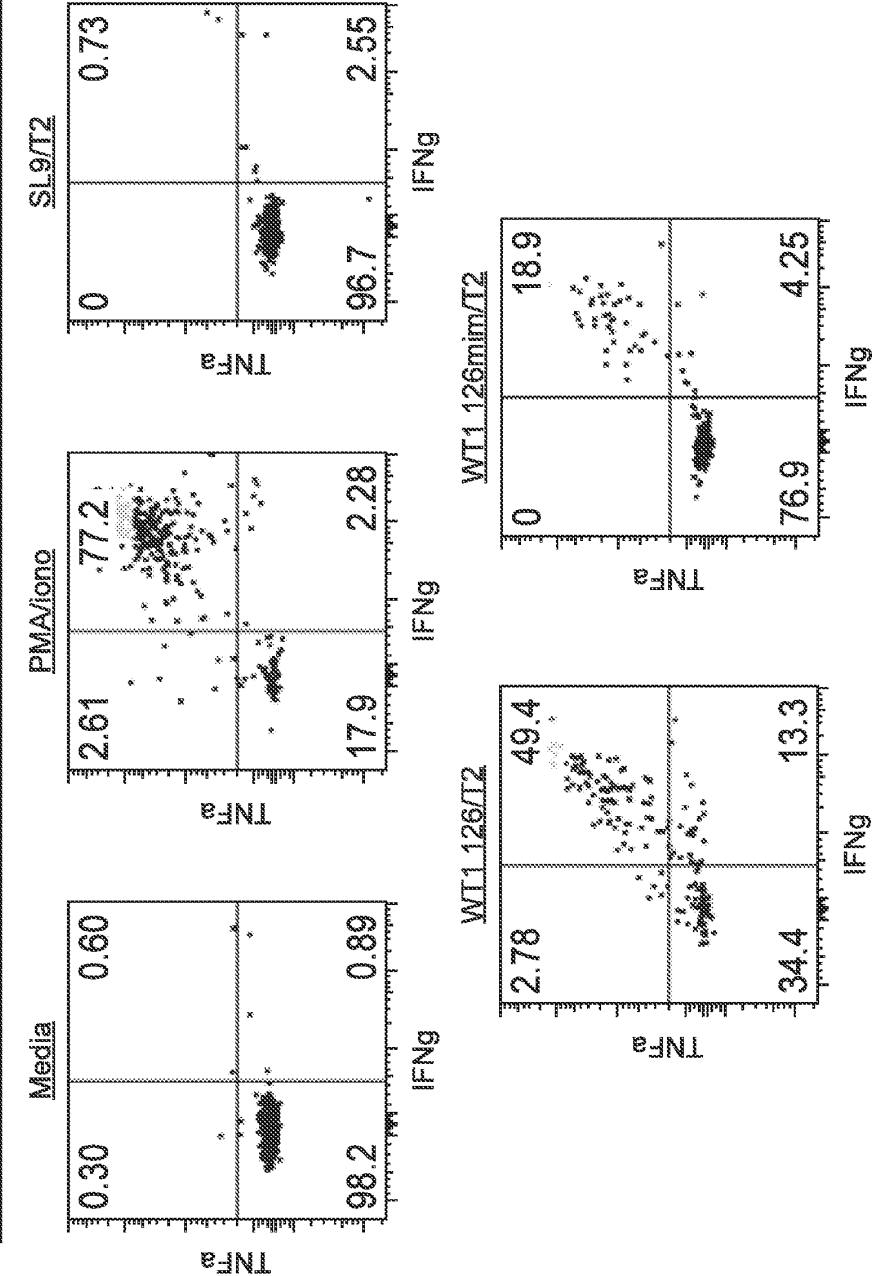
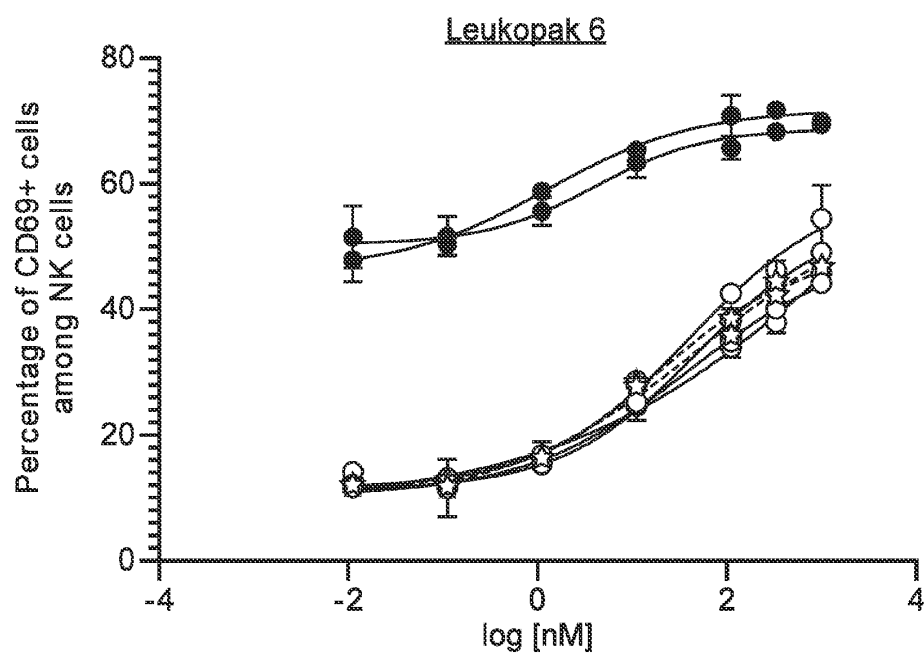


FIG. 25



Specificity	IST #	Mod position	Framework	Prism color legend
CMV	IST-1380-839-016	1	R12C	☆
MART-1	IST-1380-1571-011	1	R12C	☆
WT-1 A02 constructs	IST-1715-2380-005	37-45	R12C/G2C	○
	IST-2045-2762-004	37-45	G2C	○
	IST-1715-2381-003	126-134	R12C/G2C	○
	IST-1715-3625-004	126-134 R126Y	R12C/G2C	○
Proleukin				●
rhIL-2				●

FIG. 26

CUE-102 A02 Lead Candidates

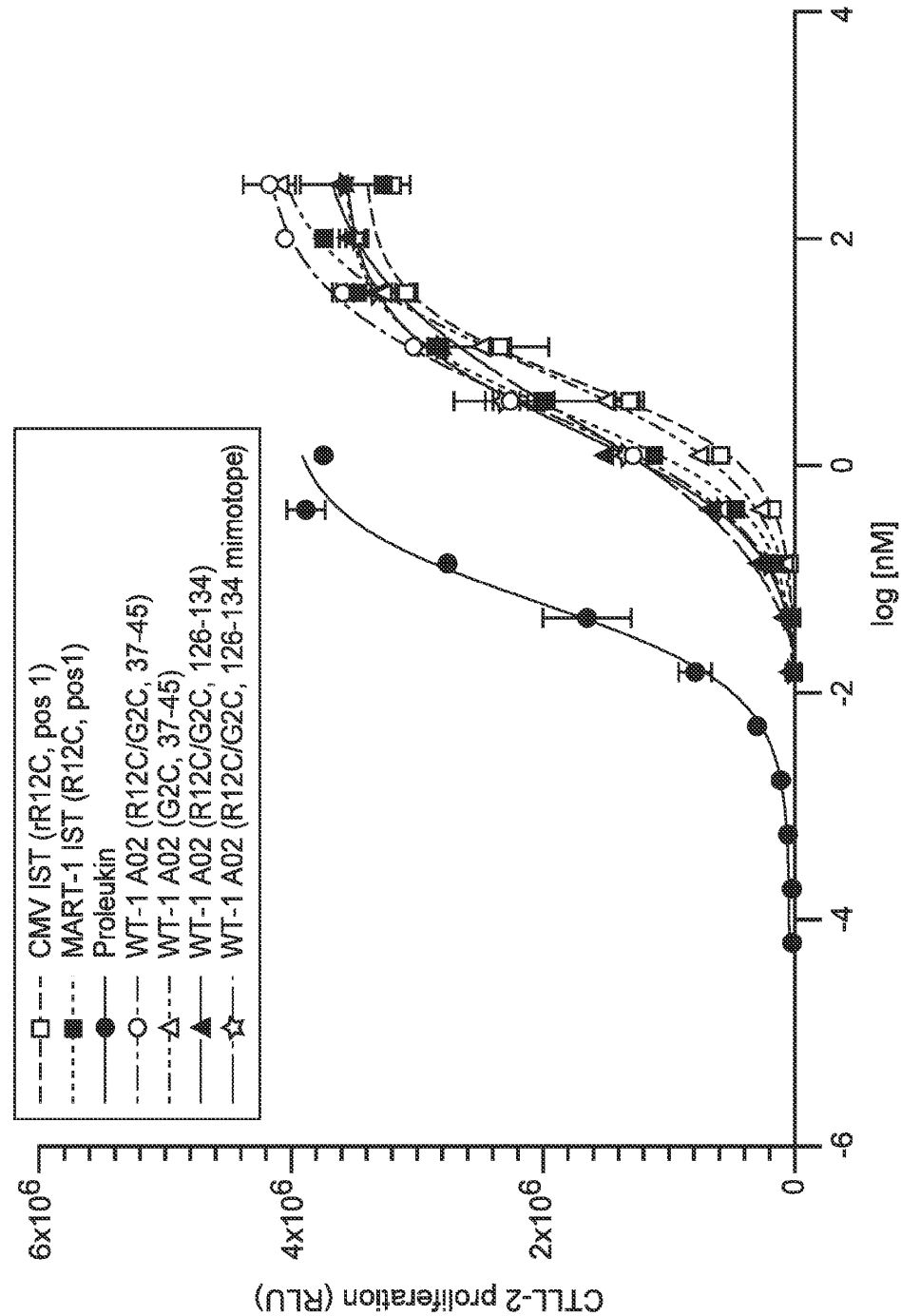


FIG. 27

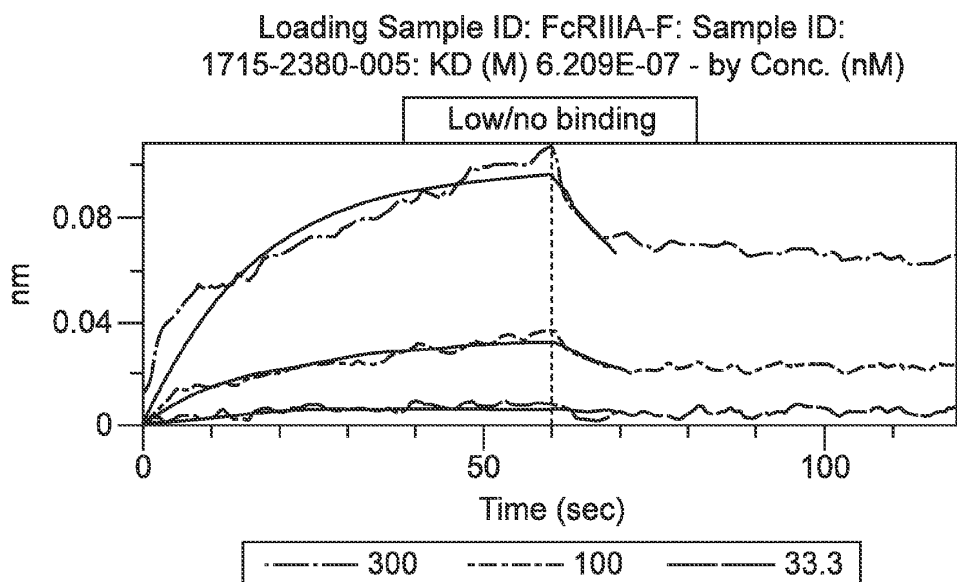
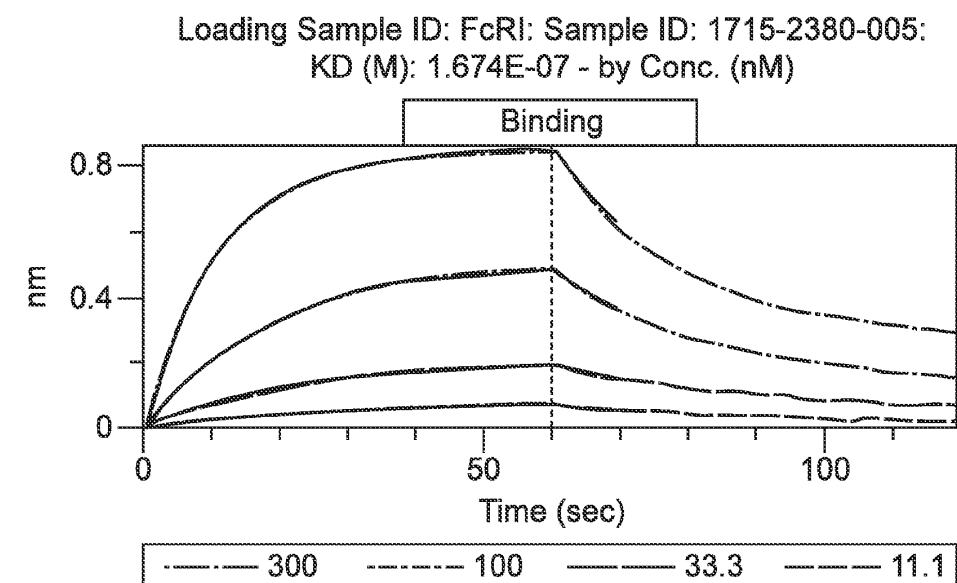
37-45 double disulfide

FIG. 27 (Cont.)

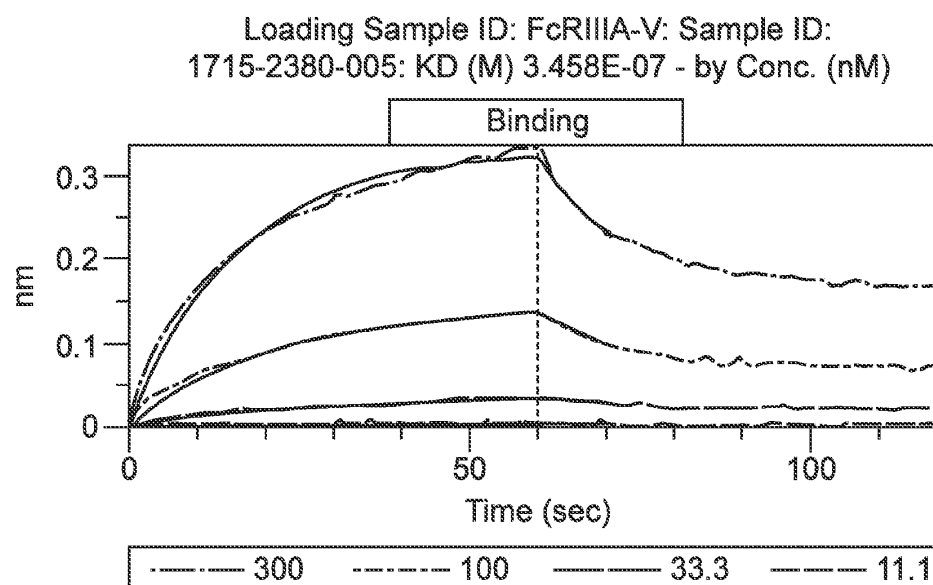
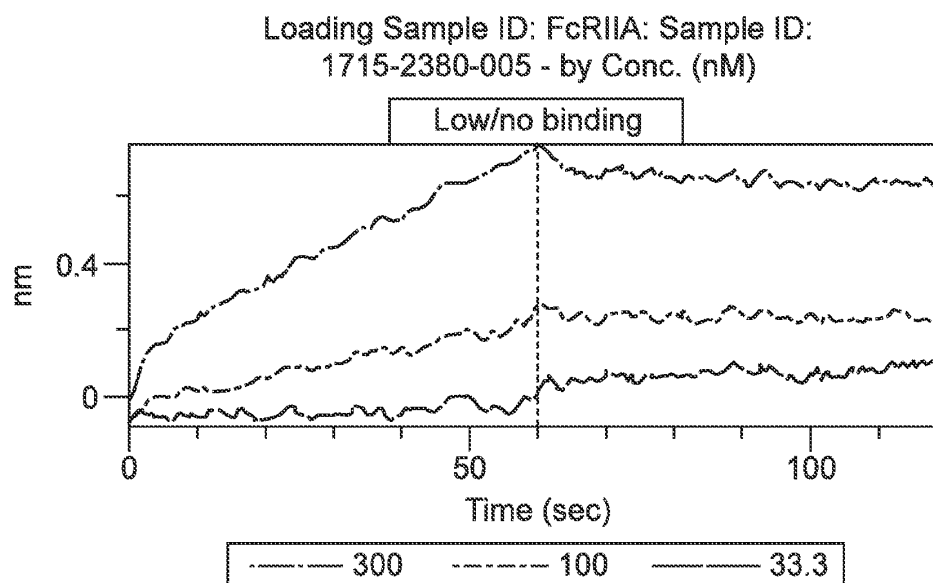
37-45 double disulfide

FIG. 27 (Cont.)

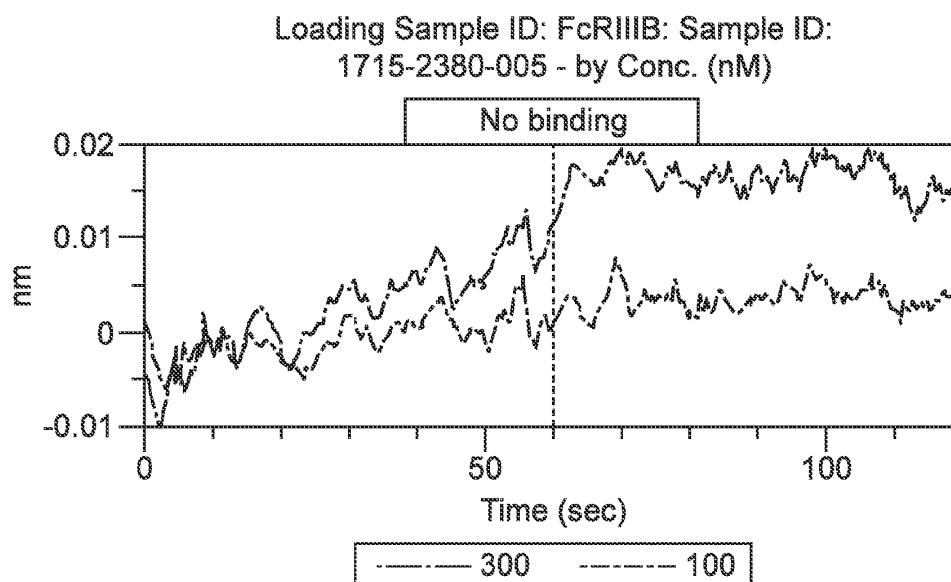
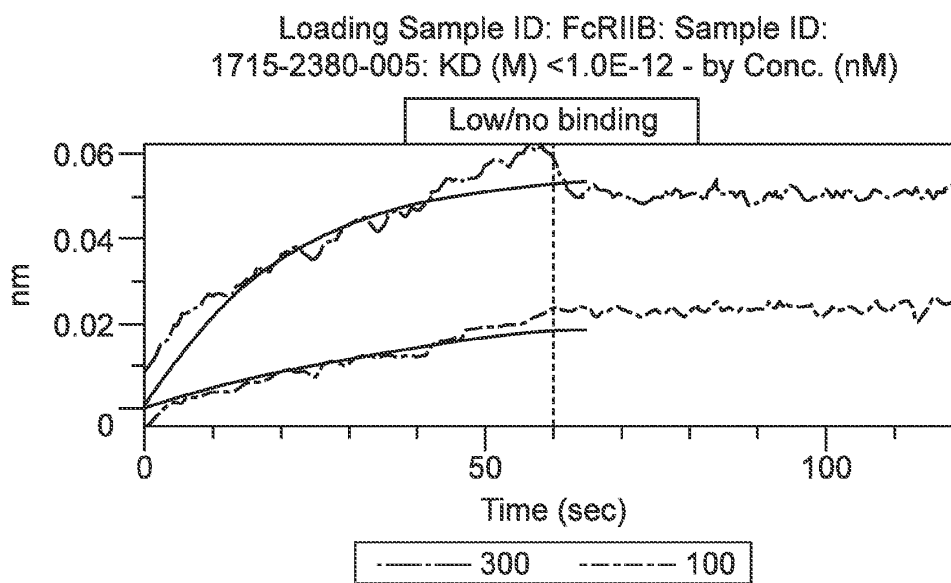
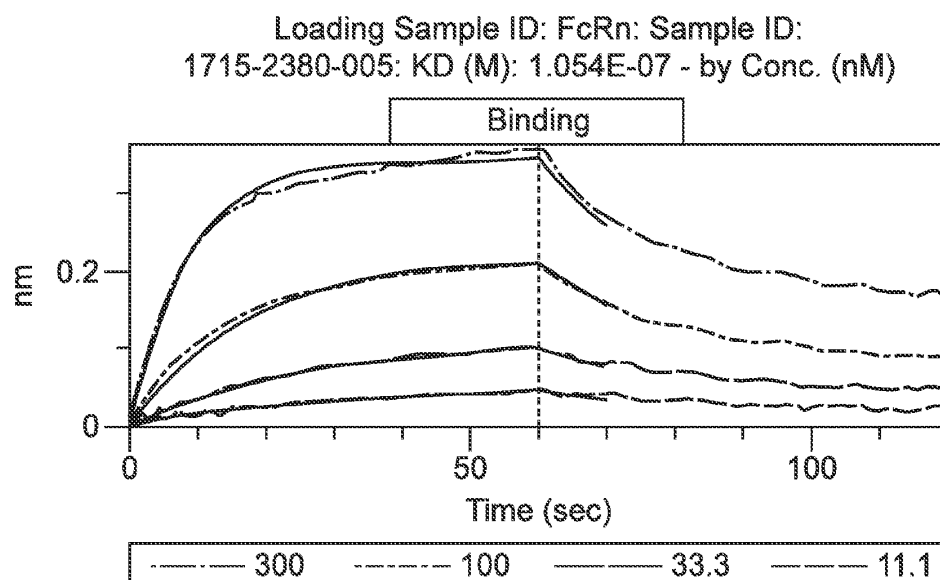
37-45 double disulfide

FIG. 27 (Cont.)

37-45 double disulfide

Loading Sample ID	Sample ID	KD (M)	kon(1/Ms)	kdis(1/s)	Full X^2	Full R^2
FcRI	1715-2380-005	1.67E-07	1.92E+05	0.03209	0.0063	0.9997
FcRIIA	1715-2380-005	No binding	--	--	--	--
FcRIIB	1715-2380-005	<1.0E-12*	1.61E+05	<1.0E+05	0.0018	0.9608
FcRIIIA-F	1715-2380-005	6.21E-07	6.61E+04	4.11E-02	0.0046	0.9793
FcRIIIA-V	1715-2380-005	3.46E-07	9.83E+04	3.40E-02	0.0089	0.9973
FcRIIIB	1715-2380-005	No Binding	--	--	--	--
FcRn (pH 6.0)	1715-2380-005	1.05E-07	2.83E+05	2.98E-02	0.0139	0.9963

FIG. 28

WT1 235-243 M236Y ISTs

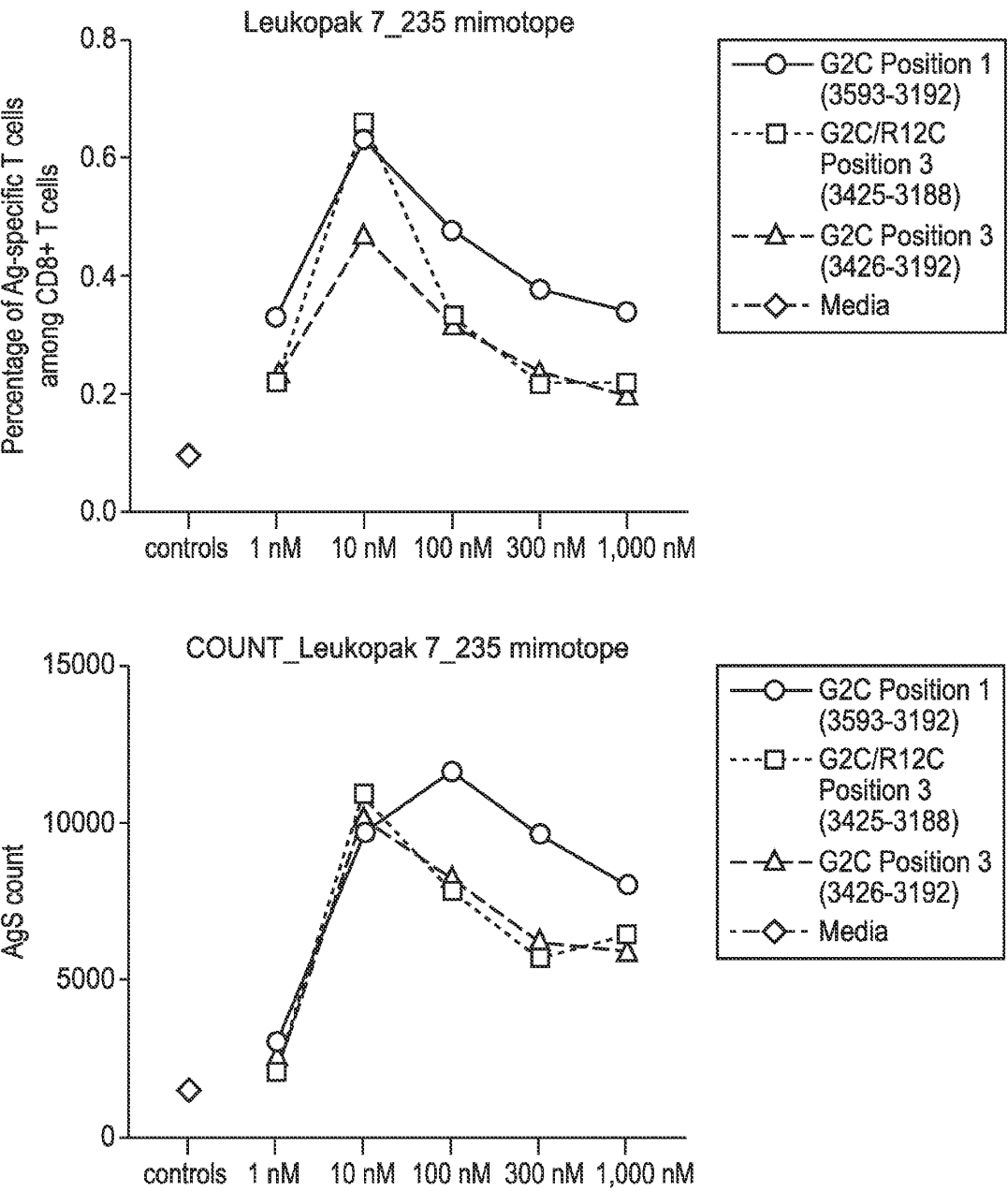


FIG. 29

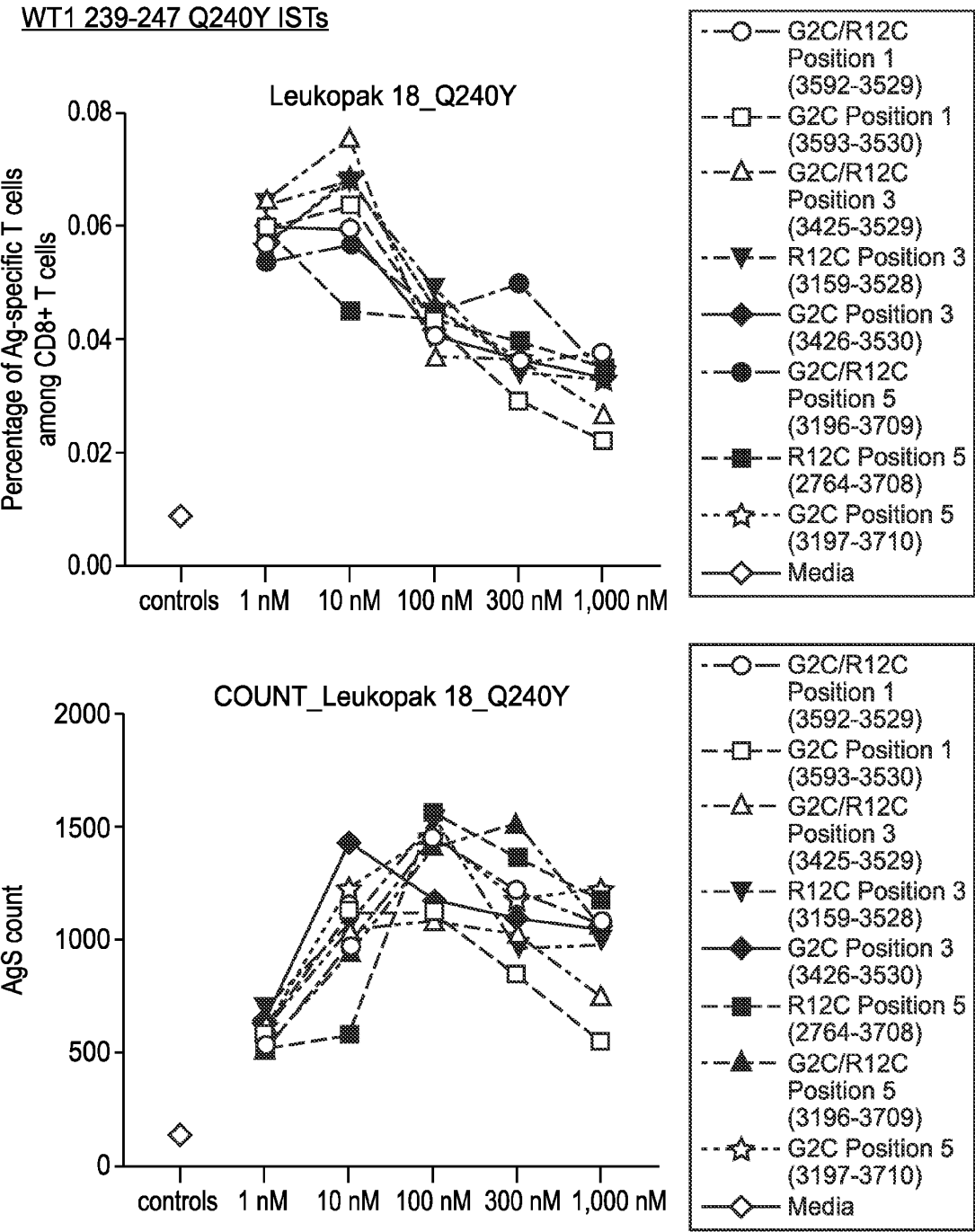


FIG. 29 (Cont.)

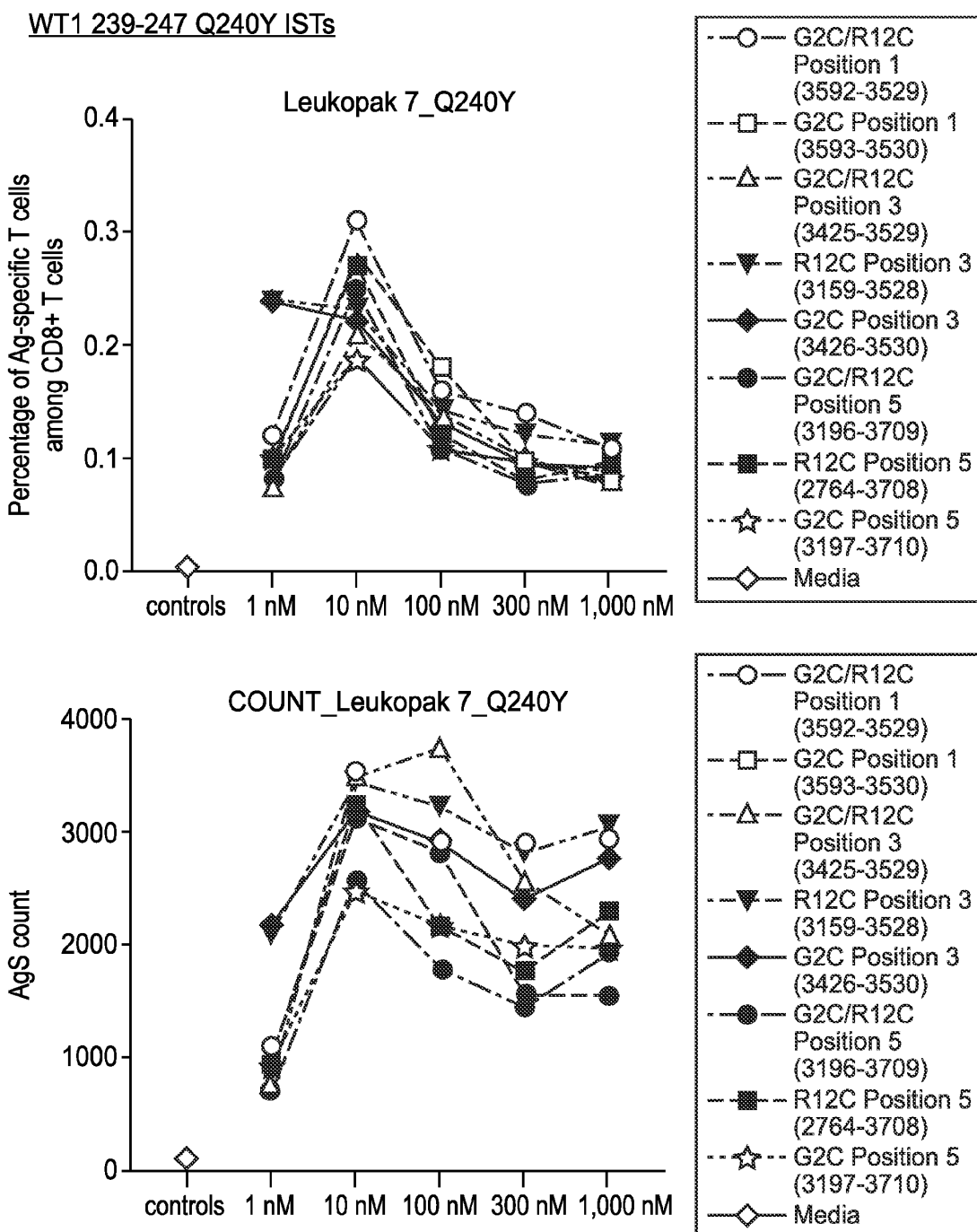
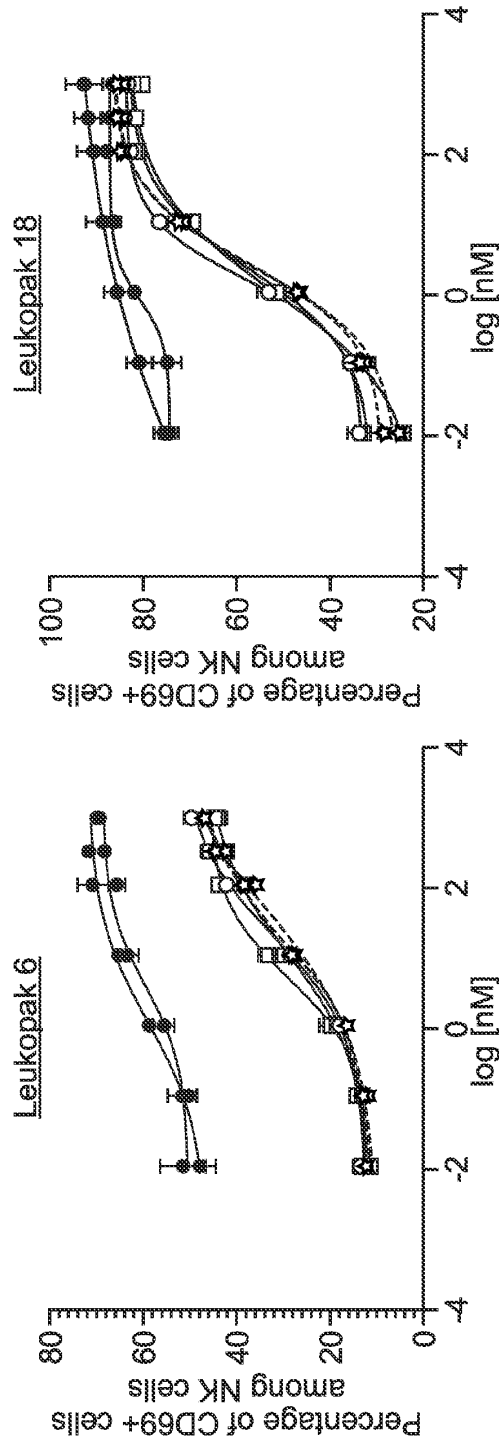


FIG. 30



Specificity	IST #	Mod position	Framework	Prism color legend
CMV	IST-1380-839-016	1	R12C	☆
	IST-1380-1571-011	1	R12C	☆
MART-1	IST-3593-3192-002	1	G2C	○
	IST-3425-3188-003	3	R12C/G2C	□
	IST-3426-3192-002	3	G2C	□
Proleukin				●
rhlL-2				●

FIG. 31

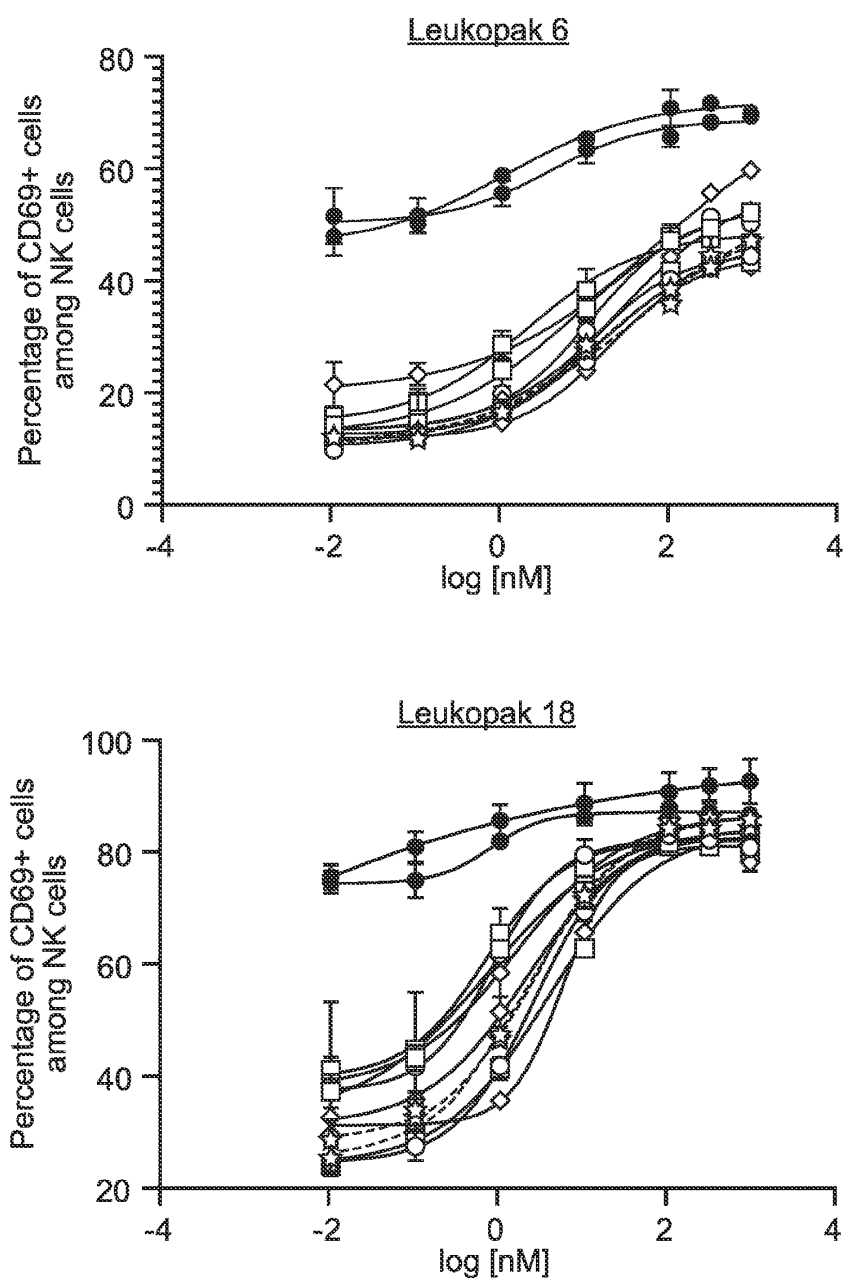


FIG. 31 (Cont.)

Specificity	IST #	Mod position	Framework	Prism color legend
CMV	IST-1380-839-016	1	R12C	☆
MART-1	IST-1380-1571-011	1	R12C	☆
WT-1 A24 (239-247; Q240Y)	IST-3592-3529-002	1	R12C/G2C	○
	IST-3425-3529-001	3	R12C/G2C	□
	IST-3196-3709-001	5	R12C/G2C	◇
	IST-3159-3528-001	3	R12C	□
	IST-2764-3708-002	5	R12C	◇
	IST-3593-3530-001	1	G2C	○
	IST-3426-3530-001	3	G2C	□
	IST-3197-3710-002	5	G2C	◇
Proleukin				●
rhIL-2				●

FIG. 32

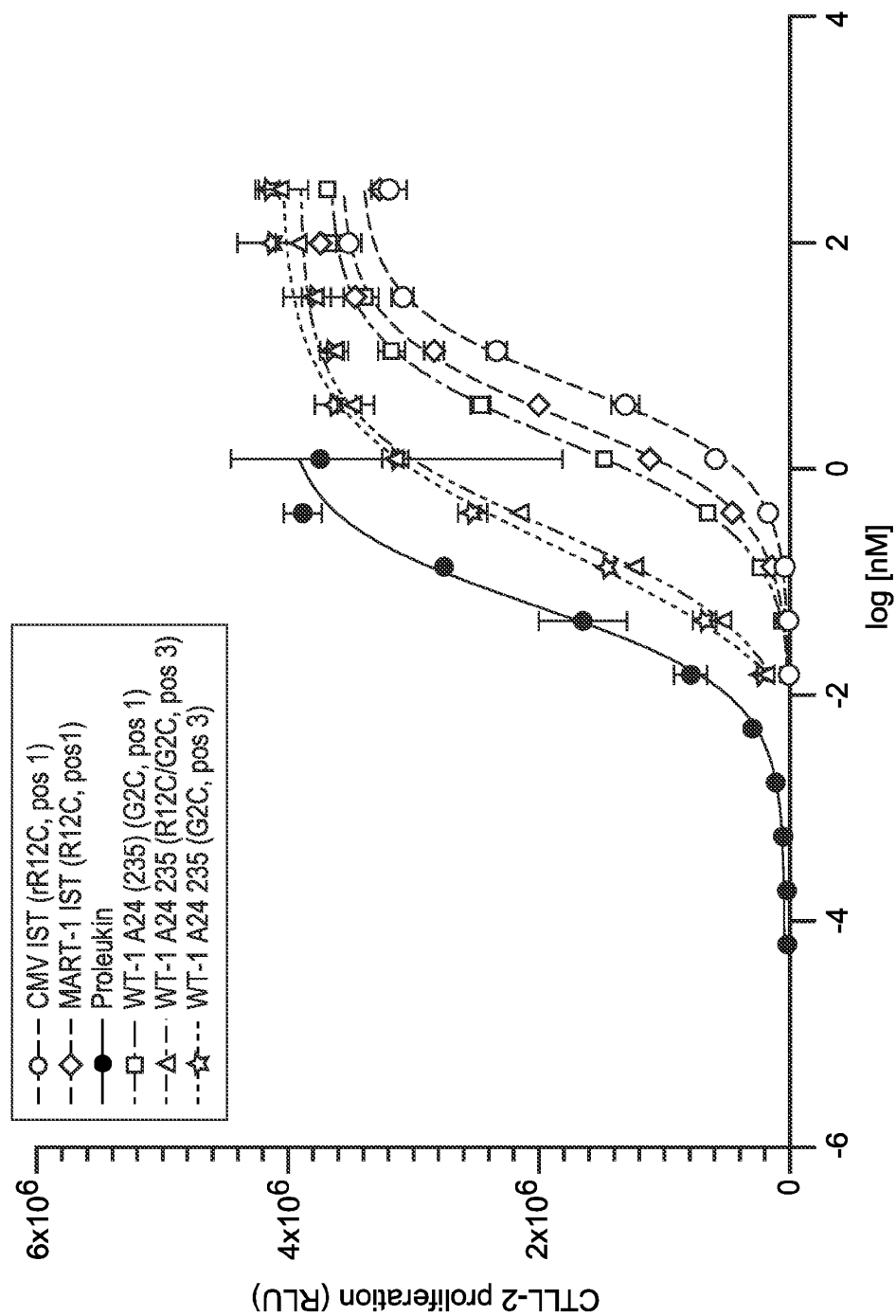


FIG. 33

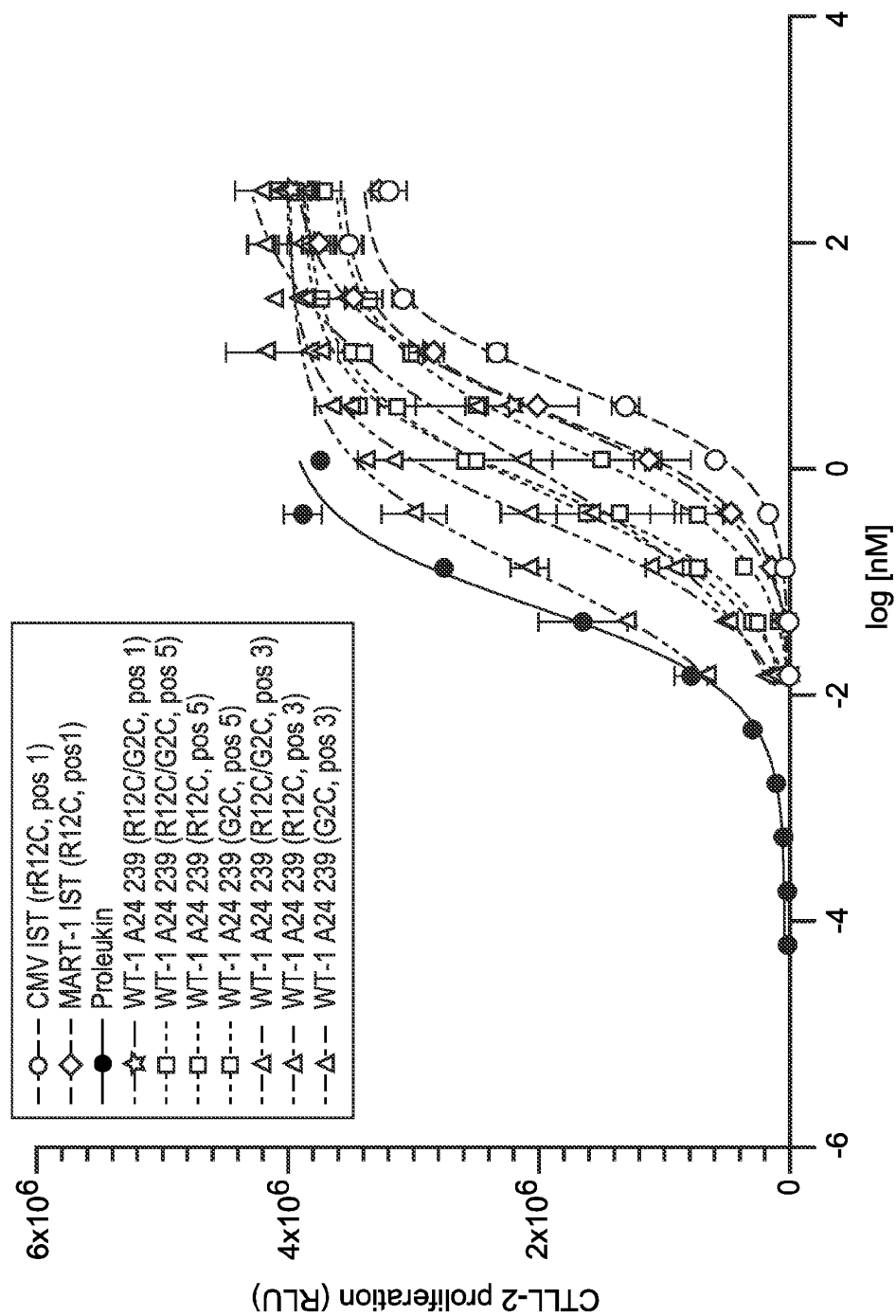


FIG. 34

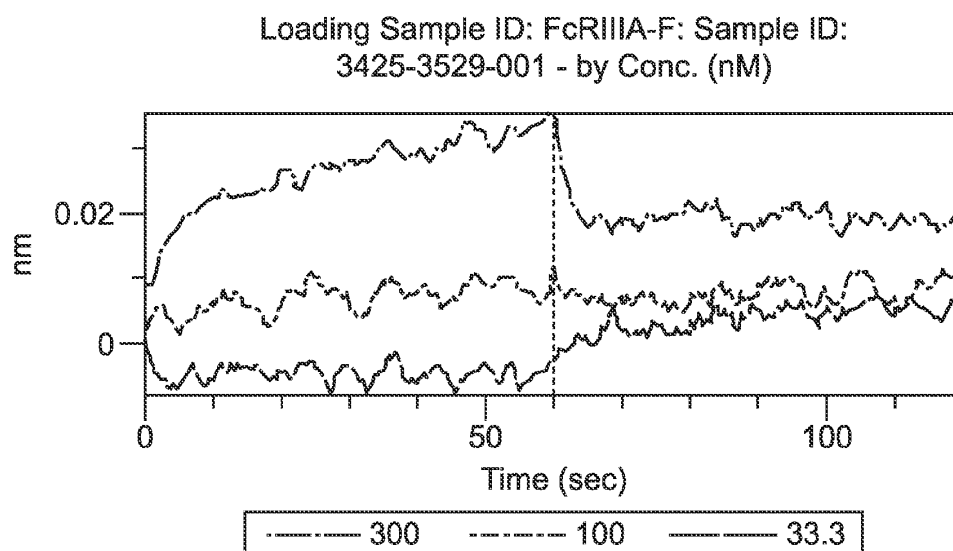
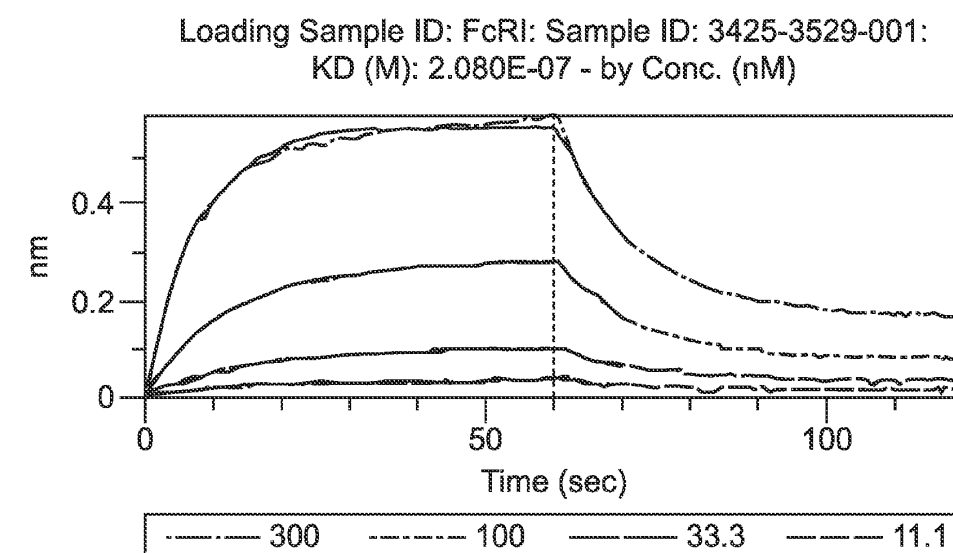


FIG. 34 (Cont.)

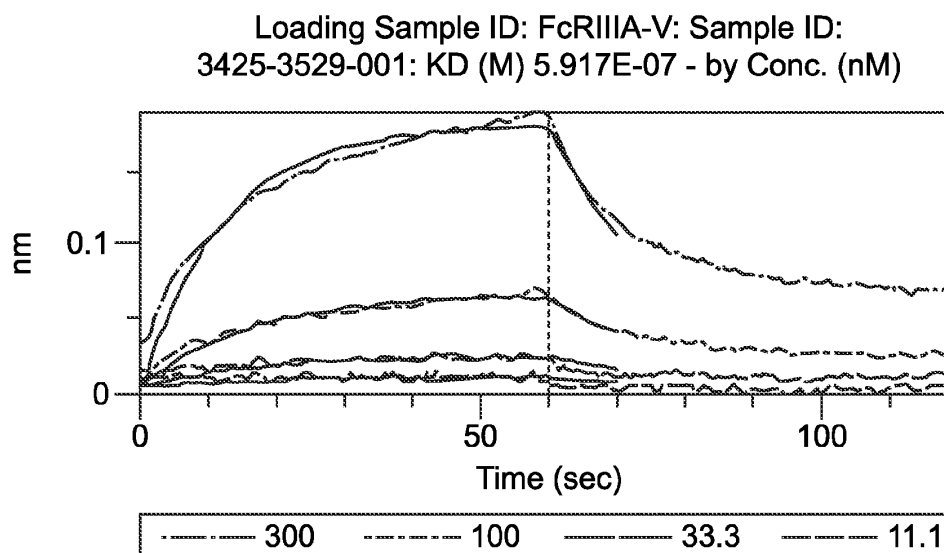
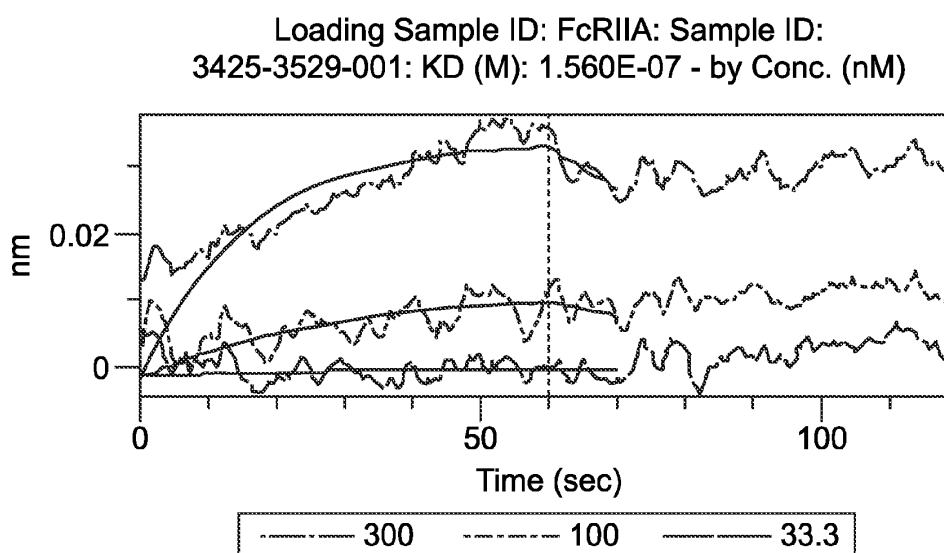


FIG. 34 (Cont.)

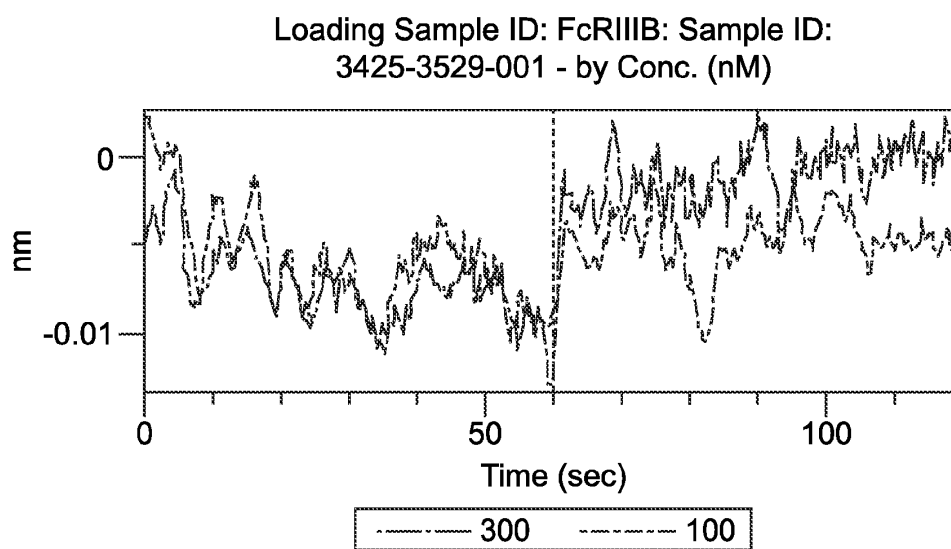
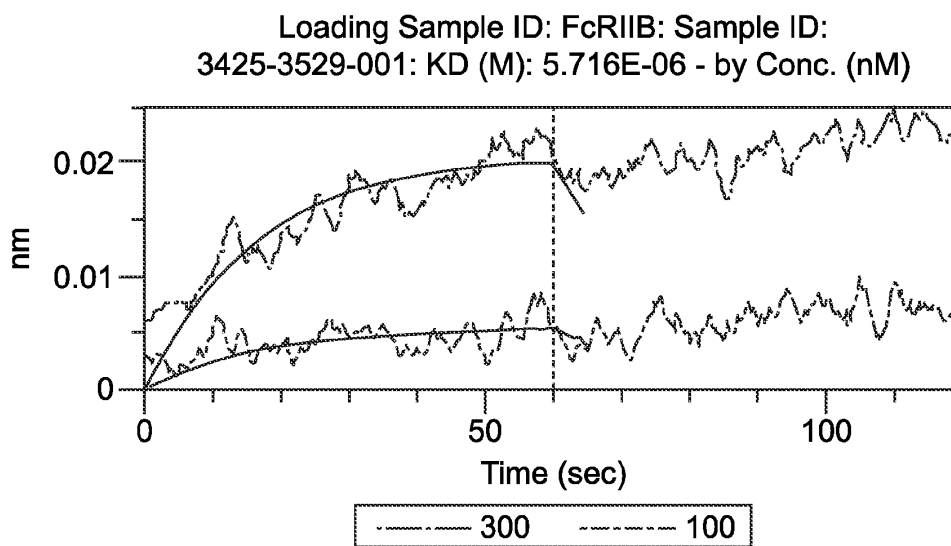
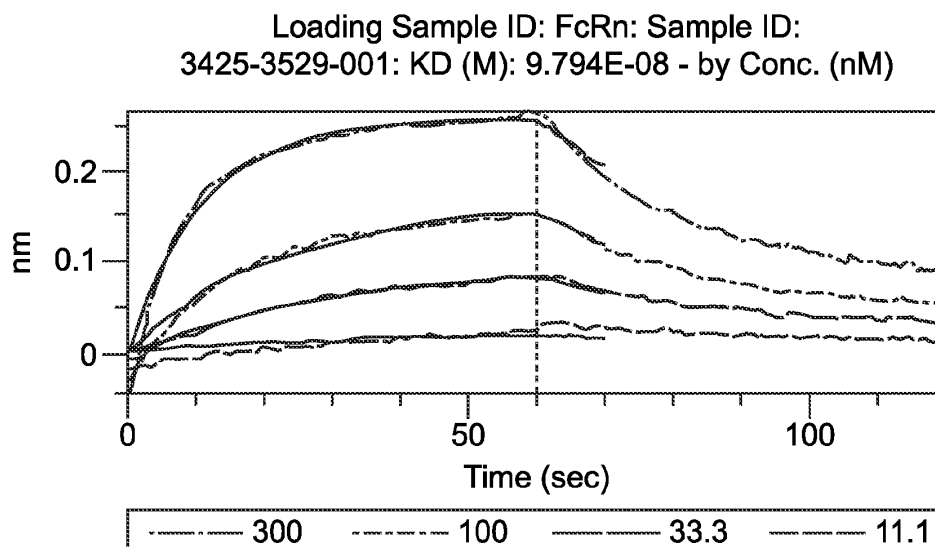


FIG. 34 (Cont.)



Loading Sample ID	Sample ID	KD (M)	kon(1/Ms)	kdis(1/s)	Full X^2	Full R^2
FcRI	3425-3529-001	2.08E-07	2.50E+05	5.20E-02	0.00687	0.9991
FcRIIA	3425-3529-001	1.56E-07*	1.36E+05	2.12E-02	0.002	0.9269
FcRIIB	3425-3529-001	5.72E-06*	1.00E+04	5.74E-02	0.0004	0.9277
FcRIIIA-F	3425-3529-001	No binding	--	--	--	--
FcRIIIA-V	3425-3529-001	5.92E-07	9.10E+04	5.39E-02	0.0078	0.9924
FcRIIIB	13425-3529-001	No Binding	--	--	--	--
FcRn (pH 6.0)	3425-3529-001	9.79E-08	2.31E+05	2.26E-02	0.0177	0.9922

FIG. 35A

SMTWNQMNLGCGGSGGGGSGGGGSI*QRTPKIQVYS*CHPAENGKSNFLNCYVSGFHPSDIE
VDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTL*SQ*PKIVKWDRDM
(SEQ ID NO:462)

epitope: SMTWNQMNL – WT1 (235-243; C235S) (SEQ ID NO:451)
(G4S)3 – underlined (SEQ ID NO:379)
 β 2M (R12C) – italicized (R12C in bold and underlined)

FIG. 35B

SMTWNQMNLGCGGSGGGGSGGGGSI*QRTPKIQVYS*CHPAENGKSNFLNCYVSGFHPSDIEV
DLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTL*SQ*PKIVKWDRDM
(SEQ ID NO:463)

epitope: SMTWNQMNL – WT1 (235-243; C235S) (SEQ ID NO:451)
GCGGS(G4S)2 – underlined (SEQ ID NO:317)
 β 2M (R12C) – italicized (R12C in bold and underlined)

FIG. 35C

SMTWNQMNLGCGGSGGGGSGGGGSI*QRTPKIQVYS*RHPAENGKSNFLNCYVSGFHPSDIEV
DLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTL*SQ*PKIVKWDRDM
(SEQ ID NO:464)

epitope: SMTWNQMNL – WT1 (235-243; C235S) (SEQ ID NO:451)
GCGGS(G4S)2 – underlined (SEQ ID NO:317)
 β 2M (R12) – italicized (R12 in bold and underlined)

FIG. 35D

SMTWNQMNLGCGGSGGGGSGGGGSIQRTPKIQVYS**R**HPAENGKSNFLNCYVSGFHPSDIEV
 DLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTL**S**QPKIVKWDRDMG
 GGGSGGGGSGGGGSAPTSSSTKKTQLQLE**A**LLLDLQMILNGINNYKNPKLTRMLTA
 KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGS
 ETTFMCEYADETATIVEFLNRWITFCQSIISTLTGCGGSGGGGSGGGGSGGGGSAPTS
 SSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCL
 EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSSETTFMCEYADETATIVEF
 LNRWITFCQSIISTLT (SEQ ID NO:465)

epitope: SMTWNQMNL – WT1 (235-243; C235S) (SEQ ID NO:451)
 (GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)
 β2M (R12) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 35E

SMTWNQMNLGCGGSGGGGSGGGGSIQRTPKIQVYS**R**HPAENGKSNFLNCYVSGFHPSDIEV
 DLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTL**S**QPKIVKWDRDMG
 GGGSGGGGSGGGGSAPTSSSTKKTQLQLE**A**LLLDLQMILNGINNYKNPKLTRMLTA
 KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGS
 ETTFMCEYADETATIVEFLNRWITFCQSIISTLTGCGGSGGGGSGGGGSGGGGSAPTS
 SSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCL
 EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSSETTFMCEYADETATIVEF
 LNRWITFCQSIISTLT (SEQ ID NO:466)

epitope: SMTWNQMNL – WT1 (235-243; C235S) (SEQ ID NO:451)
 (GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)
 β2M (R12C) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 35F

SMTWNQMNLGGGGSGGGGSGGGGSIQRTPKIQVYS[□]HPAENGKSNFLNCYVSGFHPSDIE
VDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRDM
GGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLT
AKFYMPKKATELKHLQCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKG
SETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAPT
SSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQC
LEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE
FLNRWITFCQSIISTLT (SEQ ID NO:467)

epitope: SMTWNQMNL – WT1 (235-243; C235S) (SEQ ID NO:451)

(G4S)₃ and (G4S)₄ – underlined (SEQ ID NOs:379-380)

β2M (R12C) – italicized

IL-2 (H16A; F42A) – bold

FIG. 36A

GCMTWNQMNLGGGGSGGGSGGGGSI*QRTPKIQVYS*CHPAENGKSNFLNCYVSGFHPSDI
 EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRD
 M (SEQ ID NO:468)

epitope: GCMTWNQMNL – WT1 (235-243; G-1) (SEQ ID NO:452)
 (G4S)3 – underlined (SEQ ID NO:379)
 β 2M (R12C) – italicized (R12C in bold and underlined)

FIG. 36B

GCMTWNQMNLGCGGSGGGSGGGGSI*QRTPKIQVYS*CHPAENGKSNFLNCYVSGFHPSDI
 EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRD
 M (SEQ ID NO:469)

epitope: GCMTWNQMNL – WT1 (235-243; G-1) (SEQ ID NO:452)
 GCGGS(G4S)2 – underlined (SEQ ID NO:317)
 β 2M (R12C) – italicized (R12C in bold and underlined)

FIG. 36C

GCMTWNQMNLGCGGSGGGSGGGGSI*QRTPKIQVYS*RHPAENGKSNFLNCYVSGFHPSDI
 EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRD
 M (SEQ ID NO:470)

epitope: GCMTWNQMNL – WT1 (235-243; G-1) (SEQ ID NO:452)
 GCGGS(G4S)2 – underlined (SEQ ID NO:317)
 β 2M (R12) – italicized (R12 in bold and underlined)

FIG. 36D

GCMTWNQMNLGCGGSGGGSGGGGSI*QRTPKIQVYS***R**HPAENGKSNFLNCYVSGFHPSDI
 EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRD
 MGGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRML
TAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK
 GSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGGSAP
 TSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQ
 CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIV
 EFLNRWITFCQSIISTLT (SEQ ID NO:471)

epitope: GCMTWNQMNL – WT1 (235-243; G-1) (SEQ ID NO:452)

(GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)

β2M (R12) – italicized

IL-2 (H16A; F42A) – bold

FIG. 36E

GCMTWNQMNLGCGGSGGGSGGGGSI*QRTPKIQVYS***R**HPAENGKSNFLNCYVSGFHPSDI
 EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRD
 MGGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRML
TAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK
 GSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGGSAP
 TSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQ
 CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIV
 EFLNRWITFCQSIISTLT (SEQ ID NO:472)

epitope: GCMTWNQMNL – WT1 (235-243; G-1) (SEQ ID NO:452)

(GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)

β2M (R12C) – italicized

IL-2 (H16A; F42A) – bold

FIG. 36F

GCMTWNQMNLGGGGSGGGSGGGSGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDI
EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWRD
MGGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRML
TAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK
GSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGGSAP
TSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQ
CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIV
EFLNRWITFCQSIISTLT (SEQ ID NO:473)

epitope: GCMTWNQMNL – WT1 (235-243; G-1) (SEQ ID NO:452)

(G4S)₃ and (G4S)₄ – underlined (SEQ ID NOs:379-380)

β2M (R12C) – italicized

IL-2 (H16A; F42A) – bold

FIG. 37A

SYTWNQMNLGGGGSGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDIEV
 DLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRDM
 (SEQ ID NO:474)

epitope: SYTWNQMNL – WT1 (235-243; C235S; M236Y) (SEQ ID NO:453)
 (G4S)3 – underlined (SEQ ID NO:379)
 β 2M (R12C) – italicized (R12C in bold and underlined)

FIG. 37B

3973

SYTWNQMNLGCGGSGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDIEV
 DLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRDM
 (SEQ ID NO:475)

epitope: SYTWNQMNL – WT1 (235-243; C235S; M236Y) (SEQ ID NO:453)
 GCGGS(G4S)2 – underlined (SEQ ID NO:317)
 β 2M (R12C) – italicized (R12C in bold and underlined)

FIG. 37C

SYTWNQMNLGCGGSGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEV
 DLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRDM
 (SEQ ID NO:476)

epitope: SYTWNQMNL – WT1 (235-243; C235S; M236Y) (SEQ ID NO:453)
 GCGGS(G4S)2 – underlined (SEQ ID NO:317)
 β 2M (R12) – italicized (R12 in bold and underlined)

FIG. 37D

SYTWNQMNLGCGGSGGGGSGGGGSIQRTPKIQVYS**R**HPAENGKSNFLNCYVSGFHPSDIEV
 DLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTL**S**QPKIVKWDRDMG
 GGGSGGGGSGGGGSAPTSSSTKKTQLQLE**A**LLLDLQMILNGINNYKNPKLTRMLTA
 KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGS
 ETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAPTS
 SSTKKTQLQLE**A**LLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCL
 EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSSETTFMCEYADETATIVEF
 LNRWITFCQSIISTLT (SEQ ID NO:477)

epitope: SYTWNQMNL – WT1 (235-243; C235S; M236Y) (SEQ ID NO:453)
 (GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)
 β2M (R12) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 37E

SYTWNQMNLGCGGSGGGGSGGGGSIQRTPKIQVYS**R**HPAENGKSNFLNCYVSGFHPSDIEV
 DLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTL**S**QPKIVKWDRDMG
 GGGSGGGGSGGGGSAPTSSSTKKTQLQLE**A**LLLDLQMILNGINNYKNPKLTRMLTA
 KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGS
 ETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAPTS
 SSTKKTQLQLE**A**LLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCL
 EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSSETTFMCEYADETATIVEF
 LNRWITFCQSIISTLT (SEQ ID NO:478)

epitope: SYTWNQMNL – WT1 (235-243; C235S; M236Y) (SEQ ID NO:453)
 GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)
 β2M (R12C) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 37F

SYTWNQMNLGGGGSGGGSGGGGSIQRTPKIQVYS[□]HPAENGKSNFLNCYVSGFHPSDIEV
DLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRDMG
GGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTA
KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGS
ETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGGSAPTS
SSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCL
EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSSETTFMCEYADETATIVEF
LNRWITFCQSIISTLT (SEQ ID NO:479)

epitope: SYTWNQMNL – WT1 (235-243; C235S; M236Y) (SEQ ID NO:453)

(G4S)₃ and (G4S)₄ – underlined (SEQ ID NOs:379-380)

β2M (R12C) – italicized

IL-2 (H16A; F42A) – bold

FIG. 38A

GCYTWNQMNLGCGGSGGGSGGGGSI*QRTPKIQVYS*CHPAENGKSNFLNCYVSGFHPSDI
 EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRD
 M (SEQ ID NO:480)

epitope: GCYTWNQMNL– WT1 (235-243; G-1; M236Y) (SEQ ID NO:454)

(G4S)3 – underlined (SEQ ID NO:379)

β2M (R12C) – italicized (R12C in bold and underlined)

FIG. 38B

GCYTWNQMNLGCGGSGGGSGGGGSI*QRTPKIQVYS*CHPAENGKSNFLNCYVSGFHPSDI
 EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRD
 M (SEQ ID NO:481)

epitope: GCYTWNQMNL– WT1 (235-243; G-1; M236Y) (SEQ ID NO:454)

GCGGS(G4S)2 – underlined (SEQ ID NO:317)

β2M (R12C) – italicized (R12C in bold and underlined)

FIG. 38C

GCYTWNQMNLGCGGSGGGSGGGGSI*QRTPKIQVYS*RHPAENGKSNFLNCYVSGFHPSDI
 EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRD
 M (SEQ ID NO:482)

epitope: GCYTWNQMNL– WT1 (235-243; G-1; M236Y) (SEQ ID NO:454)

GCGGS(G4S)2 – underlined (SEQ ID NO:317)

β2M (R12) – italicized (R12 in bold and underlined)

FIG. 38D

GCYTWNQMNLGCGGSGGGGSGGGGSIQRTPKIQVYS^βHPAENGKSNFLNCYVSGFHPSDIE
 VDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPEKDEYACRVNHVTLSPKIVKWDRDM
 GGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLT
AKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKG
SETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAPT
SSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQC
LEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVE
FLNRWITFCQSIISTLT (SEQ ID NO:483)

epitope: GCYTWNQMNL– WT1 (235-243; G-1; M236Y) (SEQ ID NO:454)
 (GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)
 β2M (R12) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 38E

GCYTWNQMNLGCGGSGGGGSGGGGSIQRTPKIQVYS^βHPAENGKSNFLNCYVSGFHPSDI
 EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPEKDEYACRVNHVTLSPKIVKWDRD
 MGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRML
TAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK
GSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAP
TSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQ
CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIV
EFLNRWITFCQSIISTLT (SEQ ID NO:484)

epitope: GCYTWNQMNL– WT1 (235-243; G-1; M236Y) (SEQ ID NO:454)
 (GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined (SEQ ID NOs:317, 379 and 380)
 β2M (R12C) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 38F

GCYTWNQMNLGGGGSGGGSGGGSGGG*SIQRTPKIQVYS***C***HPAENGKSNFLNCYVSGFHPSDI*
EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTTEKDEYACRVNHVTLSPKIVKWDRD
MGGGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRML
TAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK
GSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGGGGSAP
TSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQ
CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK**GSETTFMCEYADETATIV**
EFLNRWITFCQSIISTLT (SEQ ID NO:485)

epitope: GCYTWNQMNL– WT1 (235-243; G-1; M236Y) (SEQ ID NO:454)

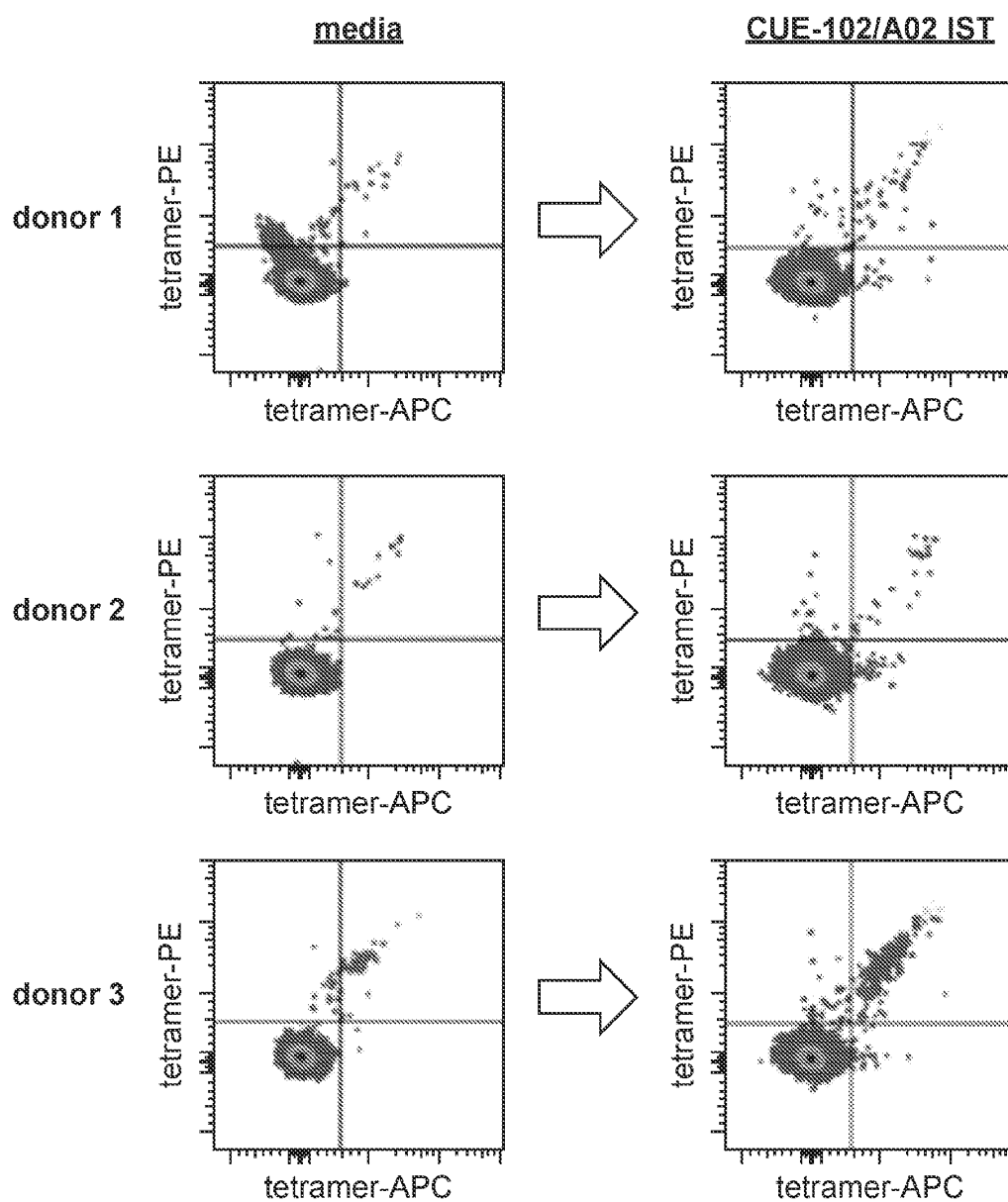
(G4S)₃ and (G4S)₄ – underlined (SEQ ID NOs:379-380)

β2M (R12C) – italicized

IL-2 (H16A; F42A) – bold

FIG. 39

Day 0 - Day 10 (priming)



Healthy donor PBMCs expanded 10 days
with CUE-102/A02 WT₁₃₇₋₄₅ Immuno-STAT

FIG. 39 (Cont.)

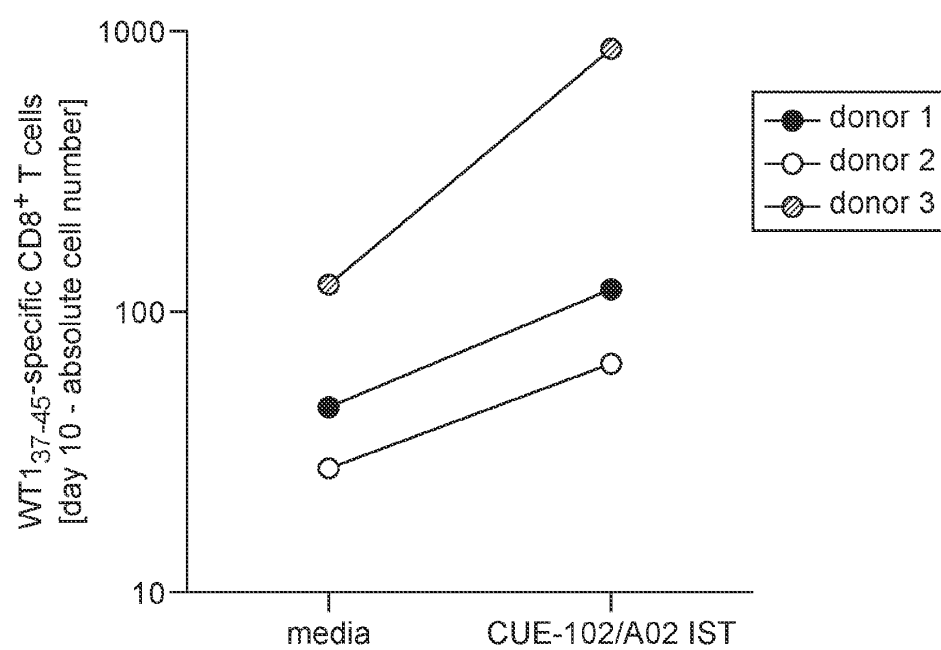
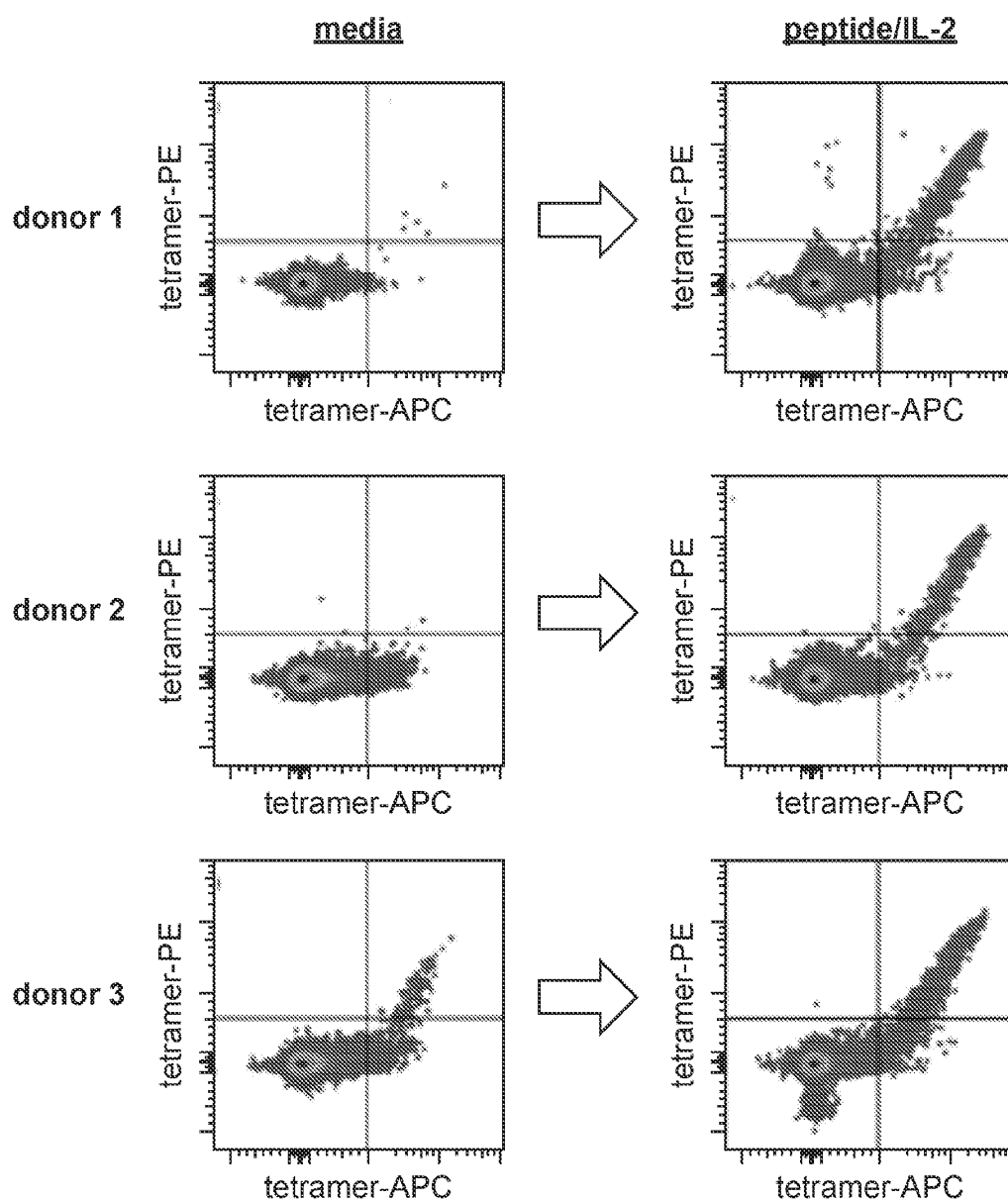


FIG. 40A

Day 0 - Day 10 (priming)

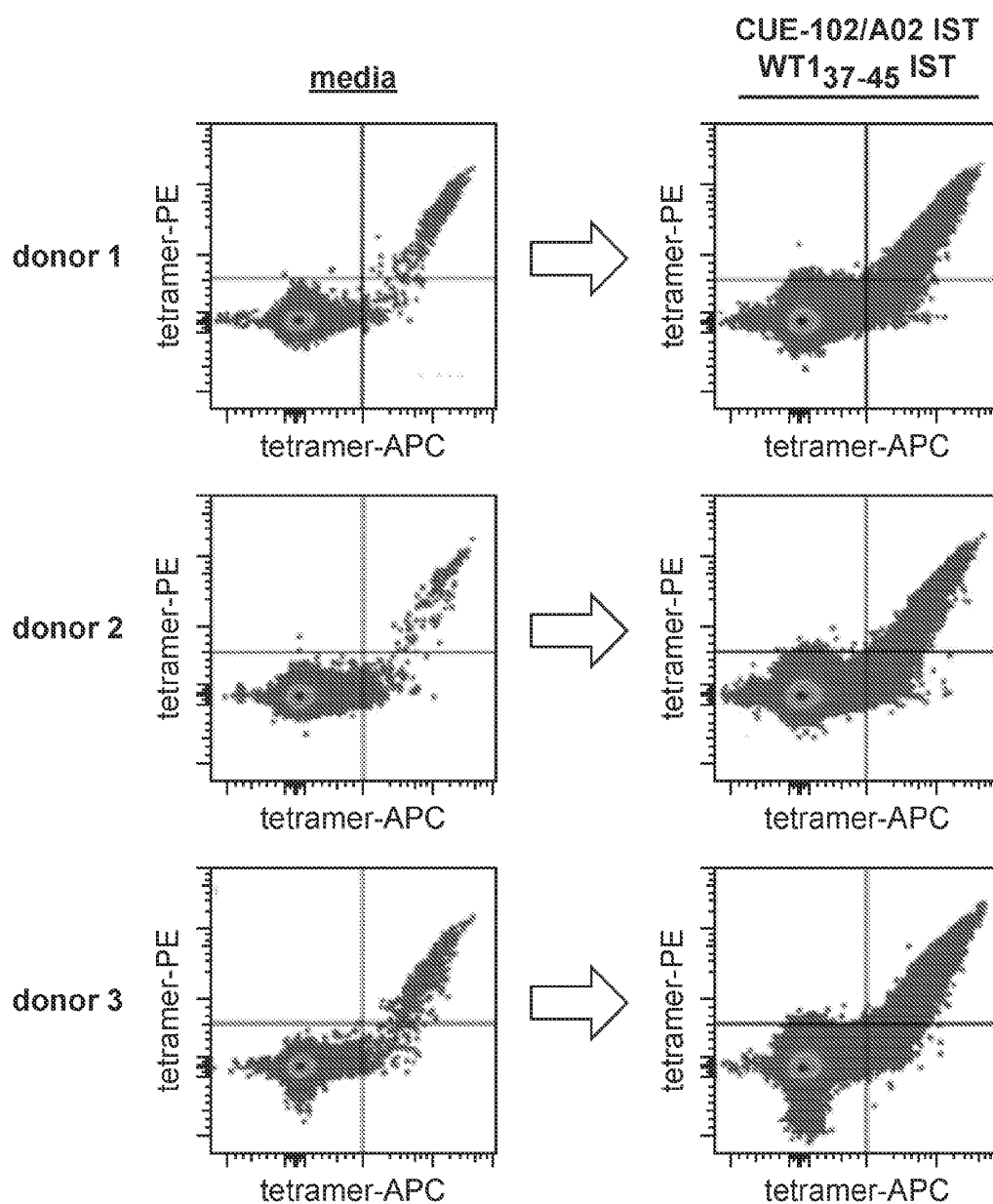


Healthy donor PBMCs expanded 10 days
with WT₁₃₇₋₄₅ peptide + rhIL-2

SUBSTITUTE SHEET (RULE 26)

FIG. 40A (Cont.)

Day 10 - Day 18 (restimulation)



CD8⁺ T cells enriched by magnetic beads are 'diluted' with mitomycin C-treated autologous PBMCs and restimulated for 8 days with CUE-102/A02 WT1₃₇₋₄₅ IST

SUBSTITUTE SHEET (RULE 26)

FIG. 40B

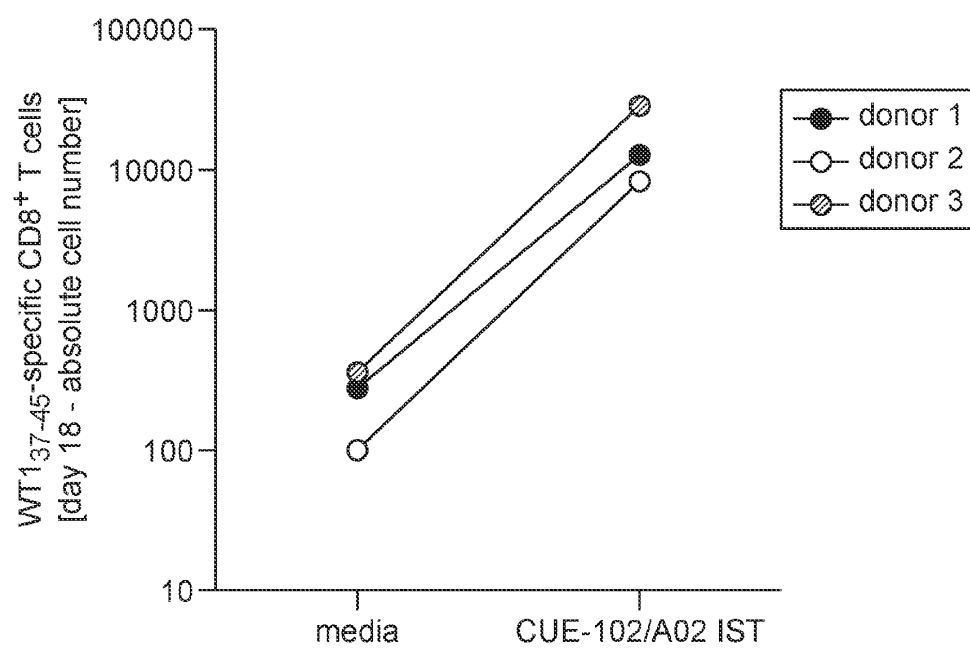


FIG. 41A

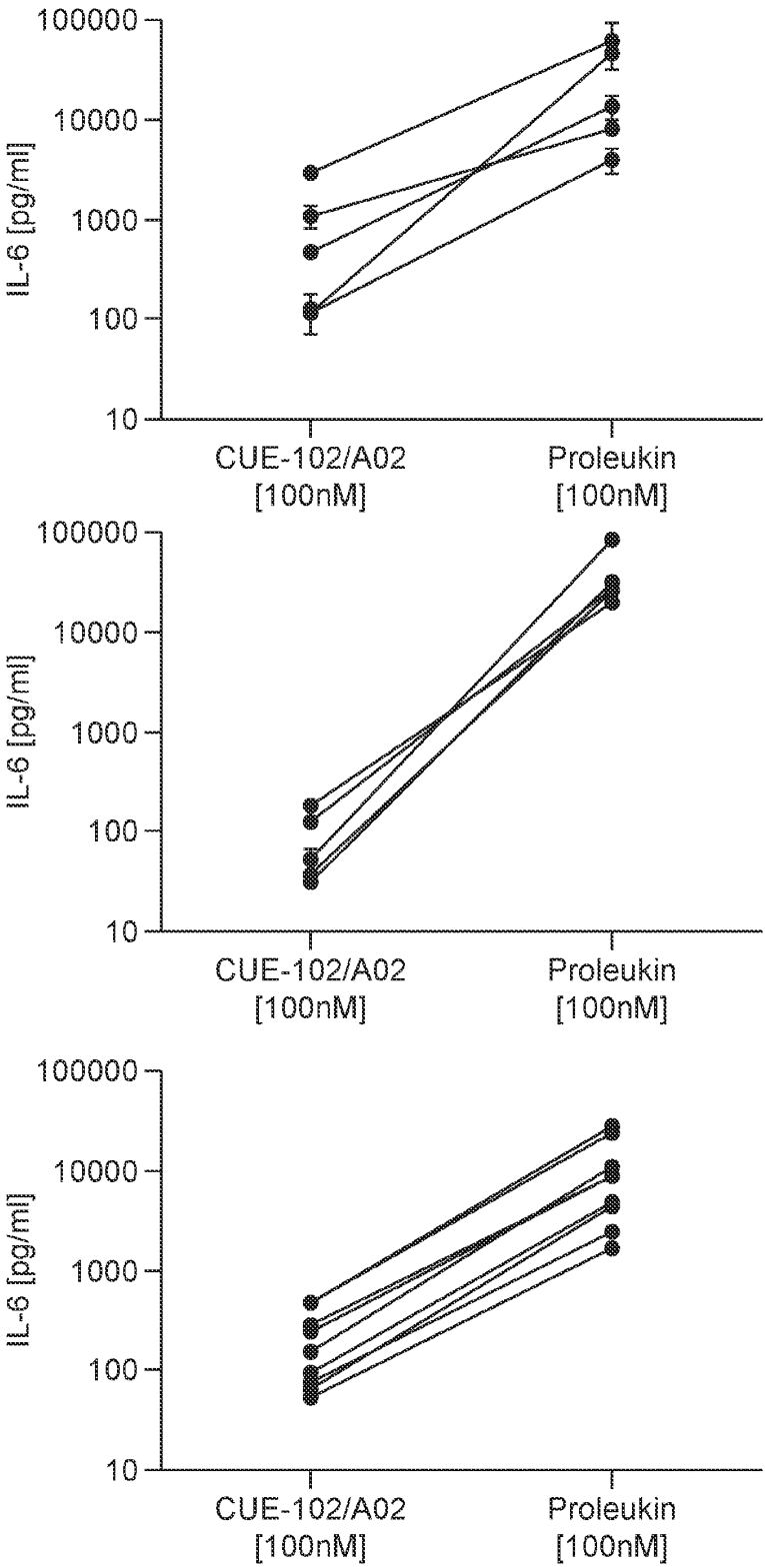


FIG. 41B

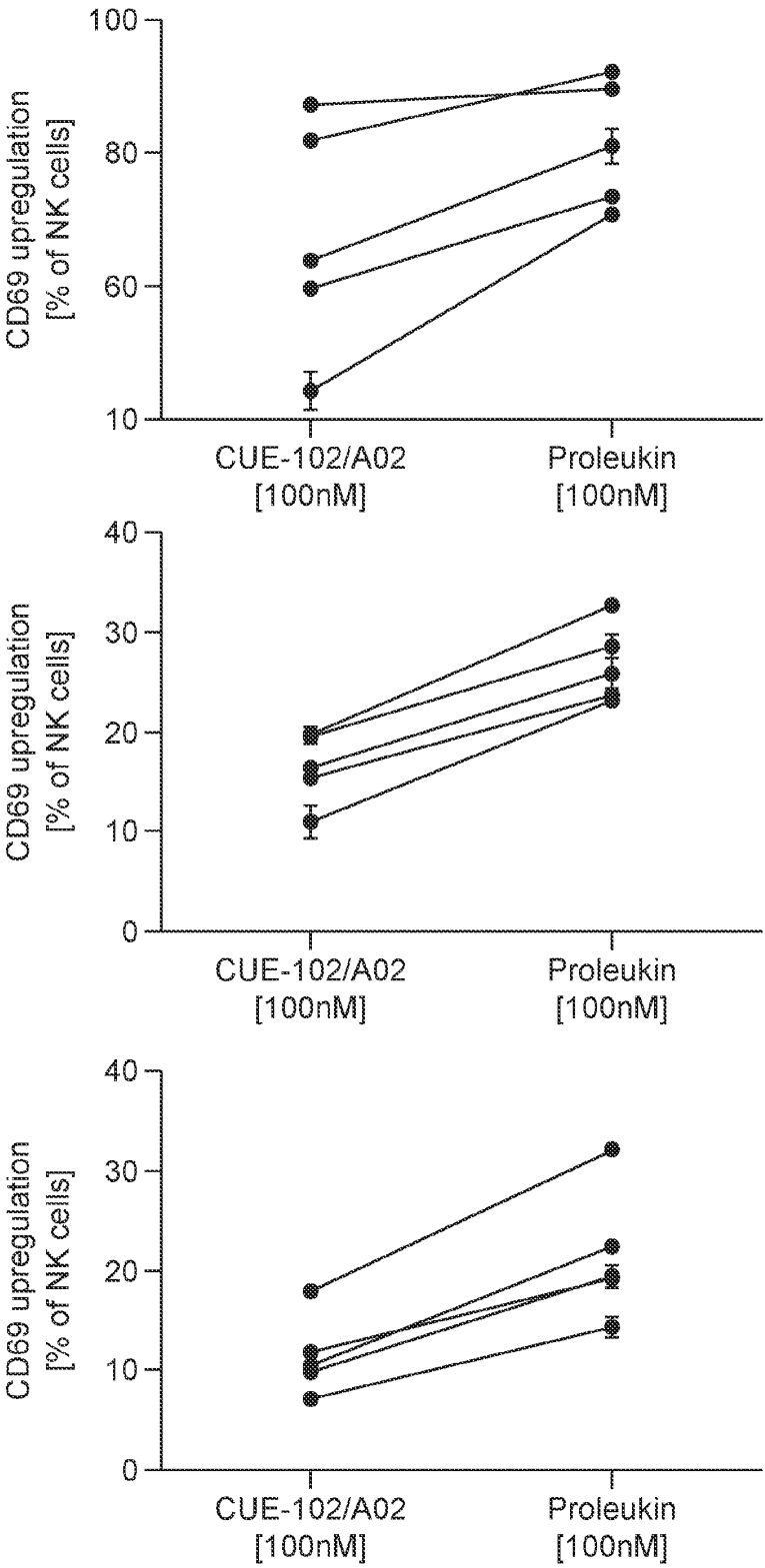


FIG. 42A

donor 1

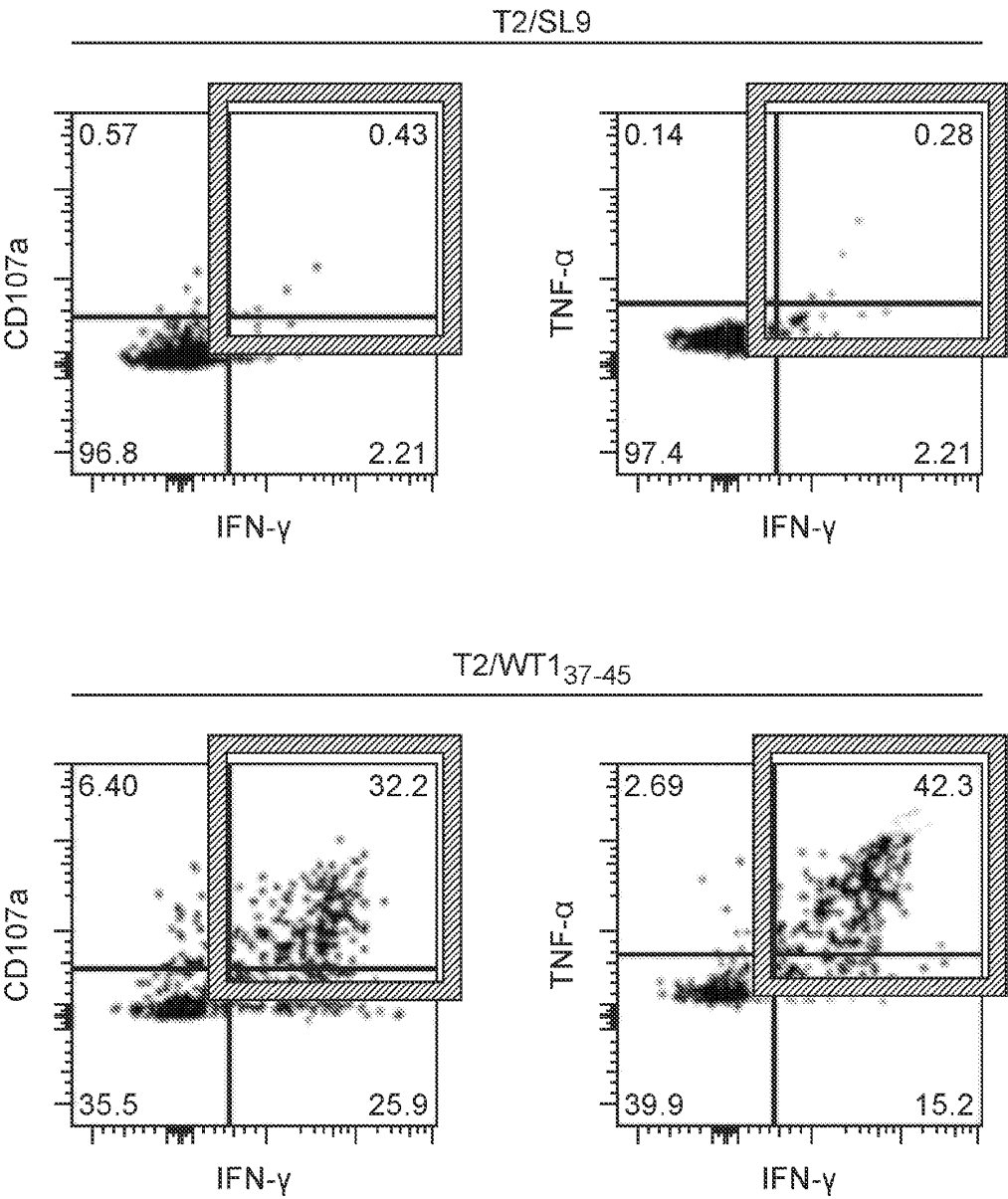


FIG. 42A (Cont.)

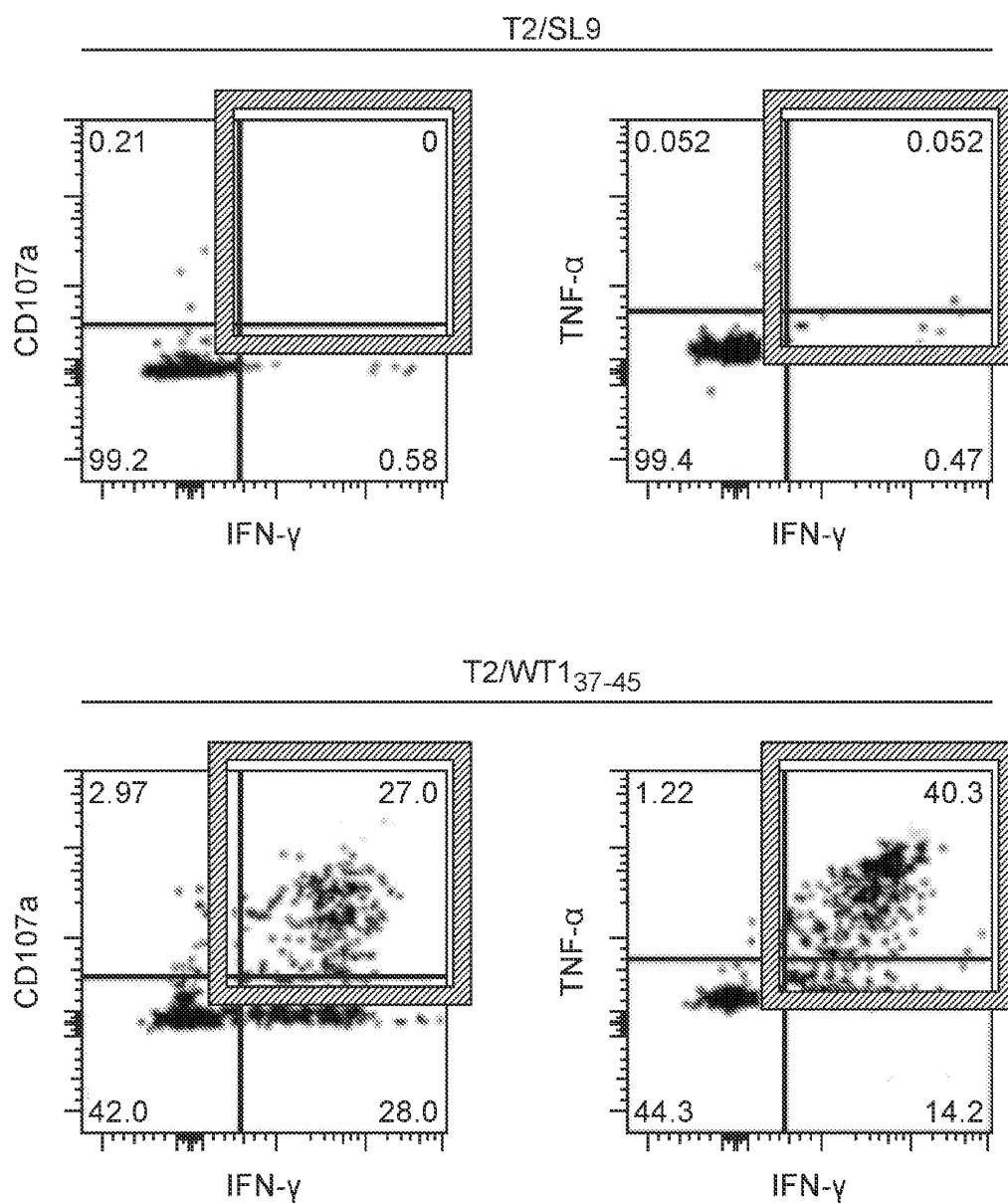
donor 2

FIG. 42B

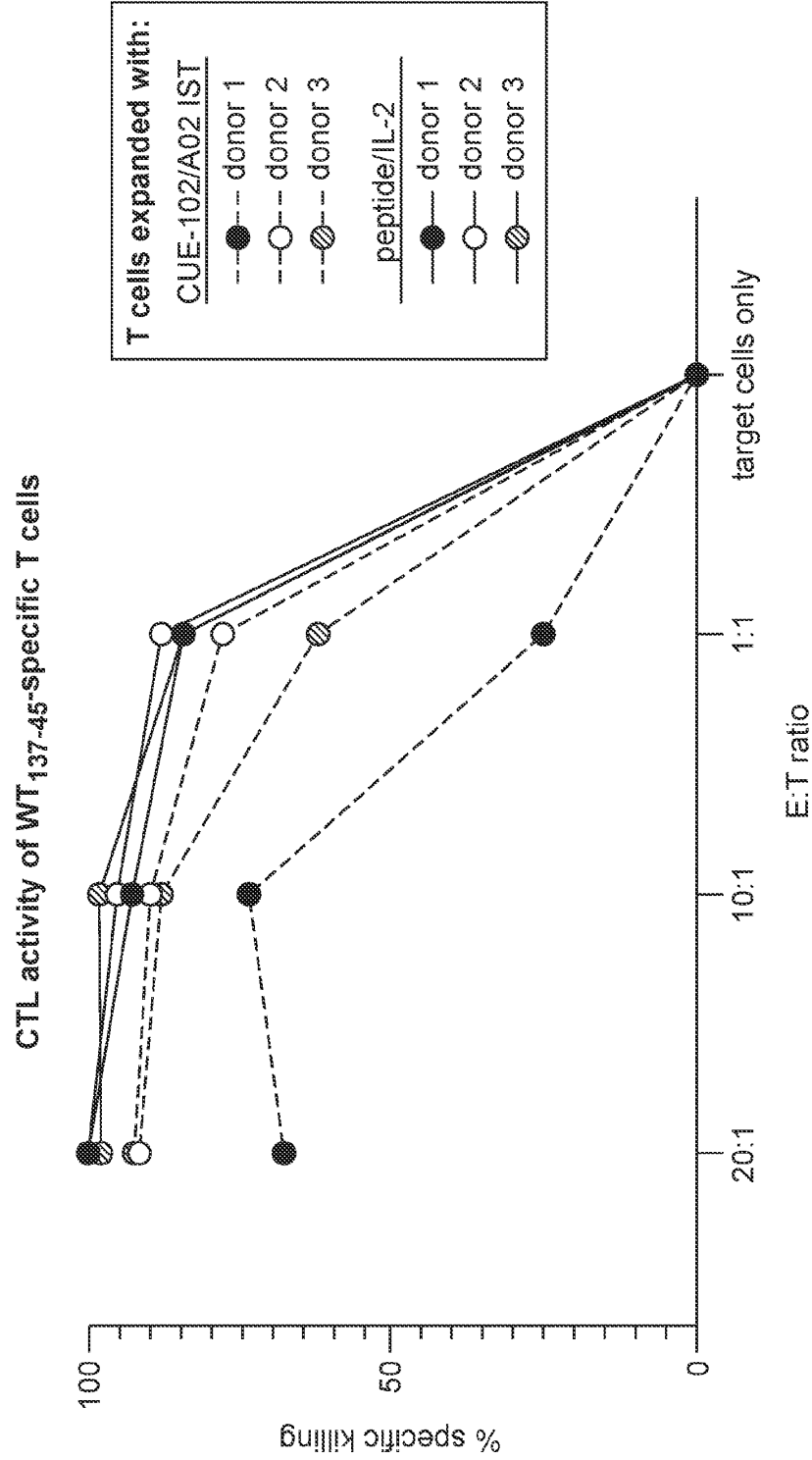


FIG. 43

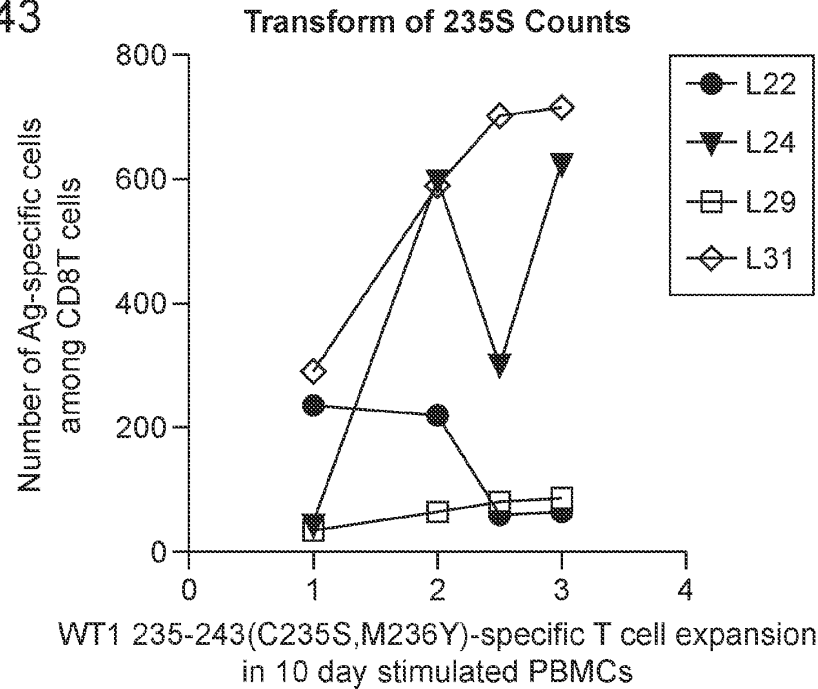


FIG. 44

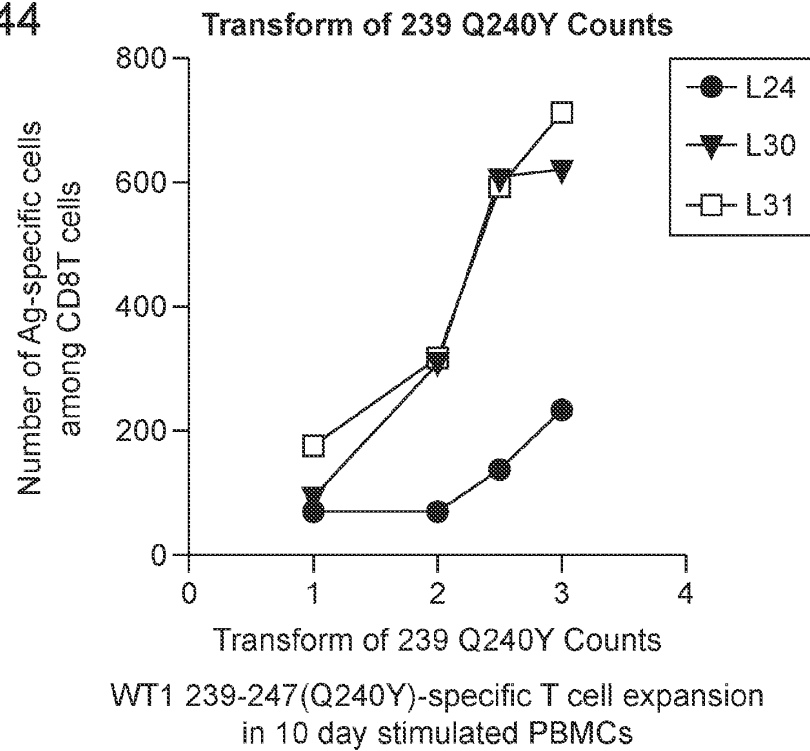


FIG. 45

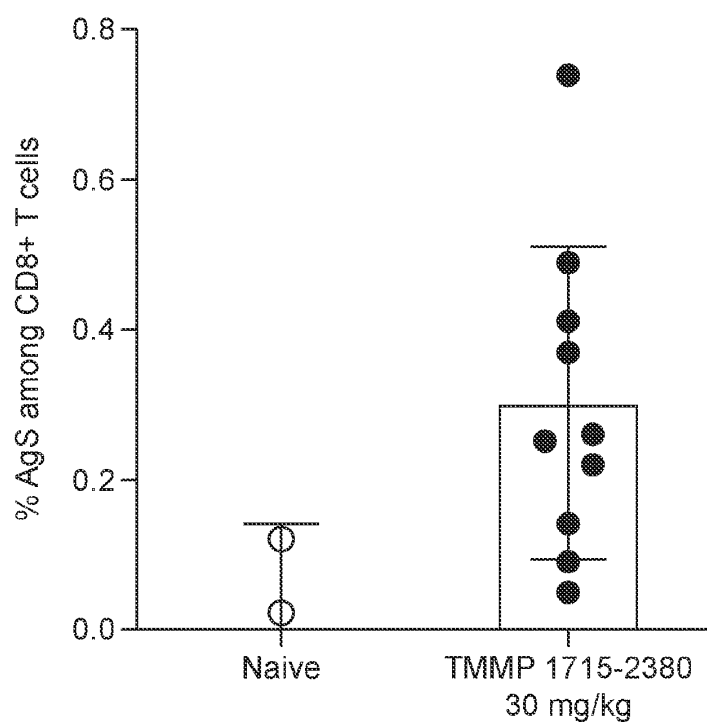


FIG. 46A

HLA-E*01:01 (Y84; A236) (R107 in bold) (wild-type)

GSHSLKYFHTSVSRPGRGEPFISVGYVDDTQFVRFDNDAASPRMVPRAPWMEQEGSEYWDRE
TRSARDTAQIFRVNLRTLRGYYNQSEAGSHTLQWMHGCELGPDRRFLRGYEQFAYDGKDYLTL
NEDLRSWTAVDTAAQISEQKSNDASEAEHQRAYLEDTCVEWLHKYLEKGKETLLHLEPPKTHV
THHPISDHEATLRCWALGFYPAEITLTWQQDGEGHTQDTELVETRPAGDGTQKWA AVVPSG
EEQRYTCHVQHEGLPEPVTLRWK (SEQ ID NO:492)

FIG. 46B

HLA-E*01:01 (Y84C; A236C) (R107 in bold)

GSHSLKYFHTSVSRPGRGEPFISVGYVDDTQFVRFDNDAASPRMVPRAPWMEQEGSEYWDRE
TRSARDTAQIFRVNLRTLRGCYYNQSEAGSHTLQWMHGCELGPDRRFLRGYEQFAYDGKDYLTL
NEDLRSWTAVDTAAQISEQKSNDASEAEHQRAYLEDTCVEWLHKYLEKGKETLLHLEPPKTHV
THHPISDHEATLRCWALGFYPAEITLTWQQDGEGHTQDTELVETRPCGDGTQKWA AVVPSG
EEQRYTCHVQHEGLPEPVTLRWK (SEQ ID NO:493)

FIG. 46C

HLA-E*01:03 (Y84; A236) (G107 in bold) (wild-type)

GSHSLKYFHTSVSRPGRGEPFISVGYVDDTQFVRFDNDAASPRMVPRAPWMEQEGSEYWDRE
TRSARDTAQIFRVNLR~~TL~~RGYYNQSEAGSHTLQWMHGCELGPDGRFLRGYEQFAYDGKDYLTL
NEDLRSWTAVDTAQISEQKSNDASEAEHQRAYLEDTCVEWLHKYLEKGKETLLHLEPPKTHV
THHPISDHEATLRCWALGFYPAEITLTWQQDGEGHTQDTELVETRPAGDGTQKWA~~AV~~VVPSG
EEQRYTCHVQHEGLPEPVTLRWK (SEQ ID NO:494)

FIG. 46D

HLA-E*01:03 (Y84C; A236C) (G107 in bold)

GSHSLKYFHTSVSRPGRGEPFISVGYVDDTQFVRFDNDAASPRMVPRAPWMEQEGSEYWDRE
TRSARDTAQIFRVNLR~~TL~~RGCYNQSEAGSHTLQWMHGCELGPDGRFLRGYEQFAYDGKDYLTL
NEDLRSWTAVDTAQISEQKSNDASEAEHQRAYLEDTCVEWLHKYLEKGKETLLHLEPPKTHV
THHPISDHEATLRCWALGFYPAEITLTWQQDGEGHTQDTELVETRPCGDGTQKWA~~AV~~VVPSG
EEQRYTCHVQHEGLPEPVTLRWK (SEQ ID NO:495)

FIG. 47A

HLA-G*01:01 (Y84; A236) (L110 in bold) (wild-type)

GSHSMRYFSAAVSRPGRGEPRFIAMGYVDDTQFVRFDSDSACPRMEPRAPWVEQEGPEYWEEE
TRNTKAHAQTDRMNLQTLRGYYNQSEASSHTLQWMIGCDLGSDGRLLRGYEQYAYDGKDYLA
LNEDLRSWTAADTAAQISKRKCEAANVAEQRRAYLEGTCVEWLHRYLENGKEMLQRADPPKT
HVTHHPVFDYEATLRCWALGFYPAEIIITWQRDGEDQTQDVELVETRPAGDGTQKWAAVVVP
SGEEQRYTCHVQHEGLPEPLMLRWK (SEQ ID NO:496)

FIG. 47B

HLA-G*01:01 (Y84C; A236C) (L110 in bold)

GSHSMRYFSAAVSRPGRGEPRFIAMGYVDDTQFVRFDSDSACPRMEPRAPWVEQEGPEYWEEE
TRNTKAHAQTDRMNLQTLRGCYNQSEASSHTLQWMIGCDLGSDGRLLRGYEQYAYDGKDYLA
LNEDLRSWTAADTAAQISKRKCEAANVAEQRRAYLEGTCVEWLHRYLENGKEMLQRADPPKT
HVTHHPVFDYEATLRCWALGFYPAEIIITWQRDGEDQTQDVELVETRPCGDGTQKWAAVVVP
SGEEQRYTCHVQHEGLPEPLMLRWK (SEQ ID NO:497)

FIG. 47C

HLA-G*01:04 (Y84; A236) (I110 in bold) (wild-type)

GSHSMRYFSAAVSRPGRGEPRFIAMGYVDDTQFVRFDSDSACPRMEPRAPWVEQEGPEYWEEE
TRNTKAHAQTDRMNLQTLRGYYNQSEASSHTLQWMIGCDLGSDGRLIRGYEQYAYDGKDYLA
LNEDLRSWTAADTAAQISKRKCEAANVAEQRRAYLEGTCVEWLHRYLENGKEMLQRADPPKT
HVTHHPVFDYEATLRCWALGFYPAEIIITWQRDGEDQTQDVELVETRPAGDGTQKWA AVVVP
SGEEQRYTCHVQHEGLPEPLMLRWK (SEQ ID NO:498)

FIG. 47D

HLA-G*01:04 (Y84C; A236C) (I110 in bold) (wild-type)

GSHSMRYFSAAVSRPGRGEPRFIAMGYVDDTQFVRFDSDSACPRMEPRAPWVEQEGPEYWEEE
TRNTKAHAQTDRMNLQTLRGCYNQSEASSHTLQWMIGCDLGSDGRLIRGYEQYAYDGKDYLA
LNEDLRSWTAADTAAQISKRKCEAANVAEQRRAYLEGTCVEWLHRYLENGKEMLQRADPPKT
HVTHHPVFDYEATLRCWALGFYPAEIIITWQRDGEDQTQDVELVETRPCGDGTQKWA AVVVP
SGEEQRYTCHVQHEGLPEPLMLRWK (SEQ ID NO:499)