

FIG.1A

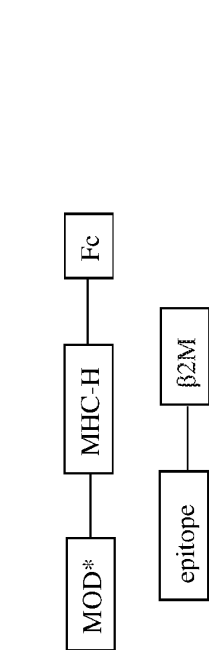


FIG.1B

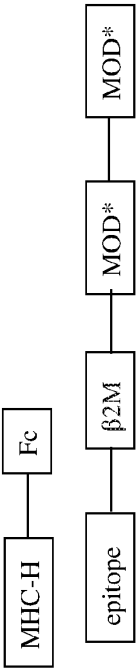
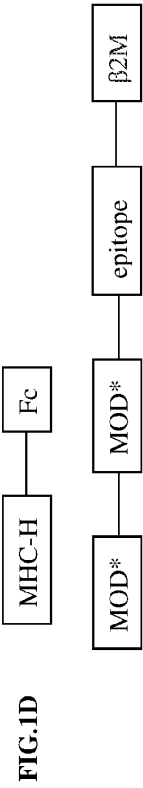
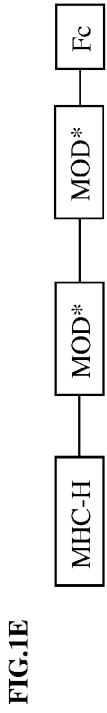
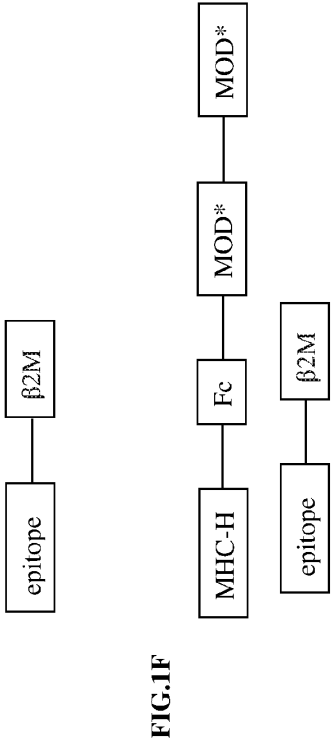


FIG.1C



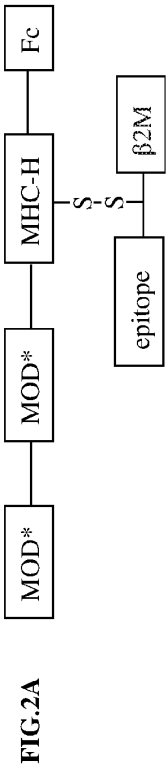
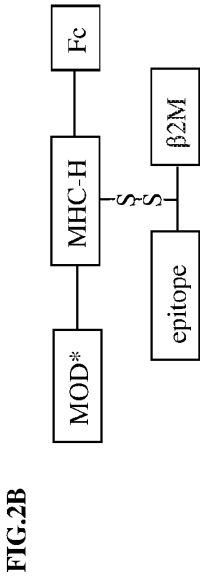
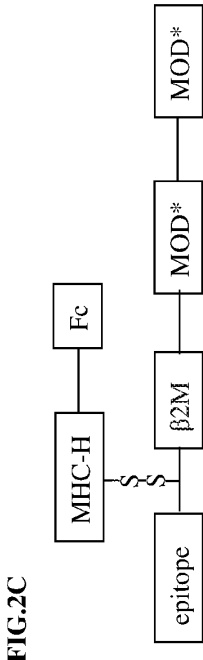


FIG.2D

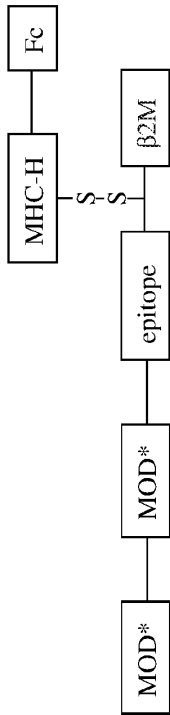


FIG.2E

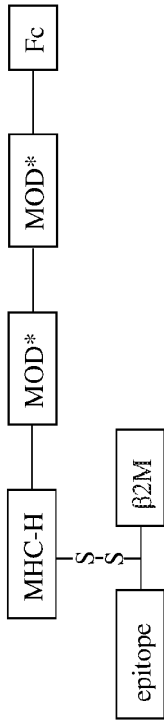


FIG.2F

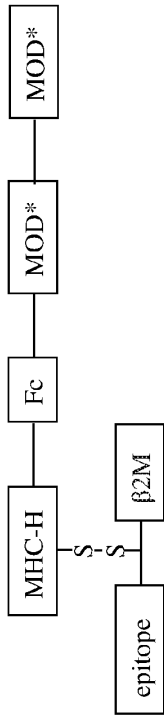


FIG. 3A**WT-1 isoform A**

```
1  MDFLLLLQDPA  STCVPEPASQ  HTLRSGPGCL  QQPEQQGVRD  PGGIWAKLGA  AEASAERLQG
61  RRSRGASGSE  PQQMGSDVRD  LNALLPAVPS  LGGGGGCALP  VSGAAQWAPV  LDFAPPGASA
121 YGSLGGPAPP  PAPPFFFFFFP  PHSFIKQEPS  WGAEPHEEQ  CLSAFTVHFS  GQFTGTAGAC
181 RYGPFPGPPP  SQASSGQARM  FPNAPYLPSC  LESQPAIRNQ  GYSTVTFDGT  PSYGHTPSHH
241 AAQFPNHSFK  HEDPMGQQGS  LGEQQYSVPP  PVYGCHTPTD  SCTGSQALLL  RTPYSSDNLY
301 QMTSQLECMT  WNQMNLGATL  KGHSTGYESD  NHTTPILCGA  QYRIHTHGVF  RGIQDVRRVP
361 GVAPTLVRSA  SETSEKRPFM  CAYPGCNKRY  FKLSHLQMHS  RKHTGEKPYQ  CDFKDCERRF
421 SRSDQLKRHQ  RRHTGVKPFQ  CKTCQRKFSS  SDHLKTHTRT  HTGEKPFSCR  WPSCQKKFAR
481 SDELVRHHNM  HQRNMTKLQL  AL
```

FIG. 3B**WT-1 isoform B**

```
1  MDFLLLLQDPA  STCVPEPASQ  HTLRSGPGCL  QQPEQQGVRD  PGGIWAKLGA  AEASAERLQG
61  RRSRGASGSE  PQQMGSDVRD  LNALLPAVPS  LGGGGGCALP  VSGAAQWAPV  LDFAPPGASA
121 YGSLGGPAPP  PAPPFFFFFFP  PHSFIKQEPS  WGAEPHEEQ  CLSAFTVHFS  GQFTGTAGAC
181 RYGPFPGPPP  SQASSGQARM  FPNAPYLPSC  LESQPAIRNQ  GYSTVTFDGT  PSYGHTPSHH
241 AAQFPNHSFK  HEDPMGQQGS  LGEQQYSVPP  PVYGCHTPTD  SCTGSQALLL  RTPYSSDNLY
301 QMTSQLECMT  WNQMNLGATL  KGVAAGSSSS  VKWTEGQSNH  STGYESDNHT  TPILCGAQYR
361 IHTHGVFRGI  QDVRRVPGVA  PTLVRSASET  SEKRPFMCAY  PGCNKRYFKL  SHLQMHSRKH
421 TGEKPYQCDF  KDCERRFSRS  DQLKRHQRRH  TGVKPFQCKT  CQRKFSSRDH  LKTHTRTHTG
481 EKPFSRWPS  CQKKFARSDE  LVRHHNMHQR  NMTKLQLAL
```

FIG. 3C**WT-1 isoform D**

1 MDFLLLLQDPA STCVPEPASQ HTLRSGPGCL QQPEQQGVRD PGGIWAKLGA AEASAERLQG
61 RRSRGASGSE PQQMGSDVRD LNALLPAVPS LGGGGGCALP VSGAAQWAPV LDFAPPGASA
121 YGSLGGPAPP PAPPPIPPPP PHSFIKQEPS WGAEPHEEQ CLSAFTVHFS GQFTGTAGAC
181 RYGFFGPPPP SQASSGQARM FPNAPYLPSC LESQPAIRNQ GYSTVTFDGT PSYGHTPSHH
241 AAQFPNHSEK HEDPMGQQGS LGEQQYSVPP PVYGCHTPTD SCTGSQALLL RTPYSSDNLY
301 QMTSQLECMT WNQMNLGATL KGVAAGSSSS VKWTEGQSNH STGYESDNHT TPILCGAQYR
361 IHTHGVFRGI QDVRVPQVA PTLVRSASET SEKRPFMCAY PGCNKRYFKL SHLQMHSRKH
421 TGEKPYQCDF KDCERRFSRS DQLKRHRH RHQRRHTGVK PFQCKTCQRK FSRSDHLKTH
481 KTSEKPFSCR WPSCQKKFAR SDELVRHHNM HQRNMTKLQL AL

FIG. 3D**WT-1 isoform E**

1 MEKGYSTVTF DGTPSYGHTP SHHAAQFPNH SFKHEDPMGQ QGSLGEQQYS VPPPVYGCHT
61 PTDSCGSGQA LLLRTPYSSD NLYQMTSQLE CMTWNQMNLG ATLKGVAAGS SSSVKWTEGQ
121 SNHSTGYESD NHTTPILCGA QYRIHTHGVF RGIQDVRVP GVAPTLVRS SETSEKRPFM
181 CAYPGCNKRY FKLSHLQMHS RKHTGEKPYQ CDFKDCERRF SRSDQLKRHQ RRHTGVKPFQ
241 CKTCQKFSR SDHLKTHTRT HTGEKPFSCR WPSCQKKFAR SDELVRHHNM HQRNMTKLQL
301 AL

FIG. 3E**WT-1 isoform F**

1 MEKGYSTVTF DGTPSYGHTP SHHAAQFPNH SFKHEDPMGQ QGSLGEQQYS VPPPVYGCHT
61 PTDSCGSGQA LLLRTPYSSD NLYQMTSQLE CMTWNQMNLG ATLKGHSTGY ESDNHTTPIL
121 CGAQYRIHTH GVFRGIQDVR RVPGVAPTLV RSASETSEKR PFMCAYPGCN KRYFKLSHLQ
181 MHSRKHTGEK PYQCDFKDCE RRFSDQLK RHQRRHTGVK PFQCKTCQRK FSRSDHLKTH
241 TRHTGKTSE KPFSCRWPSC QKKFARSDEL VRHHNMHQRN MTKLQLAL

FIG. 4A

Construct 3158

GSHSMRYFSTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASORMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRIALRAYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWORDGEDOTQDTELVETRPCGDGTFQKWAAVVVPSGEEQRYTCHVOHEGLP
KPLTLRWEGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKN
PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGG
GGGGSGGGGSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
SLSLSPG

HLA-A*24:02 – double underlined

(G4S)₃ and (G4S)₄ – underlined

IL-2 (H16A; F42A) – bold

Human IgG1 Fc (LALA) – italicized

FIG. 4B

Construct 2750

APTSSSTKKTQLEALLLDLQMI^{LN}GINNYKNPKLTRMLTAKFYMPKKATELKHLQCL
 EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL
 NRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGGGSGAPTSSSTKKTQLEALLLDLQMI
 L^{NG}GINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
 DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGG
 SGGGGSGGGSGSGSHSMRYFSTSVSRPGRGEPRFIAVG^YVDDTQFVRFDSDAASQRMEPR
 APWIEQEGPEYWDEETGKVK^{HS}QTDRENLR^{IAL}RAYNQSEAGSHTLQMMFGCDVGS^{DG}
 RFLRGYHQYAYDGKD^YIALKEDLRSWTAADMAAQITKRKWEAAHVAEQRAYLEGTCVD
 GLRRYLENGKETLQRTDPPKTHMTHPI^{SD}HEATLRCWALGFYPAEITLTWQRDGEDQT
 QDTEL^VETRPCGDGTFQKWA^{AV}VVPSGEEQRYTCHVQHEGLPKPLTLRWEAAAGGDKTH
 TCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
 VHN^{AK}TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD
 GSFFLYSKLTV^{DK}SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK**

IL2(H16A; F42A) – bold

(G4S)₄ linker – italicized

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

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FIG. 4C

Construct 3159

GSHSMRYFSTSVSRPGRGEPREFIAVGYVDDTQFVRFDSDAASQRM
EPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLR
IALRAYNQSEAGSHTLQMMFGCDVGS
DGR
FLRGYHQYAYDGKDYLKEDLR
SWTAADMAAQITKRKWEAAHVAEQ
QRAYL
EGTCVDGLRRYLENGKETLORTD
PPKTHMTHHPISDHEATLRCWAL
GFYPAEITL
TWORDGEDQTQDTEL
VETRPCGDGTFQKWA
AVVVPSGEEQRYTCHVQHEGLP
KPLTLRWE
AAAGGDKTHTCPPCPAPEAAGG
PSVFLFPPKPKDTLMISRTPEV
TCVV
VDVSHEDPEVKFNWYVDG
VEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQ
SLTCLVKGFYPSDIA
VEWESNGQPENNYKTPPVLD
SDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHN
HYTQKSLSLSPGGGGSGGGG
SGGGGSAPTSSSTKKTQLQLE
ALLDLQMILN
GINNYKNPKLTRMLTAKFYMPKKATEL
KHLQCLEEELKPLEEVLNLAQSK
NFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIS
TLTGGGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
NYKNPKLTRMLTAKFYMPKKATEL
KHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

HLA-A*24:02 – double underlined
Human IgG1 Fc (LALA) – italicized
(G4S)₃ and (G4S)₄ – underlined
IL-2 (H16A; F42A) – bold

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FIG. 4D**Construct 2752**

CMTWNQMNLGGGGSGGGSGGGGS*I*QRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDI
EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVK
WDRDM

epitope: CMTWNQMNL – WT1 (235-243)
(G4S)3 – underlined
β2M (R12C) – italicized

FIG. 4E**Construct 2753**

CYTWNQMNLGGGGSGGGSGGGGS*I*QRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDIE
VDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKW
DRDM

epitope: CYTWNQMNL – WT1 (235-243)
(G4S)3 – underlined
β2M (R12C) – italicized

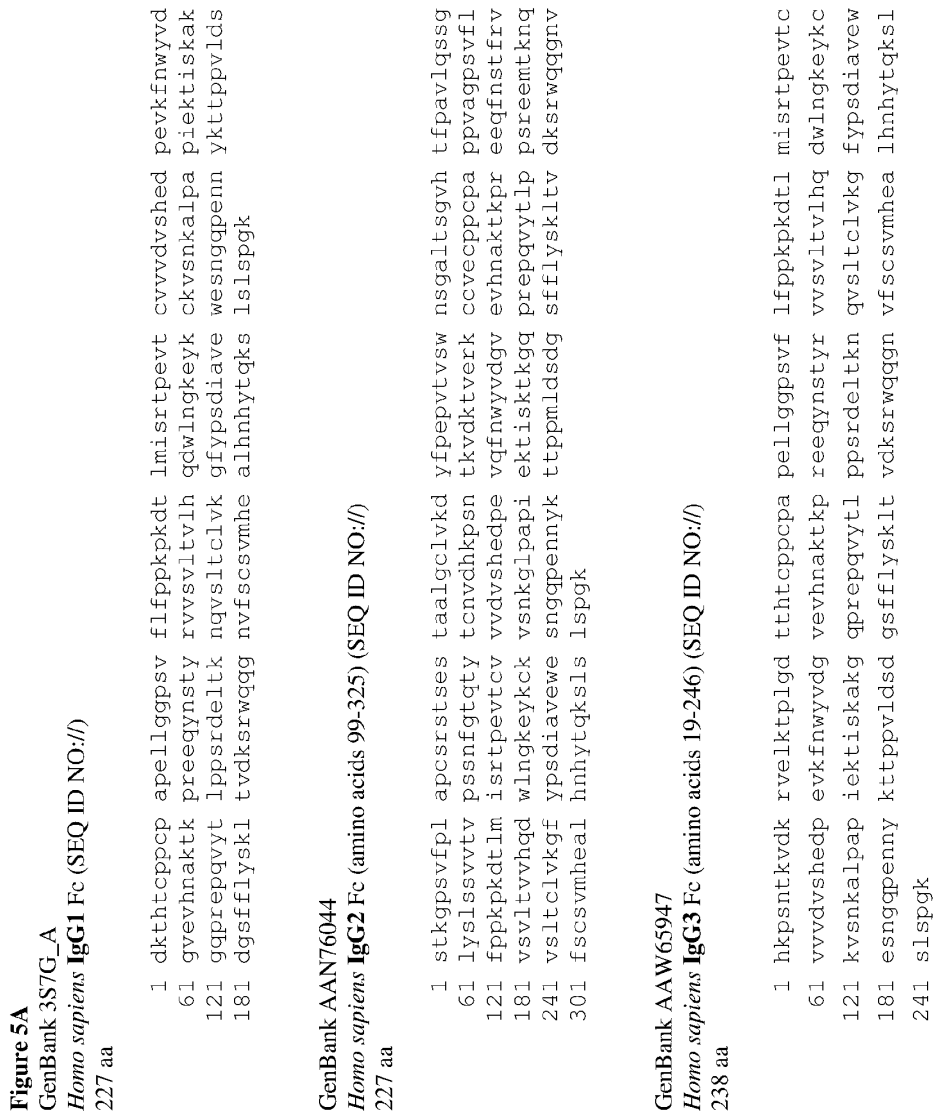


Figure 5B

GenBank AAA52770
Homo sapiens **IgD** Fc (amino acids 162-383) (SEQ ID NO://)
222 aa

1 ptkapdvfpi isgcrhpkdn spvvlaclit gyhptsvtvt wymgtqsqpq rtfpeiqrdr
61 syymtssqls tplqgwrqge ykcvvqhtas kskkeifrwp espkqaassv ptaqpqaegs
121 lakattapat trntgrggee kkekekeeq eeretkpec pshtqplgvy lltpavqdlw
181 lrdkatftcf vvgSDLkdah ltwevagkvp tggveeglle rhsgsgsqsh srllprslw
241 nagtsvtctl nhpslppqrl malrepaaqa pvklslnlla ssdppeaasw llcevsqfsp
301 pnillmwled grevntsgfa parpppqrpr ttfwawsvlr vpappspqpa tytccvvhed
361 srlllnasrs levsyvtldhg pmk

GenBank 0308221A
Homo sapiens **IgM** Fc (SEQ ID NO://)
276 aa

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

Figure 5C

GenBank P01876	
<i>Homo sapiens</i> IgA Fc (amino acids 120-353) (SEQ ID NO:1)	
234 aa	
	1 asptspkvfp lslcstqpdg nvviacvlvqg ffpgeplsvt wsegggvta rnfpssqdas
	61 gdllyttssql tlpatqclag ksvtchvkhy tnpdqdvtp cpvstpptp spstpptp
	121 scchprlslh rpaledlllg seanlctlt glrdasgvtf twtpssgksa vqgpperdlc
	181 gcysvsvlp gcaepwnhgk tftctaaype sktpltatls ksgntfirpev hllpppseel
	241 alnelvtltc largfspkdv lvrwlqgsqe lprekyltwa srqepsqgtt tfavtsilrv
	301 aaedwkkgt fscmvgheal plaftqktid rlagkpthvn vsvmaevdg tcy
GenBank 1F6A_B	
<i>Homo sapiens</i> IgE Fc (amino acids 6-222) (SEQ ID NO:1)	
212 aa	
	1 adpcdsnprg vsaylsrpsp fdlfirkspt itclvvdlap skgtvnltws rasgkpvnhs
	61 trkeekqrng tltvtstlpv gtrdwieget yqcrvthphl pralmrsttk tsgraaapev
	121 yafatpewpg srdkrtlacl iqnfmpedis vqwlhnevql pdarhsttqp rktkgsqffv
	181 fsrlevtrae weqkdeficr avheaaspsq tvqgravsvnp gk
GenBank P01861	
<i>Homo sapiens</i> IgG4 Fc (amino acids 100-327) (SEQ ID NO:1)	
228 aa	
	1 astkgpsvfp lapcsrstse staaqlclvk dyfpepvtvs wnsгалtsgv htfpavliqss
	61 glyslssvvt vpssslgtkt ytcnvdhkps ntkvdkrves kygpppcscp afeilggpsv
	121 flfppkpkdt lmsrtpevt cvvvdvsqed pevqfnwyvd gvevhnaktk preeqfnsty
	181 rvsvltvlh qdwlngkeyk ckvsnkgpls siektiskak gqprepqvyt lppsgeemtk
	241 nvsltclvk gfypsdiave wesngqpenn ykttppvlds dgsfflysr1 tvdksrwqeg
	301 nvfscsvmhe alnhytqks lslslgk

FIG. 5D

WT Human IgG1 Fc Sequence: (SEQ ID NO: //)
DKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK

FIG. 5E

Human IgG1 Fc Mutant: L234F/L235E/P331S (Triple Mutant "TM") (SEQ ID NO: //)
DKHTCPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK

FIG. 5F

Human IgG1 Fc Mutant: N297A (SEQ ID NO: //)
DKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK

FIG. 5G

Human IgG1 Fc Mutant: L234A/L235A ("LALA") (SEQ ID NO: //)
DKHTCPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK

Residue numbered according to EU index (Kabat Numbering)

FIG. 6

NP_004039.1	msrsvalavlallslsgleaiqrtpkiqvysrhpengksnflncyvsgfhpsdievdll	60
NP_001009066.1	msrsvalavlallslsgleaiqrtpkiqvysrhpengksnflncyvsgfhpsdievdll	60
NP_001040602.1	msrsvalavlallslsgleaiqrtpkiqvysrhpengksnflncyvsgfhpsdievdll	60
NP_776318.1	marfvalvllgllslsgldaiqrppkiqvysrhpdpdkpnylncyvvgfhppqgieidl	60
NP_033865.2	marsvtlvflvsltglyaiqktbpqiqvysrhpengkpni lncvytqfhpphieiqml	60
	: *:*..* *:*:*:* *:*:*:* *:*:*:* *:*:*:* *:*:*:* *:*:*:*	
NP_004039.1	kngeriekvehsdlsfskdwsfylllytteftptekdeyacrnhvtlsqpkivkwdrdm	119
NP_001009066.1	kngeriekvehsdlsfskdwsfylllytteftptekdeyacrnhvtlsqpkivkwdrdm	119
NP_001040602.1	kngkmgkvehsdlsfskdwsfylllytteftptekdeyacrnhvtlsqprtivkwdrdm	119
NP_776318.1	kngelik-seqsdlsfskdwsfyllshaeftpnksdqscrkvhtleqprivkwdrdl	118
NP033865	kngkkipkvemsdmsfskdwsfylahteftptetdtacrvkhasmaepktvywdrdm	119
	***::: * **:*:*:*:*:*:*:* *:*:*:*:*:*:* *:*:*:*:*:*:*	

FIG. 7A *Homo sapiens* HLA-A

7A.1	HLA-A*01:01:01:01 NCBI (National Center for Biotechnology Information) Accession NP_001229687.1 (SEQ ID NO:1)	1 MAVMAPRTL LLLSGALALT QTWAGSHSMR YFFTSVSRPG RGEPRFIAG YVDDTQFVRF 61 DSDAASQKME PRAPWIEQEG PEYWDQETRN MKAHSQTDRA NLGLRGYNN QSEEDGSHTIQ 121 IMYGCDVGPD GRELRGYRQD AYDGKDYIAL NEDLRSTWAA DMAAQITKRK WEAAHAAEQQ 181 RYLEGRGCDV GLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT 241 WQDGEDQTQ DTELVE ^A TRPA GDGTFQK ^{WAA} VVPSGEEQR YTCHVQHEGL PKPLTLRWEL 301 SSQPTIPIVG ILAGLVLLGA VITGAVVA ^V MWRNKSSDRK GGSYTQAASS DSAQGS ^{DVSL} 361 TACKV
7A.2	HLA-A*1101 NCBI Accession P13746.1 (SEQ ID NO:1)	1 MAVMAPRTL LLLSGALALT QTWAGSHSMR YFYTSVSRPG RGEPRFIAG YVDDTQFVRF 61 DSDAASQKME PRAPWIEQEG PEYWDQETRN VKAQSDTRV DLGLRGYNN QSEEDGSHTIQ 121 IMYGCDVGPD GRELRGYRQD AYDGKDYIAL NEDLRSTWAA DMAAQITKRK WEAAHAAEQQ 181 RYLEGRGCDV GLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT 241 WQDGEDQTQ DTELVE ^A TRPA GDGTFQK ^{WAA} VVPSGEEQR YTCHVQHEGL PKPLTLRWEL 301 SSQPTIPIVG ILAGLVLLGA VITGAVVA ^V MWRNKSSDRK GGSYTQAASS DSAQGS ^{DVSL} 361 TACKV
7A.3	HLA-A*2402 NCBI Accession P05534.2 (SEQ ID NO:1)	1 MAVMAPRTL LLLSGALALT QTWAGSHSMR YFSTS ^V SRPG RGEPRFIAG YVDDTQFVRF 61 DSDAASQKME PRAPWIEQEG PEYWD ^E ETGK VKAHSQTDRE NLRIALRYNN QSEAGSHTIQ 121 MMFGCDVGS ^D GRELRGYHQY AYDGKDYIAL KEDLRSTWAA DMAAQITKRK WEAAHVAEQQ 181 RYLEGT ^C VD GLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT 241 WORDGEDOTQ DTELVE ^A TRPA GDGTFQK ^{WAA} VVPSGEEQR YTCHVQHEGL PKPLTLRWEP 301 SSQPTIVP ^I VG ILAGLVLLGA VITGAVVA ^V MWRN ^S SSDRK GGSYSQAASS DSAQGS ^{DVSL} 361 TACKV

FIG. 7wA, continued

7A.4 HLA-A*3303 NCBI Accession AAA79865.1 (SEQ ID NO:1)

1 MAVMAPRTLL LLLLGALALT QTWAGSHSMR YFTTSVSRPG RGEPRFIAVG YVDDTQFVRF
61 DSDAASQRM EPRAPWIEQEG PEYWDNTRN VKAHSQIDRV DLGTLRGYN QSEAGSHTIQ
121 MMYGCDVGS DGRFLRGYQD AYDGKDYIAL NEDLRSWTAA DAAQITQRK WEAAARVAEQ
181 RAYLEGTCE WLRRYLENGK ETLQRTDPPK THMTHAVSD HEATLRWAL SFYPAEITLT
241 WQRDGEDQT DTELVEITRPA GDGTFQKWA VVPSGQEQR YTCVQHEGL PKPLTLRWE
301 SSQPTIPVG ILAGLVFGA VFAGAVVA VVRRKSSDRK GGSYSQAASS DSAQGSMSL
361 TACKV

FIG. 7B *Homo sapiens* HLA-B*07:02:01 HLA-B GenBank Accession NP_005505.2 (SEQ ID NO:1)

1 MLVMAPRTVL LLLSAALALT ETWAGSHSMR YFYTSVSRPG RGEPRFISVG YVDDTQFVRF
61 DSDAASPRE PRAPWIEQEG PEYWDNTRN YKAQAGTDRE SLNLRGYN QSEAGSHTLQ
121 SMYGC DVGPD GRLLRGHDGY AYDGKDYIAL NEDLRSWTAA DAAQITQRK WEAAAREAEQR
181 RAYLEGECE WLRRYLENGK DKLERADPPK THVTHPISD HEATLRWAL GFYPAEITLT
241 WQRDGEDQT DTELVEITRPA GDRTFQKWA VVPSGQEQR YTCVQHEGL PKPLTLRWE
301 SSQSTVPVG IVAGLAVLV VVIGAVVA VVRRKSSGK GGSYSQAACS DSAQGSMSL
361 TA

FIG. 7C *Homo sapiens* HLA-C HLA-C GenBank Accession NP_00129971.1,

w (SEQ ID NO:1)

1 MRVMAPRALL LLLSGGLALT ETWAGSHSMR YFDTAVSRPG RGEPRFISVG YVDDTQFVRF
61 DSDAASPRG PRAPWIEQEG PEYWDRETQ YKRQAGADV SLNLRGYN QSEAGSHTLQ
121 RMYGCDLGP GRLLRGYDGS AYDGKDYIAL NEDLRSWTAA DAAQITQRK LEAARAAEQ
181 RAYLEGTCE WLRRYLENGK ETLGRAEPPK THVTHPISD HEATLRWAL GFYPAEITLT
241 WQRDGEDQT DTELVEITRPA GDGTFQKWA VVPSGQEQR YTCVQHEGL GEPLTISWEP
301 SSQPTIPVG IVAGLAVLV LAVIGAVTA MNCIRKSSG KGSQSQAAC SNSAQGSDES
361 LITCK

FIG. 8

HLA-A	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQKMEPRAPWIEQEGPEYW
HLA-B	GSHSMRYFYTSVSRPGRGEPRIISVGIVDDTQFVRFDSDAASPRPEPRAPWIEQEGPEYW
HLA-C	CSHSMRYFDTAVSRPGRGEPRIISVGIVDDTQFVRFDSDAASPRGEPRAPWVEQEGPEYW
HLA-A*0201	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYW
Mouse H2K	GPHSLRYFVTAVSRPGLGEPRIAVGYVDDTQFVRFDSADNPRFEPRAPWMEQEGPEYW
HLA_A(var. 2)	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYW
HLA_A(var. 2C)	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYW
HLA-A(var. 2CP)	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYW
HLA-A*1101	GSHSMRYFYTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYW
HLA-A*2402	GSHSMRYFSTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYW
HLA-A*3303	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYW

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HLA-A	DQETRNKAHSQTDRLNLGTLRGYINQSEAGSHTIQIMYGCDVGPDRFLRGYRQDAYDG
HLA-B	DRNTQIYKAQAQTDRESLRNLRGYINQSEAGSHTLQSMYGCDVGPDRLLRGHDQYAYDG
HLA-C	DRETQNYKRQAQADRVSLRNLRGYINQSEAGSHTLQRMYGCDLGPDRLLRGYDQSAIDG
HLA-A*0201	DGETRKVKAHSQTHRVDLGTLRGYINQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDG
MOUSE H2K	EEQTQRAKSDEQWFRVSLRTAQRYINQSKGGSHTFQRMFGCDVGSWDRLLRGYQQFAYDG
HLA_A(var. 2)	DGETRKVKAHSQTHRVDLGTLRGYINQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDG
HLA_A(var. 2C)	DGETRKVKAHSQTHRVDLGTLRGYINQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDG
HLA-A(var. 2CP)	DGETRKVKAHSQTHRVDLGTLRGYINQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDG
HLA-A*1101	DQETRNKAHSQTDRLNLGTLRGYINQSEAGSHTIQIMYGCDVGPDRFLRGYRQDAYDG
HLA-A*2402	DEETGKVKHAHSQTDRENLRALRYINQSEAGSHTLQMMFGCDVGSWDRFLRGYHQYAYDG
HLA-A*3303	DRNTRNVKAHSQIDRVDLGTLRGYINQSEAGSHTIQMMYGCDVGSWDRFLRGYQQDAYDG

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HLA-A	KDYIALNEDLRSWTAADMAAQITKRKWEAVHAAEQRRVYLEGRCVDGLRRYLENGKETLQ
HLA-B	KDYIALNEDLRSWTAADTAQAQITQRKWEAAREAEQRRAYLEGECEVWLRRLYLENGKDKLE
HLA-C	KDYIALNEDLRSWTAADTAQAQITQRKLEAARAAEQRLRAYLEGTCEVWLRRLYLENGKETLQ
HLA-A*0201	KDYIALKEDLRSWTAADMAAQITTKHKWEAAHVAEQRLRAYLEGTCEVWLRRLYLENGKETLQ
MOUSE H2K	RDYIALNEDLKTWTAADTAALITRKRWEQAGDAEYRYRAYLEGECEVWLRRLYLELGNETLL
HLA_A(var. 2)	KDYIALKEDLRSWTAADMAAQITTKHKWEAAHVAEQRLRAYLEGTCEVWLRRLYLENGKETLQ
HLA_A(var. 2C)	KDYIALKEDLRSWTAADMAAQITTKHKWEAAHVAEQRLRAYLEGTCEVWLRRLYLENGKETLQ
HLA-A(var. 2CP)	KDYIALKEDLRSWTAADMAAQITTKHKWEAAHVAEQRLRAYLEGTCEVWLRRLYLENGKETLQ
HLA-A*1101	KDYIALNEDLRSWTAADMAAQITKRKWEAAHAAEQRRAYLEGRCVWLRRLYLENGKETLQ
HLA-A*2402	KDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQRRAYLEGTCDGLRRYLENGKETLQ
HLA-A*3303	KDYIALNEDLRSWTAADMAAQITQRKWEAARVAEQRLRAYLEGTCEVWLRRLYLENGKETLQ

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FIG. 8 (continued)

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HLA-A	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDGT
HLA-B	RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDRT
HLA-C	RAEPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDGT
HLA-A*0201	RTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDGT
MOUSE H2K	RTDSPKAHVITYHPRSQVDVILRCWALGFYPADITLTWQLNGEDLTQDMEL	VETRPAGDGT
HLA_A(var. 2)	RTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL	VETRPCGDGT
HLA_A(var. 2C)	RTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL	VETRPCGDGT
HLA-A(var. 2CP)	RTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL	VETRPCGDGT
HLA-A*1101	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDGT
HLA-A*2402	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDGT
HLA-A*3303	RTDPPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDGT

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HLA-A	QKWAADVVPSPGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-B	QKWAADVVPSPGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-C	QKWAADVVPSPGEEQRYTCHVQHEGLQEPPLTLRWE (SEQ ID NO://)
HLA-A*0201	QKWAADVVPSPGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
MOUSE H2K	QKWAADVVPSPGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA_A(var. 2)	QKWAADVVPSPGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA_A(var. 2C)	QKWAADVVPSPGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A(var. 2CP)	QKWAADVVPSPGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A*1101	QKWAADVVPSPGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A*2402	QKWAADVVPSPGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A*3303	QKWAADVVPSPGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)

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

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A*0101 DGETRNMKAHSQTDFANLSTLRGYNQSEAGSHTIQIMYGCDDVSPDGRFLPGYQQDAYDG 120
A*0201 DGETRNVKVAHSQTDFANLSTLRGYNQSEAGSHTVQRMYSGLVSGDWRLAGYHQYAYDG 120
A*0301 DGETRNVKVAQSQTDFVDLSTLRGYNQSEAGSHTIQIMYGCDDVSSDGRFLPGYQQDAYDG 120
A*1101 DGETRNVKVAQSQTDFVDLSTLRGYNQSEAGSHTIQIMYGCDDVSGDGRFLAGYHQYAYDG 120
A*2301 DEETGKVKAHSQTDFENIRIALRNTNQSEAGSHTLQMFMFGCDVSSDGRFLPGYHQYAYDG 120
A*2402 DEETGKVKAHSQTDFENIRIALRNTNQSEAGSHTLQMFMFGCDVSSDGRFLAGYHQYAYDG 120
A*2407 DEETGKVKAQSQTDFENIRIALRNTNQSEAGSHTLQMFMFGCDVSSDGRFLPGYHQYAYDG 120
A*3303 DNTRNPKVKAQSQTDFVDLSTLRGYNQSEAGSHTIQMMYGCDVSGDGRFLAGYQQDAYDG 120
A*3401 DNTRNPKVKAQSQTDFVDLSTLRGYNQSEAGSHTIQMNYGCDVSPDGRFLPGYQQDAYDG 120
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A*0101 KDYLALNEDLRSWTAADNAQITTKRWEEAAHVAAEQRRVYLEGRCVDDLRRYLENGKETLQ 180
A*0201 KDYLALKEDLRSWTAADNAQITTKRWEEAAHVAAEQQLRAYLEGTCVWELRRYLENGKETLQ 180
A*0301 KDYLALNEDLRSWTAADNAQITTKRWEEAAHAEQQLRAYLDGTCEWLRRYLENGKETLQ 180
A*1101 KDYLALNEDLRSWTAADNAQITTKRWEEAAHAEQQRAYLEGGCVWELRRYLENGKETLQ 180
A*2301 KDYLALKEDLRSWTAADNAQITTKRWEEAAHVAAEQQLRAYLEGTCVDDLRRYLENGKETLQ 180
A*2402 KDYLALKEDLRSWTAADNAQITTKRWEEAAHVAAEQQRAYLEGTCVDDLRRYLENGKETLQ 180
A*2407 KDYLALKEDLRSWTAADNAQITTKRWEEAAHVAAEQQRAYLEGTCVDDLRRYLENGKETLQ 180
A*3303 KDYLALNEDLRSWTAADNAQITTKRWEEAAHVAAEQQLRAYLEGTCVWELRRYLENGKETLQ 180
A*3401 KDYLALNEDLRSWTAADNAQITTKRWETAHAEQWRAYLEGTCVWELRRYLENGKETLQ 180

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A*0101 RTDPFKTHMTNHHPISDHEATLCWALGFYPFAEITLTWQRDGEDQTQDTIELVETRAADGTF 241
A*0201 RTDAFKTHMTNHAVSDHEATLCWALSFPFAEITLTWQRDGEDQTQDTIELVETRAADGTF 241
A*0301 RTDPFKTHMTNHHPISDHEATLCWALGFYPFAEITLTWQRDGEDQTQDTIELVETRAADGTF 241
A*1101 RTDPFKTHMTNHHPISDHEATLCWALGFYPFAEITLTWQRDGEDQTQDTIELVETRAADGTF 241
A*2301 RTDPFKTHMTNHHPISDHEATLCWALGFYPFAEITLTWQRDGEDQTQDTIELVETRAADGTF 241
A*2402 RTDPFKTHMTNHHPISDHEATLCWALGFYPFAEITLTWQRDGEDQTQDTIELVETRAADGTF 241
A*2407 RTDPFKTHMTNHHPISDHEATLCWALGFYPFAEITLTWQRDGEDQTQDTIELVETRAADGTF 241
A*3303 RTDPFKTHMTNHAVSDHEATLCWALSFPFAEITLTWQRDGEDQTQDTIELVETRAADGTF 241
A*3401 RTDAFKTHMTNHAVSDHEATLCWALSFPFAEITLTWQRDGEDQTQDTIELVETRAADGTF 241
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A*0101 QKWAAVVVPSSGEQRYTCHVQHESGLPKPLTLRWEL 276
A*0201 QKWAAVVVPSSGEQRYTCHVQHESGLPKPLTLRWEF 276
A*0301 QKWAAVVVPSSGEQRYTCHVQHESGLPKPLTLRWEL 276
A*1101 QKWAAVVVPSSGEQRYTCHVQHESGLPKPLTLRWEL 276
A*2301 QKWAAVVVPSSGEQRYTCHVQHESGLPKPLTLRWEF 276
A*2402 QKWAAVVVPSSGEQRYTCHVQHESGLPKPLTLRWEF 276
A*2407 QKWAAVVVPSSGEQRYTCHVQHESGLPKPLTLRWEF 276
A*3303 QKWASVVVPSSGEQRYTCHVQHESGLPKPLTLRWEF 276
A*3401 QKWASVVVPSSGEQRYTCHVQHESGLPKPLTLRWEF 276

FIG. 9B

GSHSMRYFX1TSVSRPGRGEPFRFIAVGIVDDTQFVRFDSDAASQX2MEPRAPWIEQEGPEYWDX
3X4TX5X6X7KX8SQX9X10RX11X12LX13X14X15X16X17YYNQSEX18GSHTX19QX20
 MX21GCDVGX22DX23RFLRGYX24QX25AYDGKDYIALX26EDLRSWTAADMAAAQX27TX287
X29KWEX30X31X32EAEQX33RX34YLX35GX36CVX37X38LRRYLENGKETILQRTDX39PK
 THMTHHX40X41SDHEATLRCWALX42FYPAEITLWQRDGEDQTQDTIELVETRPAGDGTFQKW
 AX43VVVVPSGX44EQRYTCHVQHEGLPKPLTLRWEX45

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 L, 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.

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FIG. 10A

B*0702	GSNSMKYFYTSVSRPGRGEPFISVGYVDDTQFVRFDSDAASPRKEPPRAPWIEQEGPEYW	60
B*0801	GSNSMKRYFDTAMSRPGRGEPFISVGYVDDTQFVRFDSDAASPRKEPPRAPWIEQEGPEYW	60
B*1502	GSNSMKRYFYTAMSRPGRGEPFISVGYVDDTQFVRFDSDAASPRMAEPRAPWIEQEGPEYW	60
B*3802	GSNSMKRYFYTSVSRPGRGEPFISVGYVDDTQFVRFDSDAASPRKEPPRAPWIEQEGPEYW	60
B*4001	GSNSMKRYFHTAMSRPGRGEPFISVGYVDDTLFVRFDSDATSPKEPPRAPWIEQEGPEYW	60
B*4601	GSNSMKRYFYTAMSRPGRGEPFISVGYVDDTQFVRFDSDAASPRMAEPRAPWIEQEGPEYW	60
B*5301	GSNSMPYFYTAMSRPGRGEPFISVGYVDDTQFVRFDSDAASPRTEPPRAPWIEQEGPEYW	60
	***** *;:*****;***** *****;*** *****	
B*0702	DRNTQIYKAQAQTDRRESINLNGYNQSEAGSHTLQSMYGCDEVGPDGRLRGHDQYAYDG	120
B*0801	DRNTQIFKTNQTQDRRESINLNGYNQSEAGSHTLQSMYGCDEVGPDGRLRGHDQYAYDG	120
B*1502	DRNTQISKTNQTQTYRESINLNGYNQSEAGSHTLQSMYGCDEVGPDGRLRGHDQYAYDG	120
B*3802	DRNTQICKTNQTQTYRESINLNGYNQSEAGSHTLQSMYGCDEVGPDGRLRGHDQYAYDG	120
B*4001	DRETQISKTNQTQTYRESINLNGYNQSEAGSHTLQSMYGCDEVGPDGRLRGHDQYAYDG	120
B*4601	DRETQIKYKQAQTDRVSIENLNGYNQSEAGSHTLQSMYGCDEVGPDGRLRGHDQYAYDG	120
B*5301	DRNTQIFKTNQTQTYRESINLNGYNQSEAGSHTLQSMYGCDEVGPDGRLRGHDQYAYDG	120
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	aac1 aac2	
B*0702	KDYIALNEDLSSMTAADTAQITQKKWEAAREAEQRAYLEGECEVWLRRYLENGKDKLE	180
B*0801	KDYIALNEDLSSMTAADTAQITQKKWEAARVAEQDRAYLEGECEVWLRRYLENGKDKLE	180
B*1502	KDYIALNEDLSSMTAADTAQITQKKWEAAREAEQLRAYLEGLCEVWLRRYLENGKETLQ	180
B*3802	KDYIALNEDLSSMTAADTAQITQKKWEAARVAEQRLAYLEGECEVWLRRYLENGKETLQ	180
B*4001	KDYIALNEDLSSMTAADTAQISQKKLEAARVAEQRAYLEGECEVWLRRYLENGKDKLE	180
B*4601	KDYIALNEDLSSMTAADTAQITQKKWEAAREAEQRAYLEGLCEVWLRRYLENGKETLQ	180
B*5301	KDYIALNEDLSSMTAADTAQITQKKWEAARVAEQRAYLEGLCEVWLRRYLENGKETLQ	180
	***** *****;***** ***** *****;*****;*****;*****	
	aac3 aac4	
B*0702	RADFPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLIVETRPAGDRTF	241
B*0801	RADFPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLIVETRPAGDRTF	241
B*1502	RADFPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLIVETRPAGDRTF	241
B*3802	RADFPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLIVETRPAGDRTF	241
B*4001	RADFPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLIVETRPAGDRTF	241
B*4601	RADFPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLIVETRPAGDRTF	241
B*5301	RADFPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTLIVETRPAGDRTF	241
	*****;***** ***** ***** ***** ***** *****	
	aac5 aac6	
B*0702	QKWAAVVVPSCGEEQRYTCHVQHEGLPKPLTLRWEF	276
B*0801	QKWAAVVVPSCGEEQRYTCHVQHEGLPKPLTLRWEF	276
B*1502	QKWAAVVVPSCGEEQRYTCHVQHEGLPKPLTLRWEF	276
B*3802	QKWAAVVVPSCGEEQRYTCHVQHEGLPKPLTLRWEF	276
B*4001	QKWAAVVVPSCGEEQRYTCHVQHEGLPKPLTLRWEF	276
B*4601	QKWAAVVVPSCGEEQRYTCHVQHEGLPKPLTLRWEF	276
B*5301	QKWAAVVVPSCGEEQRYTCHVQHEGLPKPLTLRWEF	276

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FIG. 10B

GSHSMRYFX1TX2X3SRPGRGEPFIX4VGYVDDTX5FVRFDSDAX6SPRX7X8PRAPWIEQEG
 PEYWDRX9TQX10X11KTX12X13TQX14YX15X16NLX17X18X19X20YYNQSEAGSHX21X
22QX23MYGCDLGPDGRLLRGHDQSAYDGKDYIALNEDLX24SWTAADTAAQIX25QRKX26EA
 ARX27AEQX28RX29YLEGX30CVEWLRRYLENGKX31X32LX33RADPPKTHVTHHPX34SDH
 EATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRTFQKWA AVVVP SGEEQRYTCHV
 QHEGLPKPLTLRWEF

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	CSHSMRYFFTSVSRPGNGEPHFISVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0303	GSHSMRYFFYTAVERPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0304	GSHSMRYFFYTAVERPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0401	GSHSMRYFFTSVSRPGNGEPHFIAVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0602	CSHSMRYFFDTAVSRPGRGEPHFISVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0701	CSHSMRYFFDTAVSRPGRGEPHFISVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0702	CSHSMRYFFDTAVSRPGRGEPHFISVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0801	CSHSMRYFFYTAVERPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*1502	CSHSMRYFFYTAVERPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
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94		
C*0102	DRETQKYKRQAQTDVSLRLNLRGTYNQSSAGSHILQWMCGLGPDGRLRGYDQYAYDG	120
C*0303	DRETQKYKRQAQTDVSLRLNLRGTYNQSSARSHLIQRMYGCDVGFPGRLRGYDQYAYDG	120
C*0304	DRETQKYKRQAQTDVSLRLNLRGTYNQSSAGSHIIQRMYGCDVGFPGRLRGYDQYAYDG	120
C*0401	DRETQKYKRQAQADRVNLRKLRLGTYNQSSDGSHTLQRMFGCDLGFPGRLRGYDQYAYDG	120
C*0602	DRETQKYKRQAQADRVNLRKLRLGTYNQSSDGSHTLQWMYGCDLGFPGRLRGYDQYAYDG	120
C*0701	DRETQKYKRQAQADRVNLRKLRLGTYNQSSDGSHTLQRMFGCDLGFPGRLRGYDQYAYDG	120
C*0702	DRETQKYKRQAQADRVNLRKLRLGTYNQSSDGSHTLQRMFGCDLGFPGRLRGYDQYAYDG	120
C*0801	DRETQKYKRQAQTDVSLRLNLRGTYNQSSAGSHILQRMYGCDLGFPGRLRGYDQYAYDG	120
C*1502	DRETQKYKRQAQTDVSLRLNLRGTYNQSSAGSHIIQRMYGCDLGFPGRLRGYDQYAYDG	120
*****;*****;***;***;*****;*****;*****;*****;*****;*****		
aac1 aac2		
139		
C*0102	KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQBRAYLEGTCVEWLKRYLNGKETLQ	180
C*0303	KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQLRAYLEGTCVEWLKRYLNGKETLQ	180
C*0304	KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQLRAYLEGTCVEWLKRYLNGKETLQ	180
C*0401	KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQBRAYLEGTCVEWLKRYLNGKETLQ	180
C*0602	KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQBRAYLEGTCVEWLKRYLNGKETLQ	180
C*0701	KDYIALNEDLRSWTAADTAQITCRKLEAARAADQLRAYLEGTCVEWLKRYLNGKETLQ	180
C*0702	KDYIALNEDLRSWTAADTAQITCRKLEAARAADQLRAYLEGTCVEWLKRYLNGKETLQ	180
C*0801	KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQLRAYLEGTCVEWLKRYLNGKETLQ	180
C*1502	KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQLRAYLEGTCVEWLKRYLNGKETLQ	180
*****;*****;*****;*****;*****;*****;*****;*****;*****;*****		
aac3 aac4		
236		
C*0102	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTLVEYTRAGDGT	241
C*0303	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTLVEYTRAGDGT	241
C*0304	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTLVEYTRAGDGT	241
C*0401	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTLVEYTRAGDGT	241
C*0602	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTLVEYTRAGDGT	241
C*0701	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTLVEYTRAGDGT	241
C*0702	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTLVEYTRAGDGT	241
C*0801	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTLVEYTRAGDGT	241
C*1502	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTLVEYTRAGDGT	241
;**;*****;*****;*****;*****;*****;*****;*****;*****		
aac5 aac6		
C*0102	QKWAADVVPSSGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0303	QKWAADVVPSSGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0304	QKWAADVVPSSGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0401	QKWAADVVPSSGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0602	QKWAADVVPSSGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0701	QKWAADVVPSSGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0702	QKWAADVVPSSGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0801	QKWAADVVPSSGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*1502	QKWAADVVPSSGEEQRYTCHVQHEGLPEPLTLRWEP	276
*****;*****;*****;*****;*****;*****;*****;*****;*****;*****		

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FIG. 11B

X1SHSMX2YFX3TAVSX4PGRGEPX5FIX6VGyvDDTQFVX7FDSDAASPRGEPRX8PWVEQEG
 PEYWDRETQX9YKRQAQX10DRVX11LRX12LRGYNQSEX13X14SHX15X16QX17MX18GC
 DX19GPDGRLLRGX20X21QX22AYDGKDYLALNEDLRSWTAADTAAQITQRKX23EAARX24A
 EQX25RAYLEGX26CVEWLRRYLX27NGKX28TLQRAEX29PKTHVTHHPX30SDHEATLRCWA
 LGFYPAEITLTWQX31DGEDQTQDTELVEITRPAGDGTfQKWAAVX32VPSGX33EQRYTCHX34
 QHEGLX35EPLTLX36WX37P

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	RFISVGIVDD	TQFVRFNDNA	ASPRMVPRAP
WMEQEGSEYW	DRETRSARDT	AQIFRVNLRT	LRG <u>Y</u> YNQS <u>X1</u> A	GSHTLQWMHG
CELGPD <u>X2</u> RFL	RGYEQFAYDG	KDYLTNLNEDL	RSWTAVDT <u>A</u> A	QISEQKSND
SEAEHQ <u>X3X4</u> YL	EDTCVEWLHK	YLEKGKETLL	HLEPPKTHVT	HHPISDHEAT
LRCWALGFYP	AEITLTWQQD	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	EWITGYAKAN	AQTDRLVALRN	LLR <u>R</u> YNQSEA	GSHTLQGMNG
CDMGPDGRLL	RGYHQHAYDG	KDYISLNEDL	RSWTAADT <u>V</u> A	QITQRFYAE
EYAEFRFTYL	EGECLELLRR	YLENGKETLQ	RADPPKAHVA	HHPISDHEAT
LRCWALGFYP	AEITLTWQRD	GEEQTQDTEL	VETRP <u>A</u> GDGT	FQKWAAVVVP
<u>X3</u> GEEQRYTCH	VQHEGLPQPL	ILRWEQS <u>X4</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	AQTDRLNLQT	<u>X6</u> RG <u>Y</u> YNQSEA	SSHTLQWMI <u>X7</u>
CDL <u>X8X9</u> DGRL <u>X10</u>	RGYEQYAYDG	KDYALNEDL	RSWTAADT <u>A</u> A	QISKRKCEAA
NVAEQRRAX <u>11</u> L	EGTCVEWL <u>X12</u> R	<u>X13</u> LENGKE <u>X14</u> LQ	RADP <u>X15</u> KTHVT	HHPVFDYEAT
LRCWALGFYP	AEIILTQW <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				

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FIG. 13

HLA-A	GSHSMRYFXTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQXMEPRAPWIEQEGPEYW	60
HLA-B	GSHSMRYFXTXSRPGRGEPRIXVGYVDDTXFVRFDSDAASPRXXPRAPWIEQEGPEYW	60
HLA-C	XSHSMXYFXTAVSXPGRGEPXIXVGYVDDTQFVXFDSDAASPRGEPXPFVWEQEGPEYW	60
HLA-E	GSHSLKYFHTSVSRPGRGEPRIISVGYVDDTQFVRFNDAAASPRMVPAPFWMEQEGSEYW	60
HLA-F	GSHSLRXFSTAVSRPGRGEPRIAVEYVDDTQFLRFDSDAAPRMEPREXWVEQEGPQYW	60
HLA-G	GSHSMRYFSAAVXRPGRGEPRIAMGXVDDXQFXRFDSDSACPRMEPRAPFWVEXEGPEYW	60
	: * : ** : * : *** * **.: ** *: * ** : **	
84		
HLA-A	DXXTXXXKAXSQXXRXIXXXXXYINQSEKGSHTXQXMXGCDVGXDXRFLRGYXQXAYDG	120
HLA-B	DRXTQXXKTXXTQXYXXNLXXXXYINQSEAGSHXXQXMYGCDLGPDGRLLRGHDSAYDG	120
HLA-C	DRETQXYKRQAQXDRVXIRXLRGYINQSEKXSHXXQXMXGCDXGPDGRLLRGXQXAYDG	120
HLA-E	DRETRSARDTAQIFRVNIRTLRGYINQSXAGSHTLQWMHGCELGPDXRFLRGYEQFAYDG	120
HLA-F	EWTTGYAKANAQTDRVAIRNLLRFINQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG	120
HLA-G	EEETRNTKAHAQTDRMNIQTXRGYINQSEASSHTLQWMIXCDLXXDGRLXRGYEQYAYDG	120
	: * : ***** ** * * : ** : ** * ****	
	aac1 aac2	
139		
HLA-A	KDYIALXEDLRSWTAADMAAQXTXKKWEXXXEAEQXRYLXGXCVXXLRRYLENGKETLQ	180
HLA-B	KDYIALNEDLRSWTAADTAAQIXQKXEAARXAEQXRYLEGXCVEWLRRYLENGKXXLX	180
HLA-C	KDYIALNEDLRSWTAADTAAQITQKXEAARXAEQXRAYLEGXCVEWLRRYLXNGKXTLQ	180
HLA-E	KDYLTNEDLRSWTAVDTAAQISEQKSNDASEAHEQXXYLEDTCVEWLHKYLEKGKETLL	180
HLA-F	KDYISLNEDLRSWTAADTAAQITQRFYEAEEYAEFRTYLEGECLELLRRYLENGKETLQ	180
HLA-G	KDYIALNEDLRSWTAADTAAQISKRKCEAANVAEQRRAXLEGTCVEWLXRXLENGKEXLQ	180
	***: * ** * ** * . ** : ** . * . : * : * : ** *	
	aac3 aac4	
236		
HLA-A	RTDXPKTHMTHHXXSDHEATLRCWALXFYPAEITLTWQRDGEDQTQDTEIVETRPAGDGTG	241
HLA-B	RADPPKTHVTHHPXSDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEIVETRPAGDRTG	241
HLA-C	RAEXPKTHVTHHPXSDHEATLRCWALGFYPAEITLTWQXDGEDQTQDTEIVETRPAGDGTG	241
HLA-E	HLEPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEQHTQDTEIVETRPAGDGTG	241
HLA-F	RADPPKAHVHHPISDHEATLRCWALGFYPAEITLTWQRDGEQHTQDTEIVETRPAGDGTG	241
HLA-G	RADPPKTHVTHHPVFDYEATLRCWALGFYPAEIILTQXDGEDQTQDTEIVETRPAGDGTG	241
	: : *: *: ** *: ***** ***** ** * : ** . ** ***** **	
	ac5 aac6	
HLA-A	QKWAXVVVPSGXEQRYTCHVQHEGLPKPLTLRWEX-----	276
HLA-B	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEP-----	276
HLA-C	QKWAAXVVVPSGXEQRYTCHXQHEGLXEPPLTLXWXP-----	276
HLA-E	QKWAAVVVPSGEEQRYTCHVQHEGLXEPVTLRWKPASQPTIPI	284
HLA-F	QKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRWEQSXQPTIPI	284
HLA-G	QKWAAVVVPSGEEQRYXCHVQHEGLPEPLMLRWXQSSLPTIPI	284
	*** * ** * * * * * : * : *	

FIG. 14A

1715

APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIS
TLTGGGGSGGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTA
KFYMPKKATELKHLQCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGGGGSGSHSMRYFFTSVSRPGRGE
PRFIAVGyvDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETRKVKAHSQIHRVDLGTLRGC
YNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEA
AHVAEQLRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFPAEIT
LTWQRDGEDQTQDTELVETRPCGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWEAAAG
GDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

hIL2 (H16A; F42A) -- underlined

(G4S)_n – bold

HLA A0202 (Y84C; A236C) – double underlined

AAAGG – bold

IgG1 Fc (LALA) -- italicized

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FIG. 14B

2380

VLDFAPPGAGCGGSGGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM

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

G2C linker – bold

 β 2M (R12C) – underlined

FIG. 14C

2381

RMFPNAPYLGCGGSGGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM

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

G2C linker -- bold

 β 2M (R12C) – underlined

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FIG. 14D

2405

APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIS
TLTGGGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTA
KFYMPKKATELKHLQCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGSHSMRYFFTSVSRPGRGE
PRFIAGYVDDTQFVRFSDAASQRMERAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRG
YNQSEAGSHTVQRMYGCDVGSDFRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEA
AHVAEQLRAYLEGTCVEWLRRLYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEIT
LTWQRDGEDQTQDTELVETRPAAGDGTQKWAAVVVP SGQEQR YTCHVQHEGLPKPLTLRWEAAAG
GDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

hIL2 (H16A; F42A) -- underlined

(G4S)_n – bold

HLA A0202 (Y84C) – double underlined

AAAGG – bold

IgG1 Fc (LALA) -- italicized

FIG. 14E

1380

APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIS
TLTGGGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTA
KFYMPKKATELKHLQCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGSHSMRYFFTSVSRPGRGE
PRFIAGVYVDDTQFVRFSDAASQRMERAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRGA
YNQSEAGSHTVQRMYGCDVGS DWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQT TKHKWEA
AHVAEQRLRAYLEGTCVEWLRRLYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEIT
LTWQRDGEDQTQDTELVE TRPCGDGTFQKWA AVVVP SGQEQR YTCHVQHEGLPKPLTLRWEAAAG
GDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

hIL2 (H16A; F42A) -- underlined
 (G4S)n – bold
 HLA A0202 (A236C) – double underlined
 AAAGG – bold
 IgG1 Fc (LALA) -- italicized

FIG. 14F**2762**

VLDFAPPGAG**CGGSGGGGSGGGG**SIQRTPKIQVYSRHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM

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

G2C linker – bold

β2M – underlined

FIG. 14G**2763**

RMFPNAPYL**CGGSGGGGSGGGG**SIQRTPKIQVYSRHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM

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

G2C linker – bold

β2M – underlined

FIG. 14H**3625**

YMFPNAPYL**CGGSGGGGSGGGG**SIQRTPKIQVYSCHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM

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

G2C linker – bold

β2M (R12C) – underlined

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FIG. 14I

3626

YMFPNAPYL**GCGGSGGGGSGGGGSI**QRTPKIQVYSRHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM

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

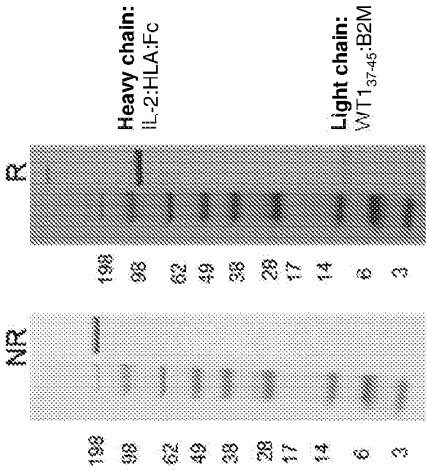
G2C linker – bold

β2M – underlined

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 (28d @ 37 °C / 42 °C)*	51/2
Freeze-thaw (3x)	Stable, No Change
T _m ** (°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 = unformulated, 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 = unformulated, PBS + 365 mM NaCl, pH 7.4

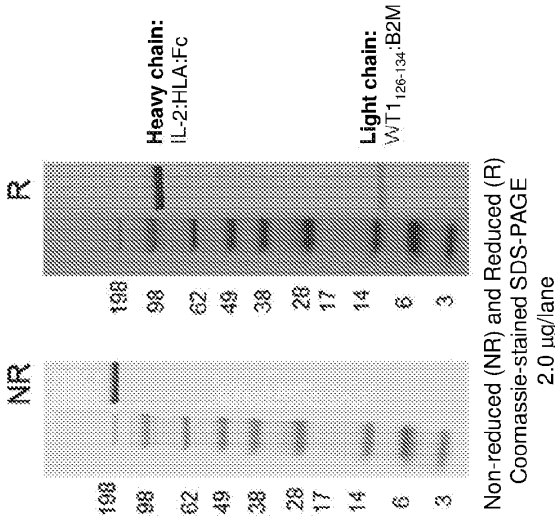


FIG. 17A

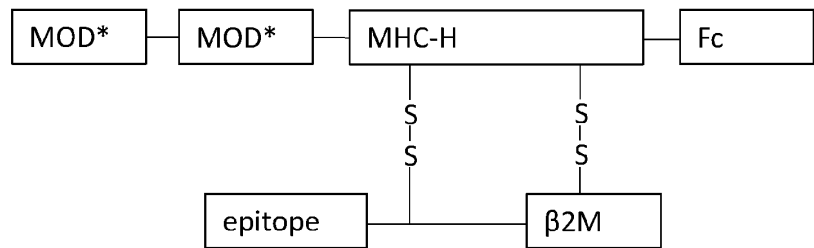


FIG. 17B

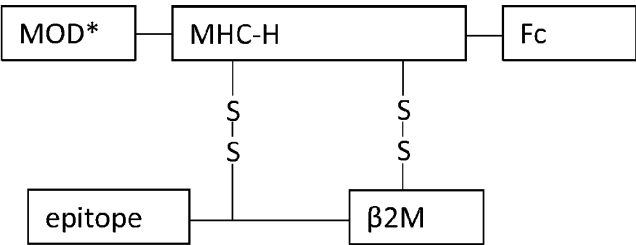


FIG. 17C

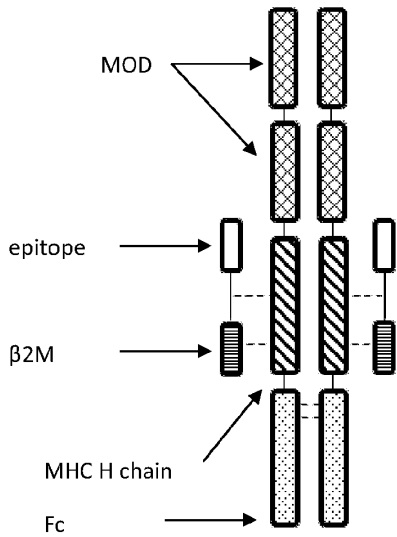


FIG. 17D

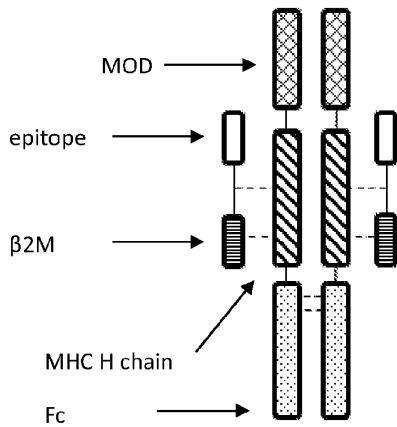


FIG. 18A

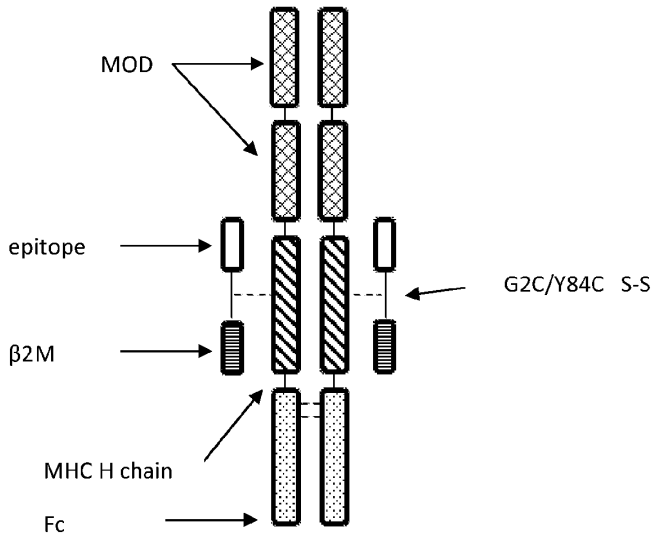
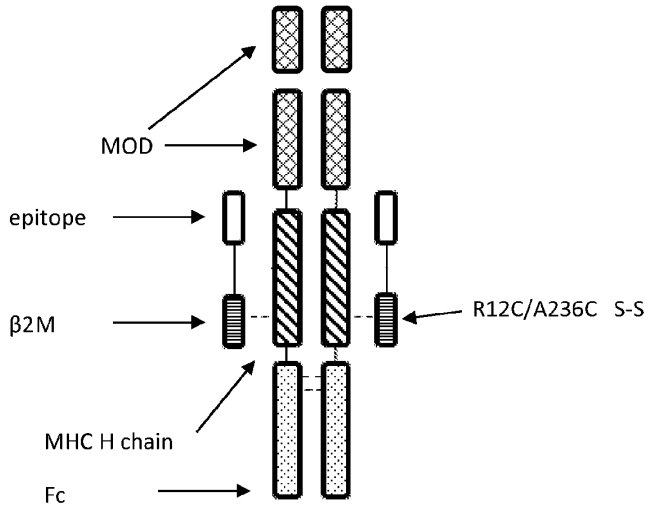
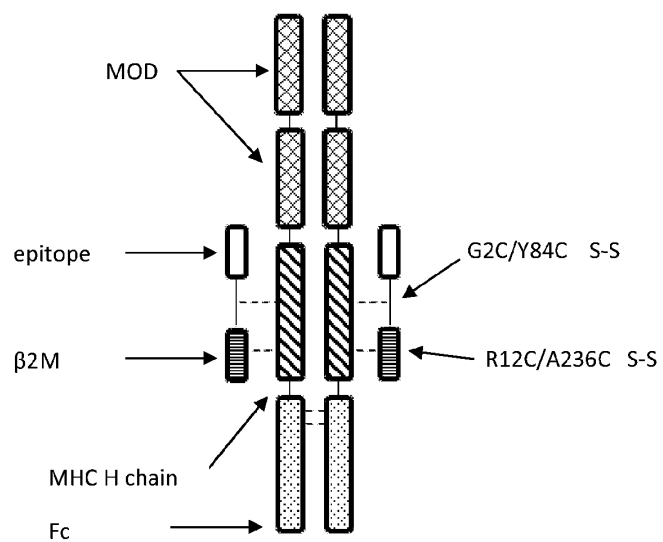


FIG. 18B

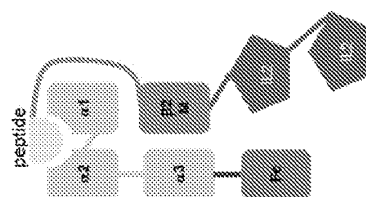


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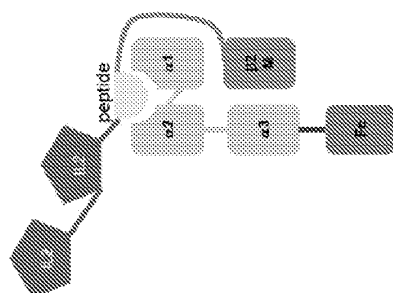
FIG. 18C



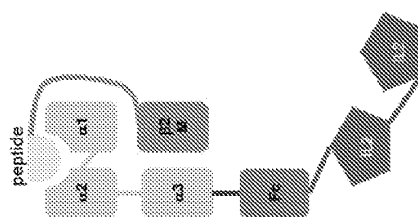
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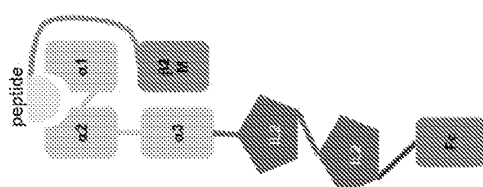
Position 5



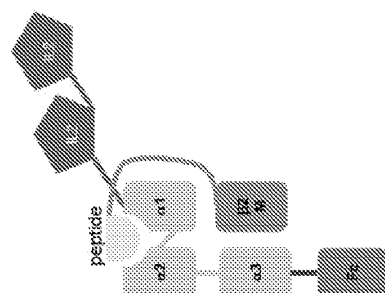
Position 4



Position 3



Position 2



Position 1

FIG. 19

FIG. 20A

3592

APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLT**AKFYMPKKAT**
ELKHLQCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFM
CEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAPTSS
STKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKH
LQCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYA
DETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSGSHSMRYFS
TSVSRPGRGEPRFIAVGYYDDTQFVRFSDAASQRMETPRAPWIEQEGPEYWDEE
TGKVKAHSQTDRENLRALRCYNQSEAGSHTLQMMFGCDVGS DGRFLRGYHQY
AYDGKDYLKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYLEGTCVDGL
RRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWORDGE
DQTQDELVETRPGDGTFOKWA AVVVPSGEEQRYTCHVQHEGLPKPLTLRWE
AAAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPG

IL-2 (H16A; F42A) – bold

(G4S)₄ – underlined

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

AAAGG linker – bold and italicized

hlgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20B

3425

GSHSMRYFSTSVSRPGRGEPREIAVGYVDDTQFVREDSDAASQRMENRAPWIEQE
GPEYWDEETGKVKAHSOTDRENLRALRCYNQSEAGSHTLQMMFGCDVGS DGR
FLRGYHOYAYDGDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGEYP AEITL
TWORDGEDQTQDTELVETRPGDGTFOKWA AVVVPSGEEQRYTCHVQHEGLP
KPLTLRWE**AAAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT**
CVVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT VHL
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQOGN VFSCSVMH EALHNHYTQKSLSLSPG**GGGGSGGGGSGGGGSAPT**
SSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELK
HLQCLEEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAPTSSSTK
KTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQC
LEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
ATIVEFLNRWITFCQSIISTLT

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

(G4S)₃ and (G4S)₄ – underlined

IL-2 (H16A; F42A) – bold

FIG. 20C

3196

GSHSMRYFSTSVSRPGRGEPREFIAVGYVDDTQFVRFDSDAASQRMENRAPWIEQE
GPEYWDEETGKVKAHSOTDRENLRALRCYNQSEAGSHTLQMMFGCDVGS DGR
FLRGYHQYAYDGGDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWORDGEDQTQDTELVETRPCGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWE**AAAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT**
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQOGN VFSCSV MHEALHNHYTQKSLSLSPG

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20D

2764

GSHSMRYFSTSVSRPGRGEPREIAVG YVDDTQFVREDSDAASQRM EPRAPWIEQE
GPEYWDEETGKVK AHSQTDRENLR IALRAYNQSEAGSHTLQMMFGCDVGS DGR
FLRGYHOYAYDGKD YIALKEDLR SWTAADMAAQITKRKWEAAHVAEQORAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGEYPAEITL
TWORDGEDQTQDTELVETR PCGDGTFQKWA AVVVPSGEEQRYTCHVQHEGLP
KPLTLRWE**AAAG****DKTHTCPCPAPEAAAGPSVFLFPPKPKDTLMISRTPEVT**
CVVV**DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH**
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFLYSKLTVD
KSRWQOGN VFSCSV MHEALHNHYTQKSLSLSPGK

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20E

3593

APTSSSTKKTQLQLE**ALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKAT**
ELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFM
CEYADETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGGGSGAPTSS
STKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKH
LQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYA
DETATIVEFLNRWITFCQSIISTLTGGGGSGGGSGGGSGGGSGGGSGSHSMRYFS
TSVSRPGRGEPRFIAVGYVDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYWDEE
TGKVKAHSQTDRENLRALRCYNQSEAGSHTLQMMFGCDVGSDGRFLRGYHQY
AYDGKDYLKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYLEGTCVDGL
RRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGEYPAEITLTWORDGE
DOTQDELVETRPAGDGTFOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE
AAAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTOKSLSLSPG

IL-2 (H16A; F42A) – bold

(G4S)₄ – underlined

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20F

3426

GSHSMRYFSTSVSRPGRGEPRFIAVGYVDDTQFVREDSDAASQRMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRIALRCYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGEYPAEITL
TWORDGEDQTDTELVETRPAGDGTFOKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWEAAAGGDKTHTCPPCPAPEAAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLH
QDWLNGKEYKCKVSNKALPAIEKTISKAKGOPREPQVYTLPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQOGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGGGGSAPT
SSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELK
HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSISTLTGGGGSGGGGSGGGGSGGGGSAPTSSSTK
KTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQC
LEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
ATIVEFLNRWITFCQSISTLT

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

(G4S)₃ and (G4S)₄ – underlined

IL-2 (H16A; F42A) – bold

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FIG. 20G

3197

GSHSMRYFSTSVSRPGRGEPREIAVG YVDDTQFVREDSDAASQRM EPRAPWIEQE
GPEYWDEETGKVK AHSQTDRENLR IALRCYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHOYAYDGKD YIALKEDLR SWTAADMAAQITKRKWEAAHVAEQORAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGEYPAEITL
TWORDGEDQTQDTELVETRPAGDGTFOKWA AVVVVPSGEEQRYTCHVQHEGLP
KPLTLRWE**AAAG****DKTHTCPCPAPEAAAGPSVFLFPPKPKDTLMISRTPEVT**
CVVV**DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH**
QDWLNGKEYKCKVSNKALPAPIEKTISKAKG**OPREPQVYTLPPSREEMTKN**
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQOGNVFSCSVMHEALHNHYTQKSLSLSPG

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

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FIG. 20H

3188

CYTWNQMNLGCGGSGGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDM

epitope: CYTWNQMNL – WT1 (235-243; M236Y)
 (GCGGS)(G4S)₂ – underlined
 β2M (R12C) – italicized

FIG. 20I

3604

CYTWNQMNLGCGGSGGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDMGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGIN
 NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
 LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSHSTLTG
 GGGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGINNYKN
 PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
 DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSHSTLT

epitope: CYTWNQMNL – WT1 (235-243; M236Y)
 (GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined
 β2M (R12C) – italicized
 IL-2 (H16A; F42A) – bold

FIG. 20J

3603

CYTWNQMNLGGGGSGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSGFH
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
KIVKWDRDMGGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKN
PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

epitope: CYTWNQMNL – WT1 (235-243; M236Y)
(G4S)₃ and (G4S)₄ – underlined
β2M (R12C) – italicized
IL-2 (H16A; F42A) – bold

FIG. 20K

3192

CYTWNQMNLGCGGSGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNCYVSGFH
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
KIVKWDRDM

epitope: CYTWNQMNL – WT1 (235-243; M236Y)
(GCGG)(G4S)₂ – underlined
β2M (R12) – italicized

FIG. 20L

3605

CYTWNQMNLGCGGSGGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNCYVSGFH
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQP
KIVKWDRDMGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
GGGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYK
NPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRP
RDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

epitope: CYTWNQMNL – WT1 (235-243; M236Y)
(GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined
β2M (R12) – italicized
IL-2 (H16A; F42A) – bold

FIG. 20M

3529

NYMNLGATLGCGGSGGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSGFH
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQP
KIVKWDRDM

epitope: NYMNLGATL – WT1 (239-247; Q240Y)
(GCGGS)(G4S)₂ – underlined
β2M (R12C) – italicized

FIG. 20N

3709

NYMNLGATLGCGGSGGGGSGGGGSI*QRTPKIQVYSCHPAENGKSNFLNCYVSGFH*
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
*KIVKWDRDMGGGSGGGGSGGGGSAPTSSSTKKTQLQLE***A**LLLDLQMILNGIN
NYKNPKLTRMLT**A**KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT**G**
GGGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLE**A**LLLDLQMILNGINNYKN
PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

epitope: NYMNLGATL – WT1 (239-247; Q240Y)
(GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined
β2M (R12C) – italicized
IL-2 (H16A; F42A) – bold

FIG. 20O

3528

NYMNLGATLGGGGSGGGGSGGGGSI*QRTPKIQVYSCHPAENGKSNFLNCYVSGFH*
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
KIVKWDRDM

epitope: NYMNLGATL – WT1 (239-247; Q240Y)
(G4S)₃ – underlined
β2M (R12C) – italicized

FIG. 20P

3708

NYMNLGATLGGGGSGGGSGGGGS***IQ***RTPK***IQ***VYSCHPAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDMGGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
 NYKNPKLTRML***TAK***FYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
 LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
 GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPK
 LTRML***TAK***FYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN
 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

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

FIG. 20Q

3530

NYMNLGATL***GCGGS***GGGGSGGGGS***IQ***RTPK***IQ***VYSRHPAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDM

epitope: NYMNLGATL – WT1 (239-247; Q240Y)
 (GCGGS)(G4S)₂ – underlined
 β2M (R12) – italicized

FIG. 20R

3710

NYMNLGATLGCGGSGGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTKEDEYACRVNHVTLSP
 KIVKWDRDMGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGIN
 NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
 LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMILNGINNYKN
 PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
 DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

epitope: NYMNLGATL – WT1 (239-247; Q240Y) (GCGGS)(G4S)₂, (G4S)₃, and (G4S)₄ – underlined
β2M (R12) – italicized
IL-2 (H16A; F42A) – bold

FIG. 21

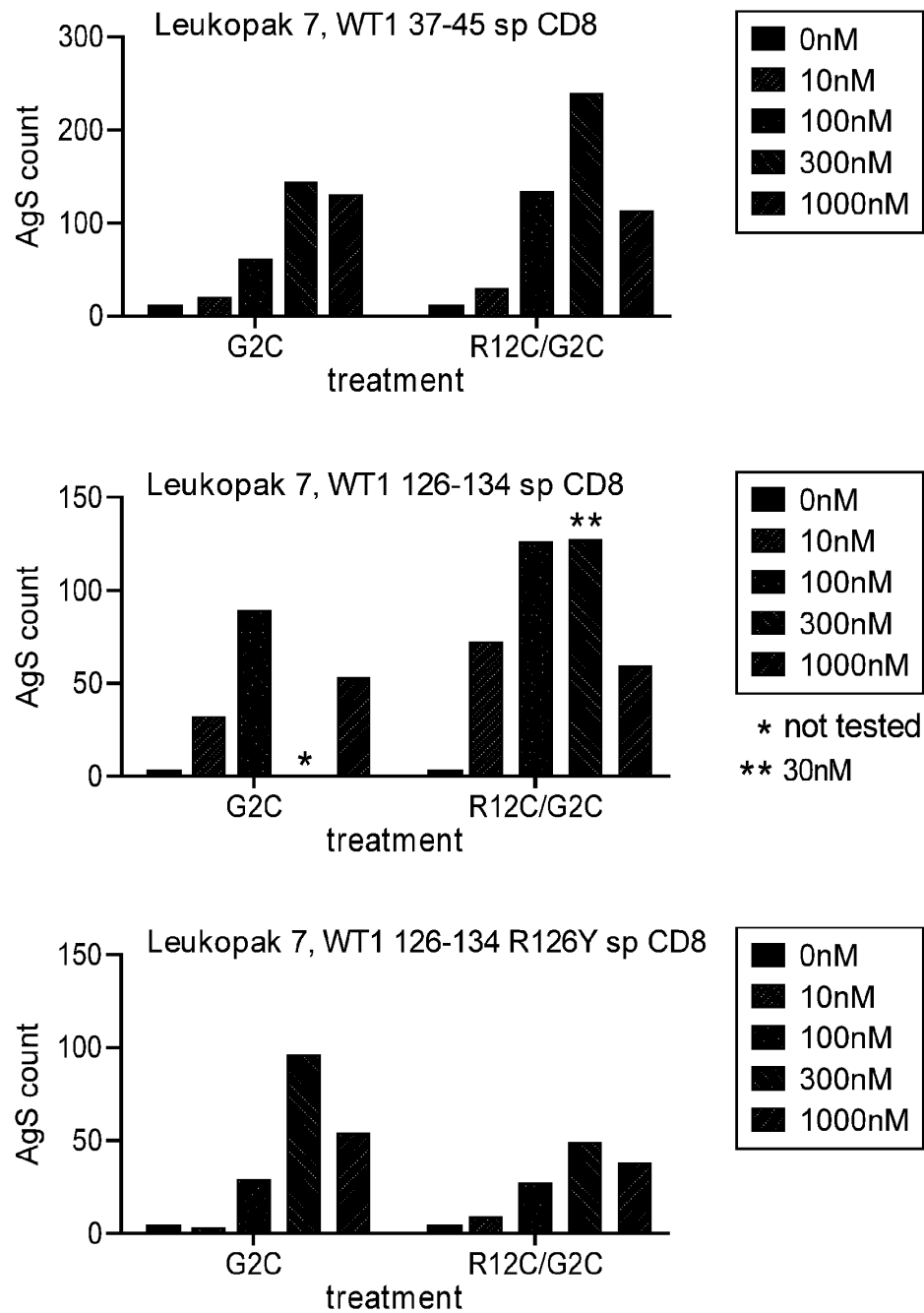


FIG. 21 (Cont.)

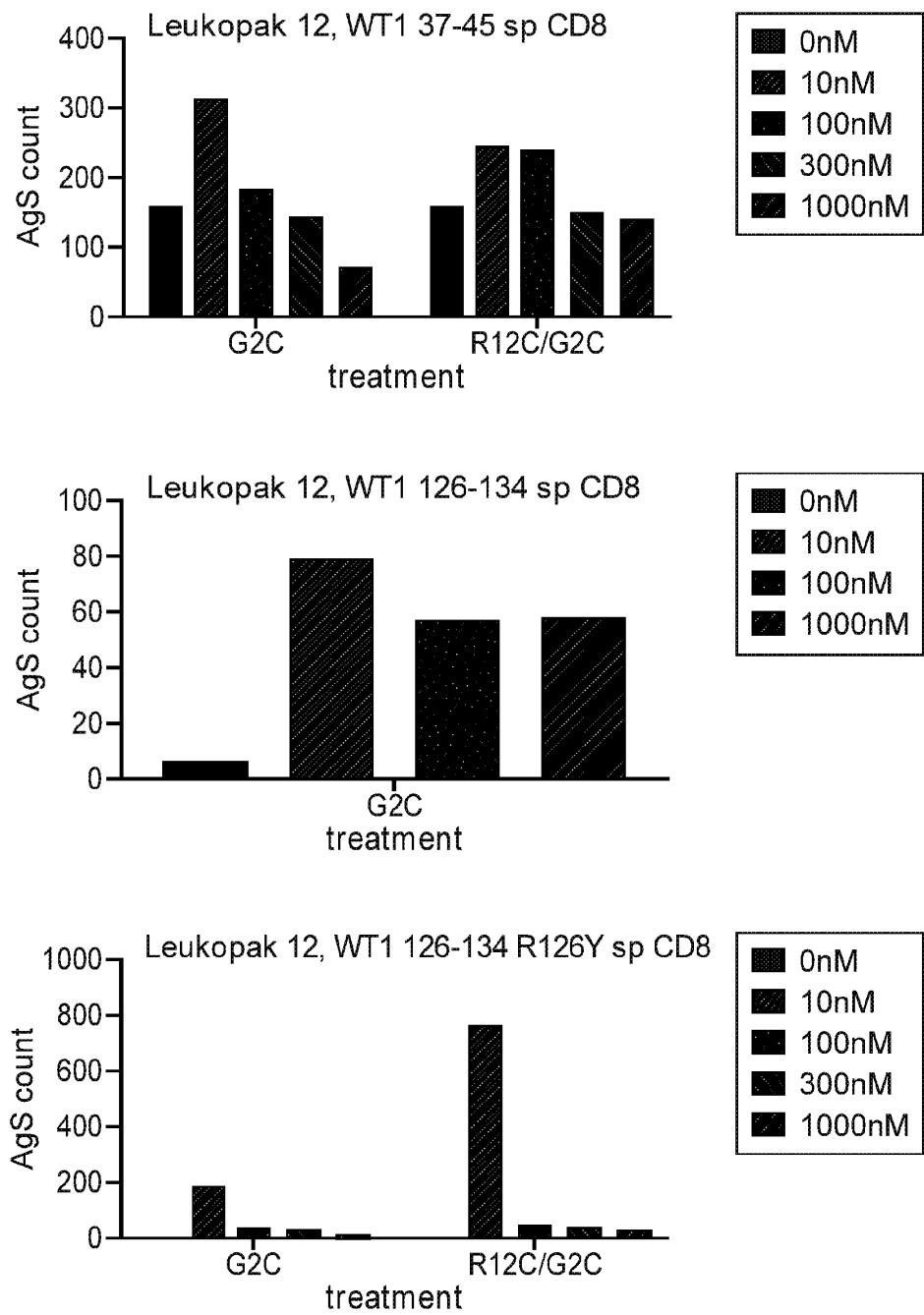
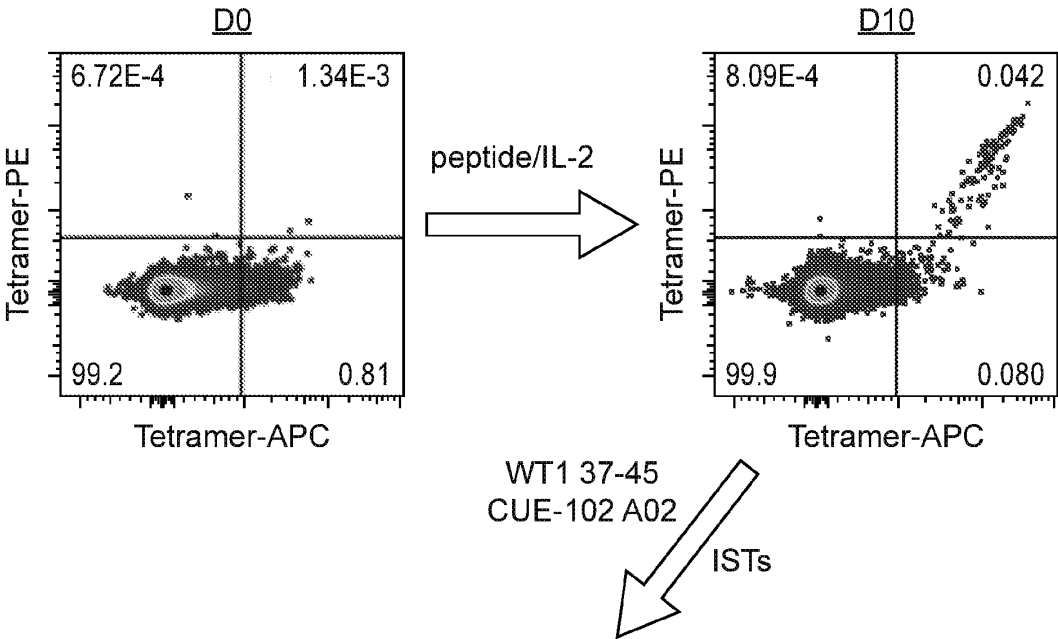


FIG. 22

WT1 37-45



WT1 37-45
CUE-102 A02

ISTs

D18 analysis

Total number of Ag-specific T cells

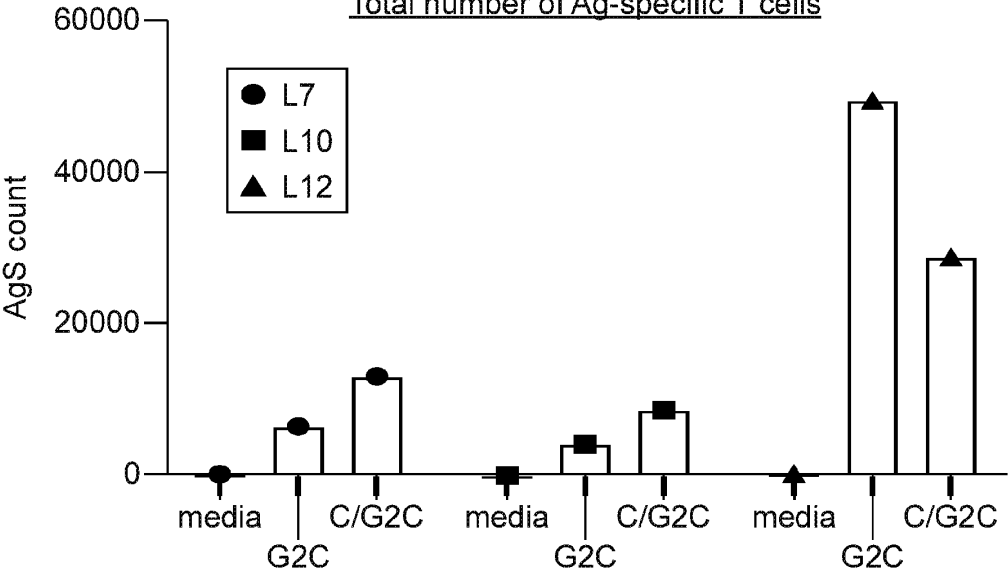


FIG. 22 (Cont.)

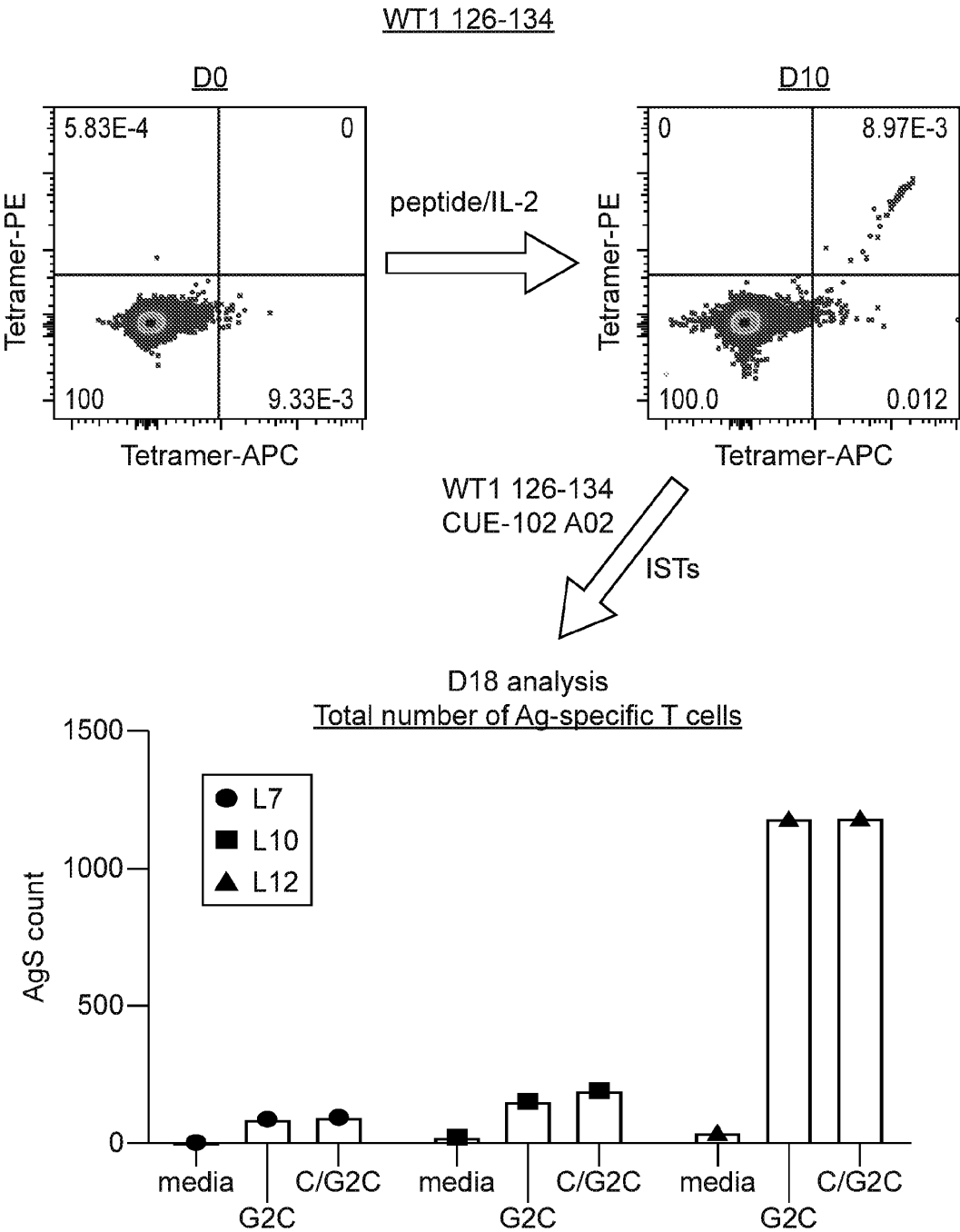
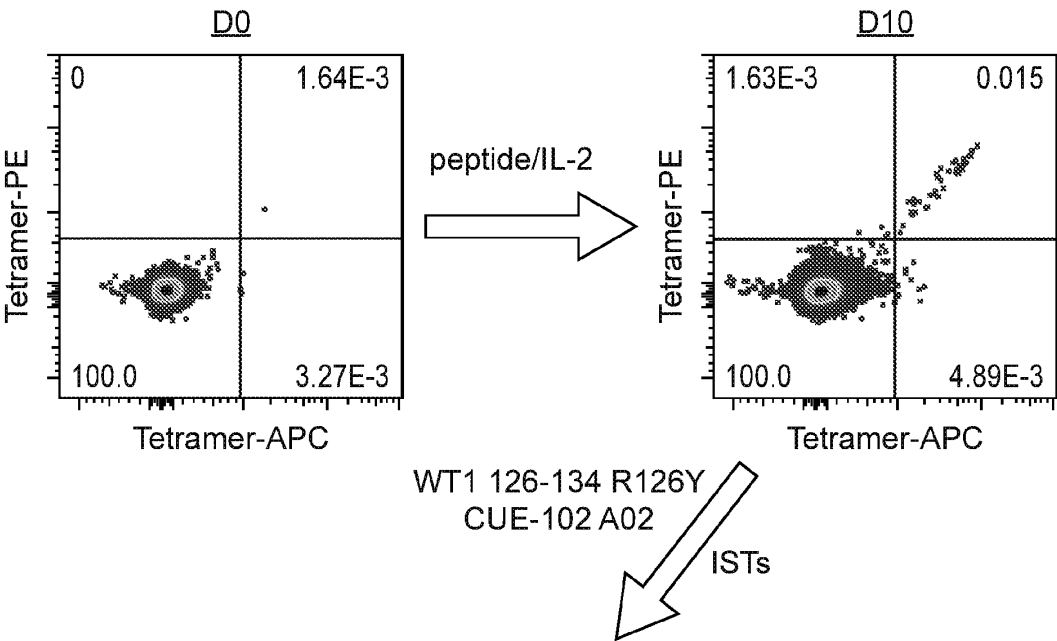


FIG. 22 (Cont.)

WT1 126-134 R126Y



WT1 126-134 R126Y
CUE-102 A02

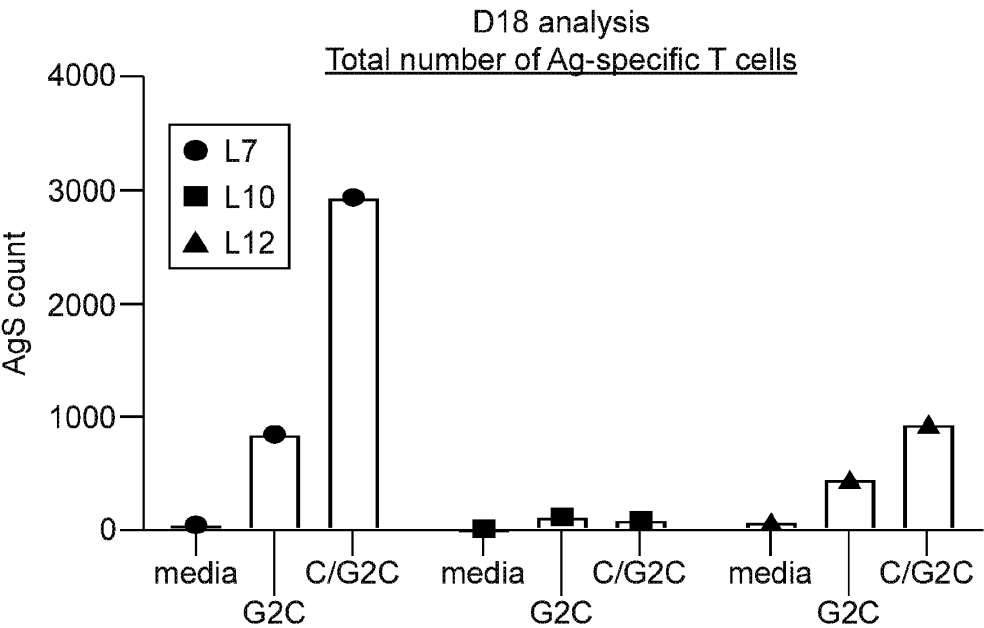


FIG. 23

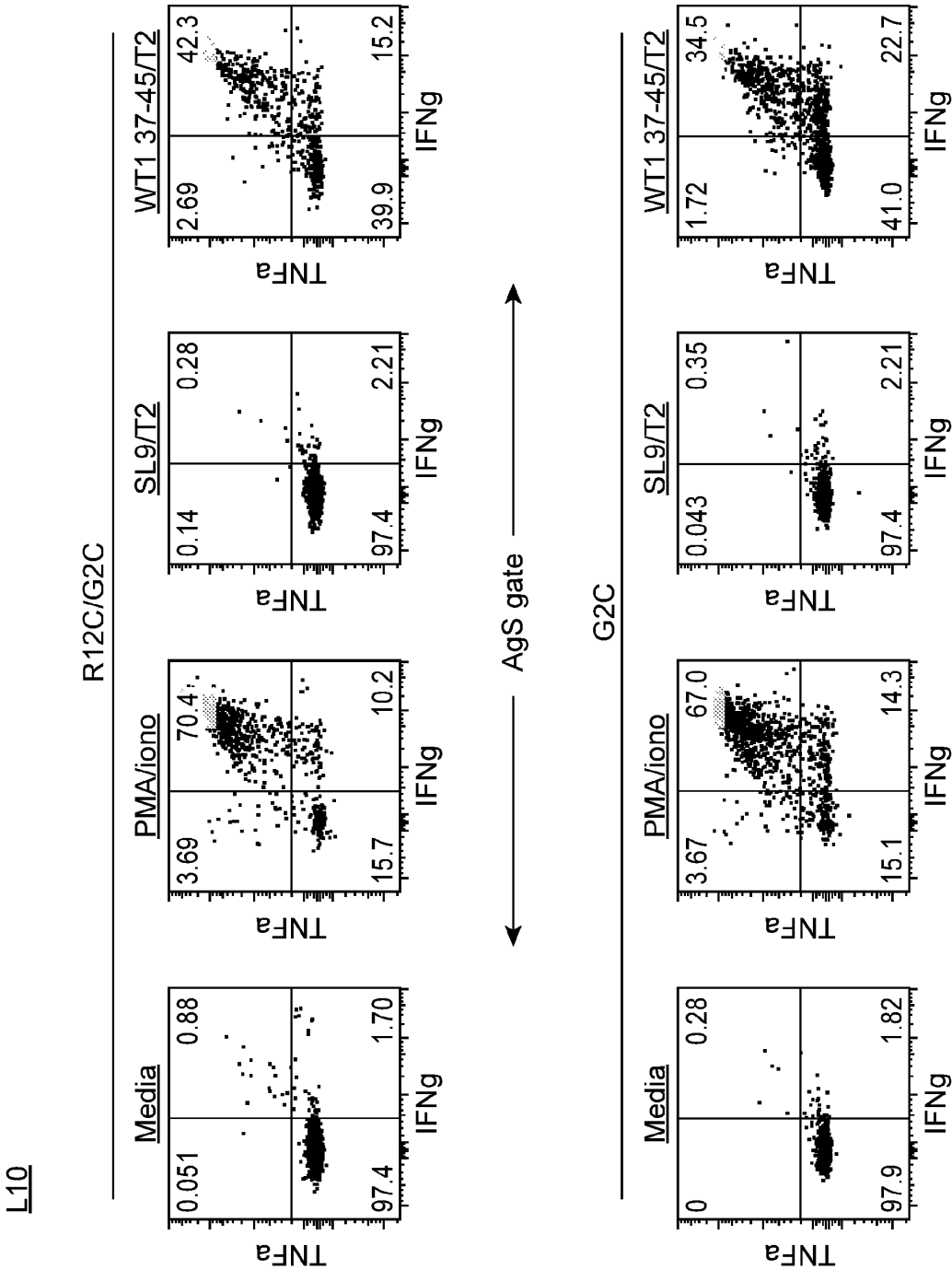


FIG. 24

L10

← AgS gate →

R12C/G2C

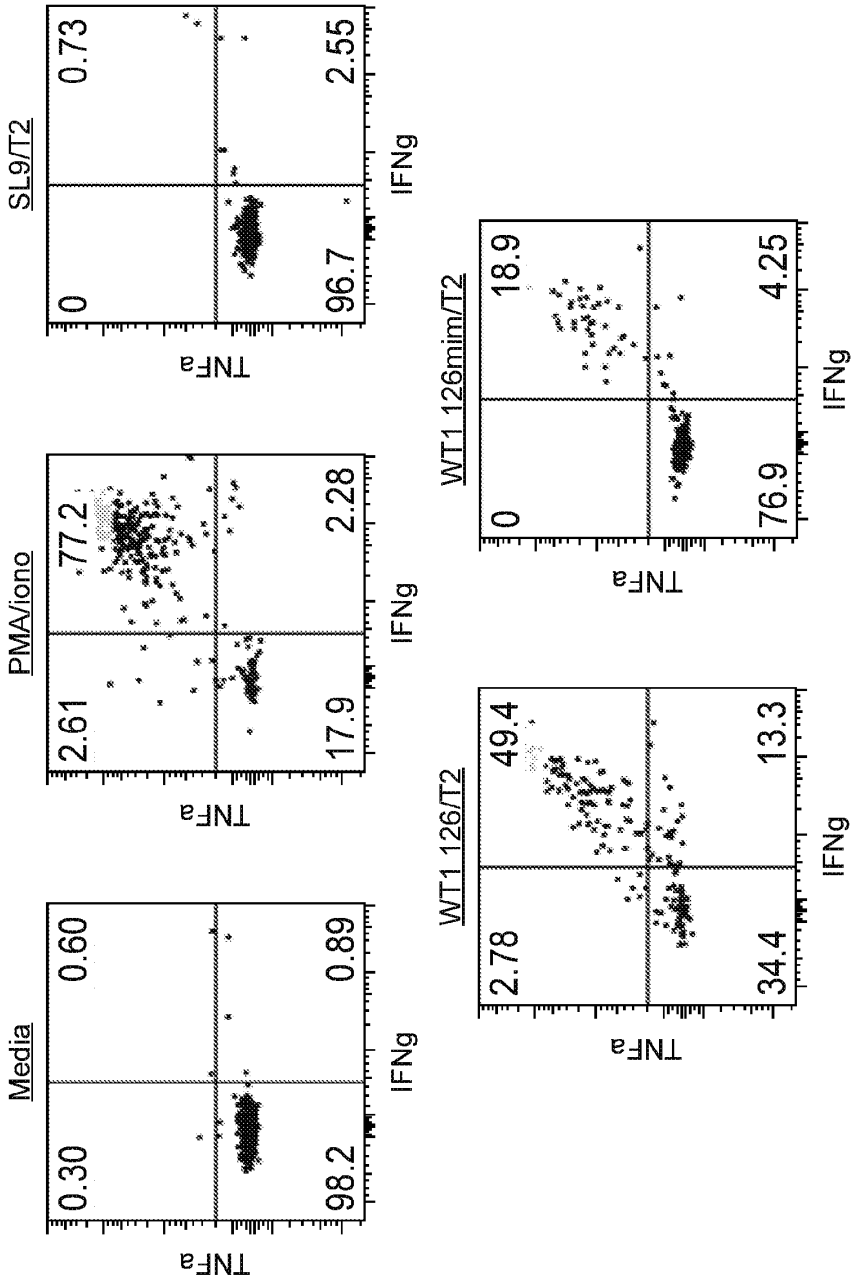
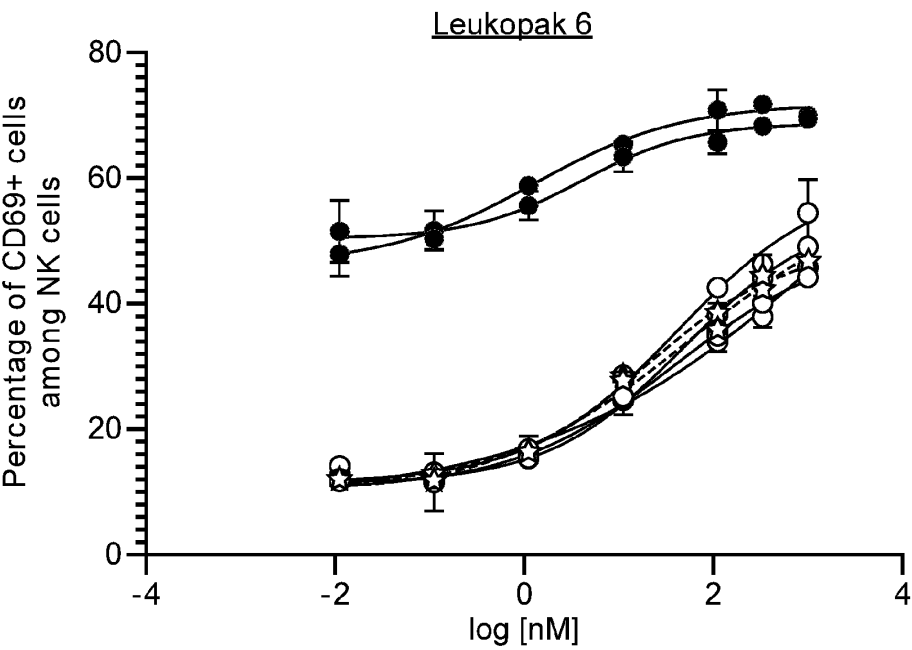


FIG. 25



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

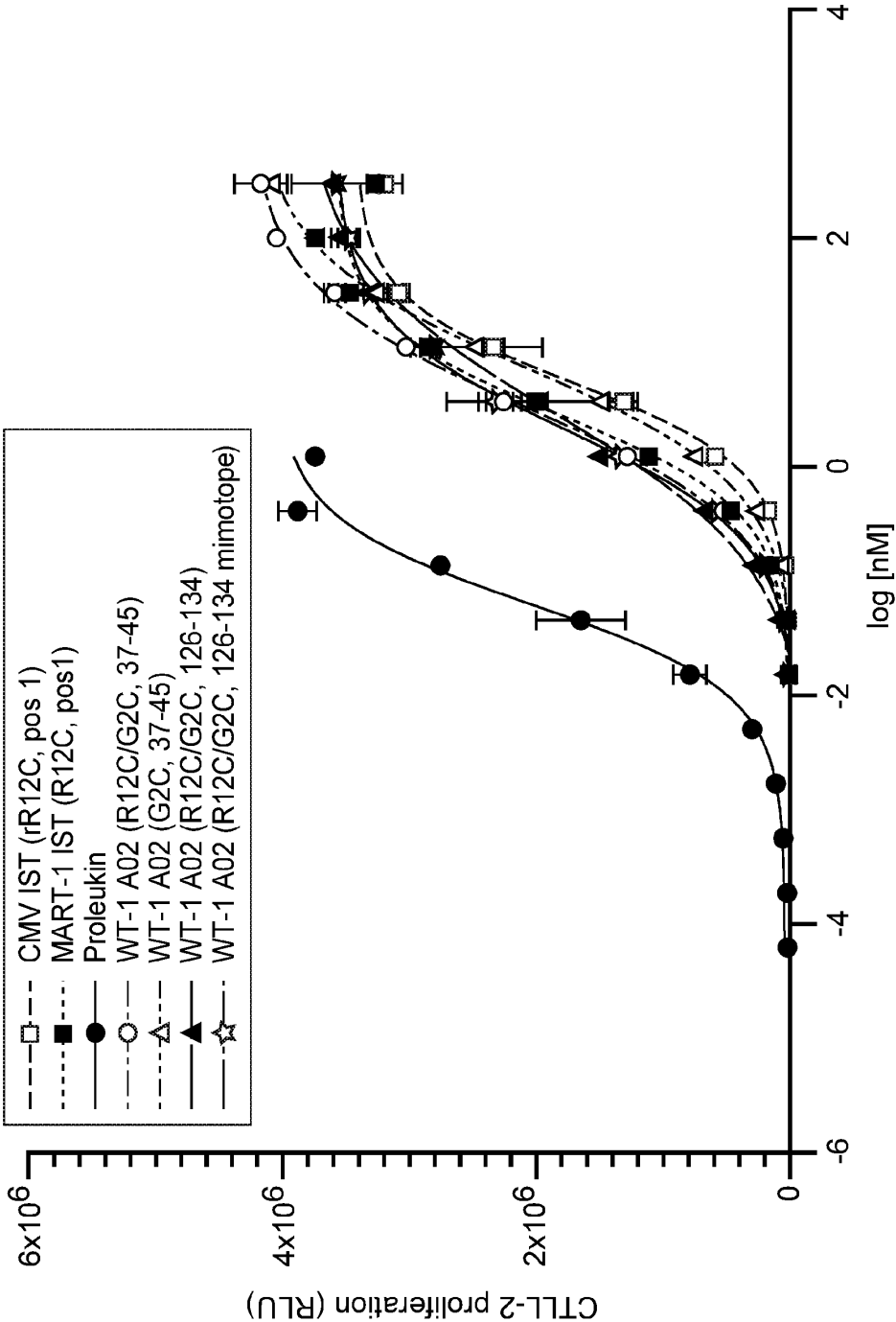


FIG. 27

37-45 double disulfide

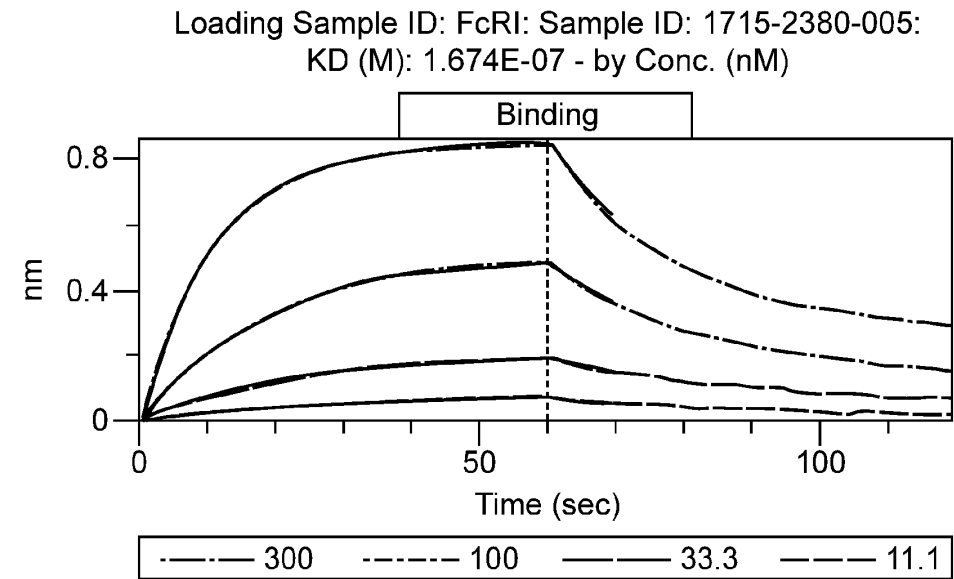
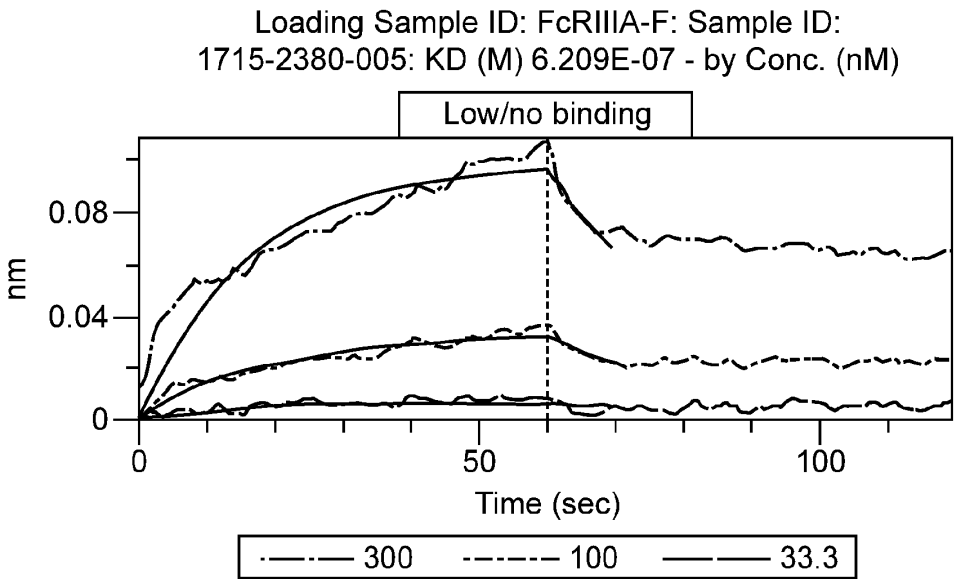
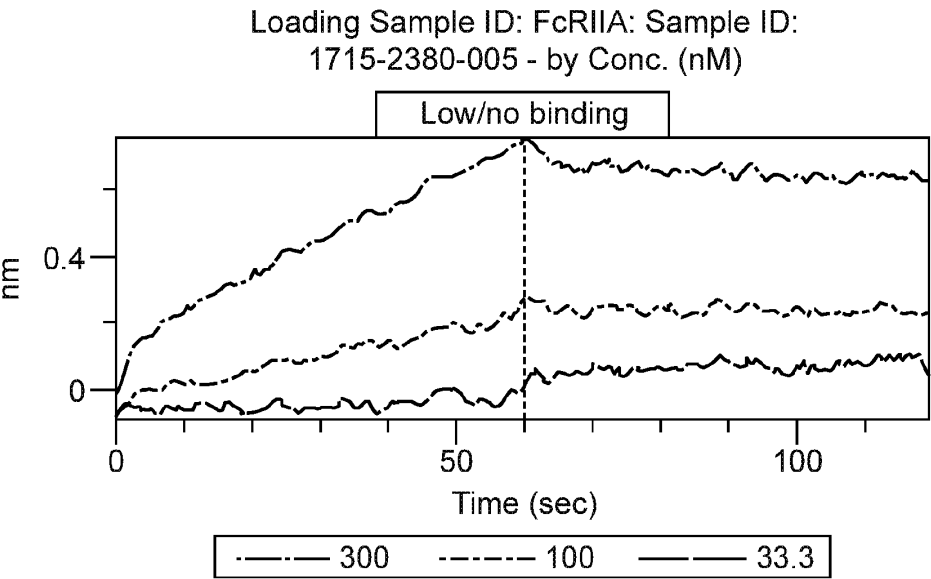
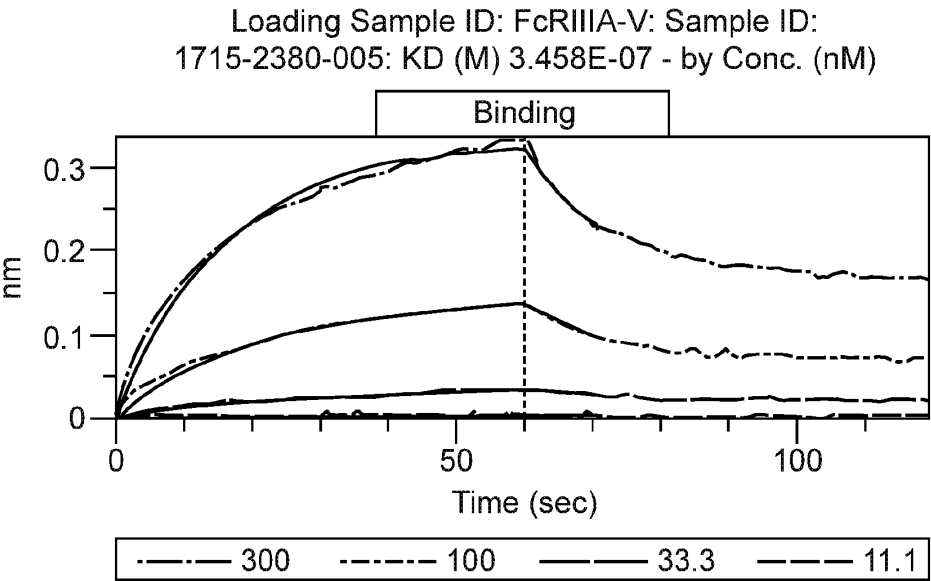


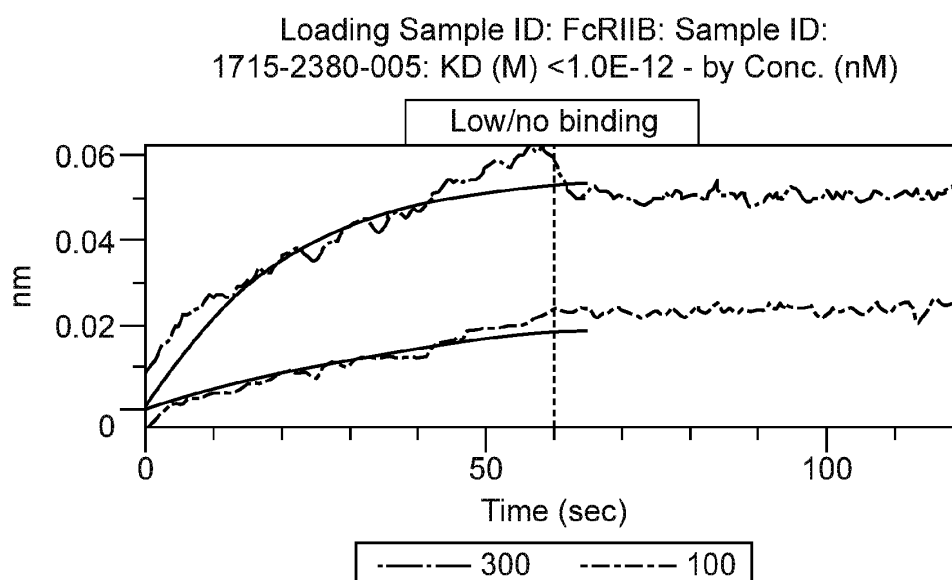
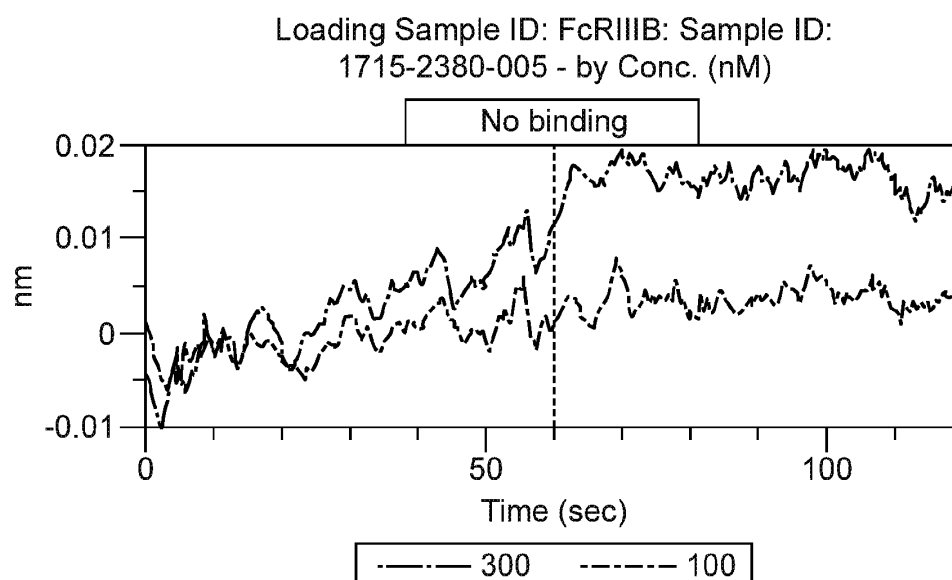
FIG. 27 (Cont.)

37-45 double disulfide



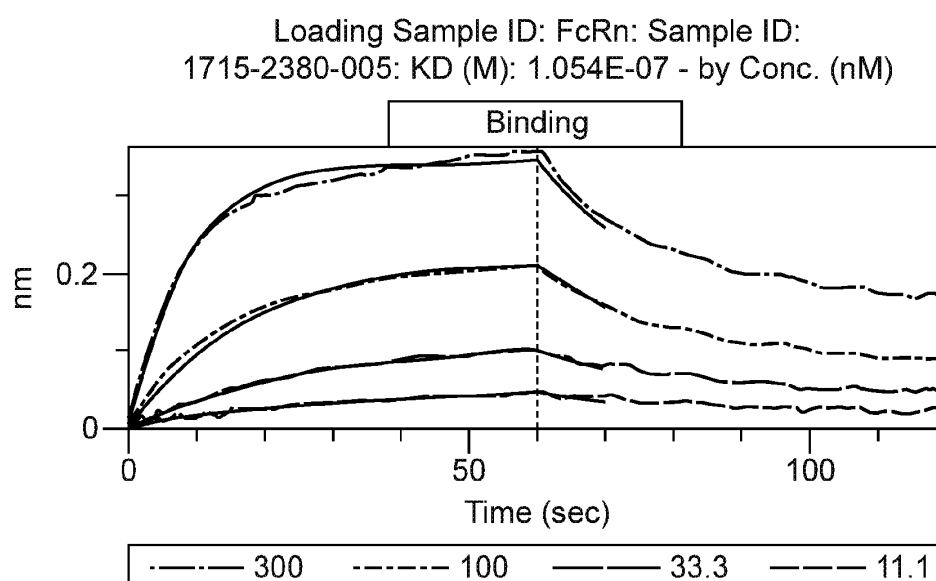
65/66

FIG. 27 (Cont.)

37-45 double disulfide

66/66

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