

FIG.2A

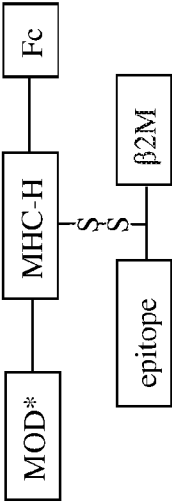


FIG.2B

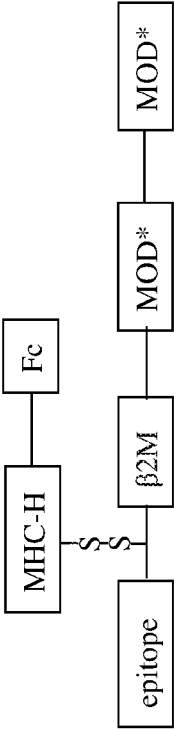


FIG.2C

FIG.2D

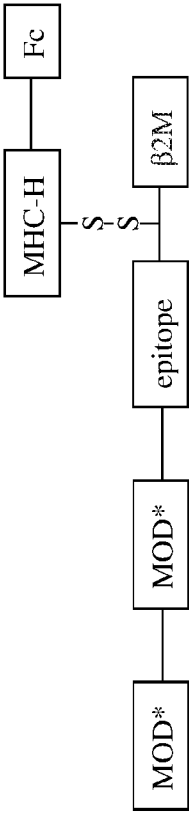


FIG.2E

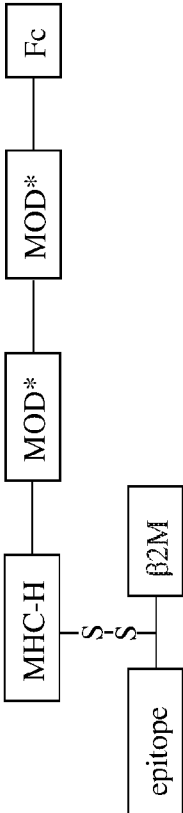


FIG.2F

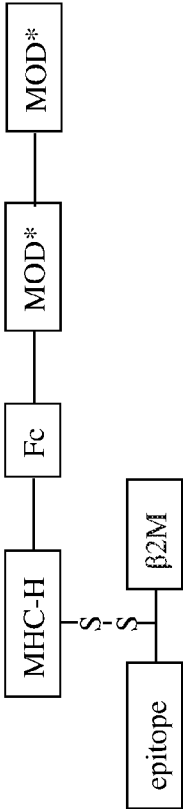


FIG. 3A**WT-1 isoform A**

1 MDFLLLLQDPA STCVPEPASQ HTLRSGPGCL QQPEQQGVDR PGGIWAKLGA AEASAERLQG
61 RRSRGASGSE PQQMGSDVRD LNALLPAVPS LGGGGGCALP VSGAAQWAPV LDFAPPGASA
121 YGSLGGPAPP PAPPPIPPPP PHSFIKQEPS WGGAEPEHEEQ CLSAFTVHFS GQFTGTAGAC
181 RYGFPGPPPP SQASSGQARM FPNAPYLPSC LESQPAIRNQ GYSTVTFDGT PSYGHTPSHH
241 AAQFPNHSFK HEDPMGQQGS LGEQQYSVPP PVYGCHTPTD SCTGSQALLL RTPYSSDNLY
301 QMTSQLECMT WNQMNLGATL KGHSTGYESD NHTTPILCGA QYRIHTHGVF RGIQDVRRVP
361 GVAPTLVRS A SETSEKRPFM CAYPGCNKRY FKLSHLQMHS RKHTGEKPYQ CDFKDCERRF
421 SRSDQLKRHQ RRHTGVKPFQ CKTCQRKFSR SDHLKTHTRT HTGEKPFSCR WPSCQKKFAR
481 SDELVRHHNM HQNMNMTKLQAL AL

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

1 MDFLLLLQDPA STCVPEPASQ HTLRSGPGCL QQPEQQGVDR PGGIWAKLGA AEASAERLQG
61 RRSRGASGSE PQQMGSDVRD LNALLPAVPS LGGGGGCALP VSGAAQWAPV LDFAPPGASA
121 YGSLGGPAPP PAPPPIPPPP PHSFIKQEPS WGGAEPEHEEQ CLSAFTVHFS GQFTGTAGAC
181 RYGFPGPPPP 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 CQRKFSRSDH LKTHTRHTGT
481 EKPFSRWPS CQKKFARSDE LVRHHNMHQ NMTKLQALAL

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

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1  MDFLLLQDPA STCVPEPASQ HTLRSGPGCL QQPEQQGVVD PGGIWAKLGA AEASAERLQG
61  RRSRGASGSE PQQMGSDVVD LNALLPAVPS LGGGGGCALP VSGAAQWAPV LDFAPPGASA
121 YGSLGGPAPP PAPPPPPPPP PHSFIKQEPS WGGAEPEHEQ CLSAFTVHFS GQFTGTAGAC
181 RYGFPGPPPP SQASSGQARM FPNAPYLPSC LESQPAIRNQ GYSTVTFDGT PSYGHTPSHH
241 AAQFPNHSFK HEDPMQQGS LGEQQYSVPP PVYGCHTPTD SCTGSQALLL RTPYSSDNLV
301 QMTSQLECMT WNQMNLGATL KGVAAGSSSS VKWTEGQSNH STGYESDNHT TPILCGAQYR
361 IHTHGVFRGI QDVRRVPGVA PTLVRSASET SEKRPFMCAY PGCNKRYFKL SHLQMHRSKH
421 TGEKPYQCDF KDCERRFSRS DQLKRHQRRH TGVKPFQCKT CQRKFSRSDH LKTHTRHTTG
481 KTSEKPFSCR WPSCQKKFAR SDELVRHHNM HQRNMTKLQL AL

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

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1  MEKGYSTVTF DGTPSYGHTP SHHAAQFPNH SFKHEDPMGQ QGSLGEQQYS VPPPVYGCHT
61  PTDSCTGSQA LLLRTPYSSD NLYQMTSQLE CMTWNQMNLG ATLKGVAAGS SSSVKWTEGQ
121 SNHSTGYESD NHTTPILCGA QYRIHTHGVF RGIQDVRRVP GVAPTLVRSV SETSEKRPFM
181 CAYPGCNKRY FKLSHLQMHV RKHTGEKPYQ CDFKDCERRF SRSDQLKRHQ RRHTGVKPFQ
241 CKTCQRKFSR SDHLKTHTRT HTGEKPFSCR WPSCQKKFAR SDELVRHHNM HQRNMTKLQL
301 AL

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

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1  MEKGYSTVTF DGTPSYGHTP SHHAAQFPNH SFKHEDPMGQ QGSLGEQQYS VPPPVYGCHT
61  PTDSCTGSQA 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

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FIG. 4A

Construct 3158

GSHSMRYFSTSVSRPGRGEPREFIAVGYVDDTQFVRFDSDAASORMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRIALRAYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHOYAYDGKDYLKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWORDGEDOTQDTELVETRPCGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWEGGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGIN
NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCHEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKN
PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPR
DLISNINVIVLELKGSETTFMCHEYADETATIVEFLNRWITFCQSIISTLTGGGGS
GGGSGGGSGGGSGGGSGGGGSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
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

APTSSSTKKTQLQLEALLLDLQMLINGINNYKNPKLTRMLTAKFYMPKKATELKHLOCL
EELKPLEEVLNLAQSKNFHLRPDLISNINVIVLELKGSETTFMCEYADETATIVEFL
NRWITFCQSIISTLTGGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQML
LINGINNYKNPKLTRMLTAKFYMPKKATELKHLOCLEELKPLEEVLNLAQSKNFHLRP
DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTGGGSGGGG
SGGGSGGGSGSGSHSMRYFSTSVSRPGRGEPRIAGVYVDDTQFVRFDSDAASQRMENR
APWIEQEGPEYWDEETGKVKAHSQTDRENLRALRAYNQSEAGSHTLOMMFGCDVGS
RFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYLEGTCVD
GLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQT
QDTELVETRPCGDGTQKWAAVVVPSSGEEQRYTCHVQHEGLPKPLTLRWEAAAGGDKTH
TCPPCPAPEAAGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK**

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

FIG. 4C

Construct 3159

GSHSMRYFSTSVSRPGRGEPREIAVG YVDDTQFVRFDSDAASQRM
EPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLR
IALRAYNQSEAGSHTLOMMFGCDVGSDGR
FLRGYHQYAYDGKD YIALKEDLR
SWTAADMAAQITKRKWEAAHVAEQ
QRAYL
EGTCVDGLRRYLENGKETLQRTDPPK
THMTHHPISDHEATLRCWALGFYPAEITL
TWQRDGEDQTQDTEL VETRPCGDGTFQK
WAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWEAAAGGDKTHTCPPCPAPEA
AGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNV FSCSVMHEALHN
HYTQKSLSLSPGGGGSGGGGSGGGGS
APTSSSTKKTQLQLEALLLDLQ MILN
GINNYKNPKLTRMLTAKFYMPKKATEL
KHLQCLEEELKPLEEVLNLAQSK
NFHLRPRDLISNINVIVLELKGSETTFM
CEYADETATIVEFLNRWITFCQSIIS
TLTGGGGSGGGGSGGGGSGGGGS
APTSSSTKKTQLQLEALLLDLQ MILNGIN
NYKNPKLTRMLTAKFYMPKKATEL
KHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFM
CEYADETATIVEFLNRWITFCQSIISTLT

HLA-A*24:02 – double underlined

Human IgG1 Fc (LALA) – italicized

(G4S)₃ and (G4S)₄ – underlined

IL-2 (H16A; F42A) – bold

10/66

FIG. 4D**Construct 2752**

CMTWNQMNLGGGGSGGGSGGGGS*IQRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDI*
EVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVK
WDRDM

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

FIG. 4E**Construct 2753**

CYTWNQMNLGGGGSGGGSGGGGS*IQRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDIE*
VDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVKW
DRDM

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

Figure 5A
GenBank 3S7G_A
Homo sapiens IgG1 Fc (SEQ ID NO:1)
227 aa

1 dkthtcppcp apellggpsv flfppkpkdt lmisrtpevt cvvvdvshed pevknwyvd
61 gvevhnatk preeqynsty rvsvltvlh qdwlngkeyk ckvsnkappa piektiskak
121 gqprepqvvt lpsrdeltk ngvsltclvk gfypsdiave wesngqpenn ykttppvlds
181 dgsfflyskl tvdksrwqgg nvfscsvmhe alhnyhtqks lslspgk

GenBank AAN76044
Homo sapiens IgG2 Fc (amino acids 99-325) (SEQ ID NO:1)
227 aa

1 stkgpsvfpl apcsrsts taalgclvkd yfpepvtvsw nsgaltsgvh tfpavlqssg
61 lyslssvvtv pssnfgtgty tcnvdhkpsn tkvdktkverk ccvecpcpa ppvagpsvfl
121 fppkpkdtlm isrtpevtcv vdvshedpe vqfnwyvdgv evhnaktkpr eeqfnstfrv
181 vsvltvvhq wlngkeykck vsnkglpapi ektisktkgg prepqvtylp psreemtknq
241 vsltclvkgf ypsdiavewe sngqpennyk ttpmldsdg sfllyskltv dksrwqggv
301 fscsvmheal hnyhtqksl lspgk

GenBank AAW65947
Homo sapiens IgG3 Fc (amino acids 19-246) (SEQ ID NO:1)
238 aa

1 hkpsntkvdk rvelktplgd tthtcppcpa pellggpsvf lfppkpkdtl misrtpevtc
61 vvvdvshedp evkfnwyvdg vevhnaktkp reeqynstyr vsvltvlhq dwlngkeykc
121 kvsnkappa iektiskakg qprepqvtyl ppsrdeltkn qvsltclvkg fypsdiavew
181 esngqpenny kttppvlds gsfflysklt vdksrwqggv vfscsvmhea lhnhytqksl
241 slspgk

Figure 5B

GenBank AAA52770
Homo sapiens **IgD** Fc (amino acids 162-383) (SEQ ID NO:1/)

222 aa

1 ptkapdvfpi isgcrhpkdn spvvlacilit gyhptsvtvt wymgtqsqpq rtfpeiqrdrd
61 syymtssqls tplqqrqge ykcvvqhtas kskkeifrwp espkaqassv ptaqpqaegs
121 lakattapat trntgrggee kkekekeeq eeretktpec pshtqplgvy lltpavqdlw
181 lrdkatftcf vvgSDLkdah ltwevagkvp tggveeglle rhnsgsqsqh srlltlprslw
241 nagtsvtctl nhpslppqrl malrepaaqa pvklslnlla ssdppeaaaw llcevsqgfs
301 pnillmwled grevntsgfa parpppqprs ttfwawsvlr vpappspqpa tytcvvhed
361 srlllnasrs levsyvtldhg pmk

GenBank 0308221A
Homo sapiens **IgM** Fc (SEQ ID NO:1/)

276 aa

1 vtstltikzs dwlgesmftc rvdhrgltfq qnassmcvpd qdtairvfai ppsfasiflt
61 kstkltlclvt dltybsvti swtreengav kthtnishes pnatfsavge asicedbdws
121 gerftctvth tdlpsplkqt isrpkgvalh rpbvylppa rzzlnlresa titclvtgfs
181 padvfvevmq rgeplspqky vtsapmpepq apgryfahsi ltvseeewnt ggtytcvvh
241 ealpnrvter tvdkstgkpt lynvslvmsd tagtocy

Figure 5C

GenBank P01876	
<i>Homo sapiens</i>	IgA Fc (amino acids 120-353) (SEQ ID NO: //)
234 aa	
	1 asptspkvfp lslcstqpdg nvviacvlvg ffpqeplsvt wsesgggvta rnfppsqdas
	61 gdlyttssql tlpatqclag ksvtchvkhy tnpdqdvtp cpvpstpptp spstpptp
	121 scchprlslh rpaledlllg seanltctlt glrdasgvtf twtpssgksa vggpperdlc
	181 gcysvssvlp gcaepwnhgk tftctaaype sktpltatls ksgntfirpev hllpppseel
	241 alnelvtltc largfspkdv lvrwlqgsqe lprekyltwa srqepsqgtt tfavtsilrv
	301 aeedwkkgdt fscmvghcal plaftqktid rlagkpthvn vsvvmaevdg tcy
GenBank 1F6A_B	
<i>Homo sapiens</i>	IgE Fc (amino acids 6-222) (SEQ ID NO: //)
212 aa	
	1 adpdsnpgrg vsaylsrpsp fdlfirkcpt itclvvdlap skgtvnltws rasgkpvnhs
	61 trkeekqgrng tltvtstlpv gtrdwieget yqcrvthphl pralmrsttk tsgpaaapev
	121 yafatpewpg srdkrtlac1 ignfmpedis vqwlhnevql pdarhsttqp rktkgsqgffv
	181 fsrlevtrae weqkdeficr avheaaspsq tvqravsvnp gk
GenBank P01861	
<i>Homo sapiens</i>	IgG4 Fc (amino acids 100-327) (SEQ ID NO: //)
228 aa	
	1 astkgpsvfp lapcsrstse staaalgclvk dyfpepvtvs wnsгалtsgv htfpavlqss
	61 glyslssvvt vpssslgtkt ytcnvdhkps ntkvdkrves kygppcpscp apeflggpsv
	121 flfppkpkdt lmisrtpevt cvvvdvsqed pevqfnwyvd gvevhnaktk preeqfnsty
	181 rvsvltvlh qdwlngkeyk ckvsnkglps siektiskak gqprepqvyt lppsqeemtk
	241 nqvsltclvk gfypsdiave wesngqpenn ykttppvlds dgsfflysr1 tvdksrwqeg
	301 nvfscsvmhe alhnhytqks lslslgk

FIG. 5D

WT Human IgG1 Fc Sequence: (SEQ ID NO: //)
 DKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
 ESNQQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

FIG. 5E

Human IgG1 Fc Mutant: L234F/L235E/P331S (Triple Mutant "TM") (SEQ ID NO: //)
 DKHTCPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVLHQDWLNGKEYCKVSNKALPAP~~S~~IEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
 ESNQQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

FIG. 5F

Human IgG1 Fc Mutant: N297A (SEQ ID NO: //)
 DKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTY
 RVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
 ESNQQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

FIG. 5G

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

Residue numbered according to EU index (Kabat Numbering)

FIG. 7A *Homo sapiens* HLA-A

7A.1 HLA-A*01:01:01 NCBI (National Center for Biotechnology Information) Accession NP_001229687.1 (SEQ ID NO:1)

1 MAVMAPRTLL LLLSGALALT QTWAGSHSMR YFFTSVSRPG RGEPRFIAVG YVDDTQFVRF
61 DSDAASQKME PRAPWIEQEG PEYWDQETRN MKAHSQIDRA NLGTLRGYIN QSEEDGSHTIQ
121 IMYGCDVGPD GRFLRGYRQD AYDGKDYIAL NEDLRSWTAA DAAQITKRK WEAAHVAEQQ
181 RYLEGRCVD GLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT
241 WQDGEDQTQ DTELVEPTRPA GDGTFQKWA VVVPSGEEQR YTCHVQHEGL PKPLTLRWEL
301 SSQPTIPIVG ILAGLVLLGA VITGAVVA V MWRKSSDRK GGSYTQAASS DSAQGS DVS L
361 TACKV

7A.2 HLA-A*1101 NCBI Accession P13746.1 (SEQ ID NO:2)

1 MAVMAPRTLL LLLSGALALT QTWAGSHSMR YFYTSVSRPG RGEPRFIAVG YVDDTQFVRF
61 DSDAASQKME PRAPWIEQEG PEYWDQETRN VKAQSQIDRV DLGTLRGYIN QSEEDGSHTIQ
121 IMYGCDVGPD GRFLRGYRQD AYDGKDYIAL NEDLRSWTAA DAAQITKRK WEAAHVAEQQ
181 RYLEGRCVE WLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT
241 WQDGEDQTQ DTELVEPTRPA GDGTFQKWA VVVPSGEEQR YTCHVQHEGL PKPLTLRWEL
301 SSQPTIPIVG ILAGLVLLGA VITGAVVA V MWRKSSDRK GGSYTQAASS DSAQGS DVS L
361 TACKV

7A.3 HLA-A*2402 NCBI Accession P05534.2 (SEQ ID NO:3)

1 MAVMAPRTLV LLLSGALALT QTWAGSHSMR YFSTSVSRPG RGEPRFIAVG YVDDTQFVRF
61 DSDAASQKME PRAPWIEQEG PEYWDEETGK VKAHSQIDRE NLRIALRYIN QSEAGSHTLQ
121 MMFGCDVGS D GRFLRGYHQY AYDGKDYIAL KEDLRSWTAA DAAQITKRK WEAAHVAEQQ
181 RYLEGTCVD GLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT
241 WQDGEDQTQ DTELVEPTRPA GDGTFQKWA VVVPSGEEQR YTCHVQHEGL PKPLTLRWEP
301 SSQPTVPIVG ILAGLVLLGA VITGAVVA V MWRNSSDRK GGSYSQAASS DSAQGS DVS L
361 TACKV

FIG. 7wA, continued

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

1 MAVMAPRTLL LLLLGALALT QTWAGSHSMR YFTTSVSRPG RGEPRFIavg YVDDTQFVRF
61 DSDAASQRME PRAPWIEQEG PEYWDRNTRN VKAHSQIDRV DLGTLRGYNN QSEAGSHTIQ
121 MMYGCDVGS D GRFLRGYQD AYDGKDYIAL NEDLRSWTAA DMAAQITQRK WEAAARVAEQL
181 RAYLEGTcve WLRYLENGK ETLQRTDPPK THMTHHAVSD HEATLRCWAL SFYPAEITLT
241 WQRDGEDQTQ DTELVEITRPA GDGTFQKWA VVVPsgGEQR YtCHVQHEGL PKPLTLRWEP
301 SSQPTIPIVG IIAGLVLFGA VFAGAVVAav RWRKSSDRK GGSYSQAASS DSAQGSDMSL
361 TACKV

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

1 mlvmaprtvl lllsaalalt etwagshsmr yfytsvsrpg rgeprfisvg yvddtqfvrf
61 dsdaaspree prapwieqeg peywdrntqi ykaqaqt dre slnrlrgyyn qseagshtlq
121 smygcdvgsd grllrgyq aydgkdyial nedlrswtaa dtaaqitqrk weaareaeqr
181 raylegecve wlrrylengk dkleradppk thvthhpisd heatlrcwal gfypaeitlt
241 wqrddgedqtq dtelvetrpa gdrtfqkwa vvpssgeeqr ytchvqhegl pkpltlrwep
301 ssqstvpivg ivaglavlav vvigavvaav mcrkssggk ggsysqaacs dsaggsdvs1
361 ta

FIG. 7C *Homo sapiens* HLA-C HLA-C GenBank Accession NP_001229971.1, w (SEQ ID NO://)

1 mrvmapprall lllsgglalt etwacshsmr yfdtavsrpg rgeprfisvg yvddtqfvrf
61 dsdaasprge prapwveqeg peywdretqn ykrqaqadv slnrlrgyyn qsedgshtlq
121 rmygcdlgsd grllrgyq aydgkdyial nedlrswtaa dtaaqitqrk leaaraaeql
181 raylegtcve wlrrylengk etlqraepk thvthhpisd heatlrcwal gfypaeitlt
241 wqrddgedqtq dtelvetrpa gdrtfqkwa vvpssgeeqr ytchmhegl qepltlswep
301 ssqptipimg ivaglavlv lavlgavvta mmcrkssgg kggsqsaacs snsaqgsdes
361 litck

FIG. 8

HLA-A	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFSDAASQKMEPRAPWIEQEGPEYW
HLA-B	GSHSMRYFYTSVSRPGRGEPRIISVGYVDDTQFVRFSDAASPREEPRAPWIEQEGPEYW
HLA-C	CSHSMRYFDTAVSRPGRGEPRIISVGYVDDTQFVRFSDAASPRGEPRAPWIEQEGPEYW
HLA-A*0201	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYW
Mouse H2K	GPHSLRYFVTAVSRPGLGEPRIAVGYVDDTQFVRFSDADNPRFEPRAPWMEQEGPEYW
HLA_A(var. 2)	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYW
HLA_A(var. 2C)	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYW
HLA-A(var.2CP)	GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYW
HLA-A*1101	GSHSMRYFYTSVSRPGRGEPRIAVGYVDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYW
HLA-A*2402	GSHSMRYFSTSVSRPGRGEPRIAVGYVDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYW
HLA-A*3303	GSHSMRYFTTSVSRPGRGEPRIAVGYVDDTQFVRFSDAASQRMPEPRAPWIEQEGPEYW

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84

HLA-A	DQETRNMKAHSQTDRLNLGTLRGYYNQSEAGSHTIQIMYGCDVGPDRFLRGYRQDAYDG
HLA-B	DRNTQIYKAQAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCVDGPDGRLLRGHDQYAYDG
HLA-C	DRETQNYKRQAQADRVSLRNLRGYYNQSEAGSHTLQRMYGCDLGPDGRLLRGYDQSAAYDG
HLA-A*0201	DGETRKVKAHSQTHRVDLGLTRGYYNQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDG
MOUSE H2K	EEQTQRAKSDEQWFRVSLRTAQRYYNQSKGGSHTFQRMFGCDVGSWDRLLRGYQQFAYDG
HLA_A(var. 2)	DGETRKVKAHSQTHRVDLGLTRGAYNQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDG
HLA_A(var. 2C)	DGETRKVKAHSQTHRVDLGLTRGCYNQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDG
HLA-A(var.2CP)	DGETRKVKAHSQTHRVDLGLTRGAYNQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDG
HLA-A*1101	DQETRNKVAQSQTDRLNLGTLRGYYNQSEAGSHTIQIMYGCDVGPDRFLRGYRQDAYDG
HLA-A*2402	DEETGKVKAHSQTDRENLRALRYYNQSEAGSHTLQMMFGCDVGSWDRFLRGYHQYAYDG
HLA-A*3303	DRNTRNVKAHSQIDRVLDLGLTRGYYNQSEAGSHTIQMMYGCDVGSWDRFLRGYQQDAYDG

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139

HLA-A	KDYIALNEDLRSWTAADMAAQITKRKWEAVHAAEQRRVYLEGRCVDGLRRYLENGKETLQ
HLA-B	KDYIALNEDLRSWTAADTAAQITQRKWEAAREAEQRRAYLEGECEVWLRRLYLENGKDKLE
HLA-C	KDYIALNEDLRSWTAADTAAQITQRKLEAARAAEQRLAYLEGTCEVWLRRLYLENGKETLQ
HLA-A*0201	KDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQRLAYLEGTCEVWLRRLYLENGKETLQ
MOUSE H2K	RDYIALNEDLKTWTAADTAALITRRKWEQAGDAEYRAYLEGECEVWLRRLYLELGNETLL
HLA_A(var. 2)	KDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQRLAYLEGTCEVWLRRLYLENGKETLQ
HLA_A(var. 2C)	KDYIALKEDLRSWTAADMCAQTTKHKWEAAHVAEQRLAYLEGTCEVWLRRLYLENGKETLQ
HLA-A(var.2CP)	KDYIALNEDLRSWTAADMAAQITKRKWEAAHVAEQRLAYLEGTCEVWLRRLYLENGKETLQ
HLA-A*1101	KDYIALNEDLRSWTAADMAAQITKRKWEAAHAAEQRAYLEGRCVEWLRRLYLENGKETLQ
HLA-A*2402	KDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQRAYLEGTCEVDGLRRYLENGKETLQ
HLA-A*3303	KDYIALNEDLRSWTAADMAAQITQRKWEAARVAEQRLAYLEGTCEVWLRRLYLENGKETLQ

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FIG. 8 (continued)

236
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HLA-A	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDGTF
HLA-B	RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDRTF
HLA-C	RAEPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDGTF
HLA-A*0201	RTDAPKTHMTHHAVSDHEATLRCWALSFPYAEITLTWQRDGEDQTQDTEL	VETRPAGDGTF
MOUSE H2K	RTDSPKAHVTYHPRSQVDVTLRCWALGFYPADITLTWQLNGEDLTQDMEL	VETRPAGDGTF
HLA_A(var. 2)	RTDAPKTHMTHHAVSDHEATLRCWALSFPYAEITLTWQRDGEDQTQDTEL	VETRPAGDGTF
HLA_A(var. 2C)	RTDAPKTHMTHHAVSDHEATLRCWALSFPYAEITLTWQRDGEDQTQDTEL	VETRPAGDGTF
HLA-A(var. 2CP)	RTDAPKTHMTHHAVSDHEATLRCWALSFPYAEITLTWQRDGEDQTQDTEL	VETRPAGDGTF
HLA-A*1101	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDGTF
HLA-A*2402	RTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL	VETRPAGDGTF
HLA-A*3303	RTDPPKTHMTHHAVSDHEATLRCWALSFPYAEITLTWQRDGEDQTQDTEL	VETRPAGDGTF
	*:: **:*:*:* * : :.*****.*****:***** :*** ** *	*****. ** **
		aac5 aac6

HLA-A	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-B	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-C	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A*0201	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
MOUSE H2K	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA_A(var. 2)	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA_A(var. 2C)	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A(var. 2CP)	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A*1101	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A*2402	QKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
HLA-A*3303	QKWAASVVPSGEEQRYTCHVQHEGLPKPLTLRWE (SEQ ID NO://)
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[illegible]

FIG. 9B

GSHSMRYFX1TSVSRPGRGEPFRFIAVGIVDDTQFVRFDSDAASQX2MEPRAPWIEQEGPEYWDX
3X4TX5X6X7KAX8SQX9X10RX11X12LX13X14X15X16X17YYNQSEX18GSHTX19QX20
MX21GCDVGX22DX23RFLRGYX24QX25AYDGKDYLX26EDLRSWTAADMAAQX27TX287
X29KWEX30X31X32EAEQX33RX34YLYX35GX36CVX37X38LRRYLENGKETLQRTDX39PK
 THMTHHX40X41SDHEATLRCWALX42FYPAEITLIWQRDGEDQTQDTELVEPTRPAGDGTFQKW
 AXX43VVVPSGX44EQRYTCHVQHEGLPKPLTLRWEXX45

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 F or L.

aacl aaaz

8202 8202

8805 8806

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FIG. 10B

GSHSMRYFX1TX2X3SRPGRGEPFIX4VGYVDDTX5FVRFDSDAX6SPRX7X8PRAPWIEQEG
 PEYWDRX9TQX10X11KTX12X13TQX14YX15X16NLX17X18X19X20YYNQSEAGSHX21X
22QX23MYGCDLGPDRLLRGHDQSAYDGKDYIALNEDLX24SWTAADTAAQIX25QRKX26EA
 ARX27AEQX28RX29YLEGX30CVEWLRRYLENGKX31X32LX33RADPPKTHVTHHPX34SDH
 EATLRCWALGFYPAEITLTWQRDGEDQTQDTELVEITRPAGDRTFQKWA AVVVPSGEEQRYTCHV
 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.

FIG. 11A

C*0102	CSHSMKYFFTSVSRPGRGEPHFISVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0303	GSHSMRYFYTAVSRRPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0304	GSHSMRYFYTAVSRRPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0401	GSHSMRYFSTSVSRPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0602	CSHSMRYFYTAVSRRPGRGEPHFISVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0701	CSHSMRYFYTAVSRRPGRGEPHFISVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0702	CSHSMRYFYTAVSRRPGRGEPHFISVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*0801	CSHSMRYFYTAVSRRPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
C*1502	CSHSMKYFFTSVSRPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPAPWVEQEGPEYW	60
***** ** * : * * ***** ; * : ***** ; ***** *****		
94		
C*0102	DRETQKYKRQAQTDREVSLRNLRGTYNQSEAGSHTLQWMCGLGPDGRLLRGYDQYAYDG	120
C*0303	DRETQKYKRQAQTDREVSLRNLRGTYNQSEARSHIIQRMYGCDVGFDPGRLLRGYDQYAYDG	120
C*0304	DRETQKYKRQAQTDREVSLRNLRGTYNQSEAGSHIIQRMYGCDVGFDPGRLLRGYDQYAYDG	120
C*0401	DRETQKYKRQAQADRVNLRKLRGTYNQSEAGSHTLQRMFGCDLGPDPGRLLRGYNQFAYDG	120
C*0602	DRETQKYKRQAQADRVNLRKLRGTYNQSEAGSHTLQWMYGCDLGPDPGRLLRGYDQYAYDG	120
C*0701	DRETQNYKRFQAQADRVNLRNLRGTYNQSEAGSHTLQRMYGCDLGPDPGRLLRGYDQYAYDG	120
C*0702	DRETQKYKRQAQADRVNLRNLRGTYNQSEAGSHTLQRMFGCDLGPDPGRLLRGYDQYAYDG	120
C*0801	DRETQKYKRQAQTDREVSLRNLRGTYNQSEAGSHTLQRMYGCDLGPDPGRLLRGYNQFAYDG	120
C*1502	DRETQNYKRFQAQADRVNLRKLRGTYNQSEAGSHIIQRMYGCDLGPDPGRLLRGYDQYAYDG	120
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aac1 aac2		
139		
C*0102	KDYIALNEDLRSWTAADTAQITQKKWEAAREAEQRRAYLEGTCVEWLRRLRYLNGKETLQ	180
C*0303	KDYIALNEDLRSWTAADTAQITQKKWEAAREAEQLRAYLEGTCVEWLRRLRYLNGKETLQ	180
C*0304	KDYIALNEDLRSWTAADTAQITQKKWEAAREAEQLRAYLEGTCVEWLRRLRYLNGKETLQ	180
C*0401	KDYIALNEDLRSWTAADTAQITQKKWEAAREAEQRRAYLEGTCVEWLRRLRYLNGKETLQ	180
C*0602	KDYIALNEDLRSWTAADTAQITQKKWEAAREAEQRRAYLEGTCVEWLRRLRYLNGKETLQ	180
C*0701	KDYIALNEDLRSWTAADTAQITQKKLEAAREAEQLRAYLEGTCVEWLRRLRYLNGKETLQ	180
C*0702	KDYIALNEDLRSWTAADTAQITQKKLEAAREAEQLRAYLEGTCVEWLRRLRYLNGKETLQ	180
C*0801	KDYIALNEDLRSWTAADTAQITQKKWEAAREAEQLRAYLEGTCVEWLRRLRYLNGKETLQ	180
C*1502	KDYIALNEDLRSWTAADTAQITQKKWEAAREAEQLRAYLEGTCVEWLRRLRYLNGKETLQ	180
***** ***** ; * : * * ***** ; * : ***** ; * : *****		
aac3 aac4		
236		
C*0102	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRAAGDGTG	241
C*0303	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRAAGDGTG	241
C*0304	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRAAGDGTG	241
C*0401	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRAAGDGTG	241
C*0602	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRAAGDGTG	241
C*0701	RAEPPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRAAGDGTG	241
C*0702	RAEPPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRAAGDGTG	241
C*0801	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRAAGDGTG	241
C*1502	RAEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRAAGDGTG	241
*** ***** ; * : * * ***** ; * : ***** ; * : *****		
aac5 aac6		
C*0102	QKWAAMVVPFGGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0303	QKWAAMVVPFGGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0304	QKWAAMVVPFGGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0401	QKWAAMVVPFGGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0602	QKWAAMVVPFGGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0701	QKWAAMVVPFGGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0702	QKWAAMVVPFGGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*0801	QKWAAMVVPFGGEEQRYTCHVQHEGLPEPLTLRWEP	276
C*1502	QKWAAMVVPFGGEEQRYTCHVQHEGLPEPLTLRWEP	276
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FIG. 11B

X1SHSMX2YFX3TAVSX4PGRGEPX5FIX6VGYVDDTQFVX7FDSDAASPRGEPRX8PWVEQEG
 PEYWDRETQX9YKRQAQX10DRVX11LRX12LRGYYNQSEX13X14SHX15X16QX17MX18GC
 DX19GPDGRLLRGX20X21QX22AYDGKDYIALNEDLRSWTAADTAX23EAARX24A
 EQX25RAYLEGX26CVEWLRRYLX27NGKX28TLQRAEX29PKTHVTHHPX30SDHEATLRCWA
 LGFYPAEITLTWQX31DGEDQTQDTELVEITRPAGDGTQKWA~~AV~~X32VPSGX33EQRYTCHX34
 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.

FIG. 12

HLA-E				
GSHSLKYFHT	SVSRPGRGEP	RFISVGYVDD	TQFVRFDNDA	ASPRMVPRAP
WMEQEGSEYW	DRETRSARDT	AQIFRVNLRT	LRG <u>Y</u> YNQS <u>X1</u> A	GSHTLQWMHG
CELGPD <u>X2</u> RFL	RGYEQFAYDG	KDYLTNLNEDL	RSWTAVDT <u>AA</u>	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	EWTTGYAKAN	AQTDRVALRN	LLR <u>R</u> YNQSEA	GSHTLQGMNG
CDMGPDGRLL	RGYHQHAYDG	KDYISLNEDL	RSWTAADT <u>VA</u>	QITQRFYEA
EYAEFFRTYL	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>AA</u>	QISKRKCEAA
NVAEQRR <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	GSHSMRYFXTSVSRPGRGEPRI	IAVGYVDDTQFVRF	DSDAASQXMEPRAPWIEQEGPEYW	60
HLA-B	GSHSMRYFXTXXSRPGRGEPRI	IXVGYVDDTXFVRF	SDAXSPRXXPRAPWIEQEGPEYW	60
HLA-C	XSHSMXYFXTAVSXPRGEPXFI	IXVGYVDDTQFVXF	SDAASPRGEPXPWVEQEGPEYW	60
HLA-E	GSHSLKYFHTSVSRPGRGEPRI	ISVGYVDDTQFVRF	DNDAAAPRMVPRAPWMEQEGSEYW	60
HLA-F	GSHSLRXFSTAVSRPGRGEPRI	IAVEYVDDTQFLRF	SDAAIPRMEPREXWVEQEGPQYW	60
HLA-G	GSHSMRYFSAAVXRPGRGEPRI	IAMGXVDDXQFXRF	SDSACPRMEPRAPWVEXEGPEYW	60
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84				
HLA-A	DXXTXXXKAXSQXXRXIX	XXXXXXYNQSEKGSHTXQXMXGCDVGXD	XRFLRGYXQXAYDG	120
HLA-B	DRXTQXXKTXXTQXYXXN	LXXXXXXYNQSEAGSHXXQXMYGCDLGPD	GRLLRGHDQSAYDG	120
HLA-C	DRETQXYKRQAQXDRVXLR	XLRCGYYNQSEKXSHXXQXMXGCDXGPD	GRLLRGXXQXAYDG	120
HLA-E	DRETRSARDTAQIFRVNIR	TLRCGYYNQSXAGSHTLQWMHGCELGPD	XRFLRGYEQFAYDG	120
HLA-F	EWTTGYAKANAQTDRVAIR	NLLFRYNQSEAGSHTLQGMNGCDMGPD	GRLLRGYHQHAYDG	120
HLA-G	EEETRNTKAHAQTDRMNI	QTXRCGYYNQSEASSHTLQWMI	XCGLXRGYEQYAYDG	120
	:	*	:	**** ** * * *: * *: * * ****
	aac1		aac2	
139				
HLA-A	KDYIALXEDLRSWTAADMA	AQXTXKKWEXXXEAEQXRXYLXGXC	VXXLRRYLENGKETLQ	180
HLA-B	KDYIALNEDLXSWTAADT	AAQIXQRKXEAARXAEQXRXYLEGXC	VEWLRRYLENGKXXLX	180
HLA-C	KDYIALNEDLRSWTAADT	AAQITQRKXEAARXAEQXRAYLEGXC	VEWLRRYLXNGKXTLQ	180
HLA-E	KDYLTNLNEDLRSWTAVDT	AAQISEQKSNDAEAEHQXXYLEDTC	VEWLHKYLEKGKETLL	180
HLA-F	KDYISLNEDLRSWTAADT	VAQITQRFYEAEEYAEFFRTYLEGEC	LELLRRYLENGKETLQ	180
HLA-G	KDYIALNEDLRSWTAADT	AAQISKRKCEANVAEQRRAXLEGTC	VEWLXRXLENGKEXLQ	180
	***: *	*** *	***.*	: ** . * . *: * : * : ** *
	aac3		aac4	
236				
HLA-A	RTDXPKTHMTHHXXSDHEAT	LRCWALXFYP	AEITLTWQRDGEDQTQDTEL	VETRPAGDGTTF 241
HLA-B	RADPPKTHVTHHPXSDHEAT	LRCWALGFYP	AEITLTWQRDGEDQTQDTEL	VETRPAGDRTTF 241
HLA-C	RAEXPKTHVTHHPXSDHEAT	LRCWALGFYP	AEITLTWQXDGEDQTQDTEL	VETRPAGDGTTF 241
HLA-E	HLEPPKTHVTHHPISDHEAT	LRCWALGFYP	AEITLTWQDGEHTQDTEL	VETRPAGDGTTF 241
HLA-F	RADPPKAHVHHPISDHEAT	LRCWALGFYP	AEITLTWQRDGEETQDTEL	VETRPAGDGTTF 241
HLA-G	RADPXKTHVTHHPVFDYEAT	LRCWALGFYP	AEIILTWQXDGEDQTQDTEL	VETRPAGDGTTF 241
	:	:	* : * : * *	* : * : * : * : * : * : * : * : * : *
	aac5		aac6	
HLA-A	QKWAXVVVPSGXEQRYTCHV	QHEGLPKPLTLRWEX	-----	276
HLA-B	QKWAAVVVPSGEEQRYTCHV	QHEGLPKPLTLRWEP	-----	276
HLA-C	QKWAAVXVPSGXEQRYTCHX	QHEGLXEPLTLXWXP	-----	276
HLA-E	QKWAAVVVPSGEEQRYTCHV	QHEGLXEPVTLRWKPASQ	PTIPI	284
HLA-F	QKWAAVVVPSGEEQRYTCHV	QHEGLPQPLILRWEQSXQ	PTIPI	284
HLA-G	QKWAAVVVPSGEEQRYXCHV	QHEGLPEPLMLRWXQSSL	PTIPI	284
	**** *	*** *	**** *	**** *

28/66

FIG. 14A**1715**

APTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIS
TLT**GGGGS****GGGGS****GGGGS****GGGGS**APTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTA
KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLT**GGGGS****GGGGS****GGGGS****GGGGS**GSHSMRYFFTSVSRPGRGE
PRFIAVGYYDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRGC
YNQSEAGSHTVQORMYGCDVGSDWRFLRGYHQYAYDGKDYLKEDLRSWTAADMAAQTTKHKWEA
AHVAEQLRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEIT
LTWQRDGEDQTQDTELVEVTRPCGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE**AAAG**
GDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

hIL2 (H16A; F42A) -- underlined

(G4S)n – bold

HLA A0202 (Y84C; A236C) – double underlined

AAAGG – bold

IgG1 Fc (LALA) -- italicized

29/66

FIG. 14B

2380

VLDFAPPGAGCGGSGGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWRDM

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

G2C linker – bold

 β 2M (R12C) – underlined

FIG. 14C

2381

RMFPNAPYL**GCGGSGGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSG**
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWRDM

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

G2C linker -- bold

 β 2M (R12C) – underlined

FIG. 14D**2405**

APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIIS
TLT**GGGGS****GGGGS****GGGGS****GGGGS**APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTA
KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLT**GGGGS****GGGGS****GGGGS****GGGGS**GSHSMRYFFTSVSRPGRGE
PRFIAVGYYDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRGC
YNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEA
AHVAEQLRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFPYAEIT
LTWQRDGEDQTQDTELVETRP**AGDGT****FQKWA****AVVVP****SGQE****QRYTCHVQHEGLPKPLTLRWE****AAAG**
GDK**TH****TCPP****CPAPEA****AAGPS****SVFL****FPPKPKD****TL****MI****SR****TP****EV****TC****VV****VD****VS****HE****D****PE****V****K****F****N****W****Y****V****D****G****V****E****V**
H**N****A****K****T****K****P****R****E****E****Q****Y****N****S****T****Y****R****V****S****V****L****T****V****L****H****Q****D****W****L****N****G****K****E****Y****K****C****K****V****S****N****K****A****L****P****A****P****I****E****K****T****I****S****K****A****G****Q****P****R****E****P****Q****V****Y**
TL**PP****S****R****E****E****M****T****K****N****Q****V****S****L****T****C****L****V****K****G****F****Y****P****S****D****I****A****V****E****W****E****S****N****G****Q****P****E****N****N****Y****K****T****T****P****V****L****D****S****D****G****S****F****F****L****Y****S****K****L****T****V****D****K**
SR**W****Q****Q****G****N****V****F****S****C****S****V****M****H****E****A****L****H****N****H****Y****T****Q****K****S****L****S****L****S****P****G**

hIL2 (H16A; F42A) -- underlined

(G4S)_n – bold

HLA A0202 (Y84C) – double underlined

AAAGG – bold

IgG1 Fc (LALA) -- italicized

1380

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

32/66

FIG. 14F**2762**

VLDFAPPGAGCGGSGGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM

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

G2C linker – bold

β2M – underlined

FIG. 14G**2763**

RMFPNAPYLGCGGSGGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM

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

G2C linker – bold

β2M – underlined

FIG. 14H**3625**

YMFPNAPYLGCGGSGGGGSGGGGSIQRTPKIQVYSCHPAENGKSNFLNCYVSG
FHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNH
VTLSQPKIVKWDRDM

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

G2C linker – bold

β2M (R12C) – underlined

33/66

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
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 = unfornulated, PBS + 365 mM NaCl, pH 7.4

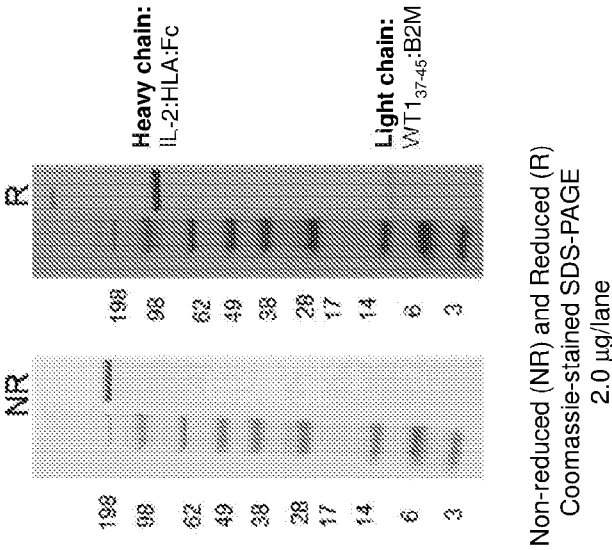
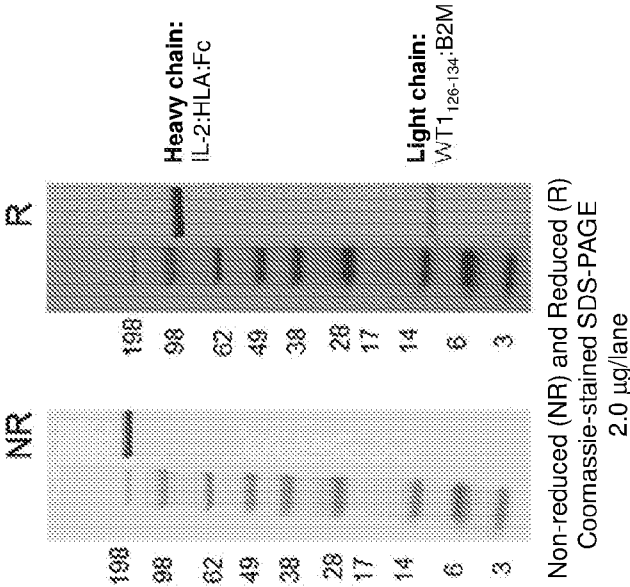


FIG. 16

	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
Tm (°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 = unfornulated, PBS + 365 mM NaCl, pH 7.4



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

FIG. 17A

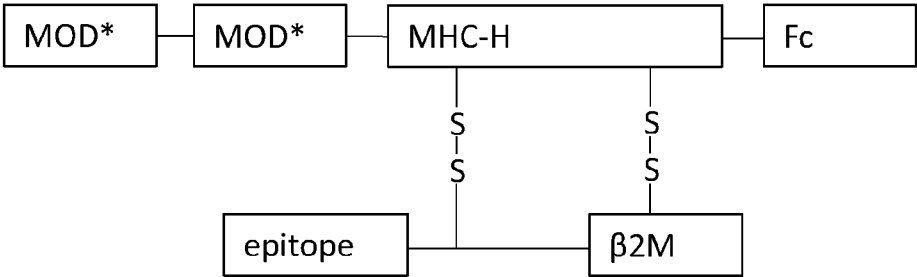


FIG. 17B

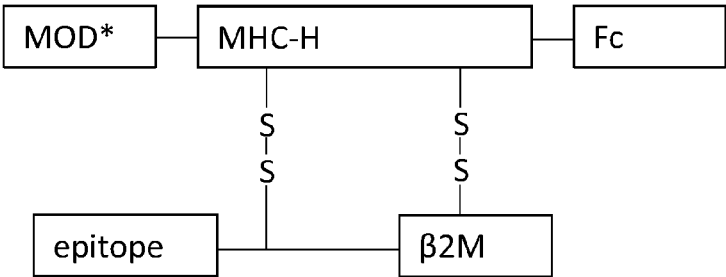


FIG. 17C

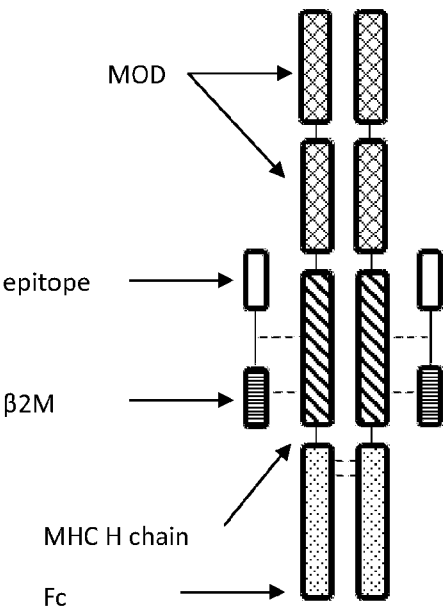


FIG. 17D

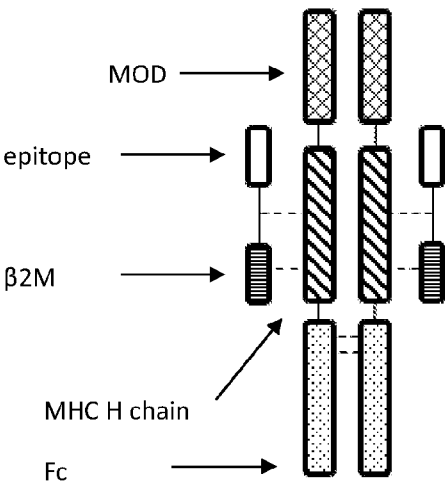


FIG. 18A

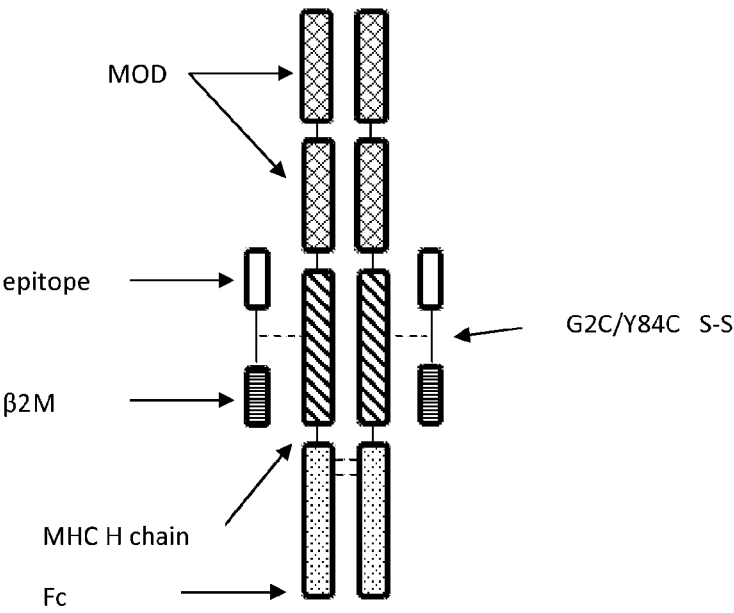


FIG. 18B

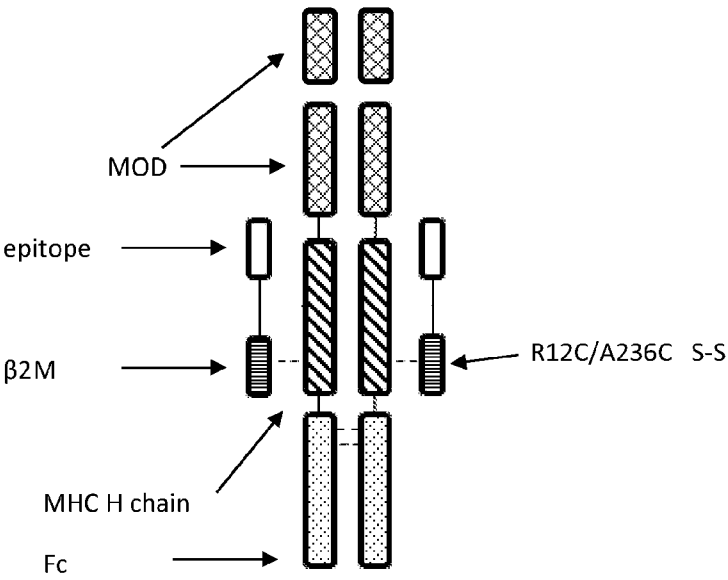
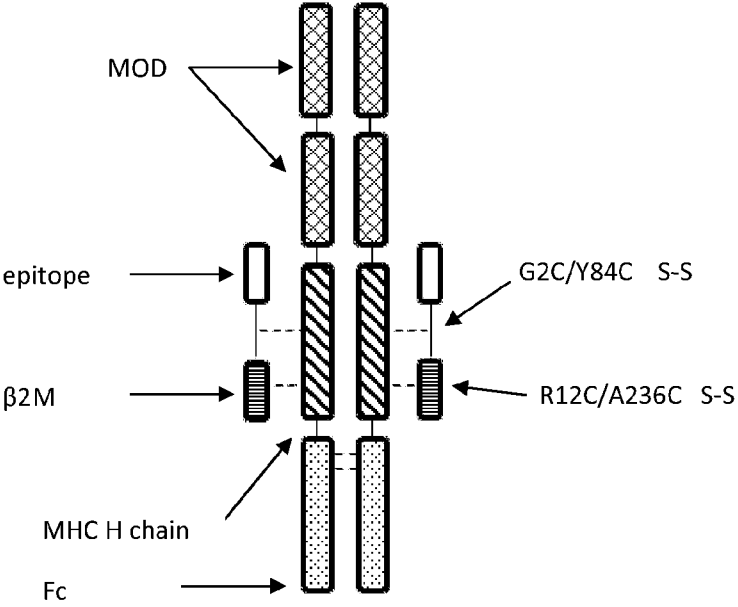


FIG. 18C



40/66

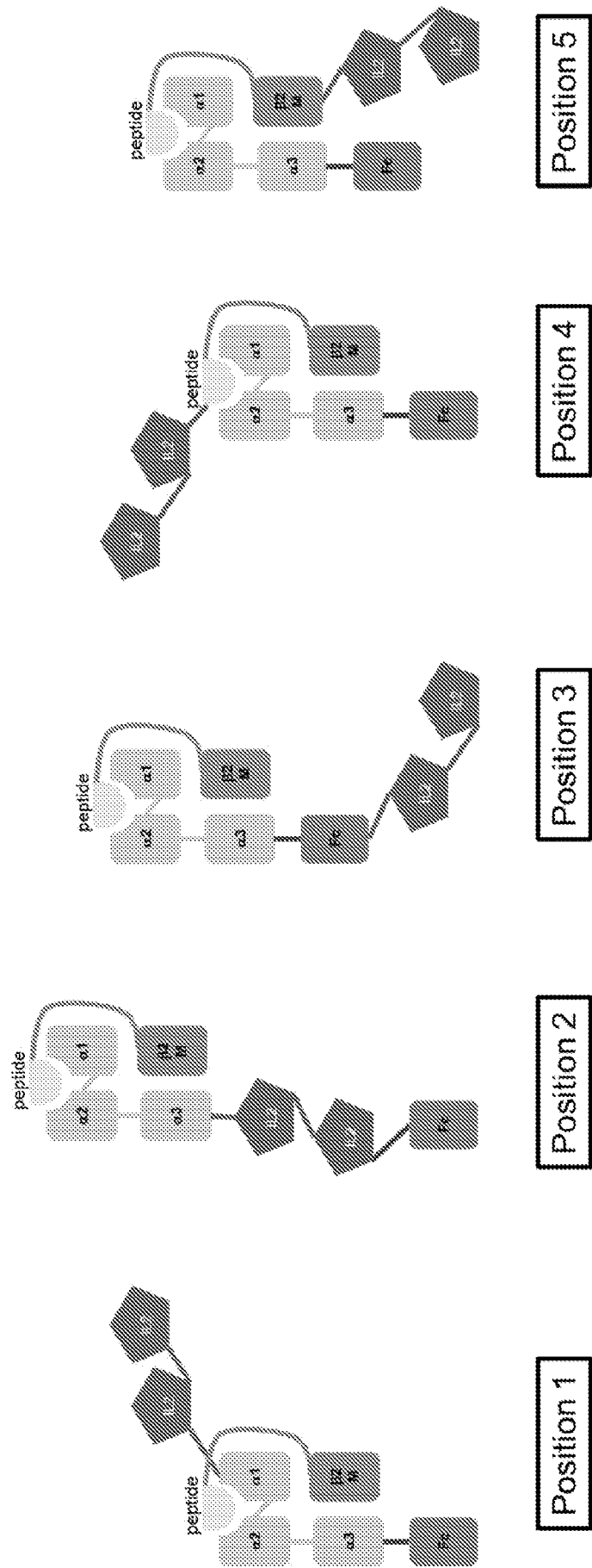


FIG. 19

FIG. 20A

3592

APTSSSTKKTQLQLE**A****ALLDLQMILNGINNYKNPKLTRMLT****A****KFYMPKKAT**
ELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFM
CEYADETATIVEFLNRWITFCQSIISTLT**TGGGGSGGGGSGGGGSGGGGSAPTSS**
STKKTQLQLE**A****ALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKH**
LQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYA
DETATIVEFLNRWITFCQSIISTLT**TGGGGSGGGGSGGGGSGGGGSGSHSMRYFS**
TSVSRPGRGEPRIA**VG****YVDDTQFVRFDSDAASQRM****EP****APWIEQEGPEYWDEE**
TGKVKAHSQTDRENLR**IALRCYNQSEAGSHTLQMMFGCDVGSDGRFLRGYHQY**
AYDGKD**YIALKEDLR****SWTAADMAAQITKRKWEAAHVAEQORAYLEGTCVDGL**
RRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWORDGE
DQTQDTEL**VE****TRPCGDGTFQKWA****AVVVP****SGEEQRYTCHVQHEGLPKPLTLRWE**
AAAGGDKTHTC**PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS**
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL
VKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPG

IL-2 (H16A; F42A) – bold

(G4S)₄ – underlined

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20B

3425

GSHSMRYFSTSVSRPGRGEPREIAVG YVDDTQFVREDSDAASQORMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRIALRCYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWQRDGEDQTQDTELVETRPCGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWE**AAAGGDK**THTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSSGSFFLYSKLTVD
KSRWQOGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGGGGSAPT
SSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELK
HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAPTSSSTK
KTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQC
LEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
ATIVEFLNRWITFCQSIISTLT

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

AAAGG linker – bold and italicized

hlgG1 Fc (L234A; L235A) – bold and underlined

(G4S)₃ and (G4S)₄ – underlined

IL-2 (H16A; F42A) – bold

FIG. 20C

3196

GSHSMRYFSTSVSRPGRGEPRFIAVGYVDDTQFVRFSDSDAASQRMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRIALRCYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWQRDGEDQTQDTELVETRPCGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWE***AAAGGDK***THTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQOGNVFSCSVMHEALHNHYTQKSLSLSPG

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20D

2764

GSHSMRYFSTSVSRPGRGEPREIAVG YVDDTQFVREDSDAASQRMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRIALRAYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWQRDGEDQTQDTELVETRPCGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP
KPLTLRWE**AAAGGDK**THTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

FIG. 20E

3593

APTSSSTKKTQLQLE**A****ALLDLQMILNGINNYKNPKLTRMLT****A****KFYMPKKAT**
ELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFM
CEYADETATIVEFLNRWITFCQSIISTLT**TGGGGSGGGSGGGSGGGGSAPTSS**
STKKTQLQLE**A****ALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKH**
LQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYA
DETATIVEFLNRWITFCQSIISTLT**TGGGGSGGGSGGGSGGGSGSHSMRYFS**
TSVSRPGRGEPREFIAVGYYDDTQFVRESDAASQRMERAPWIEQEGPEYWDEE
TGKVKAHSQTDRENLRALRCYNQSEAGSHTLQMMFGCDVGSDGRELRGYHQY
AYDGKDYLKEDLRSWTAADMAAQITKRKWEAAHVAEQORAYLEGTCVDGL
RRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWORDGE
DQTQDTELVETRPAGDGTQKWA**AVVVP****SGEEQRYTCHVQHEGLPKPLTLRWE**
AAAGG**DKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS**
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL
VKGFYP**SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ**
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

GSHSMRYFSTSVSRPGRGEPREIAVG YVDDTQFVREDSDAASQORMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRIALRCYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQRAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWQRDGEDQTQDTELVETRPAGDGTFOKWAAVVVPSGEEQRYTCHVOHEGLP
KPLTLRWEAAAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQOGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGGGGSAPT
SSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELK
HLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEY
ADETATIVEFLNRWITFCQSIISTLTGGGGSGGGGSGGGGSGGGGSAPTSSSTK
KTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQC
LEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
ATIVEFLNRWITFCQSIISTLT

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

AAAGG linker – bold and italicized

hlgG1 Fc (L234A; L235A) – bold and underlined

(G4S)₃ and (G4S)₄ – underlined

IL-2 (H16A; F42A) – bold

47/66

FIG. 20G

3197

GSHSMRYFSTSVSRPGRGEPREIAVGYYVDDTQFVREDSDAASQORMEPRAPWIEQE
GPEYWDEETGKVKAHSQTDRENLRALRCYNQSEAGSHTLQMMFGCDVGSDGR
FLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQITKRKWEAAHVAEQQRAYL
EGTCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITL
TWQRDGEDQTQDTELVETRPAGDGTFOKWA AVVVPSGEEQRYTCHVOHEGLP
KPLTLRWEAAAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

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

AAAGG linker – bold and italicized

hIgG1 Fc (L234A; L235A) – bold and underlined

48/66

FIG. 20H**3188**

CYTWNQMNLGCGGSGGGGSGGGGSI*QRTPKIQVYSCHPAENGKSNFLNCYVSGFH*
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
KIVKWDRDM

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

FIG. 20I**3604**

CYTWNQMNLGCGGSGGGGSGGGGSI*QRTPKIQVYSCHPAENGKSNFLNCYVSGFH*
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
*KIVKWDRDM*GGGGSGGGGSGGGGS**A**P**TSSSTKKTQLQLE**A**LLLDLQMILNGIN**
NYKNPKLTRMLTA**KFYMPKKATELKHLQC**LEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGGSGGGGSGGGGSA**P**TSSSTKKTQLQLE**A**LLLDLQMILNGIN**NYKN**
PKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH**LRPR**
DLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

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

49/66

FIG. 20J

3603

CYTWNQMNLGGGGSGGGGSGGGGS*IQRTPKIQVYSCH*PAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDMGGGGSGGGGSGGGGSAPTSSSTKKTQLQLE**A**LLLDLQMILNGIN
NYKNPKLTRMLT**A**KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT**G**
GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLE**A**LLLDLQMILNGINNYKN
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

CYTWNQMNLGCGGSGGGGSGGGGS*IQRTPKIQVYSR*HPAENGKSNFLNCYVSGFH
 PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
 KIVKWDRDM

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

50/66

FIG. 20L

3605

CYTWNQMNLGCGGSGGGGSGGGGS*IQRTPKIQVYSRHPAENGKSNFLNCYVSGFH*
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
*KIVKWDRDMGGGSGGGGSGGGGS***APTSSSTKKTQLQLEALLDLQMILNGIN**
NYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
GGGSGGGGSGGGGSGGGGS**APTSSSTKKTQLQLEALLDLQMILNGINNYK**
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

NYMNLGATLGCGGSGGGGSGGGGS*IQRTPKIQVYSCHPAENGKSNFLNCYVSGFH*
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
KIVKWDRDM

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

51/66

FIG. 20N

3709

NYMNLGATLGCGGSGGGGSGGGGSI*QRTPKIQVYSCHPAENGKSNFLNCYVSGFH*
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
*KIVKWDRDMGGGSGGGGSGGGGS***APTSSSTKKTQLQLE****A****LLLDLQMILNGIN**
NYKNPKLTRMLT**A****KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH**
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT**G**
GGGSGGGGSGGGGSGGGGS**APTSSSTKKTQLQLEALLLDLQMILNGINNYKN**
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

52/66

FIG. 20P

3708

NYMNLGATLGGGGSGGGSGGGGSI*QRTPKIQVYSCHPAENGKSNFLNCYVSGFH*
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
*KIVKWDRDMGGGGSGGGSGGGGS*APTSSSTKKTQLQLE**A**ALLDLQMILNGIN
NYKNPKLTRMLTA**KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFH**
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPK
LTRMLTAKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN
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

NYMNLGATLGCGGSGGGSGGGGSI*QRTPKIQVYSRHPAENGKSNFLNCYVSGFH*
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
KIVKWDRDM

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

FIG. 20R

3710

NYMNLGATLGCGGSGGGGSGGGGSI*QRTPKIQVYSRHPAENGKSNFLNCYVSGFH*
PSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSP
*KIVKWDRDMGGGSGGGGSGGGGS***APTSSSTKKTQLQLE**A**LLLDLQMILNGIN**
NYKNPKLTRMLTA**KFYMPKKATELKHLQC****LEEELKPLEEVLNLAQSKNFH**
LRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGGSGGGGSGGGGS**APTSSSTKKTQLQLE****A****LLLDLQMILNGINNYKN**
PKLTRMLTAKFYMPKKATELKHLQC**LEEELKPLEEVLNLAQSKNFHLRPR**
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

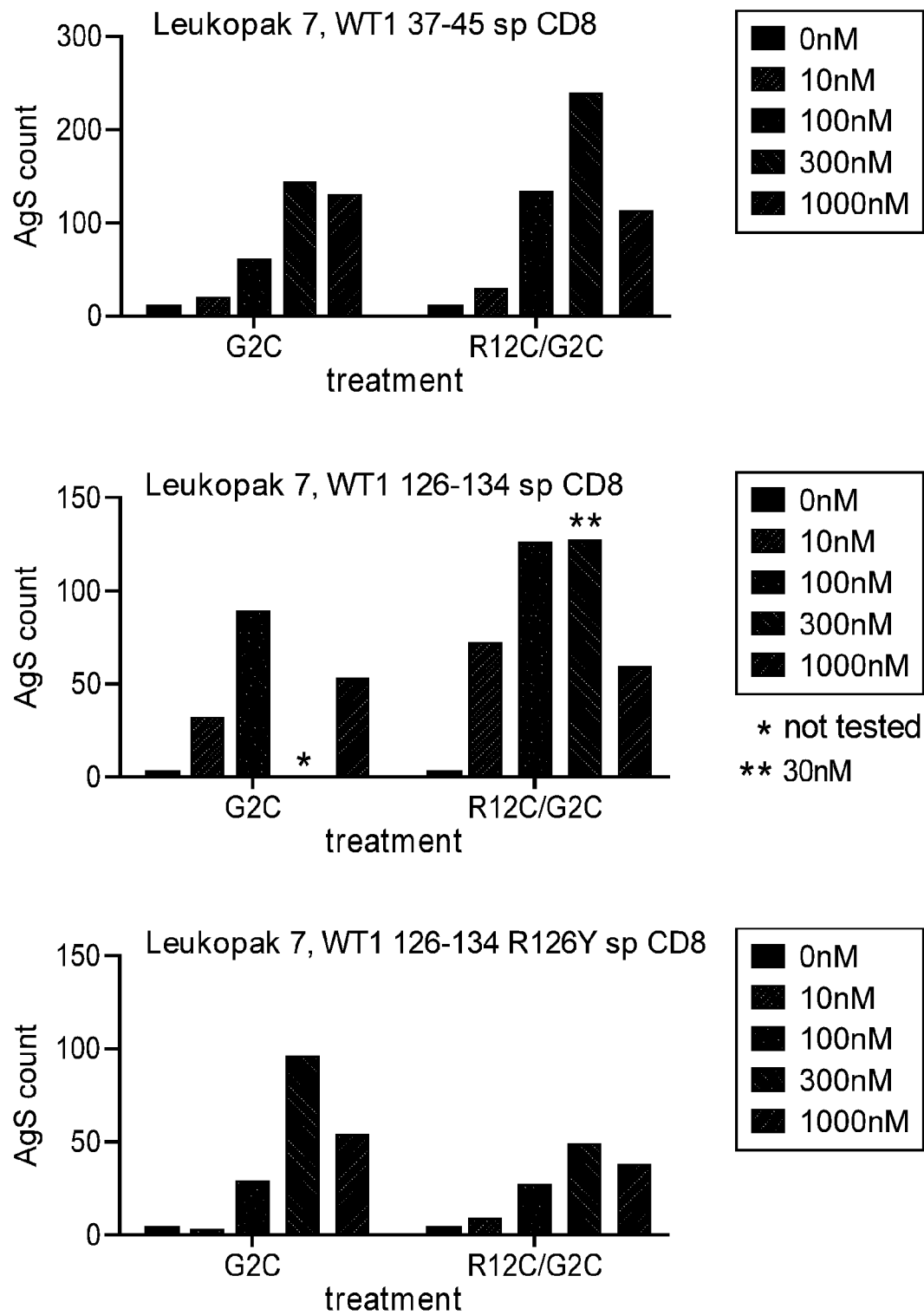
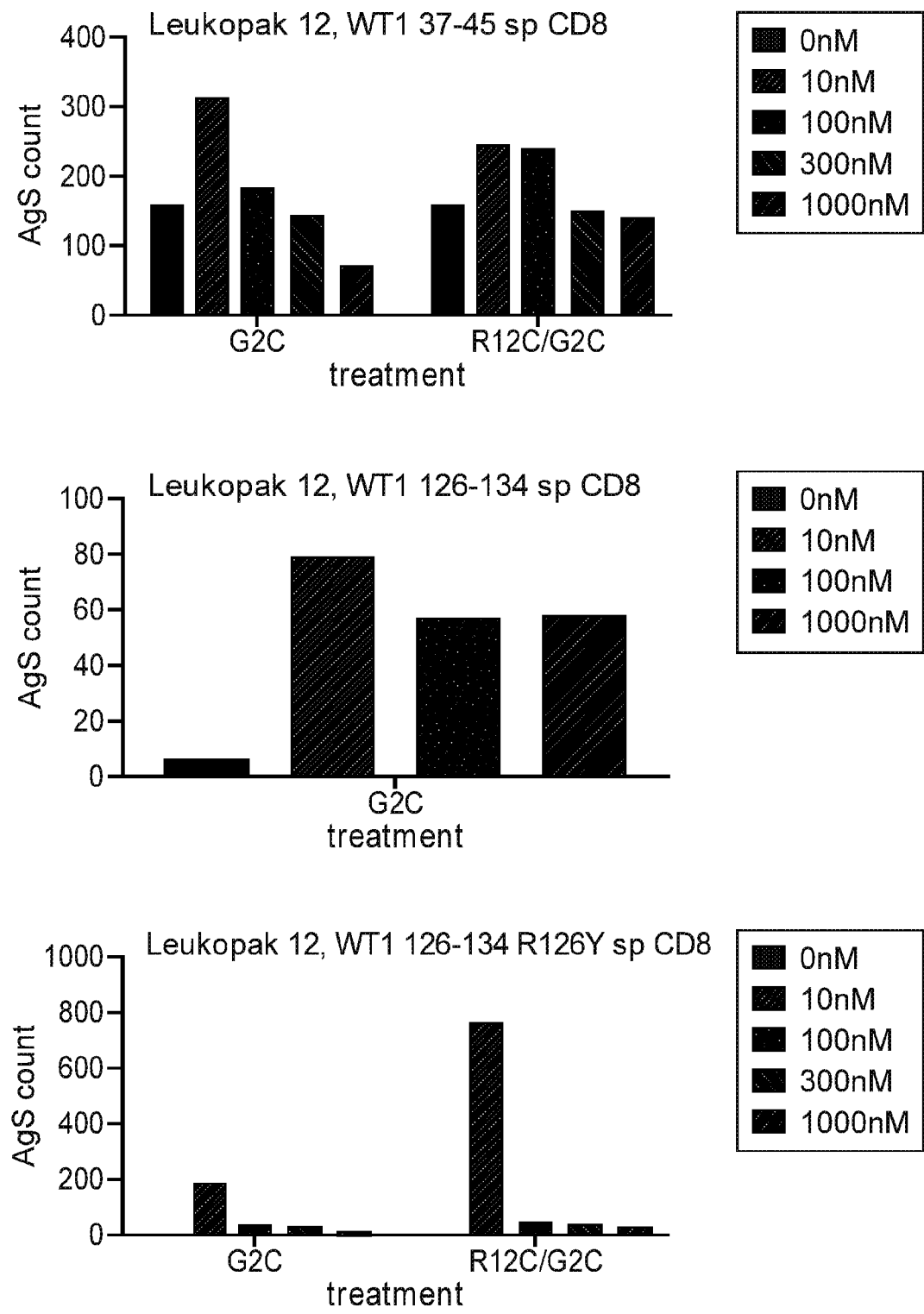
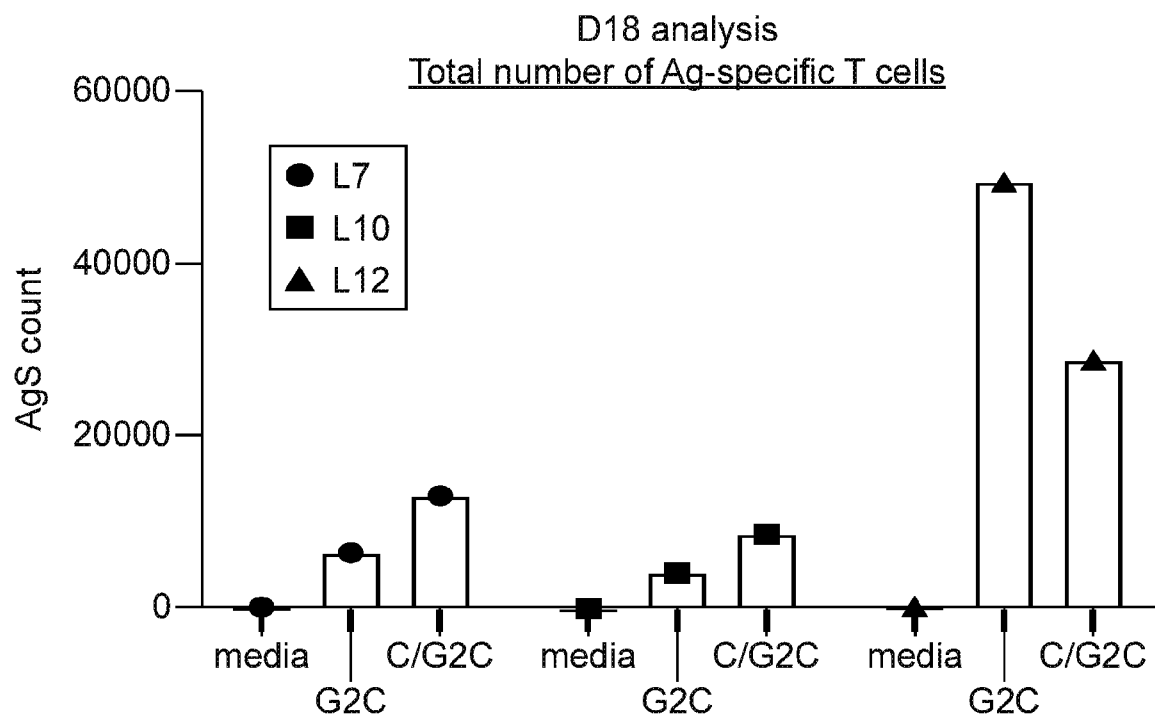
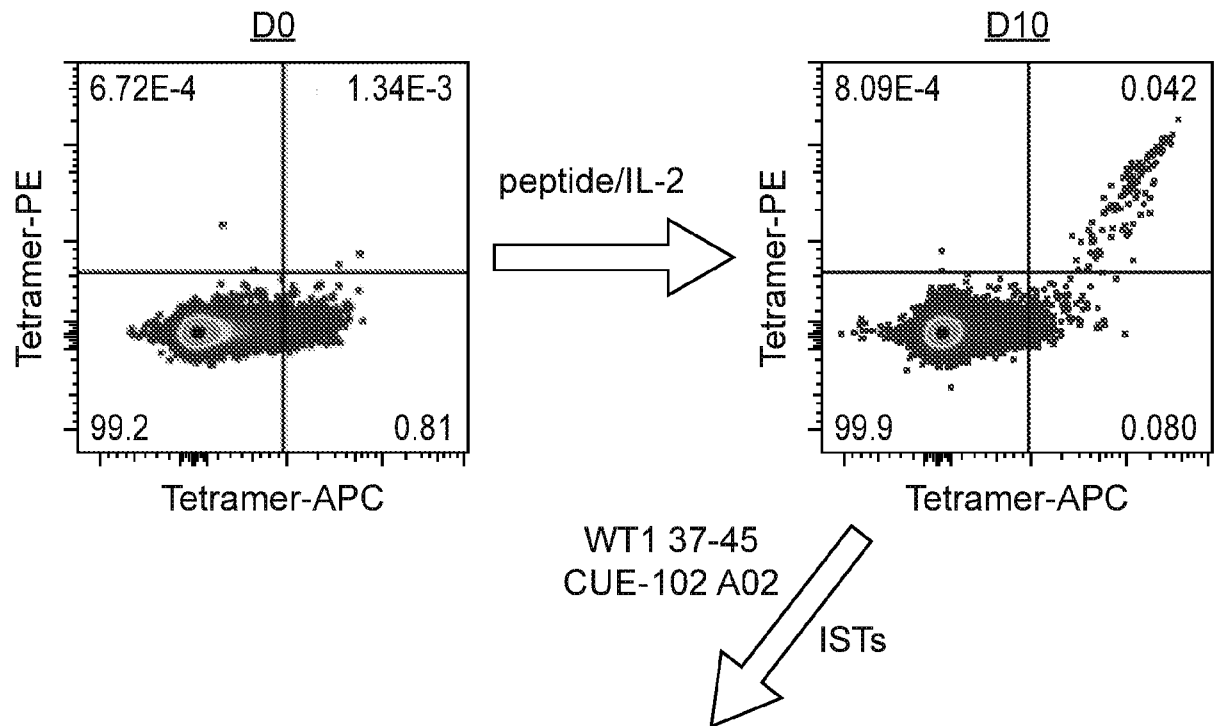


FIG. 21 (Cont.)



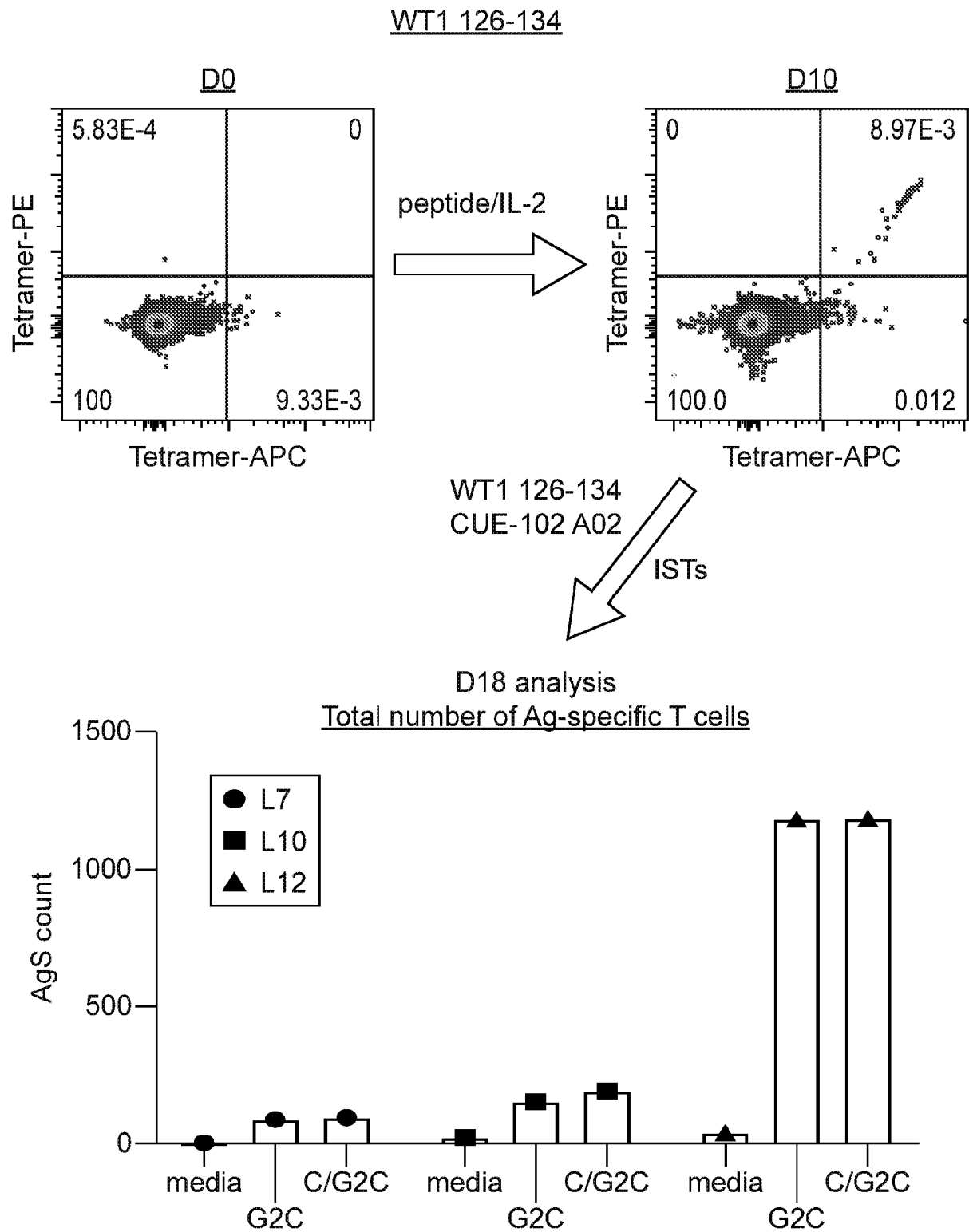
56/66

FIG. 22

WT1 37-45

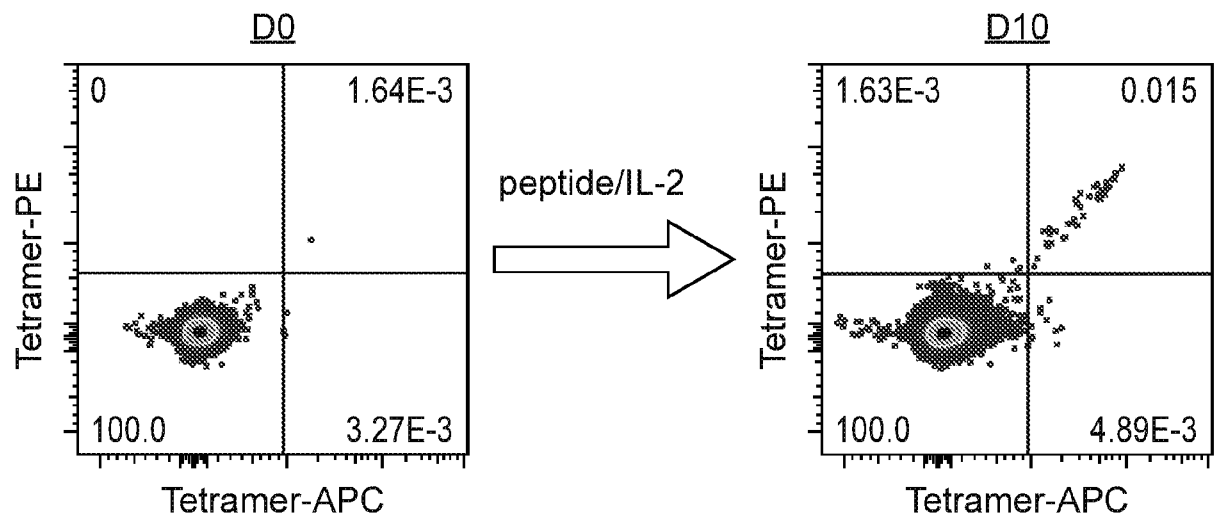
57/66

FIG. 22 (Cont.)



58/66

FIG. 22 (Cont.)

WT1 126-134 R126Y

WT1 126-134 R126Y
CUE-102 A02

ISTs

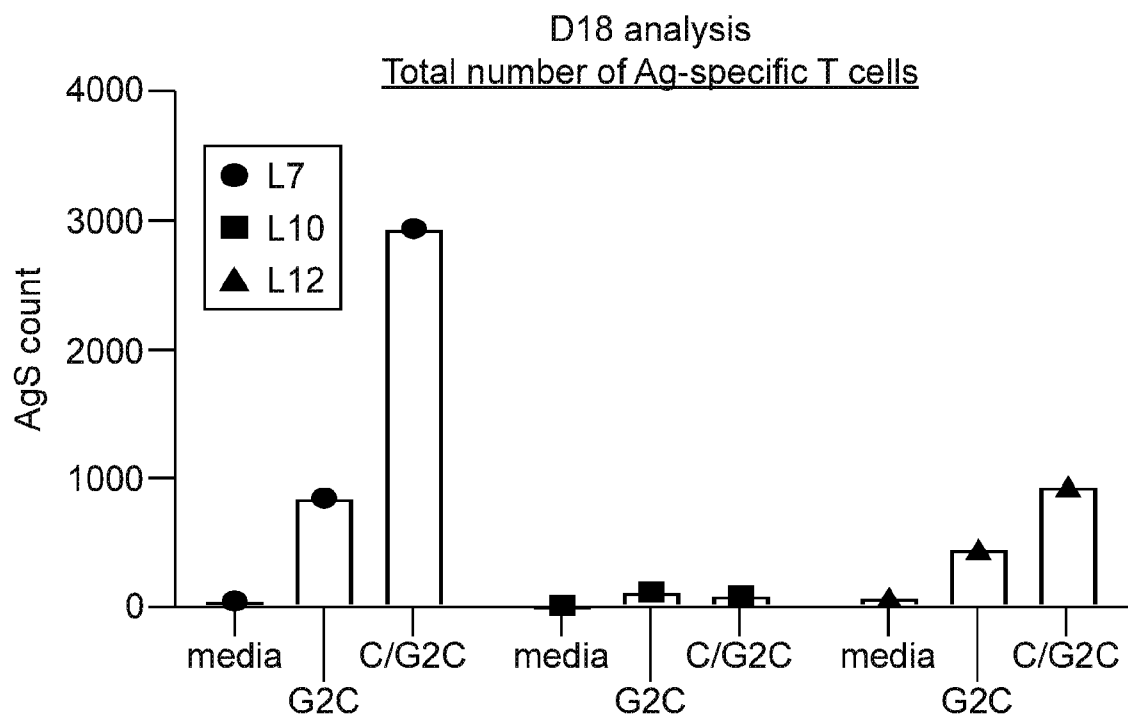


FIG. 23

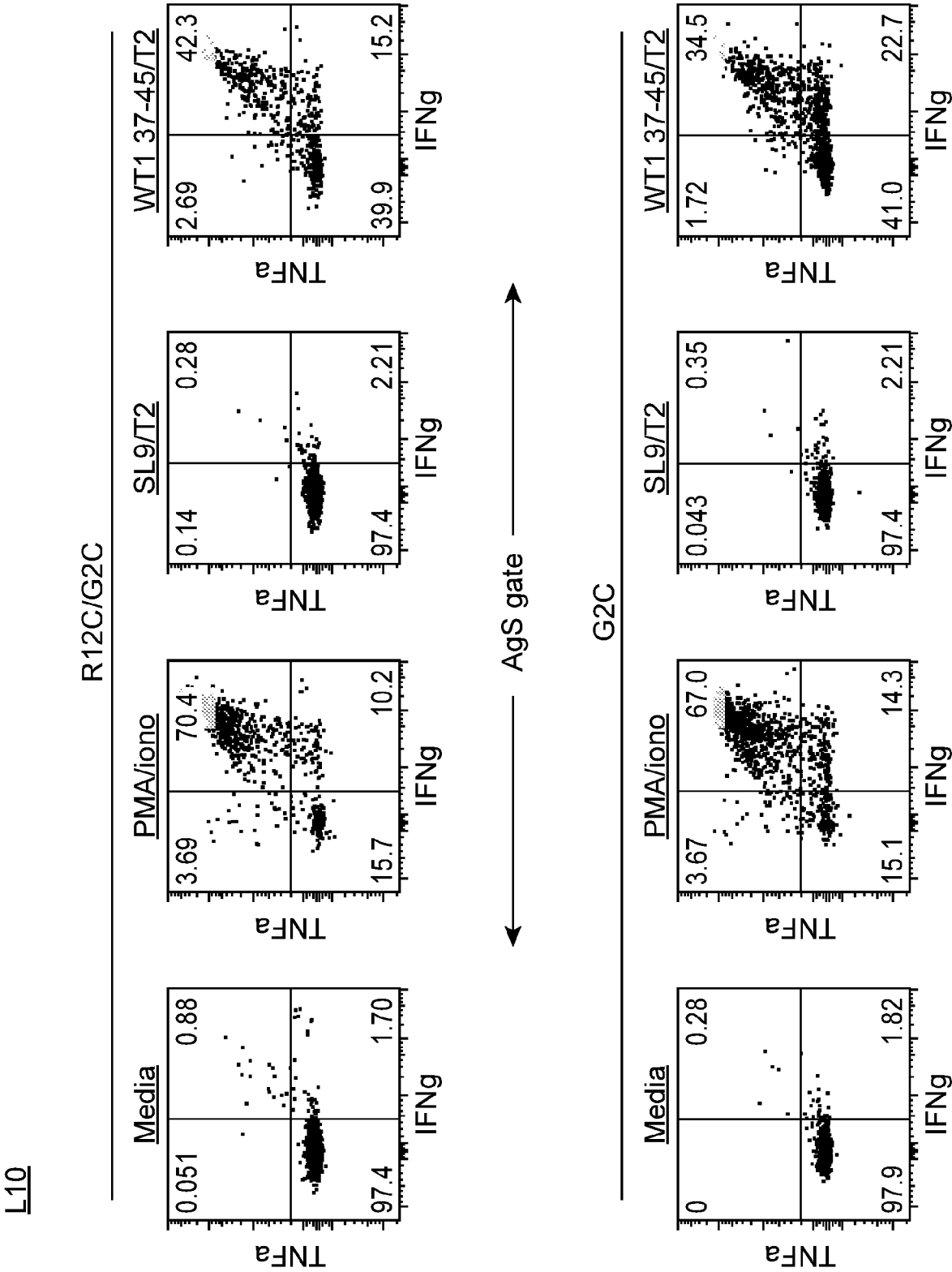
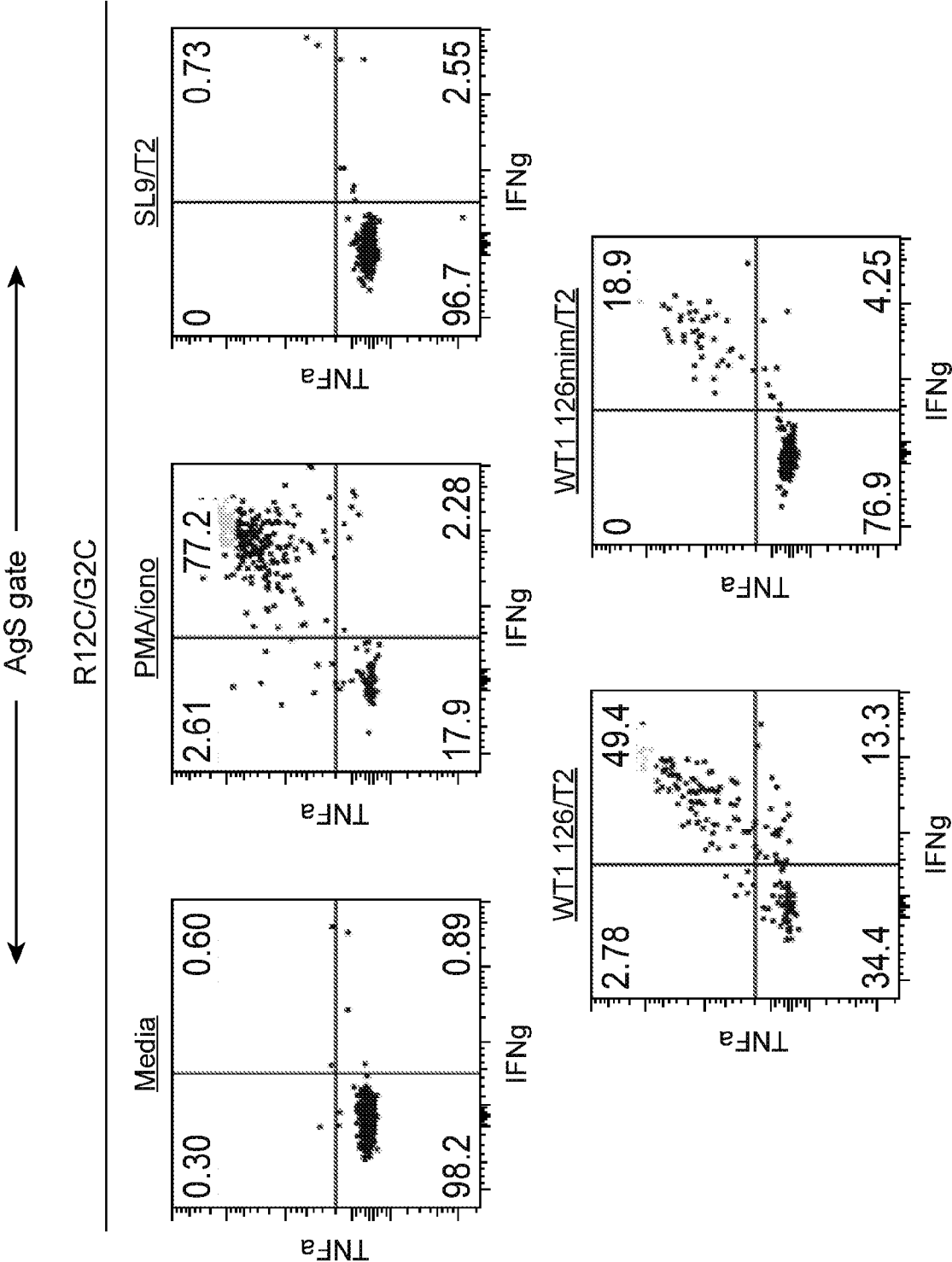


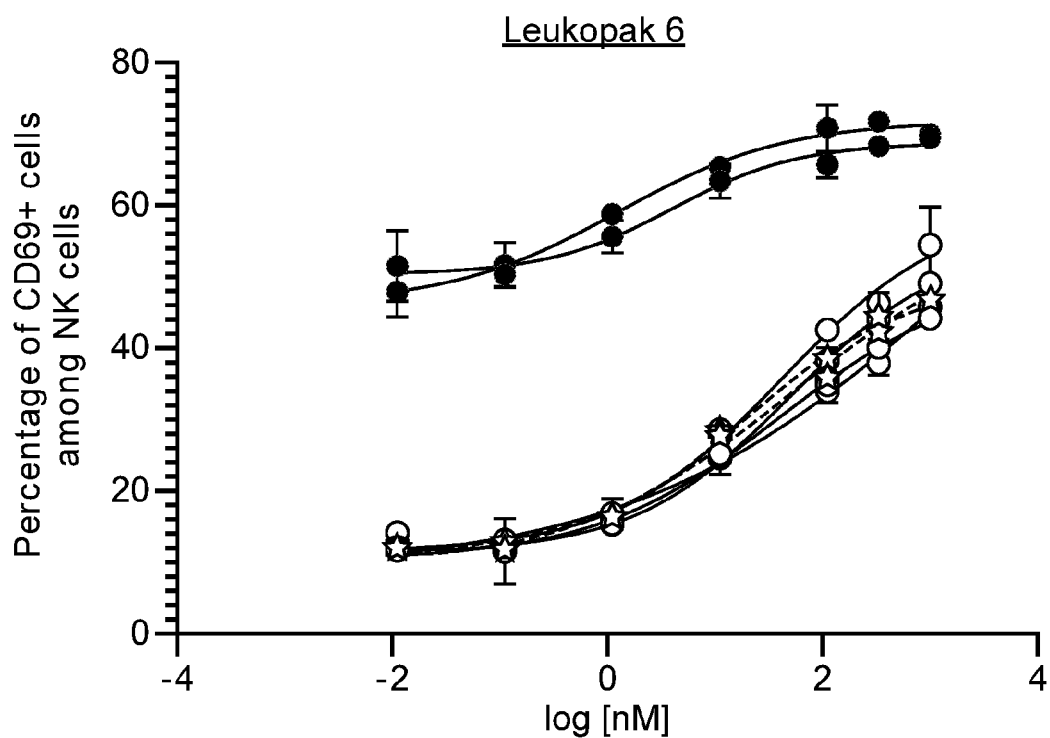
FIG. 24

L10



61/66

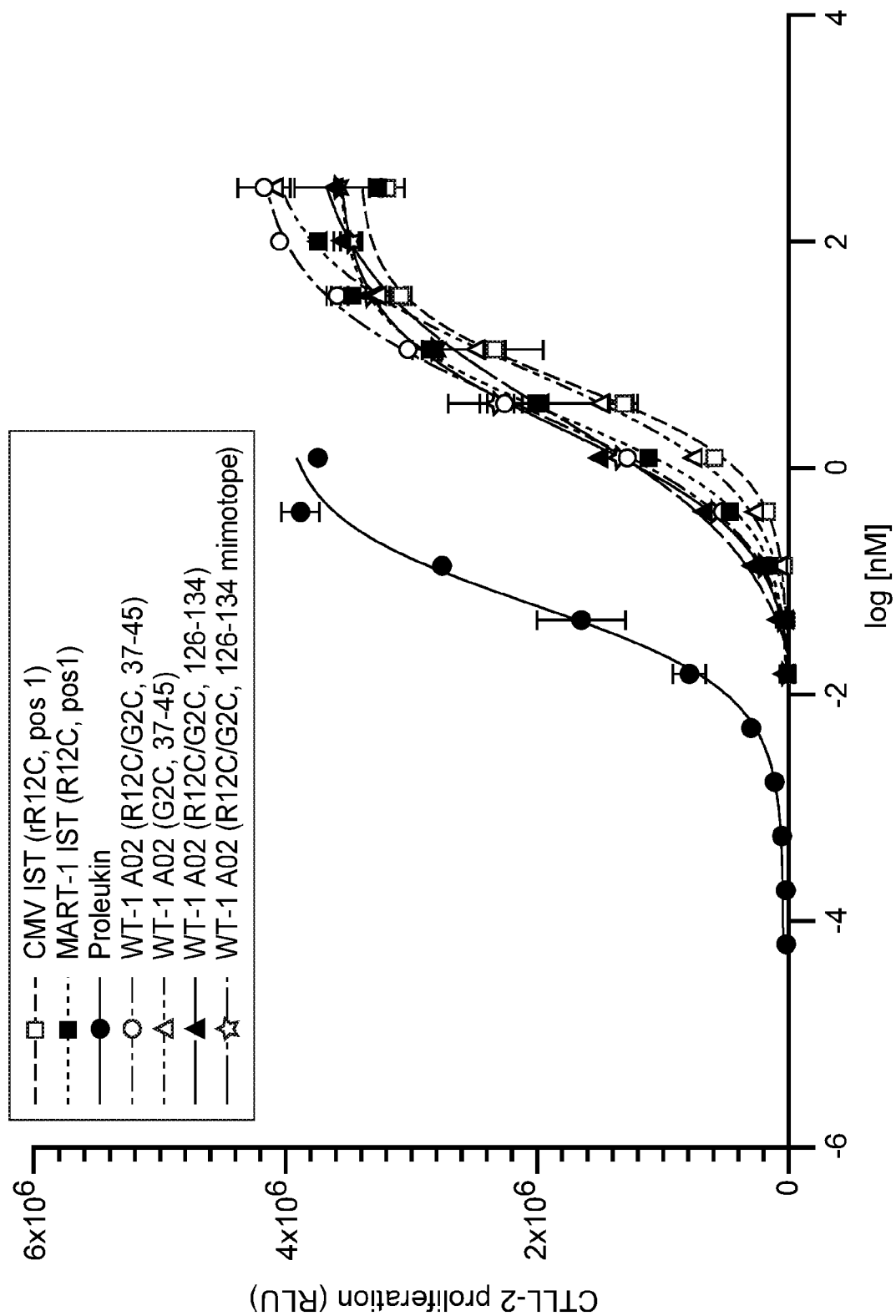
FIG. 25



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

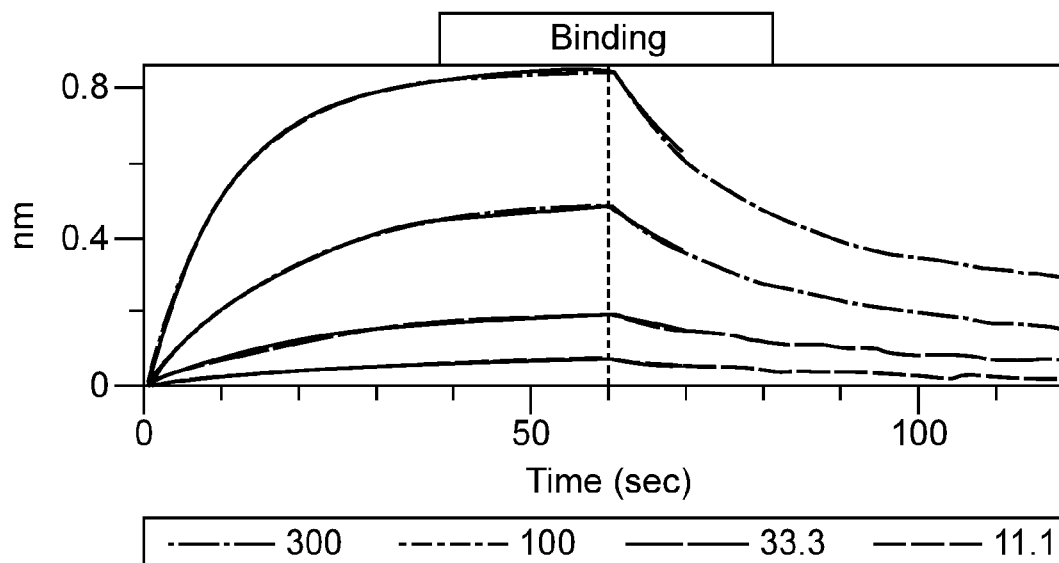


63/66

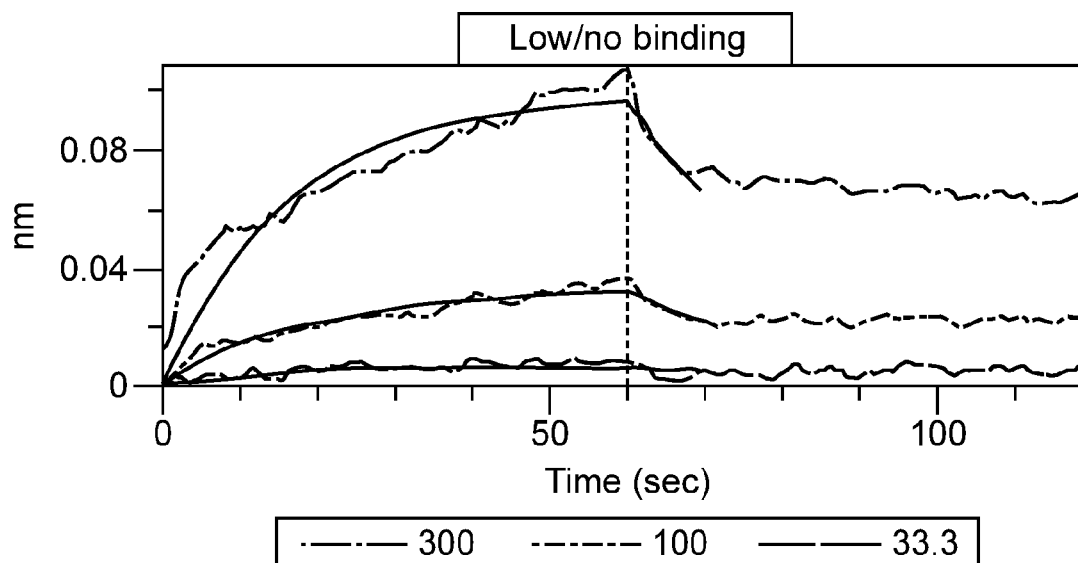
FIG. 27

37-45 double disulfide

Loading Sample ID: FcRI: Sample ID: 1715-2380-005:
KD (M): $1.674\text{E-}07$ - by Conc. (nM)



Loading Sample ID: FcRIIIA-F: Sample ID:
1715-2380-005: KD (M) $6.209\text{E-}07$ - by Conc. (nM)

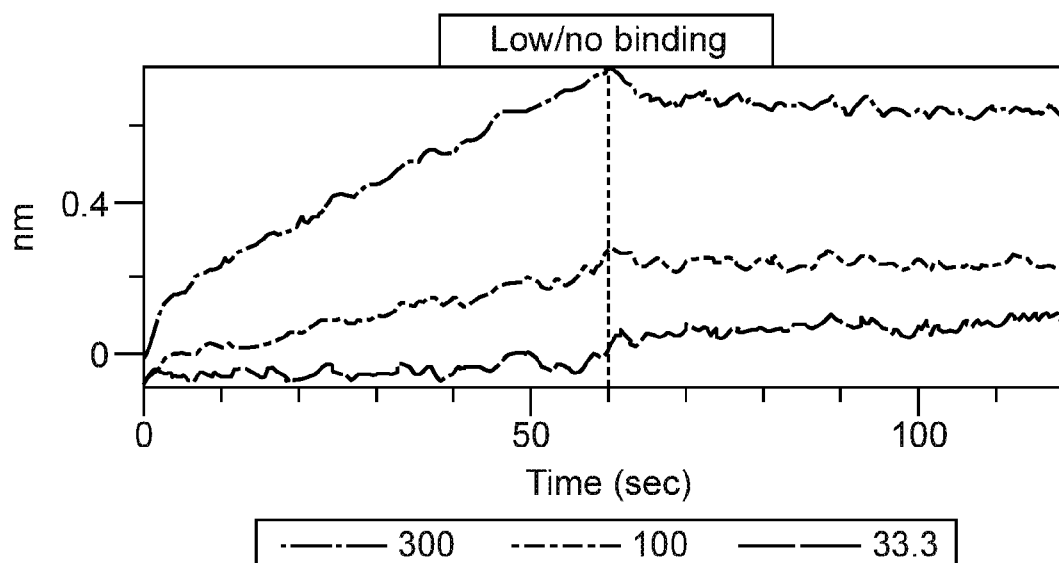


64/66

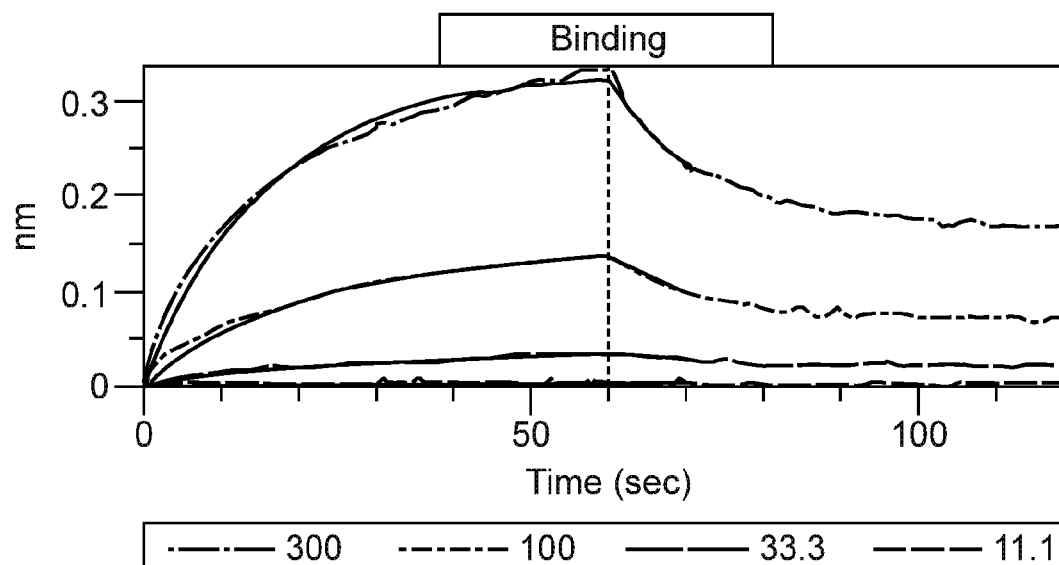
FIG. 27 (Cont.)

37-45 double disulfide

Loading Sample ID: FcRIIA: Sample ID:
1715-2380-005 - by Conc. (nM)



Loading Sample ID: FcRIIIA-V: Sample ID:
1715-2380-005: KD (M) 3.458E-07 - by Conc. (nM)

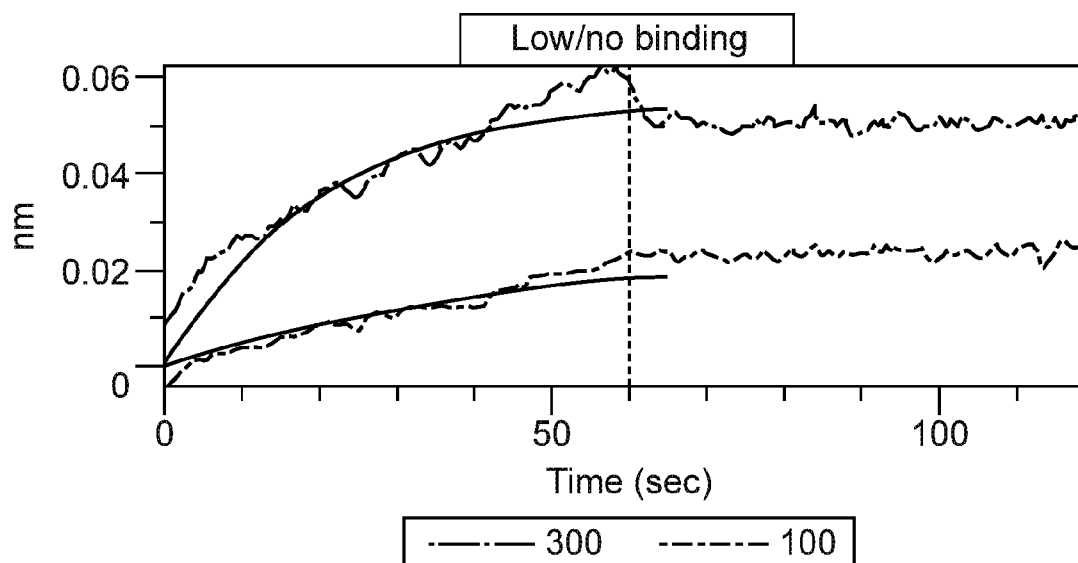


65/66

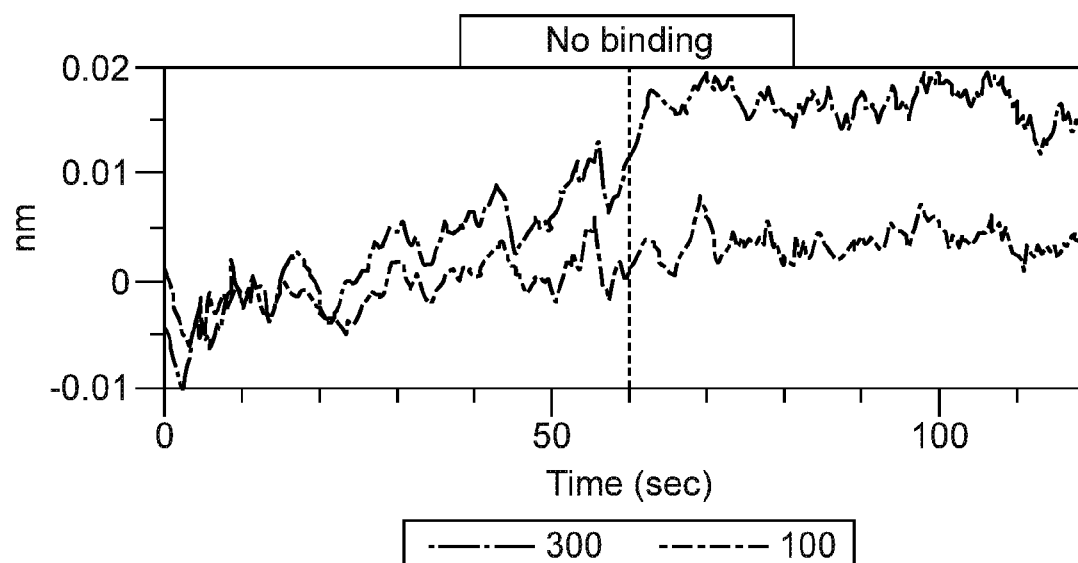
FIG. 27 (Cont.)

37-45 double disulfide

Loading Sample ID: FcRIIB: Sample ID:
1715-2380-005: KD (M) <1.0E-12 - by Conc. (nM)

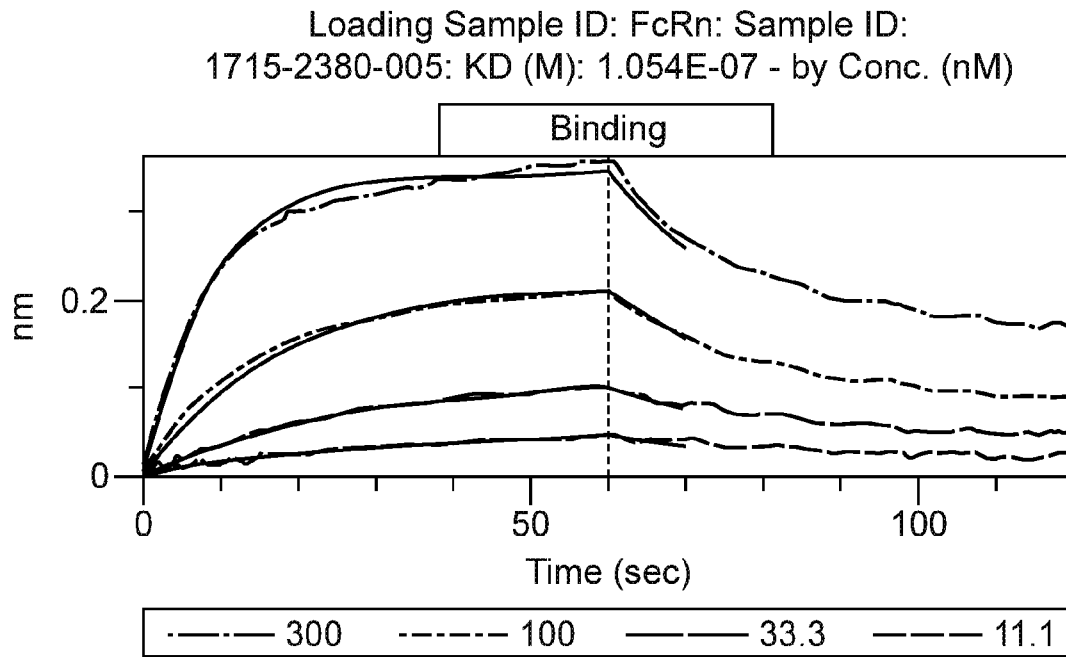


Loading Sample ID: FcRIIB: Sample ID:
1715-2380-005 - by Conc. (nM)



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