

FIG. 1

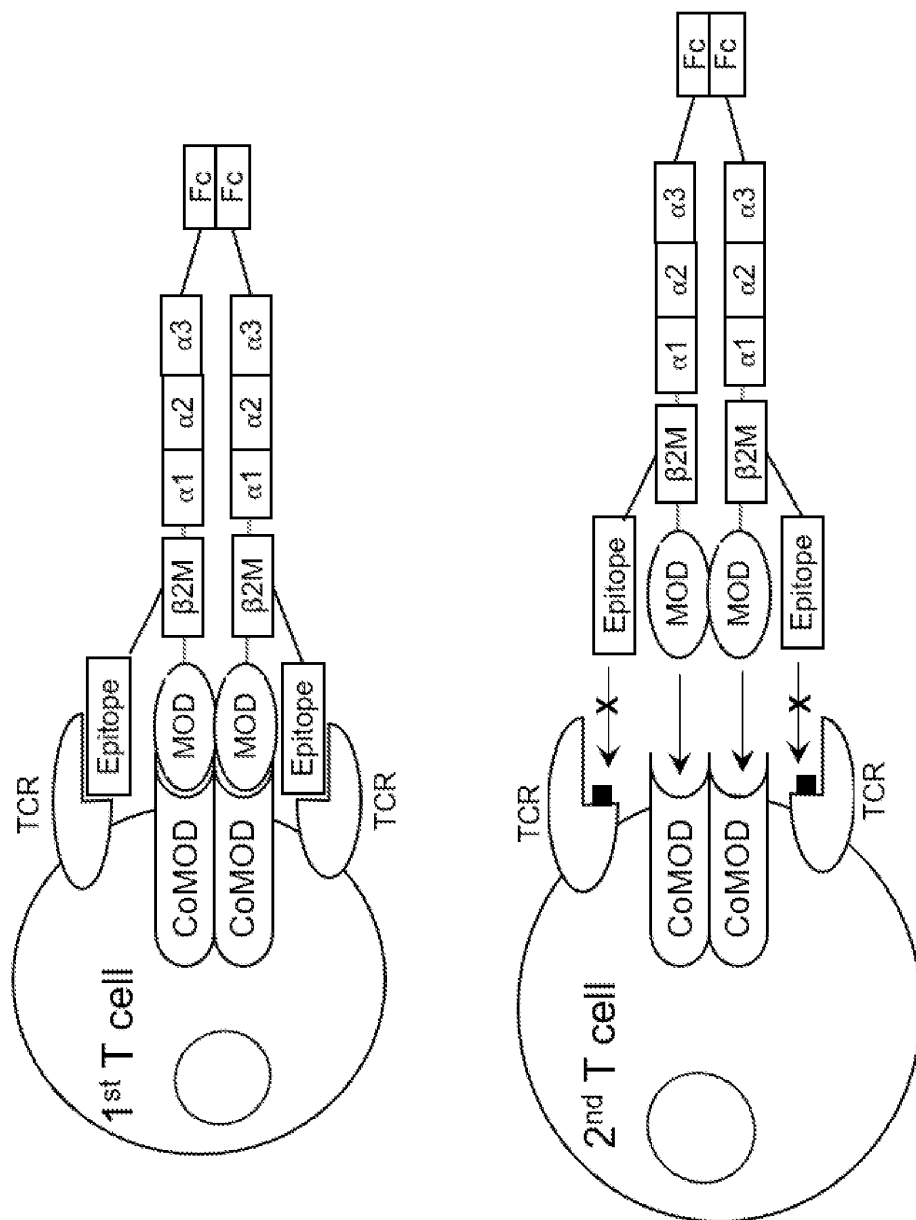


FIG. 2A***Homo sapiens* IgA (partial sequence) GenBank P01876 (SEQ ID NO:1)**

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1   ASPTSPVFPP LSLCSTQPDG NVVIACLVQG FFPQEPLSVT WSESGQGVTA RNFPPSQDAS
61  GDLYTTSSQL TLPATQCLAG KSVTCHVKHY TNPSQDVTVP CPVPSTPPTP SPSTPPTPSP
121 SCCHPRLSLH RPALEDLLLG SEANLTCTLT GLRDASGVTF TWTPSSGKSA VQGPPERDLC
181 GCYSVSSVLP GCAEPWNHGK TFTCTAAYPE SKTPLTATLS KSGNTFRPEV HLLPPPSEEL
241 ALNELVTLTC LARGFSPKDV LVRWLQGSQE LPREKYLTWA SRQEPSQGT TFAVTSILRV
301 AAEDWKKGDT FSCMVGHEAL PLAFTQKTID RLAGKPTHVN VSVVMAEVDG TCY

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CH1 aas 6-98, Hinge aas 99-121, CH2 aas 122-219, CH3 aas 220-253, (Fc aas 124-353, 210 aa)

FIG. 2B***Homo sapiens* IgD (partial sequence) GenBank AAA52770 (SEQ ID NO:2)**

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1   PTKAPDVFP I ISGCRHPKDN SPVVLACLIT GYHPTSVTVT WYMGTSQSPQ RTFPEIQRRD
61  SYYMTSSQLS TPLQWRQGE YKCVVQHTAS KSKKEIFRWP ESPKAQASSV PTAQPQAECS
121 LAKATTAPAT TRNTGRGGEE KKKEKEKEEQ EERETKTPEC PSHTQPLGVY LLTPAVQDLW
181 LRDKATFTCF VVGSDLKDAH LTWEVAGKVP TGGVEEGLLE RHSNGSQSQH SRLTLPRSLW
241 NAGTSVTCTL NHPSLPPQRL MALREPAAQA PVKLSLNL LA SSDPPEAASW LLCEVSGFSP
301 PNILLMWLED QRENTSGFA PARPPPQRS TTFWAWSVLR VPAPPSPQPA TYTCVVSHE
361 SRTLLNASRS LEVSYVTDHG PMK

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CH1 aas _1-97, Hinge aas 98-161, CH2 aas 162-267, CH3 aas 268-383 (Fc aas 162-383, 222 aas)

FIG. 2C***Homo sapiens* IgE (partial sequence) GenBank 1F6A_B (SEQ ID NO:3) 217**

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1   ADPCDSNPRG VSAYLSRPSP FDLFIRKSPT ITCLVVDLAP SKGTVNLTWS RASGKPVNHS
61  TRKEEKQRNG TLTVTSTLPV GTRDWIEGET YQCRVTHPHL PRALMRSTTK TSGPRAAPEV
121 YAFATPEWPG SRDKRTLACL IQNFMPEDIS VQWLHNEVQL PDARHSTTQP RKTGSGGFFV
181 FSRLEVTRA EWEQKDEFICR AVHEAASPSQ TVQRAVSVNP GK

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CH2 aas 5-114, CH3 aas 113-222 (Fc aas 6-222, 217aas)

FIG. 2D

WT. Homo sapiens IgG1 (partial sequence) (SEQ ID NO:4)

1 DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
 61 GVEVHNAKTK PREEQYNSTY RVVSVLTIVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK
 121 GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS
 181 DGSFFLYSKL TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK

Hinge aas 1-10, CH2 aas 11-120, CH3 aas 121-227 (Fc aas 11-227, 217 aas)

Homo sapiens IgG1 (partial sequence) Fc GenBank 3S7G_A (SEQ ID NO:5)

1 DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
 61 GVEVHNAKTK PREEQYNSTY RVVSVLTIVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK
 121 GQPREPQVYT LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS
 181 DGSFFLYSKL TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK

Hinge aas 1-10, CH2 aas 11-120, CH3 aas 121-227 (Fc aas 11-227, 217 aas)

Homo sapiens IgG1 (partial sequence) Fc Mutant: L234F/L235E/P331S (Triple Mutant "TM") (SEQ ID NO:6)

DKTHTCPPCP APE**FE**GGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
 GVEVHNAKTK PREEQYNSTY RVVSVLTIVLH QDWLNGKEYK CKVSNKALPA **S**IEKTISKAK
 GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS
 DGSFFLYSKL TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK

Hinge aas 1-10, CH2 aas 11-120, CH3 aas 121-227 (Fc aas 11-227, 217 aas)

Homo sapiens IgG1 (partial sequence) Fc Mutant: N297A (SEQ ID NO:7)

DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
 GVEVHNAKTK PREEQY**A**STY RVVSVLTIVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK
 GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS
 DGSFFLYSKL TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK

Hinge aas 1-10, CH2 aas 11-120, CH3 aas 121-227 (Fc aas 11-227, 217 aas)

Homo sapiens IgG1 (partial sequence) Fc Mutant: L234A/L235A ("LALA") (SEQ ID NO:8)

DKTHTCPPCP APE**AA**GGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
 GVEVHNAKTK PREEQYNSTY RVVSVLTIVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK
 GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS
 DGSFFLYSKL TVDKSRWQQG NVFSCSVME ALHNHYTQKS LSLSPGK

Hinge aas 1-10, CH2 aas 11-120, CH3 aas 121-227 (Fc aas 11-227, 217 aas)

FIG. 2E

Homo sapiens IgG2 (partial sequence) GenBank AAN76044 (SEQ ID NO:9)

1 STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTISW NSGALTSGVH TFPVQLQSSG
 61 LYSLSSTVTV PSSNFGTQTY TCNVDHKPSN TKVDKTVKCK CCVECPPEPA PPVAGPSVFL
 121 FPPKPKDTLM ISRTPEVTCV VVDVSHEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTFRV
 181 VSVLTVVHQD WLNGKEYKCK VSNKGLPAPI EKTISKTKGQ PREPQVYITLP PSREEMTKNQ
 241 VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPMLDSDG SFFLYSKLTV DKSRWQQGNV
 301 FSCSVMEAL HNHYTQKSLS LSPGK

CH1 aas 1-97, Hinge aas 98-109, CH2 aas 110-218, CH3 aas 219-325 (Fc aas 110-325, 216 aas)

FIG. 2F

***Homo sapiens* IgG3 (partial sequence) GenBank AAW65947 (SEQ ID NO:10)**

1 HKPSNTKVDK RVELKTPLGD TTHTCPPCPA PELLGGPSVF LFPPKPKDTL MISRTPEVTC
 61 VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR VVSVLTVLHQ DWLNGKEYKC
 121 KVSNAKALPAP IEKTISKAKG QPREPQVYTL PPSRDELTKN QVSLTCLVKG FYPSDIAVEW
 181 ESNGQPENNY KTTTPVLDSG GSFFLYSKLT VDKSRWQQGN VFSCSVMEHA LHNHYTQKSL
 241 SLSPGK

CH1 aas 1-12, Hinge aas 13-29, CH2 aas 30-139, CH3 aas 140-246 (Fc aas 30-246, 217 aas)

FIG. 2G

***Homo sapiens* IgG4 (partial sequence) GenBank P01861 (SEQ ID NO:11)**

1 ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPTVS WNSGALTSGV HTFPAVLQSS
 61 GLYSLSSVVT VPSSSLGTKT YTCNVDPKPS NTKVDKRVES KYGPPCPSCP APEFLGGPSV
 121 FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY
 181 RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK
 241 NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSRL TVDKSRWQEG
 301 NVFSCSVMEH ALHNHYTQKS LSLSLGK

CH1 aas 1-98, Hinge aas 99-110, CH2 aas 111-220, CH3 aas 221-327 (Fc aas 111-327, 217 aas)

***Homo sapiens* IgG4 (partial sequence) Segment (SEQ ID NO:12) 223 aa**

1 PPCPSCPAPF FLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVQEDPEV QFNWYVDGVE
 61 VHNAKTKPRE EQFNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP
 121 REPQVYTLPP SQEEMTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSGGS
 181 FFLYSRLTVD KSRWQEGNVF SCSVMHEALH NHYTQKSLSL SPG

Hinge aas 1-7, CH2 aas 8-117, CH3 aas 118-223 (Fc aas 8-223, 216 aas)

FIG. 2H

***Homo sapiens* IgM (partial sequence) UniProtKB P01871.4 (SEQ ID NO:13)**

1 GSASAPTLFP LVSCENSPSD TSSVAVGCLA QDFLPDSITF SWKYKNNSDI SSTRGFPSVL
 61 RGGKYAATSQ VLLPSKDVMQ GTDEHVCKV QHPNGNKEKN VPLPVIAELP PKVSFVPPR
 121 DGFFGNPRKS KLICQATGFS PRQIQVSWLR EGKQVGSVGT TDQVQAEAKE SGPTTYKVTS
 181 TLTIKESDWL GQSMFTCRVD HRGLTFQNA SSMCVDPQDT AIRVFAIPPS FASIFLTKST
 241 KLTCLVTDLT TYDSVTISWT RQNGEAVKTH TNISESHPNA TFSAVGEASI CEDDWNNGER
 301 FTCTVTHTDL PSPLKQTISR PKGVALHRPD VYLLPPAREQ LNLRESATIT CLVTGFSPAD
 321 VFVQWMQRGQ PLSPEKYVTS APMPEPQAPG RYFAHSILTV SEEEWNTGET YTCVVAHEAL
 381 PNRVTERTV D KSTGKPTLYNVSLVMSDTAGT CY

CH1 aas 1-105, CH2 aas 106-217, CH3 aas 218-323, CH4 aas 324-452

FIG. 2I

***Homo sapiens* Ig J-chain (amino acids 23-259) (SEQ ID NO:14)**

1 MKNHLLFWGV LAVFIKAVHV KAQEDERIVL VDNKCKCARI TSRIIRSSD PNEDIVERNI
 61 RIIIVPLNRE NISDPTSPLR TRFVYHLSL CKKCDPTEVE LDNQIVTATQ SNICDEDSAT
 121 ETCYTYDRNK CYTAVVPLVY GGETKMOVETA LTPDACYPD
 SIGNAL SEQUENCE AMINO ACIDS 1-22

FIG. 2J***Ig CH1 domain (SEQ ID NO:15)***

1 FTVRETASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP
 61 AVLQSSGLYS LSSVVTVPSS SLGTQTYICN VNHKPSNTKV DKKVEPKSCD KT

FIG. 2K***Ig κ chain constant region (SEQ ID NO:16)***

1 TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS
 61 KDSTYSLSST LTLKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC

Ig λ chain constant region (SEQ ID NO:17)

1 GQPKANPTVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADGSPVK AGVETTKPSK
 61 QSNNKYAASS YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS

FIG. 3A *Homo sapiens* HLA-A**3A.1 *Homo sapiens* HLA-A*01:01:01:01 NCBI (National Center for Biotechnology Information) Accession NP_001229687.1 (SEQ ID NO:18)**

1 MAVMAPRTLL LLLSGALALT QTWAGSHSMR YFTTSVSRPG RGEPRFIAVG YVDDTQFVRF
 61 DSDAASQKME PRAPWIEQEG PEYWDQETRN MKAHSQTDRA NLGTLRGYYN QSEDGSHTIQ
 121 IMYGCDVGPD GRFLRGYRQD AYDGKDYIAL NEDLRSWTAA DMAAQITKRK WEAVHAAEQR
 181 RYLEGRGCV DGLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT
 241 WQRDGEDQTQ DTELVEPTRPA GDGTFQKWAA VVPSGEEQR YTCHVQHEGL PKPLTLRWEL
 301 SSQPTIPIVG IIAGLVLLGA VITGAVVA V MWRKSSDRK GGSYQAASS DSAQGSVDVSL
 361 TACKV

3A.2 *Homo sapiens* HLA-A*1101 NCBI Accession P13746.1 (SEQ ID NO:19)

1 MAVMAPRTLL LLLSGALALT QTWAGSHSMR YFYTSVSRPG RGEPRFIAVG YVDDTQFVRF
 61 DSDAASQKME PRAPWIEQEG PEYWDQETRN VKAQSQTDRA DLGTLRGYYN QSEDGSHTIQ
 121 IMYGCDVGPD GRFLRGYRQD AYDGKDYIAL NEDLRSWTAA DMAAQITKRK WEAAHAAEQQ
 181 RYLEGRGCV WLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT
 241 WQRDGEDQTQ DTELVEPTRPA GDGTFQKWAA VVPSGEEQR YTCHVQHEGL PKPLTLRWEL
 301 SSQPTIPIVG IIAGLVLLGA VITGAVVA V MWRKSSDRK GGSYQAASS DSAQGSVDVSL
 361 TACKV

3A.3 *Homo sapiens* HLA-A*2402 NCBI Accession P05534.2 (SEQ ID NO:20)

1 MAVMAPRTL V LLLSGALALT QTWAGSHSMR YFSTSVSRPG RGEPRFIAVG YVDDTQFVRF
 61 DSDAASQKME PRAPWIEQEG PEYWDDEETGK VKAHSQTDRE NLRIALRYYN QSEAGSHTIQ
 121 MMFGCDVGS DGRFLRGYHQY AYDGKDYIAL KEDLRSWTAA DMAAQITKRK WEAAHVAEQQ
 181 RYLEGRGCV DGLRRYLENGK ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT
 241 WQRDGEDQTQ DTELVEPTRPA GDGTFQKWAA VVPSGEEQR YTCHVQHEGL PKPLTLRWEP
 301 SSQPTVPIVG IIAGLVLLGA VITGAVVA V MWRNNSDRK GGSYSQAASS DSAQGSVDVSL
 361 TACKV

3A.4 *Homo sapiens* HLA-A*3303 NCBI Accession AAA79865.1 (SEQ ID NO:21)

1 MAVMAPRTLL LLLLGALALT QTWAGSHSMR YFTTSVSRPG RGEPRFIAVG YVDDTQFVRF
 61 DSDAASQKME PRAPWIEQEG PEYWDNRNTRN VKAHSQIDRV DLGTLRGYYN QSEAGSHTIQ
 121 MMYGCDVGS DGRFLRGYQQD AYDGKDYIAL NEDLRSWTAA DMAAQITQRK WEAAARVAEQL
 181 RYLEGRGCV WLRRYLENGK ETLQRTDPPK THMTHHAVSD HEATLRCWAL SFYPAEITLT
 241 WQRDGEDQTQ DTELVEPTRPA GDGTFQKWA V VVPSGEEQR YTCHVQHEGL PKPLTLRWEP
 301 SSQPTIPIVG IIAGLVLF GA VFAGAVVA V RWRRKSSDRK GGSYSQAASS DSAQGS DMSL
 361 TACKV

FIG. 3B***Homo sapiens* HLA-B*07:02:01 GenBank Accession NP_005505.2****Amino Acids 25-362 (SEQ ID NO:22)**

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1   MLVMAPRTVL LLLSAALALT ETWAGSHSMR YFYTSVSRPG RGEPRFISVG YVDDTQFVRF
61  DSDAASPREE PRAPWIEQEG PEYWDRNTQI YKAQAQTDRE SLRNLRGYYN QSEAGSHTLQ
121 SMYGCDVGPD GRLLRGHDQY AYDGKDYIAL NEDLRSWTAA DTAAQITQRK WEAAREAEQR
181 RAYLEGECVE WLRRYLENGK DKLERADPPK THVTHHPISD HEATLRCWAL GFYPAEITLT
241 WQRDGEDQTQ DTELVETRPA GDRTFQKWAA VVPSGEEQR YTCHVQHEGL PKPLTLRWEF
301 SSQSTVPIVG IVAGLAVLAV VVIGAVVAHV MCRRKSSGGK GGSYSQAACS DSAQGSVDVSL
361 TA

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FIG. 3C *Homo sapiens* HLA-C*701 (HLA-C*07:01) GenBank Accession NP_001229971.1, Amino acids 25-366 (SEQ ID NO:23)

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1   MRVMAPRALL LLLSGGLALT ETWACSHSMR YFDTAVSRPG RGEPRFISVG YVDDTQFVRF
61  DSDAASPRGE PRAPWVEQEG PEYWDRETQN YKRQAQADRV SLRNLRGYYN QSEAGSHTLQ
121 RMYGCDLGPD GRLLRGYDQS AYDGKDYIAL NEDLRSWTAA DTAAQITQRK LEAARAAEQL
181 RAYLEGTCVE WLRRYLENGK ETLQRAEPPK THVTHHPLSD HEATLRCWAL GFYPAEITLT
241 WQRDGEDQTQ DTELVETRPA GDGTFQKWAA VVPSGQEQR YTCHMQHEGL QEPLTLSWEP
301 SSQPTIPIMG IVAGLAVLVV LAVLGAVVTA MMCRRKSSGG KGGSCSQAAC SNSAQGSDES
361 LITCK

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Fig. 3D.

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HLA-A      GSHSMRYFFTSVSRPGRGEPFPIAVGYVDDTQFVRFDSDAASQKMEPRAPWIEQEGPEYW
HLA-B      GSHSMRYFFTSVSRPGRGEPFISVGYVDDTQFVRFDSDAASPREEPAPWIEQEGPEYW
HLA-C      CSHSMRYFDTAVSRPGRGEPFISVGYVDDTQFVRFDSDAASPRGEPAPWIEQEGPEYW
HLA-A*0201 GSHSMRYFFTSVSRPGRGEPFPIAVGYVDDTQFVRFDSDAASQKMEPRAPWIEQEGPEYW
Mouse H2K  GPHSLRYFVTIAVSRPGLGEPFPIAVGYVDDTQFVRFDSDADNPRFEPRAPWMEQEGPEYW
HLA_A (var. 2) GSHSMRYFFTSVSRPGRGEPFPIAVGYVDDTQFVRFDSDAASQKMEPRAPWIEQEGPEYW
HLA_A (var. 2C) GSHSMRYFFTSVSRPGRGEPFPIAVGYVDDTQFVRFDSDAASQKMEPRAPWIEQEGPEYW
HLA-A (var. 2CP) GSHSMRYFFTSVSRPGRGEPFPIAVGYVDDTQFVRFDSDAASQKMEPRAPWIEQEGPEYW
HLA-A*1101  GSHSMRYFFTSVSRPGRGEPFPIAVGYVDDTQFVRFDSDAASQKMEPRAPWIEQEGPEYW
HLA-A*2402  GSHSMRYFFTSVSRPGRGEPFPIAVGYVDDTQFVRFDSDAASQKMEPRAPWIEQEGPEYW
HLA-A*3303  GSHSMRYFFTSVSRPGRGEPFPIAVGYVDDTQFVRFDSDAASQKMEPRAPWIEQEGPEYW
          **;*** *;***** *****;*****

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84

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HLA-A      DQETRNMKAHSQTDRLNLTTLRGYNQSEAGSHTIQIMYGCDVGFDPGRFLRGYRQDAYDG
HLA-B      DRNTQIYKAQAQTDRSLNLRGYNQSEAGSHTLQSMYGCDFGPDGRLLRGHDQYAYDG
HLA-C      DRNTQNYKRQAQADRVSLNLRGYNQSEAGSHTLQEMYGCDLGEDGRLLRGYDQSAAYDG
HLA-A*0201 DGETRNVKAHSQTHRVDLSTLRGYNQSEAGSHTVQRMYGCDVGSDFWRFLRGYHQAAYDG
MOUSE H2K  EEQTQRAKSEDEQWFFVSLRTAQRYNQSEAGSHTFQRMFGCDVGSDFWRLLRGYQQFAYDG
HLA_A (var. 2) DGETRNVKAHSQTHRVDLSTLRGYNQSEAGSHTVQRMYGCDVGSDFWRFLRGYHQAAYDG
HLA_A (var. 2C) DGETRNVKAHSQTHRVDLSTLRGYNQSEAGSHTVQRMYGCDVGSDFWRFLRGYHQAAYDG
HLA_A (var. 2CP) DGETRNVKAHSQTHRVDLSTLRGYNQSEAGSHTVQRMYGCDVGSDFWRFLRGYHQAAYDG
HLA-A*1101 DQETRNVKAHSQTDRLNLTTLRGYNQSEAGSHTIQIMYGCDVGFDPGRFLRGYRQDAYDG
HLA-A*2402 DEETGKVKAHSQTDRENLAIALRINQSEAGSHTLQMMFGCDVGSDFGRFLRGYHQAAYDG
HLA-A*3303 DRNTRNVKAHSQIDRVDLSTLRGYNQSEAGSHTIQMMYGCDVGSDFGRFLRGYQQDAYDG
          :;* * . * * . * *****; *****;*****; * * *; * * *; * * *

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aac1 aac2

139

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HLA-A      KDYIALNEDLRSWTAADMAAQITTKWEAAHVAEQRRVYLEGRCVDGLRRYLENGKETLQ
HLA-B      KDYIALNEDLRSWTAADTAQITTKWEAAHVAEQRRAYLEGECEVWLRRYLENGKDKLE
HLA-C      KDYIALNEDLRSWTAADTAQITTKLEAARAAEQRLRAYLEGTCEVWLRRYLENGKETLQ
HLA-A*0201 KDYIALKEDLRSWTAADMAAQITTKWEAAHVAEQRLRAYLEGTCEVWLRRYLENGKETLQ
MOUSE H2K  RDYIALNEDLRTWTAADTAALITTKWEAQAGDAEYRAYLEGECEVWLRRYLENGNETLL
HLA_A (var. 2) KDYIALKEDLRSWTAADMAAQITTKWEAAHVAEQRLRAYLEGTCEVWLRRYLENGKETLQ
HLA_A (var. 2C) KDYIALKEDLRSWTAADMAAQITTKWEAAHVAEQRLRAYLEGTCEVWLRRYLENGKETLQ
HLA_A (var. 2CP) KDYIALKEDLRSWTAADMAAQITTKWEAAHVAEQRLRAYLEGTCEVWLRRYLENGKETLQ
HLA-A*1101 KDYIALNEDLRSWTAADMAAQITTKWEAAHVAEQRRAYLEGECEVWLRRYLENGKETLQ
HLA-A*2402 KDYIALKEDLRSWTAADMAAQITTKWEAAHVAEQRRAYLEGTCEVWLRRYLENGKETLQ
HLA-A*3303 KDYIALNEDLRSWTAADMAAQITTKWEAAHVAEQRLRAYLEGTCEVWLRRYLENGKETLQ
          :*****;*****;***** *;*****;*****;*****;*****;*****;*****

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aac3 aac4

236

aac5	aac6
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HLA-A      QKWAAVVVVPSGEEQRYTCHVQHESGLPKPLTLRWE
HLA-B      QKWAAVVVVPSGEEQBYTTCBVQHESGLPKPLTLRWE
HLA-C      QKWAAVVVVPSGGEQERYTCHMQHESGLQEPLTLRWE
HLA-A*0201 QKWAAVVVVPSGGEQRYTCHVQHESGLPFLTLRWEP
MOUSE H2K  QKWAAVVVVPLGKEQNYYTCHVHHHESLPEPLTLRW
HLA_A (var.2) QKWAAVVVVPSGGEQRYTCHVQHESGLPKPLTLRWE
HLA_A (var.2C) QKWAAVVVVPSGAEGQRYTCHVQHESGLPKPLTLRWE
HLA-A(var.2CF) QKWAAVVVVPSGGEQRYTCHVQHESGLPKPLTLRWEP
HLA-A*1101  QKWAAVVVVPSGEEQRYTCHVQHESGLPKPLTLRLWL
HLA-A*2402  QKWAAVVVVPSGEEQRYTCHVQHESGLPKPLTLRWEP
HLA-A*3303  QKWASVVVVPSGGEQBYTTCBVQHESGLPKPLTLRWF
***.**** * ** *****.*****
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HLA-A*0101, SEQ ID NO:24; HLA-B*0702, SEQ ID NO:25; HLA-C, SEQ ID NO:26; HLA-A*0201, SEQ ID NO:27; a mouse H2K protein sequence, SEQ ID NO:28; three variants of HLA-A (var.2, var.2C, and var.2CP, SEQ ID NOs:29, 30, and 31); (HLA-A*1101 (HLA-A11), SEQ ID NO:32; HLA-A*2402 (HLA-A24), SEQ ID NO:33; HLA-A*3303 (HLA-A33), SEQ ID NO:34.

[illegible]

9/43

FIG. 3E (continued) HLA-A ALLELE CONSENSUS SEQUENCE

GSHSMRYFX1TSVSRPGRGEPFRFIAVGYYDDTQFVRFDSDAASQX2MEPRAPWIEQEGPEYWDX
3X4TX5X6X7KAX8SQX9X10RX11X12LX13X14X15X16X17YYNQSEX18GSHTX19QX20
MX21GCDVGX22DX23RFLRGYX24QX25AYDGKDYIALX26EDLRSWTAADMAAAQX27TX287
X29KWEX30X31X32EAEQX33RX34YLX35GX36CVX37X38LRRYLENGKETLQRTDX39PK
 THMTHHX40X41SDHEATLRCWALX42FYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKW
AX43VVVPSGX44EQRYTCHVQHEGLPKPLTLRWEXX45

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

SEQ ID NO:39.

FIG. 3F HLA-B ALLELES

B*0702	GSHSMRYFYTSVSRPGRGCEPRFISVGYVDDTQFVKFDSDAASPREEPKAPWIEQEGPEYW	60
B*0801	GSHSMRYFYTAMSRPGRGCEPRFISVGYVDDTQFVKFDSDAASPREEPKAPWIEQEGPEYW	60
B*1502	GSHSMRYFYTAMSRPGRGCEPRFIAVGYVDDTQFVKFDSDAASPREEPKAPWIEQEGPEYW	60
B*3802	GSHSMRYFYTSVSRPGRGCEPRFISVGYVDDTQFVKFDSDAASPREEPKAPWIEQEGPEYW	60
B*4001	GSHSMRYFHTAMSRPGRGCEPRFITVGYVDDTLFVRFDSDATSPRKEPKAPWIEQEGPEYW	60
B*4601	GSHSMRYFYTAMSRPGRGCEPRFIAVGYVDDTQFVKFDSDAASPREEPKAPWIEQEGPEYW	60
B*5301	GSHSMRYFYTAMSRPGRGCEPRFIAVGYVDDTQFVKFDSDAASPREEPKAPWIEQEGPEYW	60
	***** *;*****;***** *****;*** *****	
89		
B*0702	DRNTQIYKAQAQTDRESIRNLKQYNQSEAGSHTLQSMYGC DVGPDGRLLRGHDQYAYDG	120
B*0801	DRNTQIFKTNQTDRSIRNLKQYNQSEAGSHTLQSMYGC DVGPDGRLLRGHNQYAYDG	120
B*1502	DRNTQISKTNQTQYRESIRNLKQYNQSEAGSHIIQRMYGCDVGPDKLLRGYDQSAIDG	120
B*3802	DRNTQICKTNQTQYRENLRTALRQYNQSEAGSHTLQRMYGCDVGPDKLLRGHNQFAYDG	120
B*4001	DRNTQISKTNQTQYRESIRNLKQYNQSEAGSHTLQRMYGCDVGPDKLLRGHNQYAYDG	120
B*4601	DRNTQIKYKQAQTDVRSIRNLKQYNQSEAGSHTLQRMYGCDVGPDKLLRGHDQSAIDG	120
B*5301	DRNTQIFKTNQTQYRENLRTALRQYNQSEAGSHTIQRMYGCDLGPDKLLRGHDQSAIDG	120
	;* * ; * ;* *****;*****;*****;*****;*****	
aac1 aac2		
139		
B*0702	KDYIALNEDLRSWTAADTAQITQKKWEAAREAEQRAYLEGECEVWLRRLRYLENGKDKLE	180
B*0801	KDYIALNEDLRSWTAADTAQITQKKWEAARVAEQRAYLEGECEVWLRRLRYLENGKDTLE	180
B*1502	KDYIALNEDLSSWTAADTAQITQKKWEAAREAEQLRAYLEGLCEVWLRRLRYLENGKETLQ	180
B*3802	KDYIALNEDLSSWTAADTAQITQKKWEAARVAEQRLTYLEGECEVWLRRLRYLENGKETLQ	180
B*4001	KDYIALNEDLRSWTAADTAQISQKLEAARVAEQRAYLEGECEVWLRRLRYLENGKDKLE	180
B*4601	KDYIALNEDLSSWTAADTAQITQKKWEAAREAEQRAYLEGLCEVWLRRLRYLENGKETLQ	180
B*5301	KDYIALNEDLSSWTAADTAQITQKKWEAARVAEQRAYLEGLCEVWLRRLRYLENGKETLQ	180
	***** *****;***** ***** *;***** *****;*****;*****	
aac3 aac4		
236		
B*0702	RADPFKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEIVETRPAGDRTF	241
B*0801	RADPFKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEIVETRPAGDRTF	241
B*1502	RADPFKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEIVETRPAGDRTF	241
B*3802	RADPFKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEIVETRPAGDRTF	241
B*4001	RADPFKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEIVETRPAGDRTF	241
B*4601	RADPFKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEIVETRPAGDRTF	241
B*5301	RADPFKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEIVETRPAGDRTF	241
	***** *****;***** *****;***** *****;***** *****	
aac5 aac6		
B*0702	QKWAAVVVPSSGEEQRYTCHVQHEGLPKPLTLRWEP	276
B*0801	QKWAAVVVPSSGEEQRYTCHVQHEGLPKPLTLRWEP	276
B*1502	QKWAAVVVPSSGEEQRYTCHVQHEGLPKPLTLRWEP	276
B*3802	QKWAAVVVPSSGEEQRYTCHVQHEGLPKPLTLRWEP	276
B*4001	QKWAAVVVPSSGEEQRYTCHVQHEGLPKPLTLRWEP	276
B*4601	QKWAAVVVPSSGEEQRYTCHVQHEGLPKPLTLRWEP	276
B*5301	QKWAAVVVPSSGEEQRYTCHVQHEGLPKPLTLRWEP	276

HLA-B*0702, SEQ ID NO:40; HLA-B*0801, SEQ ID NO:41; HLA-B*1502, SEQ ID NO:42; HLA-B*3802, SEQ ID NO:43; HLA-B*4001, SEQ ID NO:44; HLA-B*4601, SEQ ID NO:45; and HLA-B*5301, SEQ ID NO:46.

FIG. 3F (continued) HLA-B ALLELE CONSENSUS

GSHSMRYFX1TX2X3SRPGRGEPRIX4VGyvDDTX5FVRFDSDAX6SPRX7X8PRAPWIEQEG
 PEYWDRX9TQX10X11KTX12X13TQX14YX15X16NLX17X18X19X20YYNQSEAGSHX21X
22QX23MYGCDLGPDGRLLRGHDQSAYDGKDYIALNEDLX24SWTAADTAAQIX25QRKX26EA
 ARX27AEQX28RX29YLEGX30CVEWLRRYLENGKX31X32LX33RADPPKTHVTHHPX34SDH
 EATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRTFQKWA^{AVV}PSGEEQRYTCHV
 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.

SEQ ID NO:47.

FIG. 3G HLA-C ALLELES

C*0102 CSHSMKYFFYTSVSRKPGRGEPFFLAVGYVDDTQFVRFDSDAASPRGEPFRAPWVEQEGPEYW 60
C*0303 GSHSMKYFFYTAVERPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPFRAPWVEQEGPEYW 60
C*0304 GSHSMKYFFYTAVERPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPFRAPWVEQEGPEYW 60
C*0401 GSHSMKYFFTSVSWPGRGEPFFLAVGYVDDTQFVRFDSDAASPRGEPFRAPWVEQEGPEYW 60
C*0602 CSHSMKYFDTAVSRKPGRGEPFFLAVGYVDDTQFVRFDSDAASPRGEPFRAPWVEQEGPEYW 60
C*0701 CSHSMKYFDTAVSRKPGRGEPFFLAVGYVDDTQFVRFDSDAASPRGEPFRAPWVEQEGPEYW 60
C*0702 CSHSMKYFDTAVSRKPGRGEPFFLAVGYVDDTQFVRFDSDAASPRGEPFRAPWVEQEGPEYW 60
C*0801 CSHSMKYFFYTAVERPGRGEPFFLAVGYVDDTQFVRFDSDAASPRGEPFRAPWVEQEGPEYW 60
C*1502 CSHSMKYFFYTAVERPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPFRAPWVEQEGPEYW 60
*****;*****;*****;*****;*****;*****;*****;*****;*****;*****

84

C*0102 DRETQKYKQQAQTDKVSILNLRLGTYNQSSAGSHTLQWMCGLGPDGRLLRGYDQYAYDG 120
C*0303 DRETQKYKQQAQTDKVSILNLRLGTYNQSSARSHIIQRMYGCDVGFDPGRLLRGYDQYAYDG 120
C*0304 DRETQKYKQQAQTDKVSILNLRLGTYNQSSAGSHIIQRMYGCDVGFDPGRLLRGYDQYAYDG 120
C*0401 DRETQKYKQQAQADRVNLIKLRGTYNQSSDGSHTLQRMFGCDLGPDPGRLLRGYDQYAYDG 120
C*0602 DRETQKYKQQAQADRVNLIKLRGTYNQSSDGSHTLQWMYGCDLGPDPGRLLRGYDQYAYDG 120
C*0701 DRETQKYKQQAQADRVNLIKLRGTYNQSSDGSHTLQRMYGCDLGPDPGRLLRGYDQYAYDG 120
C*0702 DRETQKYKQQAQADRVNLIKLRGTYNQSSDGSHTLQRMYGCDLGPDPGRLLRGYDQYAYDG 120
C*0801 DRETQKYKQQAQTDKVSILNLRLGTYNQSSAGSHTLQRMYGCDLGPDPGRLLRGYDQYAYDG 120
C*1502 DRETQKYKQQAQTDKVSILNLRLGTYNQSSAGSHIIQRMYGCDLGPDPGRLLRGYDQYAYDG 120
*****;*****;*****;*****;*****;*****;*****;*****;*****;*****

aac1 aac2

139

C*0102 KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQRRAYLESTCVEWLRRYLENGKETLQ 180
C*0303 KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQLRAYLEGLCVEWLRRYLENGKETLQ 180
C*0304 KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQLRAYLEGLCVEWLRRYLENGKETLQ 180
C*0401 KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQRRAYLESTCVEWLRRYLENGKETLQ 180
C*0602 KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQRRAYLESTCVEWLRRYLENGKETLQ 180
C*0701 KDYIALNEDLRSWTAADTAQITCRKLEAAREAEQLRAYLESTCVEWLRRYLENGKETLQ 180
C*0702 KDYIALNEDLRSWTAADTAQITCRKLEAAREAEQLRAYLESTCVEWLRRYLENGKETLQ 180
C*0801 KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQLRAYLESTCVEWLRRYLENGKETLQ 180
C*1502 KDYIALNEDLRSWTAADTAQITCRKWEAAREAEQLRAYLESTCVEWLRRYLENGKETLQ 180
*****;*****;*****;*****;*****;*****;*****;*****;*****;*****

aac3 aac4

236

C*0102 RAENPKTHVTHHPVSDHEATLRCAWLGFFYPAEITLTWQWDGSDGTQDTLQVETRAAGDGT 241
C*0303 RAENPKTHVTHHPVSDHEATLRCAWLGFFYPAEITLTWQWDGSDGTQDTLQVETRAAGDGT 241
C*0304 RAENPKTHVTHHPVSDHEATLRCAWLGFFYPAEITLTWQWDGSDGTQDTLQVETRAAGDGT 241
C*0401 RAENPKTHVTHHPVSDHEATLRCAWLGFFYPAEITLTWQWDGSDGTQDTLQVETRAAGDGT 241
C*0602 RAENPKTHVTHHPVSDHEATLRCAWLGFFYPAEITLTWQWDGSDGTQDTLQVETRAAGDGT 241
C*0701 RAENPKTHVTHHPVSDHEATLRCAWLGFFYPAEITLTWQWDGSDGTQDTLQVETRAAGDGT 241
C*0702 RAENPKTHVTHHPVSDHEATLRCAWLGFFYPAEITLTWQWDGSDGTQDTLQVETRAAGDGT 241
C*0801 RAENPKTHVTHHPVSDHEATLRCAWLGFFYPAEITLTWQWDGSDGTQDTLQVETRAAGDGT 241
C*1502 RAENPKTHVTHHPVSDHEATLRCAWLGFFYPAEITLTWQWDGSDGTQDTLQVETRAAGDGT 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
*****;*****;*****;*****;*****;*****;*****;*****;*****;*****

FIG. 3G (continued)

HLA-C*0102, SEQ ID NO:48; HLA-C*0303, SEQ ID NO:49; HLA-C*0304, SEQ ID NO:50; HLA-C*0401, SEQ ID NO:51; HLA-C*0602, SEQ ID NO:52; HLA-C*0701, SEQ ID NO:53; HLA-C*0702, SEQ ID NO:54; HLA-C*0801, SEQ ID NO:55; and HLA-C*1502, SEQ ID NO:56.

HLA-C ALLELE CONSENSUS

X1SHSMX2YFX3TAVSX4PGRGEPX5FIX6VGYYDDTQFVX7FDSDAASPRGEPRX8PWVEQEG
 PEYWDRETQX9YKRQAQX10DRVX11LRX12LRGYYNQSEX13X14SHX15X16QX17MX18GC
 DX19GPDGRLLRGX20X21QX22AYDGKDYLALNEDLRSWTAADTAAQITQRKX23EAARX24A
 EQX25RAYLEGX26CVEWLRRLX27NGKX28TLQRAEX29PKTHVTHHPX30SDHEATLRCWA
 LGFYPAEITLTWQX31DGEDQTQDTELVTETRPAGDGTFQKWAAYX32VPSGX33EQRYTCHX34
 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.

SEQ ID NO:57.

FIG. 3H - HLA-E, HLA-F, and HLA-G ALLELE CONSENSUS SEQUENCES**SEQUENCE****HLA-E**

GSHSLKYFHT SVSRPGRGEP RFISVGIVDD TQFVRFDNDA ASPRMVPRAP
 WMEQEGSEYW DRETRSARDT AQIFRVNLRT LRGYYNQSX1A GSHTLQWMHG
 CELGPDX2RFL RGYEQFAYDG KDYLTLNEDL RSWTAVDTAA QISEQKSNDA
 SEAEHQX3X4YL EDTCVELLHK YLEKGGKETLL HLEPPKTHVT HHPISDHEAT
 LRCWALGFYP AEITLTWQQD GEGHTQDTEL VETRPAGDGT FQKWAAVVVP
 SGEEX5RYTCH VQHEGLX6EPV TLRWKPASQP TIPI

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 SEQ ID NO:58

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

GSHSLRX1FST AVSRPGRGEP RYIAVEYVDD TQFLRFDSDA AIPRMEPREX2
 WVEQEGPQYW EWTTGYAKAN AQTDRLVALRN LLRRYNQSEA GSHTLQGMNG
 CDMGPDGRLL RGYHQHAYDG KDYISLNEDL RSWTAADTVA QITQRFYEA
 EYAEFRFTYL EGECELELLR YLENGKETLQ RADPPKAHVA HHPISDHEAT
 LRCWALGFYP AEITLTWQRD GEEQTQDTEL VETRPAGDGT FQKWAAVVVP
X3GEEQRYTCH VQHEGLPQPL ILRWEQSX4QP TIPI

X1= Y or F; X2= P or Q; X3= S or P; and X4= P or L SEQ ID NO:59

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 AVX1RPGRGEP RFIAMGX2VDD X3QFX4RFDSDS ACPRMEPRAP
 WVEX5EGPEYW EEETRNTKAH AQTDRMNLQT X6RGYYNQSEA
 SSHTLQWMX7 CDLX8X9DGRLX10 RGYEQYAYDG KDYLALNEDL
 RSWTAADTAA QISKRKCEAA NVAEQRRX11L EGTCVEWLX12R
X13LENGKEX14LQ RADPX15KTHVT HHPVFDYEAT LRCWALGFYP
 AEIILTQWX16D GEDQTQDVEL VETRPAGDGT FQKWAAVVVP SGEEQRYX17CH
 VQHEGLPEPL MLRWX18QSSLP TIPI

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; SEQ ID NO:60

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. 3I

CONSENSUS SEQUENCE ALIGNMENT

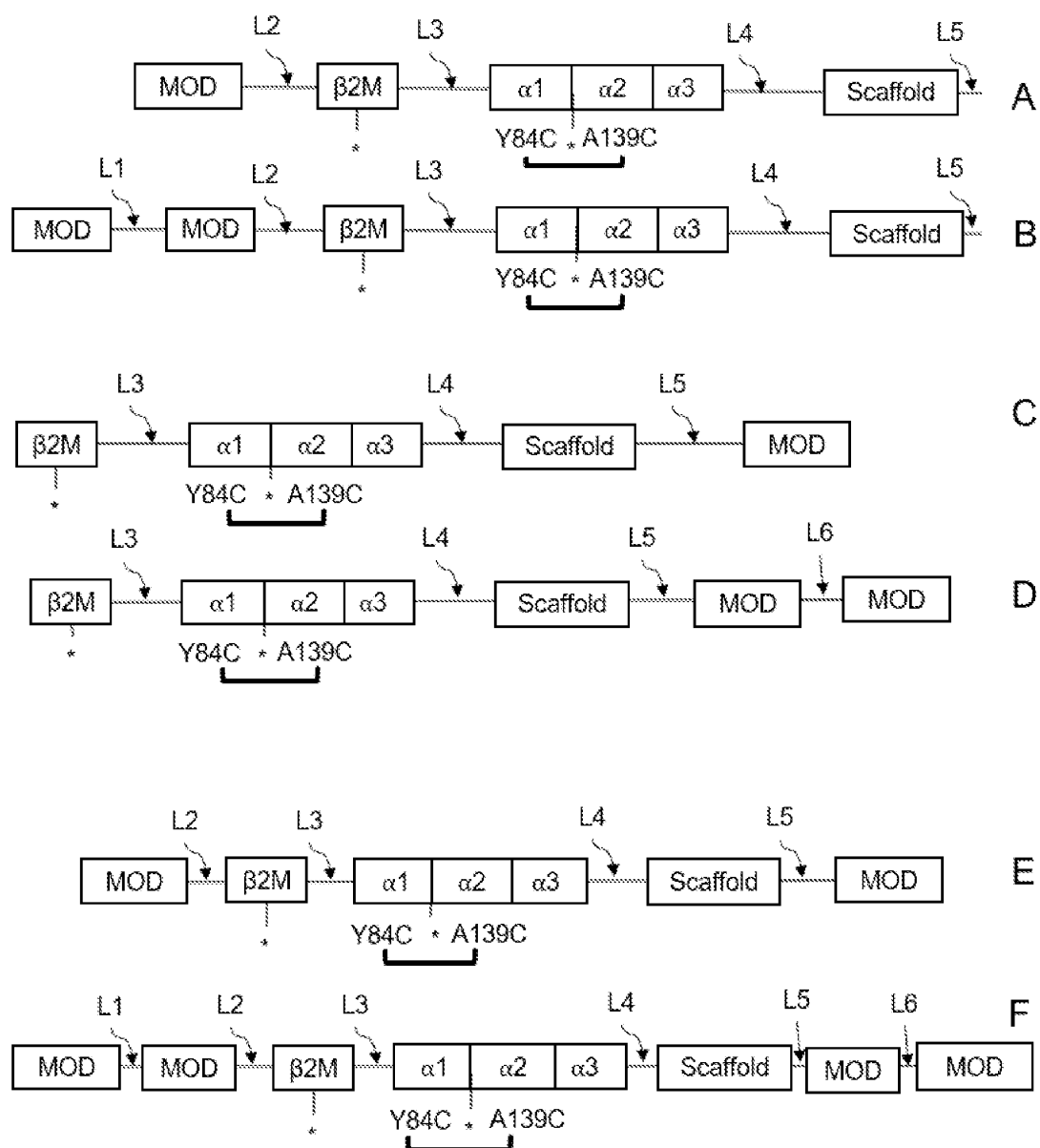
HLA-A	GSHSMRYFXTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQXMEPRAPWIEQEGPEYW	60
HLA-B	GSHSMRYFXTXXSRPGRGEPRFIXVGYVDDTXFVRFDSDAASPRXXPRAPWIEQEGPEYW	60
HLA-C	XSHSMXYFXTAVSXPRGEPXFI XVGYVDDTQFVXFDSDAASPRGEPXPWVEQEGPEYW	60
HLA-E	GSHSLKYFHTSVSRPGRGEPRFISVGYVDDTQFVRFDNDAASPRMVPRAPWMEQEGSEYW	60
HLA-F	GSHSLRXFSTAVSRPGRGEPRIAVEYVDDTQFLRFDSDAAI PRMEPREXWVEQEGPQYW	60
HLA-G	GSHSMRYFSAAVXRPGRGEPRFIAMGXVDDXQFXRFDSDSACPRMEPRAPWVEGPEYW	60
	: * : ** : * : *** * **.*: ** *: * ** : **	
84		
HLA-A	DXXTXXXKAXSQXXRXLI XXXXXYNQSEKGSHTXQXMXGCDVGXD XRFLRGYXQXAYDG	120
HLA-B	DRXTQXXKTXTTQYXXNL XXXXXYNQSEAGSHXXQXMYGCDLGP DGRLLRGHDQSAYDG	120
HLA-C	DRETQYKRQAQXDRVXIRXLRGYYNQSEKXSHXXQXMXGCDXGPDGRLLRGXXQXAYDG	120
HLA-E	DRETRSARDTAQIFRVNIRTLRGYYNQSXAGSHTLQWMHGCELGPDXRFLRGYEQFAYDG	120
HLA-F	EWTTGYAKANAQTDRVAIRNLLFRYNQSEAGSHTLQGMNGCDMGP DGRLLRGYHQHAYDG	120
HLA-G	EEETRNTKAHAQTDRMNIQT XRGYYNQSEASSHTLQWMIXCDLXXDGRLLXRGYEQYAYDG	120
	: * : ***** ** * * * : * *: ** * ****	
	aac1 aac2	
139		
HLA-A	KDYIALXEDLRSWTAADMAAQXTXKKWEXXXEAEQXRXYLXGXCVXXLR RYLENGKETLQ	180
HLA-B	KDYIALNEDLXSWTAADTAAQIXQRKXEAARXAEQXRXYLEGXCV EWLRRYLENGKXXIX	180
HLA-C	KDYIALNEDLRSWTAADTAAQITQRKXEAARXAEQXRAYLEGXCV EWLRRYLXNGKXTLQ	180
HLA-E	KDYLTINEDLRSWTAVDTAAQISEKSNDAEAEHQXXYLEDTCEW LHKYLEKGKETLL	180
HLA-F	KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEFRTYLEGECL ELLRRYLENGKETLQ	180
HLA-G	KDYIALNEDLRSWTAADTAAQISKRKCEAANVAEQRRAXLEGTCV EWLXRXLENGKEXLQ	180
	***: * ** * ** * . ** : ** . * . *: * : * : * *	
	aac3 aac4	
236		
HLA-A	RTDXPKTHMTHHXXSDHEATLRCWALGFYP AEITLTWQRDGEDQTQDTEIVETRPAGDGT F	241
HLA-B	RADPPKTHVTHHPXSDHEATLRCWALGFYP AEITLTWQRDGEDQTQDTEIVETRPAGDRT F	241
HLA-C	RAEXPKTHVTHHPXSDHEATLRCWALGFYP AEITLTWQXDGEDQTQDTEIVETRPAGDGT F	241
HLA-E	HLEPPKTHVTHHPISDHEATLRCWALGFYP AEITLTWQQDGEGHTQDTEIVETRPAGDGT F	241
HLA-F	RADPPKAHVHHPISDHEATLRCWALGFYP AEITLTWQRDGEEQTQDTEIVETRPAGDGT F	241
HLA-G	RADPXKTHVTHHPVFDYEATLRCWALGFYP AEIILTWQXDGEDQTQDVEIVETRPAGDGT F	241
	: : *: *: ** *: ***** ***** ***** *: **.* ***** ** *	
	ac5 aac6	
HLA-A	QKWAXVVVPSGXEQRYTCHVQHEGLPKPLTLRWEX-----	276
HLA-B	QKWA AVVVP SGEEQRYTCHVQHEGLPKPLTLRWEP-----	276
HLA-C	QKWA AVVVP SGXEQRYTCHXQHEGLXEP LTLXWXP-----	276
HLA-E	QKWA AVVVP SGEE XRYTCHVQHEGLXEPVTLRWKPASQPTIPI	284
HLA-F	QKWA AVVVP XGEEQRYTCHVQHEGLPQPLILRWEQSXQPTIPI	284
HLA-G	QKWA AVVVP SGEEQRYXCHVQHEGLPEPLMLRWXQSSLPTIPI	284
	***** * * * * * * * * * * : *: * *	

FIG. 4

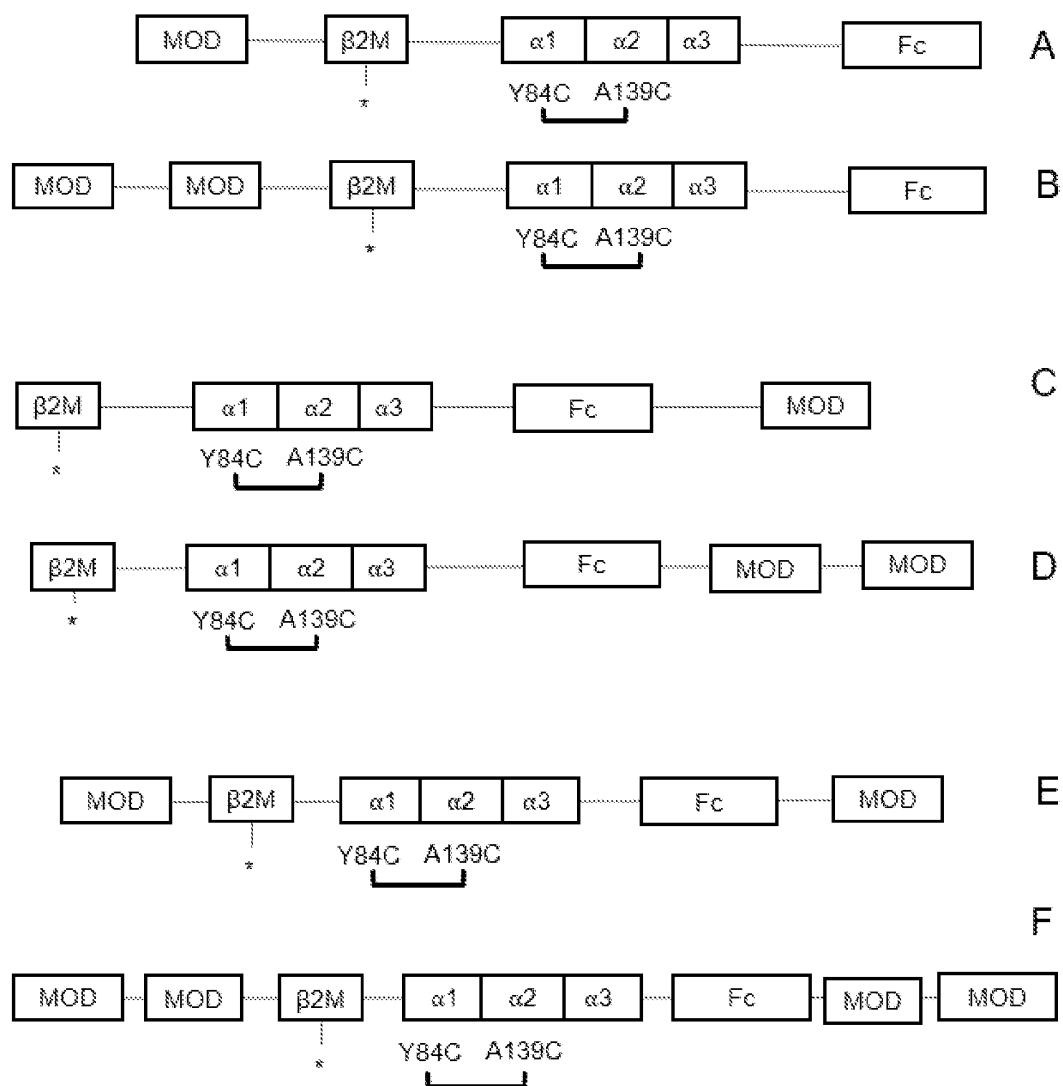
NP_004039.1	MSRSVALAVLALLSLSGLEAIQRTPKIQVYSRHPAENCKSNFLNCYVSGHFPSDIEVDLL 60
NP_001009066.1	MSRSVALAVLALLSLSGLEAIQRTPKIQVYSRHPAENCKSNFLNCYVSGHFPSDIEVDLL 60
NP_001040602.1	MSRSVALAVLALLSLSGLEAIQRTPKIQVYSRHPAENCKSNFLNCYVSGHFPSDIEVDLL 60
NP_776318.1	MARFVALVLLGLLSLGLDAIQRPDKIQVYSRHPFEDCKPNVILNCYVYGFHPDQIEIDL 60
NP_033865.2	MARSVTLVFLVLVSLTGLYAIQKTPQIQVYSRHPPECKPNILNCYVTQFHPPHIEIQML 60
	: *:.* * *:***:.*:*****.*:***.* ***** ***.**.*:***
NP_004039.1	KNGERIEKVHSDLSFSKDWSFYLLYYTEFTPTTEKDEYACRVNHVTLTSQLKIVKWRDM 119
NP_001009066.1	KNGERIEKVHSDLSFSKDWSFYLLYYTEFTPTTEKDEYACRVNHVTLTSQLKIVKWRDM 119
NP_001040602.1	KNGEKMCKVHSDLSFSKDWSFYLLYYTEFTENEXDEYACRVNHVTLTSGPRIVKWRDM 119
NP_776318.1	KNGEKI-KSEQDLSFSKDWSFYLLSHAETENSKDQYSCRVKHVTLTQPRIVKWRDL 118
NP_033865.2	KNGKKIEKVMDSMSFSKDWSFYILAHTETFTTETDTYACRVKHASMAEEKTVYWRDM 119
	::: * * *:**:* :*****.* * :*****.*: * : * *****

FIG. 4

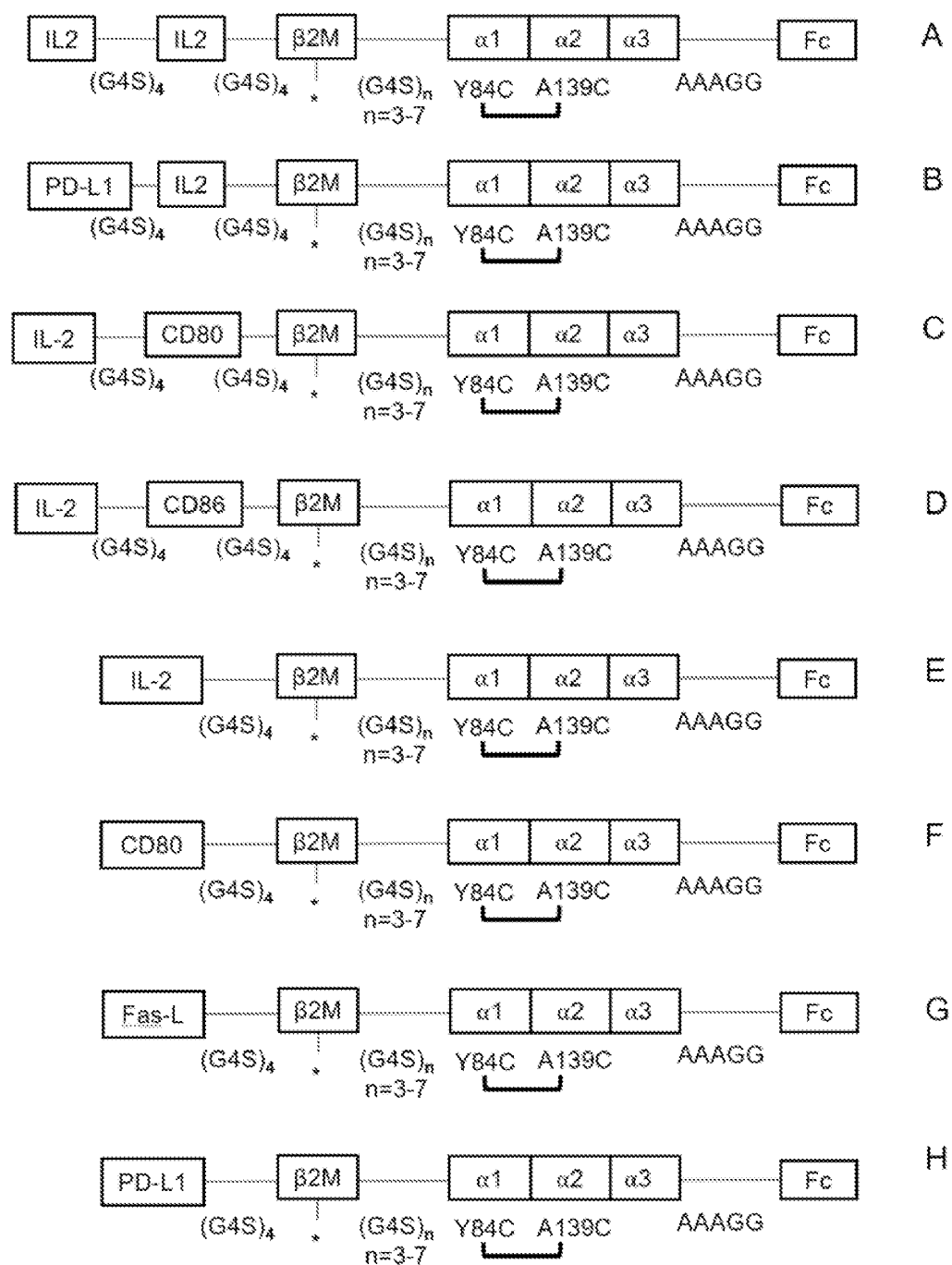
NP_004039.1	<u>MSRSVALAVLALLSLSGLEAIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLL</u>	60
NP_001009066.1	<u>MSRSVALAVLALLSLSGLEAIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLL</u>	60
NP_001040602.1	<u>MSRSVALAVLALLSLSGLEAIQRTPKIQVYSRHPENGKPNFLNCYVSGFHPSDIEVDLL</u>	60
NP_776318.1	<u>MARFVALVLLGLLSLSGLDAIQRPPIQVYSRHPPEDEGKPNYLNCYVYGFHPPQIEIDL</u>	60
NP_033865.2	<u>MARSVTLVFLVLVSLTGLYAIQKTPQIQVYSRHPPEDEGKPNILNCYVTQFHPHIEIQML</u>	60
	: *:*..* *:*:* *:*:*..*:*:*:*:*:*:* *:*:*..*:*:*:*	
NP_004039.1	KNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPEKDEYACRVNHVTLSQPKIVKWDRDM	119
NP_001009066.1	KNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPEKDEYACRVNHVTLSQPKIVKWDRDM	119
NP_001040602.1	KNCEKMGKVEHSDLSFSKDWSFYLLYYTEFTPEKDEYACRVNHVTLSGPRIVKWDRDM	119
NP_776318.1	KNGEKI - KSEQSDLSFSKDWSFYLLSHAEFTPNQSKDQYSCRVKHVTLEQPRIVKWDRDM	118
NP_033865.2	KNKKKI PKVEMSDMSFSKDWSFYILAHTFTPTETDTYACRVKHASMAEPKTVYWDMDM	119
	::: * * **:***:* :***** * :*****::: * * *****:	

FIG. 5

* represents a conjugation site e.g., E44C of β2M and/or a site in the MHC H binding pocket

FIG. 6

* represents a conjugation site in β2M
e.g., E44C of β2M

FIG. 7

* represents a conjugation site e.g., E44C of β2M and/or a site in the MHC H binding pocket

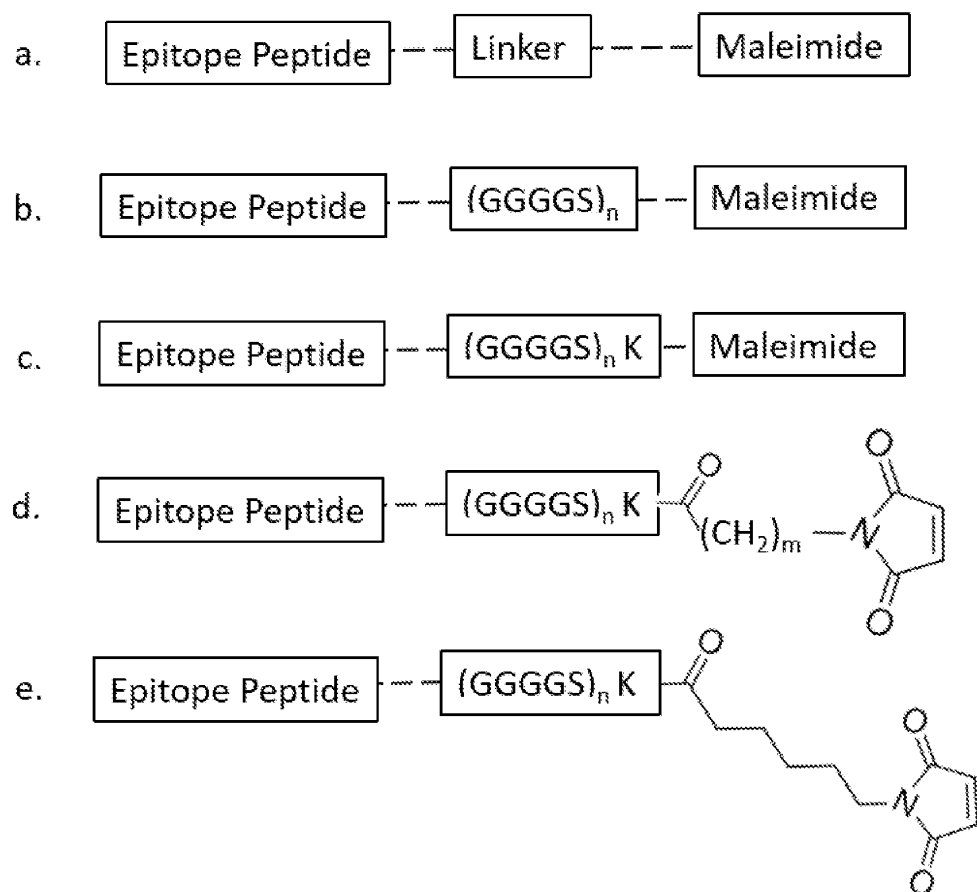
FIG. 8

FIG. 9

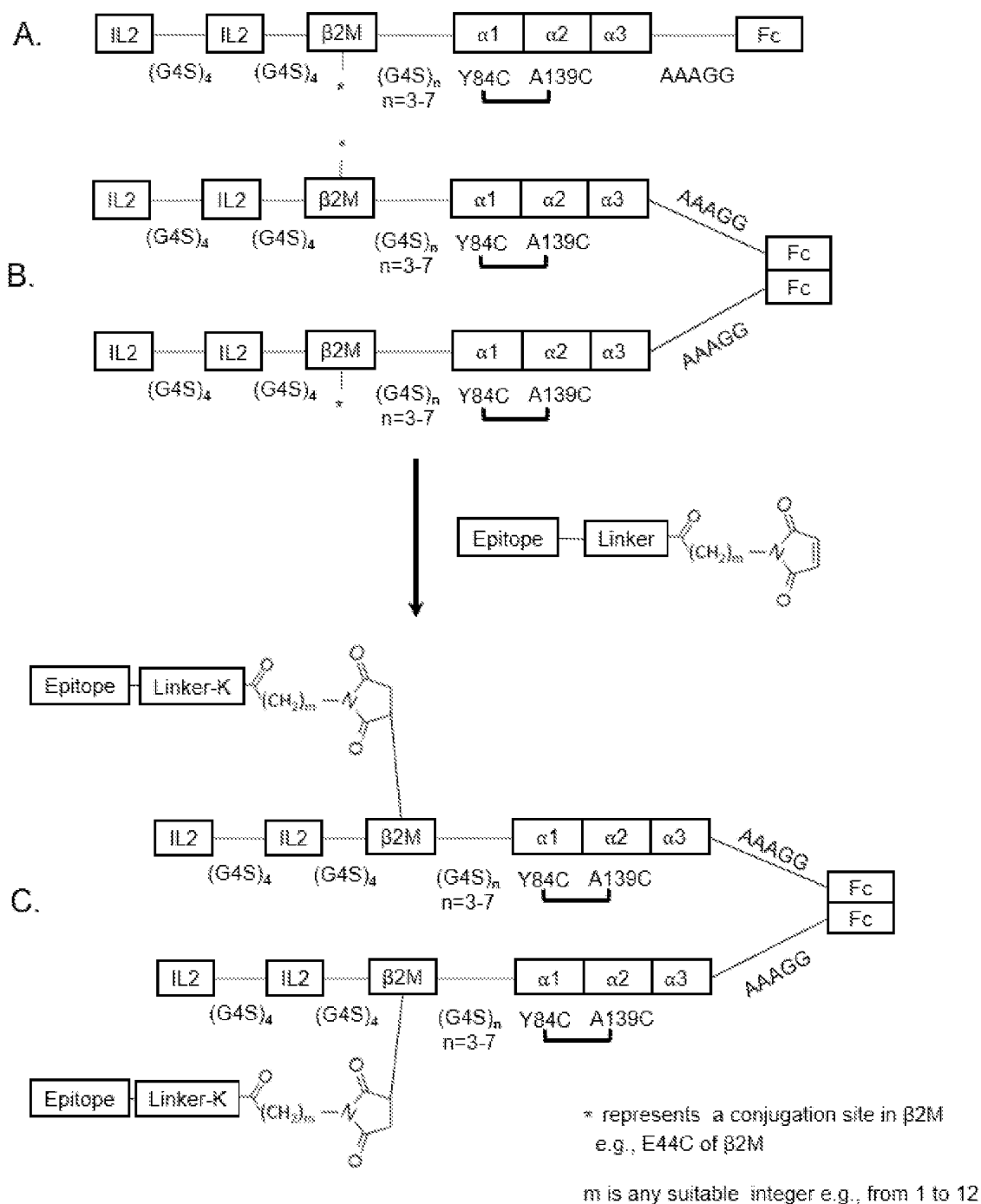


FIG. 10

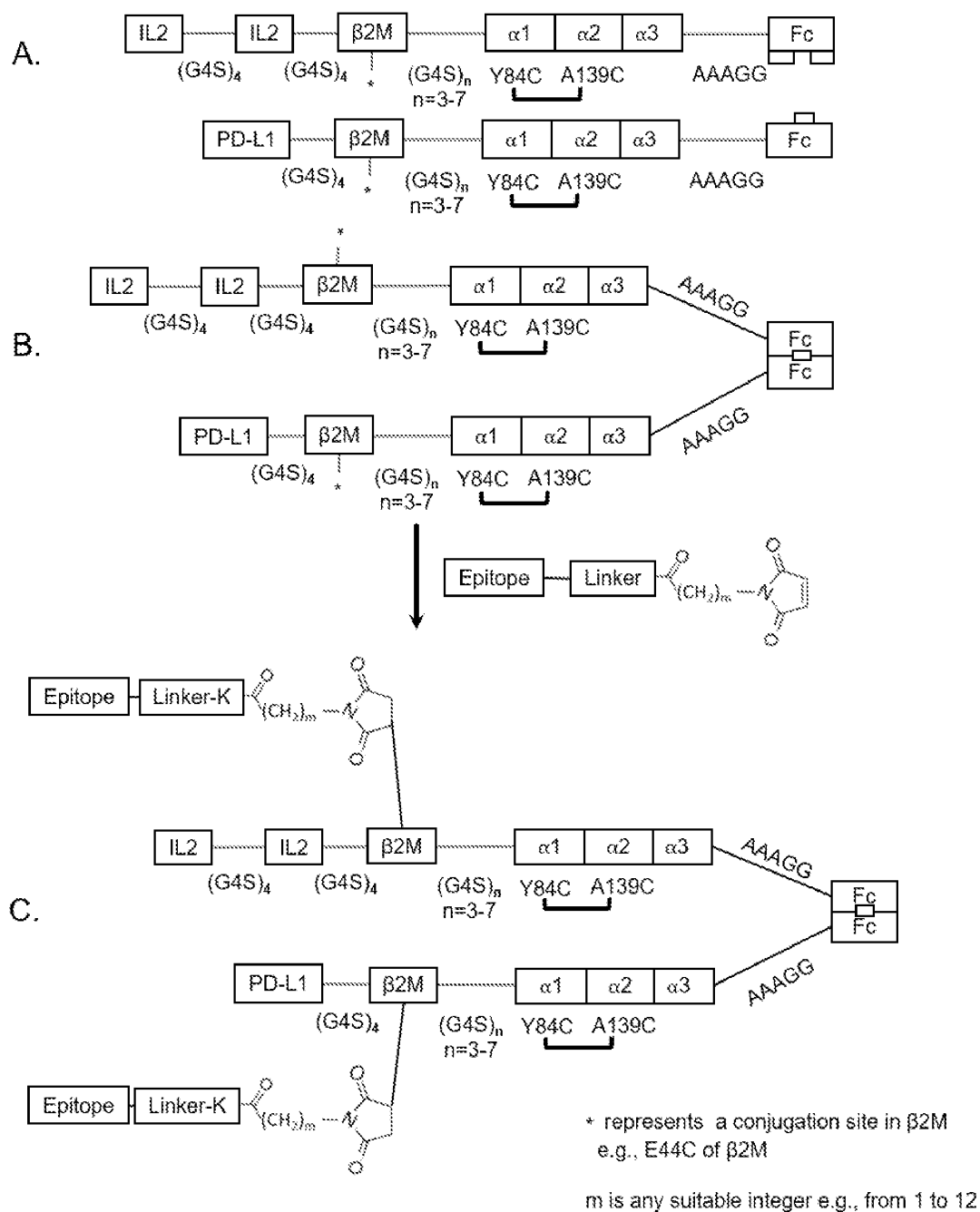


FIG. 11

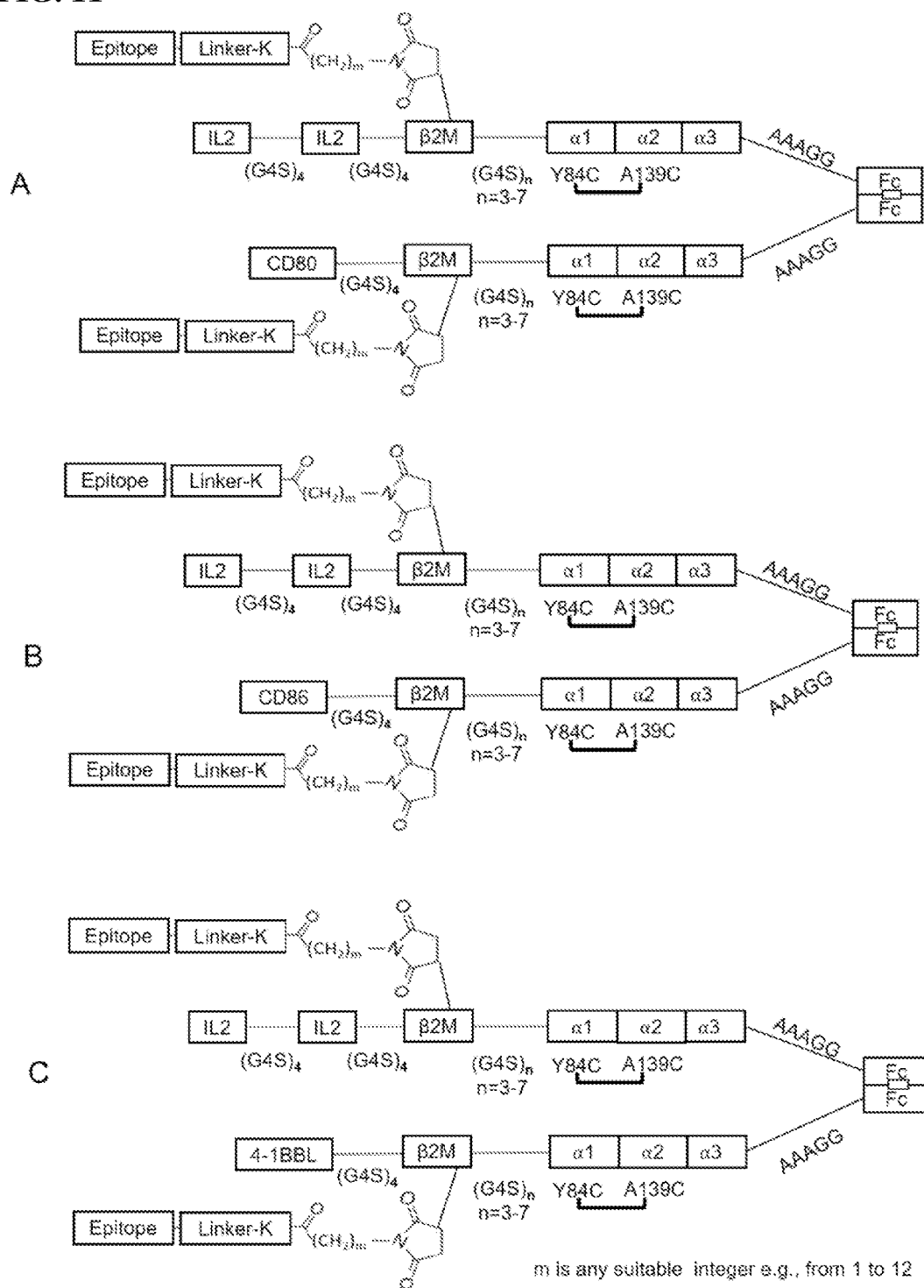


FIG. 12

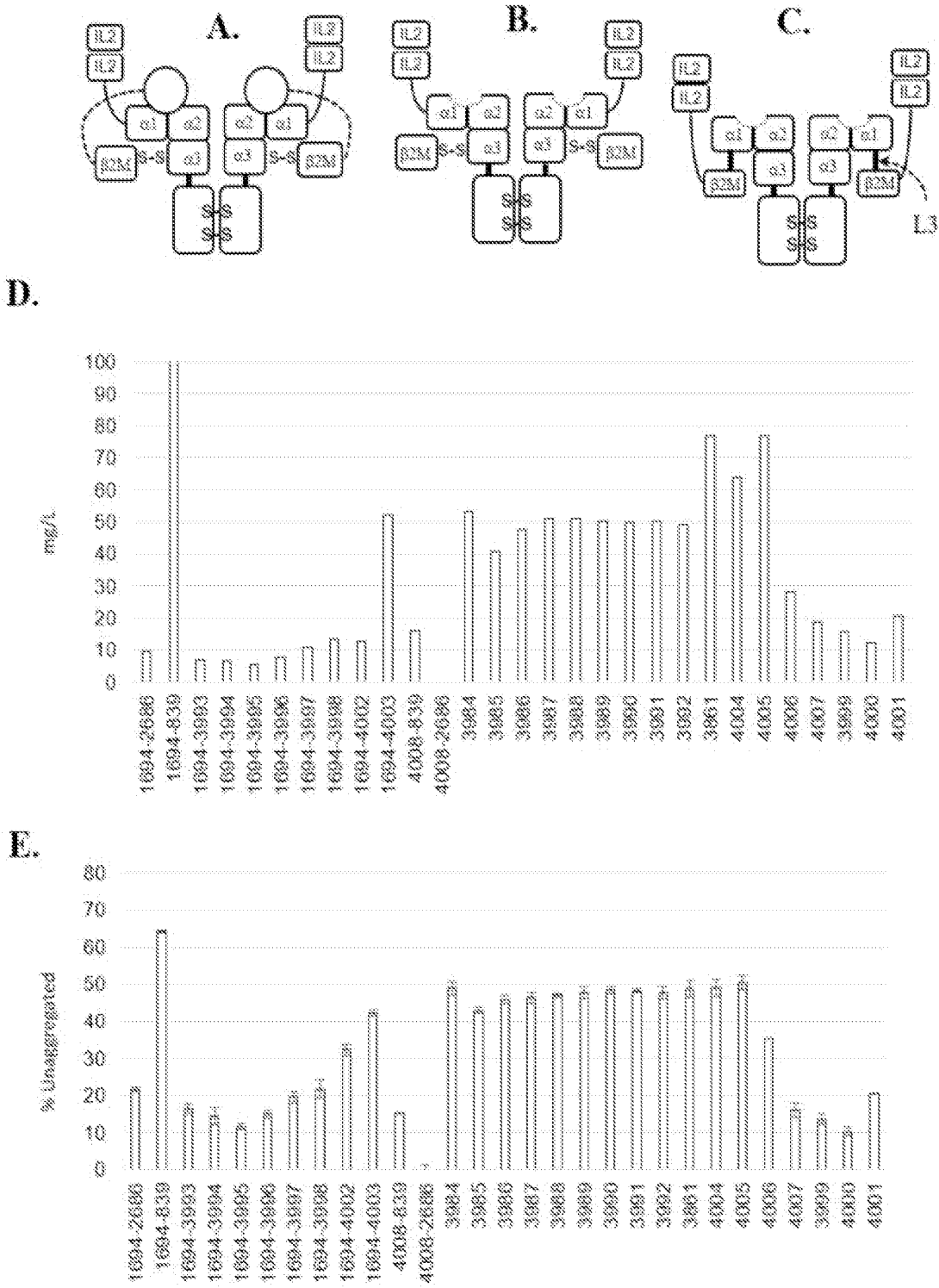


FIG. 13

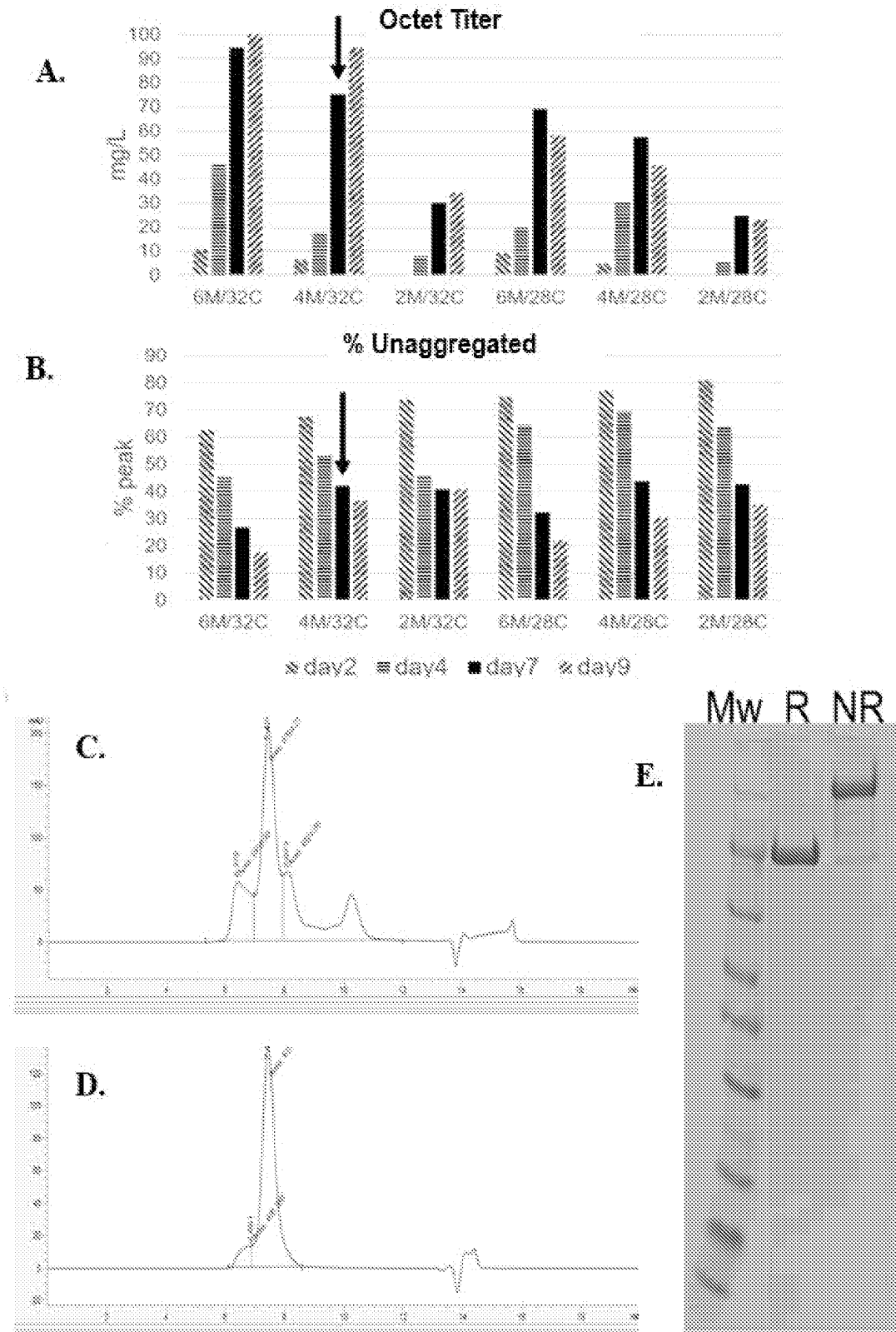
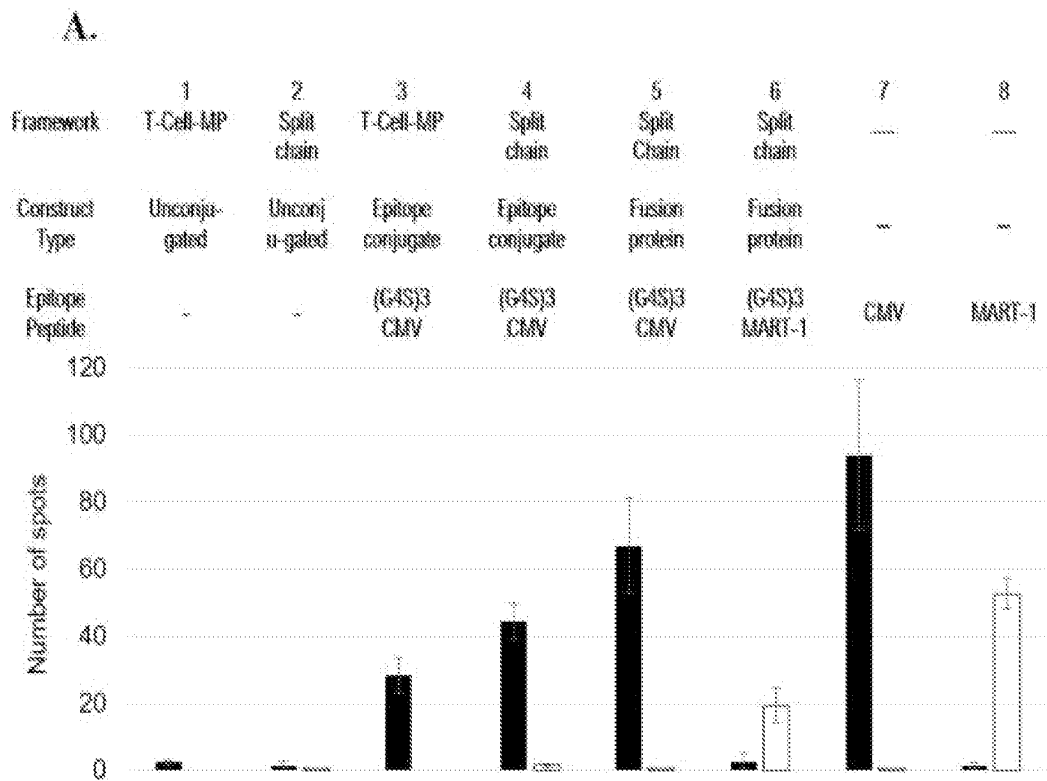
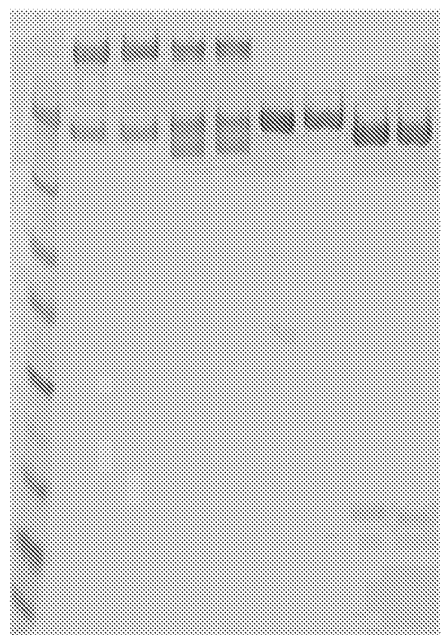


FIG. 14



B.



Non-Reduced
0- MW Standards
1- T-Cell-MP-CMV epitope conjugate
2- T-Cell-MP-MART-1 epitope conjugate
3- Split-chain fusion protein with CMV
4- Split-chain fusion protein with MART1

Reduced
5- T-Cell-MP-CMV epitope conjugate
6- T-Cell-MP-MART-1 epitope conjugate
7- Split-chain fusion protein with CMV
8- Split-chain fusion protein with MART1

FIG. 15

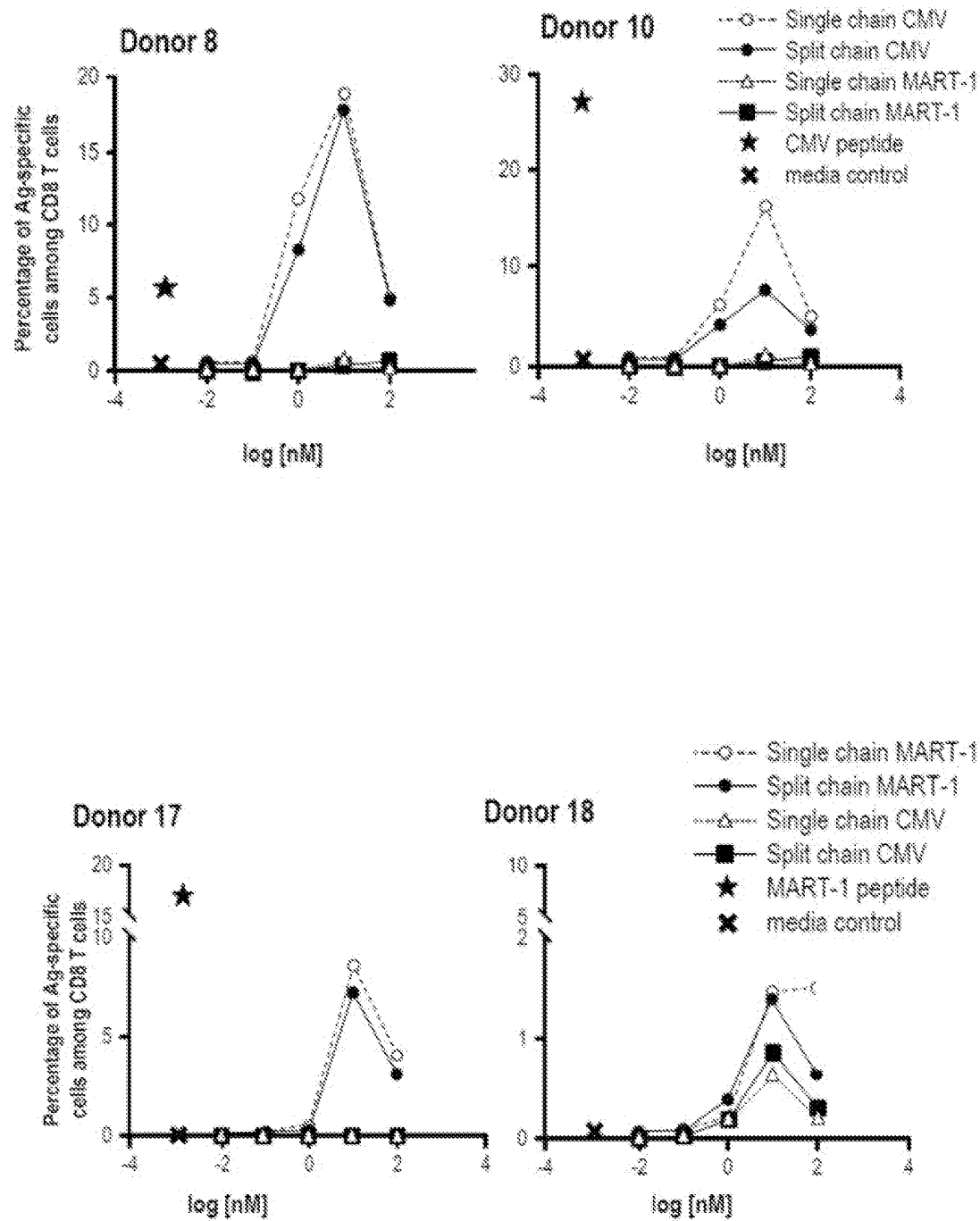


FIG. 16

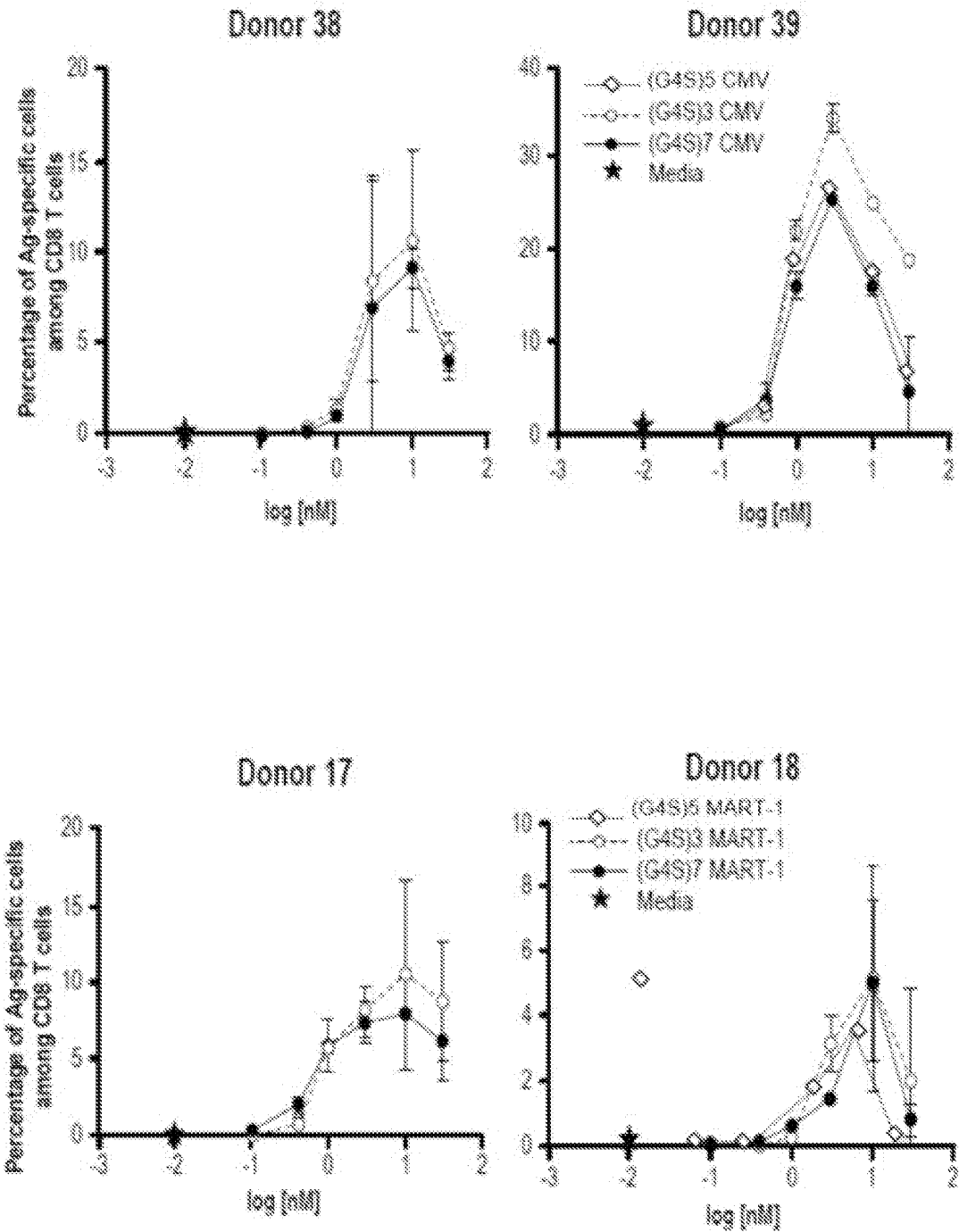


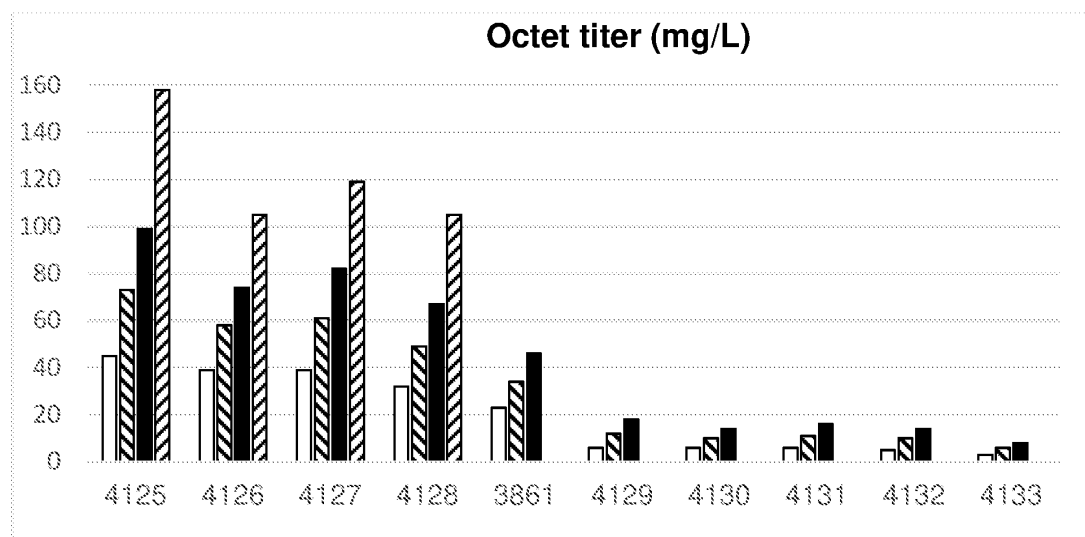
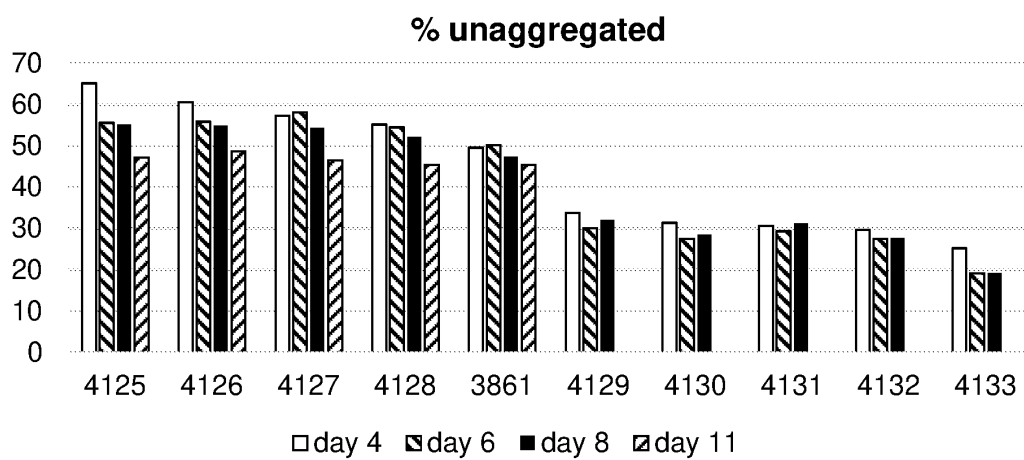
FIG. 17**A.****B.**

FIG. 18

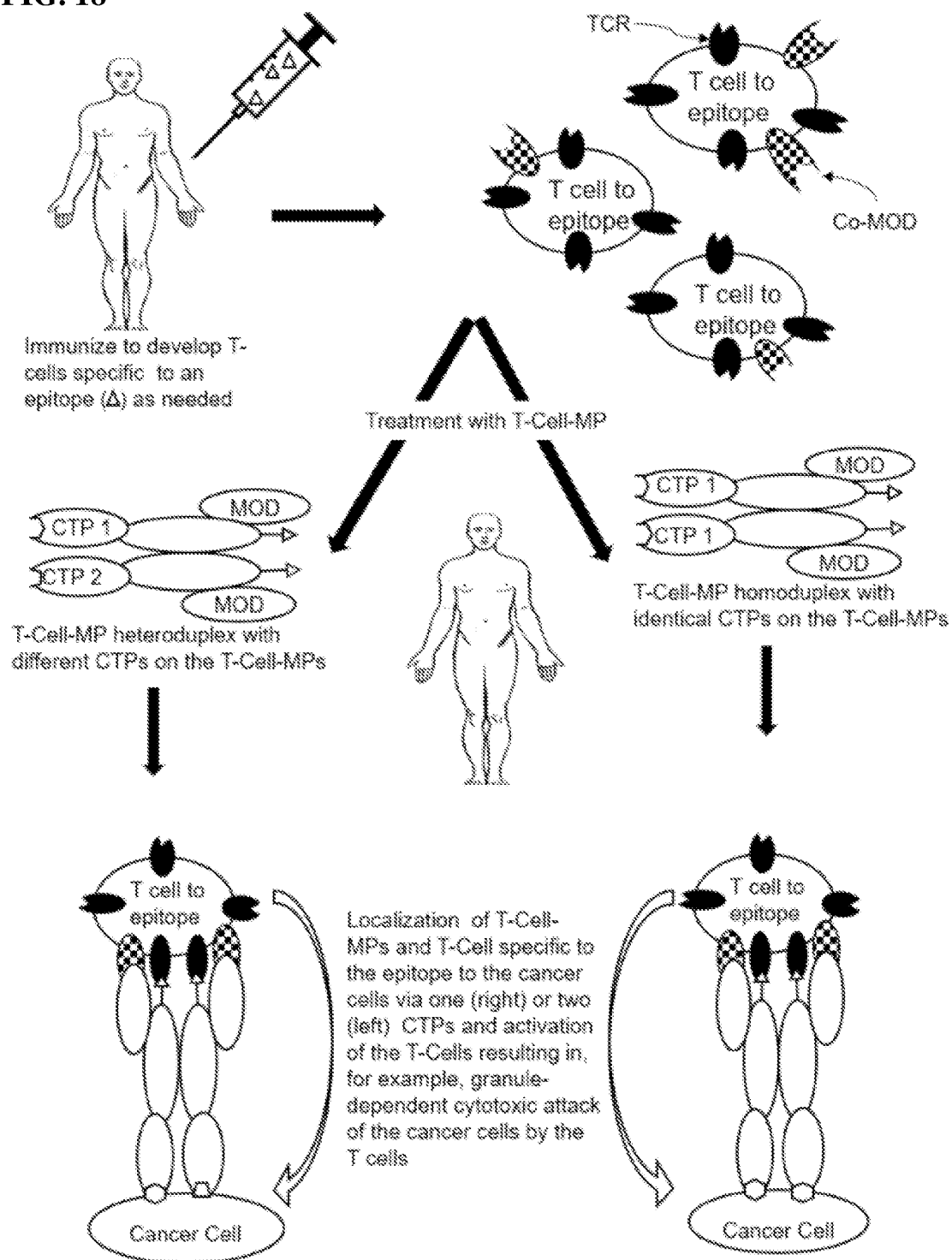


FIG. 19**Construct 839 CMV-GGGASGGGSGGGGS-β2M (R12C)**

NLVPMVATVGGGASGGGSGGGGSSIQRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDIEVDLLK
 NGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPKIVKWDRDM (SEQ ID
 NO:497)

**Construct 1694 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-HLA-A02 (A236C, Y84C,
 A139C)-AAAGG-IgG1 (L234A, L235A)**

APTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
 LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFY
 MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
 ATIVEFLNRWITFCQSIISTLTGGGSGGGSGGGSGGGGSSGSHSMRYFFTSVSRPGRGEPRFIAV
 GYVDDTQFVRFDSDAASQRMPEPRAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLRGCYNQS
 EAGSHTVQRMYGCDVGS DWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMCAQTTKHKWEA
 AHVAEQLRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEI
 TLTWQRDGEDQTQDTEL VETRPCGDGTFQKWA AVVPSGQEQRYTCHVQHEGLPKPLTLRWEA
AAGGDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT
 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:493)

Construct 2686 β2M (R12C, E44C)

IQRTPKIQVYSCHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWSFYLLYY
 TEFTPTEKDEYACRVNHVTLSPKIVKWDRDM (SEQ ID NO:495)

**Construct 3861 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)₃-HLA-
 A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)**

APTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
 LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFY
 MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
 ATIVEFLNRWITFCQSIISTLTGGGSGGGSGGGSGGGGSSIQRTPKIQVYSRHPAENGKSNFLNC
 YVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSPK
 IVKWDRDMGGGSGGGSGGGSGGGGSSGSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAA
 SQRMPEPRAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLRGCYNQSEAGSHTVQRMYGCDVG
 SDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMCAQTTKHKWEAAHVAEQLRAYLEGTCVE
 WLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL
 VETRPAGDGTQKWA AVVPSGQEQRYTCHVQHEGLPKPLTLRWEAAAGGDKTHTCPPCPAPEA
 AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
 LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
 EALHNHYTQKSLSLSPG (SEQ ID NO:496)

Construct 3984 1xhIL2(F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)₃-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)

Construct 3985 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)-GLGGS-(G₄S)₂-β2M (E44C)-(G₄S)₃-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)

Construct 3986 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₂-GLGGS-(G₄S)-β2M (E44C)-(G₄S)₃-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)

APTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGGAPTSSSTKKTQLQLEALLDLQMILNGINNYKNPKLTRMLTAKFY
MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
ATIVEFLNRWITFCQSIISTLTGGGSGGGSGGLGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNC
YVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWFSFYLLYYTEFTPTKDEYACRVNHVTLSPK
IVKWDRDMGGGSGGGSGGGGGSHSMRYFFT SVSRPGRGEPRIA VGYVDDTQFVRFDSDA
SQRMEPRAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRGCYNQSEAGSHTVQRMYGCDVG
SDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMCAQTTKHKWEAAHVAEQLRAYLEGTCVE
WLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL
VETRPAGDGT FQKWA AVVP SGQEQR YTCHVQHEGLPKPLTLRWEAAAGGDKHTHTCPPCPAPEA
AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
LTCLVKGFPYSDHDAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMH
EALHNHYTOKLSLSLSPG (SEO ID NO:500)

FIG. 19 (continued)

Construct 3990 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)-GGGGSMGGGS-(G₄S)-β2M (E44C)-(G₄S)₃-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)

APTSSSTKKTQLQLEALLLDLQMLNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMLNGINNYKNPKLTRMLTAKFY
MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
ATIVEFLNRWITFCQSIISTLTGGGSGGGSGGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNC
YVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWSFYLLYYTEFTPTTEKDEYACRVNHVTLSPK
IVKWDRDMGGGSGGGSGGGSGGGGSGSHSMRYFFTSVSRPGRGEPRFIAVGYYDDTQFVRFSDAA
SQRMPEPRAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLRGCYNQSEAGSHTVQRMYGCDVG
SDWRFLRGYHQYAYDGKDIALKEDLRSWTAADMCAQTTKHKWEAAHVAEQLRAYLEGTCVE
WLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFPYAEITLTWQRDGEDQTQDTEL
VETRPAGDGTQKWA AVVVP SGQEQR YTCHVQHEGLPKPLTLRWEAAAGGDKTHTCPPCPAPEA
AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPG (SEQ ID NO:504)

Construct 3991 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)-GGGGSGMGGGS-(G₄S)-β2M (E44C)-(G₄S)₃-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)

APTSSSTKKTQLQLEALLLDLQMLNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMLNGINNYKNPKLTRMLTAKFY
MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
ATIVEFLNRWITFCQSIISTLTGGGSGGGSGMGGSGGGGSIQRTPKIQVYSRHPAENGKSNFLNC
YVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWSFYLLYYTEFTPTTEKDEYACRVNHVTLSPK
IVKWDRDMGGGSGGGSGGGSGGGGSGSHSMRYFFTSVSRPGRGEPRFIAVGYYDDTQFVRFSDA/
SQRMPEPRAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLRGCYNQSEAGSHTVQRMYGCDV/
SDWRFLRGYHQYAYDGKDIALKEDLRSWTAADMCAQTTKHKWEAAHVAEQLRAYLEGTCVE
WLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFPYAEITLTWQRDGEDQTQDTEL
VETRPAGDGTQKWA AVVVP SGQEQR YTCHVQHEGLPKPLTLRWEAAAGGDKTHTCPPCPAPEA
AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPG (SEQ ID NO:505)

Construct 3992 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)-GGGGSGGGGM-(G₄S)-β2M (E44C)-(G₄S)₃-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)

APTSSSTKKTQLQLEALLLDLQMLNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGGSAPTSSSTKKTQLQLEALLLDLQMLNGINNYKNPKLTRMLTAKFY
MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
ATIVEFLNRWITFCQSIISTLTGGGSGGGSGGGGMGGGSIQRTPKIQVYSRHPAENGKSNFLNC
YVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWSFYLLYYTEFTPTTEKDEYACRVNHVTLSPK
IVKWDRDMGGGSGGGSGGGSGGGGSGSHSMRYFFTSVSRPGRGEPRFIAVGYYDDTQFVRFSDAA
SQRMPEPRAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLRGCYNQSEAGSHTVQRMYGCDVG
SDWRFLRGYHQYAYDGKDIALKEDLRSWTAADMCAQTTKHKWEAAHVAEQLRAYLEGTCVE
WLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFPYAEITLTWQRDGEDQTQDTEL
VETRPAGDGTQKWA AVVVP SGQEQR YTCHVQHEGLPKPLTLRWEAAAGGDKTHTCPPCPAPEA
AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPG (SEQ ID NO:506)

Construct 3993 GM-(G₄S)₃-β2M (R12C, E44C)

Construct 3994 GMGGS-(G₄S)₂-β2M (R12C, E44C)

Construct 3995 GMS-(G₄S)₂-β2M (R12C, E44C)

Construct 3996 GMGGGS-(G₄S)-β2M (R12C, E44C)

Construct 3997 GMGS-(G₄S)-β2M (R12C, E44C)

Construct 3998 GM-(G₄S)-β2M (R12C, E44C)

Construct 3999 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)₃-HLA-A02(Y84C, A139C, T143L)-AAAGG-IgG1(L234A, L235A)

37/43

Construct 4000 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)₃-HLA-A02(Y84C, A139C, T143M)-AAAGG-IgG1(L234A, L235A)

Construct 4001 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)₃-HLA-A02(L81M, Y84C, A139C)-AAAGG-IgG1(L234A, L235A)

Construct 4002 CMV-(G₃AS)-(G₄S)₂-β2M (R12C, E44C)

Construct 4003 CMV-(G₃AS)-(G₄S)-FC1-(G₄S)-β2M (R12C, E44C)

NLVPMVATVGGGASGGGGSHVVVPYGLGSPRSKRALENLLGGGGSIQRTPKIQVYSCHPAENGKS
NFLNCYVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDW SFYLLYYTEFTPTEKDEYACRVNHVT
LSQPKIVKWRDMD (SEQ ID NO:517)

[illegible][illegible]

Construct 4006 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)₂-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)
 APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
 LEEVLNLAQSKNFHLRPRDLISININIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGSGGGGAPTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFY
 MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISININIVLELKGSETTFMCEYADET
 ATIVEFLNRWITFCQSIISTLTGGGSGGGSGGGSGGGSGGGGIQRTPKIQVYSRHPAENGKSNFLNC
 YVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWFSFYLLYYTEFTPTKEDEYACRVNHVTLSPK
 IVKWDRDMGGGSGGGSGSGSHSMRYFFTSVSRPGRGEPRIA VGYVDDTQFVRFDSDAASQRME
 PRAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGLTRGCYNQSEAGSHTVQRMYGCDVGS DWRF
 LRGYHQYAYDGKDYIALKEDLRSWTAADMCAQTTKHKWEAAHVAEQLRAYLEGTCVEWLRRY
 LENGKETLQRTDAPKTHMTHHAVSDHEATLRWALSFPYAEITLTWQRDGEDQTQDTELVETRP
 AGDGTFFQKWA AVVVPSPGEQRYTCHVQHEGLPKPLTLRWEAAAGGDKTHTCPPCPAPEAAGGPS
 VFLFPPPKPDTLMISRTPEVTCVVVDVSDHEPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
 SVLTVLHQDWLNGKEYKCKVSNKALPAIEKTIKAKGQPREPQVYITLPSREEMTKNQVSLTCL
 VKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMHEAL
 HNHYTOKSLSLSPG (SEQ ID NO:520)

Construct 4007 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)

Construct 4008 2xhIL2 (F42A, H16A)-(G₄S)₄-HLA-A02 (A236C, Y85C, D137C)-AAAGG-IgG1 (L234A, L235A)

Construct 4125 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)₇-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)

40/43

Construct 4126 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)₆-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)
 APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKKATELKHLQCLEEELKP
 LEEVLNLAQSKNFHLRPRDLISNINIVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT**G**
GGGSGGGSGGGSGGGSGGGSGAPTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFY
 MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINIVIVLELKGSETTFMCEYADET
 ATIVEFLNRWITFCQSIISTLT**GGGSGGGSGGGSGGGSGGGSG**IQRTPKIQVYSRHPAENGKSNFLNC
 YVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWFSFYLLYYTEFTPTTEKDEYACRVNHVTLSPK
 IVKWDRDM**GGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSG**GSHSMRYFFTSVSRPGRGEPRFIAVG
 YVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGLTRG**C**YNQSE
 AGSHTVQRMYGCDVGSWDRFLRGYHQYAYDGKDYLKEDLRSWTAADM**C**AQTTKHKWEAA
 HVAEQLRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFPYAEIT
 LTWQRDGEDQTQDELVETRPAGDGTQFKWA AVVVPSGQEQRYTCHVQHEGLPKPLTLRWE**AA**
AGGDKHTHTCPPCPAPEAAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
 EVHNATPKPREEQKYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTKISKAKGQPREP
 QVYATLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGPENNYKTTTPPVLDSDGSFFLYSKLTV
 DKSRWOOGNVYFSCSMYHEALHNHYTOKSLSLSPG (SEO ID NO:524)

Construct 4127 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)₅-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)
 APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKP
 LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT**G**
GGGSGGGSGGGSGGGSGGGSGAPTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFY
 MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
 ATIVEFLNRWITFCQSIISTLT**GGGSGGGSGGGSGGGSGGGSG**IQRTPKIQVYSRHPAENGKSNFLNC
 YVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWFSFYLLYYTEFTPTKDEYACRVNHVTLSPH
 IVKWDRDM**GGGSGGGSGGGSGGGSGGGSG**GSHSMRYFFTSVSRPGRGEPRFIAVGYYDD
 QFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETRKYKAHSQTHRVDLGTLRG**C**YNQSEAGSHT
 VQRMYGCDVGSDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADM**C**AQTTKHKWEAAHVAEQ
 LRAYLEGTVCVEWLRRLRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQR
 DGEDQTQDELVETRPAGDGTFFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE**AAAGG**DK
 THTCPCPAPEAAGGPSVDFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVEVHNA
 KTKPREEQNKQYVRSVSLTVLHQDWLNGKEYKCKVSNKALPAIEKTISKAKGQPREPQVYITLP
 PSREEMTKNQVSLTCLVKGFYPSDIAVWESNGKCPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW
 QOQNVFSCSVMEALHNHYTOKSLSLSPG (SEQ ID NO:525)

Construct 4128 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (E44C)-(G₄S)₄-HLA-A02(Y84C, A139C)-AAAGG-IgG1(L234A, L235A)
 APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKKATELKHLQCLEELKPL
 LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT**GGGGSGGGSGGGSGGGSGGGSG**APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFY
 MPKKATELKHLQCLEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADET
 ATIVEFLNRWITFCQSIISTLT**GGGGSGGGSGGGSGGGSGGGSG**IQRTPKIQVYSRHPAENGKSNFLNC
 YVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWFSFYLLYYTEFTPTTEKDEYACRVNHVTLSPK
 IVKWDRDM**GGGGSGGGSGGGSGGGSGGGSG**GSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRF
 DSDAASQRMENRAPWIEQEGPEYWDGETRKVKAHQSQTHRVLDGLTRGC**C**YNQSEAGSHTVQRM
 YGCDVGSQDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADM**C**AQTTKHKWEAAHVAEQLRAYL
 EGTCVEWLRRLRYLENGKETLQRTDAPKTHMTHHA VSDHEATLRCWALSFYPAEITLTWQRDGED
 QTQDTEL VETRPAGDGTFFQKWA AAVVVP SGQEQR YTCHVQHEGLPKPLTLRWE**AAAGG**DKHTHC
 PPCPAPEAAAGGSPVLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVLTPLSPRE
 EMTKQNVSLTCLVKGFYPSDIAVEWESNGKPENNYKATTPPVLDSDGSFFLYSKLTVDKSRWQQG
 NVFSCSVMHREALHNHYTOKSLSLSPG (SEO ID NO:526)

Construct 4131 hIL2 (F42A, H16A)-(G₄S)₄-hIL2 (F42A, H16A)-(G₄S)₄-β2M (R12C, E44C)-(G₄S)₅-HLA-A02(Y84C, A139C, A236C)-AAAGG-IgG1(L234A, L235A)
 APTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFYMPKKKATELKHLQCLEEELKP
 LEEVLNLAQSKNFHLRPRDLISNINIVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTG
GGGSGGGSGGGSGGGSGGGSGAPTSSSTKKTQLQLEALLLDLQMILNGINNYKNPKLTRMLTAKFY
 MPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINIVIVLELKGSETTFMCEYADET
 ATIVEFLNRWITFCQSIISTLTGGGSGGGSGGGSGGGSGGGSGIQRTPKIQVYSCHPAENGKSNFLNC
 YVSGFHPSDIEVDLLKNGCRIEKVEHSDLSFSKDWFSFYLLYYTEFTPTKDEYACRVNHVTLSPQK
 IVKWDRDMGGGSGGGSGGGSGGGSGGGSGGSHSMRYFFTSVSRPGRGEPRFIAVGYYDDT
 QFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRGCYNQSEAGSHT
 VQRMYGCDVGSDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMCAQTTKHKWEAAHVAEQ
 LRAYLEGTVCVEWLRRLRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQR
 DGEDQTDTELVETRPCGDGTFQKWAAVVPSGQEQRYTCHVQHEGLPKPLTLRWEAAAGGDK
 THTCPQPAEAAAGPSVGLFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAIEKTISKAKGQPREPQVYITLP
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRW
 QOQNVFSCSVMEALHNHYTOKSLSLSPG (SEQ ID NO:529)

