HSQRRQDILDLWIYHTQGYF

QUERY	HSQRRQDILDLWIYHTQGYF
CONSENSUS_A	y-rk--E-----V-?-----
A.FR.HIV232956	Y-R---E-----V-N-----
A.FR.HIV232957	Y--K-RE-----V-N-----
A.FR.HIV232959	---K--E-----V-N-----
A.KE.Q23-CXC-CG	Y-RK--E-----V-------
A.SE.SE6594	Y-RK--E-----VH-I--F-
A.SE.SE7253	Y-R---E-----V-N-----
A.SE.SE7535	Y-KK--E-----VH------
A.SE.SE8131	Y-RK--E-----V-------
A.SE.SE8538	Y-RK--E-----V-N--x--
A.SE.SE8891	Y-R---E-----V-N-----
A.UG.92UG037	Y-KK--E-----V-------
A.UG.U455	---K--E-----V-----F-
CONSENSUS_B	y--k--------v-------
B.-.E90NEF	----------V-N-----
B.-.HIV232997	---K--E-----V-------
B.-.HIV233002	Y-PK-KE-----V-----F-
B.-.HIV233009	Y-PK--E-----V-----F-
B.-.HIV233016	---K--------V-------
B.-.HIV233020	---Q--------V-----F-
B.-.HIV233023	---G----------F-
B.-.HIV233029	Y--K--E----SV-------
B.-.HIV233030	Y--K-K------V-N-----
B.-.HIV233032	Y--K-K------V-------
B.-.HIV233037	Y----------
B.-.HIV233038	-F-Q--------V-------
B.-.HIV233043	Y--K--------V-------
B.-.HIV233045	Y-----G-----V-------
B.-.HIV233046	Y----------
B.AU.1062-1-NEF	---K--E----------
B.AU.93JW-3	---K--------V-------
B.AU.93LW-3	-T-K----------
B.AU.AF064660	Y--K--------V-------
B.AU.AF064667	W--K--------V-------
B.AU.AF064676	Y----------
B.AU.MBC200	Y--E--------V-D-----
B.AU.MBC925	Y--K----------
B.CN.AF033570	---K--------V-------
B.CN.AF033572	---K--------V-------
B.CN.PRC8	Y--K--------V-------
B.CN.RL42	Y----------V-------
B.DE.D31	---K--------V-------
B.DE.HAN	Y-PK--E-----V-------
B.DE.HEI28CS	Y--x--------V-N-----
B.DE.HEI3BL	Y--K--------V-------
B.DE.HEI4BL	W--K--------V-------
B.DE.HIVU52491	Y--K--E-----V-------
B.DE.NEFCC	Y--K--E-----V-------
B.DE.NEFCG	Y-----E-----V-------
B.DE.NH53	F--K--E----------
B.ES.89SP061	W--K--------VH------
B.ES.AF082355	Y--K----------
B.ES.AF082357	Y----------V-------
B.ES.AF082358	Y--K--------V-------
B.ES.AF082359	Y--K--------V-------
B.ES.AF082363	Y----------F-
B.ES.AF082364	Y-PK--E-----V-N-----
B.ES.AF082366	Y----------V-------
B.ES.AF082368	Y--K--------V-------
B.ES.AF082370	Y----------V-------
B.ES.AF082375	Y--K--------V-------
B.ES.AF082376	Y--K----------N-----
B.ES.AF082377	---K----------
B.ES.AF082378	Y--K--------V-------
B.ES.AF082380	---K--------V-------
B.ES.AF082383	Y--K--------V-------
B.ES.AF082386	Y-HK--------V-----F-
B.FR.HIV232961	---K--------V-------
B.FR.HIV232962	Y--K-RE-----V-N-----
B.FR.HIV232963	C--K--E----------
B.FR.HIV232964	W--Q--E-----V-N---F-
B.FR.HIV232965	---K--------V-------
B.FR.HXB2	----------
B.FR.NE100	---K--E-----V-------
B.FR.SWB884	---K--E-----V-------
B.GA.OYI	Y--K--------V-------
B.GB.001GH-93(1)	---K--------V-N-----
B.GB.002EM-93(1)	W--K--------V-------
B.GB.003PW-93(1)	Y--K--------V-N-----
B.GB.005PF1-93(1)	Y--Q--E-----V------L
B.GB.006DC-93(1)	Y----------V-------
B.GB.010JW-93(1)	Y--K--------V-------
B.GB.011JR-93(4)	Y--K--------V-------
B.GB.012WM-93(1)	Y-RK--E-----V-------
B.GB.013PP-94(2)	---Q--------V-------
B.GB.016GB-93(1)	Y--K--------V-----F-
B.GB.023PA-93(1)	----------V-----F-
B.GB.025JN-93(1)	Y--K--------V-------
B.GB.027SL-93(1)	---K--E-----FH------
B.GB.028JH-94(1)	Y--K--------V-------
B.GB.030JG-93(1)	--LK--E---------P---
B.GB.031DA-93(1)	W--K--------V-N-----
B.GB.032AN-93(1)	---K--------V-------
B.GB.037BS-94(2)	Y--K------Q-V-------
B.GB.039NM-94(1)	Y-LK--------V-------
B.GB.044C1-94(2)	Y--K--------V-------
B.GB.046JM-94(1)	W----------V-N-----
B.GB.048AD-94(1)	---KG-------V-------
B.GB.056RP-94B(1)	---K--------V-------
B.GB.057DR-94(1)	Y-RK--E-----V-N-----
B.GB.065RK-94(1)	---K--------V-------
B.GB.067MM-94(2)	Y--K--------V-------
B.GB.068JB-94(1)	---K--------V-----F-
B.GB.098MS-94(1)	Y-HK--------V-------
B.GB.103CD-94(1)	Y----------V---E---
B.GB.104RT-94(1)	Y--Q--------V-N-----
B.GB.105AS-94(1)	W--K--E----------
B.GB.112CR-94(2)	Y-PK--E-----V-------
B.GB.117CH-94(2)	---Q----------
B.GB.122PS-95(1)	Y--K--------V-------
B.GB.124PD-95(1)	Y--K--------V-------
B.GB.127RG-96(1)	Y--K----------
B.GB.130WDC-95(1)	Y--Q--------V-------
B.GB.131MVS-95(1)	Y-----E----------
B.GB.143PL-95(1)	---K--------V-------
B.GB.151DH-95(1)	Y----------VH----F-
B.GB.157GT-95(1)	Y--K--------V-------
B.GB.160KO-95(1)	Y----------N-----
B.GB.161KC-95(1)	Y--Q--------V-N--D--
B.GB.162BB-95(1)	Y----------
B.GB.163NG-95(1)	Y-----E-----V-------
B.GB.164SZ-95(1)	Y--K--------V-------
B.GB.165DH-95(1)	Y-RK--E-----V-------
B.GB.166PW-95(1)	Y--K--E-----V-------
B.GB.167RW-95(1)	Y-RK--E-----M-------
B.GB.168MB-95(1)	Y--K--------V-------
B.GB.CAM1	Y----------
B.GB.GLNEF1	-A----------
B.GB.MANC	Y--K--------V-------
B.GB.NEF2	---K--------V-------
B.GB.NEF3	---K--------V-------
B.GB.NEF5	Y--K----------
B.IN.HIVP35A	Y--K--------V-------
B.IT.AF011471	----------V-------
B.IT.AF011474	---K--------V-------
B.IT.AF011477	Y--K--------V-------
B.IT.AF011478	Y--K--------V-N--ASS
B.IT.AF011480	----------V-------
B.IT.AF011482	---K--------V-------
B.IT.AF011483	Y--K--------V----xF-
B.IT.AF011486	----------V-------
B.IT.AF011488	Y----------V---E---
B.IT.AF011492	Y--K--------V-------
B.IT.AF047080	Y--K--------V-----F-
B.IT.AF047081	Y--Q--------V-N-----
B.IT.B.IT-L1	Y--Q--------V-N---F-
B.IT.B.IT-L2	Y----------V-------
B.IT.B.IT-L3	Y--K--E-----V-N-----
B.IT.B.IT-L4	Y--K--------V-------
B.IT.B.IT-L5	---K--x-----V-------
B.IT.B.IT-R1	Y--Q-K------V-------
B.IT.B.IT-R2	Y-----E-----V-------
B.IT.B.IT-R3	---K--------V-------
B.IT.B.IT-R4	----------VH------
B.IT.B.IT-R5	W--K----------
B.KR.AF063915	Y--K--------V-------
B.KR.AF063916	Y-PK--------V-----F-
B.KR.AF063919	---K--------V-------
B.KR.AF063921	Y--K--------V-------
B.KR.AF063926	Y--K--------V-N-----
B.KR.AF063927	Y--K--------V-------
B.KR.AF063931	Y--K--------V-------
B.KR.HIVZ98019	Y--K--------V-------
B.KR.HIVZ98022	---K--------V-------
B.KR.HIVZ98024	Y--K--------V-------
B.KR.HIVZ98025	---K--------V------L
B.KR.HIVZ98027	Y--K--------V#----F-
B.KR.HIVZ98029	Y--K--------V-------
B.KR.HIVZ98030	Y--KS----------

```
B.KR.HIVZ98032        Y--K--------V-------
B.KR.HIVZ98034        Y--K--------------F-
B.NL.3202A21          Y-------------------
B.NL.NEFA             Y--K-K------V-------
B.NL.NEFD             Y--K-K------V-------
B.NL.NEFE             ------------V-------
B.SE.AF047082         Y--K-RE-------N-----
B.SE.AF047083         Y--K--------V-------
B.SE.AF047085         ------------V-------
B.TH.28-19            ---K--E-----V-------
B.TH.AF082838         Y--K--------V-------
B.TH.AF082839         --HK--------V-------
B.TH.AF082841         F--K--------V-------
B.TW.LM49             Y--KKE------------F-
B.US.HIV1U03375       Y--------E--V-------
B.US.005PF-96(1)      Y--Q--E-------N-----
B.US.AD-93(1)         Y----R------V-N-----
B.US.AD8              ---K--E-----V-------
B.US.BC               F-----------T-------
B.US.BIB              Y--N----------------
B.US.BJ-93(1)         Y--Q--------V-------
B.US.BO1              -------------------
B.US.BRVA             ---Q--------V-------
B.US.BT-94(1)         Y--Q-R------V-------
B.US.CD1              Y--K-----N--V-------
B.US.D8511            Y--K--------V-------
B.US.DH1              Y----------$V-------
B.US.DH123            Y--K--------V-N-----
B.US.DJ-93(1)         ---K--------------F-
B.US.E1               Y--K--------V-------
B.US.E81NEF           ------------V-------
B.US.E88NEF           -------------------
B.US.EP-94(1)         Y-RK--E-----V-------
B.US.FA-93(1)         Y--K--------V-N-----
B.US.HIV1U16893       Y-------------------
B.US.HIV1U24455       Y--K--------V-------
B.US.HIV1U26074       ---K----------------
B.US.HIV1U26098       Y--K----------------
B.US.HIV1U26112       Y--K--------V-------
B.US.HIV1U26119       Y--K-R------V-------
B.US.HIV1U26141       Y-----------V-------
B.US.HIVU44444        -------------------
B.US.HIVU44450        Y--K--------V-N-----
B.US.HIVU44456        ---K------M$--------
B.US.HIVU44465        Y-----E-----V-------
B.US.HIVU44468        ---K----------------
B.US.HP87B1           Y-RK--E-----V-------
B.US.HS-93(1)         Y--K--E-----V-------
B.US.JRCSF            Y--K----------------
B.US.JRFL             ---K--------V-------
B.US.LM1              Y-----------V-------
B.US.LT-87-1(1)       Y--K-R------V-------
B.US.MB-94(1)         Y--K--------V-------
B.US.MNCG             Y--K--------V-------
B.US.NC7              W-------------------
B.US.NEF              -------------------
B.US.NEF164B          Y--K--E-----V-------
B.US.NEF166E          Y--K----------------
B.US.NEF179C          Y--Q--------V-N-----
B.US.NEF226B          ---Q--------V-------
B.US.P102A13          ------E-----V-------
B.US.P233A17          Y--K--------V-N-----
B.US.P248A01          Y--K--------V-------
B.US.P357A01          ---K--G-----V-------
B.US.P896             ---K--------V-----F-
B.US.PC-93(1)         Y--K----------------
B.US.PRISO(1)         ---Q--------V-N-----
B.US.RF               F--K--------V-------
B.US.RP12             Y--K--------V-------
B.US.RR1              Y--K--------V-N-----
B.US.SC               -------------------
B.US.SF2              W-----E-------------
B.US.U16917           ---K----------------
B.US.WEAU160          Y--K--------V-----F-
B.US.WR27             Y--K--------V-------
B.US.YU2              ---Q--------V-------

CONSENSUS_C           Y-kk--e-----v-------
C.BR.92BR025          Y-KK--------V-N-----
C.BW.96BW01B21        Y-KK--E-----V-N---V-
C.BW.96BW0402         Y-KK--------V-N-----
C.BW.96BW0502         Y-KK--E-----V-----F-
C.BW.96BW1104         Y-RK--E-----V-----F-
C.BW.96BW1210         Y-KK--E-----V-N-----
C.BW.96BW15B03        Y-PK--E-----V-----F-
C.BW.96BW16B01        Y-KK--------V-N-R-FL
C.BW.96BW17A09        Y-KK--E-----V-----F-
C.ET.ETH2220          Y-KK--E-----V-N---F-
C.FR.HIV232966        Y-R---E-----V-----F-
C.FR.HIV232967        Y-KK-KE-----V-N-----
C.FR.HIV232968        Y-KK--E-----V-----F-
C.FR.HIV232969        Y-KK--E-----V-N---F-
C.FR.HIV232970        Y-KK--E-----V-------
C.FR.HIV232971        Y-KN--E-----V-------
C.FR.HIV232972        Y-RK--E-----V-----F-
C.FR.HIV232973        Y-KK--E-----V-----F-
C.FR.HIV232976        Y-KQ--------V-N---F-
C.FR.HIV232977        Y-KK--E-------------
C.FR.HIV232978        Y-KK--------V-------
C.FR.HIV232979        Y-KK--E-----V-N-----
C.FR.HIV232980        Y--K--------V-----F-
C.FR.HIV232996        Y--K--E-----V-N-----
C.IN.21068            Y-KK--E-----V-------
C.IN.301904           Y-KK--E-----V-------
C.IN.301999           Y-KK--E-----V-----F-
C.IN.94IN11246        Y-KK--E-----V-------
C.IN.HIVY15117        Y-KK--E-----V-------
C.IN.HIVY17884        Y-KK--E-----V-------
C.IN.HIVY17891        Y-KK--E-----V-------
C.IN.HIVY17892        Y-KK--E-----V-------

CONSENSUS_D           w-kK--e-----V-?---?-
D.CD.84ZR085          Y--K--------V-----F-
D.CD.ELI              W-KK--E-----V-N---I-
D.CD.NDK              W-KK--E-----V-N---I-
D.UG.94UG1141         W-PK--E-----V-----F-

CONSENSUS_F           Y-kK--E-----V-------
F.CM.HIV232985        Y-KK--E-----V-------
F.CM.HIV232986        Y-RK--E-----V-------
F.FR.HIV232987        Y-KK--E-----V-----F-

CONSENSUS_F1          Y-Kk--e-----v-------
F1.BE.VI850           Y-KK-G-T----V-------
F1.BR.93BR020.1       Y-K---E-----V-------
F1.FI.FIN9363         Y-KK--E-----L-------
F1.FR.MP411           Y-KK--E-----V-----F-

CONSENSUS_F2          Y-?K--E-----V-------
F2.CM.MP255           Y-KK--E-----V-------
F2.CM.MP257           Y-RK--E-----V-------

CONSENSUS_G           y-Kk--------V-n---f-
G.BE.DRCBL            Y-KK--E-----V-----F-
G.FI.HH8793           Y-KK--------V-N---F-
G.ML.HIV232990        --KQ--------V-N---F-
G.NG.92NG083          Y-K---------V-N---F-
G.NG.HIV232991        Y-KQ----P---V-N-----
G.NG.HIV232992        Y-KK--E-----V-N---F-
G.SE.SE6165           Y-KK--E-----V-N-----

CONSENSUS_H           Y-Kk--e-----V-N-----
H.BE.VI991            Y-KK--E-----V-N-----
H.BE.VI997            Y-KK--E-----V-N-----
H.CD.HIV232994        Y-KK--E-----V-N---F-
H.CD.HIV232995        Y-KK--E---F-V-N-----
H.CF.90CF056          Y-KQ--------V-N-----

CONSENSUS_J           Y-KK--E-----VHN-----
J.SE.SE9173           Y-KK--E-----VHN-----
J.SE.SE9280           Y-KK--E-----VHN-----

CONSENSUS_K           Y-K?--E-----V-----F-
K.CD.EQTB11C          Y-K---E-----V-----F-
K.CM.MP535            Y-KK--E-----V-----F-
N.CM.YBF30            W-RK--------M-----IL

CONSENSUS_O           Y-HK-AE-----?-?---F-
O.CM.ANT70C           Y-HK-AE-----V-N---F-
O.CM.MVP5180          Y-HK-AE-----------F-
CRF01_AE.CF.90CF402   --K---E-----VHN-----
CRF01_AE.FR.232982    Y-K---E-----V-N---F-
CRF01_AE.FR.232983    Y-KK--E-----V-----F-
CRF01_AE.FR.232984    Y-KK--E-----V-N---F-
CRF01_AE.TH.1-2       Y-K---E-----V-N---F-
CRF01_AE.TH.1-3       Y-K---E-----V-N---F-
CRF01_AE.TH.11-25     Y-K---E-----V-N---F-
CRF01_AE.TH.11-31     Y-K---E-----V-N---F-
CRF01_AE.TH.122-21    Y-K---E-----V-N---F-
CRF01_AE.TH.18-47     Y-KK--E-----V-N---F-
CRF01_AE.TH.235-3     Y-K---E-----V-N---F-
CRF01_AE.TH.235-32    Y-K---E-----V-N---F-
CRF01_AE.TH.24-54     --KK--E-----V-N---FL
CRF01_AE.TH.240-12    Y-KK--E-----V-N---F-
```

```
CRF01_AE.TH.26-3      Y-K---E-----V-----F-
CRF01_AE.TH.35-6      Y-K---E-----V-N---F-
CRF01_AE.TH.6-9       Y-K---E-----V-N---F-
CRF01_AE.TH.73-44     Y-KK--E-----V-N---F-
CRF01_AE.TH.74-26     Y-KK--E-----V-N---F-
CRF01_AE.TH.89-30     Y-KK--E-----V-N---F-
CRF01_AE.TH.9-3       Y-K---E-----V-N---F-
CRF01_AE.TH.93TH253   Y-KK--E-----V-----F-
CRF01_AE.TH.98-4      Y-KK--E-----V-N---F-
CRF01_AE.TH.CM240     Y-KK--E-----V-N---F-
CRF01_AE.TH.TH022     Y-KK--E-----V-N---F-
CRF01_AE.TH.TH047     Y-KK--E-----V-N---F-
CRF02_AG.FR.DJ263     Y-KK--E-----V-----F-
CRF02_AG.FR.DJ264     Y-KK--E-----V-----F-
CRF02_AG.NG.IBNG      Y-KK--E-----V-N---F-
CRF03_AB.RU.KAL1532   Y-KK--E-----V-------
CRF04_cpx.CY.94CY03   Y-KK--E-----V-----F-
CRF04_cpx.GR.97PVCH   Y-KQ--------V-N-----
CRF04_cpx.GR.97PVMY   Y-KK--E-----V-N-----
AC.IN.21301           Y-RK--E-----V-----F-
AC.RW.92RW009         Y-KK--------V-N-----
AC.SE.SE9488          Y--Q--------V-N-----
AC.ZM.ZAM184          Y-----E-----V-------
ACD.SE.SE8603         Y-KK--------V-N---F-
AD.SE.SE6954          W-PK--E-----V-------
AD.SE.SE7108          Y-RK-A------V-----F-
ADHU.NO.NOGIL3        Y-KK--E-----VHN---F-
ADU.CD.MAL            W-PK--E-----V-------
AF.GA.HIV232981       Y-RK--E-----V-------
AG.NG.G3              Y-KK--------V-N-----
AG.SE.SE7812          Y-KK--E-----V-----F-
AGHU.GA.VI354         ---K--------V-------
AGJ.AU.BFP90          Y-KK--E-----V-N---F-
AGJ.ML.95ML84         Y-KK--------V-----F-
AGU.CD.Z321           Y-KK--E-----V-----F-
BF.BR.93BR029.4       Y-KK--E-----V-------
DF.BE.VI961           W-RK--K-----V-N-----
GH.GA.HIV232993       Y-KK--E-----V-----F-
GU.FR.HIV232974       Y-KK--E-----V-N---F-
U.CD.VI1126           Y-KK--E-----V-N-----
U.CM.HIV232988        Y-KK--E-----V-----F-
U.FR.HIV232958        Y-KK--E-----V-------
U.FR.HIV232960        Y-KK--E-----V-------

CONSENSUS_CPZ         Y-R---E-----V-----?-
CPZ.GA.CPZGAB         Y-R---E-----V-----F-
CPZ.US.CPZUS          Y-R---E-----V-----I-
```

YNVLPQGWKGSPAIFQSSMT

```
QUERY                YNVLPQGWKGSPAIFQSSMT

CONSENSUS_A          --------------------
A.KE.Q23-CXC-CG      --------------------
A.SE.SE6594          x-------------------
A.SE.SE7253          --------------------
A.SE.SE7535          --------------------
A.SE.SE8131          --------------------
A.SE.SE8538          ------------S-------
A.SE.SE8891          -------------------I
A.UG.92UG037         ----------------A---
A.UG.U455            ------------S-------

CONSENSUS_B          --------------------
B.-.NL43E9           ----------------C---
B.AU.MBC18           --------------------
B.AU.MBC200          --------------------
B.AU.MBC925          ----------------C---
B.AU.MBCC54          --------------------
B.AU.MBCC98          ----------------Y---
B.AU.MBCD36          --------------------
B.CN.RL42            ----------------C---
B.DE.D31             --------------------
B.DE.HAN             --------------------
B.FR.HXB2            --------------------
B.GA.OYI             --------------------
B.GB.CAM1            --------------------
B.GB.MANC            --------------------
B.NL.3202A21         ----------------C---
B.TW.LM49            --------------------
B.US.AD8             --------------------
B.US.BC              --------------------
B.US.DH123           --------------------
B.US.JRCSF           --------------------
B.US.JRFL            --------------------
B.US.MNCG            --------------------
B.US.NY5CG           ----------------C---
B.US.P896            --------------------
B.US.RF              --------------------
B.US.SF2             --------------------
B.US.WEAU160         --------------------
B.US.WR27            ------------T--P----
B.US.YU2             --------------------

CONSENSUS_C          --------------------
C.BR.92BR025         ------------S-----T-
C.BW.96BW01B03       --------------------
C.BW.96BW0402        -------------------I
C.BW.96BW0502        --------------------
C.BW.96BW1104        ------------S-------
C.BW.96BW1210        --------------------
C.BW.96BW15B03       ------------S-------
C.BW.96BW1626        --------------------
C.BW.96BW17A09       --------------------
C.ET.ETH2220         ------------P------P
C.IN.21068           ----------------N---
C.IN.301904          --------------------
C.IN.301905          ----------------C---
C.IN.301999          ----------------A---
C.IN.94IN11246       --------------------

CONSENSUS_D          --------------------
D.CD.84ZR085         -------------------I
D.CD.ELI             --------------------
D.CD.NDK             --------------------
D.CD.Z2Z6            --------------------
D.UG.94UG1141        --------------------

CONSENSUS_F1         ----------------c---
F1.BE.VI850          ----------------C---
F1.BR.93BR020.1      ----------------Y---
F1.FI.FIN9363        ----------------C---
F1.FR.MP411          --------------------

CONSENSUS_F2         ----------------?--?
F2.CM.MP255          ----------------C---
F2.CM.MP257          -------------------I

CONSENSUS_G          --------------------
G.BE.DRCBL           -#..----------------
G.FI.HH8793          --------------------
G.NG.92NG083         --------------------
G.SE.SE6165          --------------------
CONSENSUS_H          --------------------
H.BE.VI991           --------------------
H.BE.VI997           --------------------
H.CF.90CF056         --------------------

CONSENSUS_J          ----------------C---
J.SE.SE9173          ----------------C---
J.SE.SE9280          ----------------C---

CONSENSUS_K          ----------------?---
K.CD.EQTB11C         ----------------C---
K.CM.MP535           ----------------H---
N.CM.YBF30           -----------------T--
CONSENSUS_O          --------------------
O.CM.ANT70C          --------------------
O.CM.MVP5180         --------------------
AC.ET.E3099G         --------------------
AC.IN.21301          ----------------A---
AC.RW.92RW009        ----------------N---
AC.SE.SE9488         --------------------
AC.ZM.ZAM184         ------------S-------
ACD.SE.SE8603        --------------------
AD.SE.SE6954         --------------------
AD.SE.SE7108         --------------------
ADU.CD.MAL           --------------------
AG.NG.G3             --------------------
AG.SE.SE7812         ----------------A---
AGHU.GA.VI354        --------------------
AGHU.NO.NOGIL3       ----------------C---
AGJ.AU.BFP90         -------------------I
AGJ.ML.95ML8         -------------------I
AGU.CD.Z321          --------------------
BF.BR.93BR029.4      --------------------
CRF01_AE.CF.90CF40   --------------------
CRF01_AE.TH.93TH25   --------------------
CRF01_AE.TH.CM240    --------------------
CRF01_AE.TH.TH022    ----------------C-T-
CRF01_AE.TH.TH047    --------------------
CRF02_AG.FR.DJ263    ----------------A---
CRF02_AG.FR.DJ264    ----------------A---
CRF02_AG.NG.IBNG     ----------------A---
CRF03_AB.RU.KAL153   --------------------
CRF04_CPX.CY.94CY0   ----------------C---
CRF04_CPX.GR.97PVC   ----------------Y---
CRF04_CPX.GR.97PVM   ----------------C---
DF.CD.VI961          ----------------C---
U.CD.VI1126          ----------------Y---

CONSENSUS_CPZ        --------------------
CPZ.CD.CPZANT        ----------------A---
CPZ.GA.CPZGAB        ------------S-------
CPZ.US.CPZUS         --------------------
```

SPAIFQSSMTKILEPFRKQN

```
QUERY                SPAIFQSSMTKILEPFRKQN

CONSENSUS_A          -----------------sk-
A.KE.Q23-CXC-CG      -----------------SK-
A.SE.SE6594          -----------------SK-
A.SE.SE7253          -----------------LK-
A.SE.SE7535          -----------------ER-
A.SE.SE8131          -----------------SK-
A.SE.SE8538          --S--------------SK-
A.SE.SE8891          ---------I-------V--
A.UG.92UG037         ------A----------SK-
A.UG.U455            --S--------------S-H

CONSENSUS_B          --------------------
B.-.NL43E9           ------C-------------
B.AU.MBC18           ----------R------R--
B.AU.MBC200          --------------------
B.AU.MBC925          ------C-------------
B.AU.MBCC54          --------------------
B.AU.MBCC98          ------Y-------------
B.AU.MBCD36          --------------------
B.CN.RL42            ------C-------------
B.DE.D31             --------------------
B.DE.HAN             --------------------
B.FR.HXB2            --------------------
B.GA.OYI             --------------------
B.GB.CAM1            --------------------
B.GB.MANC            --------------------
B.NL.3202A21         ------C-------------
B.TW.LM49            ----------R---------
B.US.AD8             --------------------
B.US.BC              --------------------
B.US.DH123           --------------------
B.US.JRCSF           --------------------
B.US.JRFL            --------------------
B.US.MNCG            --------------------
B.US.NY5CG           ------C-------------
B.US.P896            --------------------
B.US.RF              ----------------K---
B.US.SF2             --------------------
B.US.WEAU160         --------------------
B.US.WR27            --T--P----Q-------P-
B.US.YU2             ----------T---------

CONSENSUS_C          -----------------a--
C.BR.92BR025         --S-----T--------A--
C.BW.96BW01B03       -----------------AL-
C.BW.96BW0402        ---------I-------TK-
C.BW.96BW0502        -----------------L--
C.BW.96BW1104        --S--------------AK-
C.BW.96BW1210        -----------------A--
C.BW.96BW15B03       --S--------------AR-
C.BW.96BW1626        -----------------A--
C.BW.96BW17A09       -----------------A--
C.ET.ETH2220         --P------PQ------AP-
C.IN.21068           ------N---R------A--
C.IN.301904          ----------R------AR-
C.IN.301905          ------C---R------A--
C.IN.301999          ------A----------A--
C.IN.94IN11246       -----------------GR-

CONSENSUS_D          --------------------
D.CD.84ZR085         ---------I----------
D.CD.ELI             --------------------
D.CD.NDK             --------------------
D.CD.Z2Z6            --------------------
D.UG.94UG1141        --------------------

CONSENSUS_F1         ------c----------ak-
F1.BE.VI850          ------C----------MK-
F1.BR.93BR020.1      ------Y------D---AK-
F1.FI.FIN9363        ------C----------TR-
F1.FR.MP411          -----------------AK-

CONSENSUS_F2         ------?--?-------??-
F2.CM.MP255          ------C----------AK-
F2.CM.MP257          ---------I--------E-

CONSENSUS_G          -----------------tk-
G.BE.DRCBL           -----------------T--
G.FI.HH8793          -----------------IK-
G.NG.92NG083         ---------------S-TK-
G.SE.SE6165          ----------R------AN-

CONSENSUS_H          --------------------
H.BE.VI991           --------------------
H.BE.VI997           --------------------
H.CF.90CF056         -------------A---E--

CONSENSUS_J          ------C------K---ER-
J.SE.SE9173          ------C------K---ER-
J.SE.SE9280          ------C------K---ER-

CONSENSUS_K          ------?----------?K-
K.CD.EQTB11C         ------C----------RK-
K.CM.MP535           ------H----------IK-
N.CM.YBF30           -------T---------EKH

CONSENSUS_O          -------------D---??-
O.CM.ANT70C          -------------D---RD-
O.CM.MVP5180         -------------D----S-
AC.ET.E3099G         ----------E------TK-
AC.IN.21301          ------A----------A--
AC.RW.92RW009        ------N----------A--
AC.SE.SE9488         -------------A---S--
AC.ZM.ZAM184         --S----------D---SK-
ACD.SE.SE8603        -----------------SK-
AD.SE.SE6954         --------------------
AD.SE.SE7108         -----------------SK-
ADU.CD.MAL           -----------------TK-
AG.NG.G3             -----------------TE-
AG.SE.SE7812         ------A----------TK-
AGHU.GA.VI354        --------------------
AGHU.NO.NOGIL3       ------C----------AK-
AGJ.AU.BFP90         ---------I-------IK-
AGJ.ML.95ML8         ---------I-------TK-
AGU.CD.Z321          -----------------TK-
BF.BR.93BR029.4      --------------------
CRF01_AE.CF.90CF40   -----------------AR-
CRF01_AE.TH.93TH25   -----------------IK-
CRF01_AE.TH.CM240    -----------------IK-
CRF01_AE.TH.TH022    ------C-T--------TK-
CRF01_AE.TH.TH047    -----------------IK-
CRF02_AG.FR.DJ263    ------A---N---HY-IK-
CRF02_AG.FR.DJ264    ------A----------IK-
CRF02_AG.NG.IBNG     ------A----------TK-
CRF03_AB.RU.KAL153   --------------------
CRF04_CPX.CY.94CY0   ------C----------FK-
CRF04_CPX.GR.97PVC   ------Y----------TR-
CRF04_CPX.GR.97PVM   ------C----------TK-
DF.CD.VI961          ------C-------------
U.CD.VI1126          ------Y----------TK-

CONSENSUS_CPZ        -------------?---?k?
CPZ.CD.CPZANT        ------A------A---DKY
CPZ.GA.CPZGAB        --S--------------EK-
CPZ.US.CPZUS         -------------D-----H
```

LRPGGKKKYKLKHIVWASRE

```
QUERY                 LRPGGKKKYKLKHIVWASRE

CONSENSUS_A           ---------r---l------
A.KE.Q23-CXC-CG       ---------RM--LI-----
A.SE.SE6594           ---------R---L------
A.SE.SE7253           ---------RM--L------
A.SE.SE7535           -------Q-R---L------
A.SE.SE8131           -----N---R---L------
A.SE.SE8538           ---------RM--L------
A.SE.SE8891           -------------M---R--
A.UG.92UG037          ---------R---L------
A.UG.U455             -----N---R---L------

CONSENSUS_B           --------------------
B.AU.AF128998         -------T-Q----------
B.-.NL43E9            -------L------I-----
B.AU.MBC18            --------------------
B.AU.MBC200           -------Q-R----------
B.AU.MBC925           ---R-----Q----------
B.AU.MBCC54           ---------Q----------
B.AU.MBCC98           ---------Q----------
B.AU.MBCD36           -----R---Q----------
B.CN.RL42             ---------R---L------
B.DE.D31              ---------R----------
B.DE.HAN              ---------Q----------
B.ES.89SP061          ---------R---L------
B.FR.HXB2             --------------------
B.GA.OYI              ---------Q----------
B.GB.CAM1             --------------------
B.GB.MANC             --------------------
B.JP.JH31             --------------------
B.NL.3202A21          -------R------------
B.TW.LM49             ---------R---L------
B.US.85WCIPR54        --------------------
B.US.AD8              --------------------
B.US.BC               -------------L------
B.US.DH123            --------------------
B.US.JRCSF            ---------R----------
B.US.JRFL             ---------R----------
B.US.MNCG             -------------V------
B.US.NC7              ---------M----------
B.US.NY5CG            -------Q-R----------
B.US.P896             --------------------
B.US.RF               ---R---R------------
B.US.SF2              --------------------
B.US.WC001            --------------------
B.US.WEAU160          -----N--------------
B.US.WR27             ---------R---L------
B.US.YU2              -------Q-R----------

CONSENSUS_C           -------h-m---l------
C.BR.92BR025          -K-----H-MM--L------
C.BW.96BW01B22        -------C-M---L------
C.BW.96BW0402         -------Q-RI--L------
C.BW.96BW0502         -------H-M---L------
C.BW.96BW1104         -------R-MI--L------
C.BW.96BW1210         -------R-MM--L------
C.BW.96BW15B03        S------C-M----------
C.BW.96BW1626         -------R-M---L------
C.BW.96BW17A09        -------H-M---L------
C.ET.ETH2220          -------H-M---L---N--
C.IN.93IN904          -------H-M---L------
C.IN.93IN905          -------H-M---L------
C.IN.93IN999          -------H-M---L------
C.IN.94IN11246        -------H-M---L------
C.IN.95IN21068        -------R-M---L------

CONSENSUS_D           ---------r---l------
D.CD.84ZR085          --------------------
D.CD.ELI              ---------R----------
D.CD.NDK              ---------A---LI-----
D.CD.Z2Z6             ---------R---L------
D.UG.94UG1141         ---------R---L------

CONSENSUS_F           ---------rm--L------
F.BR.BZ162            ---------R---L------
F.CD.VI174            ---------RM--L------
F.RW.VI69             -----R----M--LI-----

CONSENSUS_F1          ---------rm--L------
F1.BE.VI850           -------R--M--LI-----
F1.BR.93BR020.1       ---------R---L------
F1.FI.FIN9363         -------Q-RI--L------
F1.FR.MP411           ---------RM--L------

CONSENSUS_F2          -?-----?-R---?------
F2.CM.MP255           -K-----R-R---L------
F2.CM.MP257           ---------R----------

CONSENSUS_G           -----x---xx--L------
G.BE.DRCBL            -------R-RM--L------
G.FI.HH8793           ---------R---L------
G.NG.92NG083          -----R--------------
G.SE.SE6165           -----R-S--I--L------

CONSENSUS_H           ---------R---L------
H.BE.VI991            -----R---R---L------
H.BE.VI997            ---------R----------
H.CF.90CF056          ---------R---L------

CONSENSUS_J           -------?-RI--L------
J.SE.SE9173           -------Q-RI--L------
J.SE.SE9280           ---------RI--L------

CONSENSUS_K           ---------r---L------
K.BE.VI325            -----S---R---L------
K.CD.EQTB11C          ---------R---L------
K.CM.MP535            -------------L------
N.CM.YBF30            ---------RM--L------

CONSENSUS_O           -?--S--?-R---L------
O.CM.ANT70C           -K--S----R---L------
O.CM.MVP5180          ----S--A-R---L------
CRF01-AE.CF.90CF40    -------Q-RM--L------
CRF01-AE.TH.93TH25    ----------M--L------
CRF01-AE.TH.CM240     -----R---R---L------
CRF01-AE.TH.TH022     -----R---RM--L------
CRF01-AE.TH.TH047     -----R---H----------
CRF02_AG.FR.DJ263     ---------R---L------
CRF02_AG.FR.DJ264     ---A-----R---L------
CRF02_AG.NG.IBNG      ---------R---L------
CRF03_AB.RU.KAL15     ------E--RI--L------
CRF04_cpx.CY.94CY0    ---------R---L------
CRF04_cpx.GR.97PVC    ---------R---L------
CRF04_cpx.GR.97PVM    -------R-RI--LI-----
AC.ET.E3099G          -----N---R---L------
AC.IN.21301           -------H-MI--L------
AC.RW.92RW009         -K-----T-MM--L------
AC.SE.SE9488          ---------RM--L------
AC.ZM.ZAM174-21       -----S-R-MI--L------
AC.ZM.ZAM184          -------Q-RM--L------
AC.ZM.ZAM716-17       -------Q-RI--L------
ACD.SE.SE8603         ---------R---L------
AD.SE.SE6954          -------R-R----------
AD.SE.SE7108          -----R--------------
ADHU.NO.NOGIL3        -------Q-R---L------
ADU.CD.MAL            ---------R---L------
AG.NG.G3              ---------RM--L------
AG.SE.SE7812          ---------R---L------
AGHU.GA.VI354         ---------QI---------
AGJ.AU.BFP90          ----------M--L------
AGJ.ML.95ML8          ---------RM--L------
AGU.CD.Z321           -------Q------------
BF.BR.93BR029.4       -----H---R----------
DF.CD.VI961           ---------R----------
U.CD.VI1126           -----R---R---L------

CONSENSUS_CPZ         ---------Mm--L------
CPZ.CD.CPZANT         ---------MI--L---RS-
CPZ.GA.CPZGAB         -----R-R-MM--L------
CPZ.US.CPZUS          ---------MM--L------
```

TNNPPIPVGEIYKRWIILGL

```
QUERY                TNNPPIPVGEIYKRWIILGL

CONSENSUS_A          -g-------D----------
A.KE.Q23-CXC-CG      -G-------D----------
A.SE.SE6594          -S-------D----------
A.SE.SE7253          -G-------D----------
A.SE.SE7535          -G-------D----------
A.SE.SE8131          -S---V---D----------
A.SE.SE8538          -S-------D----------
A.SE.SE8891          -S-------D----------
A.UG.92UG037         -G-------D-----M----
A.UG.U455            -G-------D--R-------

CONSENSUS_B          --------------------
B.AU.AF128998        -S---V--------------
B.-.NL43E9           -H------------------
B.AU.MBC18           -G--A---------------
B.AU.MBC200          --------------------
B.AU.MBC925          --------------------
B.AU.MBCC54          -S------------------
B.AU.MBCC98          ---------D----------
B.AU.MBCD36          ---------D----------
B.CN.RL42            --------------------
B.DE.D31             --------------------
B.DE.HAN             --------------------
B.ES.89SP061         --------------------
B.FR.HXB2            --------------------
B.GA.OYI             --------------------
B.GB.CAM1            --------------------
B.GB.MANC            --------------------
B.JP.JH31            -S------------------
B.NL.3202A21         -H------------------
B.TW.LM49            --------------------
B.US.85WCIPR54       --------------------
B.US.AD8             --------------------
B.US.BC              --------------------
B.US.DH123           -----------------M--
B.US.JRCSF           --------------------
B.US.JRFL            --------------------
B.US.MNCG            --------------------
B.US.NC7             -S------------------
B.US.NY5CG           -H------------------
B.US.P896            --------------------
B.US.RF              --------------------
B.US.SF2             --------------------
B.US.WC001           --------------------
B.US.WEAU160         --------------------
B.US.WR27            -Hx-----------------
B.US.YU2             --------------------

CONSENSUS_C          -s---v---d----------
C.BR.92BR025         -----V---D----------
C.BW.96BW01B22       -A---V---D----------
C.BW.96BW0402        -S-------D----------
C.BW.96BW0502        -S---V---D----------
C.BW.96BW1104        -S-------D----------
C.BW.96BW1210        -S-------D----------
C.BW.96BW15B03       -S-------D----------
C.BW.96BW1626        -S---V--------------
C.BW.96BW17A09       ---------D------TM--
C.ET.ETH2220         -G---V---D----------
C.IN.93IN904         -G---V---D----------
C.IN.93IN905         -G---V--------------
C.IN.93IN999         -G---V---D----------
C.IN.94IN11246       -S---V--------------
C.IN.95IN21068       -----V---D----------

CONSENSUS_D          -S------------------
D.CD.84ZR085         -S------------------
D.CD.ELI             -S---------------V--
D.CD.NDK             -S------------------
D.CD.Z2Z6            -S------------------
D.UG.94UG1141        -S------------------

CONSENSUS_F          -s---v--------------
F.BR.BZ162           -S---V--------------
F.CD.VI174           -----V--------------
F.RW.VI69            -S-------D----------

CONSENSUS_F1         -?---V---d----------
F1.BE.VI850          -G---V---D----------
F1.BR.93BR020.1      -G---V----M---------
F1.FI.FIN9363        -S---V---D----------
F1.FR.MP411          -S---V---D----------

CONSENSUS_F2         -?---V--------------
F2.CM.MP255          -G---V--------------
F2.CM.MP257          -S---V--------------

CONSENSUS_G          -S----------------x-
G.BE.DRCBL           -S---V--------------
G.FI.HH8793          -S------------------
G.NG.92NG083         -S------------------
G.SE.SE6165          -G------------------

CONSENSUS_H          -G--x----D----------
H.BE.VI991           -G-------D----------
H.BE.VI997           -G--S----D----------
H.CF.90CF056         -G--A----D----------

CONSENSUS_J          -G------------------
J.SE.SE9173          -G------------------
J.SE.SE9280          -G------------------

CONSENSUS_K          -s---v--------------
K.BE.VI325           -S---V--------------
K.CD.EQTB11C         -S------------------
K.CM.MP535           -S---V--------------
N.CM.YBF30           -A---V---D--R---V---

CONSENSUS_O          -R???----D--RK--V---
O.CM.ANT70C          RP-Q-----D--RK--V---
O.CM.MVP5180         RGANS----D--RK--V---
CRF01-AE.CF.90CF40   -S-----------K------
CRF01-AE.TH.93TH25   ---------D----------
CRF01-AE.TH.CM240    ---------D----------
CRF01-AE.TH.TH022    -S-------D----------
CRF01-AE.TH.TH047    ---------S----------
CRF02_AG.FR.DJ263    -S-------D----------
CRF02_AG.FR.DJ264    -S-------D----------
CRF02_AG.NG.IBNG     -S--------------V---
CRF03_AB.RU.KAL15    -S-------D----------
CRF04_cpx.CY.94CY0   -S---V--------------
CRF04_cpx.GR.97PVC   -S------------------
CRF04_cpx.GR.97PVM   -S-------D----------
AC.ET.E3099G         -H------------------
AC.IN.21301          -G---V--------------
AC.RW.92RW009        --------------------
AC.SE.SE9488         -G-------D----------
AC.ZM.ZAM174-21      -S------------------
AC.ZM.ZAM184         -S------------------
AC.ZM.ZAM716-17      -S------------------
ACD.SE.SE8603        -S-------D----------
AD.SE.SE6954         -S------------------
AD.SE.SE7108         -S-------D----------
ADHU.NO.NOGIL3       -S------------------
ADU.CD.MAL           -S-------D----------
AG.NG.G3             -S------------------
AG.SE.SE7812         -S--------------V---
AGHU.GA.VI354        -G------------------
AGJ.AU.BFP90         -S------------------
AGJ.ML.95ML8         -S------------------
AGU.CD.Z321          -S------------------
BF.BR.93BR029.4      -S---V--------------
DF.CD.VI961          --------------------
U.CD.VI1126          -S---V--------------

CONSENSUS_CPZ        -a-------D--r--v----
CPZ.CD.CPZANT        QQ-GGV---D-------M--
CPZ.GA.CPZGAB        -A-------DV-R--V----
CPZ.US.CPZUS         -A-------D--R--VV---
```

Study Subject ID:03RCH95
Study Subject Clone:
Study Subject HLA:A26,A33,B8,B82,Cw3,Cw7
Sequence: Known reactive 20Mer0: HSQRRQDILDLWIYHTQGYF Nef(102–121)

Possible HLA

A26	A*2601,A*2602,A*2603,A*2604,A*2605,A*2606,A*2607,A*2608
A33	A*3301,A*3303
B8	B*0801,B*0802,B*0803,B*0806
Cw3	Cw*0307,Cw*0301
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(1-9)	HSQRRQDIL	Cw*0301
(3-11)	QRRQDILDL	Cw*0301
(5-13)	RQDILDLWI	Cw*0301
(12-20)	WIYHTQGYF	Cw*0301
(1-8)	HSQRRQDI	Cw*0301
(2-9)	SQRRQDIL	Cw*0301
(4-11)	RRQDILDL	Cw*0301
(6-13)	QDILDLWI	Cw*0301
(13-20)	IYHTQGYF	Cw*0301
(2-11)	SQRRQDILDL	Cw*0301
(4-13)	RRQDILDLWI	Cw*0301
(11-20)	LWIYHTQGYF	Cw*0301
(1-9)	HSQRRQDIL	Cw*0702
(3-11)	QRRQDILDL	Cw*0702
(6-14)	QDILDLWIY	Cw*0702
(11-19)	LWIYHTQGY	Cw*0702
(12-20)	WIYHTQGYF	Cw*0702
(2-9)	SQRRQDIL	Cw*0702
(4-11)	RRQDILDL	Cw*0702
(7-14)	DILDLWIY	Cw*0702
(12-19)	WIYHTQGY	Cw*0702
(13-20)	IYHTQGYF	Cw*0702
(2-11)	SQRRQDILDL	Cw*0702
(5-14)	RQDILDLWIY	Cw*0702
(10-19)	DLWIYHTQGY	Cw*0702
(11-20)	LWIYHTQGYF	Cw*0702

Anchor Residues Searched

B8	XX[K]X[KR]XXX[L]
B8	XX[K]X[KR]XX[L]
B8	XX[K]X[KR]XXXX[L]
Cw*0301	XXXXXXXX[LFMI]
Cw*0301	XXXXXXX[LFMI]
Cw*0301	XXXXXXXXX[LFMI]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH95
Study Subject Clone:
Study Subject HLA:A26,A33,B8,B82,Cw3,Cw7
Sequence: Known reactive 20Mer1: YNVLPQGWKGSPAIFQSSMT RT(146–165)

Possible HLA

A26	A*2601,A*2602,A*2603,A*2604,A*2605,A*2606,A*2607,A*2608
A33	A*3301,A*3303
B8	B*0801,B*0802,B*0803,B*0806
Cw3	Cw*0307,Cw*0301
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(6-14)	QGWKGSPAI	Cw*0301
(7-15)	GWKGSPAIF	Cw*0301
(11-19)	SPAIFQSSM	Cw*0301
(7-14)	GWKGSPAI	Cw*0301
(8-15)	WKGSPAIF	Cw*0301
(12-19)	PAIFQSSM	Cw*0301
(5-14)	PQGWKGSPAI	Cw*0301
(6-15)	QGWKGSPAIF	Cw*0301
(10-19)	GSPAIFQSSM	Cw*0301
(7-15)	GWKGSPAIF	Cw*0702
(8-15)	WKGSPAIF	Cw*0702
(6-15)	QGWKGSPAIF	Cw*0702

Anchor Residues Searched

B8	XX[K]X[KR]XXX[L]
B8	XX[K]X[KR]XX[L]
B8	XX[K]X[KR]XXXX[L]
Cw*0301	XXXXXXXX[LFMI]
Cw*0301	XXXXXXX[LFMI]
Cw*0301	XXXXXXXXX[LFMI]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH95
Study Subject Clone:
Study Subject HLA:A26,A33,B8,B82,Cw3,Cw7
Sequence: Known reactive 20Mer2: SPAIFQSSMTKILEPFRKQN RT(156–175)

Possible HLA

A26	A*2601,A*2602,A*2603,A*2604,A*2605,A*2606,A*2607,A*2608
A33	A*3301,A*3303
B8	B*0801,B*0802,B*0803,B*0806
Cw3	Cw*0307,Cw*0301
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(1-9)	SPAIFQSSM	Cw*0301
(4-12)	IFQSSMTKI	Cw*0301
(5-13)	FQSSMTKIL	Cw*0301
(8-16)	SMTKILEPF	Cw*0301
(2-9)	PAIFQSSM	Cw*0301
(5-12)	FQSSMTKI	Cw*0301
(6-13)	QSSMTKIL	Cw*0301
(9-16)	MTKILEPF	Cw*0301
(3-12)	AIFQSSMTKI	Cw*0301
(4-13)	IFQSSMTKIL	Cw*0301
(7-16)	SSMTKILEPF	Cw*0301
(5-13)	FQSSMTKIL	Cw*0702
(8-16)	SMTKILEPF	Cw*0702
(6-13)	QSSMTKIL	Cw*0702
(9-16)	MTKILEPF	Cw*0702
(4-13)	IFQSSMTKIL	Cw*0702
(7-16)	SSMTKILEPF	Cw*0702

Anchor Residues Searched

B8	XX[K]X[KR]XXX[L]
B8	XX[K]X[KR]XX[L]
B8	XX[K]X[KR]XXXX[L]
Cw*0301	XXXXXXXX[LFMI]
Cw*0301	XXXXXXX[LFMI]
Cw*0301	XXXXXXXXX[LFMI]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH95
Study Subject Clone:
Study Subject HLA:A26,A33,B8,B82,Cw3,Cw7
Sequence: Known reactive 20Mer3: LRPGGKKKYKLKHIVWASRE p17(21–40)

Possible HLA

A26	A*2601,A*2602,A*2603,A*2604,A*2605,A*2606,A*2607,A*2608
A33	A*3301,A*3303
B8	B*0801,B*0802,B*0803,B*0806
Cw3	Cw*0307,Cw*0301
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(4-11)	GGKKKYKL	B8
(3-11)	PGGKKKYKL	Cw*0301
(6-14)	KKKYKLKHI	Cw*0301
(4-11)	GGKKKYKL	Cw*0301
(7-14)	KKYKLKHI	Cw*0301
(2-11)	RPGGKKKYKL	Cw*0301
(5-14)	GKKKYKLKHI	Cw*0301
(1-9)	LRPGGKKKY	Cw*0702
(3-11)	PGGKKKYKL	Cw*0702
(2-9)	RPGGKKKY	Cw*0702
(4-11)	GGKKKYKL	Cw*0702
(2-11)	RPGGKKKYKL	Cw*0702

Anchor Residues Searched

B8	XX[K]X[KR]XXX[L]
B8	XX[K]X[KR]XX[L]
B8	XX[K]X[KR]XXXX[L]
Cw*0301	XXXXXXXX[LFMI]
Cw*0301	XXXXXXX[LFMI]
Cw*0301	XXXXXXXXX[LFMI]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH95
Study Subject Clone:
Study Subject HLA:A26,A33,B8,B82,Cw3,Cw7
Sequence: Known reactive 20Mer4: TNNPPIPVGEIYKRWIILGL p24(119–138)

Possible HLA

A26	A*2601,A*2602,A*2603,A*2604,A*2605,A*2606,A*2607,A*2608
A33	A*3301,A*3303
B8	B*0801,B*0802,B*0803,B*0806
Cw3	Cw*0307,Cw*0301
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(3-11)	NPPIPVGEI	Cw*0301
(8-16)	VGEIYKRWI	Cw*0301
(9-17)	GEIYKRWII	Cw*0301
(10-18)	EIYKRWIIL	Cw*0301
(12-20)	YKRWIILGL	Cw*0301
(4-11)	PPIPVGEI	Cw*0301
(9-16)	GEIYKRWI	Cw*0301
(10-17)	EIYKRWII	Cw*0301
(11-18)	IYKRWIIL	Cw*0301
(13-20)	KRWIILGL	Cw*0301
(2-11)	NNPPIPVGEI	Cw*0301
(7-16)	PVGEIYKRWI	Cw*0301
(8-17)	VGEIYKRWII	Cw*0301
(9-18)	GEIYKRWIIL	Cw*0301
(11-20)	IYKRWIILGL	Cw*0301
(4-12)	PPIPVGEIY	Cw*0702
(10-18)	EIYKRWIIL	Cw*0702
(12-20)	YKRWIILGL	Cw*0702
(5-12)	PIPVGEIY	Cw*0702
(11-18)	IYKRWIIL	Cw*0702
(13-20)	KRWIILGL	Cw*0702
(3-12)	NPPIPVGEIY	Cw*0702
(9-18)	GEIYKRWIIL	Cw*0702
(11-20)	IYKRWIILGL	Cw*0702

Anchor Residues Searched

B8	XX[K]X[KR]XXX[L]
B8	XX[K]X[KR]XX[L]

B8	XX[K]X[KR]XXXX[L]
Cw*0301	XXXXXXXX[LFMI]
Cw*0301	XXXXXXX[LFMI]
Cw*0301	XXXXXXXXX[LFMI]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

This table lists epitopes that are experimentally observed to be presented by a HLA type carried by the patient, but the de£ned epitope has substitutions relative to the peptides from your reference strains and so might be missed by your reagents: in HXB2 for Gag, Pol; MN for Env; BRU for Nef, relative to most B clade Sequences in the database:

Protein	Epitope in Database	Epitope in Ref. strain	Epitope in Consensus B	HLA	Notes
p24(127–135)	GDIYKRWII	GEIYKRWII	GEIYKRWII	B*0801	
p24(128–135)	DIYKRWII	EIYKRWII	EIYKRWII	B8	
p24(164–172)	YVDRFFKTL	YVDRFYKTL	YVDRFYKTL	A26 or B70	
gp160(2–10)	RVKEKYQHL	RAIEAQQHM	GIRKNYQHL	B*0801	
gp160(2–10)	RVKEKYQHL	RAIEAQQHM	GIRKNYQHL	B8	

Table 1: **p24**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(127–135)	p24(259–267 SF2)	GDIYKRWII	HIV-1 infection	human(B*0801)	[McAdam (1998)]
	• GDIYKRWII speci£c CTL clone also recognized GEIYKRWII				
p24(128–135)	p24()	DIYKRWII	HIV-1 infection	human(B8)	[Goulder (2000)]
	• The CTL-dominant response was focused on this epitope in a HIV+ South African – this epitope did not fall within the £ve most recognized peptides in the study • Three peptides GSEELRSLYNTVATL (p17 residues 71-85), SALSEGATPQDLNTMLNTVG (p24 41-60), and WEKIRLRPG-GKKKYKLK(p17 16-30) contained the dominant Gag-speci£c epitope in 31 out of 44 B-clade infected individuals from Boston who showed Gag-CTL responses • Five peptides RLRPGGKKHYMIKHLVW (p17 20-36), ELRSLYNTVATLYCV (p17Gag 74-88), SALSEGATPQDLNTMLNTVG (p24 41-60), FRDYVDRFFKTLRAEQA (p24 161-177), and SILDIKQGKEPFRDY (p24 149-164) contained dominant Gag-speci£c epitopes in 32 out of 37 C-clade infected subjects from South Africa				
p24(164–172)	p24(298–306 Clade A)	YVDRFFKTL	HIV-1 infection	human(A26 or B70)	[Dorrell (1999)]
	• CTL responses in three individuals with non-clade B infections were studied, 2 with subtype A infections, 1 with subtype C – their infections all originated in East Africa • This CTL epitope is conserved in A and C subtype, and B clade sequences tend to have a change from F to Y, YVDRFYKTL – both variants showed strong CTL reactivity • CTL reacted with targets presenting either in the context A26 or B70 – the epitope has the HLA-26 motif of Val at position 2 and Leu at the carboxy terminus, and the B70 anchor residue motif is unknown				

Table 2: **gp160**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
gp160(2–10)	gp160(2–10 IIIB)	RVKEKYQHL	HIV-1 infection	human(B*0801)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*0801 epitope				
gp160(2–10)	gp160(2–10 IIIB)	RVKEKYQHL	HIV-1 infection	human(B8)	[Sipsas (1997)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by 3 lab workers accidentally infected with HIV-1 IIIB • Type-speci£c epitope, unique to the LAI and IIIB because of a deletion of three amino acids that are present in all other subtype B HIV-1s • RVKGIRKNYQHL, a variant found in JRCSF, was not recognized • This epitope is in the signal sequence of gp120				

Table 3: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
Nef(102–115)	Nef(102–115 LAI)	HSQRRQDILDLWIY	HIV-1 infection	human(B7)	[Goulder (1997b), Goulder (1997a)]
	• Identical twin hemophiliac brothers were both infected with the same batch of factor VIII • One had a strong response to this peptide, the other did not • [Goulder (1997a)] is a review of immune escape that summarizes this study				
Nef(102–121)	Nef(101–120 SF2)	HSQRRQDILDLQIYHTQGYF	HIV-1 infection	human()	[Lieberman (1997)]
	• Of 25 patients, most had CTL speci£c for more than 1 HIV-1 protein • Eleven subjects had CTL that could recognize vaccinia-expressed LAI Nef • Two of these 11 had CTL response to this peptide • The responding subjects were HLA-A2, A3, B8, B62 and HLA-A2, B21				
Nef(105–114)	Nef(105–114 LAI)	RRQDILDLWI	HIV-1 infection	human(B*2705)	[Goulder (1997c)]
	• De£ned as optimal epitope from within reactive peptide HSQRRQDILDLWIYHTQGYF [Nef(102-121 LAI)] • HLA-B*2705 is associated with slow HIV disease progression • The HLA-B*2705 binding motif includes R at position 2, and L in the C-term position				
Nef(105–114)	Nef(105–114 LAI)	RRQDILDLWI	HIV-1 infection	human(B*2705)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*2705 epitope				
Nef(106–115)	()	RQDILDLWIY		(B7)	[Brander & Goulder(2001), Goulder(1999)]

Table 4: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
Nef(102–115)	Nef(102–115 LAI)	HSQRRQDILDLWIY	HIV-1 infection	human(B7)	[Goulder (1997b), Goulder (1997a)]
	• Identical twin hemophiliac brothers were both infected with the same batch of factor VIII • One had a strong response to this peptide, the other did not • [Goulder (1997a)] is a review of immune escape that summarizes this study				
Nef(102–121)	Nef(101–120 SF2)	HSQRRQDILDLQIYHTQGYF	HIV-1 infection	human()	[Lieberman (1997)]
	• Of 25 patients, most had CTL speci£c for more than 1 HIV-1 protein • Eleven subjects had CTL that could recognize vaccinia-expressed LAI Nef • Two of these 11 had CTL response to this peptide • The responding subjects were HLA-A2, A3, B8, B62 and HLA-A2, B21				
Nef(105–114)	Nef(105–114 LAI)	RRQDILDLWI	HIV-1 infection	human(B*2705)	[Goulder (1997c)]
	• De£ned as optimal epitope from within reactive peptide HSQRRQDILDLWIYHTQGYF [Nef(102-121 LAI)] • HLA-B*2705 is associated with slow HIV disease progression • The HLA-B*2705 binding motif includes R at position 2, and L in the C-term position				
Nef(105–114)	Nef(105–114 LAI)	RRQDILDLWI	HIV-1 infection	human(B*2705)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*2705 epitope				
Nef(106–115)	()	RQDILDLWIY		(B7)	[Brander & Goulder(2001), Goulder(1999)]

Table 5: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
Nef(102–115)	Nef(102–115 LAI)	HSQRRQDILDLWIY	HIV-1 infection	human(B7)	[Goulder (1997b), Goulder (1997a)]
	• Identical twin hemophiliac brothers were both infected with the same batch of factor VIII • One had a strong response to this peptide, the other did not • [Goulder (1997a)] is a review of immune escape that summarizes this study				
Nef(102–121)	Nef(101–120 SF2)	HSQRRQDILDLQIYHTQGYF	HIV-1 infection	human()	[Lieberman (1997)]
	• Of 25 patients, most had CTL speci£c for more than 1 HIV-1 protein • Eleven subjects had CTL that could recognize vaccinia-expressed LAI Nef • Two of these 11 had CTL response to this peptide • The responding subjects were HLA-A2, A3, B8, B62 and HLA-A2, B21				
Nef(105–114)	Nef(105–114 LAI)	RRQDILDLWI	HIV-1 infection	human(B*2705)	[Goulder (1997c)]
	• De£ned as optimal epitope from within reactive peptide HSQRRQDILDLWIYHTQGYF [Nef(102-121 LAI)] • HLA-B*2705 is associated with slow HIV disease progression • The HLA-B*2705 binding motif includes R at position 2, and L in the C-term position				
Nef(105–114)	Nef(105–114 LAI)	RRQDILDLWI	HIV-1 infection	human(B*2705)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*2705 epitope				
Nef(106–115)	()	RQDILDLWIY		(B7)	[Brander & Goulder(2001), Goulder(1999)]

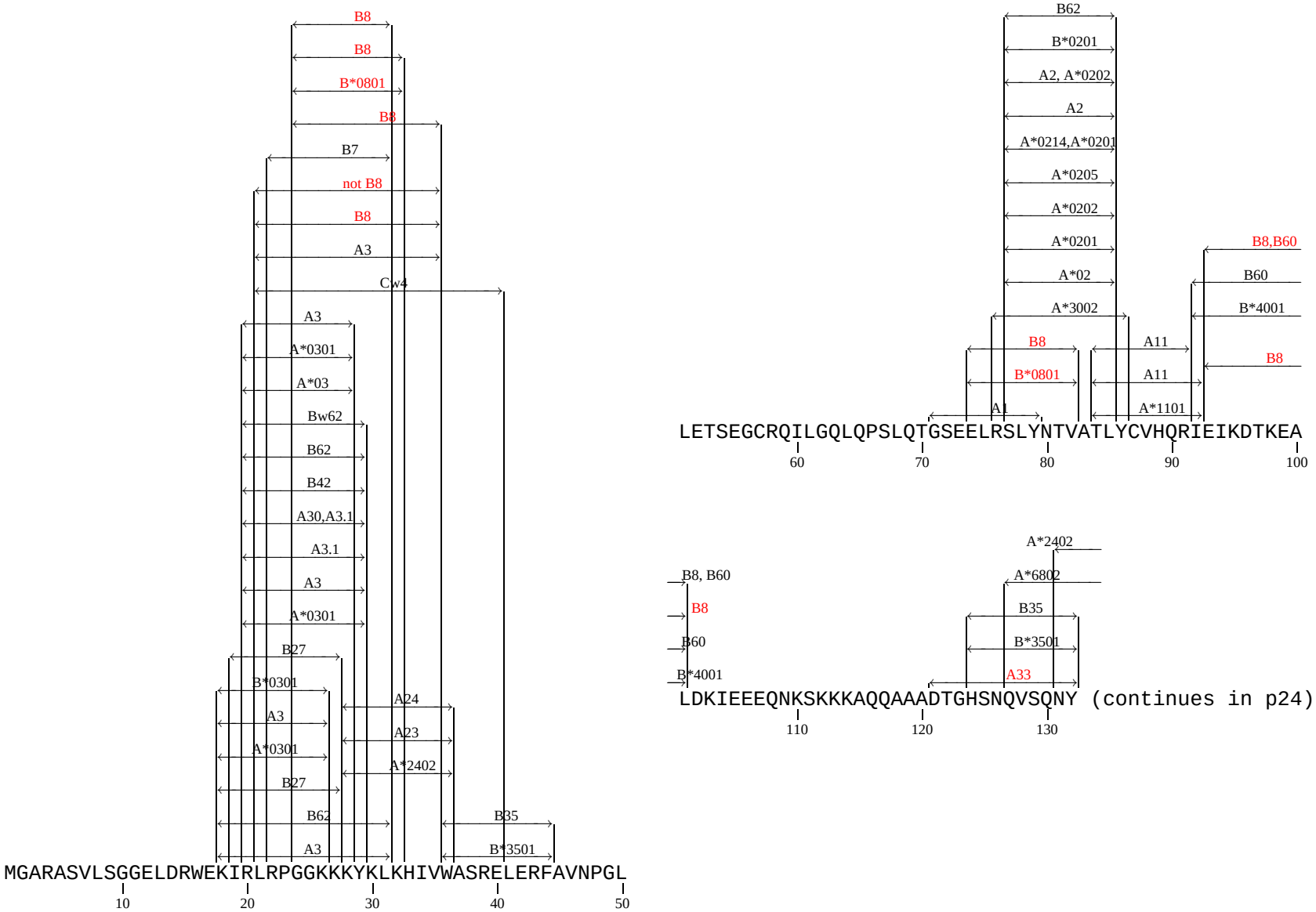
Table 6: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
Nef(102–115)	Nef(102–115 LAI)	HSQRRQDILDLWIY	HIV-1 infection	human(B7)	[Goulder (1997b), Goulder (1997a)]
	• Identical twin hemophiliac brothers were both infected with the same batch of factor VIII • One had a strong response to this peptide, the other did not • [Goulder (1997a)] is a review of immune escape that summarizes this study				
Nef(102–121)	Nef(101–120 SF2)	HSQRRQDILDLQIYHTQGYF	HIV-1 infection	human()	[Lieberman (1997)]
	• Of 25 patients, most had CTL speci£c for more than 1 HIV-1 protein • Eleven subjects had CTL that could recognize vaccinia-expressed LAI Nef • Two of these 11 had CTL response to this peptide • The responding subjects were HLA-A2, A3, B8, B62 and HLA-A2, B21				
Nef(105–114)	Nef(105–114 LAI)	RRQDILDLWI	HIV-1 infection	human(B*2705)	[Goulder (1997c)]
	• De£ned as optimal epitope from within reactive peptide HSQRRQDILDLWIYHTQGYF [Nef(102-121 LAI)] • HLA-B*2705 is associated with slow HIV disease progression • The HLA-B*2705 binding motif includes R at position 2, and L in the C-term position				
Nef(105–114)	Nef(105–114 LAI)	RRQDILDLWI	HIV-1 infection	human(B*2705)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*2705 epitope				
Nef(106–115)	()	RQDILDLWIY		(B7)	[Brander & Goulder(2001), Goulder(1999)]

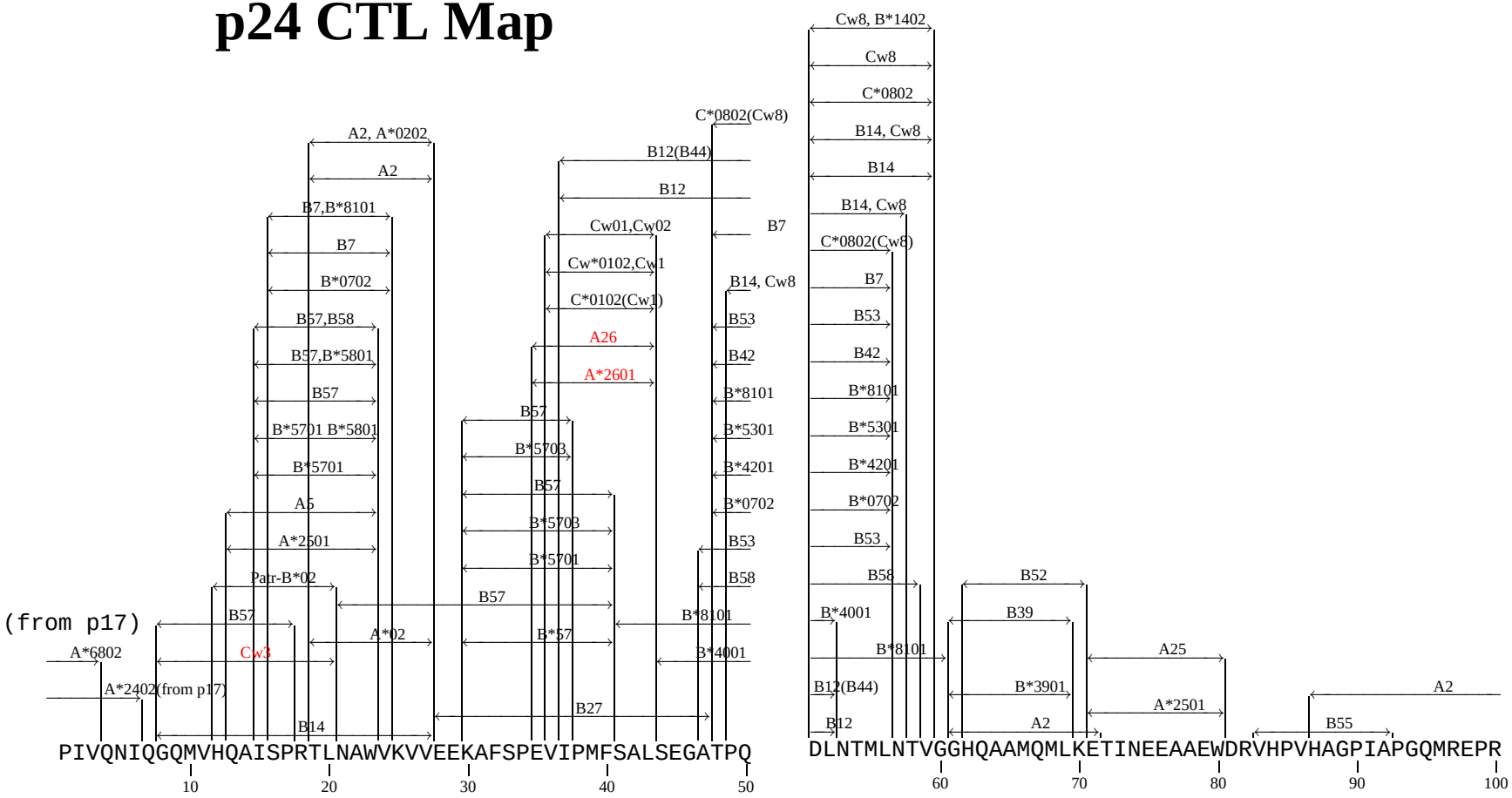
Table 7: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
Nef(102–115)	Nef(102–115 LAI)	HSQRRQDILDLWIY	HIV-1 infection	human(B7)	[Goulder (1997b), Goulder (1997a)]
	• Identical twin hemophiliac brothers were both infected with the same batch of factor VIII • One had a strong response to this peptide, the other did not • [Goulder (1997a)] is a review of immune escape that summarizes this study				
Nef(102–121)	Nef(101–120 SF2)	HSQRRQDILDLQIYHTQGYF	HIV-1 infection	human()	[Lieberman (1997)]
	• Of 25 patients, most had CTL speci£c for more than 1 HIV-1 protein • Eleven subjects had CTL that could recognize vaccinia-expressed LAI Nef • Two of these 11 had CTL response to this peptide • The responding subjects were HLA-A2, A3, B8, B62 and HLA-A2, B21				
Nef(105–114)	Nef(105–114 LAI)	RRQDILDLWI	HIV-1 infection	human(B*2705)	[Goulder (1997c)]
	• De£ned as optimal epitope from within reactive peptide HSQRRQDILDLWIYHTQGYF [Nef(102-121 LAI)] • HLA-B*2705 is associated with slow HIV disease progression • The HLA-B*2705 binding motif includes R at position 2, and L in the C-term position				
Nef(105–114)	Nef(105–114 LAI)	RRQDILDLWI	HIV-1 infection	human(B*2705)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*2705 epitope				
Nef(106–115)	()	RQDILDLWIY		(B7)	[Brander & Goulder(2001), Goulder(1999)]

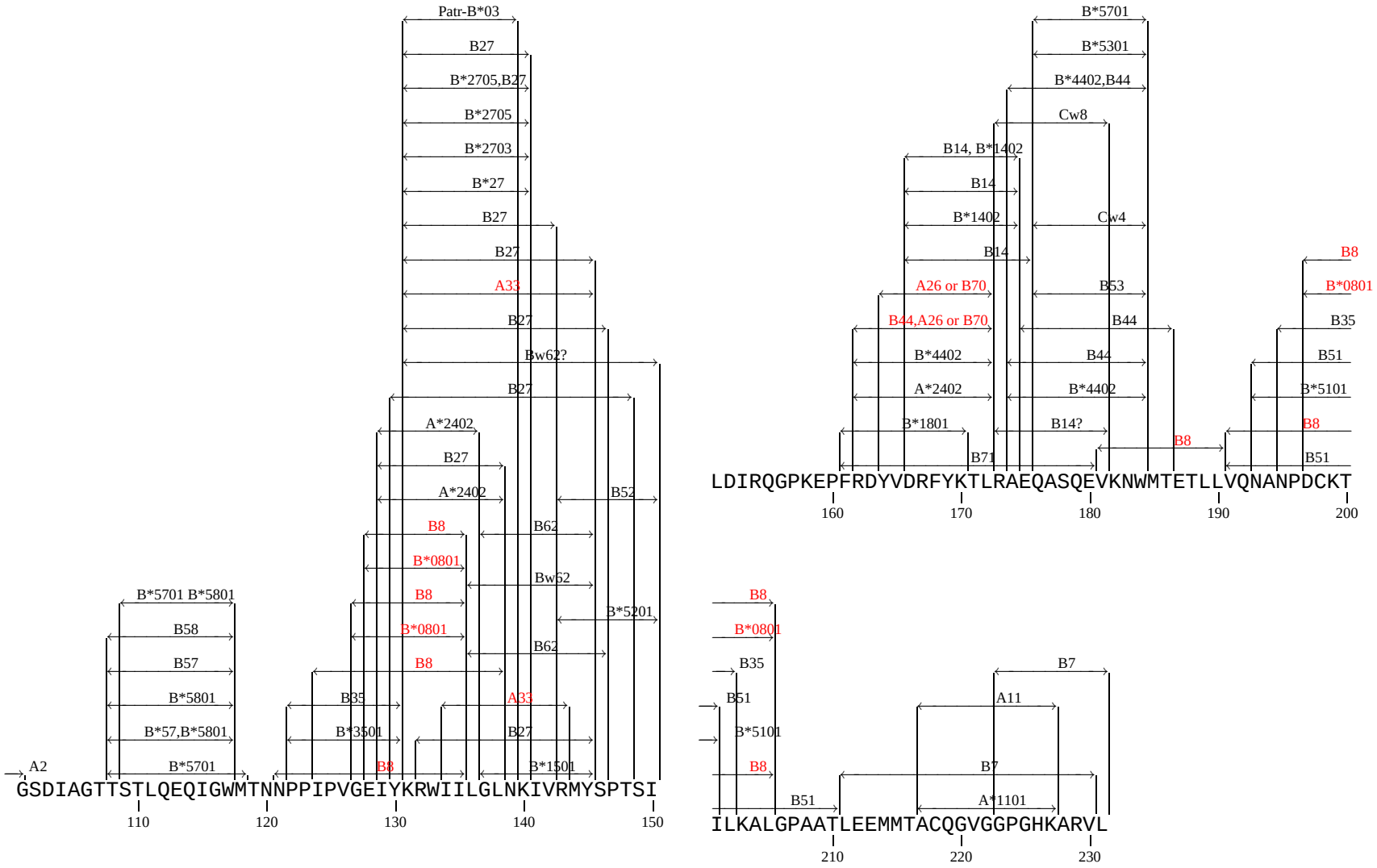
p17 CTL Map


B8
B8
B*0801
B8
B7
not B8
B8
A3
Cw4
A3
A*0301
A*03
Bw62
B62
B42
A30,A3.1
A3.1
A3
A*0301
B27
B*0301
A3
A*0301
B27
B62
A3
A24
A23
A*2402
B35
B*3501
MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERFAVNPGL
10
20
30
40
50
B62
B*0201
A2, A*0202
A2
A*0214,A*0201
A*0205
A*0202
A*0201
A*02
A*3002
B8
B*0801
A1
A11
A11
A*1101
B8,B60
B60
B*4001
B8
LETSEGCRQILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIEIKDTKEA
60
70
80
90
100
A*2402
B8, B60
A*6802
B8
B35
B60
B*3501
B*4001
A33
LDKIEEEQNKSKKKAQQAAADTGHSNQVSQNY (continues in p24)
110
120
130

p24 CTL Map



(from p17)
A*6802
A*2402(from p17)
B57
Cw3
B14
Patr-B*02
A5
A*2501
B*5701
B*5701 B*5801
B57,B*5801
B57,B58
B*0702
B7
B7,B*8101
A2
A2, A*0202
A*02
B57
B*5703
B*5701
B*57
B27
B*5703
B57
A26
A*2601
Cw01,Cw02
Cw*0102,Cw1
C*0102(Cw1)
B12
B12(B44)
C*0802(Cw8)
B7
B14, Cw8
B53
B42
B*8101
B*5301
B*4201
B*0702
B53
B58
B*8101
B*4001
PIVQNIQGQMVHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGATPQ
10
20
30
40
50
Cw8, B*1402
Cw8
C*0802
B14, Cw8
B14
B14, Cw8
C*0802(Cw8)
B7
B53
B42
B*8101
B*5301
B*4201
B*0702
B53
B58
B*4001
B*8101
B12(B44)
B12
B52
B39
B*3901
A2
A25
A*2501
A2
B55
DLNTMLNTVGGHQAAMQMLKETINEEAAEWDRVHPVHAGPIAPGQMREPR
60
70
80
90
100


Patr-B*03
B27
B*2705,B27
B*2705
B*2703
B*27
B27
B27
A33
B27
Bw62?
B27
A*2402
B27
A*2402
B52
B8
B62
B*0801
Bw62
B*5701 B*5801
B8
B*5201
B58
B*0801
B62
B57
B8
B*5801
B35
A33
B*57,B*5801
B*3501
B27
A2
B*5701
B8
B*1501
GSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNKIVRMYSPTSI
110
120
130
140
150
B*5701
B*5301
B*4402,B44
Cw8
B14, B*1402
B14
B*1402
Cw4
B14
B8
A26 or B70
B53
B*0801
B44,A26 or B70
B44
B35
B*4402
B44
B51
A*2402
B*4402
B*5101
B*1801
B14?
B8
B8
B71
B51
LDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKT
160
170
180
190
200
B8
B*0801
B35
B7
B51
A11
B*5101
B8
B7
B51
A*1101
ILKALGPAATLEEMMTACQGVGGPGHKARVL
210
220
230

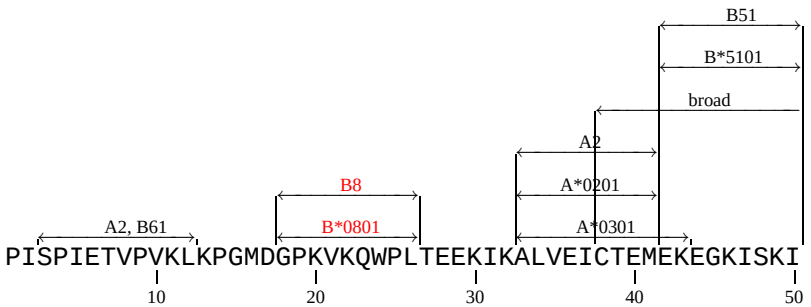
p2p7p1p6 CTL Map

```
AEAMSQVTNSATIMMQRGNFRNQRKIVKCFNCGKEGHTARNCRAPRKKGC
          10         20         30         40         50

 p2 <-          <>
start      p2 end  p7 start

                A2                          A2
WKCGKEGHQMKDCTERQANFLGKIWPSYKGRPGNFLQSRPEPTAPPEESF
          60         70         80         90        100

                    <>                <>
              p7 end  p1 start    p1  p6 start
                                 end

                          B7
RSGVETTTPPQKQEPIDKELYPLTSLRSLFGNDPSSQ
          110        120        130

                                p6 end ->
```

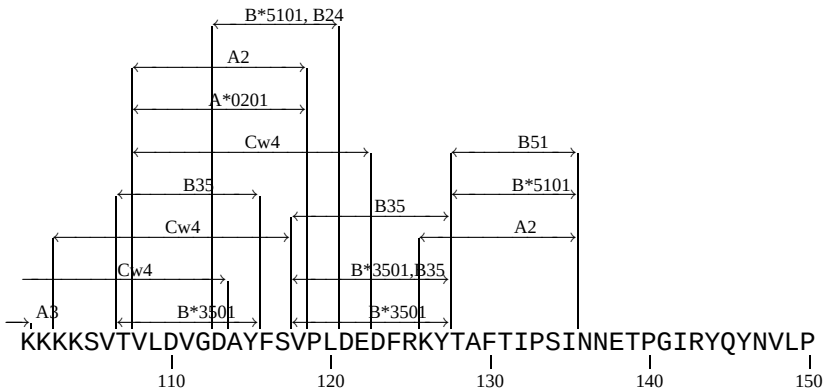
Protease CTL Map

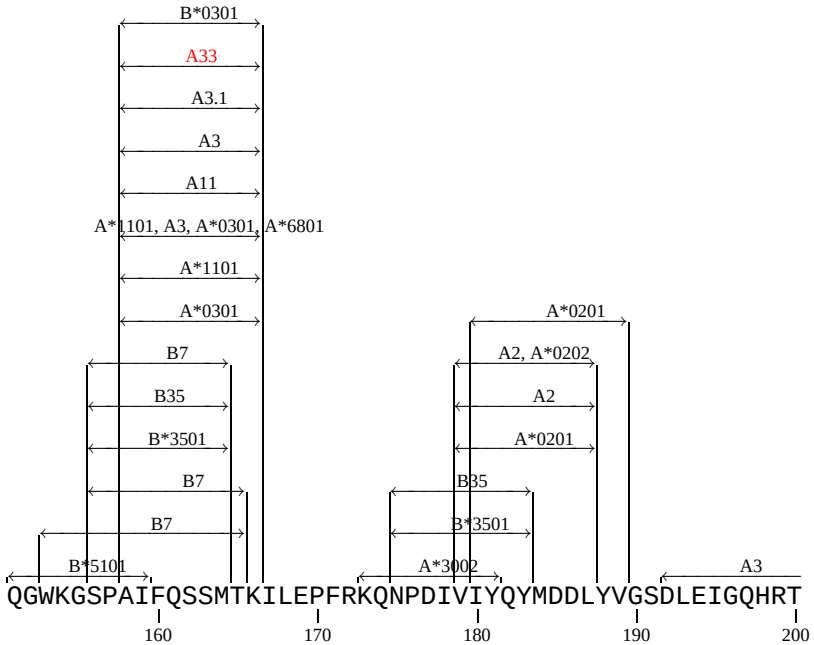
```
A*7401
A*6802,A*7401,A19
A*6802                                A*6802
PQVTLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGI
          10         20         30         40         50

                                A*0201
GGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
          60         70         80         90
```

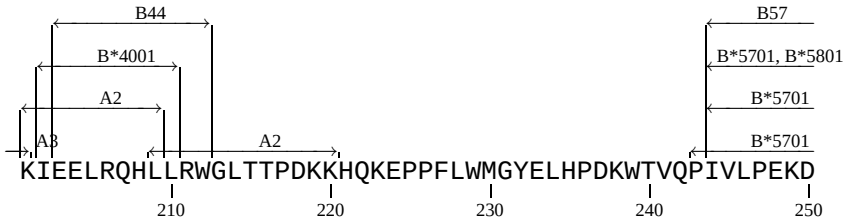
RT CTL Map

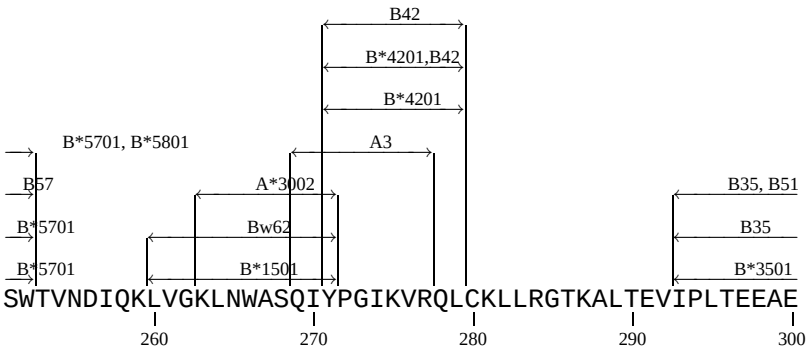

B51
B*5101
broad
A2
B8
A*0201
A2, B61
B*0801
A*0301
PISPIETVPVKLKPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKI
10
20
30
40
50

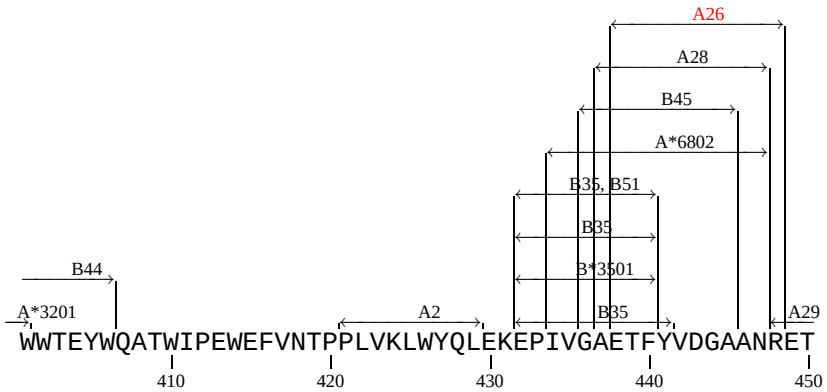
Cw4
broad
A3
GPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGL
60
70
80
90
100


B*5101, B24
A2
A*0201
Cw4
B51
B35
B*5101
B35
Cw4
A2
Cw4
B*3501,B35
A3
B*3501
B*3501
KKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLP
110
120
130
140
150

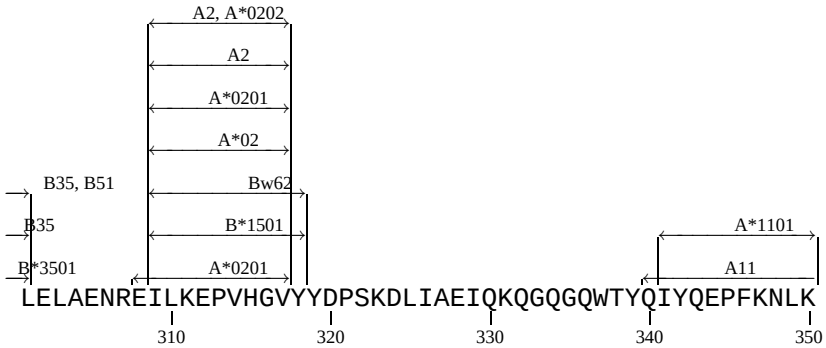

B*0301
A33
A3.1
A3
A11
A*1101, A3, A*0301, A*6801
A*1101
A*0301
A*0201
B7
A2, A*0202
B35
A2
B*3501
A*0201
B7
B35
B7
B*3501
B*5101
A*3002
A3
QGWKGSPAIFQSSMTKILEPFRKQNPDIVIYQYMDDLYVGSDLEIGQHRT
160
170
180
190
200

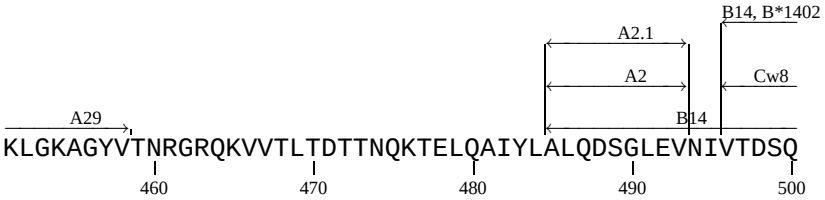

B44
B57
B*4001
B*5701, B*5801
A2
B*5701
A3
A2
B*5701
KIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWTVQPIVLPEKD
210
220
230
240
250

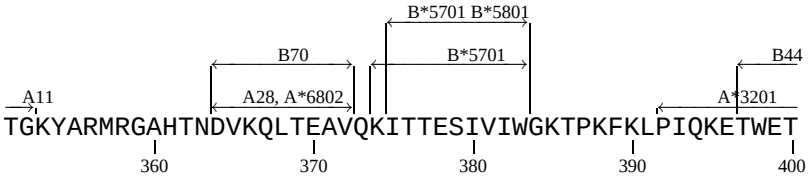


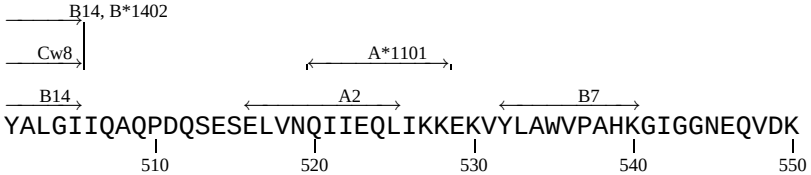


p15 RNase start <-





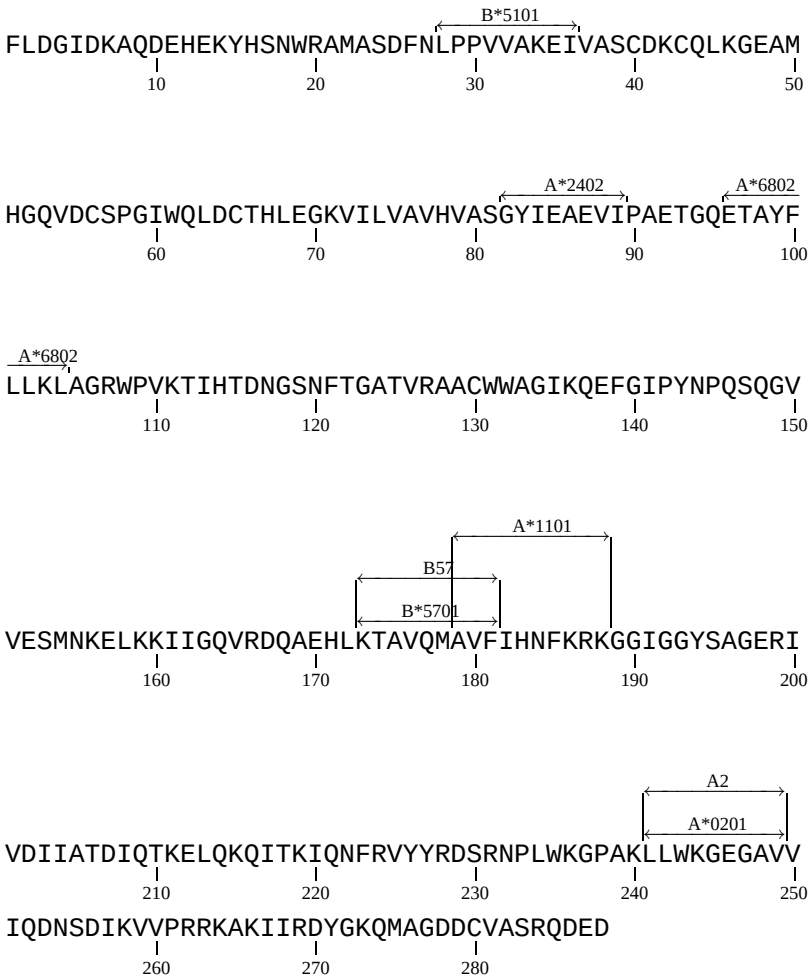




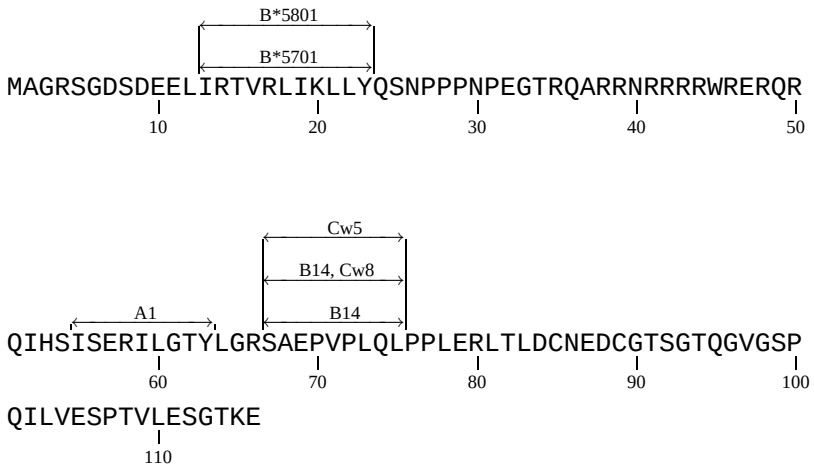
LVSAGIRKVL

-> p15 RNase end

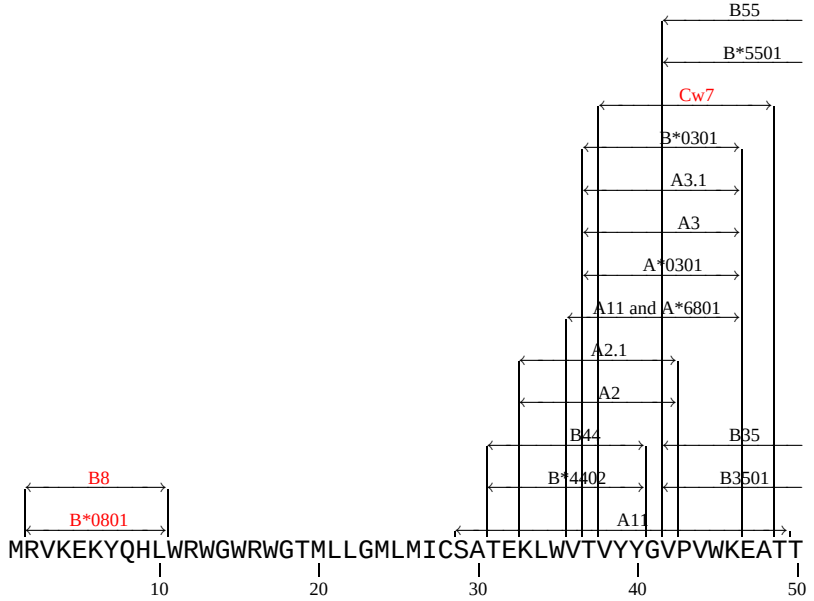
Integrase CTL Map



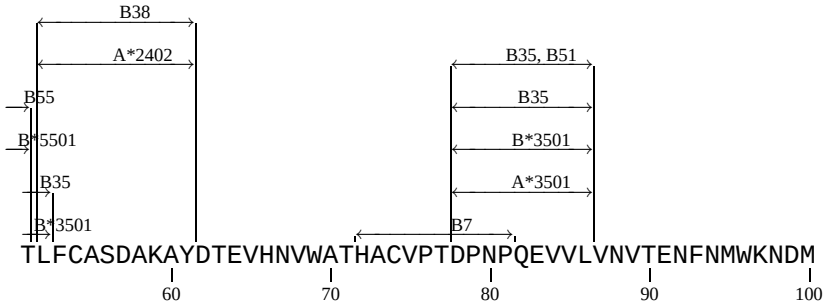
Rev CTL Map

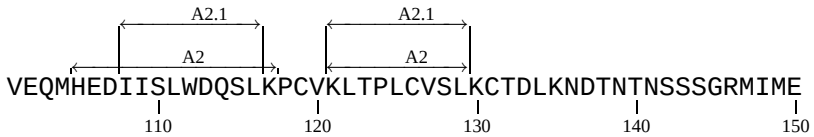


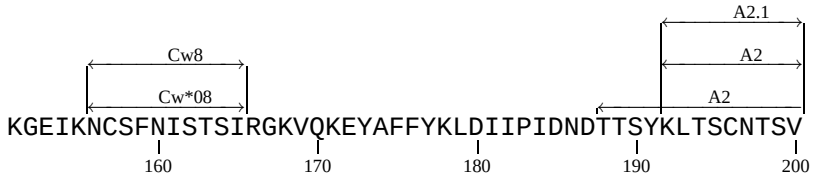
gp160 CTL Map

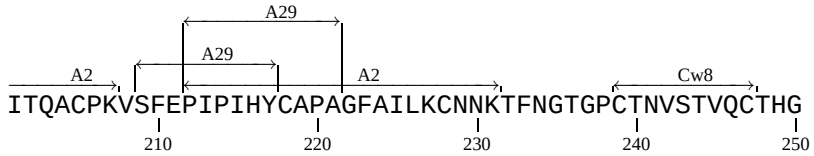


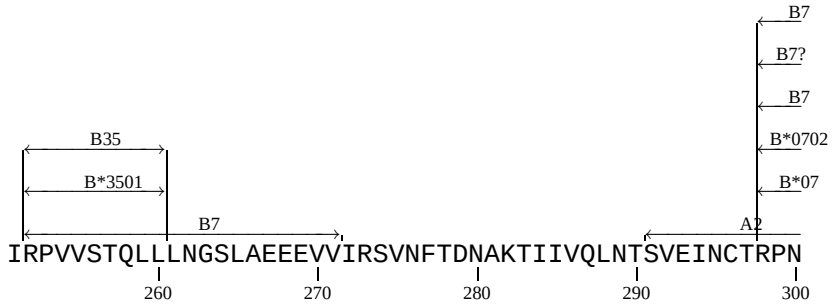
<- gp120 start

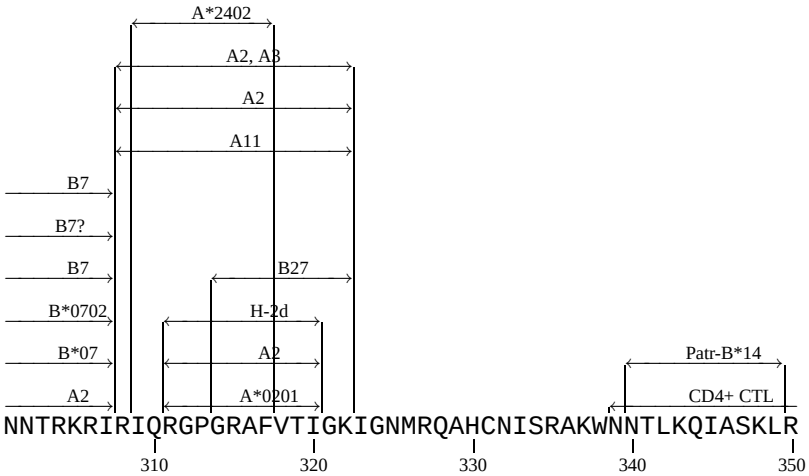


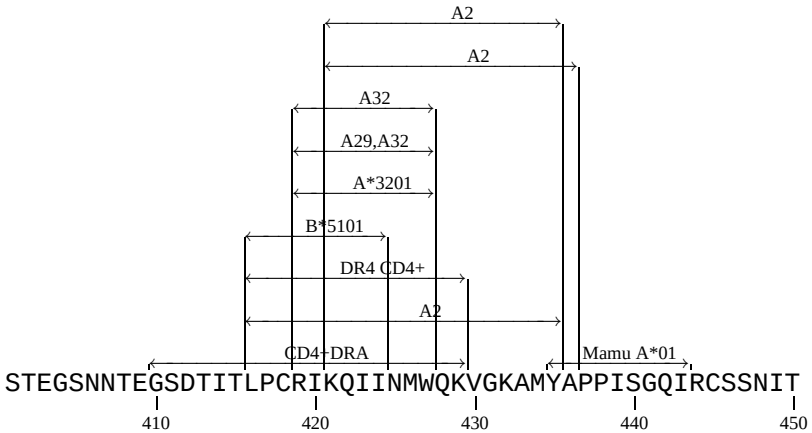


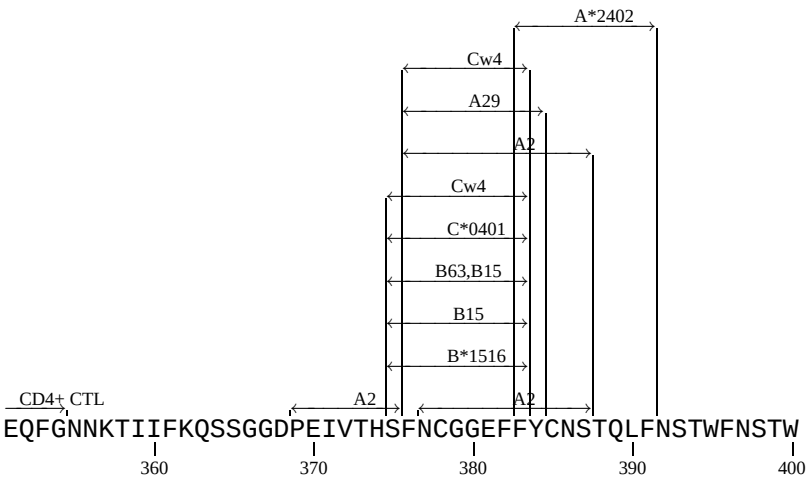


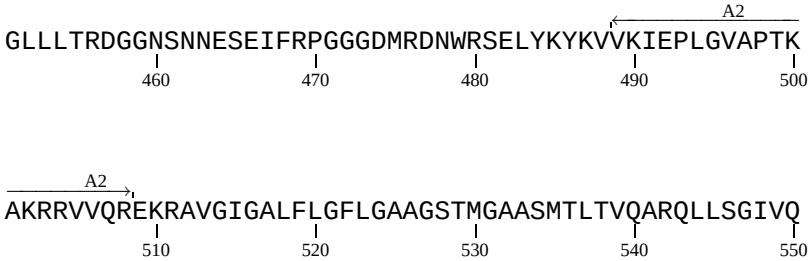




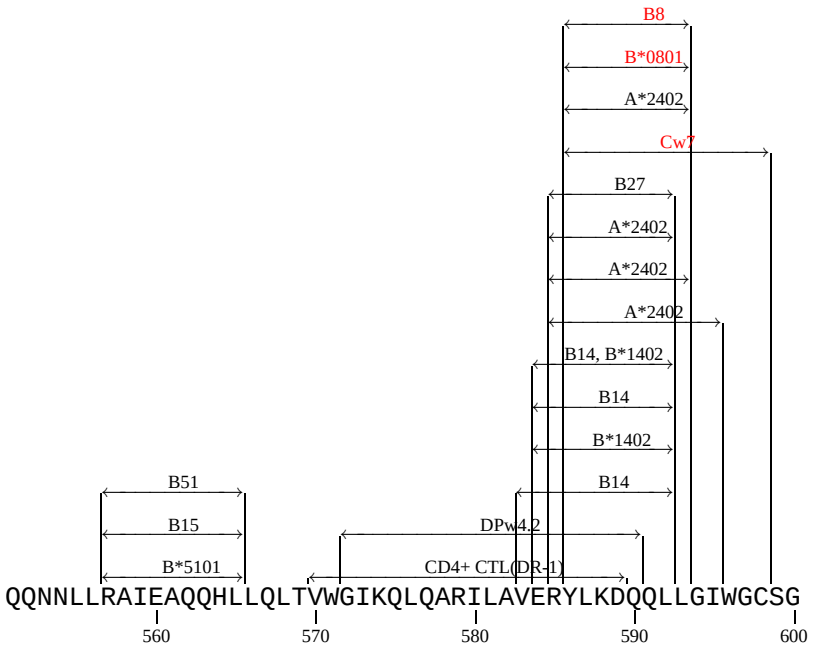


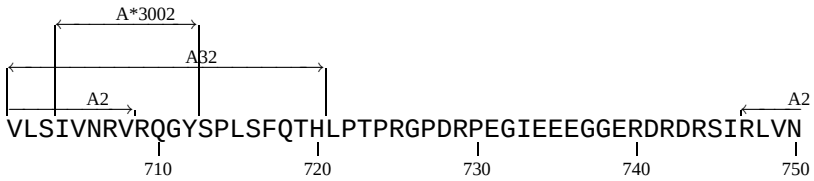


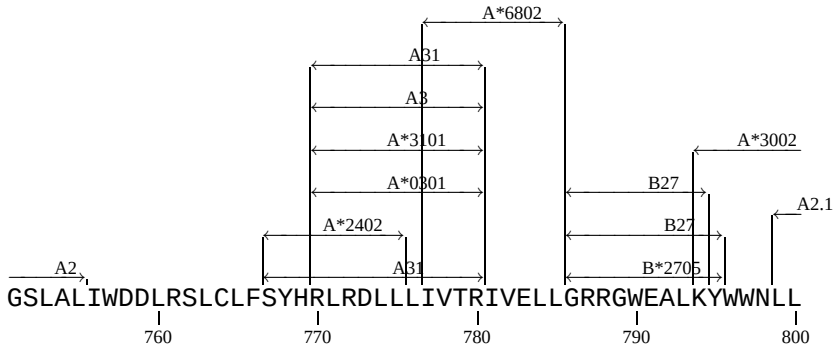




gp120 end <> gp41 start

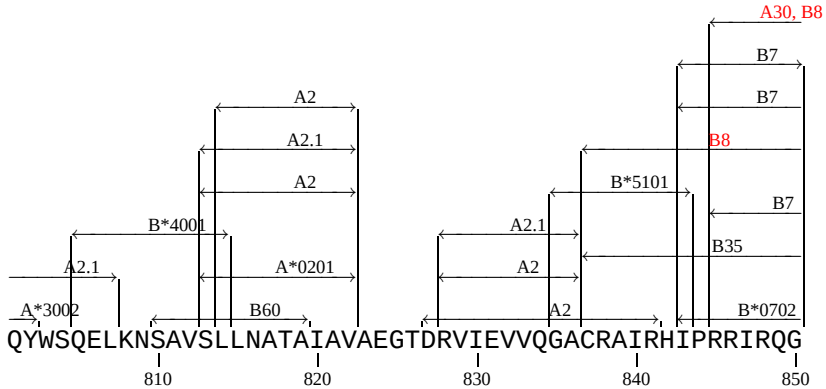

B8
B*0801
A*2402
Cw7
B27
A*2402
A*2402
A*2402
B14, B*1402
B14
B*1402
B14
B51
B15
B*5101
DPw4.2
CD4+ CTL(DR-1)
QQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSG
560
570
580
590
600

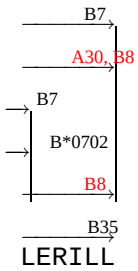

A*3002
A32
A2
A2
VLSIVNRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRLVN
710
720
730
740
750


A*6802
A31
A3
A*3101
A*0301
A*2402
A31
A*3002
B27
B27
B*2705
A2.1
A2
GSLALIWDDLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEALKYWWNLL
760
770
780
790
800

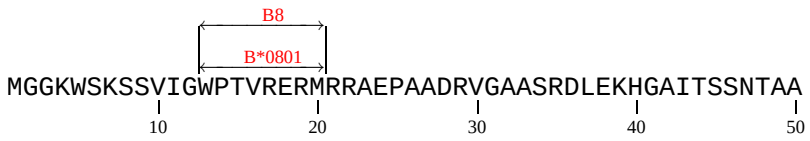
B35
B*3501
KLICTTAVPWNASWSNKSLEQIWNHTTWMEWDREINNYTSLIHSLIEESQ
610
620
630
640
650

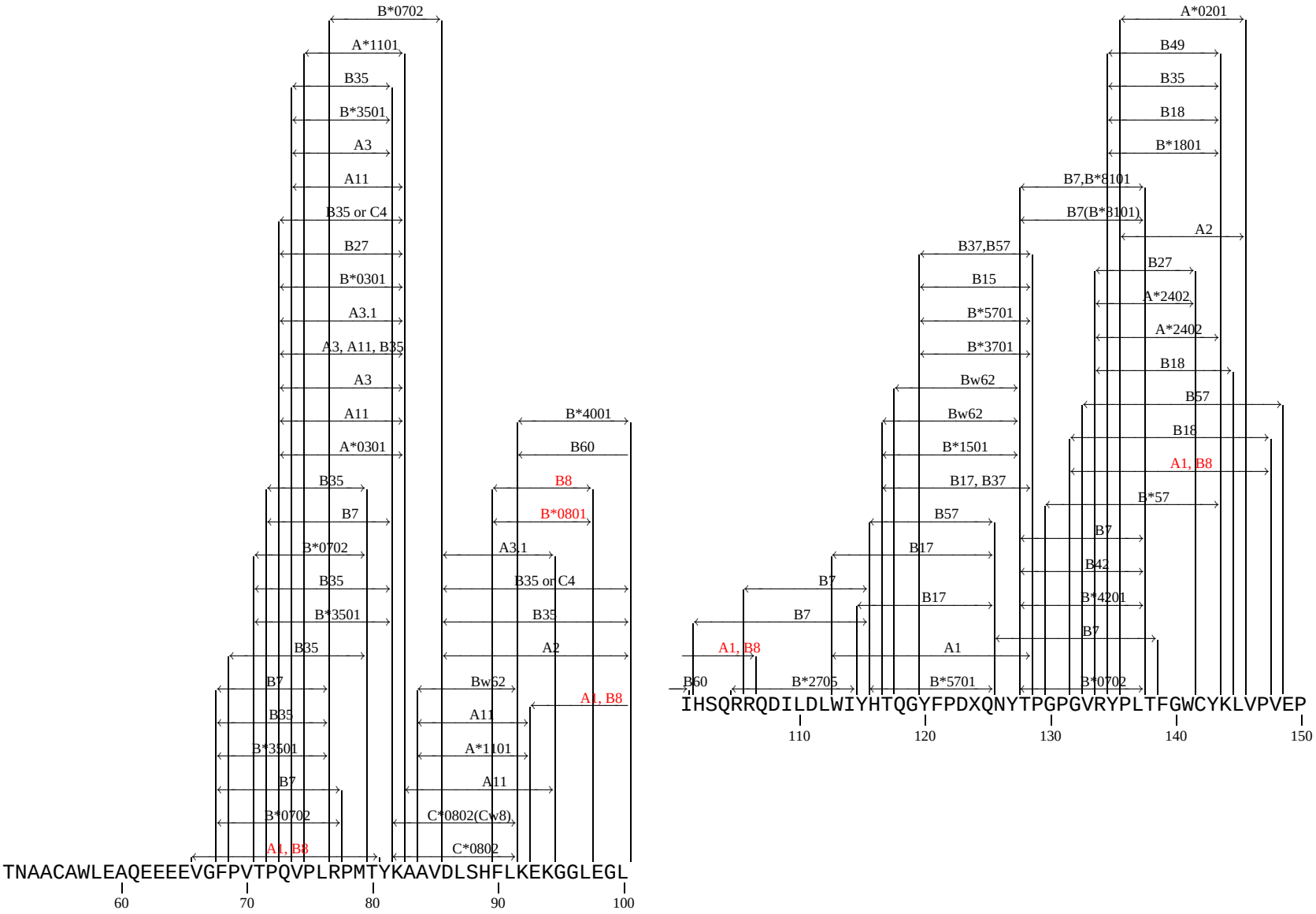
A2.1
A*2402
A2.1
A2
NQQEKNEQELLELDKWASLWNWFNITNWLWYIKLFIMIVGGLVGLRIVFA
660
670
680
690
700

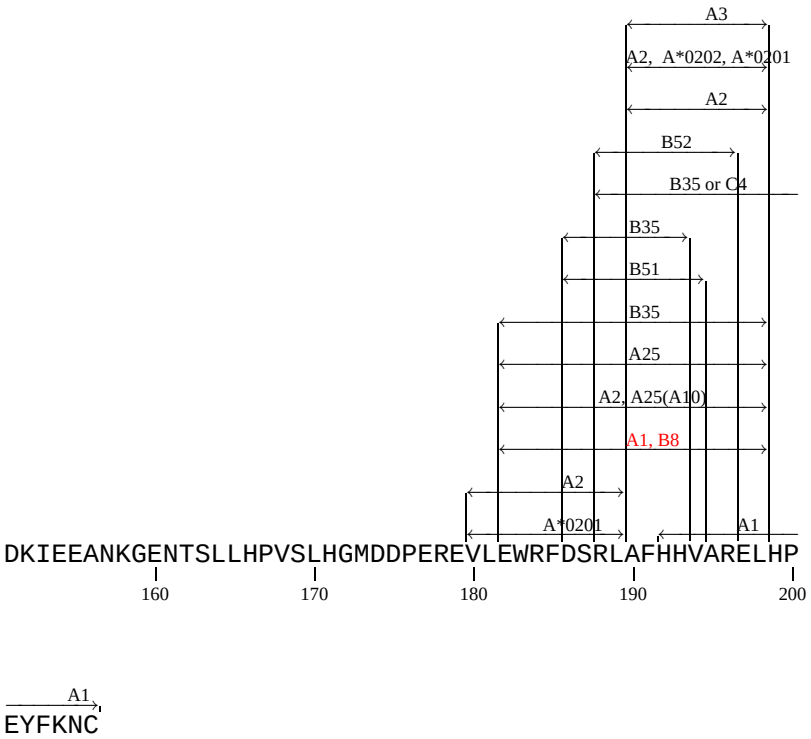

A30, B8
B7
B7
A2
A2.1
A2
B8
B*5101
B7
B*4001
A2.1
B35
A2.1
A*0201
A2
A*3002
B60
A2
B*0702
QYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQG
810
820
830
840
850


B7
A30, B8
B7
B*0702
B8
B35
LERILL
-> gp41 end

Nef CTL Map


B8
B*0801
MGGKWSKSSVIGWPTVRERMRRAEPAADRVGAASRDLEKHGAITSSNTAA
10
20
30
40
50


B*0702
A*1101
B35
B*3501
A3
A11
B35 or C4
B27
B*0301
A3.1
A3, A11, B35
A3
A11
A*0301
B35
B7
B*0702
B35
B*3501
B35
B7
B35
B*3501
B7
B*0702
A1, B8
B*4001
B60
B8
B*0801
A3.1
B35 or C4
B35
A2
Bw62
A1, B8
A11
A*1101
A11
C*0802(Cw8)
C*0802
TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGL
60
70
80
90
100
A*0201
B49
B35
B18
B*1801
B7,B*8101
B7(B*3101)
A2
B37,B57
B27
B15
A*2402
B*5701
A*2402
B*3701
B18
Bw62
B57
Bw62
B18
B*1501
A1, B8
B17, B37
B*57
B57
B7
B17
B42
B7
B17
B*4201
B7
B7
A1, B8
A1
B60
B*2705
B*5701
B*0702
IHSQRRQDILDLWIYHTQGYFPDXQNYTPGPGVRYPLTFGWCYKLVPVEP
110
120
130
140
150



[Brander & Goulder(2001)] C. Brander & P. Goulder. The evolving £eld of HIV CTL epitope mapping: New approaches to the identi£cation of novel epitopes. *HIV Molecular Immunology Database* pages IV–1, 2001. Notes: This review article in the annual HIV Molecular Immunology Compendium presents the table of Optimal CTL Epitopes that has been curated by Brander and others for several years.

[Dorrell (1999)] L. Dorrell, T. Dong, G. S. Ogg, S. Lister, S. McAdam, T. Rostron, C. Conlon, A. J. McMichael, & S. L. Rowland-Jones. Distinct recognition of non-clade B human immunode£ciency virus type 1 epitopes by cytotoxic T lymphocytes generated from donors infected in Africa. *J Virol* **73**:1708–14, 1999. (Medline: 99099071).

[Goulder (1997a)] P. Goulder, D. Price, M. Nowak, S. Rowland-Jones, R. Phillips, & A. McMichael. Co-evolution of human immunode£ciency virus and cytotoxic T-lymphocyte responses. *Immunol Rev* **159**:17–29, 1997a. (Medline: 98078460).

[Goulder (1997b)] P. Goulder, A. Sewell, D. Lalloo, D. Price, J. Whelan, J. Evans, G. Taylor, G. Luzzi, P. Giangrande, R. Phillips, & A. J. McMichael. Patterns of immunodominance in HIV-1-speci£c cytotoxic T lymphocyte responses in two human histocompatibility leukocyte antigens (HLA)-identical siblings with HLA-A*0201 are in¤uenced by epitope mutation. *J Exp Med* **8**:1423–33, 1997b. (Medline: 97272078) Notes: Primary human immunode£ciency virus (HIV) infection is controlled principally by HIV-speci£c cytotoxic T lymphocytes (CTL) to a steady- state level of virus load, which strongly in¤uences the ultimate rate of progression to disease. Epitope selection by CTL may be an important determinant of the degree of immune control over the virus. This report describes the CTL responses of two HLA-identical hemophiliac brothers who were exposed to identical batches of Factor VIII and became seropositive within 10 wk of one another. Both have HLA-A*0201. The CTL responses of the two siblings were very dissimilar, one donor making strong responses to two epitopes within p17 Gag (HLA-A*0201-restricted SLYNTVATL and HLA-A3-restricted RLRPGGKKK). The sibling responded to neither epitope, but made strong responses to two epitopes presented by HLA-B7. This was not the result of differences in presentation of the epitopes. However, mutations in both immunodominant epitopes of the p17 Gag responder were seen in proviral sequences of the nonresponder. We then documented the CTL responses to two HLA-A*0201-restricted epitopes, in Gag (SLYNTVATL) and Pol (ILKEPVHGV) in 22 other HIV-infected donors with HLA-A*0201. The majority (71%) generated responses to the Gag epitope. In the 29% of donors failing to respond to the Gag epitope in standard assays, there was evidence of low frequency memory CTL responses using peptide stimulation of PBMC, and most of these donors also showed mutations in or around the Gag epitope.

[Goulder(1999)] P. J. Goulder. personal communication. *unpublished* 1999.

[Goulder (2000)] P. J. Goulder, C. Brander, K. Annamalai, N. Mngqundaniso, U. Govender, Y. Tang, S. He, K. E. Hartman, C. A. O'Callaghan, G. S. Ogg, M. A. Altfeld, E. S. Rosenberg, H. Cao, S. A. Kalams, M. Hammond, M. Bunce, S. I. Pelton, S. A. Burchett, K. McIntosh, H. M. Coovadia, & B. D. Walker. Differential narrow focusing of immunodominant human immunode£ciency virus gag-speci£c cytotoxic T-lymphocyte responses in infected African and caucasoid adults and children. *J Virol* **74**:5679–90, 2000. (Medline: 20283828).

[Goulder (1997c)] P. J. Goulder, A. Edwards, R. E. Phillips, & A. J. McMichael. Identi£cation of a novel HLA-B*2705-restricted cytotoxic T lymphocyte epitope within a conserved region of HIV-1 Nef. *AIDS* **11**:536–538, 1997c. (Medline: 97239113).

[Lieberman (1997)] J. Lieberman, J. A. Fabry, D. M. Fong, & G. R. Parkerson 3rd. Recognition of a small number of diverse epitopes dominates the cytotoxic T lymphocytes response to HIV type 1 in an infected individual. *AIDS Res Hum Retroviruses* **13**:383–92, 1997. (Medline: 97229916).

[McAdam (1998)] S. McAdam, P. Kaleebu, P. Krausa, P. Goulder, N. French, B. Collin, T. Blanchard, J. Whitworth, A. McMichael, & F. Gotch. Cross-clade recognition of p55 by cytotoxic T lymphocytes in HIV-1 infection. *AIDS* **12**:571–9, 1998. (Medline: 98242898).

[Sipsas (1997)] N. V. Sipsas, S. A. Kalams, A. Trocha, S. He, W. A. Blattner, B. D. Walker, & R. P. Johnson. Identi£cation of type-speci£c cytotoxic T lymphocyte responses to homologous viral proteins in laboratory workers accidentally infected with HIV-1. *J Clin Invest* **99**:752–62, 1997. (Medline: 97197584) Notes: To examine a situation where the autologous strain and the reference reagents would be the same, the CTL response of three lab workers accidentally infected with HIV IIIB was studied. Both group speci£c and type speci£c epitopes were targets for CTL clones. One subject had a broadening of CTL response over time, using a broad range of restricting HLA class I alleles. Characterization of the cytotoxic T lymphocyte (CTL) response against HIV-1 has been limited by the use of target cells expressing viral proteins from laboratory isolates of HIV-1. This approach has favored identi£cation of group-speci£c CTL responses and precluded assessment of the extent of type-speci£c CTL responses directed against HIV-1. Using cells expressing viral proteins from the HIV-1 IIIB strain, we performed a detailed characterization of HIV-1-speci£c CTL response in three laboratory workers accidentally infected with HIV-1 IIIB. Eight of the epitopes identi£ed were group speci£c, lying in relatively conserved regions of Gag, reverse transcriptase, and envelope. Three type-speci£c epitopes were identi£ed, two of them in highly variable regions of envelope. In longitudinal studies in one subject, seven different epitopes and £ve different restricting HLA class I alleles were identi£ed, with a progressive increase in the number of CTL epitopes recognized by this subject over time. Our data demonstrate that type-speci£c CTL responses make up a signi£cant proportion of the host cellular immune response against HIV-1 and that a broadening of epitope speci£city may occur.