FSVPLDEDFRKYTAFTIPSI

```
QUERY                FSVPLDEDFRKYTAFTIPSI

CONSENSUS_A          -------s-----------t
A.KE.Q23-CXC-CG      -----H-E-----------T
A.SE.SE6594          -----H-------------T
A.SE.SE7253          -------S-----------T
A.SE.SE7535          -----H-G-----------T
A.SE.SE8131          -------S-----------T
A.SE.SE8538          -------S-----------T
A.SE.SE8891          ------KN------------
A.UG.92UG037         -------S-----------T
A.UG.U455            -------S------------

CONSENSUS_B          ------k-------------
B.-.NL43E9           ------K-------------
B.AU.MBC18           -------N------------
B.AU.MBC200          ------KE------------
B.AU.MBC925          -----Y-------------T
B.AU.MBCC54          -------N------------
B.AU.MBCC98          ------K-------------
B.AU.MBCD36          -------S------------
B.CN.RL42            ------K------------V
B.DE.D31             --------------------
B.DE.HAN             ------K-------------
B.FR.HXB2            --------------------
B.GA.OYI             ------K-------------
B.GB.CAM1            ------K------------T
B.GB.MANC            -----Y-------V------
B.NL.3202A21         ------K------------V
B.TW.LM49            ------K-------------
B.US.AD8             ------K-------------
B.US.BC              ------K-------------
B.US.DH123           --I----------------V
B.US.JRCSF           ------K-------------
B.US.JRFL            ------K-------------
B.US.MNCG            ------K-------------
B.US.NY5CG           ------K-------------
B.US.P896            --------------------
B.US.RF              ------KE------------
B.US.SF2             ------K-------------
B.US.WEAU160         --------------------
B.US.WR27            ---x--xEx----------x
B.US.YU2             -----H--------------

CONSENSUS_C          --------------------
C.BR.92BR025         -------G------------
C.BW.96BW01B03       -------G------------
C.BW.96BW0402        -------S------------
C.BW.96BW0502        -------G------------
C.BW.96BW1104        -------S------------
C.BW.96BW1210        -------S-----------R
C.BW.96BW15B03       --------------------
C.BW.96BW1626        -------S------------
C.BW.96BW17A09       --------------------
C.ET.ETH2220         -------G-----------T
C.IN.21068           -----Y--------------
C.IN.301904          -----Y--------------
C.IN.301905          -----Y------------V
C.IN.301999          -----Y-------------R
C.IN.94IN11246       -----Y--------------

CONSENSUS_D          --------------------
D.CD.84ZR085         --I--C--------------
D.CD.ELI             ----------------S--
D.CD.NDK             --------------------
D.CD.Z2Z6            ------K-------------
D.UG.94UG1141        -----H-------------T

CONSENSUS_F1         ------K------------v
F1.BE.VI850          ------K--K---------V
F1.BR.93BR020.1      ------K-------S----T
F1.FI.FIN9363        ------K------------V
F1.FR.MP411          ------KE-----------L

CONSENSUS_F2         ------KE------------
F2.CM.MP255          ------KE------------
F2.CM.MP257          ------KE------------

CONSENSUS_G          --------------------?
G.BE.DRCBL           -------N-----------T
G.FI.HH8793          -------S-----------T
G.NG.92NG083         ------K-------------
G.SE.SE6165          --------------------

CONSENSUS_H          ------k-------------
H.BE.VI991           -----H-------------T
H.BE.VI997           ------K-------------
H.CF.90CF056         ------KE------------

CONSENSUS_J          -----Y--------------
J.SE.SE9173          -----Y--------------
J.SE.SE9280          -----Y--------------

CONSENSUS_K          ------K-------------
K.CD.EQTB11C         ------K-------------
K.CM.MP535           ------K-------------
N.CM.YBF30           --C---K-------------

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

CONSENSUS_CPZ        --c---k------------v
CPZ.CD.CPZANT        --I---Q------------V
CPZ.GA.CPZGAB        --C---K-------------
CPZ.US.CPZUS         --C---KE-----------V
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LLMICSAT

QUERY	LLMICSAT
CONSENSUS_A	mii----a
A.GB.MA246	MII----A
A.GB.MC108	MIIF---A
A.KE.K89	MII----A
A.KE.Q23-CXC-CG	TIIF---V
A.NG.NG1935	.-I-Y--A
A.RW.KIG93	M-I---VA
A.RW.SF1703	M-I-----
A.SE.SE6594	-II---VA
A.SE.SE7253	MI----TA
A.SE.SE7535	-VI---VA
A.SE.SE8131	MII---TA
A.SE.SE8538	MII---TA
A.SE.SE8891	III----A
A.UG.92UG037	MII--NTA
A.UG.U455	-II--N-Q
A.UG.UG273A	-IT---TA
A.UG.UG275A	M-I---TA
CONSENSUS_B	m------a
B.AU.MBC18	I------A
B.AU.MBC200	M------A
B.AU.MBC925	-------A
B.AU.MBCC54	I------A
B.AU.MBCC98	M------A
B.AU.MBCD36	I------E
B.BE.SIMI84	M------V
B.CN.RL42	M----N-A
B.DE.D31	M-------
B.DE.HAN	M---S-VA
B.ES.89SP061	M----K-A
B.FR.HXB2	M-------
B.FR.PHI120	I------A
B.FR.PHI133	MF-----E
B.FR.PHI146	M-------
B.FR.PHI153	M-R--N-A
B.FR.PHI159	-----N--
B.FR.PIH155	M-------
B.FR.PIH160	M------V
B.FR.PIH309	I-------
B.FR.PIH373	I----N-A
B.FR.PIH374	I----N-K
B.GA.OYI	M------A
B.GB.AC-46	M------A
B.GB.CAM1	M------A
B.GB.GB8.C1	M-------
B.GB.JB	M------A
B.GB.M23470	I------R
B.GB.M26864	M------G
B.GB.M30156	M-------
B.GB.M737677	M------A
B.GB.M737685	M----N-A
B.GB.MANC	M------E
B.GB.MB314	I----N-A
B.GB.WB	M----K-A
B.JP.ETR	M------A
B.JP.JH32	I------A
B.NL.3202A21	M------A
B.NL.68A	M-------
B.NL.ENVVA	M------A
B.NL.ENVVF	M------A
B.NL.ENVVG	M------A
B.NL.H0320-2A12	M------A
B.TH.TH936705	M------A
B.TT.QZ4589	M-I-----
B.TW.LM49	M---S--A
B.US.85WCIPR54	M------A
B.US.92US657.1	M------E
B.US.ADA	M------V
B.US.ALA1	I-------
B.US.BC	I---Y--A
B.US.BRVA	I-------
B.US.C26-12.1BH	I-----TA
B.US.CDC452	M------A
B.US.DH123	I------A
B.US.ENVUS-R2	--------
B.US.JRCSF	T------V
B.US.JRFL	I------V
B.US.M02-3.SW	M---S---
B.US.MNCG	--------
B.US.NC7	M-------
B.US.NL43E9	I-------
B.US.NY5CG	M------A
B.US.P896	M------A
B.US.RF	M------A
B.US.SC	I------A
B.US.SC141	M-I----A
B.US.SC14C	M------A
B.US.SF128A	M-L-----
B.US.SF2	M-------
B.US.SFMHS1	I---Y--A
B.US.SFMHS11	I------E
B.US.SFMHS16	M-------
B.US.SFMHS17	I-------
B.US.SFMHS18	I-------
B.US.SFMHS19	I------A
B.US.SFMHS2	I------A
B.US.SFMHS20	T-----TA
B.US.SFMHS21	M------A
B.US.SFMHS3	M------A
B.US.SFMHS4	M-------
B.US.SFMHS5	I-------
B.US.SFMHS6	M-------
B.US.SFMHS7	I------A
B.US.SFMHS8	I------A
B.US.SFMHS9	-M-----A
B.US.US1	T------E
B.US.US2	I---S--A
B.US.US3	M------A
B.US.US4	I----R--
B.US.WC001	M-----VA
B.US.WEAU160	I------A
B.US.WMJ22	MW-----V
B.US.WR27	M----N--
B.US.YU2	M------A
CONSENSUS_C	m----nvm
C.BI.BU910112	M----NVM
C.BI.BU910213	MV---NVL
C.BI.BU910316	MV--YNVM
C.BI.BU910423	M..---VM
C.BI.BU910518	M-..-NVM
C.BI.BU910611	M--V-NVM
C.BI.BU910717	M..-YNVM
C.BI.BU910812	M-I--NVM
C.BR.92BR025	MV--YNVR
C.BW.96BW01B03	MI-L-NVM
C.BW.96BW0402	MIINGMGS
C.BW.96BW0502	M-I-S-VV
C.BW.96BW11B01	M----NVM
C.BW.96BW1210	M--V-.SK
C.BW.96BW15B03	...---GL
C.BW.96BW16B01	I-I-NNVV
C.BW.96BW17B05	M-----VL
C.DJ.DJ259A	M-L--..N
C.DJ.DJ373A	M-LM-NGM
C.ET.ETH2220	M----NGM
C.IN.21068	M----NVV
C.IN.301904	M----NVG
C.IN.301905	M----NVG
C.IN.301999	M----NVV
C.IN.94IN11246	M----NGG
C.SN.SE364A	MRL-YNVG
C.SO.SM145A	M-----GG
C.UG.UG268A2	I----NVM
CONSENSUS_D	m--t--?a
D.CD.84ZR085	-M-TY--A
D.CD.ELI	I--T---A
D.CD.JY1	I--T--VA
D.CD.NDK	M--T---A
D.CD.Z2Z6	I--T--NA
D.SN.SE365A2	M--T--VA
D.TZ.87TZ4622	M-------
D.UG.92UG024D	M-----G-
D.UG.94UG1141	M-----V-
D.UG.C971-412	M------A
D.UG.UG266A2	MII---TA
D.UG.UG269A	M----RV-
D.UG.UG274A2	M--TY-VA
D.UG.WHO15-474	M--T--TA
F.BR.BZ126A	I-I--N-E
CONSENSUS_F1	i-I--n-A
F1.BE.VI850	I-I--N-A
F1.BR.93BR020.1	T-I--N-A
F1.FI.FIN9363	M-I--K-A
F1.FR.MP411	I-I----A
CONSENSUS_F2	I-I--?-?

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F2.CM.MP255          IICNAN--
F2.CM.MP257          I-I----A

CONSENSUS_G          -VI----s
G.BE.DRCBL           -VI----E
G.FI.HH8793          -VI----S
G.GA.LBV217          -VI--N-S
G.NG.92NG083         -VI----S
G.NG.NG1928          WVI----S
G.NG.NG1929          -VI----S
G.NG.NG1937          -VI---TS
G.NG.NG1939          -VI----S
G.SE.SE6165          -VI----S

CONSENSUS_H          M-L----a
H.BE.VI991           M-L---VV
H.BE.VI997           M-L-Y--A
H.CF.90CF056         M-L----A

CONSENSUS_J          M----?-?
J.SE.SE9173          M------R
J.SE.SE9280          M----K-K

CONSENSUS_K          I-I---?A
K.CD.EQTB11C         I-I----A
K.CM.MP535           I-I---NA
N.CM.YBF30           S-IKVIGS

CONSENSUS_O          --?p-lss
O.CM.ANT70C          C-SLR...
O.CM.CM4974          C-NCK...
O.CM.HIV1CA9EN       -IIP-LSS
O.CM.MVP5180         C-SYS...
O.GA.VI686           -IIP-LSS
O.GQ.193HA           -ITP-LSS
O.GQ.276HA           C-SSKPSS
O.GQ.341HA           -TTP-LSF
O.GQ.655HA           -TTP-LSF
AC.IN.21301          M--V-NVV
AC.RW.92RW009        M-T----A
AC.SE.SE9488         M-I-----
AC.ZM.ZAM174         M-----VV
AC.ZM.ZAM184         M-----VV
AC.ZM.ZAM716-3       ...---VV
ACD.SE.SE8603        MIL----V
AD.KE.K124A2         MII--N-A
AD.SE.SE6954         M--T--V-
AD.SE.SE7108         MII---VA
AD.UG.C6080-10       MII----A
AD.UG.UG/92/035      MII----A
ADHU.NO.NOGIL3       M-L---T-
ADU.CD.MAL           M--T--IA
AG.GA.VI191A2        -GI--N-E
AG.NG.G3             -VI----S
AG.SE.SE7812         IMT----G
AGHU.GA.VI354        M----N-K
AGJ.AU.BFP90         -VI----S
AGJ.ML.95ML84        -AI-----
AGJ.NG.NG3670        -VI----S
AGU.CD.Z321          -VI----A
AU.NG.NG3678         I-I--R-A
BF.BR.93BR029.4      I-I--N-E
CD.BI.BU910905       M----NVM
CRF01_AE.CF.90CF402  -VI----S
CRF01_AE.TH.93TH253  -VIM---S
CRF01_AE.TH.A01021.  -VI----A
CRF01_AE.TH.070703   -VI----S
CRF01_AE.TH.070704   -GI----S
CRF01_AE.TH.070705   -VI----S
CRF01_AE.TH.070707   -VI----S
CRF01_AE.TH.070708   -VI----S
CRF01_AE.TH.070709   -VI----S
CRF01_AE.TH.070710   -VIM-T-S
CRF01_AE.TH.070711   -VI----S
CRF01_AE.TH.070713   -VIT--TA
CRF01_AE.TH.CM240    -VI----S
CRF01_AE.TH.E11429.  -VIM---S
CRF01_AE.TH.KH03     -VI----S
CRF01_AE.TH.KH08     -VI----S
CRF01_AE.TH.TH022    -VI----S
CRF01_AE.TH.TH047    -VI----S
CRF01_AE.TH.TH92014  -VI----S
CRF01_AE.TH.TH92111  -VI----S
CRF02_AG.DJ.DJ258A   IMI--N-K
CRF02_AG.FR.DJ263    IMI--N-E
CRF02_AG.FR.DJ264    IMI--N-E
CRF02_AG.NG.IBNG     IMI--N-E
CRF02_AG.NG.NG1921   -II--N-K
CRF02_AG.NG.NG3675   IM-L---E
CRF03_AB.RU.KAL1532  M-------
CRF03_AB.RU.KAL681   M-------
CRF03_AB.UA.UKR9700  MIIM-K-A
CRF04_cpx.CY.94CY03  -VI----S
CRF04_cpx.GR.97PVCH  -VIM---S
CRF04_cpx.GR.97PVMY  -VI----S
DF.BE.VI961          I-I----A
GH.GA.VI525          -VI-S--S
GU.NG.NG3670         M----N-A
U.CD.VI1126          IFI--N-A

CONSENSUS_CPZ        -??p???s
CPZ.CD.CPZANT        IQF-EKG-
CPZ.GA.CPZGAB        --TP-LTS
CPZ.US.CPZUS         -IIP.GLS
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IWVDLRSLFLFSYH

QUERY	IWVDLRSLFLFSYH
CONSENSUS_A	a-d-----C-----
A.GB.MA246	V-D-----C-----
A.GB.MC108	A-D-----C-----
A.KE.K89	A-D-----C-----
A.KE.Q23-CXC-CG	A-D-----C-----
A.NG.NG1935	A-D-----C-----
A.RW.KIG93	A-E---N-C-----
A.RW.SF1703	A-D-----C-----
A.SE.SE6594	A-D-----C-----
A.SE.SE7253	A-D-----C-----
A.SE.SE7535	A-E-----C-----
A.SE.SE8131	A-D-----CR----
A.SE.SE8538	A-D-----C-----
A.SE.SE8891	A-D-----C--C-R
A.UG.92UG037	A-D---N-C-----
A.UG.U455	A-D---N-C-----
A.UG.UG273A	A-D-----C-----
A.UG.UG275A	A-D-----C-----
CONSENSUS_B	--------c-----
B.AU.MBC18	F-D-----C-----
B.AU.MBC200	--------C-----
B.AU.MBC925	F-------C-----
B.AU.MBCC54	F-D-----C-----
B.AU.MBCC98	F-------C-C---
B.AU.MBCD36	F-D-----C--L--
B.BE.SIMI84	--G-----------
B.CN.RL42	--E-----C-----
B.DE.D31	--D--S--C--L--
B.DE.HAN	F-D-----C----R
B.ES.89SP061	--------C-----
B.FR.HXB2	--D-----C-----
B.FR.PHI120	--D-----C-----
B.FR.PHI133	--------C-----
B.FR.PHI146	C-D---N-C--G--
B.FR.PHI153	--E-----C-----
B.FR.PHI159	F----------R
B.FR.PIH155	--------CI----
B.FR.PIH160	F-D-----C-----
B.FR.PIH309	--------C-----
B.FR.PIH373	--I-----C-----
B.FR.PIH374	F-------C-----
B.GA.OYI	--D-----C-----
B.GB.AC-46	------N-C-----
B.GB.CAM1	--D-----C-----
B.GB.GB8.C1	F-D-----C-----
B.GB.JB	L-------C-----
B.GB.M23470	F----------
B.GB.M26864	--------C-----
B.GB.M30156	----------
B.GB.M737677	--D-----C-----
B.GB.M737685	--------C-----
B.GB.MANC	V-D-----C-----
B.GB.MB314	----------
B.GB.WB	--D-----C-----
B.JP.ETR	--------C-----
B.JP.JH32	--------C-----
B.NL.3202A21	--D-----C-----
B.NL.68A	--D----------
B.NL.ENVVA	--D-----C-----
B.NL.ENVVF	--D-----C-----
B.NL.ENVVG	--------C-----
B.NL.H0320-2A12	--D---PVC-----
B.TH.TH936705	--E--Q--C-----
B.TT.QZ4589	V-D-----C-----
B.TW.LM49	--------C-----
B.US.85WCIPR54	--------C-----
B.US.92US657.1	--------C--IC-
B.US.ADA	F-D-----C-----
B.US.ALA1	--------C-----
B.US.BC	F-D-----C-----
B.US.BRVA	F----------
B.US.C26-12.1BH	--------C-----
B.US.CDC452	V-D-----C-----
B.US.DH123	------T-------
B.US.ENVUS-R2	--------C-----
B.US.JRCSF	----------
B.US.JRFL	--------C-----
B.US.M02-3.SW	--D-----C-----
B.US.MNCG	----------
B.US.NC7	L-E---N-C-----
B.US.NL43E9	--D-----C-----
B.US.NY5CG	--------C-----
B.US.P896	F-----N-C--L--
B.US.RF	--D--WT-CS----
B.US.SC	----$---C-----
B.US.SC141	-$IN----C-----
B.US.SC14C	--I-----C-----
B.US.SF128A	--D-----C-----
B.US.SF2	--E-----C----R
B.US.SFMHS1	F-D--Q--C-----
B.US.SFMHS11	--------CI----
B.US.SFMHS16	F-DG----C-----
B.US.SFMHS17	F-------C-----
B.US.SFMHS18	--------C-----
B.US.SFMHS19	--------C-----
B.US.SFMHS2	--------C-----
B.US.SFMHS20	V-------C-----
B.US.SFMHS21	--D-----C-----
B.US.SFMHS3	--D--W--C----R
B.US.SFMHS4	--------C-----
B.US.SFMHS5	--------C-----
B.US.SFMHS6	F-D---N-C-----
B.US.SFMHS7	--------C-----
B.US.SFMHS8	--------C--N--
B.US.SFMHS9	--D-----C-----
B.US.US1	-R------C-----
B.US.US2	--D-----C-----
B.US.US3	--D-----C-----
B.US.US4	--D-----C-----
B.US.WC001	--------C-----
B.US.WEAU160	--------C--L--
B.US.WMJ22	--D-----C-----
B.US.WR27	--D-----C-----
B.US.YU2	--------C-----
CONSENSUS_C	a-d-----c-----
C.BI.BU910112	A-D-----C-----
C.BI.BU910213	A-D-----C-----
C.BI.BU910316	V-E---N-C-----
C.BI.BU910423	A-D-----C--C--
C.BI.BU910518	A-D-----C----R
C.BI.BU910611	A-D-----C--C--
C.BI.BU910717	A-D-----Y----R
C.BI.BU910812	A-D-----C--L--
C.BR.92BR025	A-D-----C-----
C.BW.96BW01B03	V-D---NPC-----
C.BW.96BW0402	V-D-----C-----
C.BW.96BW0502	A-D-----C-----
C.BW.96BW11B01	A-D-----C--C--
C.BW.96BW1210	A-D-----C-----
C.BW.96BW15B03	A-D-----C-----
C.BW.96BW16B01	A-D-----C-----
C.BW.96BW17B05	A-D-----CI-L--
C.DJ.DJ259A	A-D-----C----R
C.DJ.DJ373A	A-D----------
C.ET.ETH2220	F-D-----C-----
C.IN.21068	F-D---N-C-----
C.IN.301904	A-D---N-C-----
C.IN.301905	A-D---N-C-----
C.IN.301999	A-D-----C-----
C.IN.94IN11246	A-D-----C-----
C.SN.SE364A	A-D-----C-----
C.SO.SM145A	A-D-----C-----
C.UG.UG268A2	A-D-----C----R
CONSENSUS_D	--D---n-C-----
D.CD.84ZR085	--D---N-C-----
D.CD.ELI	--D-----C-----
D.CD.JY1	F-D---N-C-----
D.CD.NDK	F-D---N-C-----
D.CD.Z2Z6	--D---N-C-----
D.SN.SE365A2	--DG--N-C-----
D.TZ.87TZ4622	--D---N-C-----
D.UG.92UG024D	--D---N-C--R--
D.UG.94UG1141	--D---N-C-----
D.UG.C971-412	--D---N-C--G-R
D.UG.UG266A2	A-D-----C-----
D.UG.UG269A	--D---N-C-----
D.UG.UG274A2	--D---N-C----R
D.UG.WHO15-474	--D---N-C-L---
F.BR.BZ126A	V-D---N-C----R
CONSENSUS_F1	?-D---N-C----R
F1.BE.VI850	A-D---N-C----R
F1.BR.93BR020.1	A-D---N-C----R
F1.FI.FIN9363	V-D---N-C----R
F1.FR.MP411	V-D---N-C----R
CONSENSUS_F2	?-D-?---C?---?

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F2.CM.MP255          T-D-----CS---R
F2.CM.MP257          A-D-F---CV----

CONSENSUS_G          a-D-----c-----
G.BE.DRCBL           A-D-----C-----
G.FI.HH8793          A-D-----C-----
G.GA.LBV217          A-D-----C-----
G.NG.92NG083         A-D-----C-----
G.NG.NG1928          A-D-V---WI----
G.NG.NG1929          A-D-----C----R
G.NG.NG1937          A-D-----C-----
G.NG.NG1939          A-D-V---C-----
G.SE.SE6165          --D-----C-----

CONSENSUS_H          V-d-----c----R
H.BE.VI991           V-E---N-C----R
H.BE.VI997           V-D-----C----R
H.CF.90CF056         V-D-----S----R

CONSENSUS_J          A-D---?-C-----
J.SE.SE9173          A-D-----C-----
J.SE.SE9280          A-D---N-C-----

CONSENSUS_K          A-D---N-C----R
K.CD.EQTB11C         A-D---N-C----R
K.CM.MP535           A-D---N-C----R
N.CM.YBF30           V-E---N-LI-L--

CONSENSUS_O          lyt---tii-w?--
O.CM.ANT70C          LYT---TII-WT--
O.CM.CM4974          LYT---TII-WI--
O.CM.HIV1CA9EN       LYT---TII-WT--
O.CM.MVP5180         LYT---TII-WT--
O.GA.VI686           LYT---TII-WI--
O.GQ.193HA           LYT---TITVW---
O.GQ.276HA           LST---T---W---
O.GQ.341HA           LYT---TII-W---
O.GQ.655HA           .............
AC.IN.21301          F-D-----C-----
AC.RW.92RW009        A-D-----C-----
AC.SE.SE9488         A-D-----C-----
AC.ZM.ZAM174         A-D-----CR----
AC.ZM.ZAM184         A-D-----C-----
AC.ZM.ZAM716-3       A-D-----C-----
ACD.SE.SE8603        A-D-----C-----
AD.KE.K124A2         --D---D-C-----
AD.SE.SE6954         --D---N-C-----
AD.SE.SE7108         A-D-----C-----
AD.UG.C6080-10       A-D-----C-----
AD.UG.UG/92/035      A-D-----C-----
ADHU.NO.NOGIL3       V-E---N-C----R
ADU.CD.MAL           --D---N-C-----
AG.GA.VI191A2        A-D-----C-----
AG.NG.G3             A-D---N-C-----
AG.SE.SE7812         A-D-----C-----
AGHU.GA.VI354        --E---N-C----R
AGJ.AU.BFP90         A-D-----C-----
AGJ.ML.95ML84        A-D-----C-----
AGJ.NG.NG3670        A-E---N-C-----
AGU.CD.Z321          A-D-----C--C--
AU.NG.NG3678         A-D-----C-----
BF.BR.93BR029.4      V-D---N-C----R
CD.BI.BU910905       V-D-----C----R
CRF01_AE.CF.90CF402  A-D-----C-----
CRF01_AE.TH.93TH253  A-D-----C-----
CRF01_AE.TH.A01021.  A-D-----C-----
CRF01_AE.TH.070703   A-D-I---C--L--
CRF01_AE.TH.070704   A-D-----C-----
CRF01_AE.TH.070705   A-D-----C-----
CRF01_AE.TH.070707   A-D-----C----R
CRF01_AE.TH.070708   A-D-----C----R
CRF01_AE.TH.070709   A-D-----C-----
CRF01_AE.TH.070710   A-D-----------
CRF01_AE.TH.070711   A-D-----C-----
CRF01_AE.TH.070713   A-D-----C--C--
CRF01_AE.TH.CM240    A-D-----C-----
CRF01_AE.TH.E11429.  A-D-----C--L--
CRF01_AE.TH.KH03     V-D-----C-----
CRF01_AE.TH.KH08     A-D-----C-----
CRF01_AE.TH.TH022    A-D-----C--L--
CRF01_AE.TH.TH047    A-D-----C--L--
CRF01_AE.TH.TH92014  V-D-----C-----
CRF01_AE.TH.TH92111  A-D-----C-----
CRF02_AG.DJ.DJ258A   A-D-----C-----
CRF02_AG.FR.DJ263    A-D-----C-----
CRF02_AG.FR.DJ264    A-D-----C-----
CRF02_AG.NG.IBNG     A-D-----C-----
CRF02_AG.NG.NG1921   A-D-----------
CRF02_AG.NG.NG3675   A-E-----C-----
CRF03_AB.RU.KAL1532  --D-----CF-I--
CRF03_AB.RU.KAL681   --D-----C--I--
CRF03_AB.UA.UKR9700  A-D-----C----R
CRF04_cpx.CY.94CY03  --D---N-C----R
CRF04_cpx.GR.97PVCH  --D---N-C-----
CRF04_cpx.GR.97PVMY  V-D---N-C----R
DF.BE.VI961          --D---N-C-----
GH.GA.VI525          V-D--W--C----R
GU.NG.NG3670         A-D---N-C-----
U.CD.VI1126          A-D---N-C----R

CONSENSUS_CPZ        ?-?---n-?i??-?
CPZ.CD.CPZANT        .............
CPZ.GA.CPZGAB        --D---N-GIW--Q
CPZ.US.CPZUS         V-E---N-LI-L--
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GELDRWEKIRLRPGGKKKYK

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QUERY                GELDRWEKIRLRPGGKKKYK

CONSENSUS_A          -k--a--------------r
A.KE.Q23-CXC-CG      -KF-A--------------R
A.SE.SE6594          -K--A--------------R
A.SE.SE7253          -K--A--------------R
A.SE.SE7535          -K--A------------Q-R
A.SE.SE8131          -K--A----------N---R
A.SE.SE8538          -R--A--------------R
A.SE.SE8891          EKK-A---M-----------
A.UG.92UG037         -K--A--------------R
A.UG.U455            KK--S----------N---R

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

CONSENSUS_C          -K--k------------h-m
C.BR.92BR025         -K--A--R-K-K-----H-M
C.BW.96BW01B22       -K--Q------------C-M
C.BW.96BW0402        -K--A------------Q-R
C.BW.96BW0502        EK--K------------H-M
C.BW.96BW1104        -K--T------------R-M
C.BW.96BW1210        EK--T------------R-M
C.BW.96BW15B03       EK--T-----S------C-M
C.BW.96BW1626        -K--K------------R-M
C.BW.96BW17A09       -K--T------------H-M
C.ET.ETH2220         EK--A----K-------H-M
C.IN.93IN904         EK--K------------H-M
C.IN.93IN905         -K--K------------H-M
C.IN.93IN999         EK--K--R---------H-M
C.IN.94IN11246       -K--K------------H-M
C.IN.95IN21068       -K--K------------R-M

CONSENSUS_D          -K--a--------------r
D.CD.84ZR085         -K--A---------------
D.CD.ELI             -K--K--------------R
D.CD.NDK             -K--T--R-----------A
D.CD.Z2Z6            -K--A--------------R
D.UG.94UG1141        -K--E--------------R

CONSENSUS_F          -K--A--------------r
F.BR.BZ162           -K--A--------------R
F.CD.VI174           -K--A----Q---------R
F.RW.VI69            -K--A----------R----

CONSENSUS_F1         -K--a--------------r
F1.BE.VI850          -K--E----Q-------R--
F1.BR.93BR020.1      -K--A--------------R
F1.FI.FIN9363        -K--A------------Q-R
F1.FR.MP411          -K--A--R-----------R

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

CONSENSUS_G          -K--A----------x---x
G.BE.DRCBL           -K--A------------R-R
G.FI.HH8793          -K--A--------------R
G.NG.92NG083         -K--S----------R----
G.SE.SE6165          -K--A----------R-S--

CONSENSUS_H          -K--A--------------R
H.BE.VI991           -K--A----------R---R
H.BE.VI997           -R--TL-------------R
H.CF.90CF056         -K--A--------------R

CONSENSUS_J          -K--D------------?-R
J.SE.SE9173          -K--D------------Q-R
J.SE.SE9280          -K--D--------------R

CONSENSUS_K          -K--?--------------r
K.BE.VI325           -K--T----------S---R
K.CD.EQTB11C         -K--K----Q---------R
K.CM.MP535           -K--A---------------
N.CM.YBF30           -K--Q--S-Y---------R

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

CONSENSUS_CPZ        -k--?--------------M
CPZ.CD.CPZANT        EK--T--S-----------M
CPZ.GA.CPZGAB        -K------V------R-R-M
CPZ.US.CPZUS         -R--A--------------M
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LRPGGKKKYKLKHIVWASRE

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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------
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GSEELRSLYNTVATLYCVHQ

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QUERY                GSEELRSLYNTVATLYCVHQ

CONSENSUS_A          -T------------------
A.KE.Q23-CXC-CG      -T--IK--F-----------
A.SE.SE6594          -T--IK--F-----------
A.SE.SE7253          -T------F----V------
A.SE.SE7535          -T------------------
A.SE.SE8131          -T------------------
A.SE.SE8538          -T---K---------W----
A.SE.SE8891          -T------------------
A.UG.92UG037         -T------------------
A.UG.U455            -T-----------V------

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

CONSENSUS_C          -T------?----------?
C.BR.92BR025         -TK--I--H----------E
C.BW.96BW01B22       -T---K-------------E
C.BW.96BW0402        -T------F----------K
C.BW.96BW0502        -T----------------A
C.BW.96BW1104        -T--I--------------E
C.BW.96BW1210        -T---K-------------E
C.BW.96BW15B03       -T------F----------E
C.BW.96BW1626        -T---K-------V-F---A
C.BW.96BW17A09       -T---K--------------
C.ET.ETH2220         -T---K--F-----------
C.IN.93IN904         -T------H---V------A
C.IN.93IN905         -T------F----------A
C.IN.93IN999         -T------H----------E
C.IN.94IN11246       -T------F----------A
C.IN.95IN21068       -T------F----------A

CONSENSUS_D          -------------------e
D.CD.84ZR085         -------I-----------K
D.CD.ELI             -T-----------------K
D.CD.NDK             ----I-------------E
D.CD.Z2Z6            --------F----------E
D.UG.94UG1141        ----IK------V------E

CONSENSUS_F          -------------V--f---
F.BR.BZ162           -------------V--F---
F.CD.VI174           --------F--IVV--Y---
F.RW.VI69            -------------V--F---

CONSENSUS_F1         -----?--?--?-V--y---
F1.BE.VI850          -----K--F----V--Y---
F1.BR.93BR020.1      -----K-----I-V--Y---
F1.FI.FIN9363        -----------I-V--F---
F1.FR.MP411          --------F----V------

CONSENSUS_F2         -----K--?-??VV--Y---
F2.CM.MP255          -----K----A-VV--Y---
F2.CM.MP257          -----K--F--IVV--Y---

CONSENSUS_G          -T--IK--F-----------
G.BE.DRCBL           -T--IK--F-----------
G.FI.HH8793          -T--IK--F-----------
G.NG.92NG083         -T------F-----------
G.SE.SE6165          -T--IK----A---------

CONSENSUS_H          -T---Q--F----V------
H.BE.VI991           -T-D-Q-----I-V------
H.BE.VI997           -T---x--F---------L-
H.CF.90CF056         -T---K--F-L--V-----R

CONSENSUS_J          -T?-IK--------------
J.SE.SE9173          -T--IK--------------
J.SE.SE9280          -TQ-IK--------------

CONSENSUS_K          -----?--?----?------
K.BE.VI325           -----K--F---V-------
K.CD.EQTB11C         --------F-------W---
K.CM.MP535           ----IK-----I-V--F---
N.CM.YBF30           ----------AL-V-----S

CONSENSUS_O          --??-?--W-AI?V-W---N
O.CM.ANT70C          --DS-Q--W-AIVV-W---N
O.CM.MVP5180         ---D-K--W-AI-V-W---N
CRF01-AE.CF.90CF40   -----K--F--I---W----
CRF01-AE.TH.93TH25   -----K-----I---W----
CRF01-AE.TH.CM240    -L---K--F------W----
CRF01-AE.TH.TH022    --------F------W----
CRF01-AE.TH.TH047    --------F--IV--W----
CRF02_AG.FR.DJ263    -----K-----I---W---K
CRF02_AG.FR.DJ264    -----K-----I---W----
CRF02_AG.NG.IBNG     -----K--F--I---W----
CRF03_AB.RU.KAL15    -----K--------------
CRF04_cpx.CY.94CY0   -----------IT--W----
CRF04_cpx.GR.97PVC   ----VK--F--L---W----
CRF04_cpx.GR.97PVM   -----K--F-LI---W----
AC.ET.E3099G         -----K--------------
AC.IN.21301          -T------H----------A
AC.RW.92RW009        -TD-----------------
AC.SE.SE9488         -T--IK--F-----------
AC.ZM.ZAM174-21      -T------F--A-------E
AC.ZM.ZAM184         -T-DI--------V--Y---
AC.ZM.ZAM716-17      -T------F----------A
ACD.SE.SE8603        -T-------------W---K
AD.SE.SE6954         -----K--F----------A
AD.SE.SE7108         -T---K--------------
ADHU.NO.NOGIL3       -----K--F-L--V-W----
ADU.CD.MAL           ----IK--------------
AG.NG.G3             -T--IK--F-----------
AG.SE.SE7812         -----K--F--I---W----
AGHU.GA.VI354        -----K--F-----------
AGJ.AU.BFP90         -----K--F-----------
AGJ.ML.95ML8         -----K--------------
AGU.CD.Z321          -T--II--------------
BF.BR.93BR029.4      --------------------
DF.CD.VI961          -------------------E
U.CD.VI1126          --------F---V---W---

CONSENSUS_CPZ        ---g----F--l-V-W---s
CPZ.CD.CPZANT        R-P-II--F--ICV-W---K
CPZ.GA.CPZGAB        ---G----F--L-V-W-I-S
CPZ.US.CPZUS         ---G----F--L-V-W---S
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HQMKDCTERQANFLGKIWPS

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QUERY                HQMKDCTERQANFLGKIWPS

CONSENSUS_A          --------...ERQANFLGki
A.KE.Q23-CXC-CG      --------...ERQANFLGKI
A.SE.SE6594          --------...ERQANFLGKI
A.SE.SE7253          --------...ERQANFLGKM
A.SE.SE7535          --------...ERQANFLGRI
A.SE.SE8131          --------...ERQANFLGKI
A.SE.SE8538          --------...ERQANFLGKI
A.SE.SE8891          --------...ERQANFLGKI
A.UG.92UG037         --------...ERQANFLGKI
A.UG.U455            --------...ERQANFLGKI

CONSENSUS_B          -------??.eRQAnFLGkI
B.AU.AF128998        --------...ERQANFLGKI
B.-.NL43E9           --------...ERQANFLGKI
B.AU.MBC18           --------...ERQANFLGKI
B.AU.MBC200          --------...ERQANFLGKI
B.AU.MBC925          --------...ERQANFLGKI
B.AU.MBCC54          -H-T---...DRQANFLGKI
B.AU.MBCC98          ---I---...ERQANFLGKI
B.AU.MBCD36          --------...ERQANFLGKI
B.CN.RL42            -L------...ERQANFLGKI
B.DE.D31             --------...ERQANFLGKI
B.DE.HAN             --------...ERQANFLGKI
B.ES.89SP061         --------...ERQANFLGKI
B.FR.HXB2            --------...ERQANFLGKI
B.GA.OYI             --------...ERQANFLGKI
B.GB.CAM1            ------N...ERQANFLGKI
B.GB.MANC            --------...ERQANFLGKI
B.JP.JH31            ------N...ERQANFLGKI
B.NL.3202A21         --------...ERQANFLGKI
B.TW.LM49            --------...ERQANFLGKI
B.US.85WCIPR54       --------...ERQANFLGKI
B.US.AD8             --------...ERQANFLGKI
B.US.BC              --------...ERQANFLGKI
B.US.DH123           --------...ERQANFLGKI
B.US.JRCSF           ----E---...ERQANFLGKI
B.US.JRFL            --------...ERQANFLGKI
B.US.MNCG            --------...ERQANFLGKI
B.US.NC7             ------I...ERQANFLGKI
B.US.NY5CG           --------...ERQANFLGKI
B.US.P896            --------...ERQANFLGKI
B.US.RF              -------NE.GRQANFLGKI
B.US.SF2             --------...ERQANFLGKI
B.US.WC001           --------...ERQANFLGKI
B.US.WEAU160         --------...ERQANFLGKI
B.US.WR27            ---x-xx...ERQAxFLGxI
B.US.YU2             --------...ERQANFLGKI

CONSENSUS_C          --------...ErqAnFLGki
C.BR.92BR025         --V-----...ERQANFLGKI
C.BW.96BW01B22       --------...ERQANFLGKI
C.BW.96BW0402        --------...ERQANFLGKI
C.BW.96BW0502        --------...ERQANFLGKI
C.BW.96BW1104        --------...ERRANFLGKI
C.BW.96BW1210        ------S...EGQANFLGKI
C.BW.96BW15B03       --------...ERQANFLGKI
C.BW.96BW1626        --------...ERQADFLGKI
C.BW.96BW17A09       ----E---...ERQANFLGKI
C.ET.ETH2220         --------...ERQANFLGRL
C.IN.93IN904         --------...ERQANFLGKI
C.IN.93IN905         --------...ERQANFLGKI
C.IN.93IN999         --------...ERQANFLGKI
C.IN.94IN11246       --------...ERQANFLGKI
C.IN.95IN21068       --------...ERQANFLGKI

CONSENSUS_D          --------...ERQANFLGkI
D.CD.84ZR085         --------...ERQANFLGKI
D.CD.ELI             --L-----...ERQANFLGRI
D.CD.NDK             --------...ERQANFLGKI
D.CD.Z2Z6            --L-----...ERQANFLGKI
D.UG.94UG1141        --------...ERQANFLGKI

CONSENSUS_F          --------...ErQANFLGKI
F.BR.BZ162           --------...EGQANFLGKI
F.CD.VI174           --------...ERQANFLGKI
F.RW.VI69            --------...ERQANFLGKI

CONSENSUS_F1         --------...ERQANFLGKI
F1.BE.VI850          --------...ERQANFLGKI
F1.BR.93BR020.1      --------...ERQANFLGKI
F1.FI.FIN9363        --------...ERQANFLGKI
F1.FR.MP411          --------...ERQANFLGKI

CONSENSUS_F2         --------...ERQANFLGK?
F2.CM.MP255          --------...ERQANFLGKI
F2.CM.MP257          --------...ERQANFLGKM

CONSENSUS_G          ----x---...ERQANFLGKI
G.BE.DRCBL           ----E---...ERQANFLGKI
G.FI.HH8793          --------...ERQANFLGKI
G.NG.92NG083         ----E---...ERQANFLGKI
G.SE.SE6165          --------...ERQANFLGKI

CONSENSUS_H          --------...ERQANFLGKI
H.BE.VI991           --------...GRQANFLGKI
H.BE.VI997           --------...ERQANFLGKI
H.CF.90CF056         --------...ERQANFLGKI

CONSENSUS_J          --------...ERQANFLGKI
J.SE.SE9173          --------...ERQANFLGKI
J.SE.SE9280          --------...ERQANFLGKI

CONSENSUS_K          -------??.eRQANFLGKi
K.BE.VI325           --------...ERQANFLGKI
K.CD.EQTB11C         ------S...ERQANFLGKF
K.CM.MP535           --------...ERQANFLGKI
N.CM.YBF30           ------KNE.GRQANFLGK-

CONSENSUS_O          ------?N..G?QANFLGKY
O.CM.ANT70C          ------RN..GKQANFLGKY
O.CM.MVP5180         ------KN..GRQANFLGKY
CRF01-AE.CF.90CF40   --------...ERQANFLGKI
CRF01-AE.TH.93TH25   --------...ERQANFLGKI
CRF01-AE.TH.CM240    --------...ERQANFLGKI
CRF01-AE.TH.TH022    --------...ERQANFLGKI
CRF01-AE.TH.TH047    --------...ERQANFLGKI
CRF02_AG.FR.DJ263    --------...EGQANFLGKI
CRF02_AG.FR.DJ264    --------...ERQANFLGKI
CRF02_AG.NG.IBNG     --------...ERQANFLGKI
CRF03_AB.RU.KAL15    --------...ERQANFLGRI
CRF04_cpx.CY.94CY0   --------...ERQANFLGRM
CRF04_cpx.GR.97PVC   --------...ERQANFLGRM
CRF04_cpx.GR.97PVM   ------P...ERQANSLGRM
AC.ET.E3099G         --------...ERQANFLGKI
AC.IN.21301          --------...ERQANFLGKI
AC.RW.92RW009        --------...ERQANFLGKI
AC.SE.SE9488         --------...ERQANFLGKI
AC.ZM.ZAM174-21      --------...ERQANFLGKI
AC.ZM.ZAM184         --------...ERQANFLGKI
AC.ZM.ZAM716-17      --------...ERQANFLGKI
ACD.SE.SE8603        --------...ERQANFLGKI
AD.SE.SE6954         --------...ERQANFLGKI
AD.SE.SE7108         --------...ERQANFLGKI
ADHU.NO.NOGIL3       --------...ERQANFLGKI
ADU.CD.MAL           --------...ERQANFLGKI
AG.NG.G3             --------...ERQANFLGKI
AG.SE.SE7812         --------...ERQANFLGKI
AGHU.GA.VI354        --------...ERQANFLGKI
AGJ.AU.BFP90         --------...ERQANFLGKI
AGJ.ML.95ML8         --------...ERQANFLGRI
AGU.CD.Z321          -------....ERQANFLGKI
BF.BR.93BR029.4      --------...ERQANFLGKI
DF.CD.VI961          ------I...EGQANFLGRV
U.CD.VI1126          --------...ERQANFLGKI

CONSENSUS_CPZ        -------a?n?rqvNFLGK?
CPZ.CD.CPZANT        --L-N-PATNTGKVNFLGKP
CPZ.GA.CPZGAB        --------...GRQVNFLGKG
CPZ.US.CPZUS         -------AGN.RQANFLGKH
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ANFLGKIWPSYKGRPGNFLQ

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QUERY                ANFLGKIWPSYKGRPGNFLQ

CONSENSUS_A          ----------s--....RPG
A.KE.Q23-CXC-CG      ----------R--....RPG
A.SE.SE6594          ----------S--....RPG
A.SE.SE7253          ------M---S--....RPG
A.SE.SE7535          -----R----S--....RPG
A.SE.SE8131          ----------H--....RPG
A.SE.SE8538          ----------S--....RPG
A.SE.SE8891          ----------NR-....RPG
A.UG.92UG037         ----------S--....RPG
A.UG.U455            ----------N--....RPG

CONSENSUS_B          ----------h--....Rpg
B.AU.AF128998        ----------H--....RPG
B.-.NL43E9           ----------H--....RPG
B.AU.MBC18           ----------H--....RPG
B.AU.MBC200          ----------....RPG
B.AU.MBC925          ----------H--....RPG
B.AU.MBCC54          ----------....RPG
B.AU.MBCC98          ----------H--....RPG
B.AU.MBCD36          ----------H--....RQE
B.CN.RL42            ----------H--....RPG
B.DE.D31             ----------....RPG
B.DE.HAN             ----------H--....RPG
B.ES.89SP061         ----------HR-....RPG
B.FR.HXB2            ----------....RPG
B.GA.OYI             ----------H--....RPG
B.GB.CAM1            ----------H--....RPG
B.GB.MANC            ----------H--....RPG
B.JP.JH31            ----------S--....RPG
B.NL.3202A21         ----------H--....RPG
B.TW.LM49            ----------H-E....RPG
B.US.85WCIPR54       ----------H--....RPG
B.US.AD8             ----------H--....RPG
B.US.BC              ----------H--....RPG
B.US.DH123           ----------H-E....RPG
B.US.JRCSF           ----------....RPG
B.US.JRFL            ----------....RPG
B.US.MNCG            ----------C--....R.R
B.US.NC7             ----------H--....RPG
B.US.NY5CG           ----------H--....RPG
B.US.P896            ----------H--....RPG
B.US.RF              ----------H--....RPG
B.US.SF2             ----------....RPG
B.US.WC001           ----------....RPG
B.US.WEAU160         --------S-Q--....RPG
B.US.WR27            -x---x-R--Hx-....RPG
B.US.YU2             ----------H--....RPG

CONSENSUS_C          ----------h--...?RPG
C.BR.92BR025         ----------HR-....RPG
C.BW.96BW01B22       ----------H--....RPG
C.BW.96BW0402        ----------H--....RPG
C.BW.96BW0502        ----------H--....RPG
C.BW.96BW1104        ----------H--....RPG
C.BW.96BW1210        ----------H--....RPG
C.BW.96BW15B03       ----------H--....RPG
C.BW.96BW1626        -D--------H--....RPG
C.BW.96BW17A09       ----------H--...GRPG
C.ET.ETH2220         -----RL---N--....RPG
C.IN.93IN904         ----------H--....RPG
C.IN.93IN905         ----------H--....RPG
C.IN.93IN999         ----------H--....RPG
C.IN.94IN11246       ----------H--....RPG
C.IN.95IN21068       ----------H--....RPG

CONSENSUS_D          ----------H--....RPG
D.CD.84ZR085         ----------H--....RPG
D.CD.ELI             -----R----H--....RPG
D.CD.NDK             ----------H--....RPG
D.CD.Z2Z6            ----------H--....RPG
D.UG.94UG1141        ----------HN-....RPG

CONSENSUS_F          ----------n--....RPG
F.BR.BZ162           ----------H--....RPG
F.CD.VI174           ----------N--....RPG
F.RW.VI69            ----------N--....RPG

CONSENSUS_F1         ----------N--....RPG
F1.BE.VI850          ----------N--....RPG
F1.BR.93BR020.1      ----------N--....RPG
F1.FI.FIN9363        ----------N--....RPG
F1.FR.MP411          ----------N--....RPG

CONSENSUS_F2         ------?---N?-....RPG
F2.CM.MP255          ----------NR-....RPG
F2.CM.MP257          ------M---N--....RPG

CONSENSUS_G          ----------N--....RPG
G.BE.DRCBL           ----------N--....RPG
G.FI.HH8793          ----------N--....RPG
G.NG.92NG083         ----------N--....RPG
G.SE.SE6165          ----------N--....RPG

CONSENSUS_H          ----------S--....RPG
H.BE.VI991           ----------S--....RPG
H.BE.VI997           ----------S--....RPG
H.CF.90CF056         ----------S--....RPG

CONSENSUS_J          ----------S--....RPG
J.SE.SE9173          ----------S--....RPG
J.SE.SE9280          ----------S--....RPG

CONSENSUS_K          ----------n--....rPG
K.BE.VI325           ----------N--....KPG
K.CD.EQTB11C         ------F--LN-E....RPG
K.CM.MP535           ----------H--....RPG
N.CM.YBF30           ------S-SPF--....RPG

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

CONSENSUS_CPZ        v-----?--??w-????RPG
CPZ.CD.CPZANT        V-----PT-TWW-C...RPG
CPZ.GA.CPZGAB        V-----G---RS-....RPG
CPZ.US.CPZUS         ------H-SPSWSGGSKRPG
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Study Subject ID:03RCH34
Study Subject Clone:
Study Subject HLA:A2,A23,B44,Cw4,Cw7
Sequence: Known reactive 20Mer0: FSVPLDEDFRKYTAFTIPSI RT(116–135)

Possible HLA

A2	A2.1,A*0201,A*0202,A*0203,A*0204,A*0205,A*0206,A*0207,A*0208,A*0209,A*0210,A*0211,A*0212,A*0213,A*0214,A*0216,A*0217,A*0218,A*0220,A*02
A23	A*2301
B44	B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
Cw4	C4,Cw*0401,C*0401,Cw*0402
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(6-15)	DEDFRKYTAF	B*4402
(6-15)	DEDFRKYTAF	B*4403
(8-15)	DFRKYTAF	Cw*0401
(1-9)	FSVPLDEDF	Cw*0702
(4-12)	PLDEDFRKY	Cw*0702
(7-15)	EDFRKYTAF	Cw*0702
(2-9)	SVPLDEDF	Cw*0702
(5-12)	LDEDFRKY	Cw*0702
(8-15)	DFRKYTAF	Cw*0702
(3-12)	VPLDEDFRKY	Cw*0702
(6-15)	DEDFRKYTAF	Cw*0702

Anchor Residues Searched

A*0201	X[LM]XXXXXX[VL]
A*0201	X[LM]XXXXX[VL]
A*0201	X[LM]XXXXXXX[VL]
A*0202	X[L]XXXXXX[LV]
A*0202	X[L]XXXXX[LV]
A*0202	X[L]XXXXXXX[LV]
A*0204	X[L]XXXXXX[L]
A*0204	X[L]XXXXX[L]
A*0204	X[L]XXXXXXX[L]
A*0205	X[VLIMQ]XXXXXX[L]
A*0205	X[VLIMQ]XXXXX[L]
A*0205	X[VLIMQ]XXXXXXX[L]
A*0206	X[V]XXXXXX[V]
A*0206	X[V]XXXXX[V]
A*0206	X[V]XXXXXXX[V]

A*0207	X[L][D]XXXXX[L]
A*0207	X[L][D]XXXX[L]
A*0207	X[L][D]XXXXXX[L]
A*0214	X[VQL]XXXXXX[LV]
A*0214	X[VQL]XXXXX[LV]
A*0214	X[VQL]XXXXXXX[LV]
B44	X[E]XXXXXX[Y]
B44	X[E]XXXXX[Y]
B44	X[E]XXXXXXX[Y]
B*4402	X[E]XXXXXX[FY]
B*4402	X[E]XXXXX[FY]
B*4402	X[E]XXXXXXX[FY]
B*4403	X[E]XXXXXX[YF]
B*4403	X[E]XXXXX[YF]
B*4403	X[E]XXXXXXX[YF]
Cw*0401	X[YPF]XXXXXX[LF]
Cw*0401	X[YPF]XXXXX[LF]
Cw*0401	X[YPF]XXXXXXX[LF]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH34
Study Subject Clone:
Study Subject HLA:A2,A23,B44,Cw4,Cw7
Sequence: Known reactive 20Mer1: LLMICSAT gp160(24–31)

Possible HLA

A2	A2.1,A*0201,A*0202,A*0203,A*0204,A*0205,A*0206,A*0207,A*0208,A*0209,A*0210,A*0211,A*0212,A*0213,A*0214,A*0216,A*0217,A*0218,A*0220,A*02
A23	A*2301
B44	B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
Cw4	C4,Cw*0401,C*0401,Cw*0402
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

Anchor Residues Searched

A*0201	X[LM]XXXXXX[VL]
A*0201	X[LM]XXXXX[VL]
A*0201	X[LM]XXXXXXX[VL]
A*0202	X[L]XXXXXX[LV]
A*0202	X[L]XXXXX[LV]
A*0202	X[L]XXXXXXX[LV]
A*0204	X[L]XXXXXX[L]
A*0204	X[L]XXXXX[L]
A*0204	X[L]XXXXXXX[L]
A*0205	X[VLIMQ]XXXXXX[L]
A*0205	X[VLIMQ]XXXXX[L]
A*0205	X[VLIMQ]XXXXXXX[L]
A*0206	X[V]XXXXXX[V]
A*0206	X[V]XXXXX[V]
A*0206	X[V]XXXXXXX[V]
A*0207	X[L][D]XXXXX[L]
A*0207	X[L][D]XXXX[L]
A*0207	X[L][D]XXXXXX[L]
A*0214	X[VQL]XXXXXX[LV]
A*0214	X[VQL]XXXXX[LV]
A*0214	X[VQL]XXXXXXX[LV]
B44	X[E]XXXXXX[Y]
B44	X[E]XXXXX[Y]
B44	X[E]XXXXXXX[Y]
B*4402	X[E]XXXXXX[FY]
B*4402	X[E]XXXXX[FY]

B*4402	X[E]XXXXXXX[FY]
B*4403	X[E]XXXXXX[YF]
B*4403	X[E]XXXXX[YF]
B*4403	X[E]XXXXXXX[YF]
Cw*0401	X[YPF]XXXXXX[LF]
Cw*0401	X[YPF]XXXXX[LF]
Cw*0401	X[YPF]XXXXXXX[LF]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH34
Study Subject Clone:
Study Subject HLA:A2,A23,B44,Cw4,Cw7
Sequence: Known reactive 20Mer2: IWVDLRSLFLFSYH gp160(756–769)

Possible HLA

A2	A2.1,A*0201,A*0202,A*0203,A*0204,A*0205,A*0206,A*0207,A*0208,A*0209,A*0210,A*0211,A*0212,A*0213,A*0214,A*0216,A*0217,A*0218,A*0220,A*02
A23	A*2301
B44	B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
Cw4	C4,Cw*0401,C*0401,Cw*0402
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(2-10)	WVDLRSLFL	A*0205
(2-10)	WVDLRSLFL	A*0214
(1-9)	IWVDLRSLF	Cw*0702
(2-10)	WVDLRSLFL	Cw*0702
(3-11)	VDLRSLFLF	Cw*0702
(5-13)	LRSLFLFSY	Cw*0702
(1-8)	IWVDLRSL	Cw*0702
(2-9)	WVDLRSLF	Cw*0702
(3-10)	VDLRSLFL	Cw*0702
(4-11)	DLRSLFLF	Cw*0702
(6-13)	RSLFLFSY	Cw*0702
(1-10)	IWVDLRSLFL	Cw*0702
(2-11)	WVDLRSLFLF	Cw*0702
(4-13)	DLRSLFLFSY	Cw*0702

Anchor Residues Searched

A*0201	X[LM]XXXXXX[VL]
A*0201	X[LM]XXXXX[VL]
A*0201	X[LM]XXXXXXX[VL]
A*0202	X[L]XXXXXX[LV]
A*0202	X[L]XXXXX[LV]
A*0202	X[L]XXXXXXX[LV]
A*0204	X[L]XXXXXX[L]
A*0204	X[L]XXXXX[L]
A*0204	X[L]XXXXXXX[L]
A*0205	X[VLIMQ]XXXXXX[L]
A*0205	X[VLIMQ]XXXXX[L]
A*0205	X[VLIMQ]XXXXXXX[L]

A*0206	X[V]XXXXXX[V]
A*0206	X[V]XXXXX[V]
A*0206	X[V]XXXXXXX[V]
A*0207	X[L][D]XXXXX[L]
A*0207	X[L][D]XXXX[L]
A*0207	X[L][D]XXXXXX[L]
A*0214	X[VQL]XXXXXX[LV]
A*0214	X[VQL]XXXXX[LV]
A*0214	X[VQL]XXXXXXX[LV]
B44	X[E]XXXXXX[Y]
B44	X[E]XXXXX[Y]
B44	X[E]XXXXXXX[Y]
B*4402	X[E]XXXXXX[FY]
B*4402	X[E]XXXXX[FY]
B*4402	X[E]XXXXXXX[FY]
B*4403	X[E]XXXXXX[YF]
B*4403	X[E]XXXXX[YF]
B*4403	X[E]XXXXXXX[YF]
Cw*0401	X[YPF]XXXXXX[LF]
Cw*0401	X[YPF]XXXXX[LF]
Cw*0401	X[YPF]XXXXXXX[LF]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH34
Study Subject Clone:
Study Subject HLA:A2,A23,B44,Cw4,Cw7
Sequence: Known reactive 20Mer3: GELDRWEKIRLRPGGKKKYK p17(11–30)

Possible HLA

A2	A2.1,A*0201,A*0202,A*0203,A*0204,A*0205,A*0206,A*0207,A*0208,A*0209,A*0210,A*0211,A*0212,A*0213,A*0214,A*0216,A*0217,A*0218,A*0220,A*02
A23	A*2301
B44	B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
Cw4	C4,Cw*0401,C*0401,Cw*0402
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(2-11)	ELDRWEKIRL	A*0201
(2-11)	ELDRWEKIRL	A*0202
(2-11)	ELDRWEKIRL	A*0204
(2-11)	ELDRWEKIRL	A*0205
(2-11)	ELDRWEKIRL	A*0207
(2-11)	ELDRWEKIRL	A*0214
(3-11)	LDRWEKIRL	Cw*0702
(11-19)	LRPGGKKKY	Cw*0702
(4-11)	DRWEKIRL	Cw*0702
(12-19)	RPGGKKKY	Cw*0702
(2-11)	ELDRWEKIRL	Cw*0702
(10-19)	RLRPGGKKKY	Cw*0702

Anchor Residues Searched

A*0201	X[LM]XXXXXX[VL]
A*0201	X[LM]XXXXX[VL]
A*0201	X[LM]XXXXXXX[VL]
A*0202	X[L]XXXXXX[LV]
A*0202	X[L]XXXXX[LV]
A*0202	X[L]XXXXXXX[LV]
A*0204	X[L]XXXXXX[L]
A*0204	X[L]XXXXX[L]
A*0204	X[L]XXXXXXX[L]
A*0205	X[VLIMQ]XXXXXX[L]
A*0205	X[VLIMQ]XXXXX[L]
A*0205	X[VLIMQ]XXXXXXX[L]
A*0206	X[V]XXXXXX[V]
A*0206	X[V]XXXXX[V]

A*0206	X[V]XXXXXXX[V]
A*0207	X[L][D]XXXXX[L]
A*0207	X[L][D]XXXX[L]
A*0207	X[L][D]XXXXXX[L]
A*0214	X[VQL]XXXXXX[LV]
A*0214	X[VQL]XXXXX[LV]
A*0214	X[VQL]XXXXXXX[LV]
B44	X[E]XXXXXX[Y]
B44	X[E]XXXXX[Y]
B44	X[E]XXXXXXX[Y]
B*4402	X[E]XXXXXX[FY]
B*4402	X[E]XXXXX[FY]
B*4402	X[E]XXXXXXX[FY]
B*4403	X[E]XXXXXX[YF]
B*4403	X[E]XXXXX[YF]
B*4403	X[E]XXXXXXX[YF]
Cw*0401	X[YPF]XXXXXX[LF]
Cw*0401	X[YPF]XXXXX[LF]
Cw*0401	X[YPF]XXXXXXX[LF]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH34
Study Subject Clone:
Study Subject HLA:A2,A23,B44,Cw4,Cw7
Sequence: Known reactive 20Mer4: LRPGGKKKYKLKHIVWASRE p17(21–40)

Possible HLA

A2	A2.1,A*0201,A*0202,A*0203,A*0204,A*0205,A*0206,A*0207,A*0208,A*0209,A*0210,A*0211,A*0212,A*0213,A*0214,A*0216,A*0217,A*0218,A*0220,A*02
A23	A*2301
B44	B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
Cw4	C4,Cw*0401,C*0401,Cw*0402
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(2-11)	RPGGKKKYKL	Cw*0401
(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

A*0201	X[LM]XXXXXX[VL]
A*0201	X[LM]XXXXX[VL]
A*0201	X[LM]XXXXXXX[VL]
A*0202	X[L]XXXXXX[LV]
A*0202	X[L]XXXXX[LV]
A*0202	X[L]XXXXXXX[LV]
A*0204	X[L]XXXXXX[L]
A*0204	X[L]XXXXX[L]
A*0204	X[L]XXXXXXX[L]
A*0205	X[VLIMQ]XXXXXX[L]
A*0205	X[VLIMQ]XXXXX[L]
A*0205	X[VLIMQ]XXXXXXX[L]
A*0206	X[V]XXXXXX[V]
A*0206	X[V]XXXXX[V]
A*0206	X[V]XXXXXXX[V]
A*0207	X[L][D]XXXXX[L]
A*0207	X[L][D]XXXX[L]
A*0207	X[L][D]XXXXXX[L]
A*0214	X[VQL]XXXXXX[LV]
A*0214	X[VQL]XXXXX[LV]

A*0214	X[VQL]XXXXXXX[LV]
B44	X[E]XXXXXX[Y]
B44	X[E]XXXXX[Y]
B44	X[E]XXXXXXX[Y]
B*4402	X[E]XXXXXX[FY]
B*4402	X[E]XXXXX[FY]
B*4402	X[E]XXXXXXX[FY]
B*4403	X[E]XXXXXX[YF]
B*4403	X[E]XXXXX[YF]
B*4403	X[E]XXXXXXX[YF]
Cw*0401	X[YPF]XXXXXX[LF]
Cw*0401	X[YPF]XXXXX[LF]
Cw*0401	X[YPF]XXXXXXX[LF]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH34
Study Subject Clone:
Study Subject HLA:A2,A23,B44,Cw4,Cw7
Sequence: Known reactive 20Mer5: GSEELRSLYNTVATLYCVHQ p17(71–90)

Possible HLA

A2	A2.1,A*0201,A*0202,A*0203,A*0204,A*0205,A*0206,A*0207,A*0208,A*0209,A*0210,A*0211,A*0212,A*0213,A*0214,A*0216,A*0217,A*0218,A*0220,A*02
A23	A*2301
B44	B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
Cw4	C4,Cw*0401,C*0401,Cw*0402
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(4-12)	ELRSLYNTV	A*0201
(7-15)	SLYNTVATL	A*0201
(4-12)	ELRSLYNTV	A*0202
(7-15)	SLYNTVATL	A*0202
(7-15)	SLYNTVATL	A*0204
(7-15)	SLYNTVATL	A*0205
(11-18)	TVATLYCV	A*0206
(4-12)	ELRSLYNTV	A*0214
(7-15)	SLYNTVATL	A*0214
(11-18)	TVATLYCV	A*0214
(2-9)	SEELRSLY	B44
(2-9)	SEELRSLY	B*4402
(2-9)	SEELRSLY	B*4403
(8-15)	LYNTVATL	Cw*0401
(1-9)	GSEELRSLY	Cw*0702
(7-15)	SLYNTVATL	Cw*0702
(8-16)	LYNTVATLY	Cw*0702
(1-8)	GSEELRSL	Cw*0702
(2-9)	SEELRSLY	Cw*0702
(8-15)	LYNTVATL	Cw*0702
(9-16)	YNTVATLY	Cw*0702
(6-15)	RSLYNTVATL	Cw*0702
(7-16)	SLYNTVATLY	Cw*0702

Anchor Residues Searched

A*0201	X[LM]XXXXXX[VL]
A*0201	X[LM]XXXXX[VL]
A*0201	X[LM]XXXXXXX[VL]

A*0202	X[L]XXXXXX[LV]
A*0202	X[L]XXXXX[LV]
A*0202	X[L]XXXXXXX[LV]
A*0204	X[L]XXXXXX[L]
A*0204	X[L]XXXXX[L]
A*0204	X[L]XXXXXXX[L]
A*0205	X[VLIMQ]XXXXXX[L]
A*0205	X[VLIMQ]XXXXX[L]
A*0205	X[VLIMQ]XXXXXXX[L]
A*0206	X[V]XXXXXX[V]
A*0206	X[V]XXXXX[V]
A*0206	X[V]XXXXXXX[V]
A*0207	X[L][D]XXXXX[L]
A*0207	X[L][D]XXXX[L]
A*0207	X[L][D]XXXXXX[L]
A*0214	X[VQL]XXXXXX[LV]
A*0214	X[VQL]XXXXX[LV]
A*0214	X[VQL]XXXXXXX[LV]
B44	X[E]XXXXXX[Y]
B44	X[E]XXXXX[Y]
B44	X[E]XXXXXXX[Y]
B*4402	X[E]XXXXXX[FY]
B*4402	X[E]XXXXX[FY]
B*4402	X[E]XXXXXXX[FY]
B*4403	X[E]XXXXXX[YF]
B*4403	X[E]XXXXX[YF]
B*4403	X[E]XXXXXXX[YF]
Cw*0401	X[YPF]XXXXXX[LF]
Cw*0401	X[YPF]XXXXX[LF]
Cw*0401	X[YPF]XXXXXXX[LF]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH34
Study Subject Clone:
Study Subject HLA:A2,A23,B44,Cw4,Cw7
Sequence: Known reactive 20Mer6: HQMKDCTERQANFLGKIWPS p2p7p1p6(58–77)

Possible HLA

A2	A2.1,A*0201,A*0202,A*0203,A*0204,A*0205,A*0206,A*0207,A*0208,A*0209,A*0210,A*0211,A*0212,A*0213,A*0214,A*0216,A*0217,A*0218,A*0220,A*02
A23	A*2301
B44	B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
Cw4	C4,Cw*0401,C*0401,Cw*0402
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(5-13)	DCTERQANF	Cw*0702
(6-14)	CTERQANFL	Cw*0702
(6-13)	CTERQANF	Cw*0702
(7-14)	TERQANFL	Cw*0702
(4-13)	KDCTERQANF	Cw*0702
(5-14)	DCTERQANFL	Cw*0702

Anchor Residues Searched

A*0201	X[LM]XXXXXX[VL]
A*0201	X[LM]XXXXX[VL]
A*0201	X[LM]XXXXXXX[VL]
A*0202	X[L]XXXXXX[LV]
A*0202	X[L]XXXXX[LV]
A*0202	X[L]XXXXXXX[LV]
A*0204	X[L]XXXXXX[L]
A*0204	X[L]XXXXX[L]
A*0204	X[L]XXXXXXX[L]
A*0205	X[VLIMQ]XXXXXX[L]
A*0205	X[VLIMQ]XXXXX[L]
A*0205	X[VLIMQ]XXXXXXX[L]
A*0206	X[V]XXXXXX[V]
A*0206	X[V]XXXXX[V]
A*0206	X[V]XXXXXXX[V]
A*0207	X[L][D]XXXXX[L]
A*0207	X[L][D]XXXX[L]
A*0207	X[L][D]XXXXXX[L]
A*0214	X[VQL]XXXXXX[LV]
A*0214	X[VQL]XXXXX[LV]

A*0214	X[VQL]XXXXXXX[LV]
B44	X[E]XXXXXX[Y]
B44	X[E]XXXXX[Y]
B44	X[E]XXXXXXX[Y]
B*4402	X[E]XXXXXX[FY]
B*4402	X[E]XXXXX[FY]
B*4402	X[E]XXXXXXX[FY]
B*4403	X[E]XXXXXX[YF]
B*4403	X[E]XXXXX[YF]
B*4403	X[E]XXXXXXX[YF]
Cw*0401	X[YPF]XXXXXX[LF]
Cw*0401	X[YPF]XXXXX[LF]
Cw*0401	X[YPF]XXXXXXX[LF]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:03RCH34
Study Subject Clone:
Study Subject HLA:A2,A23,B44,Cw4,Cw7
Sequence: Known reactive 20Mer7: ANFLGKIWPSYKGRPGNFLQ p2p7p1p6(68–87)

Possible HLA

A2	A2.1,A*0201,A*0202,A*0203,A*0204,A*0205,A*0206,A*0207,A*0208,A*0209,A*0210,A*0211,A*0212,A*0213,A*0214,A*0216,A*0217,A*0218,A*0220,A*02
A23	A*2301
B44	B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
Cw4	C4,Cw*0401,C*0401,Cw*0402
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(10-18)	SYKGRPGNF	Cw*0401
(10-19)	SYKGRPGNFL	Cw*0401
(3-11)	FLGKIWPSY	Cw*0702
(10-18)	SYKGRPGNF	Cw*0702
(11-19)	YKGRPGNFL	Cw*0702
(4-11)	LGKIWPSY	Cw*0702
(11-18)	YKGRPGNF	Cw*0702
(12-19)	KGRPGNFL	Cw*0702
(2-11)	NFLGKIWPSY	Cw*0702
(9-18)	PSYKGRPGNF	Cw*0702
(10-19)	SYKGRPGNFL	Cw*0702

Anchor Residues Searched

A*0201	X[LM]XXXXXX[VL]
A*0201	X[LM]XXXXX[VL]
A*0201	X[LM]XXXXXXX[VL]
A*0202	X[L]XXXXXX[LV]
A*0202	X[L]XXXXX[LV]
A*0202	X[L]XXXXXXX[LV]
A*0204	X[L]XXXXXX[L]
A*0204	X[L]XXXXX[L]
A*0204	X[L]XXXXXXX[L]
A*0205	X[VLIMQ]XXXXXX[L]
A*0205	X[VLIMQ]XXXXX[L]
A*0205	X[VLIMQ]XXXXXXX[L]
A*0206	X[V]XXXXXX[V]
A*0206	X[V]XXXXX[V]
A*0206	X[V]XXXXXXX[V]

A*0207	X[L][D]XXXXX[L]
A*0207	X[L][D]XXXX[L]
A*0207	X[L][D]XXXXXX[L]
A*0214	X[VQL]XXXXXX[LV]
A*0214	X[VQL]XXXXX[LV]
A*0214	X[VQL]XXXXXXX[LV]
B44	X[E]XXXXXX[Y]
B44	X[E]XXXXX[Y]
B44	X[E]XXXXXXX[Y]
B*4402	X[E]XXXXXX[FY]
B*4402	X[E]XXXXX[FY]
B*4402	X[E]XXXXXXX[FY]
B*4403	X[E]XXXXXX[YF]
B*4403	X[E]XXXXX[YF]
B*4403	X[E]XXXXXXX[YF]
Cw*0401	X[YPF]XXXXXX[LF]
Cw*0401	X[YPF]XXXXX[LF]
Cw*0401	X[YPF]XXXXXXX[LF]
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
p17(77–85)	SLFNTVATL	SLYNTVATL	SLYNTVATL	A*0201	
p24(174–184)	AEQASQDVKNW	AEQASQEVKNW	AEQASQEVKNW	B*4402	
p24(174–184)	AEQASQDVKNW	AEQASQEVKNW	AEQASQEVKNW	B*4402,B44	
RT(179–187)	VIYQYMMDL	VIYQYMDDL	VIYQYMDDL	A2	
RT(179–187)	VIYQYMMDL	VIYQYMDDL	VIYQYMDDL	A2, A*0202	
RT(308–317)	EILKEPVGHV	EILKEPVHGV	EILKEPVHGV	A*0201	
gp160(31–40)	AENLWVTVYY	TEKLWVTVYY	AEQLWVTVYY	B*4402	
gp160(31–40)	AENLWVTVYY	TEKLWVTVYY	AEQLWVTVYY	B44	
gp160(121–129)	KLTPLCVSL	KLTPLCVTL	KLTPLCVTL	A2	
gp160(192–200)	KLTSCNTSV	RLISCNTSV	RLISCNTSV	A2	
gp160(192–200)	TLTSCNTSV	RLISCNTSV	RLISCNTSV	A2	
gp160(192–200)	TLTSCNTSV	RLISCNTSV	RLISCNTSV	A2.1	
gp160(311–320)	RGPGRAFVTI	IGPGRAFYTT	IGPGRAFYTT	A*0201	
gp160(311–320)	RGPGRAFVTI	IGPGRAFYTT	IGPGRAFYTT	A2	
gp160(311–320)	MGPKRAFYAT	IGPGRAFYTT	IGPGRAFYTT	A2	
gp160(369–375)	PEIVTHS	PEIVMHS	PEIVMHS	A2	
gp160(377–387)	NSGGEFFYSNS	NCGGEFFYCNT	NCGGEFFYCNT	A2	
gp160(700–708)	AVLSVVNRV	AVLSIVNRV	AVLSIVNRV	A2	
gp160(747–755)	RLVNGSLAL	RLVHGFLAI	RLVDGFLAL	A2	
gp160(770–778)	RLRDLLLIV	HHRDLLLIA	RLRDLLLIV	A*0201	
gp160(813–822)	SLLNATDIAV	SLLNATAIAV	SLLNATAIAV	A*0201	
gp160(813–822)	SLLNATDIAV	SLLNATAIAV	SLLNATAIAV	A2	
gp160(813–822)	SLLNATDIAV	SLLNATAIAV	SLLNATAIAV	A2.1	
gp160(814–822)	LLNATDIAV	LLNATAIAV	LLNATAIAV	A2	
Nef(73–82)	SVPLRPMTYK	QVPLRPMTYK	QVPLRPMTYK	B35 or C4	
Nef(136–145)	PLTFGWCFKL	PLTFGWCYKL	PLTFGWCFKL	A2	

Table 1: **p17**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p17(77–85)	p17(77–85 Clade A)	SLFNTVATL	HIV-1 infection	human(A*0201)	[Dorrell (1999)]
	• Epitope SL9: 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 epitope is most commonly SLYNTVATL in B subtype, and CTL from the C subtype infection did not recognize B clade gag or the 3Y form of the epitope, but do recognize the predominant A and C clade form, SLFNTVATL				

Table 2: **p24**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(174–184)	p24(306–316 LAI)	AEQASQDVKNW		human(B*4402)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*4402 epitope				
p24(174–184)	p24(306–316 LAI)	AEQASQDVKNW		human(B*4402,B44)	[Brander & Walker(1997)]
	• Pers. Comm. from D. Lewinsohn to C. Brander and B. Walker, C Brander *et al*., this database, 1999				

Table 3: **RT**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(179–187)	RT()	VIYQYMMDL	HIV-1 exposure	human(A2)	[Rowland-Jones (1998a)]
	• A CTL response was found in exposed but uninfected prostitutes from Nairobi using previously-de£ned B clade epitopes that tended to be conserved in A and D clades – such cross-reactivity could protect against both A and D and confer protection in Nairobi where both subtypes are circulating • The A and D consensus sequences are both VIYQYMMDL				
RT(179–187)	Pol()	VIYQYMMDL	HIV-1 exposure	human(A2, A*0202)	[Rowland-Jones (1998b)]
	• HIV-speci£c CTL were found in exposed seronegative prostitutes from Nairobi – these CTL may confer protection • Seroprevalence in this cohort is 90-95% and their HIV-1 exposure is among the highest in the world • Most isolated HIV strains are clade A in Nairobi, although clades C and D are also found – B clade epitopes are often cross-reactive, however stronger responses are frequently observed using A or D clade versions of epitopes • This epitope is conserved among A, B and D clade viruses				
RT(308–317)	RT()	EILKEPVGHV	HIV-1 infection	human(A*0201)	[van der Burg (1997), Menendez-Arias (1998)]
	• Recognized by CTL from a long-term survivor, SPIETVPVKL was also recognized • Recognized by CTL from a progressor, EELRQHLLRW and TWETWWTEYW were also recognized				

Table 4: **gp160**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
gp160(31–40)	gp160(30–39 WEAU)	AENLWVTVYY	HIV-1 infection	human(B*4402)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*4402 epitope				
gp160(31–40)	gp160(30–39 WEAU)	AENLWVTVYY	HIV-1 infection	human(B44)	[Borrow (1997), Goulder (1997), Borrow & Shaw(1998)]
	• Two CTL lines from the patient WEAU were studied – one had an optimal peptide of (A)AENLWVTVYY, and the other (A)AENLWVTVY, and both responded equally well with one or two N-term Alanines • Rapidly post-infection, a strong immunodominant response was observed against this epitope • The naturally occurring forms of the peptide found in WEAU were tested as targets for early WEAU CTLs – the form TENLWVTVY was as reactive as the wild type AENLWVTVY – but the forms AKNLWVTVY, AGNLWVTVY, AANLWVTVY did not serve as targets • The glutamic acid in the second position is a B44 anchor residue • [Goulder (1997)] and [Borrow & Shaw(1998)] are reviews of immune escape that summarizes this study in the context of CTL escape to £xation				
gp160(121–129)	gp120(121–129)	KLTPLCVSL	*in vitro* stimulation	human(A2)	[Zarling (1999)]
	• This study compares the ability of macrophages and dendritic cells to stimulate primary responses in CD8+ lymphocytes isolated from HLA-appropriate HIV-uninfected donors using peptide-pulsed APC – the dendritic cells performed better as APC for the stimulation of primary responses • Strong CTL responses were elicited by the epitopes DRFYKTLRA and GEIYKRWII when presented by either immature or mature dendritic cells – macrophages were not able to prime a CTL response against DRFYKTLRA • A weak response to KLTPLCVSL was stimulated using macrophages as the APC • No detectable response was observed for the following previously-de£ned HIV epitopes: KIRLRPGGK, ILKEPVHGV, IRLRPGGK, GPKVKQWPL				
gp160(192–200)	gp120(192–199 HXB2R)	KLTSCNTSV	HIV-1 infection	human(A2)	[Brander (1995)]
	• Epitope predicted on HLA binding motif, and studied in the context of inclusion in a synthetic vaccine				
gp160(192–200)	gp120(197–205)	TLTSCNTSV	no CTL shown	human(A2)	[Garboczi (1992)]
	• Crystallization of HLA-A2 molecules complexed with antigenic peptides – refers to Dadaglio *et al* 1991				
gp160(192–200)	gp120(199–207)	TLTSCNTSV	peptide immunization and HIV-1 infection	human(A2.1)	[Brander (1996)]
	• This epitope was recognized by PBMC from 6/14 HIV+ asymptomatic patients • This epitope was used along with pol CTL epitope ALQDSGLEV and a tetanus toxin T helper epitope for a synthetic vaccine • This vaccine failed to induce a CTL response, although a helper response was evident				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
gp160(311–320)	gp160(318–327 IIIB)	RGPGRAFVTI	CTL line from HIV-donor	human(A*0201)	[Alexander-Miller (1996)]
	• This immunogenic peptide does not have the known binding motif for A2.1 • The same optimal peptide for this human HLA-A2.1 epitope was observed for a murine H-2 D^d epitope				
gp160(311–320)	gp160(318–327 IIIB)	RGPGRAFVTI	vaccinia IIIB gp160	human(A2)	[Achour (1996)]
	• Individual was immunized with rec vaccinia gp160 IIIB and boosted with puri£ed gp160 • Lysis only occurs with IIIB P18 peptide pulsed onto autologous targets; MN, RF, SIMI P18 peptides fail to stimulate CTL • Restimulating immune cells from gp160 IIIB vaccinees with MN, RF, or SIMI P18 did not enhance the MN, RF, or SIMI speci£c CTL response				
gp160(311–320)	gp160(318–327 SIMI)	MGPKRAFYAT	vaccinia SIMI gp160	human(A2)	[Achour (1996)]
	• Individual was immunized with rec vaccinia gp160 SIMI and boosted with puri£ed recombinant gp160 SIMI • P18 MN and RF peptides were able to stimulate the HIV-speci£c CTL that arose in response to the SIMI vaccination, thus the P18 MN peptide (IGPGRAFYTT) and the P18 RF peptide (KGPGRVIYAT) could cross-react • The P18 IIIB peptide does not cross-react (RGPGRAFVTI in the epitope region) • gp160 SIMI primed immune cells could generate a signi£cantly broader speci£city when stimulated with P18 MN or P18RF peptides, but not P18 IIIB				
gp160(369–375)	gp120(374–380 BRU)	PEIVTHS	HIV-1 infection	human(A2)	[Dadaglio (1991)]
	• De£ned through blocking CTL activity, and Env deletions				
gp160(377–387)	gp120(377–387)	NSGGEFFYSNS		human(A2)	[Hickling (1990)]
	• Peptides recognized by class I restricted CTL can bind to class II				
gp160(700–708)	gp41(705–714)	AVLSVVNRV	HIV-1 infection	human(A2)	[Ferris (1999)]
	• This epitope is processed by a TAP1/2 dependent mechanism				
gp160(747–755)	gp41(747–755)	RLVNGSLAL	HIV-1 infection	human(A2)	[Parker (1992)]
	• Studied in the context of HLA-A2 peptide binding				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
gp160(770–778)	Env(679–777)	RLRDLLLIV	HIV-1 infection	human(A*0201)	[Kmieciak (1998)]
	• CTL responses in six patients to four Env epitopes were studied: D2: LLNATAIAV, 5.3: RLRDLLLIV, D1: KLTPLCVTL, and 4.3: QMHEDIISL – all have A2 anchor residues • The C terminal epitopes (D2 and 5.3) were highly variable and the variability was considered responsible for limited CTL response, while D1 and 4.3, N-terminal epitopes, were much more conserved and gave evidence of high levels of CTL response *in vitro* • Peptides 5.3 and D2 bound to HLA A*0201 with low af£nity and were variable, particularly D2;				
gp160(813–822)	gp41(814–823 LAI)	SLLNATDIAV	MN rec gp160	human(A*0201)	[Dupuis (1995)]
	• Of two CTL clones, one reacted only with 815-823, the other with 814-823 and 815-823 • Noted to be A*0201 in Brander *et al*., 1999 database				
gp160(813–822)	gp41(814–823)	SLLNATDIAV	HIV-1 infection	human(A2)	[Kundu (1998b)]
	• Allogeneic dendritic cells (DCs) were obtained from HLA-identical siblings, pulsed with rgp160 MN or A2-restricted HIV-1 epitope peptides, and infused monthly into six HIV-infected patients • 1/6 showed increased env-speci£c CTL and increased lymphoproliferative responses, 2/6 showed increase only in proliferative responses, and 3/6 showed no change – pulsed DCs were well tolerated • SLLNATDIAV is a conserved HLA-A2 epitope included in this study – 4/6 patients had this sequence as their HIV direct sequence, and 3 of these had a detectable CTL response – the other two had either the sequence SLFNAIDIAV or SLLNTTDIVV and no detectable CTL response • CTL demonstrated against peptide-coated target, epitope is naturally processed and enhancible with vaccine				
gp160(813–822)	Env(814–823 Clade B)	SLLNATDIAV	HIV-1 MN rgp160	human(A2.1)	[Kundu (1998a)]
	• Ten HIV-1+ HLA A2 asymptomatic individuals were given two courses of HIV-1 MN rgp160 vaccine over a 2 year period • Two hundred and £fty three HIV-1 peptides of 9 or 10 aa possessing the HLA-A2.1 binding motif (Leu at position 2, Val at the C terminus) were identi£ed in gp160, of which 25 had a high or intermediate binding af£nity • Eleven peptides were studied that had high HLA-A2 binding af£nity – a CTL response was detected to 9/11 peptides in at least 1 individual • CTL responses after reimmunization may include recall responses – only individuals with vaccine cross-reactive sequences prior to vaccination showed detectable CTL responses • CTL to overlapping peptides in this region gave a positive response in the greatest number of patients • ALTERNATIVE EPITOPES: LLNATDIAV and LLNATDIAVA – CTL were induced by vaccine in those that had the sequence SLLNATAIAVA in their own infection, but not in those with: NLLNTIAIAVA or NLFNTTAIAVA or SLLNATAITVA				
gp160(814–822)	gp41(815–823 LAI)	LLNATDIAV	MN rec gp160	human(A2)	[Dupuis (1995)]
	• Of two CTL clones, one reacted only with 815-823, the other with 814-823 and 815-823				

Table 5: **Nef**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
Nef(73–82)	Nef(73–82 LAI)	SVPLRPMTYK	HIV-1 infection	human(B35 or C4)	[Buseyne (1993)]
	• Vertical transmission of HIV ranges from 13% to 39% • Primary assays showed cytotoxic activity against at least one HIV protein was detected in 70% of infected children • Epitopes recognized in £ve children were mapped using synthetic peptides and secondary cultures • Patient EM13, who had a CTL response to three epitopes in Nef, was infected via blood transfusion after birth and went from CDC stage P2A to P2E during the study				
Nef(136–145)	Nef(136–145)	PLTFGWCFKL	HIV-1 infection	human(A2)	[Durali (1998)]
	• Cross-clade CTL response was studied by determining the CTL activity in seven patients from Bangui, (6 A subtype, and 1 AG recombinant infections) and one A subtype infection from a person living in France originally from Togo, to different antigens expressed in vaccinia • Pol reactivity: 8/8 had CTL to A subtype, and 7/8 to B subtype, and HIV-2 Pol was not tested • Gag reactivity: 7/8 reacted with A or B subtype gag, 3/8 with HIV-2 Gag • Nef reactivity: 7/8 reacted with A subtype, and 5/8 with B subtype, none with HIV-2 Nef • Env reactivity: 3/8 reacted with A subtype, 1/8 with B subtype, none with HIV-2 Env • Patient B18 had the greatest breadth and diversity of response, and recognized Gag SLYNTVATL and Nef PLTFGWCFKL				

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

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(118–127)	RT(273–282 SF2)	VPLDKDFRKY	HIV-1 infection	human(B*3501)	[Tomiyama (1997), Menendez-Arias (1998)]
	• A CTL clone responsive to this epitope was obtained • 4/7 B35-positive individuals had a CTL response to this epitope • A K to E substitution at position 5 abrogates speci£c lysis, and reduces binding to B*3501 • [Menendez-Arias (1998)], in a review, notes that a Glu to Lys (E to K) change abrogates CTL activity, but that both VPLDEDFRKY and VPLDKDFRKY can serve as HLA-B35 epitopes, so the change must alter T cell receptor binding – residues in this epitope may be important for polymerase activity				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*3501 epitope				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501,B35)	[Shiga (1996)]
	• Binds HLA-B*3501				
RT(118–127)	()	VPLDKDFRKY	HIV-1 infection	human(B35)	[Kawana (1999)]
	• HLA B35 is associated with rapid disease progression • The sequences of 9 previously described HIV-1 B35 CTL epitopes were obtained in 10 HLA B35+ and 19 HLA B35- individuals • 3/9 CTL epitopes had substitutions that were more common in B35+ individuals than in B35- individuals – only one of these reduced the binding of the peptide to B35 and was shown to be an escape mutation • ——E—- was found in 8/10 of the B35+ individuals, and three of the B35- individuals – the D –> E substituted peptide had similar binding af£nity to B35 and was equally susceptible to a CTL clone				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B35)	[Sipsas (1997)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by three lab workers accidentally infected with HIV-1 IIIB • VPLDKDFRKY, a variant found in HIV MN, was not recognized • VPHDEDFRKY, a variant found in HIV YU2, was not recognized • This epitope was type-speci£c and conserved in only one other B subtype sequence				
RT(126–135)	RT(293–302 HXB-nPLAP)	KYTAFTIPSI	HIV-1 infection	human(A2)	[Shankar (1998)]
	• A novel CTL clone was de£ned with a panel of recombinant vaccinia-RT-infected B-LCL target cells using PBMCs donated by a patient who was HIV-seropositive for 6 years and had not received any antiretroviral therapy • There is evidence that some CTL epitopes are poorly presented on the surface of infected cells, but this RT epitope was recognized as effectively on HIV-infected cells as on peptide-pulsed targets				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5101 epitope				
RT(128–135)	Pol(283–290 SF2)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Tomiyama (1999)]
	• HLA-B27, -B51, and -B57 are associated with slow progression to AIDS, while HLA-B35, -B8, -B24 are associated with a rapid progression to AIDS (Nat. Med. 2:405, 1996;Lancet 22:1187, 1986;Hum Immunol 22:73, 1988;Hum Immunol 44:156, 1995) • 15% of Japanese populations carry HLA-B51 while HLA-B27 and -B57 are detected in less than 0.3% • Of the 172 HIV-1 peptides with HLA-B*5101 anchor residues, 33 bound to HLA-B*5101, seven of these peptides were reactive with CTL from 3 B*5101 positive individuals, and six were properly processed • Four of the six epitopes were highly conserved among B subtype sequences, but TAFTIPSI is somewhat variable				
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B51)	[Sipsas (1997), Menendez-Arias (1998)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by 3 lab workers accidentally infected with HIV-1 IIIB • TAFTIPST, a variant found in HIV-1 CAM1, was also recognized but 100-fold more peptide was needed • TAFTIPSV, a variant found in HIV-1 VE1RT, was also recognized, but 10-fold more peptide was needed • TVFTIPSI, a variant found in HIV-1 MANC, was also recognized • [Menendez-Arias (1998)], in a review, notes that this epitope includes a region near the active site of RT – the substitution of the position two conservative change from A to V decreases CTL recognition				
RT(128–135)	RT(295–302)	TAFTIPSI	HIV-1 infection	human(B51)	[Betts (2000)]
	• Only 4/11 HLA-A2+ HIV+ individuals had CTL that reacted to SLYNTVATL, calling into question whether it is immunodominant • Ninty £ve optimally de£ned peptides from this database were used to screen for gamma interferon responses to other epitopes • Three of the four individuals that responded to SLYNTVATL recognized additional HIV epitopes, and all three were also HLA B51 and recognized this epitope as well as other epitopes				

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

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(118–127)	RT(273–282 SF2)	VPLDKDFRKY	HIV-1 infection	human(B*3501)	[Tomiyama (1997), Menendez-Arias (1998)]
	• A CTL clone responsive to this epitope was obtained • 4/7 B35-positive individuals had a CTL response to this epitope • A K to E substitution at position 5 abrogates speci£c lysis, and reduces binding to B*3501 • [Menendez-Arias (1998)], in a review, notes that a Glu to Lys (E to K) change abrogates CTL activity, but that both VPLDEDFRKY and VPLDKDFRKY can serve as HLA-B35 epitopes, so the change must alter T cell receptor binding – residues in this epitope may be important for polymerase activity				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*3501 epitope				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501,B35)	[Shiga (1996)]
	• Binds HLA-B*3501				
RT(118–127)	()	VPLDKDFRKY	HIV-1 infection	human(B35)	[Kawana (1999)]
	• HLA B35 is associated with rapid disease progression • The sequences of 9 previously described HIV-1 B35 CTL epitopes were obtained in 10 HLA B35+ and 19 HLA B35- individuals • 3/9 CTL epitopes had substitutions that were more common in B35+ individuals than in B35- individuals – only one of these reduced the binding of the peptide to B35 and was shown to be an escape mutation • ——E—- was found in 8/10 of the B35+ individuals, and three of the B35- individuals – the D –> E substituted peptide had similar binding af£nity to B35 and was equally susceptible to a CTL clone				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B35)	[Sipsas (1997)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by three lab workers accidentally infected with HIV-1 IIIB • VPLDKDFRKY, a variant found in HIV MN, was not recognized • VPHDEDFRKY, a variant found in HIV YU2, was not recognized • This epitope was type-speci£c and conserved in only one other B subtype sequence				
RT(126–135)	RT(293–302 HXB-nPLAP)	KYTAFTIPSI	HIV-1 infection	human(A2)	[Shankar (1998)]
	• A novel CTL clone was de£ned with a panel of recombinant vaccinia-RT-infected B-LCL target cells using PBMCs donated by a patient who was HIV-seropositive for 6 years and had not received any antiretroviral therapy • There is evidence that some CTL epitopes are poorly presented on the surface of infected cells, but this RT epitope was recognized as effectively on HIV-infected cells as on peptide-pulsed targets				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5101 epitope				
RT(128–135)	Pol(283–290 SF2)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Tomiyama (1999)]
	• HLA-B27, -B51, and -B57 are associated with slow progression to AIDS, while HLA-B35, -B8, -B24 are associated with a rapid progression to AIDS (Nat. Med. 2:405, 1996;Lancet 22:1187, 1986;Hum Immunol 22:73, 1988;Hum Immunol 44:156, 1995) • 15% of Japanese populations carry HLA-B51 while HLA-B27 and -B57 are detected in less than 0.3% • Of the 172 HIV-1 peptides with HLA-B*5101 anchor residues, 33 bound to HLA-B*5101, seven of these peptides were reactive with CTL from 3 B*5101 positive individuals, and six were properly processed • Four of the six epitopes were highly conserved among B subtype sequences, but TAFTIPSI is somewhat variable				
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B51)	[Sipsas (1997), Menendez-Arias (1998)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by 3 lab workers accidentally infected with HIV-1 IIIB • TAFTIPST, a variant found in HIV-1 CAM1, was also recognized but 100-fold more peptide was needed • TAFTIPSV, a variant found in HIV-1 VE1RT, was also recognized, but 10-fold more peptide was needed • TVFTIPSI, a variant found in HIV-1 MANC, was also recognized • [Menendez-Arias (1998)], in a review, notes that this epitope includes a region near the active site of RT – the substitution of the position two conservative change from A to V decreases CTL recognition				
RT(128–135)	RT(295–302)	TAFTIPSI	HIV-1 infection	human(B51)	[Betts (2000)]
	• Only 4/11 HLA-A2+ HIV+ individuals had CTL that reacted to SLYNTVATL, calling into question whether it is immunodominant • Ninty £ve optimally de£ned peptides from this database were used to screen for gamma interferon responses to other epitopes • Three of the four individuals that responded to SLYNTVATL recognized additional HIV epitopes, and all three were also HLA B51 and recognized this epitope as well as other epitopes				

Table 8: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(118–127)	RT(273–282 SF2)	VPLDKDFRKY	HIV-1 infection	human(B*3501)	[Tomiyama (1997), Menendez-Arias (1998)]
	• A CTL clone responsive to this epitope was obtained • 4/7 B35-positive individuals had a CTL response to this epitope • A K to E substitution at position 5 abrogates speci£c lysis, and reduces binding to B*3501 • [Menendez-Arias (1998)], in a review, notes that a Glu to Lys (E to K) change abrogates CTL activity, but that both VPLDEDFRKY and VPLDKDFRKY can serve as HLA-B35 epitopes, so the change must alter T cell receptor binding – residues in this epitope may be important for polymerase activity				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*3501 epitope				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501,B35)	[Shiga (1996)]
	• Binds HLA-B*3501				
RT(118–127)	()	VPLDKDFRKY	HIV-1 infection	human(B35)	[Kawana (1999)]
	• HLA B35 is associated with rapid disease progression • The sequences of 9 previously described HIV-1 B35 CTL epitopes were obtained in 10 HLA B35+ and 19 HLA B35- individuals • 3/9 CTL epitopes had substitutions that were more common in B35+ individuals than in B35- individuals – only one of these reduced the binding of the peptide to B35 and was shown to be an escape mutation • ——E—- was found in 8/10 of the B35+ individuals, and three of the B35- individuals – the D –> E substituted peptide had similar binding af£nity to B35 and was equally susceptible to a CTL clone				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B35)	[Sipsas (1997)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by three lab workers accidentally infected with HIV-1 IIIB • VPLDKDFRKY, a variant found in HIV MN, was not recognized • VPHDEDFRKY, a variant found in HIV YU2, was not recognized • This epitope was type-speci£c and conserved in only one other B subtype sequence				
RT(126–135)	RT(293–302 HXB-nPLAP)	KYTAFTIPSI	HIV-1 infection	human(A2)	[Shankar (1998)]
	• A novel CTL clone was de£ned with a panel of recombinant vaccinia-RT-infected B-LCL target cells using PBMCs donated by a patient who was HIV-seropositive for 6 years and had not received any antiretroviral therapy • There is evidence that some CTL epitopes are poorly presented on the surface of infected cells, but this RT epitope was recognized as effectively on HIV-infected cells as on peptide-pulsed targets				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5101 epitope				
RT(128–135)	Pol(283–290 SF2)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Tomiyama (1999)]
	• HLA-B27, -B51, and -B57 are associated with slow progression to AIDS, while HLA-B35, -B8, -B24 are associated with a rapid progression to AIDS (Nat. Med. 2:405, 1996;Lancet 22:1187, 1986;Hum Immunol 22:73, 1988;Hum Immunol 44:156, 1995) • 15% of Japanese populations carry HLA-B51 while HLA-B27 and -B57 are detected in less than 0.3% • Of the 172 HIV-1 peptides with HLA-B*5101 anchor residues, 33 bound to HLA-B*5101, seven of these peptides were reactive with CTL from 3 B*5101 positive individuals, and six were properly processed • Four of the six epitopes were highly conserved among B subtype sequences, but TAFTIPSI is somewhat variable				
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B51)	[Sipsas (1997), Menendez-Arias (1998)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by 3 lab workers accidentally infected with HIV-1 IIIB • TAFTIPST, a variant found in HIV-1 CAM1, was also recognized but 100-fold more peptide was needed • TAFTIPSV, a variant found in HIV-1 VE1RT, was also recognized, but 10-fold more peptide was needed • TVFTIPSI, a variant found in HIV-1 MANC, was also recognized • [Menendez-Arias (1998)], in a review, notes that this epitope includes a region near the active site of RT – the substitution of the position two conservative change from A to V decreases CTL recognition				
RT(128–135)	RT(295–302)	TAFTIPSI	HIV-1 infection	human(B51)	[Betts (2000)]
	• Only 4/11 HLA-A2+ HIV+ individuals had CTL that reacted to SLYNTVATL, calling into question whether it is immunodominant • Ninty £ve optimally de£ned peptides from this database were used to screen for gamma interferon responses to other epitopes • Three of the four individuals that responded to SLYNTVATL recognized additional HIV epitopes, and all three were also HLA B51 and recognized this epitope as well as other epitopes				

Table 9: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(118–127)	RT(273–282 SF2)	VPLDKDFRKY	HIV-1 infection	human(B*3501)	[Tomiyama (1997), Menendez-Arias (1998)]
	• A CTL clone responsive to this epitope was obtained • 4/7 B35-positive individuals had a CTL response to this epitope • A K to E substitution at position 5 abrogates speci£c lysis, and reduces binding to B*3501 • [Menendez-Arias (1998)], in a review, notes that a Glu to Lys (E to K) change abrogates CTL activity, but that both VPLDEDFRKY and VPLDKDFRKY can serve as HLA-B35 epitopes, so the change must alter T cell receptor binding – residues in this epitope may be important for polymerase activity				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*3501 epitope				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501,B35)	[Shiga (1996)]
	• Binds HLA-B*3501				
RT(118–127)	()	VPLDKDFRKY	HIV-1 infection	human(B35)	[Kawana (1999)]
	• HLA B35 is associated with rapid disease progression • The sequences of 9 previously described HIV-1 B35 CTL epitopes were obtained in 10 HLA B35+ and 19 HLA B35- individuals • 3/9 CTL epitopes had substitutions that were more common in B35+ individuals than in B35- individuals – only one of these reduced the binding of the peptide to B35 and was shown to be an escape mutation • ——E—- was found in 8/10 of the B35+ individuals, and three of the B35- individuals – the D –> E substituted peptide had similar binding af£nity to B35 and was equally susceptible to a CTL clone				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B35)	[Sipsas (1997)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by three lab workers accidentally infected with HIV-1 IIIB • VPLDKDFRKY, a variant found in HIV MN, was not recognized • VPHDEDFRKY, a variant found in HIV YU2, was not recognized • This epitope was type-speci£c and conserved in only one other B subtype sequence				
RT(126–135)	RT(293–302 HXB-nPLAP)	KYTAFTIPSI	HIV-1 infection	human(A2)	[Shankar (1998)]
	• A novel CTL clone was de£ned with a panel of recombinant vaccinia-RT-infected B-LCL target cells using PBMCs donated by a patient who was HIV-seropositive for 6 years and had not received any antiretroviral therapy • There is evidence that some CTL epitopes are poorly presented on the surface of infected cells, but this RT epitope was recognized as effectively on HIV-infected cells as on peptide-pulsed targets				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5101 epitope				
RT(128–135)	Pol(283–290 SF2)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Tomiyama (1999)]
	• HLA-B27, -B51, and -B57 are associated with slow progression to AIDS, while HLA-B35, -B8, -B24 are associated with a rapid progression to AIDS (Nat. Med. 2:405, 1996;Lancet 22:1187, 1986;Hum Immunol 22:73, 1988;Hum Immunol 44:156, 1995) • 15% of Japanese populations carry HLA-B51 while HLA-B27 and -B57 are detected in less than 0.3% • Of the 172 HIV-1 peptides with HLA-B*5101 anchor residues, 33 bound to HLA-B*5101, seven of these peptides were reactive with CTL from 3 B*5101 positive individuals, and six were properly processed • Four of the six epitopes were highly conserved among B subtype sequences, but TAFTIPSI is somewhat variable				
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B51)	[Sipsas (1997), Menendez-Arias (1998)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by 3 lab workers accidentally infected with HIV-1 IIIB • TAFTIPST, a variant found in HIV-1 CAM1, was also recognized but 100-fold more peptide was needed • TAFTIPSV, a variant found in HIV-1 VE1RT, was also recognized, but 10-fold more peptide was needed • TVFTIPSI, a variant found in HIV-1 MANC, was also recognized • [Menendez-Arias (1998)], in a review, notes that this epitope includes a region near the active site of RT – the substitution of the position two conservative change from A to V decreases CTL recognition				
RT(128–135)	RT(295–302)	TAFTIPSI	HIV-1 infection	human(B51)	[Betts (2000)]
	• Only 4/11 HLA-A2+ HIV+ individuals had CTL that reacted to SLYNTVATL, calling into question whether it is immunodominant • Ninty £ve optimally de£ned peptides from this database were used to screen for gamma interferon responses to other epitopes • Three of the four individuals that responded to SLYNTVATL recognized additional HIV epitopes, and all three were also HLA B51 and recognized this epitope as well as other epitopes				

Table 10: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(118–127)	RT(273–282 SF2)	VPLDKDFRKY	HIV-1 infection	human(B*3501)	[Tomiyama (1997), Menendez-Arias (1998)]
	• A CTL clone responsive to this epitope was obtained • 4/7 B35-positive individuals had a CTL response to this epitope • A K to E substitution at position 5 abrogates speci£c lysis, and reduces binding to B*3501 • [Menendez-Arias (1998)], in a review, notes that a Glu to Lys (E to K) change abrogates CTL activity, but that both VPLDEDFRKY and VPLDKDFRKY can serve as HLA-B35 epitopes, so the change must alter T cell receptor binding – residues in this epitope may be important for polymerase activity				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*3501 epitope				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501,B35)	[Shiga (1996)]
	• Binds HLA-B*3501				
RT(118–127)	()	VPLDKDFRKY	HIV-1 infection	human(B35)	[Kawana (1999)]
	• HLA B35 is associated with rapid disease progression • The sequences of 9 previously described HIV-1 B35 CTL epitopes were obtained in 10 HLA B35+ and 19 HLA B35- individuals • 3/9 CTL epitopes had substitutions that were more common in B35+ individuals than in B35- individuals – only one of these reduced the binding of the peptide to B35 and was shown to be an escape mutation • —E— was found in 8/10 of the B35+ individuals, and three of the B35- individuals – the D –> E substituted peptide had similar binding af£nity to B35 and was equally susceptible to a CTL clone				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B35)	[Sipsas (1997)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by three lab workers accidentally infected with HIV-1 IIIB • VPLDKDFRKY, a variant found in HIV MN, was not recognized • VPHDEDFRKY, a variant found in HIV YU2, was not recognized • This epitope was type-speci£c and conserved in only one other B subtype sequence				
RT(126–135)	RT(293–302 HXB-nPLAP)	KYTAFTIPSI	HIV-1 infection	human(A2)	[Shankar (1998)]
	• A novel CTL clone was de£ned with a panel of recombinant vaccinia-RT-infected B-LCL target cells using PBMCs donated by a patient who was HIV-seropositive for 6 years and had not received any antiretroviral therapy • There is evidence that some CTL epitopes are poorly presented on the surface of infected cells, but this RT epitope was recognized as effectively on HIV-infected cells as on peptide-pulsed targets				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5101 epitope				
RT(128–135)	Pol(283–290 SF2)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Tomiyama (1999)]
	• HLA-B27, -B51, and -B57 are associated with slow progression to AIDS, while HLA-B35, -B8, -B24 are associated with a rapid progression to AIDS (Nat. Med. 2:405, 1996;Lancet 22:1187, 1986;Hum Immunol 22:73, 1988;Hum Immunol 44:156, 1995) • 15% of Japanese populations carry HLA-B51 while HLA-B27 and -B57 are detected in less than 0.3% • Of the 172 HIV-1 peptides with HLA-B*5101 anchor residues, 33 bound to HLA-B*5101, seven of these peptides were reactive with CTL from 3 B*5101 positive individuals, and six were properly processed • Four of the six epitopes were highly conserved among B subtype sequences, but TAFTIPSI is somewhat variable				
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B51)	[Sipsas (1997), Menendez-Arias (1998)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by 3 lab workers accidentally infected with HIV-1 IIIB • TAFTIPST, a variant found in HIV-1 CAM1, was also recognized but 100-fold more peptide was needed • TAFTIPSV, a variant found in HIV-1 VE1RT, was also recognized, but 10-fold more peptide was needed • TVFTIPSI, a variant found in HIV-1 MANC, was also recognized • [Menendez-Arias (1998)], in a review, notes that this epitope includes a region near the active site of RT – the substitution of the position two conservative change from A to V decreases CTL recognition				
RT(128–135)	RT(295–302)	TAFTIPSI	HIV-1 infection	human(B51)	[Betts (2000)]
	• Only 4/11 HLA-A2+ HIV+ individuals had CTL that reacted to SLYNTVATL, calling into question whether it is immunodominant • Ninty £ve optimally de£ned peptides from this database were used to screen for gamma interferon responses to other epitopes • Three of the four individuals that responded to SLYNTVATL recognized additional HIV epitopes, and all three were also HLA B51 and recognized this epitope as well as other epitopes				

Table 11: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(118–127)	RT(273–282 SF2)	VPLDKDFRKY	HIV-1 infection	human(B*3501)	[Tomiyama (1997), Menendez-Arias (1998)]
	• A CTL clone responsive to this epitope was obtained • 4/7 B35-positive individuals had a CTL response to this epitope • A K to E substitution at position 5 abrogates speci£c lysis, and reduces binding to B*3501 • [Menendez-Arias (1998)], in a review, notes that a Glu to Lys (E to K) change abrogates CTL activity, but that both VPLDEDFRKY and VPLDKDFRKY can serve as HLA-B35 epitopes, so the change must alter T cell receptor binding – residues in this epitope may be important for polymerase activity				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*3501 epitope				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501,B35)	[Shiga (1996)]
	• Binds HLA-B*3501				
RT(118–127)	()	VPLDKDFRKY	HIV-1 infection	human(B35)	[Kawana (1999)]
	• HLA B35 is associated with rapid disease progression • The sequences of 9 previously described HIV-1 B35 CTL epitopes were obtained in 10 HLA B35+ and 19 HLA B35- individuals • 3/9 CTL epitopes had substitutions that were more common in B35+ individuals than in B35- individuals – only one of these reduced the binding of the peptide to B35 and was shown to be an escape mutation • —E— was found in 8/10 of the B35+ individuals, and three of the B35- individuals – the D –> E substituted peptide had similar binding af£nity to B35 and was equally susceptible to a CTL clone				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B35)	[Sipsas (1997)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by three lab workers accidentally infected with HIV-1 IIIB • VPLDKDFRKY, a variant found in HIV MN, was not recognized • VPHDEDFRKY, a variant found in HIV YU2, was not recognized • This epitope was type-speci£c and conserved in only one other B subtype sequence				
RT(126–135)	RT(293–302 HXB-nPLAP)	KYTAFTIPSI	HIV-1 infection	human(A2)	[Shankar (1998)]
	• A novel CTL clone was de£ned with a panel of recombinant vaccinia-RT-infected B-LCL target cells using PBMCs donated by a patient who was HIV-seropositive for 6 years and had not received any antiretroviral therapy • There is evidence that some CTL epitopes are poorly presented on the surface of infected cells, but this RT epitope was recognized as effectively on HIV-infected cells as on peptide-pulsed targets				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5101 epitope				
RT(128–135)	Pol(283–290 SF2)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Tomiyama (1999)]
	• HLA-B27, -B51, and -B57 are associated with slow progression to AIDS, while HLA-B35, -B8, -B24 are associated with a rapid progression to AIDS (Nat. Med. 2:405, 1996;Lancet 22:1187, 1986;Hum Immunol 22:73, 1988;Hum Immunol 44:156, 1995) • 15% of Japanese populations carry HLA-B51 while HLA-B27 and -B57 are detected in less than 0.3% • Of the 172 HIV-1 peptides with HLA-B*5101 anchor residues, 33 bound to HLA-B*5101, seven of these peptides were reactive with CTL from 3 B*5101 positive individuals, and six were properly processed • Four of the six epitopes were highly conserved among B subtype sequences, but TAFTIPSI is somewhat variable				
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B51)	[Sipsas (1997), Menendez-Arias (1998)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by 3 lab workers accidentally infected with HIV-1 IIIB • TAFTIPST, a variant found in HIV-1 CAM1, was also recognized but 100-fold more peptide was needed • TAFTIPSV, a variant found in HIV-1 VE1RT, was also recognized, but 10-fold more peptide was needed • TVFTIPSI, a variant found in HIV-1 MANC, was also recognized • [Menendez-Arias (1998)], in a review, notes that this epitope includes a region near the active site of RT – the substitution of the position two conservative change from A to V decreases CTL recognition				
RT(128–135)	RT(295–302)	TAFTIPSI	HIV-1 infection	human(B51)	[Betts (2000)]
	• Only 4/11 HLA-A2+ HIV+ individuals had CTL that reacted to SLYNTVATL, calling into question whether it is immunodominant • Ninty £ve optimally de£ned peptides from this database were used to screen for gamma interferon responses to other epitopes • Three of the four individuals that responded to SLYNTVATL recognized additional HIV epitopes, and all three were also HLA B51 and recognized this epitope as well as other epitopes				

Table 12: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(118–127)	RT(273–282 SF2)	VPLDKDFRKY	HIV-1 infection	human(B*3501)	[Tomiyama (1997), Menendez-Arias (1998)]
	• A CTL clone responsive to this epitope was obtained • 4/7 B35-positive individuals had a CTL response to this epitope • A K to E substitution at position 5 abrogates speci£c lysis, and reduces binding to B*3501 • [Menendez-Arias (1998)], in a review, notes that a Glu to Lys (E to K) change abrogates CTL activity, but that both VPLDEDFRKY and VPLDKDFRKY can serve as HLA-B35 epitopes, so the change must alter T cell receptor binding – residues in this epitope may be important for polymerase activity				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*3501 epitope				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501,B35)	[Shiga (1996)]
	• Binds HLA-B*3501				
RT(118–127)	()	VPLDKDFRKY	HIV-1 infection	human(B35)	[Kawana (1999)]
	• HLA B35 is associated with rapid disease progression • The sequences of 9 previously described HIV-1 B35 CTL epitopes were obtained in 10 HLA B35+ and 19 HLA B35- individuals • 3/9 CTL epitopes had substitutions that were more common in B35+ individuals than in B35- individuals – only one of these reduced the binding of the peptide to B35 and was shown to be an escape mutation • —E— was found in 8/10 of the B35+ individuals, and three of the B35- individuals – the D –> E substituted peptide had similar binding af£nity to B35 and was equally susceptible to a CTL clone				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B35)	[Sipsas (1997)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by three lab workers accidentally infected with HIV-1 IIIB • VPLDKDFRKY, a variant found in HIV MN, was not recognized • VPHDEDFRKY, a variant found in HIV YU2, was not recognized • This epitope was type-speci£c and conserved in only one other B subtype sequence				
RT(126–135)	RT(293–302 HXB-nPLAP)	KYTAFTIPSI	HIV-1 infection	human(A2)	[Shankar (1998)]
	• A novel CTL clone was de£ned with a panel of recombinant vaccinia-RT-infected B-LCL target cells using PBMCs donated by a patient who was HIV-seropositive for 6 years and had not received any antiretroviral therapy • There is evidence that some CTL epitopes are poorly presented on the surface of infected cells, but this RT epitope was recognized as effectively on HIV-infected cells as on peptide-pulsed targets				

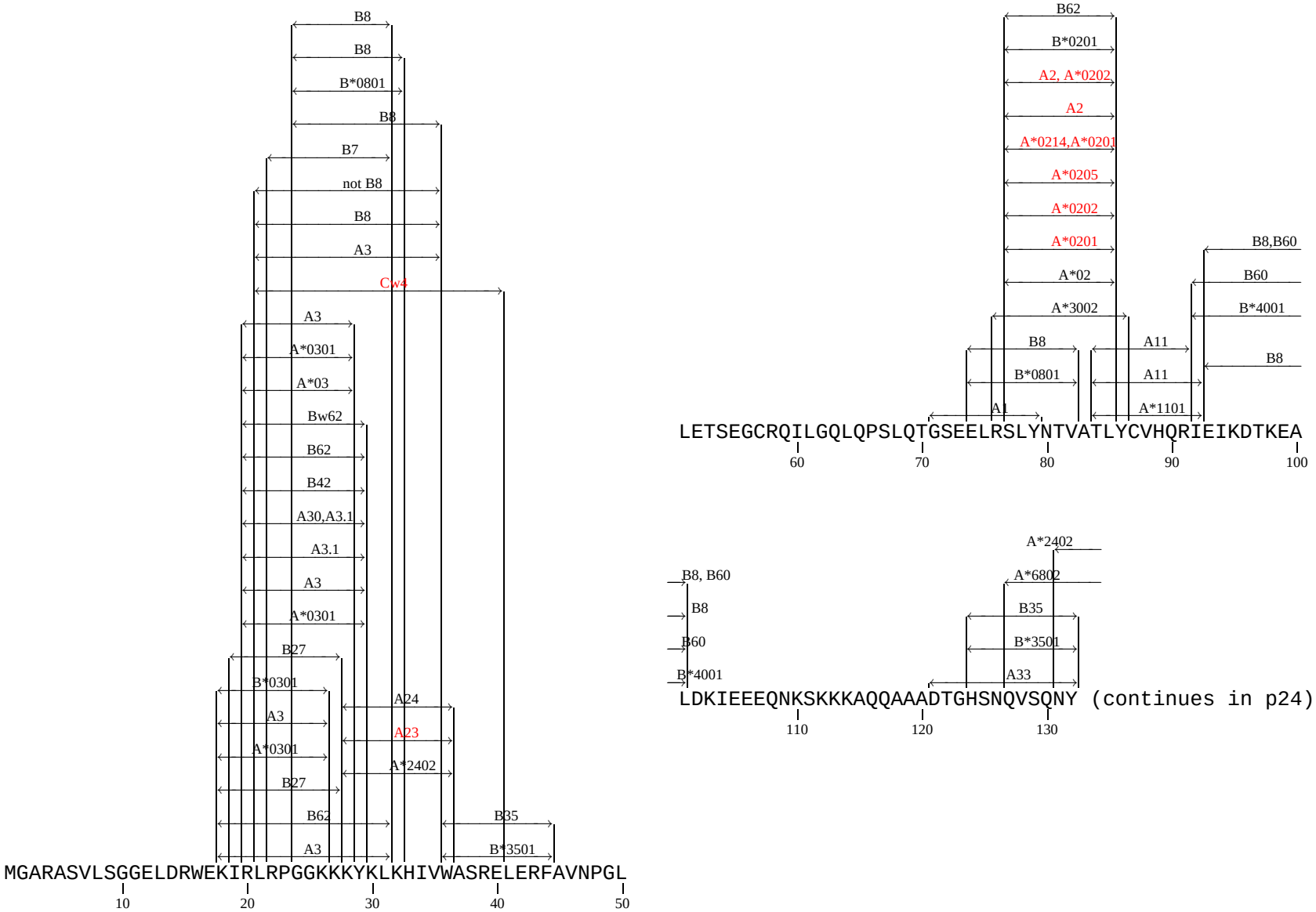
HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5101 epitope				
RT(128–135)	Pol(283–290 SF2)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Tomiyama (1999)]
	• HLA-B27, -B51, and -B57 are associated with slow progression to AIDS, while HLA-B35, -B8, -B24 are associated with a rapid progression to AIDS (Nat. Med. 2:405, 1996;Lancet 22:1187, 1986;Hum Immunol 22:73, 1988;Hum Immunol 44:156, 1995) • 15% of Japanese populations carry HLA-B51 while HLA-B27 and -B57 are detected in less than 0.3% • Of the 172 HIV-1 peptides with HLA-B*5101 anchor residues, 33 bound to HLA-B*5101, seven of these peptides were reactive with CTL from 3 B*5101 positive individuals, and six were properly processed • Four of the six epitopes were highly conserved among B subtype sequences, but TAFTIPSI is somewhat variable				
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B51)	[Sipsas (1997), Menendez-Arias (1998)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by 3 lab workers accidentally infected with HIV-1 IIIB • TAFTIPST, a variant found in HIV-1 CAM1, was also recognized but 100-fold more peptide was needed • TAFTIPSV, a variant found in HIV-1 VE1RT, was also recognized, but 10-fold more peptide was needed • TVFTIPSI, a variant found in HIV-1 MANC, was also recognized • [Menendez-Arias (1998)], in a review, notes that this epitope includes a region near the active site of RT – the substitution of the position two conservative change from A to V decreases CTL recognition				
RT(128–135)	RT(295–302)	TAFTIPSI	HIV-1 infection	human(B51)	[Betts (2000)]
	• Only 4/11 HLA-A2+ HIV+ individuals had CTL that reacted to SLYNTVATL, calling into question whether it is immunodominant • Ninty £ve optimally de£ned peptides from this database were used to screen for gamma interferon responses to other epitopes • Three of the four individuals that responded to SLYNTVATL recognized additional HIV epitopes, and all three were also HLA B51 and recognized this epitope as well as other epitopes				

Table 13: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(118–127)	RT(273–282 SF2)	VPLDKDFRKY	HIV-1 infection	human(B*3501)	[Tomiyama (1997), Menendez-Arias (1998)]
	• A CTL clone responsive to this epitope was obtained • 4/7 B35-positive individuals had a CTL response to this epitope • A K to E substitution at position 5 abrogates speci£c lysis, and reduces binding to B*3501 • [Menendez-Arias (1998)], in a review, notes that a Glu to Lys (E to K) change abrogates CTL activity, but that both VPLDEDFRKY and VPLDKDFRKY can serve as HLA-B35 epitopes, so the change must alter T cell receptor binding – residues in this epitope may be important for polymerase activity				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*3501 epitope				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B*3501,B35)	[Shiga (1996)]
	• Binds HLA-B*3501				
RT(118–127)	()	VPLDKDFRKY	HIV-1 infection	human(B35)	[Kawana (1999)]
	• HLA B35 is associated with rapid disease progression • The sequences of 9 previously described HIV-1 B35 CTL epitopes were obtained in 10 HLA B35+ and 19 HLA B35- individuals • 3/9 CTL epitopes had substitutions that were more common in B35+ individuals than in B35- individuals – only one of these reduced the binding of the peptide to B35 and was shown to be an escape mutation • —E— was found in 8/10 of the B35+ individuals, and three of the B35- individuals – the D –> E substituted peptide had similar binding af£nity to B35 and was equally susceptible to a CTL clone				
RT(118–127)	RT(273–282 IIIB)	VPLDEDFRKY	HIV-1 infection	human(B35)	[Sipsas (1997)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by three lab workers accidentally infected with HIV-1 IIIB • VPLDKDFRKY, a variant found in HIV MN, was not recognized • VPHDEDFRKY, a variant found in HIV YU2, was not recognized • This epitope was type-speci£c and conserved in only one other B subtype sequence				
RT(126–135)	RT(293–302 HXB-nPLAP)	KYTAFTIPSI	HIV-1 infection	human(A2)	[Shankar (1998)]
	• A novel CTL clone was de£ned with a panel of recombinant vaccinia-RT-infected B-LCL target cells using PBMCs donated by a patient who was HIV-seropositive for 6 years and had not received any antiretroviral therapy • There is evidence that some CTL epitopes are poorly presented on the surface of infected cells, but this RT epitope was recognized as effectively on HIV-infected cells as on peptide-pulsed targets				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5101 epitope				
RT(128–135)	Pol(283–290 SF2)	TAFTIPSI	HIV-1 infection	human(B*5101)	[Tomiyama (1999)]
	• HLA-B27, -B51, and -B57 are associated with slow progression to AIDS, while HLA-B35, -B8, -B24 are associated with a rapid progression to AIDS (Nat. Med. 2:405, 1996;Lancet 22:1187, 1986;Hum Immunol 22:73, 1988;Hum Immunol 44:156, 1995) • 15% of Japanese populations carry HLA-B51 while HLA-B27 and -B57 are detected in less than 0.3% • Of the 172 HIV-1 peptides with HLA-B*5101 anchor residues, 33 bound to HLA-B*5101, seven of these peptides were reactive with CTL from 3 B*5101 positive individuals, and six were properly processed • Four of the six epitopes were highly conserved among B subtype sequences, but TAFTIPSI is somewhat variable				
RT(128–135)	RT(295–302 IIIB)	TAFTIPSI	HIV-1 infection	human(B51)	[Sipsas (1997), Menendez-Arias (1998)]
	• HIV IIIB proteins were used to de£ne the range of CTL epitopes recognized by 3 lab workers accidentally infected with HIV-1 IIIB • TAFTIPST, a variant found in HIV-1 CAM1, was also recognized but 100-fold more peptide was needed • TAFTIPSV, a variant found in HIV-1 VE1RT, was also recognized, but 10-fold more peptide was needed • TVFTIPSI, a variant found in HIV-1 MANC, was also recognized • [Menendez-Arias (1998)], in a review, notes that this epitope includes a region near the active site of RT – the substitution of the position two conservative change from A to V decreases CTL recognition				
RT(128–135)	RT(295–302)	TAFTIPSI	HIV-1 infection	human(B51)	[Betts (2000)]
	• Only 4/11 HLA-A2+ HIV+ individuals had CTL that reacted to SLYNTVATL, calling into question whether it is immunodominant • Ninty £ve optimally de£ned peptides from this database were used to screen for gamma interferon responses to other epitopes • Three of the four individuals that responded to SLYNTVATL recognized additional HIV epitopes, and all three were also HLA B51 and recognized this epitope as well as other epitopes				

p17 CTL Map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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
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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
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60
70
80
90
100
A*2402
B8, B60
A*6802
B8
B35
B60
B*3501
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A33
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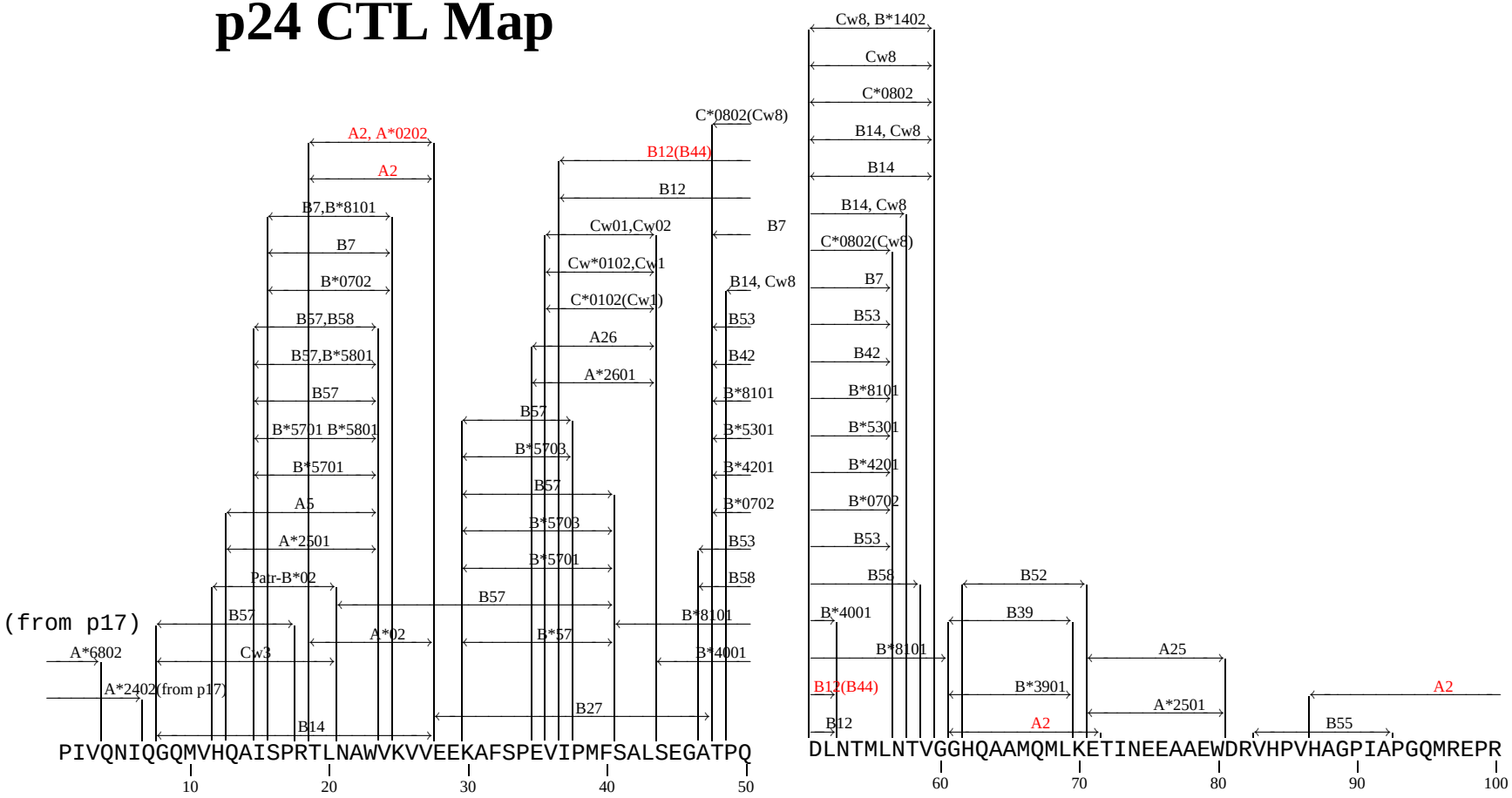
110
120
130

p24 CTL Map


(from p17)
A*6802
A*2402(from p17)
B14
Pair-B*02
B57
Cw3
A5
A*2501
B57,B58
B57,B*5801
B57
B*5701 B*5801
B*5701
B7,B*8101
B7
B*0702
A2, A*0202
A2
A*02
B57
B*5703
B57
B*5703
B57
B*5701
B*57
B27
Cw01,Cw02
Cw*0102,Cw1
C*0102(Cw1)
A26
A*2601
B12(B44)
B12
C*0802(Cw8)
B7
B14, Cw8
B53
B42
B*8101
B*5301
B*4201
B*0702
B53
B58
B*8101
B*4001
PIVQNIQGQMVHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGATPQ
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20
30
40
50
Cw8, B*1402
Cw8
C*0802
B14, Cw8
B14
B14, Cw8
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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
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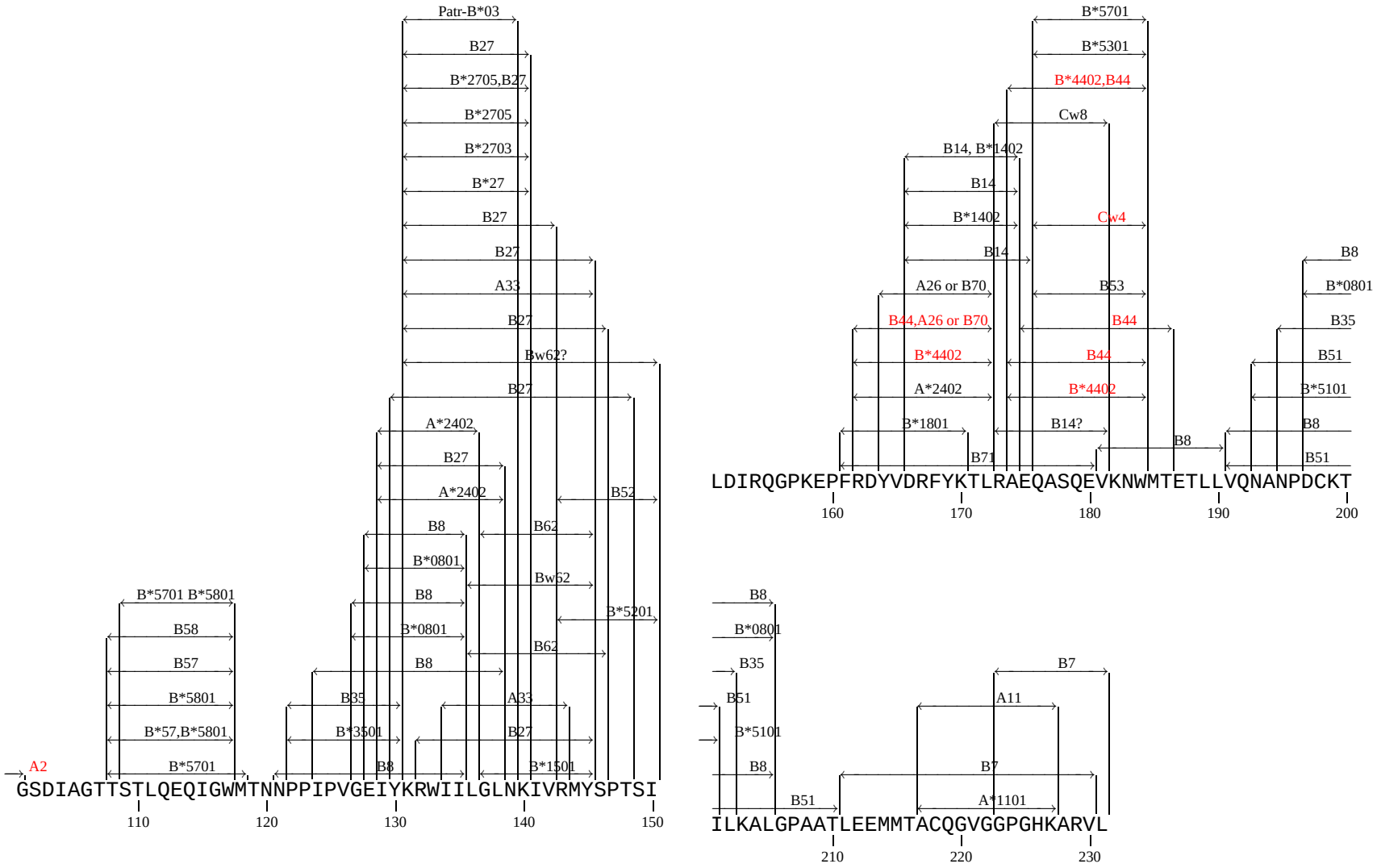
70
80
90
100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B27
B*2705,B27
B*2705
B*2703
B*27
B27
B27
A33
B27
Bw62?
B27
A*2402
B27
A*2402
B52
B8
B62
B*0801
Bw62
B8
B*5201
B*0801
B62
B8
B*5701 B*5801
B58
B57
B*5801
B*57,B*5801
B*5701
A2
B35
A33
B*3501
B27
B8
B*1501
GSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNKIVRMYSPTSI
110
120
130
140
150
B*5701
B*5301
B*4402,B44
Cw8
B14, B*1402
B14
B*1402
Cw4
B14
A26 or B70
B53
B44,A26 or B70
B44
B*4402
B44
A*2402
B*4402
B*1801
B14?
B71
B8
B8
B*0801
B35
B51
B*5101
B8
B51
LDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKT
160
170
180
190
200
B8
B*0801
B35
B51
B*5101
B8
B51
B7
A11
B7
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

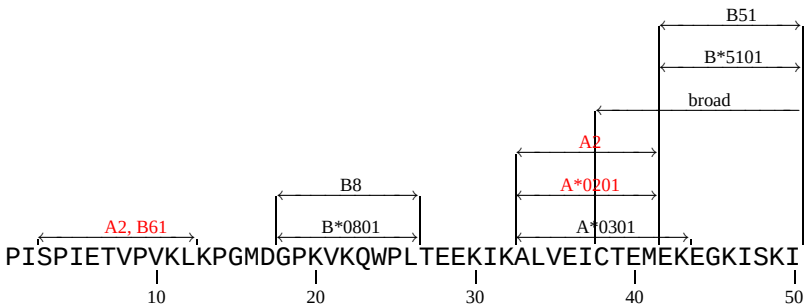
                         B7
    RSGVETTTPPQKQEPIDKELYPLTSLRSLFGNDPSSQ
              |         |         |
            110       120       130
                                p6 end ->
```

Protease CTL Map

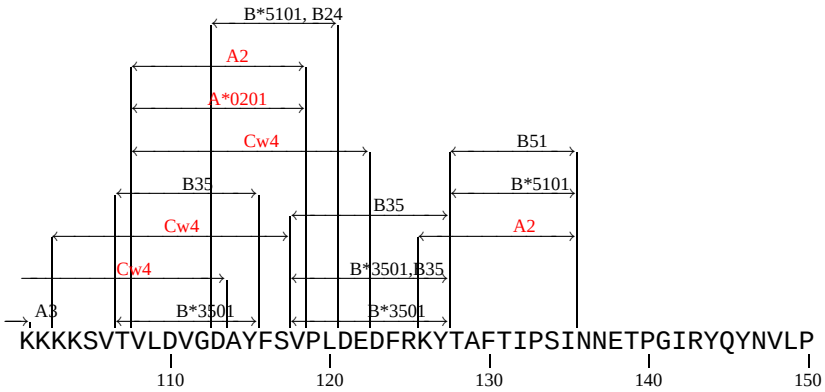
```
A*7401
A*6802,A*7401,A19
A*6802                                  A*6802
PQVTLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGI
          |         |         |         |         |
         10        20        30        40        50

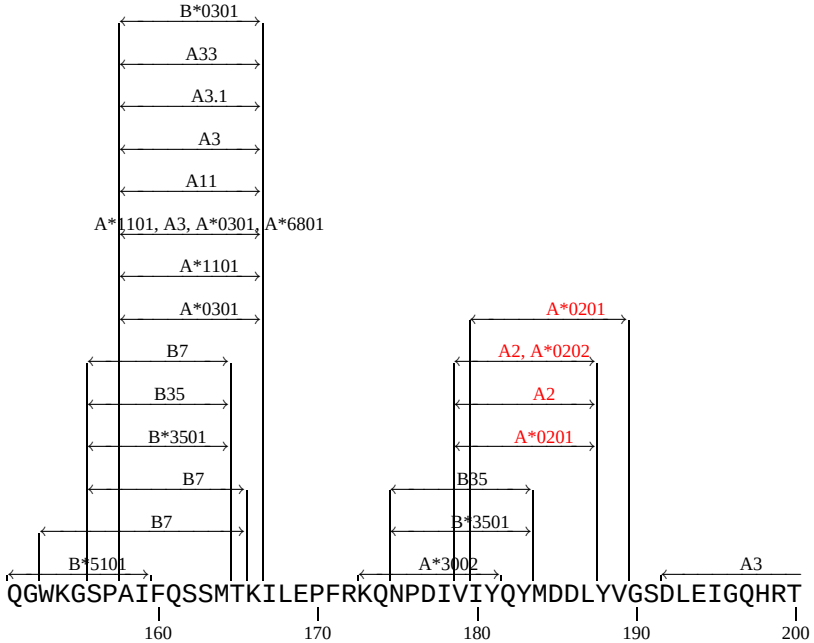
                                   A*0201
GGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
          |         |         |         |
         60        70        80        90
```

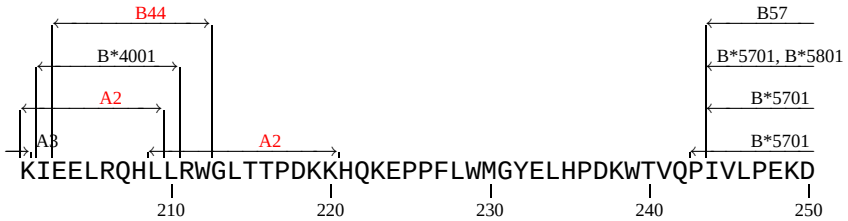
RT CTL Map

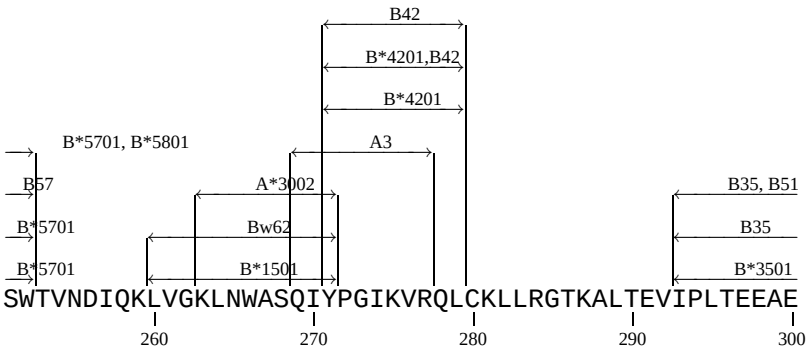

B51
B*5101
broad
A2
B8
A*0201
A2, B61
B*0801
A*0301
PISPIETVPVKLKPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKI
10
20
30
40
50

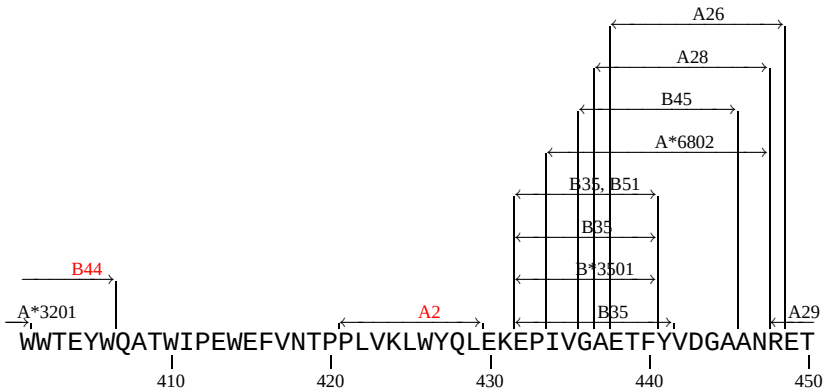
Cw4
broad
A3
GPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGL
60
70
80
90
100


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

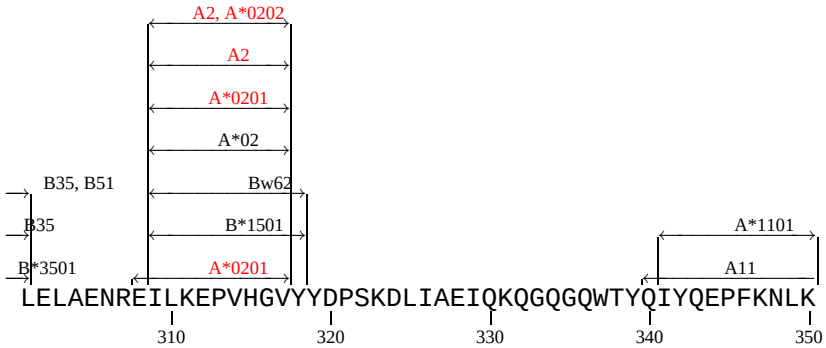

B*0301
A33
A3.1
A3
A11
A*1101, A3, A*0301, A*6801
A*1101
A*0301
A*0201
B7
A2, A*0202
B35
A2
B*3501
A*0201
B7
B35
B7
B*3501
B*5101
A*3002
A3
QGWKGSPAIFQSSMTKILEPFRKQNPDIVIYQYMDDLYVGSDLEIGQHRT
160
170
180
190
200

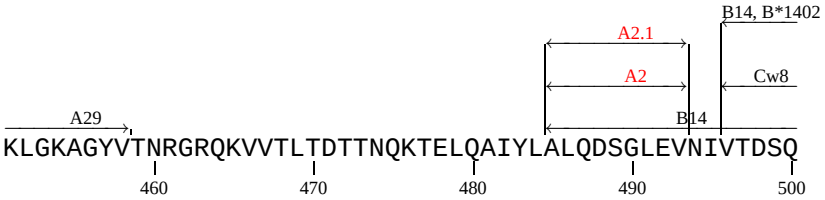

B44
B57
B*4001
B*5701, B*5801
A2
B*5701
A3
A2
B*5701
KIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWTVQPIVLPEKD
210
220
230
240
250

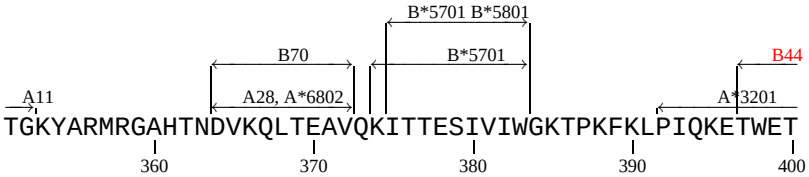


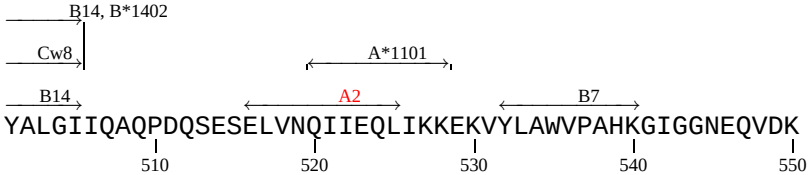


p15 RNase start <-





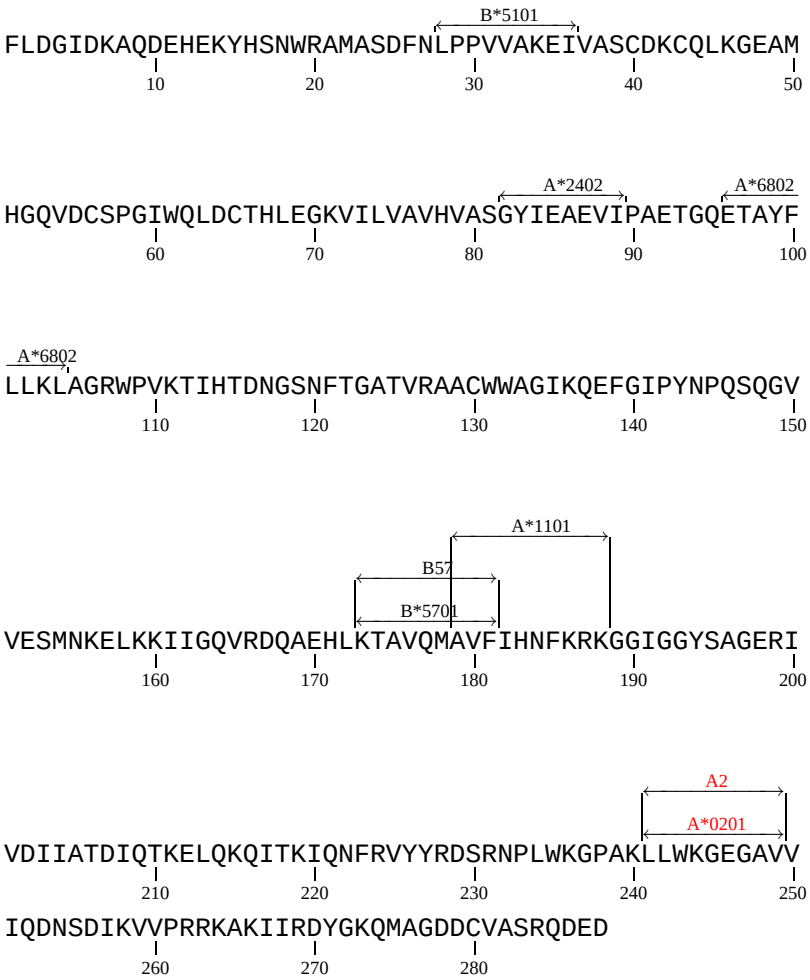




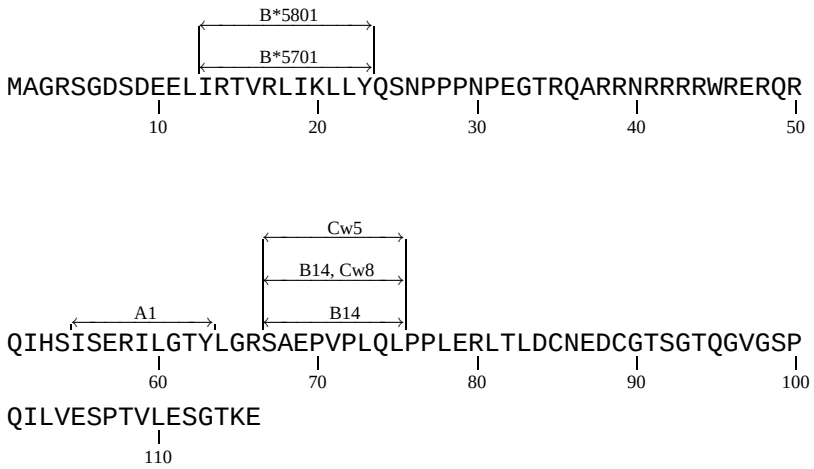
LVSAGIRKVL

-> p15 RNase end

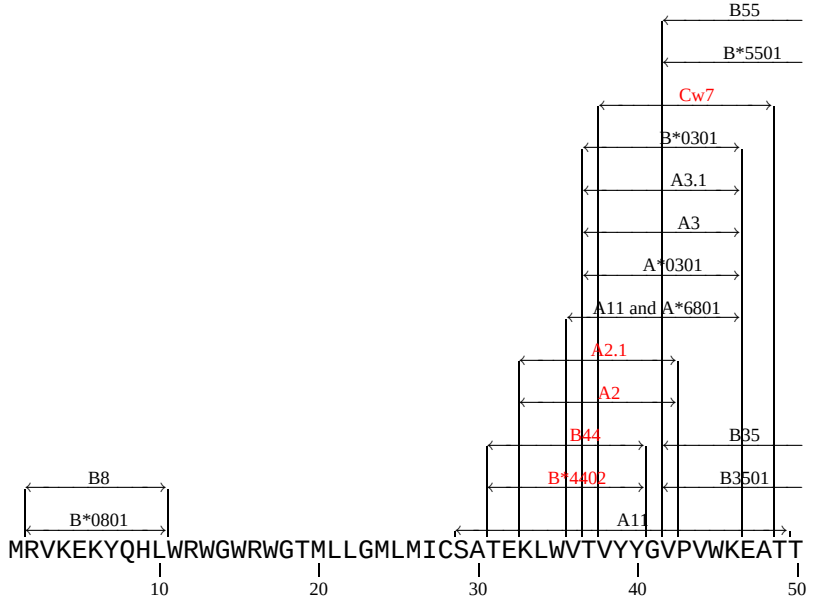
Integrase CTL Map



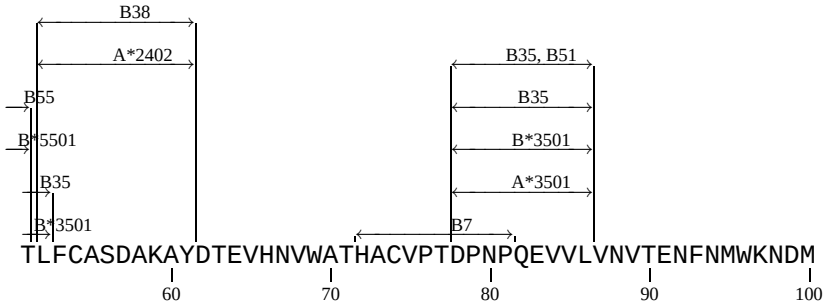
Rev CTL Map

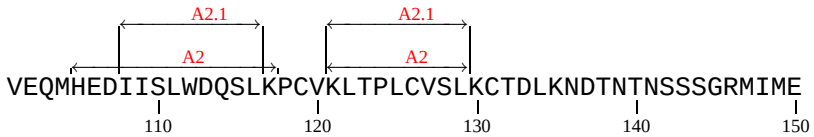


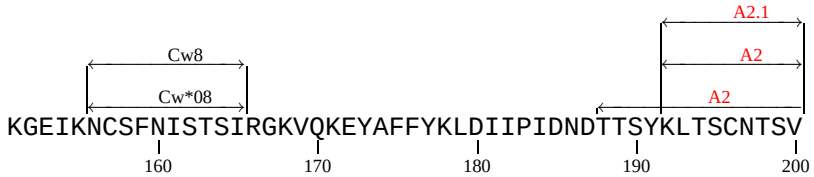
gp160 CTL Map

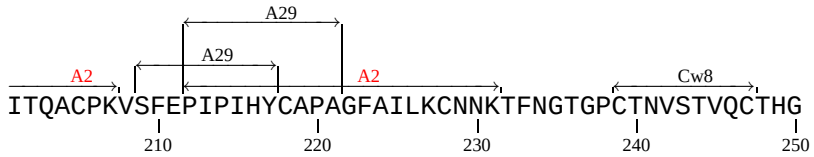


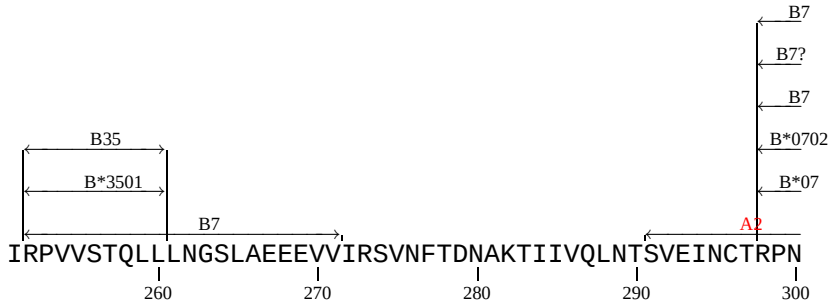
<- gp120 start

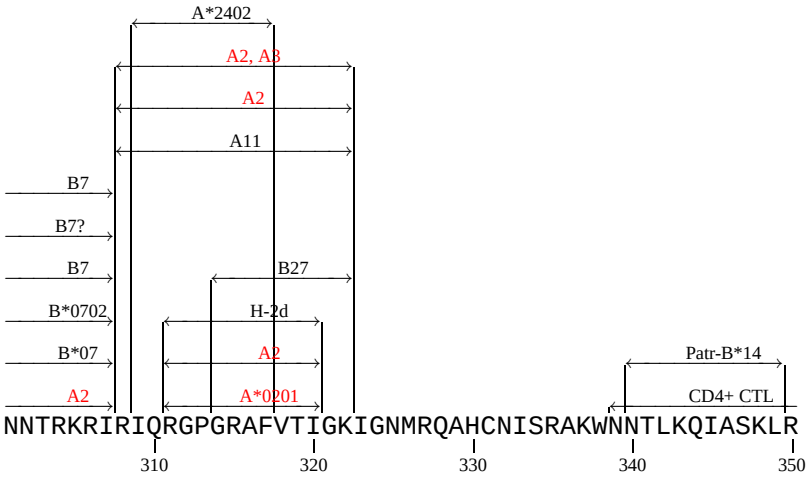


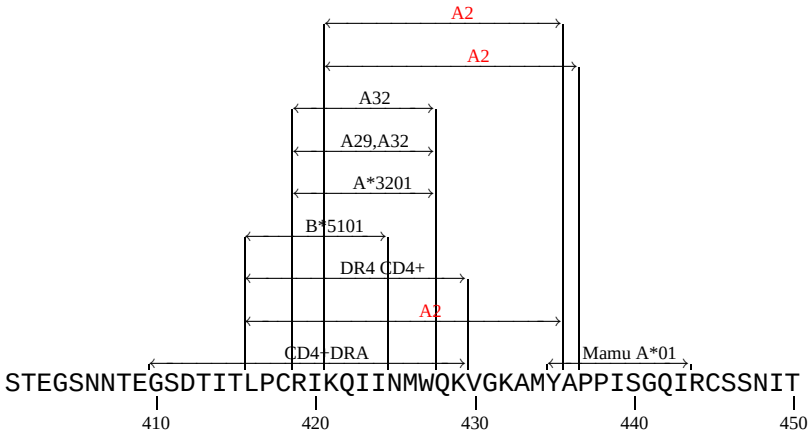


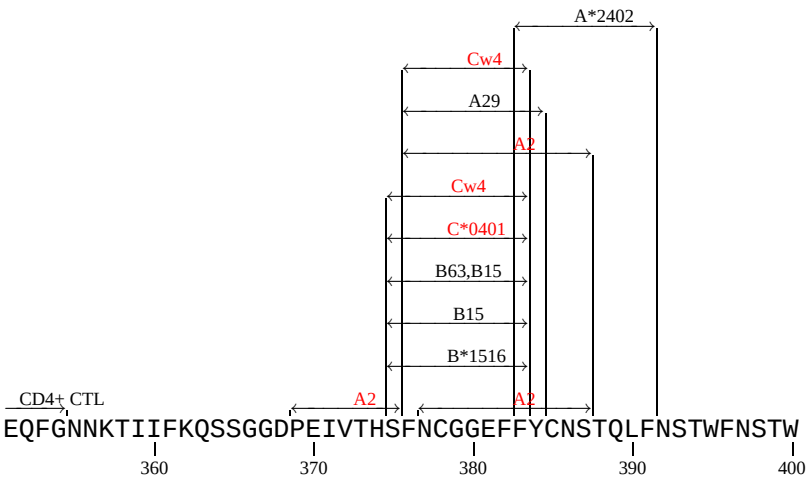


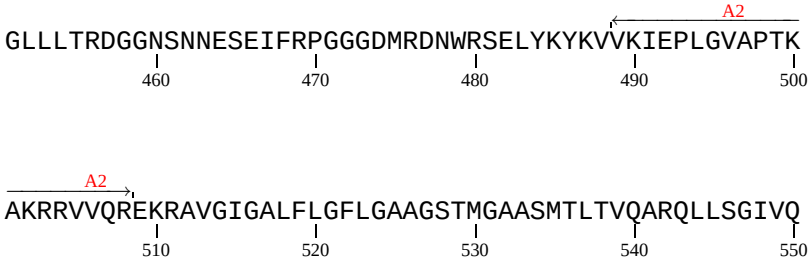




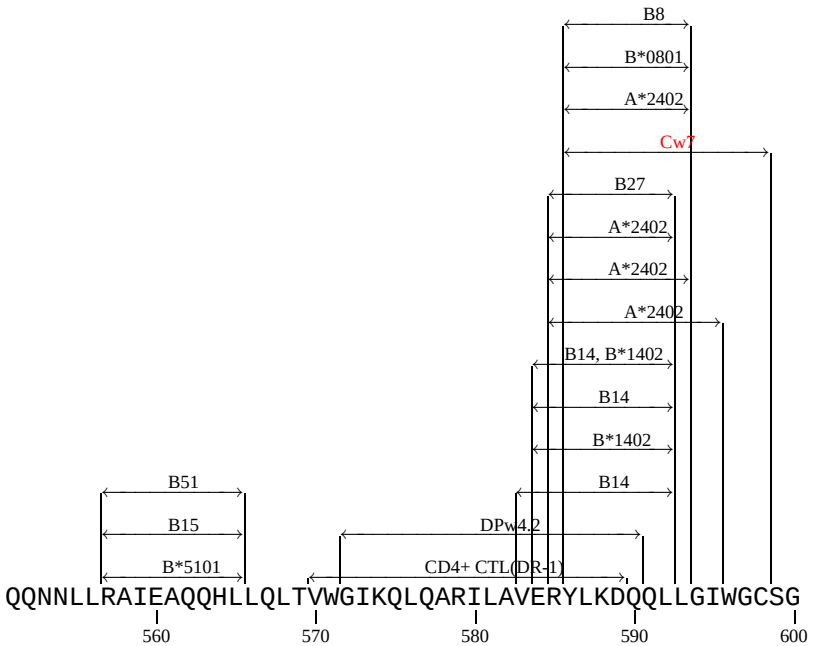


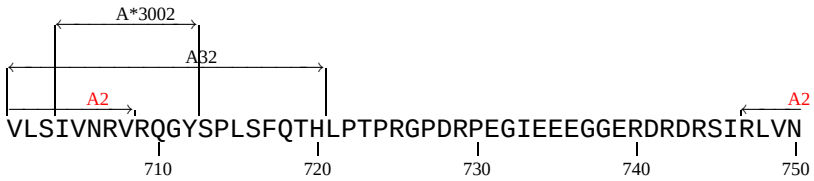


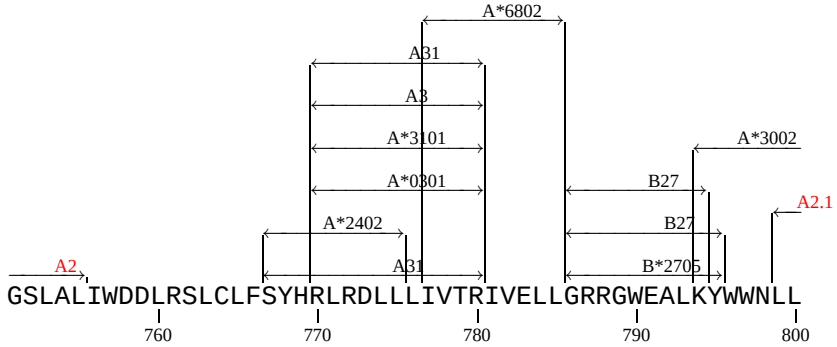




gp120 end <> gp41 start

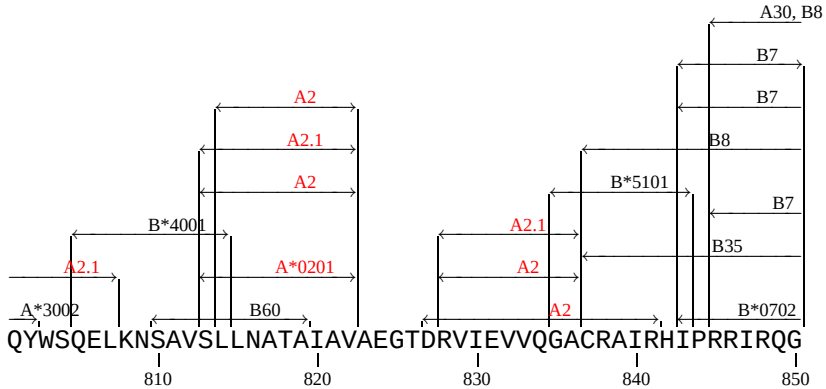

B8
B*0801
A*2402
Cw7
B27
A*2402
A*2402
A*2402
B14, B*1402
B14
B*1402
B14
B51
B15
B*5101
DPw4.2
CD4+ CTL(DR-1)
QQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSG
560
570
580
590
600

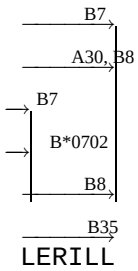

A*3002
A32
A2
A2
VLSIVNRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRLVN
710
720
730
740
750


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

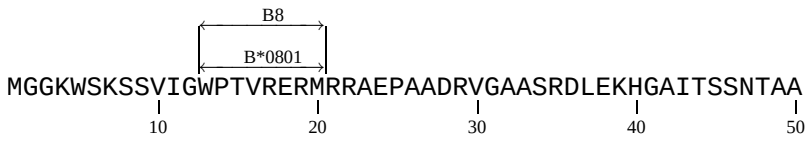
A2.1
A*2402
A2.1
A2
NQQEKNEQELLELDKWASLWNWFNITNWLWYIKLFIMIVGGLVGLRIVFA
660
670
680
690
700

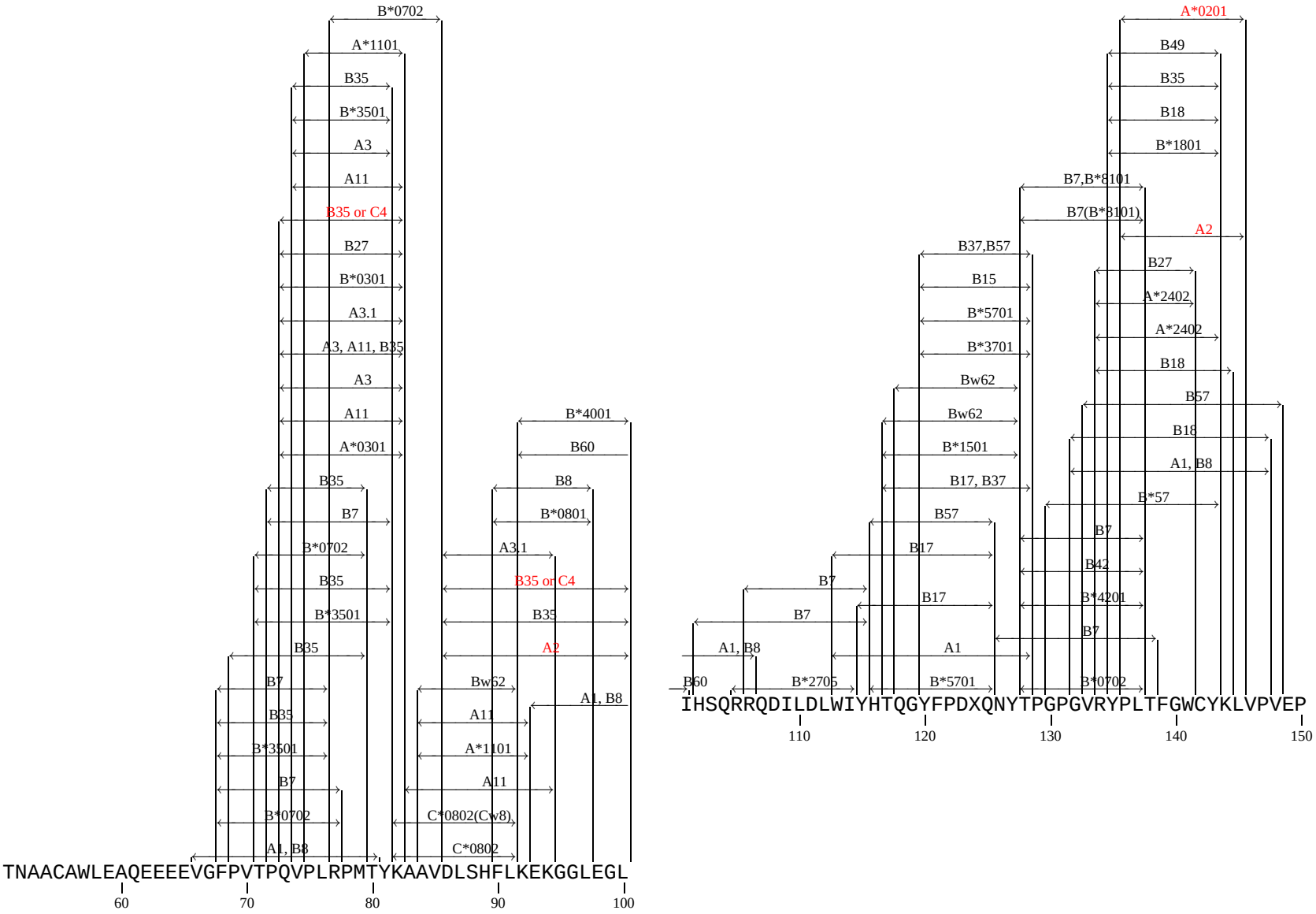

A30, B8
B7
B7
A2
A2.1
B8
A2
B*5101
B7
B*4001
A2.1
B35
A2.1
A*0201
A2
A*3002
B60
A2
B*0702
QYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQG
810
820
830
840
850

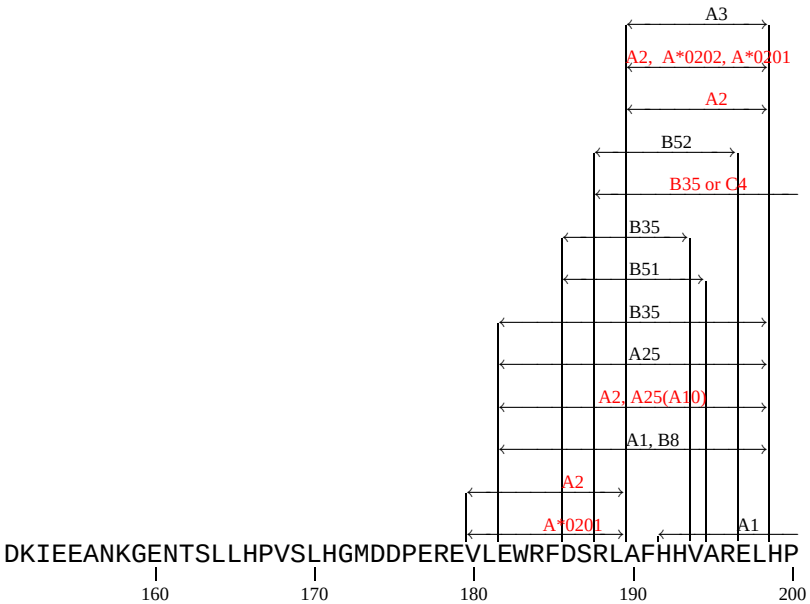


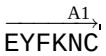
-> gp41 end

Nef CTL Map




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*8101)
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





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[Durali (1998)] D. Durali, J. Morvan, F. Letourneur, D. Schmitt, N. Guegan, M. Dalod, S. Saragosti, D. Sicard, J. P. Levy, & E. Gomard. Cross-reactions between the cytotoxic T-lymphocyte responses of human immunode£ciency virus-infected African and European patients. *J Virol* **72**:3547–53, 1998. (Medline: 98216712).

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role of cytotoxic T cells in HIV infection. *Dev Biol Stand* **92**:209–14, 1998a. (Medline: 98214896) Notes: In this paper CTL response to previously de£ned conserved epitopes was found in exposed but uninfected prostitutes in Nairobi. Subtypes A and D are circulating in this regions, and the reactive epitopes tended to be conserved. Similarly previous studies in the Gambia showed that exposed but uninfected prostitutes tended to have B35 presented CTL epitopes conserved between HIV-1 and HIV-2. It was suggested that what was special about B35 is simply that it presents epitopes found both in HIV-1 and HIV-2.

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