QMVHQAISPRTLNAWVKVVE

```
QUERY                QMVHQAISPRTLNAWVKVVE

CONSENSUS_A          -----sl-----------i-
A.KE.Q23-CXC-CG      --I--SL-----------I-
A.SE.SE6594          --I--SL-----------I-
A.SE.SE7253          -----SL-----------I-
A.SE.SE7535          -----SL-----------I-
A.SE.SE8131          -----VM-----------I-
A.SE.SE8538          --I--NL-----------I-
A.SE.SE8891          -----SL-----------I-
A.UG.92UG037         --I--SL-----------I-
A.UG.U455            -P----L-------------

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

CONSENSUS_C          ------------------i-
C.BR.92BR025         -----P--A-----------
C.BW.96BW01B22       -----PL-----------I-
C.BW.96BW0402        ------------------I-
C.BW.96BW0502        ------------------I-
C.BW.96BW1104        ------------------I-
C.BW.96BW1210        ------------------I-
C.BW.96BW15B03       ------------------I-
C.BW.96BW1626        -----------S------I-
C.BW.96BW17A09       --------------------
C.ET.ETH2220         -----P--A-----------
C.IN.93IN904         ------L-----------I-
C.IN.93IN905         ------------------I-
C.IN.93IN999         -----P------------I-
C.IN.94IN11246       ------------------I-
C.IN.95IN21068       ------------------I-

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

CONSENSUS_F          ------------------I-
F.BR.BZ162           -----S------------I-
F.CD.VI174           ------------------I-
F.RW.VI69            ------------------I-

CONSENSUS_F1         -----s?-----------I-
F1.BE.VI850          -----SL-----------I-
F1.BR.93BR020.1      -----SL-----------I-
F1.FI.FIN9363        ------------------I-
F1.FR.MP411          -----P------------I-

CONSENSUS_F2         -----?L-----------I-
F2.CM.MP255          ------L-----------I-
F2.CM.MP257          -----SL-----------I-
CONSENSUS_G          --------------------
G.BE.DRCBL           --------------------
G.FI.HH8793          --------------------
G.NG.92NG083         --I-----------------
G.SE.SE6165          -------T------------
CONSENSUS_H          --------------------
H.BE.VI991           --------------------
H.BE.VI997           -----P--x-----------
H.CF.90CF056         --------------------

CONSENSUS_J          -P----L-----------I-
J.SE.SE9173          -P----L-----------I-
J.SE.SE9280          -P----L-----------I-

CONSENSUS_K          -----?L-----------I-
K.BE.VI325           -----PL-----------I-
K.CD.EQTB11C         ------L-----------I-
K.CM.MP535           ------L-----------I-
N.CM.YBF30           -----PLT----------I-

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

CONSENSUS_CPZ        ------?----------?--
CPZ.CD.CPZANT        IAR--PLT---------C--
CPZ.GA.CPZGAB        --------------------
CPZ.US.CPZUS         ------M----------A--
```

PRGSDIAGTTSTLQEQIGWM

```
QUERY                PRGSDIAGTTSTLQEQIGWM

CONSENSUS_A          ------------p-------
A.KE.Q23-CXC-CG      ------------P-------
A.SE.SE6594          ------------P-------
A.SE.SE7253          ------------P-------
A.SE.SE7535          ------------P-------
A.SE.SE8131          -----------------A--
A.SE.SE8538          ------------P---LQ--
A.SE.SE8891          ------------P-------
A.UG.92UG037         ------------P----A--
A.UG.U455            ------------V-------

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

CONSENSUS_C          -----------------a--
C.BR.92BR025         -----------------T--
C.BW.96BW01B22       -----------N-----A--
C.BW.96BW0402        -----------------A--
C.BW.96BW0502        --------A--------A--
C.BW.96BW1104        -----------------A--
C.BW.96BW1210        -----------N-----N--
C.BW.96BW15B03       -----------------A--
C.BW.96BW1626        -----------------A--
C.BW.96BW17A09       -----------------A--
C.ET.ETH2220         -----------------A--
C.IN.93IN904         -----------S-----A--
C.IN.93IN905         -----------S-----A--
C.IN.93IN999         -----------------A--
C.IN.94IN11246       -----------------A--
C.IN.95IN21068       -----------------A--

CONSENSUS_D          -----------------a--
D.CD.84ZR085         --------------------
D.CD.ELI             -----------------A--
D.CD.NDK             -----------------A--
D.CD.Z2Z6            -----------------A--
D.UG.94UG1141        -----------N--------

CONSENSUS_F          -----------------Q--
F.BR.BZ162           -----------------Q--
F.CD.VI174           -----------------Q--
F.RW.VI69            -----------------Q--

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

CONSENSUS_F2         -----------------?--
F2.CM.MP255          -----------------T--
F2.CM.MP257          -----------------A--

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

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

CONSENSUS_J          -----------?--------
J.SE.SE9173          -----------N--------
J.SE.SE9280          --------------------

CONSENSUS_K          -----------------?--
K.BE.VI325           -----------------T--
K.CD.EQTB11C         -----------------T--
K.CM.MP535           -----------------A--
N.CM.YBF30           -------------A--VA--

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

CONSENSUS_CPZ        ----------------?---
CPZ.CD.CPZANT        -T----------V---MQ--
CPZ.GA.CPZGAB        -------------------T
CPZ.US.CPZUS         ----------------V---
```

Study Subject ID:01RCH49
Study Subject Clone:
Study Subject HLA:A30,A68,B44,B57,Cw7
Sequence: Known reactive 20Mer0: QMVHQAISPRTLNAWVKVVE p24(9–28)

Possible HLA

A30	A*3001,A*3002,A*3003,A*3004
A68	A*6801,A*6802,A*6808
B44	B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
B57	Bw57,B*57,B*5701,B*5702,B*5703,B*5704
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(10-17)	RTLNAWVK	A*6801
(2-10)	MVHQAISPR	A*6801
(4-12)	HQAISPRTL	Cw*0702
(5-12)	QAISPRTL	Cw*0702
(3-12)	VHQAISPRTL	Cw*0702

Anchor Residues Searched

A*6801	X[VT]XXXXX[RK]
A*6801	X[VT]XXXXXX[RK]
A*6801	X[VT]XXXXXXX[RK]
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*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:01RCH49
Study Subject Clone:
Study Subject HLA:A30,A68,B44,B57,Cw7
Sequence: Known reactive 20Mer1: PRGSDIAGTTSTLQEQIGWM p24(99–118)

Possible HLA

A30	A*3001,A*3002,A*3003,A*3004
A68	A*6801,A*6802,A*6808
B44	B*4402,B*4403,B*4404,B*4405,B*4406,B*4407,B*4408
B57	Bw57,B*57,B*5701,B*5702,B*5703,B*5704
Cw7	Cw*0701,Cw*0702,Cw*0704,Cw*0706

Possible Epitopes based on anchor residues

(5-13)	DIAGTTSTL	Cw*0702
(6-13)	IAGTTSTL	Cw*0702
(4-13)	SDIAGTTSTL	Cw*0702

Anchor Residues Searched

A*6801	X[VT]XXXXX[RK]
A*6801	X[VT]XXXXXX[RK]
A*6801	X[VT]XXXXXXX[RK]
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*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

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

Protein	Epitope in Database	Epitope in Ref. strain	Epitope in Consensus B	HLA	Notes
p24(15–23)	LSPRTLNAW	ISPRTLNAW	ISPRTLNAW	B57,B58	
p24(108–117)	TSTLQEQIGWF	TSTLQEQIGWM	TSTLQEQIGWM	B*57,B*5801	
p24(108–118)	TSTLQEQIGWF	TSTLQEQIGWM	TSTLQEQIGWM	B*5701	
p24(174–184)	AEQASQDVKNW	AEQASQEVKNW	AEQASQEVKNW	B*4402	
p24(174–184)	AEQASQDVKNW	AEQASQEVKNW	AEQASQEVKNW	B*4402,B44	
Protease(3–11)	ITLWQRPLV	VTLWQRPLV	ITLWQRPLV	A*6802	
Protease(3–11)	ITLWQRPLV	VTLWQRPLV	ITLWQRPLV	A*6802,A*7401,A19	
Protease(30–38)	DTVLEEMNL	DTVLEEMSL	DTVLEEMNL	A*6802	
Protease(30–38)	DTVLEDINL	DTVLEEMSL	DTVLEEMNL	A*6802	
Protease(30–38)	DTVLEEWNL	DTVLEEMSL	DTVLEEMNL	A*6802	
RT(364–372)	DVKQLTEVV	DVKQLTEAV	DVKQLTEAV	A28, A*6802	
Integrase(96–104)	ETAYFILKL	ETAYFLLKL	ETAYFLLKL	A*6802	
gp160(31–40)	AENLWVTVYY	TEKLWVTVYY	AEQLWVTVYY	B*4402	
gp160(31–40)	AENLWVTVYY	TEKLWVTVYY	AEQLWVTVYY	B44	
gp160(704–712)	IVNRNRQGY	IVNRVRQGY	IVNRVRQGY	A*3002	
gp160(777–785)	IVTRIVELL	IAARIVELL	IVTRIVELL	A*6802	
gp160(794–802)	KYCWNLLQY	KYWWNLLQY	KYWWNLLQY	A*3002	

Table 1: **p24**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(15–23)	p24()	LSPRTLNAW	HIV-1 exposed seronegative	human(B57,B58)	[Kaul (2000)]
	• 11/16 heavily HIV exposed but persistently seronegative sex-workers in Nairobi had HIV-speci£c CD8 gamma-IFN responses in the cervix – systemic CD8+ T cell responses tended to be to the same epitopes but at generally lower levels than cervical CD8+ T cell responses • Low risk individuals did not have such CD8+ cells • CD8+ epitopes T cell DTVLEDINL (3 individuals), SLYNVATL (4 individuals), LSPRTLNAW (3 individuals) and YPLTFGWCF (4 individuals) were most commonly recognized by the HIV-resistant women				
p24(108–117)	p24(240–249 LAI)	TSTLQEQIGWF	HIV-1 infection	human(B*57,B*5801)	[Goulder (1996)]
	• Response to this epitope was found in 4 slow progressing HLA-B*57 individuals, in 2 it was dominant or very strong • For one donor (from Zimbabwe) this was de£ned as the optimal peptide • This epitope can be presented in the context of the closely related HLA molecules B*5801 and B*57				
p24(108–118)	p24(240–249 LAI)	TSTLQEQIGWF	HIV-1 infection	human(B*5701)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5701 epitope				
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 2: **Protease**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
Protease(3–11)	RT(71–79 A/B/D)	ITLWQRPLV	?	human(A*6802)	[Brander & Goulder(2001)]
	• C. Brander notes this is an A*6802 epitope				
Protease(3–11)	Protease(71–79 LAI)	ITLWQRPLV		human(A*6802,A*7401,A*0201)	[Long (1998)]
	• Predicted on binding motif, no truncations analyzed • Clade A/B/D consensus, S. Rowland-Jones, pers. comm.				
Protease(30–38)	Pol()	DTVLEEMNL	HIV-1 exposure	human(A*6802)	[Rowland-Jones (1998)]
	• 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 B and D clade viruses • The Clade A version of the epitope: DTVLEDINL • This epitope was recognized by two different exposed and uninfected prostitutes • This epitope was identi£ed by screening 49 HIV-1 peptides with the predicted A*6802 anchor residue motif x(VT)xxxxxx(VL)				
Protease(30–38)	pol()	DTVLEDINL	HIV-1 exposed seronegative	human(A*6802)	[Kaul (2000)]
	• 11/16 heavily HIV exposed but persistently seronegative sex-workers in Nairobi had HIV-speci£c CD8 gamma-IFN responses in the cervix – systemic CD8+ T cell responses tended to be to the same epitopes but at generally lower levels than cervical CD8+ T cell responses • Low risk individuals did not have such CD8+ cells • CD8+ epitopes T cell DTVLEDINL (3 individuals), SLYNVATL (4 individuals), LSPRTLNAW (3 individuals) and YPLTFGWCF (4 individuals) were most commonly recognized by the HIV-resistant women				
Protease(30–38)	RT(85–93 Clade D)	DTVLEEWNL	?	human(A*6802)	[Brander & Goulder(2001)]
	• C. Brander notes this is an A*6802 epitope				

Table 3: **RT**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(364–372)	RT(518–526 U455)	DVKQLTEVV		human(A28, A*6802)	[Dong (1998), Menendez-Arias (1998)]
	• Predicted on binding motif, no truncations analyzed • Reacts with clade A consensus (U455), and with the peptide DVKQLAEAV, from the D clade				

Table 4: **Integrase**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
Integrase(96–104)	Integrase(823–831)	ETAYFILKL		human(A*6802)	[Dong & Rowland-Jones(1998)]
	• Epitope found in clade A, B, and D – Pers. Comm. S. Rowland-Jones and T. Dong				

Table 5: **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(704–712)	gp160(704–712 LAI)	IVNRNRQGY		human(A*3002)	[Brander & Goulder(2001), Goulder (2001)]
	• C. Brander notes this is an A*3002 epitope				
gp160(777–785)	gp41(782–790 LAI)	IVTRIVELL	?	human(A*6802)	[Brander & Goulder(2001)]
	• C. Brander notes this is an A*6802 epitope				
gp160(794–802)	gp160(794–802 LAI)	KYCWNLLQY		human(A*3002)	[Brander & Goulder(2001), Goulder (2001)]
	• C. Brander notes this is an A*3002 epitope				

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

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(11–24)	p24()	VQHAISPRTLNAWV	HIV-1 infection	human()	[Goulder (2000)]
	• The CTL-dominant response was focused on this epitope in an HIV+ Haitian living in Boston, who was A34/68 B57/71 Cw3/7 – this epitope fell outside the most recognized peptides in the study • Three peptides GSEELRSLYNTVATL (p17 residues 71-85), SALSEGATPQDLNTMLNTVG (p24 41-60), and WEKIRLRPG-GKKKYKLK(p17 16-30) contained the dominant Gag-speci£c epitope in 31 out of 44 B-clade infected individuals from Boston who showed Gag-CTL responses • Five peptides RLRPGGKKHYMIKHLVW (p17 20-36), ELRSLYNTVATLYCV (p17Gag 74-88), SALSEGATPQDLNTMLNTVG (p24 41-60), FRDYVDRFFKTLRAEQA (p24 161-177), and SILDIKQGKEPFRDY (p24 149-164) contained dominant Gag-speci£c epitopes in 32 out of 37 C-clade infected subjects from South Africa			
p24(12–20)	Gag(146–154)	HQAISPRTL	HIV-1 infection	chimpanzee(Patr-B*02)	[Balla-Jhagjhoorsingh (1999)]
	• Certain HLA-alleles have been associated with long-term survival – among them are HLA-B*27 and HLA-B*57 • Of more than 150 chimpanzees that have been reported to be infected with HIV-1, only one has developed AIDS • CTL responses were studied in two HIV-1 infected chimpanzees that have strong CTL responses, and they were found to respond to highly conserved epitopes that are recognized in humans in the context of HLA-B*27 and HLA-B*57 • The human HLA protein which presents this Patr-B*02 epitope is HLA-B*5701 but the amino acid sequences in the binding pockets of HLA-B*5701 and Patr-B*02 are distinctive			
p24(13–23)	p24(145–155)	QAISPRTLNAW	HIV-1 infection	human()	[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 • 1/11 of the A2+ individuals was HLA A*0201, A1, B57 and responded to QAISPRTLNAW noted previously to be A25				
p24(13–23)	p24(145–155 LAI)	QAISPRTLNAW		human(A*2501)	[Brander & Goulder(2001)]
	• C. Brander notes that this is an A*2501 (Pers. Comm. I. Kurane and K. West)				
p24(13–23)	p24(145–155 LAI)	QAISPRTLNAW		human(A5)	[Kurane & West(1998)]
p24(15–23)	p24(147–155 IIIB)	ISPRTLNAW	HIV-1 infection	human(B*5701)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5701 epitope				
p24(15–23)	Gag(147–155 LAI)	ISPRTLNAW	HIV-1 infection	human(B*5701 B*5801)	[Klein (1998)]
	• B57 has been associated with long-term non-progression in the Amsterdam cohort • The most pronounced CTL responses in HLA B*5701 LTS were to RT and Gag				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(15–23)	p24(147–155)	ISPRTLNAW	HIV-1 infection	human(B57)	[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 • 1/11 of the A2+ individuals was HLA A*0201, A1, B57 and responded to four B57 epitopes and two others, but not SLYNTVATLjt				
p24(15–23)	p24(147–155 IIIB)	ISPRTLNAW	HIV-1 infection	human(B57,B*5801)	[Goulder (1996)]
	• Five slow progressors made a response to this epitope, and in two it was the dominant response • Peptide de£ned on the basis of B*5801 binding motif, yet not cross-restricted except at high concentrations				
p24(15–23)	p24()	LSPRTLNAW	HIV-1 exposed seronegative	human(B57,B58)	[Kaul (2000)]
	• 11/16 heavily HIV exposed but persistently seronegative sex-workers in Nairobi had HIV-speci£c CD8 gamma-IFN responses in the cervix – systemic CD8+ T cell responses tended to be to the same epitopes but at generally lower levels than cervical CD8+ T cell responses • Low risk individuals did not have such CD8+ cells • CD8+ epitopes T cell DTVLEDINL (3 individuals), SLYNVATL (4 individuals), LSPRTLNAW (3 individuals) and YPLTFGWCF (4 individuals) were most commonly recognized by the HIV-resistant women				
p24(16–24)	p24()	SPRTLNAWV	HIV-1 infection	chimpanzee()	[Santra (1999)]
	• 3/4 animals displayed HIV-1 Gag-speci£c CTL activity • Effector cells from two chimpanzees were able to recognize epitopes also recognized by human HIV-1 Gag-speci£c CTL (SPRTL-NAWV, HLA-B7, and DLNTMLNTV, HLA-B14) • No chimpanzee CTL were detected to the following human HIV-1 speci£c Gag epitopes, although they were embedded within 20mer peptides that contained a reactive epitope: ISPRTLNAW, HLA-B57; KRWIILGLNK, HLA-B27; and DRFYKTLRA, HLA-B14				
p24(16–24)	p24(148–156)	SPRTLNAWV		human(B*0702)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*0702 epitope • Optimal peptide mapped by titration, Pers. Comm. from D. Lewinsohn to C. Brander and B. Walker				
p24(16–24)	p24(148–156)	SPRTLNAWV		human(B7)	[Brander & Walker(1997)]
	• Optimal peptide mapped by titration, Pers. Comm. from D. Lewinsohn to C. Brander and B. Walker				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(16–24)	p24(148–156)	SPRTLNAWV	HIV infection	human(B7)	[Brodie (2000)]
	• Study tracks and quanti£es *in vivo* migration of neo-marked CD8 HIV-speci£c CTL • Adoptively transferred gene-marked HIV-speci£c CTL homed to speci£c lymph node sites, colocalizing within the parafollicular regions of the lymph node adjacent to cells expressing HIV tat-fusion transcripts, indicative of viral replication • The CTL clones expressed CCR5 and localized among HIV-1 infected cells expressing MIP-1alpha and MIP-1beta, CC-chemokines produced at sites of viral replication, suggesting a possible homing mechanism • This study provides a methodology for tracking and studying antigen speci£c CTL *in vivo*				
p24(16–24)	p24()	SPRTLNAWV	HIV-1 exposed seronegative	human(B7,B*8101)	[Kaul (2000)]
	• 11/16 heavily HIV exposed but persistently seronegative sex-workers in Nairobi had HIV-speci£c CD8 gamma-IFN responses in the cervix – systemic CD8+ T cell responses tended to be to the same epitopes but at generally lower levels than cervical CD8+ T cell responses • Low risk individuals did not have such CD8+ cells • CD8+ epitopes T cell DTVLEDINL (3 individuals), SLYNVATL (4 individuals), LSPRTLNAW (3 individuals) and YPLTFGWCF (4 individuals) were most commonly recognized by the HIV-resistant women				
p24(16–24)	Gag()	SPRTLNAWV	HIV-1 exposure	human(B7,B*8101)	[Rowland-Jones (1998)]
	• 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				
p24(19–27)	p24(151–159)	TLNAWVKVV	HIV-1 infection	human(A*02)	[Huang (2000)]
	• The single cell ELISPOT assay was optimized and highly speci£c, and found to work well even after the primary cells had been frozen and thawed • Increases in gamma interferon producing cells were observed in response to anti-retroviral therapy using single cell IFN-gamma-production ELISPOT • In 3/3 HLA-A*02 B*27 subjects the immunodominant epitope was against HLA B*27 Gag p24 epitope KRWIILGL, not A2 Gag epitopes				
p24(19–27)	p24(151–159)	TLNAWVKVV	HIV-1 infection	human(A2)	[Parker (1992), Parker (1994)]
	• Study of sequence motifs preferred for peptide binding to class I HLA-A2				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(19–27)	p24()	TLNAWVKVV	HIV-1 exposure	human(A2, A*0202)	[Rowland-Jones (1998)]
	• 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				

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

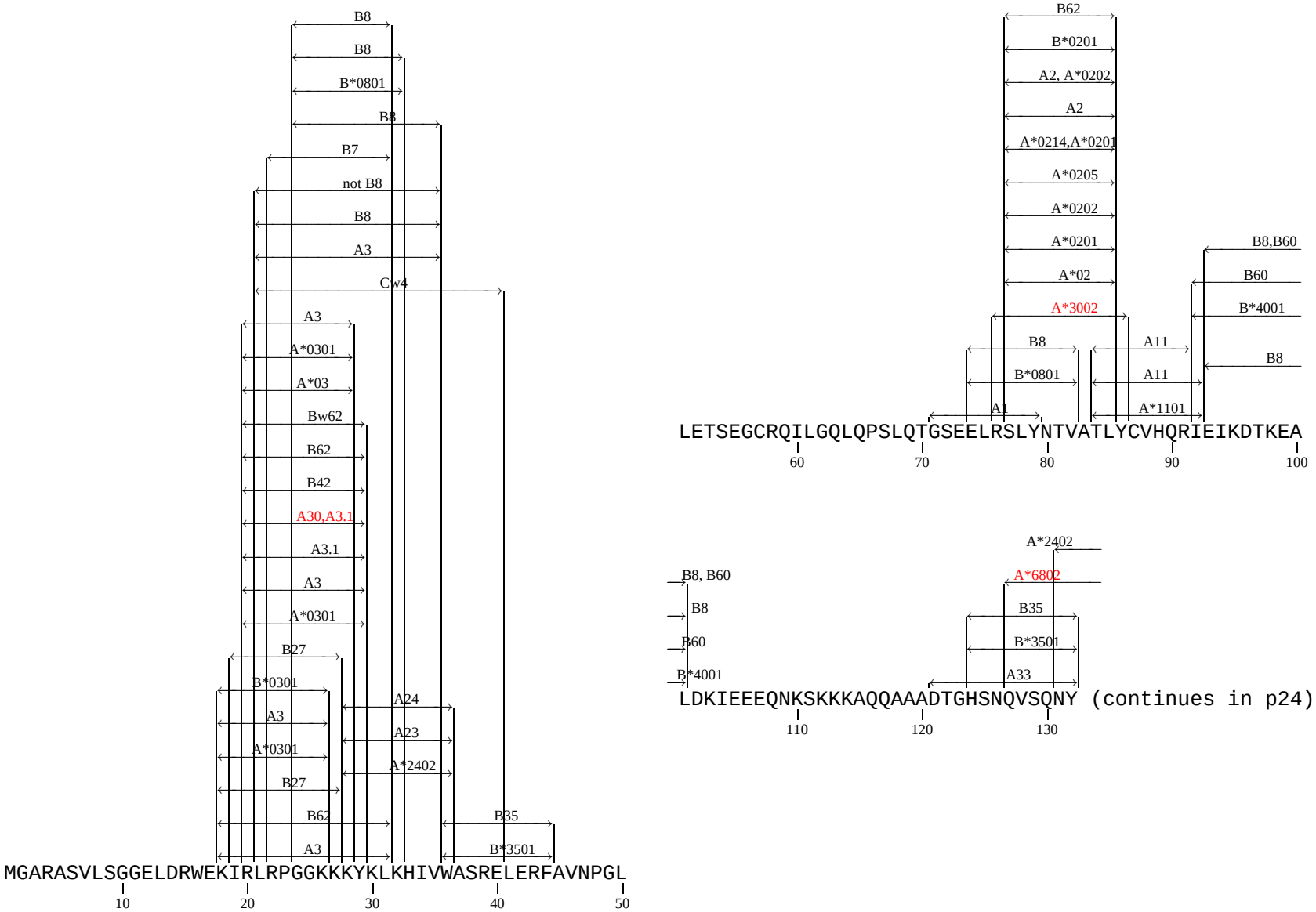
HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(11–24)	p24()	VQHAISPRTLNAWV	HIV-1 infection	human()	[Goulder (2000)]
	• The CTL-dominant response was focused on this epitope in an HIV+ Haitian living in Boston, who was A34/68 B57/71 Cw3/7 – this epitope fell outside the most recognized peptides in the study • Three peptides GSEELRSLYNTVATL (p17 residues 71-85), SALSEGATPQDLNTMLNTVG (p24 41-60), and WEKIRLRPG-GKKKYKLK(p17 16-30) contained the dominant Gag-speci£c epitope in 31 out of 44 B-clade infected individuals from Boston who showed Gag-CTL responses • Five peptides RLRPGGKKHYMIKHLVW (p17 20-36), ELRSLYNTVATLYCV (p17Gag 74-88), SALSEGATPQDLNTMLNTVG (p24 41-60), FRDYVDRFFKTLRAEQA (p24 161-177), and SILDIKQGKEPFRDY (p24 149-164) contained dominant Gag-speci£c epitopes in 32 out of 37 C-clade infected subjects from South Africa			
p24(12–20)	Gag(146–154)	HQAISPRTL	HIV-1 infection	chimpanzee(Patr-B*02)	[Balla-Jhagjhoorsingh (1999)]
	• Certain HLA-alleles have been associated with long-term survival – among them are HLA-B*27 and HLA-B*57 • Of more than 150 chimpanzees that have been reported to be infected with HIV-1, only one has developed AIDS • CTL responses were studied in two HIV-1 infected chimpanzees that have strong CTL responses, and they were found to respond to highly conserved epitopes that are recognized in humans in the context of HLA-B*27 and HLA-B*57 • The human HLA protein which presents this Patr-B*02 epitope is HLA-B*5701 but the amino acid sequences in the binding pockets of HLA-B*5701 and Patr-B*02 are distinctive				
p24(13–23)	p24(145–155)	QAISPRTLNAW	HIV-1 infection	human()	[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 • 1/11 of the A2+ individuals was HLA A*0201, A1, B57 and responded to QAISPRTLNAW noted previously to be A25				
p24(13–23)	p24(145–155 LAI)	QAISPRTLNAW		human(A*2501)	[Brander & Goulder(2001)]
	• C. Brander notes that this is an A*2501 (Pers. Comm. I. Kurane and K. West)				
p24(13–23)	p24(145–155 LAI)	QAISPRTLNAW		human(A5)	[Kurane & West(1998)]
p24(15–23)	p24(147–155 IIIB)	ISPRTLNAW	HIV-1 infection	human(B*5701)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*5701 epitope				
p24(15–23)	Gag(147–155 LAI)	ISPRTLNAW	HIV-1 infection	human(B*5701 B*5801)	[Klein (1998)]
	• B57 has been associated with long-term non-progression in the Amsterdam cohort • The most pronounced CTL responses in HLA B*5701 LTS were to RT and Gag				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(15–23)	p24(147–155)	ISPRTLNAW	HIV-1 infection	human(B57)	[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 • 1/11 of the A2+ individuals was HLA A*0201, A1, B57 and responded to four B57 epitopes and two others, but not SLYNTVATLjt				
p24(15–23)	p24(147–155 IIIB)	ISPRTLNAW	HIV-1 infection	human(B57,B*5801)	[Goulder (1996)]
	• Five slow progressors made a response to this epitope, and in two it was the dominant response • Peptide de£ned on the basis of B*5801 binding motif, yet not cross-restricted except at high concentrations				
p24(15–23)	p24()	LSPRTLNAW	HIV-1 exposed seronegative	human(B57,B58)	[Kaul (2000)]
	• 11/16 heavily HIV exposed but persistently seronegative sex-workers in Nairobi had HIV-speci£c CD8 gamma-IFN responses in the cervix – systemic CD8+ T cell responses tended to be to the same epitopes but at generally lower levels than cervical CD8+ T cell responses • Low risk individuals did not have such CD8+ cells • CD8+ epitopes T cell DTVLEDINL (3 individuals), SLYNVATL (4 individuals), LSPRTLNAW (3 individuals) and YPLTFGWCF (4 individuals) were most commonly recognized by the HIV-resistant women				
p24(16–24)	p24()	SPRTLNAWV	HIV-1 infection	chimpanzee()	[Santra (1999)]
	• 3/4 animals displayed HIV-1 Gag-speci£c CTL activity • Effector cells from two chimpanzees were able to recognize epitopes also recognized by human HIV-1 Gag-speci£c CTL (SPRTL-NAWV, HLA-B7, and DLNTMLNTV, HLA-B14) • No chimpanzee CTL were detected to the following human HIV-1 speci£c Gag epitopes, although they were embedded within 20mer peptides that contained a reactive epitope: ISPRTLNAW, HLA-B57; KRWIILGLNK, HLA-B27; and DRFYKTLRA, HLA-B14				
p24(16–24)	p24(148–156)	SPRTLNAWV		human(B*0702)	[Brander & Goulder(2001)]
	• C. Brander notes this is a B*0702 epitope • Optimal peptide mapped by titration, Pers. Comm. from D. Lewinsohn to C. Brander and B. Walker				
p24(16–24)	p24(148–156)	SPRTLNAWV		human(B7)	[Brander & Walker(1997)]
	• Optimal peptide mapped by titration, Pers. Comm. from D. Lewinsohn to C. Brander and B. Walker				

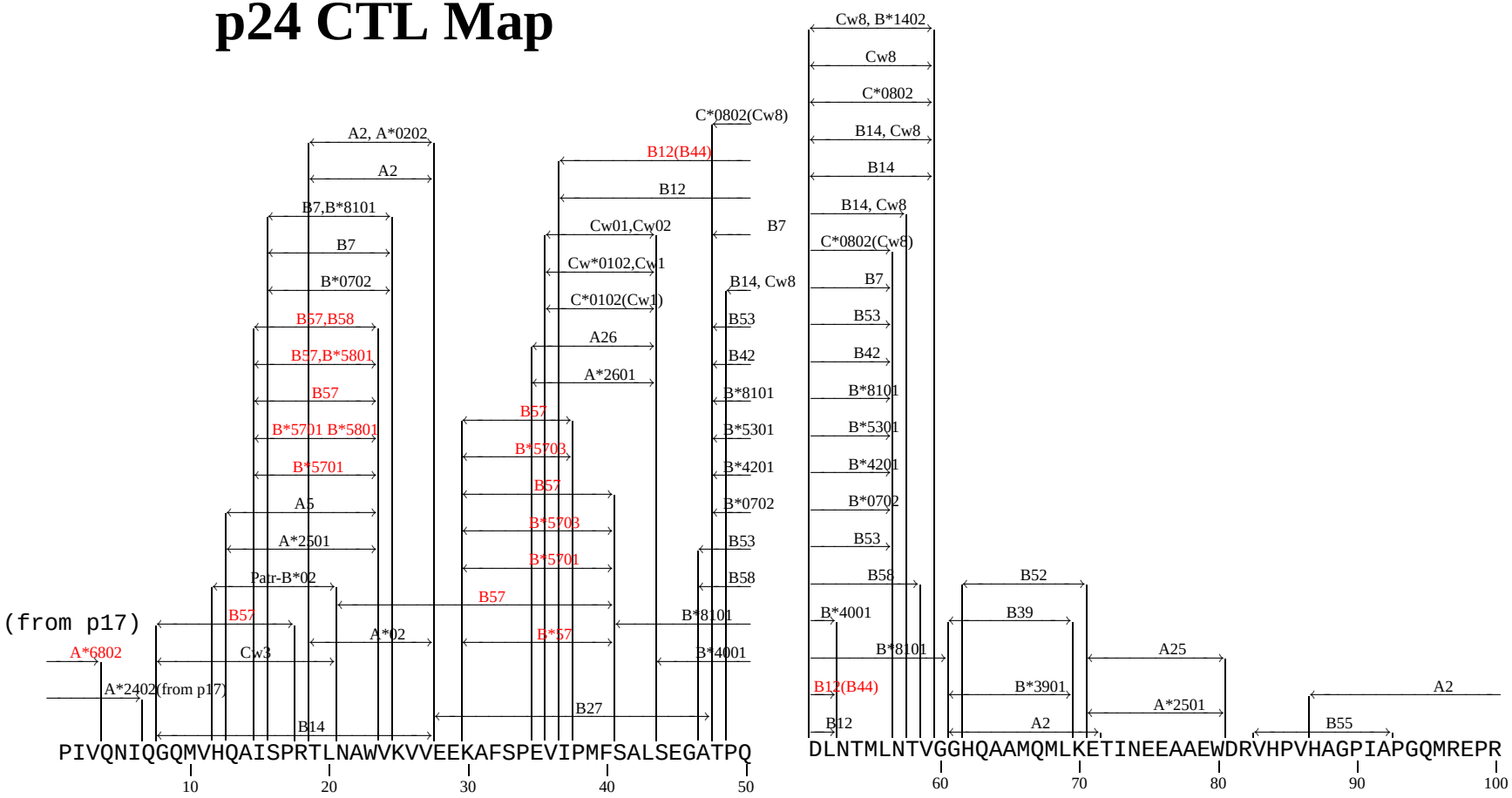
HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(16–24)	p24(148–156)	SPRTLNAWV	HIV infection	human(B7)	[Brodie (2000)]
	• Study tracks and quanti£es *in vivo* migration of neo-marked CD8 HIV-speci£c CTL • Adoptively transferred gene-marked HIV-speci£c CTL homed to speci£c lymph node sites, colocalizing within the parafollicular regions of the lymph node adjacent to cells expressing HIV tat-fusion transcripts, indicative of viral replication • The CTL clones expressed CCR5 and localized among HIV-1 infected cells expressing MIP-1alpha and MIP-1beta, CC-chemokines produced at sites of viral replication, suggesting a possible homing mechanism • This study provides a methodology for tracking and studying antigen speci£c CTL *in vivo*				
p24(16–24)	p24()	SPRTLNAWV	HIV-1 exposed seronegative	human(B7,B*8101)	[Kaul (2000)]
	• 11/16 heavily HIV exposed but persistently seronegative sex-workers in Nairobi had HIV-speci£c CD8 gamma-IFN responses in the cervix – systemic CD8+ T cell responses tended to be to the same epitopes but at generally lower levels than cervical CD8+ T cell responses • Low risk individuals did not have such CD8+ cells • CD8+ epitopes T cell DTVLEDINL (3 individuals), SLYNVATL (4 individuals), LSPRTLNAW (3 individuals) and YPLTFGWCF (4 individuals) were most commonly recognized by the HIV-resistant women				
p24(16–24)	Gag()	SPRTLNAWV	HIV-1 exposure	human(B7,B*8101)	[Rowland-Jones (1998)]
	• 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				
p24(19–27)	p24(151–159)	TLNAWVKVV	HIV-1 infection	human(A*02)	[Huang (2000)]
	• The single cell ELISPOT assay was optimized and highly speci£c, and found to work well even after the primary cells had been frozen and thawed • Increases in gamma interferon producing cells were observed in response to anti-retroviral therapy using single cell IFN-gamma-production ELISPOT • In 3/3 HLA-A*02 B*27 subjects the immunodominant epitope was against HLA B*27 Gag p24 epitope KRWIILGL, not A2 Gag epitopes				
p24(19–27)	p24(151–159)	TLNAWVKVV	HIV-1 infection	human(A2)	[Parker (1992), Parker (1994)]
	• Study of sequence motifs preferred for peptide binding to class I HLA-A2				

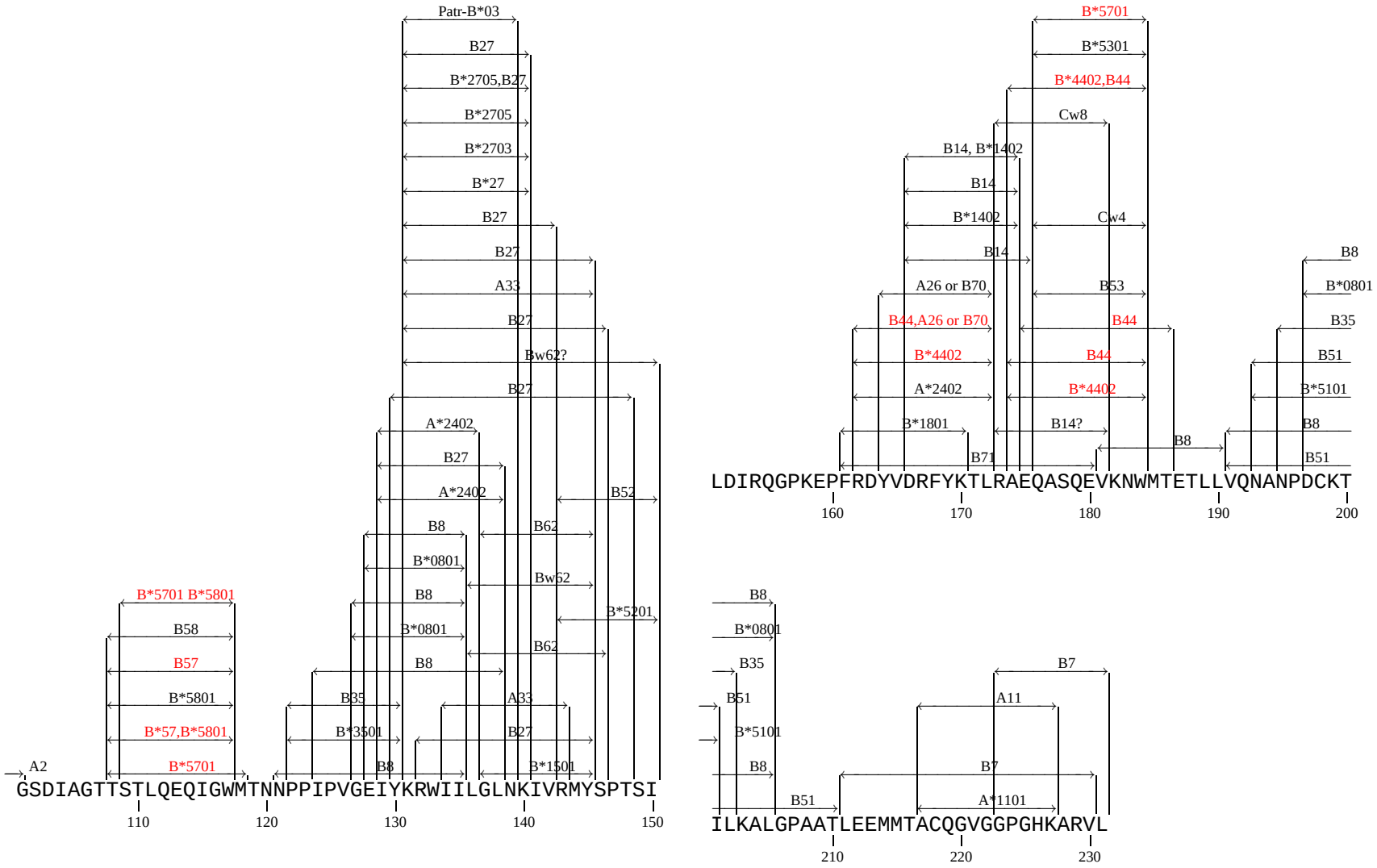
HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p24(19–27)	p24()	TLNAWVKVV	HIV-1 exposure	human(A2, A*0202)	[Rowland-Jones (1998)]
	• HIV-speci£c CTL were found in exposed seronegative prostitutes from Nairobi – these CTL may confer protection • Seroprevalence in this cohort 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				

p17 CTL Map


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

p24 CTL Map


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


Patr-B*03
B27
B*2705,B27
B*2705
B*2703
B*27
B27
B27
A33
B27
Bw62?
B27
A*2402
B27
A*2402
B52
B8
B62
B*0801
Bw62
B8
B*5201
B*0801
B62
B8
B35
A33
B*3501
B27
B8
B*1501
B*5701 B*5801
B58
B57
B*5801
B*57,B*5801
B*5701
A2
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

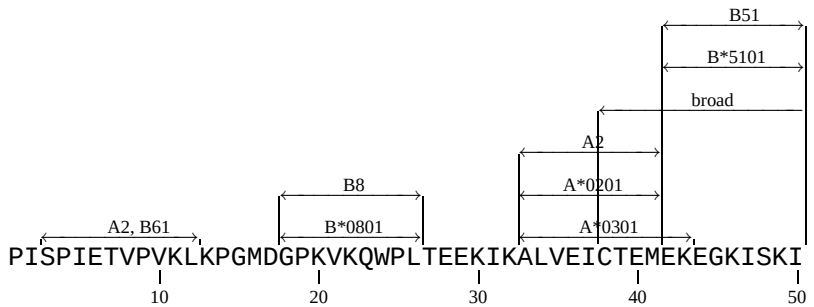
p2p7p1p6 CTL Map

```
    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 ->
```

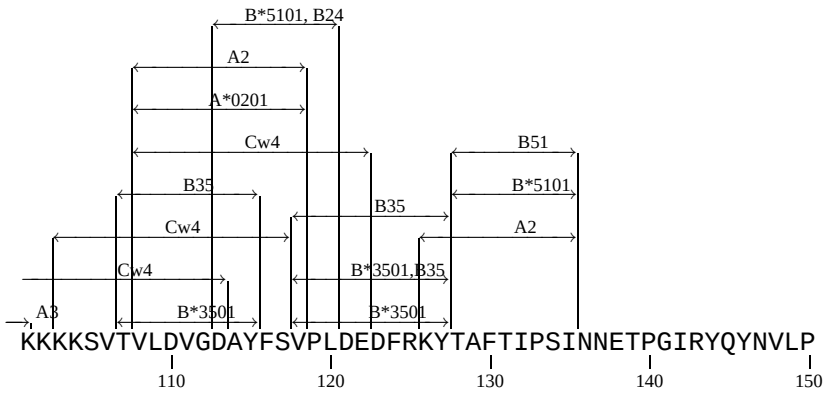
Protease CTL Map

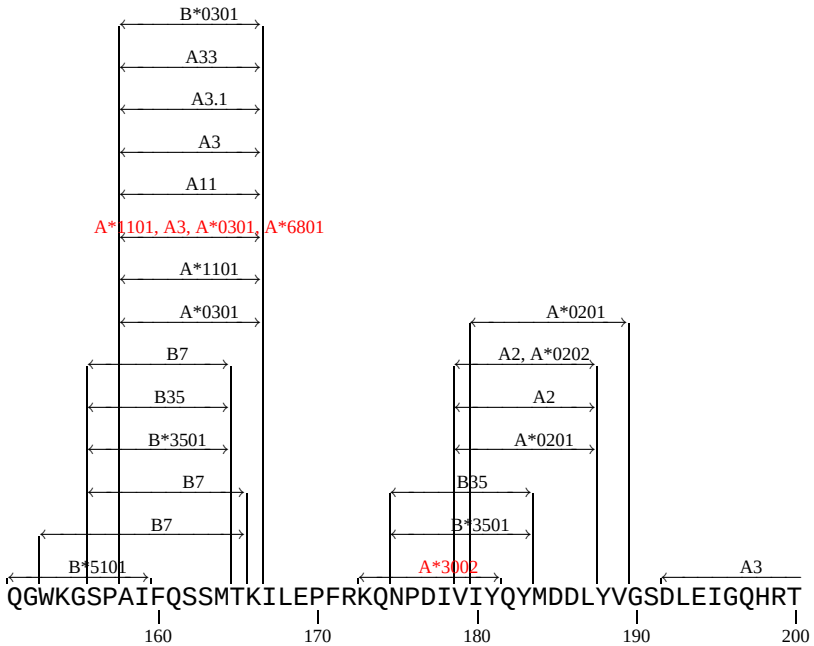
```
A*7401
A*6802,A*7401,A19
A*6802                                  A*6802
PQVTLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGI
          |         |         |         |         |
         10        20        30        40        50

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

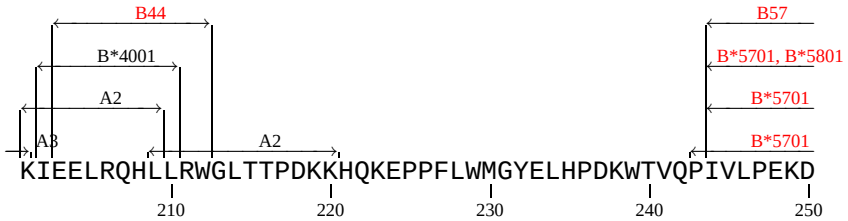
RT CTL Map

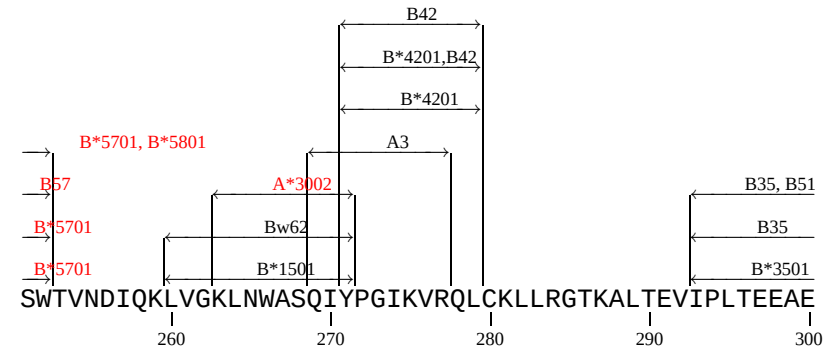

B51
B*5101
broad
A2
B8
A*0201
A2, B61
B*0801
A*0301
PISPIETVPVKLKPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKI
10
20
30
40
50

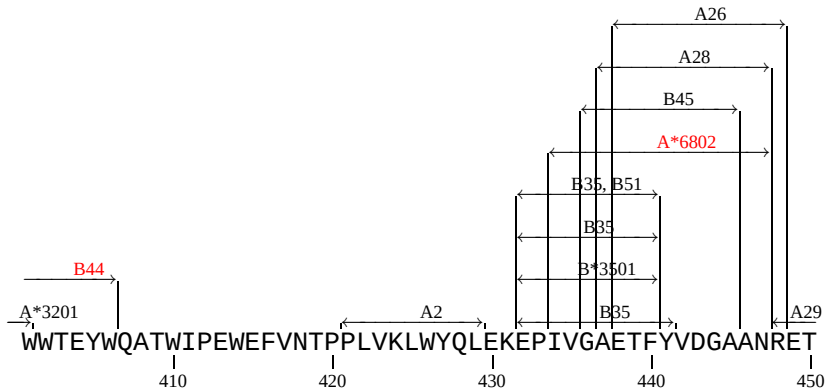
Cw4
broad
A3
GPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGL
60
70
80
90
100


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

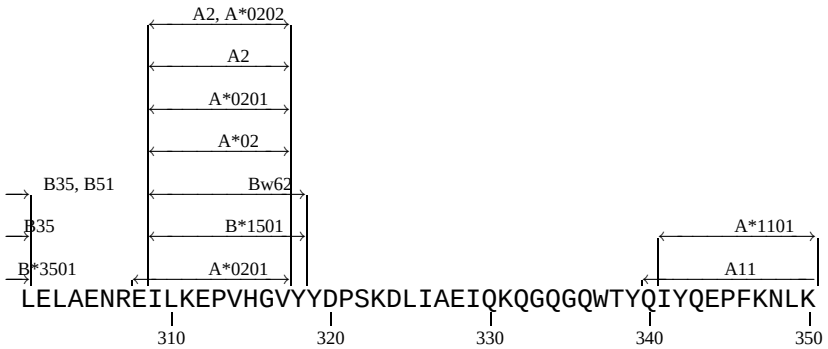

B*0301
A33
A3.1
A3
A11
A*1101, A3, A*0301, A*6801
A*1101
A*0301
A*0201
B7
A2, A*0202
B35
A2
B*3501
A*0201
B7
B35
B7
B*3501
B*5101
A*3002
A3
QGWKGSPAIFQSSMTKILEPFRKQNPDIVIYQYMDDLYVGSDLEIGQHRT
160
170
180
190
200

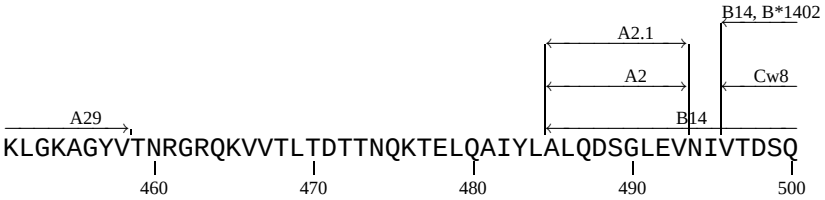

B44
B57
B*4001
B*5701, B*5801
A2
B*5701
A3
A2
B*5701
KIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWTVQPIVLPEKD
210
220
230
240
250

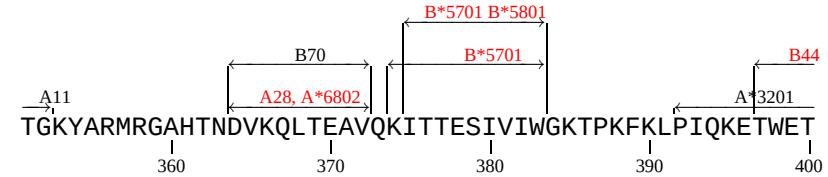


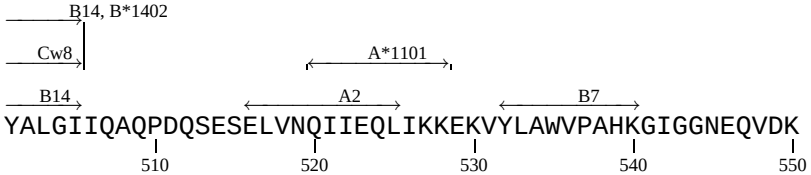


p15 RNase start <-









LVSAGIRKVL

-> p15 RNase end

Integrase CTL Map

B*5101

FLDGIDKAQDEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLKGEAM

10 20 30 40 50

A*2402 A*6802

HGQVDCSPGIWQLDCTHLEGKVILVAVHVASGYIEAEVIPAETGQETAYF

60 70 80 90 100

A*6802

LLKLAGRWPVKTIHTDNGSNFTGATVRAACWWAGIKQEFGIPYNPQSQGV

110 120 130 140 150

A*1101

B57

B*5701

VESMNKELKKIIGQVRDQAEHLKTAVQMAVFIHNFKRKGGIGGYSAGERI

160 170 180 190 200

A2

A*0201

VDIIATDIQTKELQKQITKIQNFRVYYRDSRNPLWKGPAKLLWKGEGAVV

210 220 230 240 250

IQDNSDIKVVPRRKAKIIRDYGKQMAGDDCVASRQDED

260 270 280

Rev CTL Map

B*5801

B*5701

MAGRSGDSDEELIRTVRLIKLLYQSNPPPNPEGTRQARRNRRRRWRERQR

10 20 30 40 50

Cw5

B14, Cw8

A1

B14

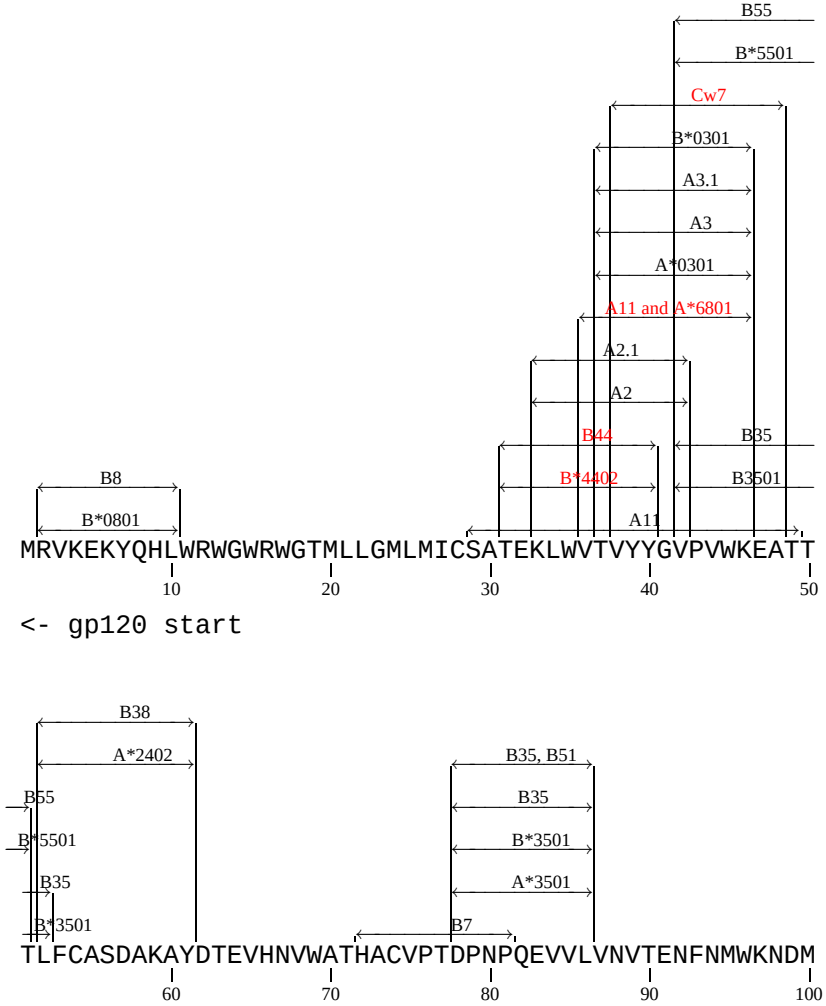
QIHSISERILGTYLGRSAEPVPLQLPPLERLTLDCNEDCGTSGTQGVGSP

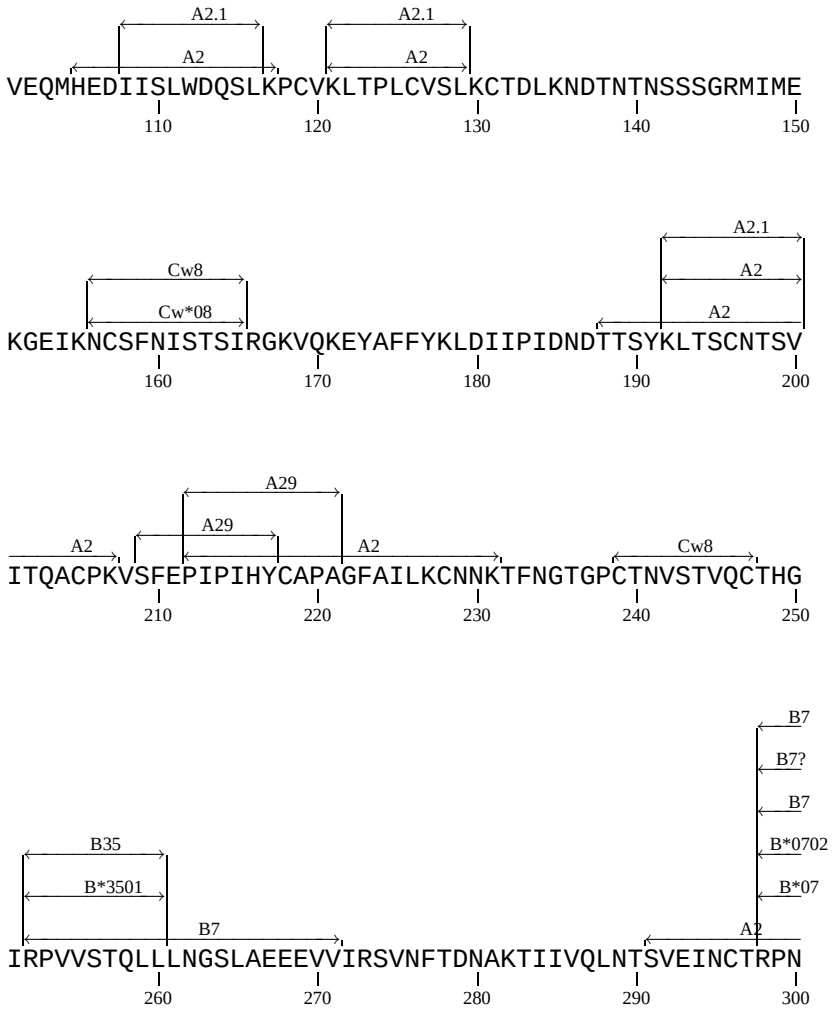
60 70 80 90 100

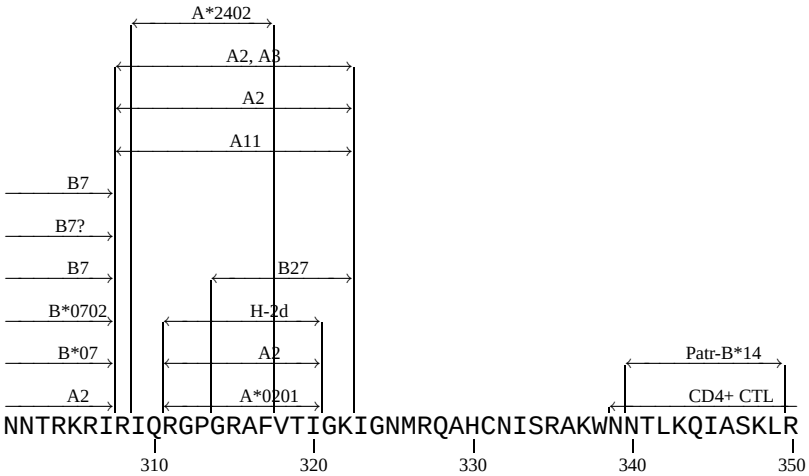
QILVESPTVLESGTKE

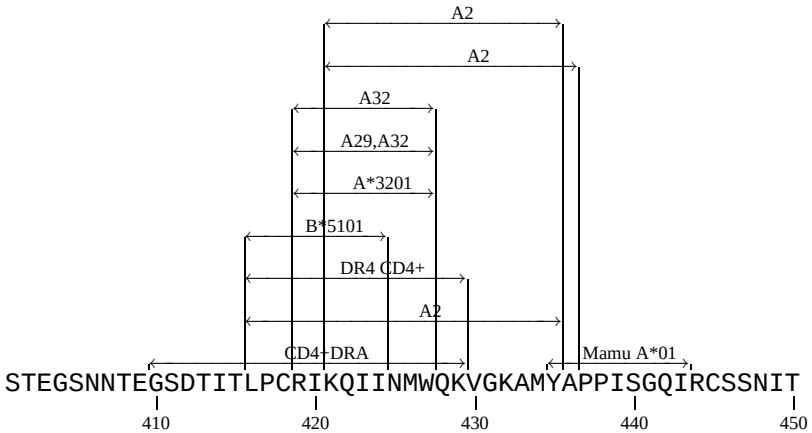
110

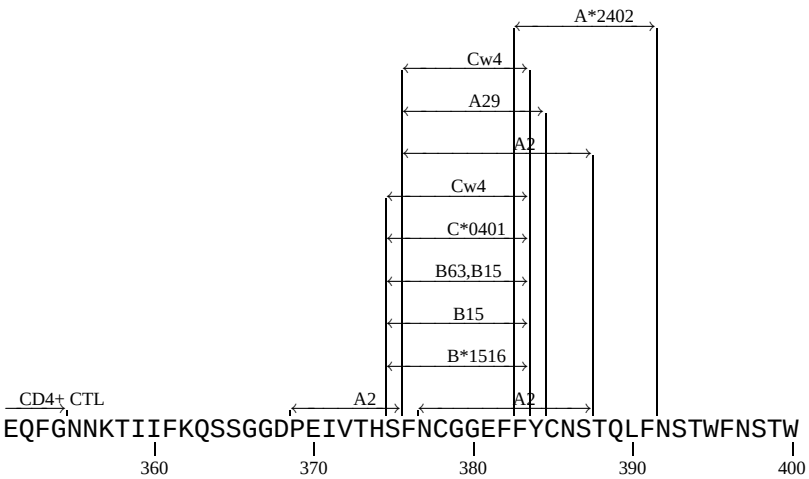
gp160 CTL Map

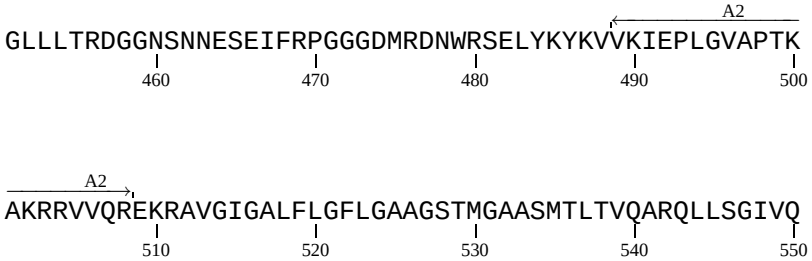




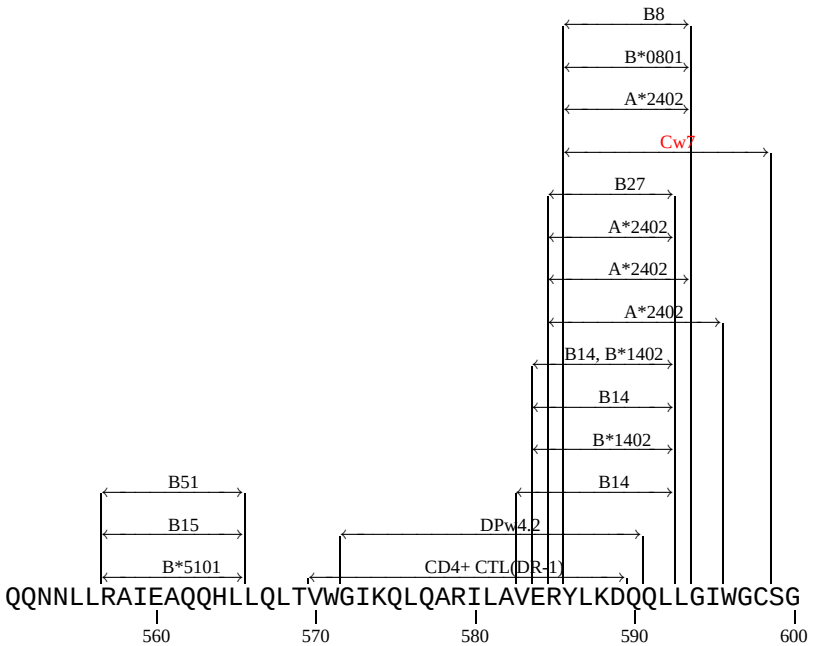


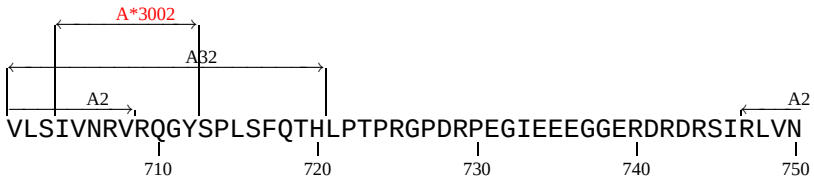


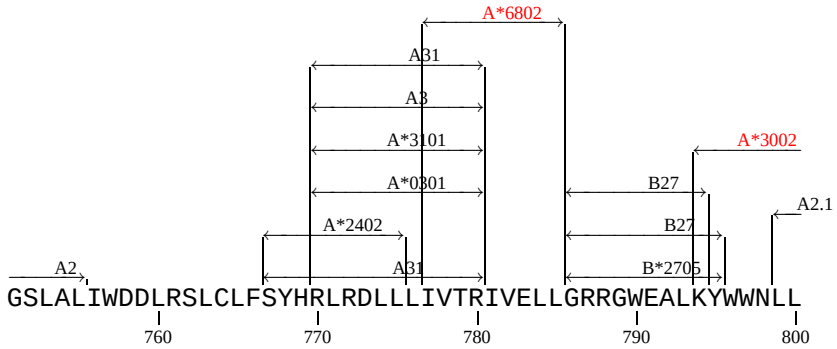




gp120 end <> gp41 start

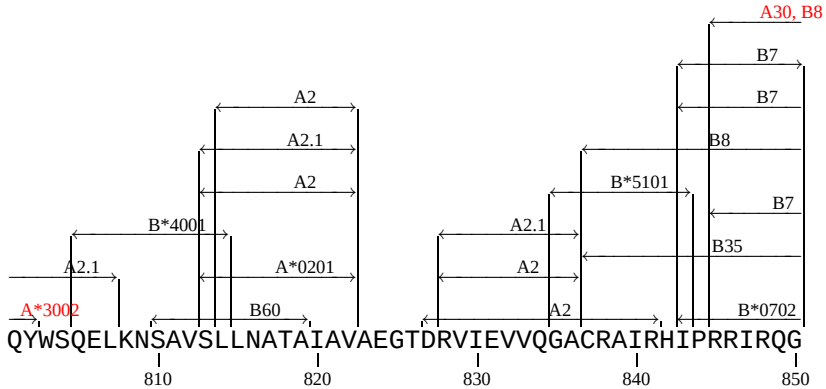

B8
B*0801
A*2402
Cw7
B27
A*2402
A*2402
A*2402
B14, B*1402
B14
B*1402
B14
B51
B15
B*5101
DPw4.2
CD4+ CTL(DR-1)
QQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSG
560
570
580
590
600

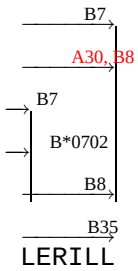

A*3002
A32
A2
A2
VLSIVNRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRLVN
710
720
730
740
750


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

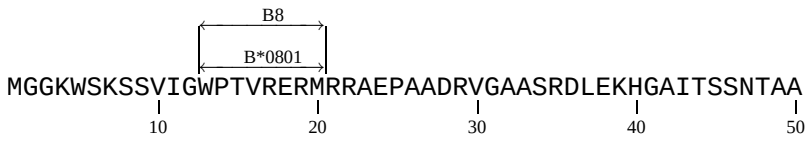
A2.1
A*2402
A2.1
A2
NQQEKNEQELLELDKWASLWNWFNITNWLWYIKLFIMIVGGLVGLRIVFA
660
670
680
690
700

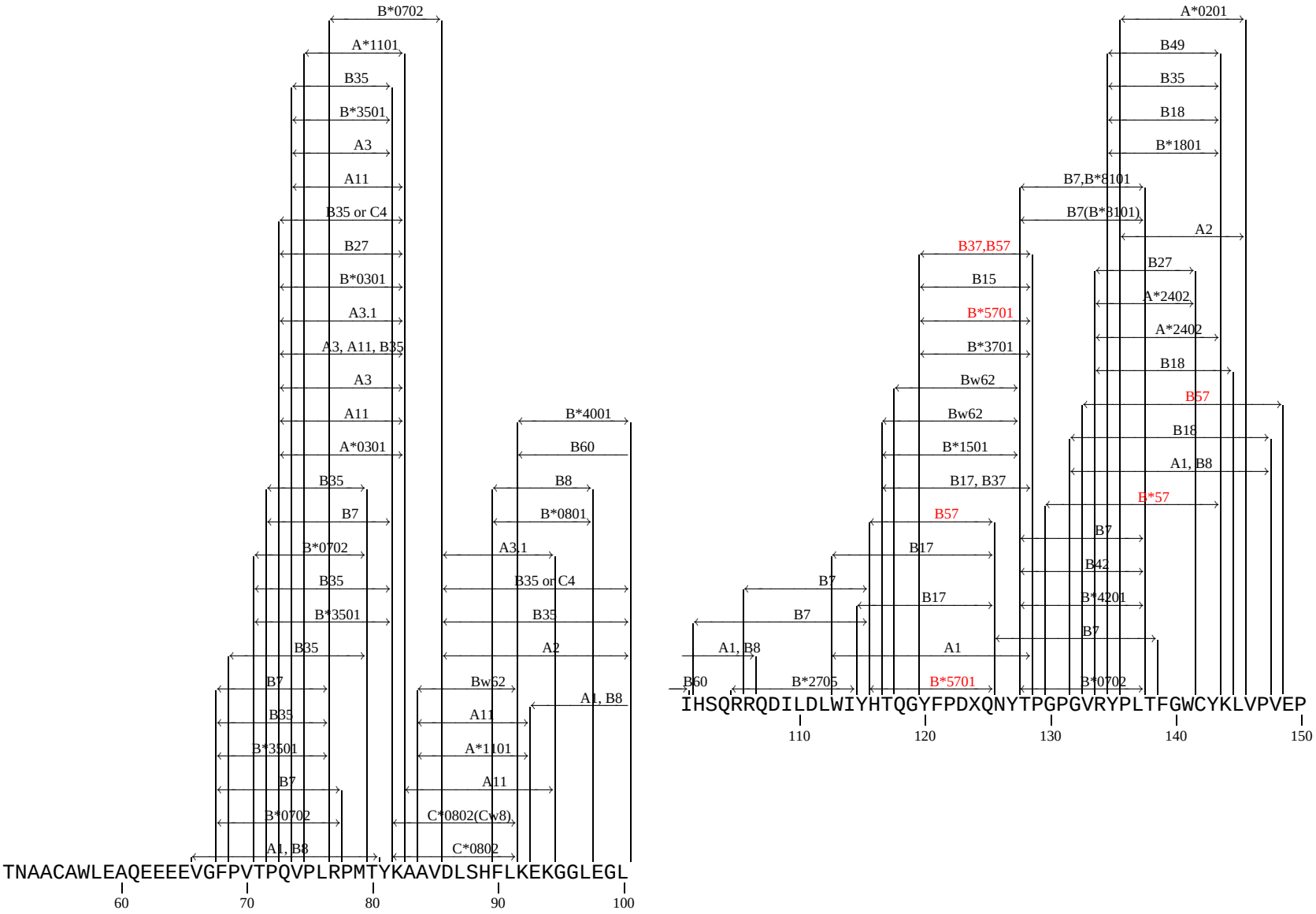

A30, B8
B7
B7
A2
A2.1
B8
A2
B*5101
B7
B*4001
A2.1
B35
A2.1
A*0201
A2
A*3002
B60
A2
B*0702
QYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQG
810
820
830
840
850

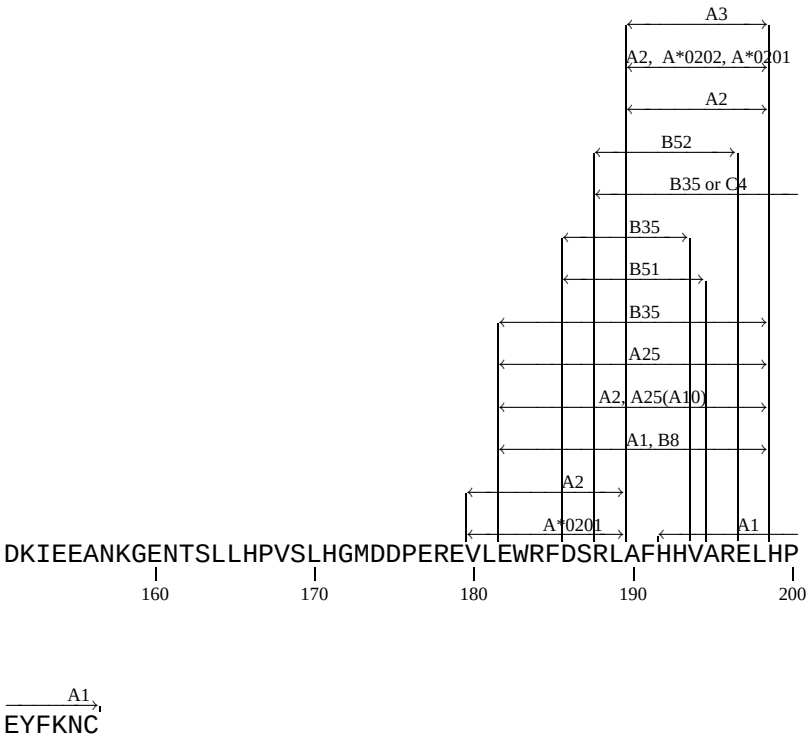


-> gp41 end

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*3101)
A2
B37,B57
B27
B15
A*2402
B*5701
A*2402
B*3701
B18
Bw62
B57
Bw62
B18
B*1501
A1, B8
B17, B37
B*57
B57
B7
B17
B42
B7
B17
B*4201
B7
B7
A1, B8
A1
B60
B*2705
B*5701
B*0702
IHSQRRQDILDLWIYHTQGYFPDXQNYTPGPGVRYPLTFGWCYKLVPVEP
110
120
130
140
150



[Balla-Jhagjhoorsingh (1999)] S. S. Balla-Jhagjhoorsingh, G. Koopman, P. Mooij, T. G. Haaksma, V. J. Teeuwsen, R. E. Bontrop, & J. L. Heeney. Conserved CTL epitopes shared between HIV-infected human long-term survivors and chimpanzees. *J Immunol* **162**:2308–14, 1999. (Medline: 99138931).

[Betts (2000)] M. R. Betts, J. P. Casazza, B. A. Patterson, S. Waldrop, W. Trigona, T.-M. Fu, F. Kern, L. J. Picker, & R. A. Koup. Putative immunodominant human imunode£ciency virus-speci£c CD8+ T cell responses cannot be predicted by major histocompatibility complex class I haplotype. *J Virol* **74**:9144–9151, 2000. (Medline: 20438112).

[Borrow (1997)] P. Borrow, H. Lewicki, X. Wei, M. S. Horwitz, N. Peffer, H. Meyers, J. A. Nelson, J. E. Gairin, B. H. Hahn, M. B. Oldstone, & G. M. Shaw. Anti-viral pressure exerted by HIV-1-speci£c cytotoxic T lymphocytes (CTLs) during primary infection demonstrated by rapid selection of CTL escape virus. *Nat Med* **3**:205–11, 1997. (Medline: 97170967) Notes: Genetic pathways of virus escape from CTL pressure resembled virus escape from antiretroviral therapy.

[Borrow & Shaw(1998)] P. Borrow & G. M. Shaw. Cytotoxic T-lymphocyte escape viral variants: how important are they in viral evasion of immune clearance in vivo? *Immunol Rev* **164**:37–51, 1998. (Medline: 99011854).

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

[Brander & Walker(1997)] C. Brander & B. Walker. Systematic identi£cation of optimal HIV-1 CTL epitopes. *HIV Molecular Immunology Database* pages IV–1 to IV–11, 1997.

[Brodie (2000)] S. J. Brodie, B. K. Patterson, D. A. Lewinsohn, K. Diem, D. Spach, P. D. Greenberg, S. R. Riddell, & L. Corey. HIV-speci£c cytotoxic T lymphocytes traf£c to lymph nodes and localize at sites of HIV replication and cell death. *J Clin Invest* **105**:1407–17, 2000. (Medline: 20273932).

[Dong (1998)] T. Dong . Personal Communication 1998. Notes: Personal Communication.

[Dong & Rowland-Jones(1998)] T. Dong & S. Rowland-Jones. Personal communication 1998. Notes: Personal communication.

[Goulder (2001)] P. Goulder, M. Addo, M. Altfeld, & et al. Rapid de£nition of £ve novel HLA-A*3002 restricted HIV speci£c CTL epitopes by intracellular cytokine staining and Elispot assays. *J. Virol* **75(3)**:1339–1347, 2001. (Medline: 11152507).

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

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

[Goulder (1996)] P. J. R. Goulder, M. Bunce, P. Krausa, K. McIntyre, S. Crowley, B. Morgan, A. Edwards, P. Giangrande, R. E. Phillips, & A. J. McMichael. Novel, cross-restricted, conserved and immunodominant cytotoxic T lymphocyte epitopes in slow HIV Type 1 infection. *AIDS Res and Hum Retroviruses* **12**:1691–1698, 1996. (Medline: 97118362) Notes: HLA-B*57 is over-represented in slow progressors. HLA*5801 is a closely related molecule, and while the de£ned anchor residues of HLA*5801 can be used to predict epitopes in HIV-1 proteins, the CTL from HLA-B*57 positive individuals have limited cross-presentation capacity with HLA*5801 targets. In this paper £ve new HLA-B*57 epitopes were de£ned.

[Huang (2000)] X. L. Huang, Z. Fan, C. Kalinyak, J. W. Mellors, & C. R. Rinaldo. CD8(+) T cell gamma interferon production speci£c for human immunode£ciency virus type 1 (HIV-1) in HIV-1-infected subjects. *Clin Diagn Lab Immunol* **7**:279–87, 2000. (Medline: 20169431).

[Kaul (2000)] R. Kaul, F. A. Plummer, J. Kimani, T. Dong, P. Kiama, T. Rostron, E. Njagi, K. S. MacDonald, J. J. Bwayo, A. J. McMichael, & S. L. Rowland-Jones. HIV-1-speci£c mucosal CD8+ lymphocyte responses in the cervix of HIV-1- resistant prostitutes in Nairobi. *J Immunol* **164**:1602–11, 2000. (Medline: 20109119).

[Klein (1998)] M. R. Klein, S. H. van der Burg, E. Hovenkamp, A. M. Holwerda, J. W. Drijfhout, C. J. Melief, & F. Miedema. Characterization of HLA-B57-restricted human immunode£ciency virus type 1 Gag- and RT-speci£c cytotoxic T lymphocyte responses . *J Gen Virol* **79 (Pt 9)**:2191–201, 1998. (Medline: 98418500).

[Kurane & West(1998)] I. Kurane & K. West. 1998. Notes: Personal communication.

[Menendez-Arias (1998)] L. Menendez-Arias, A. Mas, & E. Domingo. Cytotoxic T-lymphocyte responses to HIV-1 reverse transcriptase (review). *Viral Immunol* **11**:167–81, 1998. (Medline: 99203068).

[Parker (1994)] K. C. Parker, M. A. Bednarek, & J. E. Coligan. Scheme for ranking potential HLA-A2 binding peptides based on independent binding of individual peptide side-chains. *J Immunol* **152**, 1994. (Medline: 94075819) Notes: The authors conclude that peptide amino acid side-chain binding to the HLA-A2 molecule is independent of the sequence of the peptide, and developed a table of coef£cients that can be used to help predict peptide binding to HLA-A2.

[Parker (1992)] K. C. Parker, M. A. Bednarek, L. K. Hull, U. Utz, B. C. H. J. Zweerink, W. E. Biddison, & J. E. Coligan. Sequence motifs important for peptide binding to the human MHC class I molecule, HLA-A2. *J Immunol* **149**, 1992. (Medline: 93056532).

[Rowland-Jones (1998)] S. L. Rowland-Jones, T. Dong, K. R. Fowke, J. Kimani, P. Krausa, H. Newell, T. Blanchard, K. Ariyoshi, J. Oyugi, E. Ngugi, J. Bwayo, K. S. MacDonald, A. J. McMichael, & F. A. Plummer. Cytotoxic T cell responses to multiple conserved HIV epitopes in HIV- resistant prostitutes in Nairobi [see comments]. *J Clin Invest* **102**:1758–65, 1998. (Medline: 99021675).

[Santra (1999)] S. Santra, P. N. Fultz, & N. L. Letvin. Virus-speci£c cytotoxic T lymphocytes in human immunode£ciency virus type 1-infected chimpanzees. *J Virol* **73**:7065–9, 1999. (Medline: 99329238).