GAETFYVDGAANRETKLGKA

QUERY	GAETFYVDGAANRETKLGKA
CONSENSUS_A	--------------------
A.KE.Q23-CXC-CG	--------------------
A.SE.SE6594	--DS-F-E---KEK-Lx-TG
A.SE.SE7253	--------------------
A.SE.SE7535	--------------------
A.SE.SE8131	-V------------------
A.SE.SE8538	--------------------
A.SE.SE8891	--------------------
A.UG.92UG037	--------------------
A.UG.U455	--------------------
CONSENSUS_B	--------------------
B.-.NL43E9	--------------------
B.AU.MBC18	--------------------
B.AU.MBC200	--------------------
B.AU.MBC925	--------------------
B.AU.MBCC54	----------------I---
B.AU.MBCC98	------------K-------
B.AU.MBCD36	-------N--------VK--
B.CN.RL42	E-------------------
B.DE.D31	--------------------
B.DE.HAN	--------------------
B.FR.HXB2	--------------------
B.GA.OYI	--------------------
B.GB.CAM1	--------------R----
B.GB.MANC	--------------------
B.NL.3202A21	--------------------
B.TW.LM49	--------------------
B.US.AD8	--------------------
B.US.BC	--------------------
B.US.DH123	-----------S---R----
B.US.JRCSF	--------------------
B.US.JRFL	--------------------
B.US.MNCG	----------------K---
B.US.NY5CG	--------------------
B.US.P896	-------------D--S---
B.US.RF	--------------------
B.US.SF2	--------------------
B.US.WEAU160	------------K-------
B.US.WR27	-----------S--------
B.US.YU2	--------------------
CONSENSUS_C	----------------i---
C.BR.92BR025	--------------I-M---
C.BW.96BW01B03	----------------I---
C.BW.96BW0402	--------------------
C.BW.96BW0502	-V------------------
C.BW.96BW1104	----------------I---
C.BW.96BW1210	-V--------------M---
C.BW.96BW15B03	----------------I---
C.BW.96BW1626	--------------------
C.BW.96BW17A09	--------------------
C.ET.ETH2220	-V----------------I---
C.IN.21068	----------------I---
C.IN.301904	-V--------------K---
C.IN.301905	-V-----------D--I---
C.IN.301999	-V--------------I---
C.IN.94IN11246	-------------D--I---
CONSENSUS_D	--------------------
D.CD.84ZR085	------------K-------
D.CD.ELI	--------------------
D.CD.NDK	--------------------
D.CD.Z2Z6	--------------------
D.UG.94UG1141	----------------I---
CONSENSUS_F1	----------S-----K---
F1.BE.VI850	--D-------S-----K---
F1.BR.93BR020.1	----------S-----K---
F1.FI.FIN9363	----------S-----K---
F1.FR.MP411	----------S-----K---
CONSENSUS_F2	--------------------
F2.CM.MP255	--------------------
F2.CM.MP257	--------------------
CONSENSUS_G	----Y---------------
G.BE.DRCBL	-V--Y---------------
G.FI.HH8793	----Y---------------
G.NG.92NG083	----Y---------------
G.SE.SE6165	----Y---------------
CONSENSUS_H	----Y-----------?---
H.BE.VI991	----Y-----------M---
H.BE.VI997	----Y-----------I---
H.CF.90CF056	----Y-I-------------
CONSENSUS_J	----------S-----?---
J.SE.SE9173	----------S-----V---
J.SE.SE9280	----------S-----T---
CONSENSUS_K	----------------?---
K.CD.EQTB11C	----------------Q---
K.CM.MP535	-----------H----K-R-
N.CM.YBF30	--------------------
CONSENSUS_O	----?--------?------
O.CM.ANT70C	----Y---------------
O.CM.MVP5180	-------------N------
AC.ET.E3099G	-------xDT----------
AC.IN.21301	----------------I---
AC.RW.92RW009	----------------I---
AC.SE.SE9488	--------------------
AC.ZM.ZAM184	R-------------------
ACD.SE.SE8603	--------------------
AD.SE.SE6954	--------------------
AD.SE.SE7108	-V------------------
ADU.CD.MAL	----------------K---
AG.NG.G3	----Y-------K-------
AG.SE.SE7812	----------------I---
AGHU.GA.VI354	----------------Q---
AGHU.NO.NOGIL3	----------------K---
AGJ.AU.BFP90	----------------Q---
AGJ.ML.95ML8	------------K---K---
AGU.CD.Z321	----------------Q---
BF.BR.93BR029.4	--------------------
CRF01_AE.CF.90CF40	-----------S----Q---
CRF01_AE.TH.93TH25	-----------S--------
CRF01_AE.TH.CM240	-----------S--------
CRF01_AE.TH.TH022	-----------S--------
CRF01_AE.TH.TH047	-----------S--------
CRF02_AG.FR.DJ263	--------------------
CRF02_AG.FR.DJ264	------------K-------
CRF02_AG.NG.IBNG	----------------I---
CRF03_AB.RU.KAL153	----------------S---
CRF04_CPX.CY.94CY0	----------------Q---
CRF04_CPX.GR.97PVC	-----------S---RR---
CRF04_CPX.GR.97PVM	-----------S---NQ---
DF.CD.VI961	--------------------
U.CD.VI1126	----------------K-R-
CONSENSUS_CPZ	?---------------?---
CPZ.CD.CPZANT	E------------NSQ----
CPZ.GA.CPZGAB	TTD-Y-----------T---
CPZ.US.CPZUS	-----------Q----K---

EKASFPEVIPMFSALSEGAT

QUERY	EKASFPEVIPMFSALSEGAT
CONSENSUS_A	---fs----------
A.KE.Q23-CXC-CG	---FS----------
A.SE.SE6594	--GFN----------
A.SE.SE7253	---FS-----V---------
A.SE.SE7535	---FS----------
A.SE.SE8131	-R-FS----------
A.SE.SE8538	--GFN----------
A.SE.SE8891	--GFS----------
A.UG.92UG037	---LS----------
A.UG.U455	D--FS----------
CONSENSUS_B	---FS----------
B.AU.AF128998	---FS----------
B.-.NL43E9	---FS----------
B.AU.MBC18	---FS----------
B.AU.MBC200	---FS----------
B.AU.MBC925	---FS----------
B.AU.MBCC54	---FS----------
B.AU.MBCC98	---FS----------
B.AU.MBCD36	---FS-------T-------
B.CN.RL42	---FS----------
B.DE.D31	---FS----------
B.DE.HAN	---FS----------
B.ES.89SP061	---FS----------
B.FR.HXB2	---FS----------
B.GA.OYI	---FS----------A----
B.GB.CAM1	---FS----------
B.GB.MANC	---FS----------I
B.JP.JH31	---FS----------
B.NL.3202A21	---FS----------
B.TW.LM49	---FS----------
B.US.85WCIPR54	---FS----------
B.US.AD8	---FS----------
B.US.BC	---FS----------
B.US.DH123	---FS----------
B.US.JRCSF	---FS----------
B.US.JRFL	---FS----------
B.US.MNCG	---FS----------
B.US.NC7	---FS----------
B.US.NY5CG	---FS----------
B.US.P896	---FS----------
B.US.RF	---FS----------
B.US.SF2	---FS----------
B.US.WC001	---FS----------
B.US.WEAU160	---FS----------
B.US.WR27	---FS----------
B.US.YU2	---FS----------
CONSENSUS_C	---FS-------T-------
C.BR.92BR025	---FS-------T-------
C.BW.96BW01B22	---FS-------T-------
C.BW.96BW0402	---FS-------T-------
C.BW.96BW0502	---FS-------T-------
C.BW.96BW1104	---FS-------T-------
C.BW.96BW1210	---FS--I----T-------
C.BW.96BW15B03	---FS-------T-------
C.BW.96BW1626	---FS-------T-------
C.BW.96BW17A09	---FS-------T-------
C.ET.ETH2220	---FS-------T-------
C.IN.93IN904	---FS-------T-------
C.IN.93IN905	---FS-------T-------
C.IN.93IN999	---FS-------T-------
C.IN.94IN11246	---FS-------T-------
C.IN.95IN21068	---FS-------T-------
CONSENSUS_D	---Fs----------
D.CD.84ZR085	---FN----------
D.CD.ELI	---FS----------
D.CD.NDK	---FS----------
D.CD.Z2Z6	---FS----------
D.UG.94UG1141	---FN----------
CONSENSUS_F	---FS----------
F.BR.BZ162	---FS----------
F.CD.VI174	---FS----------
F.RW.VI69	---FS----------
CONSENSUS_F1	---FS----------
F1.BE.VI850	---FS----------
F1.BR.93BR020.1	---FS----------
F1.FI.FIN9363	---FS----------
F1.FR.MP411	---FS----------
CONSENSUS_F2	---FS----------
F2.CM.MP255	---FS----------
F2.CM.MP257	---FS----------
CONSENSUS_G	---FS----------
G.BE.DRCBL	---FS-------T-------
G.FI.HH8793	---FS----------
G.NG.92NG083	---FS----------
G.SE.SE6165	---FS----------
CONSENSUS_H	---FS----------
H.BE.VI991	---FS----------
H.BE.VI997	---FS----------
H.CF.90CF056	---FS----------
CONSENSUS_J	---FS----------
J.SE.SE9173	---FS----------
J.SE.SE9280	---FS----------
CONSENSUS_K	---FS----------
K.BE.VI325	---FS----------AD---
K.CD.EQTB11C	---FS----------
K.CM.MP535	---FS-------T-------
N.CM.YBF30	---FS-------M-------
CONSENSUS_O	---FN--I----M------?
O.CM.ANT70C	---FN--I----M------I
O.CM.MVP5180	---FN--I----M------V
CRF01-AE.CF.90CF40	--GFN----------
CRF01-AE.TH.93TH25	--GFN----------
CRF01-AE.TH.CM240	--GFN----------
CRF01-AE.TH.TH022	--GFN----------
CRF01-AE.TH.TH047	--GFS----------
CRF02_AG.FR.DJ263	---FS-------T-------
CRF02_AG.FR.DJ264	---FS-------T-------
CRF02_AG.NG.IBNG	--GFS----------
CRF03_AB.RU.KAL15	---FS----------
CRF04_cpx.CY.94CY0	---FS----------
CRF04_cpx.GR.97PVC	---FS----------
CRF04_cpx.GR.97PVM	--GFS----------
AC.ET.E3099G	---FS----------
AC.IN.21301	---FS--I----T-------
AC.RW.92RW009	---FSQ------T-------
AC.SE.SE9488	D--FS-------T-------
AC.ZM.ZAM174-21	---FS-------T-------
AC.ZM.ZAM184	---FS----------
AC.ZM.ZAM716-17	---FS-------T-------
ACD.SE.SE8603	---FS----------
AD.SE.SE6954	---FS----------A
AD.SE.SE7108	---FS----------
ADHU.NO.NOGIL3	---FS-----------D---
ADU.CD.MAL	---FS----------
AG.NG.G3	--NFS-------T-------
AG.SE.SE7812	---FS----------
AGHU.GA.VI354	--GFS----------
AGJ.AU.BFP90	D--FS-------T-------
AGJ.ML.95ML8	---FS----------
AGU.CD.Z321	--NFS----------
BF.BR.93BR029.4	---FS----------
DF.CD.VI961	---FS-------T-------
U.CD.VI1126	---FS-------T-------
CONSENSUS_CPZ	---Fn----------
CPZ.CD.CPZANT	--NFN----------
CPZ.GA.CPZGAB	---FS----------L
CPZ.US.CPZUS	---FN-------M-------

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--

Study Subject ID:01RCH22
Study Subject Clone:
Study Subject HLA:A2,A66,B45,B57,Cw7,Cw16
Sequence: Known reactive 20Mer0: GAETFYVDGAANRETKLGKA RT(436–455)

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
A66	A*6601,A*6602
B45	B*4501,B*5002
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

(9-17)	GAANRETKL	Cw*0702
(10-17)	AANRETKL	Cw*0702
(8-17)	DGAANRETKL	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]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]

Cw*0702 XXXXXXXXX[YFL]

Study Subject ID:01RCH22
Study Subject Clone:
Study Subject HLA:A2,A66,B45,B57,Cw7,Cw16
Sequence: Known reactive 20Mer1: EKASFPEVIPMFSALSEGAT p24(29–48)

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
A66	A*6601,A*6602
B45	B*4501,B*5002
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

(7-15)	EVIPMFSAL	A*0205
(8-15)	VIPMFSAL	A*0205
(7-15)	EVIPMFSAL	A*0214
(4-12)	SFPEVIPMF	Cw*0702
(7-15)	EVIPMFSAL	Cw*0702
(5-12)	FPEVIPMF	Cw*0702
(8-15)	VIPMFSAL	Cw*0702
(3-12)	ASFPEVIPMF	Cw*0702
(6-15)	PEVIPMFSAL	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]
Cw*0702	XXXXXXXX[YFL]
Cw*0702	XXXXXXX[YFL]
Cw*0702	XXXXXXXXX[YFL]

Study Subject ID:01RCH22
Study Subject Clone:
Study Subject HLA:A2,A66,B45,B57,Cw7,Cw16
Sequence: Known reactive 20Mer2: QMVHQAISPRTLNAWVKVVE p24(9–28)

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
A66	A*6601,A*6602
B45	B*4501,B*5002
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

(11-19)	TLNAWVKVV	A*0201
(11-18)	TLNAWVKV	A*0201
(11-19)	TLNAWVKVV	A*0202
(11-18)	TLNAWVKV	A*0202
(4-12)	HQAISPRTL	A*0205
(4-12)	HQAISPRTL	A*0214
(11-19)	TLNAWVKVV	A*0214
(11-18)	TLNAWVKV	A*0214
(4-12)	HQAISPRTL	Cw*0702
(5-12)	QAISPRTL	Cw*0702
(3-12)	VHQAISPRTL	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]
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(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	
RT(179–187)	VIYQYMMDL	VIYQYMDDL	VIYQYMDDL	A2	
RT(179–187)	VIYQYMMDL	VIYQYMDDL	VIYQYMDDL	A2, A*0202	
RT(308–317)	EILKEPVGHV	EILKEPVHGV	EILKEPVHGV	A*0201	
RT(436–445)	GVETFYVDGA	GAETFYVDGA	GAETFYVDGA	B45	
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(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(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				

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				
RT(436–445)	Pol(591–600 IIIB)	GVETFYVDGA	HIV-1 infection	human(B45)	[Wilson (1999)]
	• This study describes maternal CTL responses in the context of mother-to-infant transmission • Detection of CTL escape mutants in the mother was associated with transmission, but the CTL-susceptible forms of the virus tended to be found in infected infants • No variants of this epitope were found in a non-transmitting mother who had a CTL response to it • This epitope spans the Pol p66 RT – p15 (RNAse) domain				

Table 4: **gp160**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
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				
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				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
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				
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				

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
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(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(436–445)	RT(591–600 IIIB)	GAETFYVDGA	HIV-1 infection	human(B45)	[Menendez-Arias (1998)]
	• This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(436–445)	Pol(591–600 IIIB)	GVETFYVDGA	HIV-1 infection	human(B45)	[Wilson (1999)]
	• This study describes maternal CTL responses in the context of mother-to-infant transmission • Detection of CTL escape mutants in the mother was associated with transmission, but the CTL-susceptible forms of the virus tended to be found in infected infants • No variants of this epitope were found in a non-transmitting mother who had a CTL response to it • This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(437–447)	RT(592–602 LAI)	AETFYVDGAAN		human(A28)	[Brander & Walker(1996), Menendez-Arias (1998)]
	• P. Johnson, pers. comm. • This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(438–448)	RT(593–603 IIIB)	ETFYVDGAANR	HIV-1 infection	human(A26)	[Menendez-Arias (1998)]
	• This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(438–448)	Pol(593–603 IIIB)	ETFYVDGAANR	HIV-1 infection	human(A26)	[Wilson (1999)]
	• This study describes maternal CTL responses in the context of mother-to-infant transmission • Detection of CTL escape mutants in the mother was associated with transmission, but the CTL-susceptible forms of the virus tended to be found in infected infants • One other variant was found that gave a positive, though reduced, CTL response: ETYYVNGAANR • This epitope spans the Pol p66 RT – p15 (RNAse) domain				

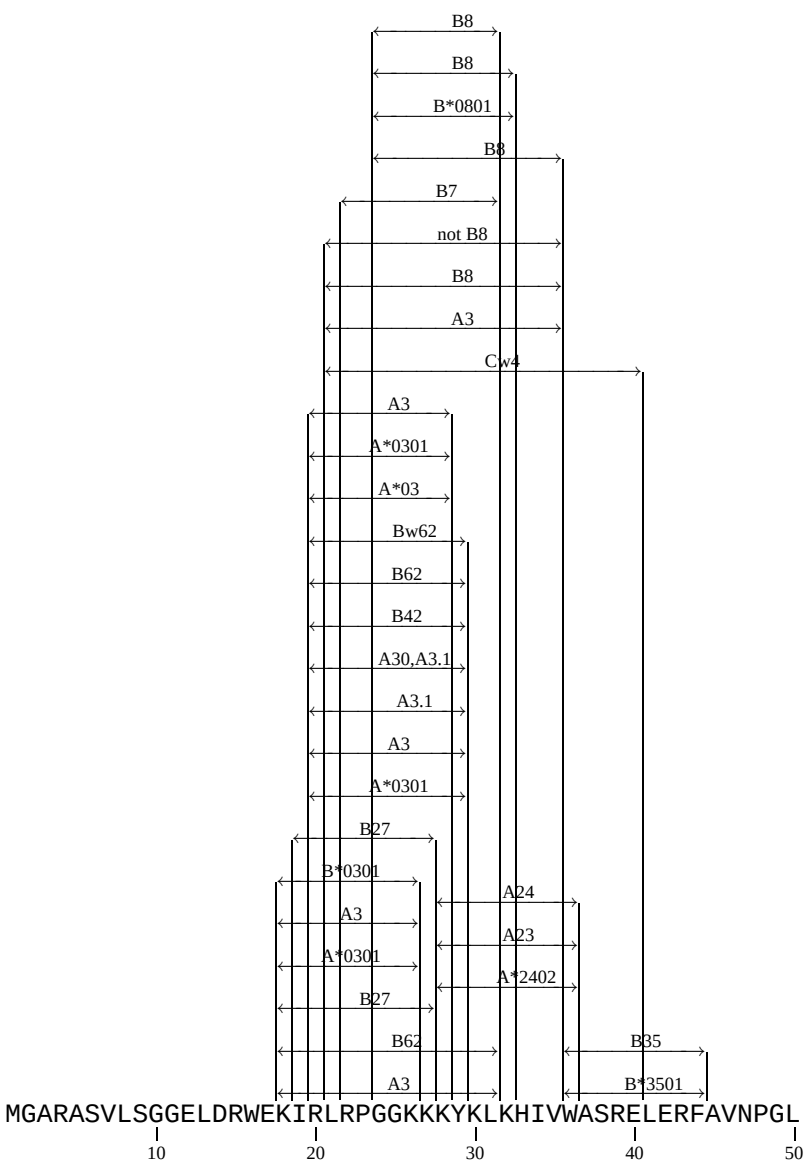
Table 7: **All De£ned Epitopes within the 20mer, regardless of HLA type**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(436–445)	RT(591–600 IIIB)	GAETFYVDGA	HIV-1 infection	human(B45)	[Menendez-Arias (1998)]
	• This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(436–445)	Pol(591–600 IIIB)	GVETFYVDGA	HIV-1 infection	human(B45)	[Wilson (1999)]
	• This study describes maternal CTL responses in the context of mother-to-infant transmission • Detection of CTL escape mutants in the mother was associated with transmission, but the CTL-susceptible forms of the virus tended to be found in infected infants • No variants of this epitope were found in a non-transmitting mother who had a CTL response to it • This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(437–447)	RT(592–602 LAI)	AETFYVDGAAN		human(A28)	[Brander & Walker(1996), Menendez-Arias (1998)]
	• P. Johnson, pers. comm. • This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(438–448)	RT(593–603 IIIB)	ETFYVDGAANR	HIV-1 infection	human(A26)	[Menendez-Arias (1998)]
	• This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(438–448)	Pol(593–603 IIIB)	ETFYVDGAANR	HIV-1 infection	human(A26)	[Wilson (1999)]
	• This study describes maternal CTL responses in the context of mother-to-infant transmission • Detection of CTL escape mutants in the mother was associated with transmission, but the CTL-susceptible forms of the virus tended to be found in infected infants • One other variant was found that gave a positive, though reduced, CTL response: ETYYVNGAANR • This epitope spans the Pol p66 RT – p15 (RNAse) domain				

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

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
RT(436–445)	RT(591–600 IIIB)	GAETFYVDGA	HIV-1 infection	human(B45)	[Menendez-Arias (1998)]
	• This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(436–445)	Pol(591–600 IIIB)	GVETFYVDGA	HIV-1 infection	human(B45)	[Wilson (1999)]
	• This study describes maternal CTL responses in the context of mother-to-infant transmission • Detection of CTL escape mutants in the mother was associated with transmission, but the CTL-susceptible forms of the virus tended to be found in infected infants • No variants of this epitope were found in a non-transmitting mother who had a CTL response to it • This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(437–447)	RT(592–602 LAI)	AETFYVDGAAN		human(A28)	[Brander & Walker(1996), Menendez-Arias (1998)]
	• P. Johnson, pers. comm. • This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(438–448)	RT(593–603 IIIB)	ETFYVDGAANR	HIV-1 infection	human(A26)	[Menendez-Arias (1998)]
	• This epitope spans the Pol p66 RT – p15 (RNAse) domain				
RT(438–448)	Pol(593–603 IIIB)	ETFYVDGAANR	HIV-1 infection	human(A26)	[Wilson (1999)]
	• This study describes maternal CTL responses in the context of mother-to-infant transmission • Detection of CTL escape mutants in the mother was associated with transmission, but the CTL-susceptible forms of the virus tended to be found in infected infants • One other variant was found that gave a positive, though reduced, CTL response: ETYYVNGAANR • This epitope spans the Pol p66 RT – p15 (RNAse) domain				

p17 CTL Map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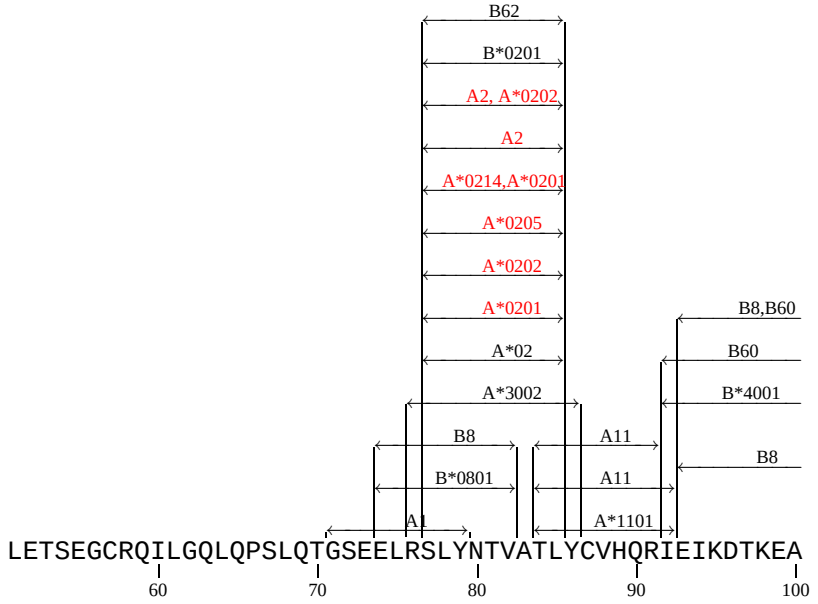
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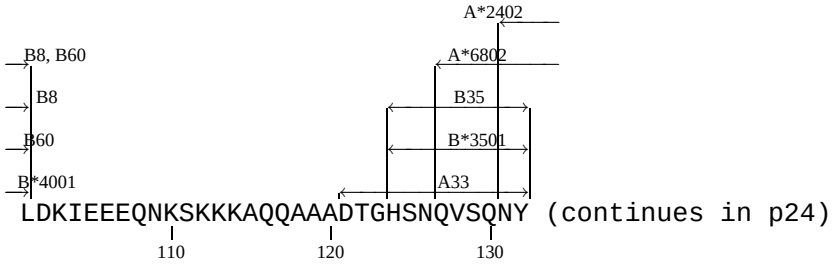
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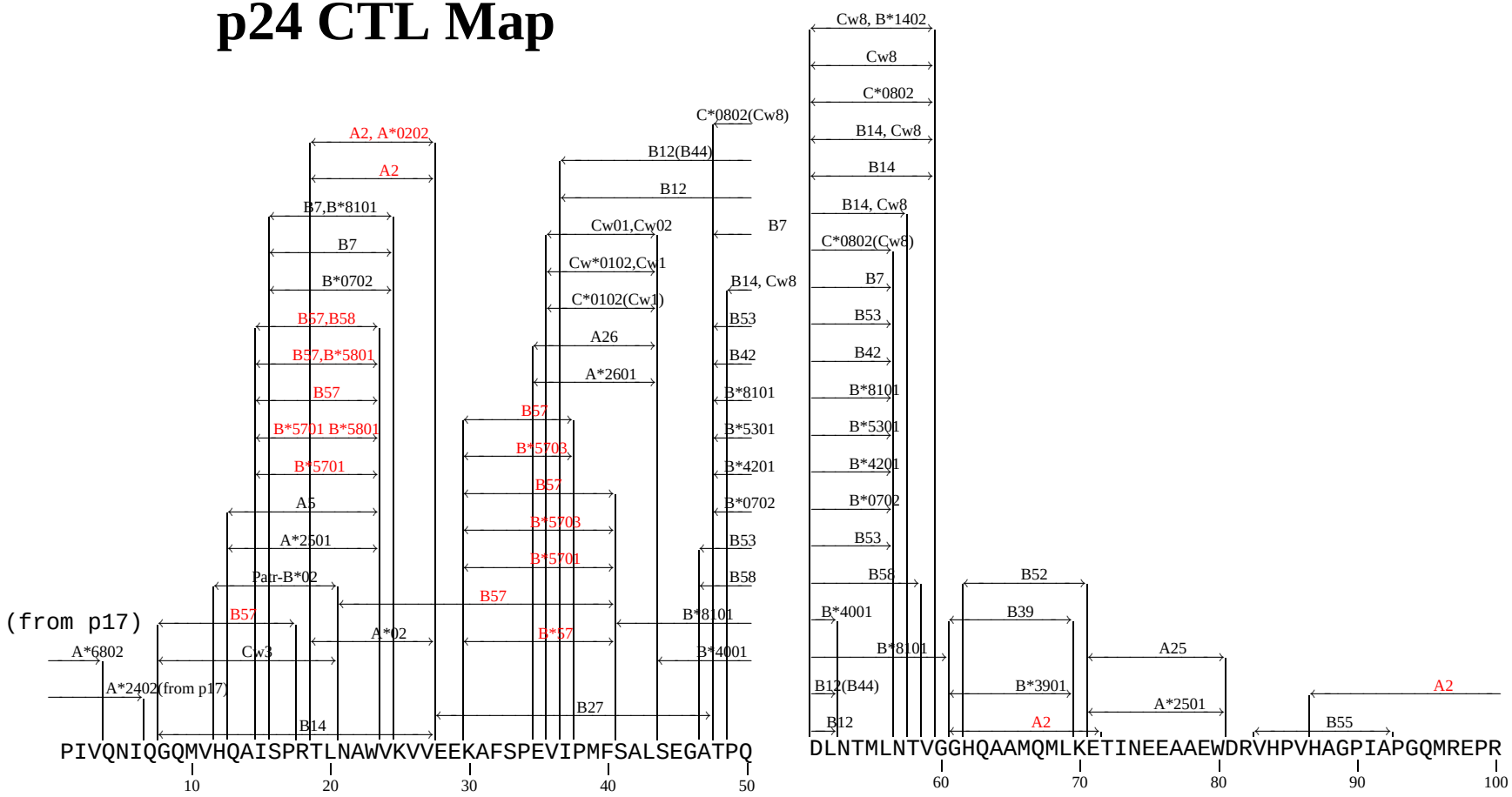
130

p24 CTL Map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B57
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A*2501
Pair-B*02
B57
B57
Cw3
A*02
B14
C*0802(Cw8)
B12(B44)
B12
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Cw*0102,Cw1
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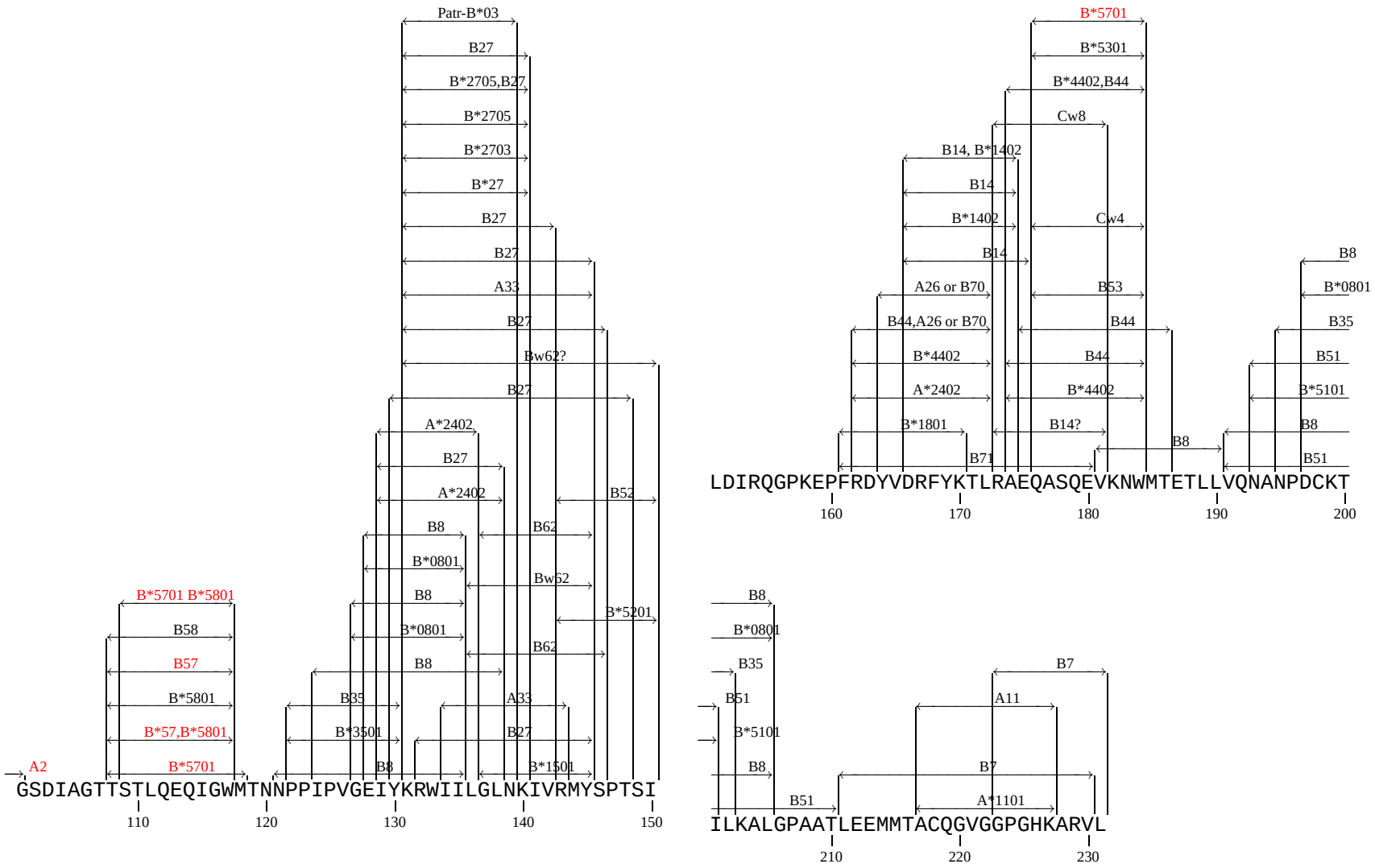
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B35
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B44
B51
A*2402
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B14?
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B8
B71
B51
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170
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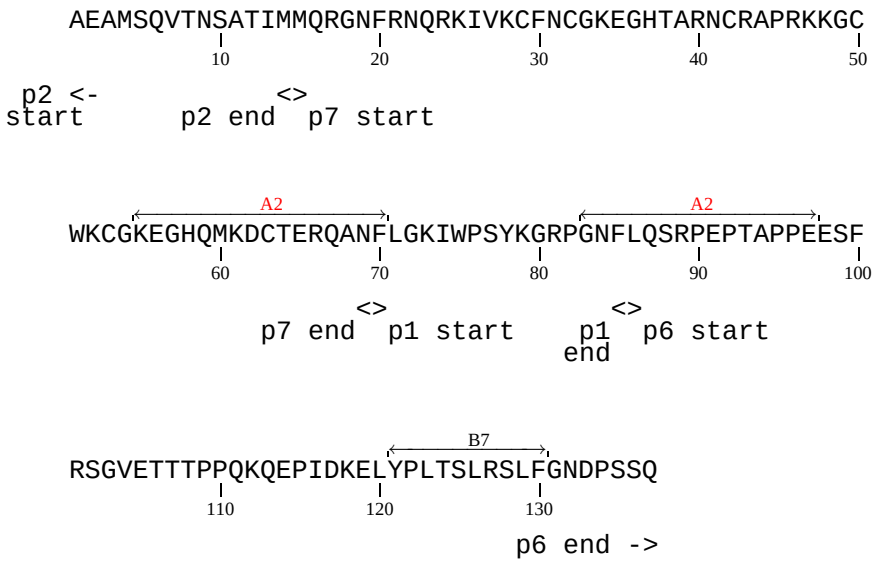
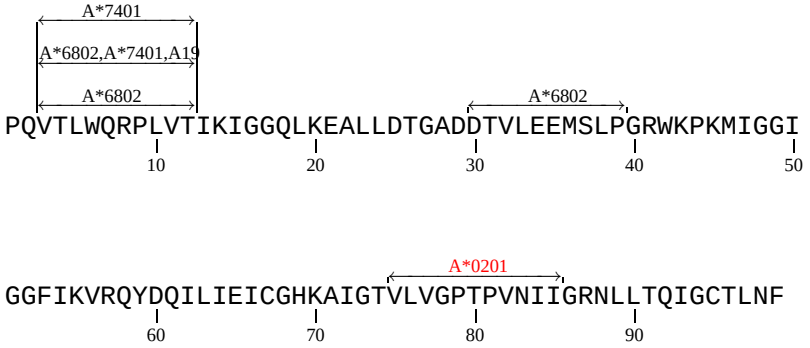
B7
A11
B7
A*1101

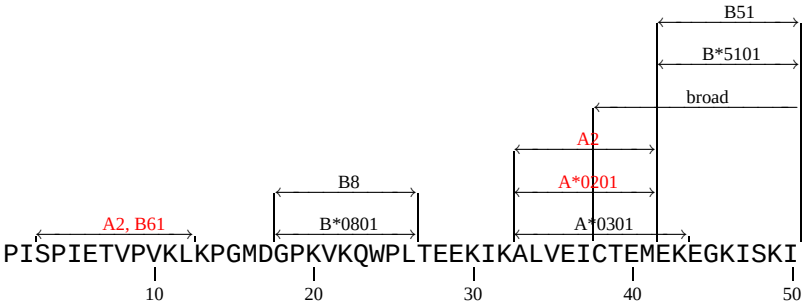
p2p7p1p6 CTL Map

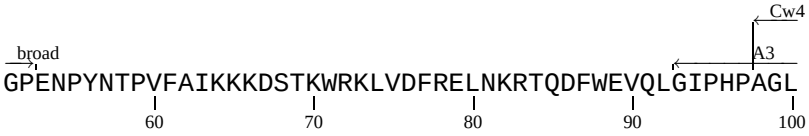


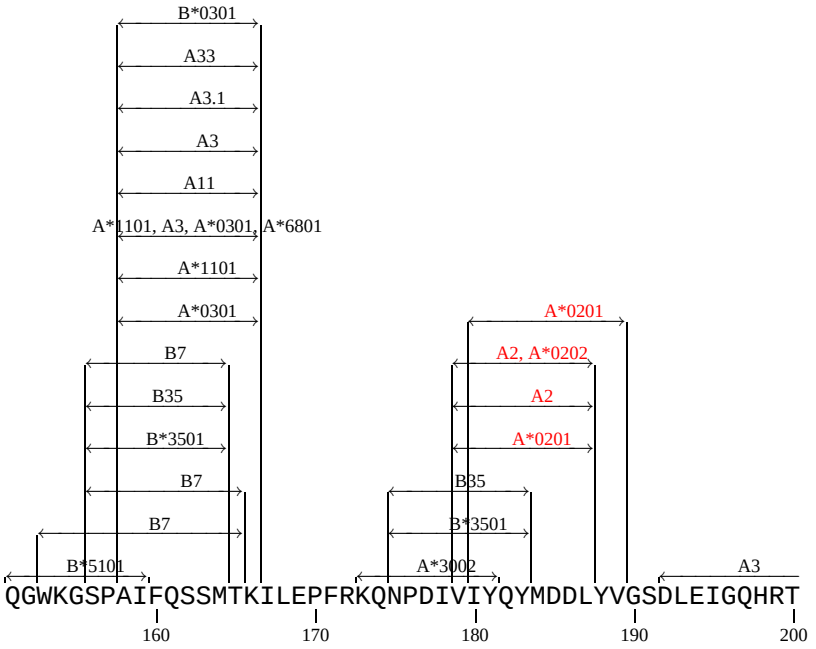
Protease CTL Map

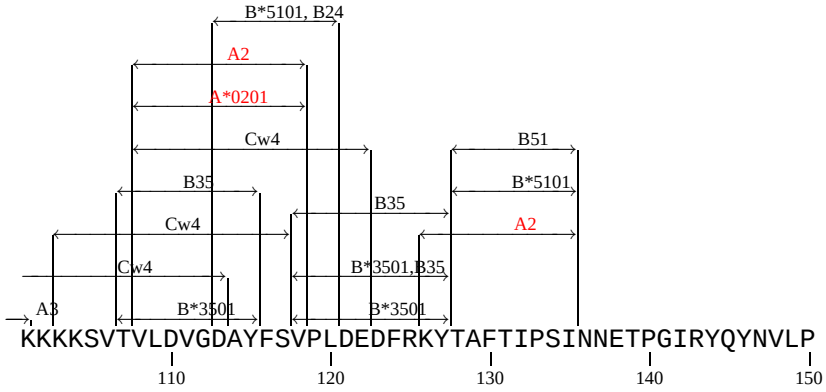


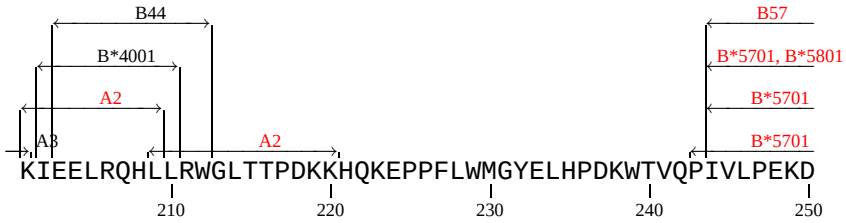
RT CTL Map

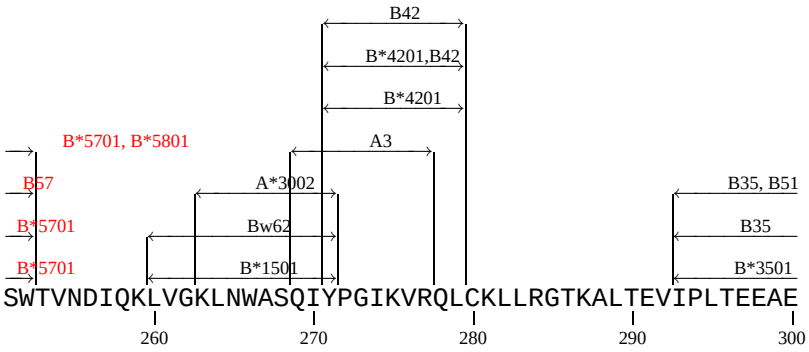

B51
B*5101
broad
A2
B8
A*0201
A2, B61
B*0801
A*0301
PISPIETVPVKLKPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKI
10
20
30
40
50

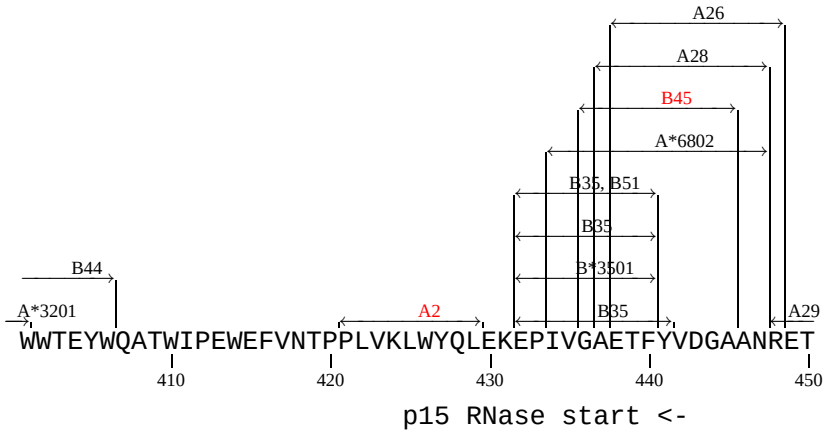

Cw4
broad
A3
GPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGL
60
70
80
90
100


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

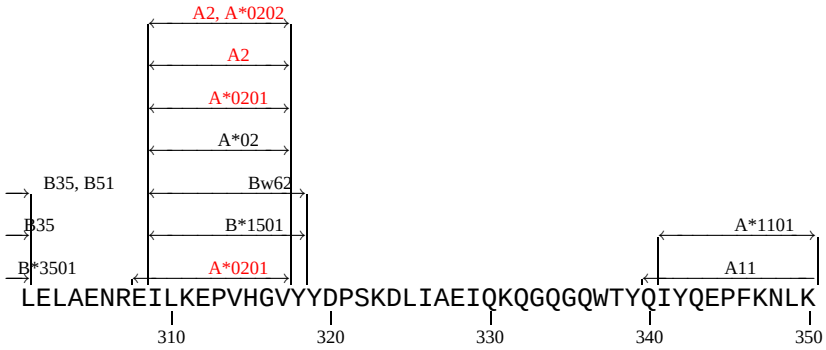

B*5101, B24
A2
A*0201
Cw4
B51
B35
B*5101
B35
Cw4
A2
Cw4
B*3501,B35
A3
B*3501
B*3501
KKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLP
110
120
130
140
150

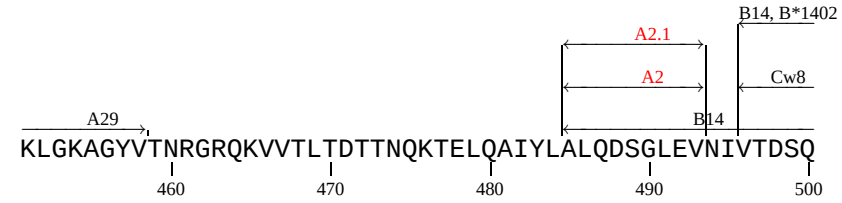

B44
B57
B*4001
B*5701, B*5801
A2
B*5701
A3
A2
B*5701
KIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWTVQPIVLPEKD
210
220
230
240
250

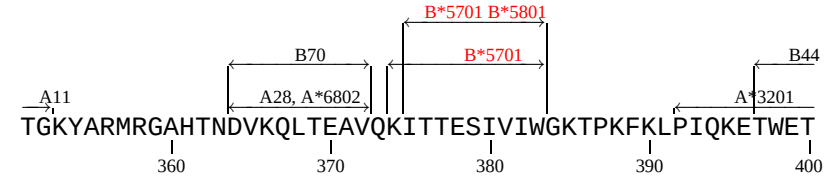


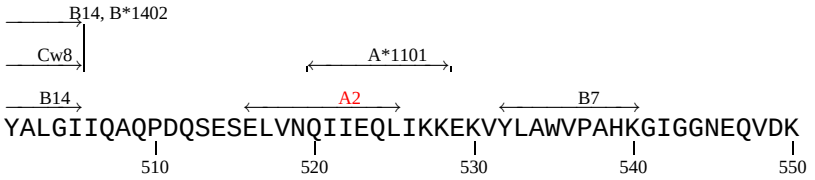


p15 RNase start <-





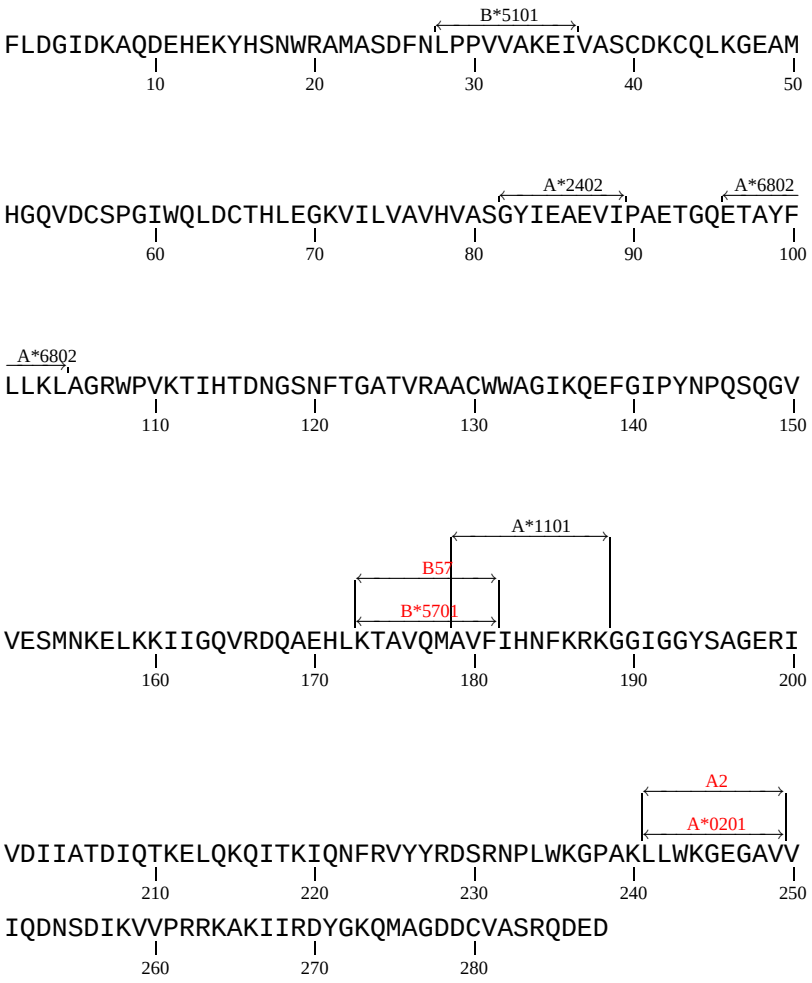




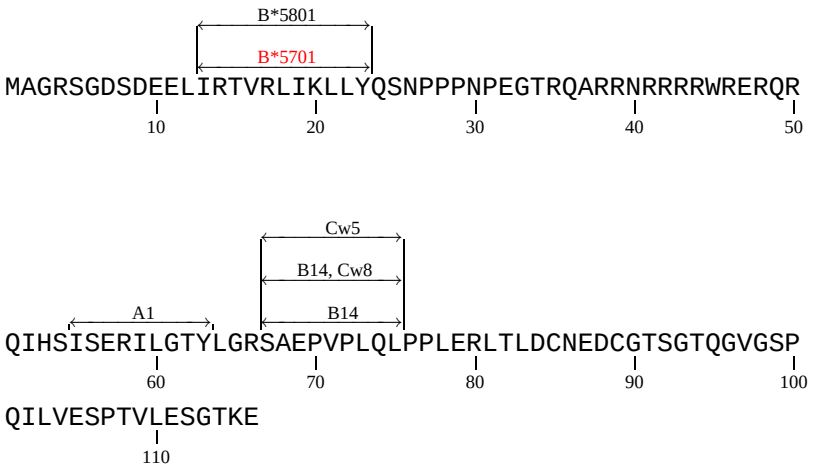
LVSAGIRKVL

-> p15 RNase end

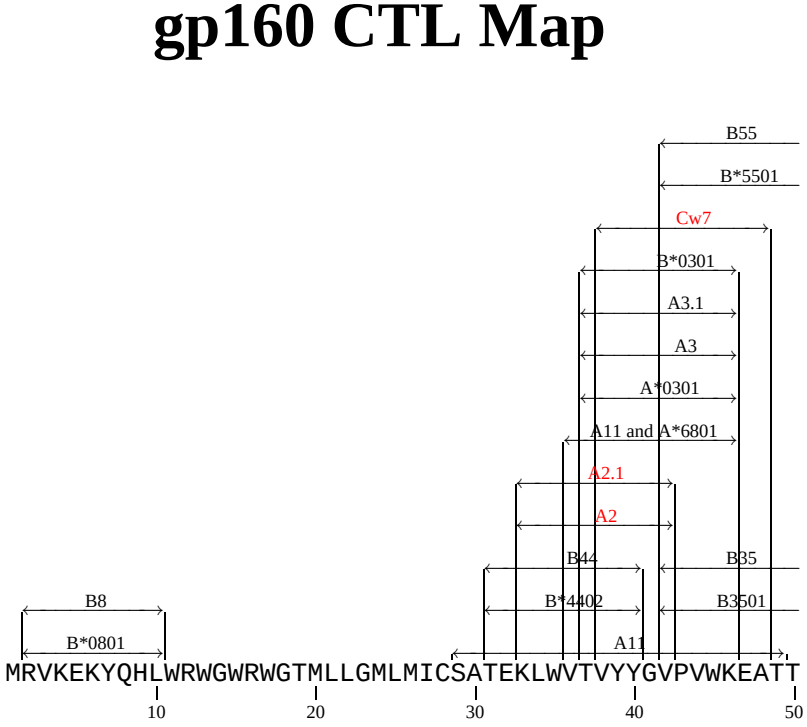
Integrase CTL Map



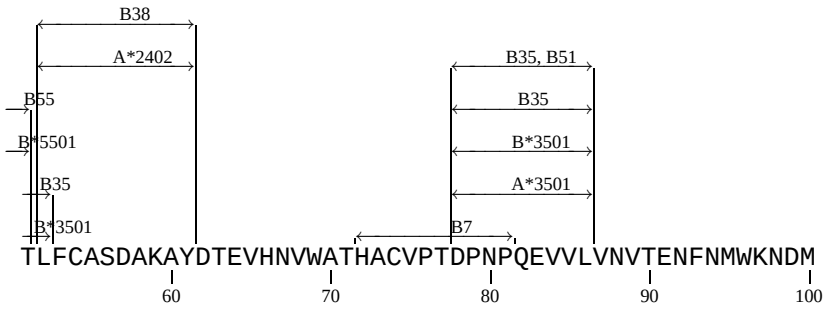
Rev CTL Map

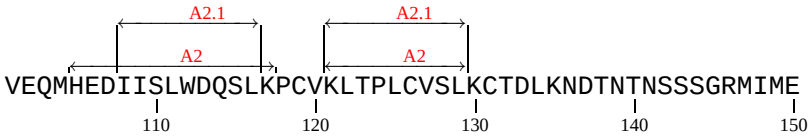


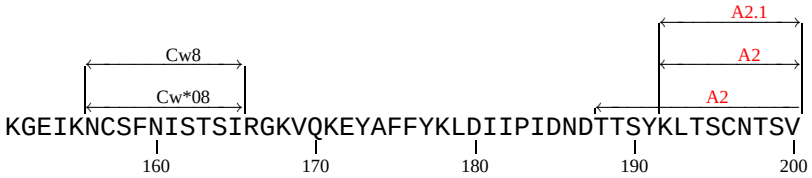
gp160 CTL Map

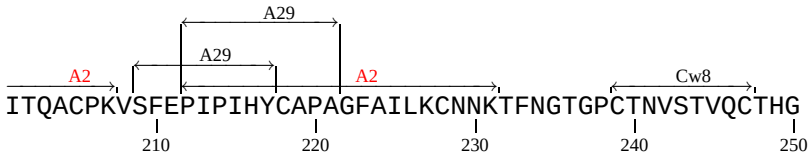


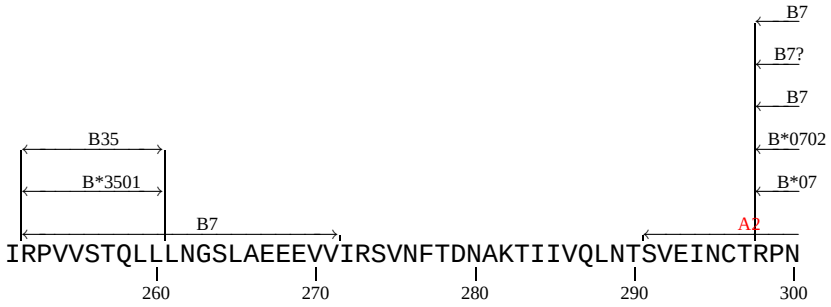
<- gp120 start

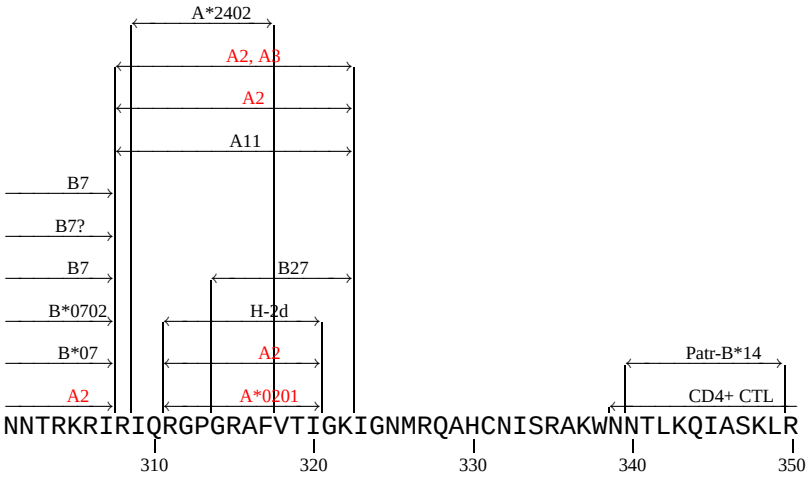


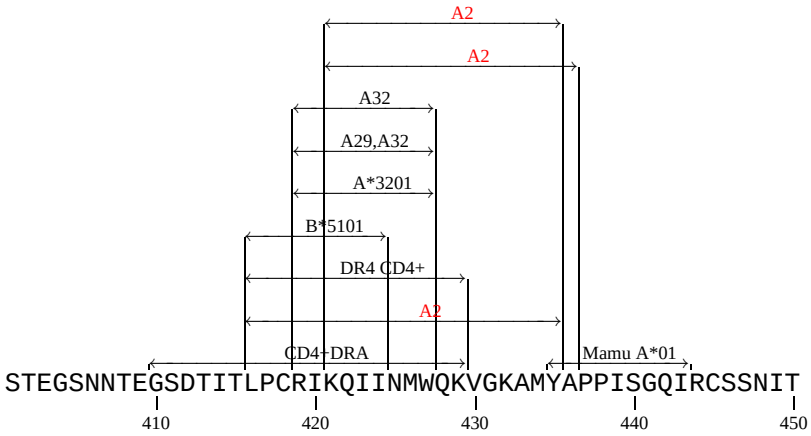


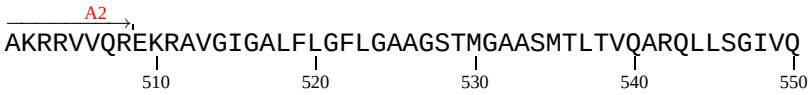




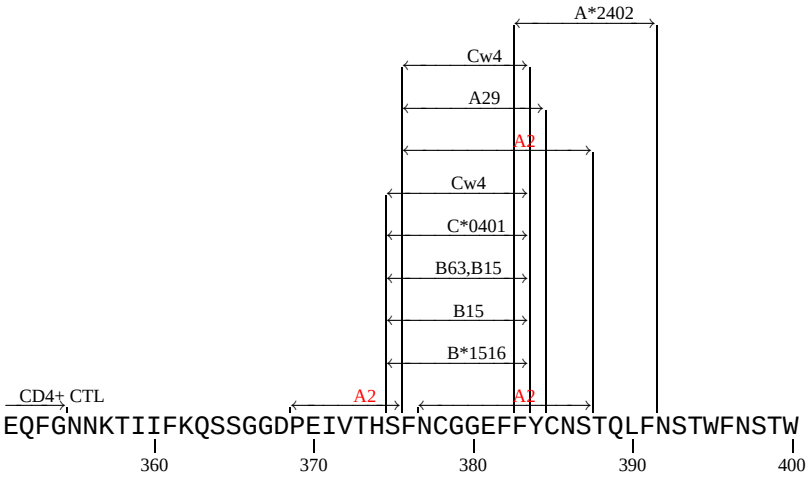


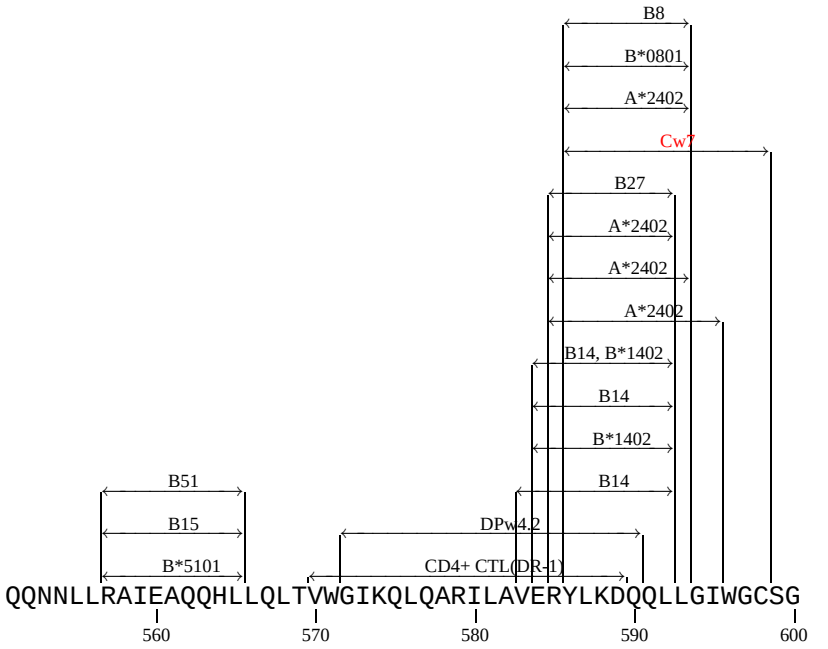


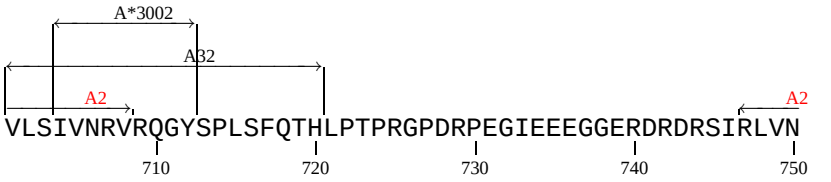


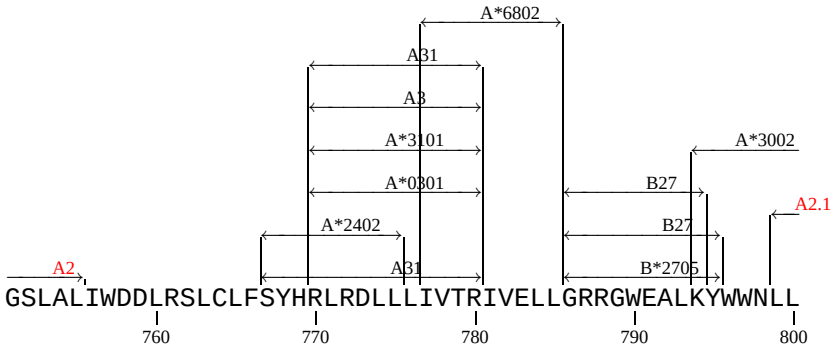


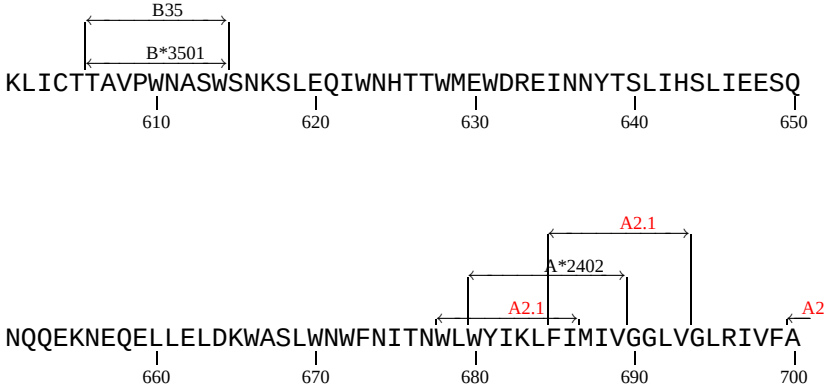
gp120 end <> gp41 start



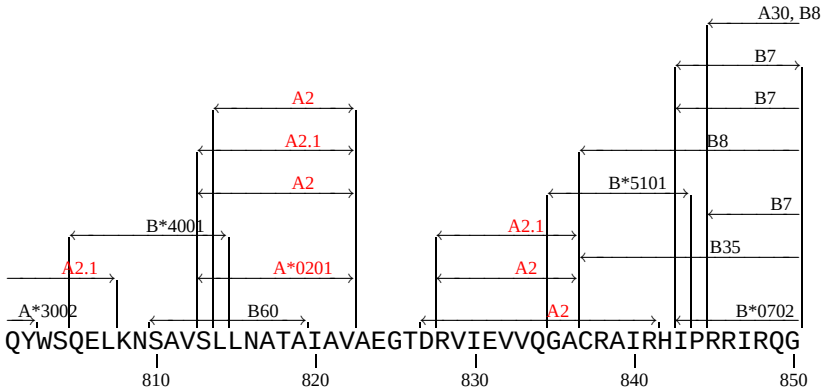

B8
B*0801
A*2402
Cw7
B27
A*2402
A*2402
A*2402
B14, B*1402
B14
B*1402
B14
B51
B15
B*5101
DPw4.2
CD4+ CTL(DR-1)
QQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGIWGCSG
560
570
580
590
600

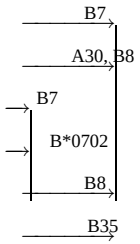

A*3002
A32
A2
A2
VLSIVNRVRQGYSPLSFQTHLPTPRGPDRPEGIEEEGGERDRDRSIRLVN
710
720
730
740
750


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

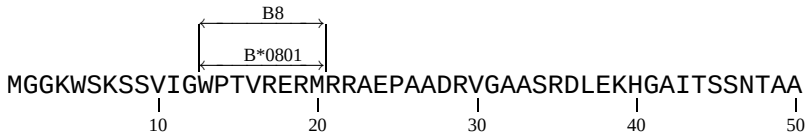

A30, B8
B7
B7
A2
A2.1
B8
A2
B*5101
B7
B*4001
A2.1
B35
A2.1
A*0201
A2
A*3002
B60
A2
B*0702
QYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQGACRAIRHIPRRIRQG
810
820
830
840
850

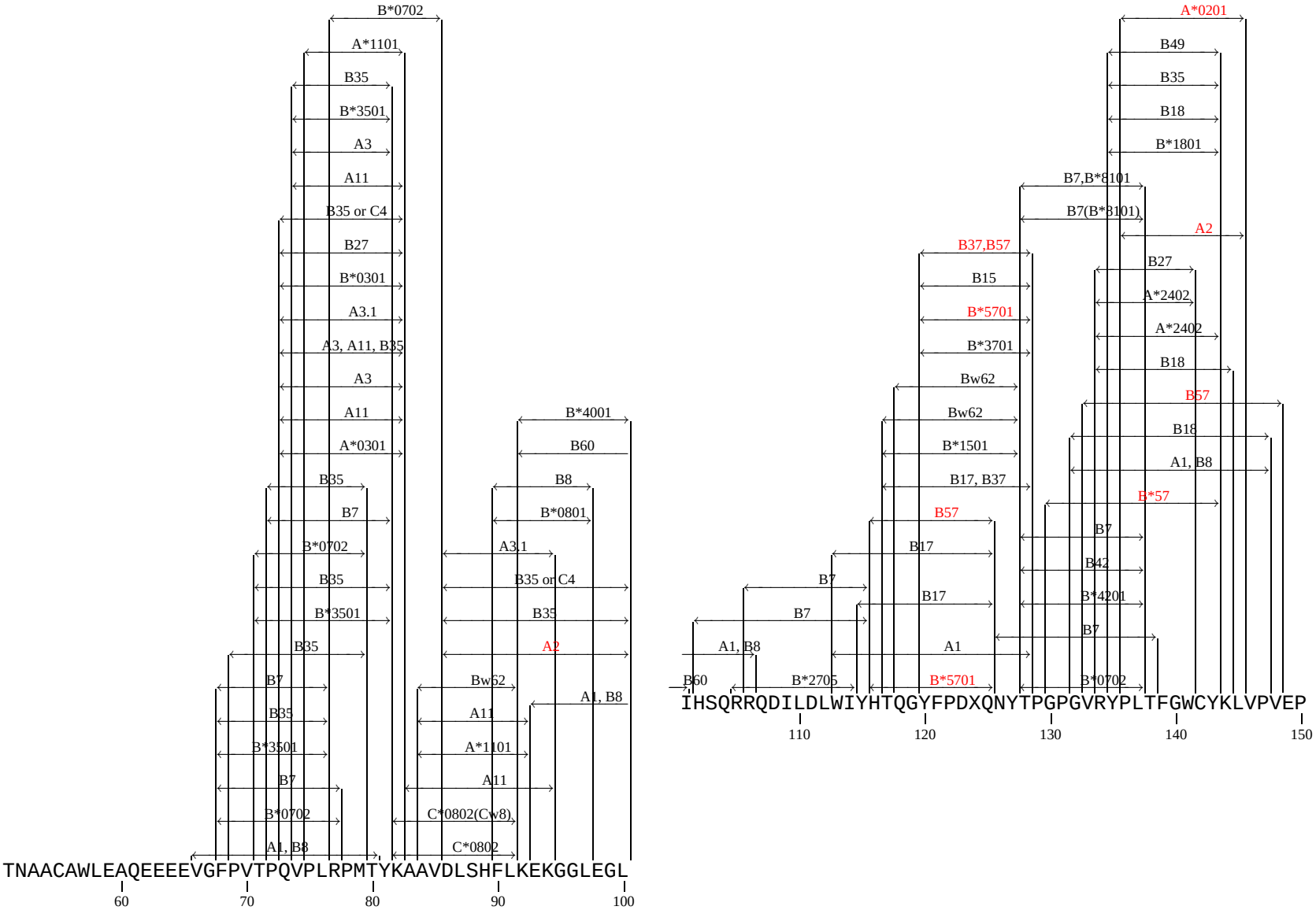


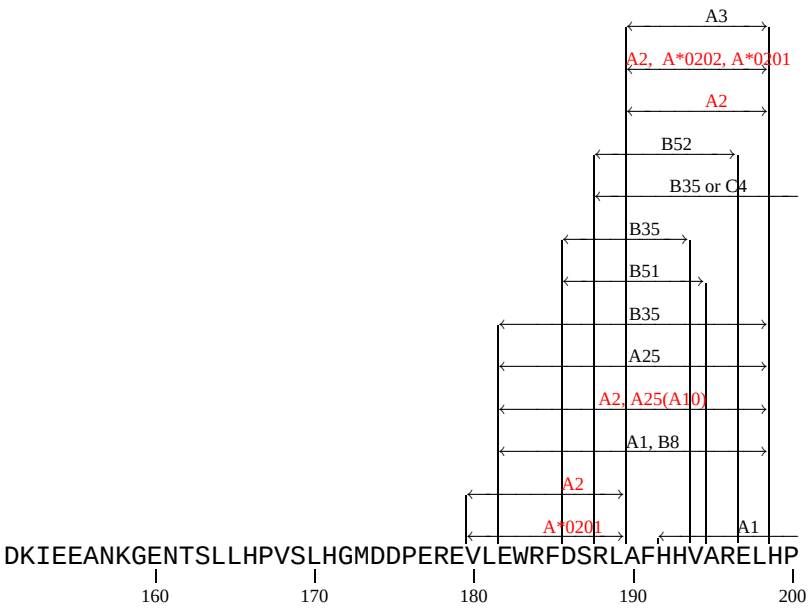
LERILL

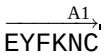
-> gp41 end

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
A1, B8
B*4001
B60
B8
B*0801
A3.1
B35 or C4
B35
A2
Bw62
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





[Achour (1996)] A. Achour, F. Bex, P. Hermans, A. Burny, & D. Zagury. Induction of anti-gp160 cytotoxic T cells cross-reacting with various V3 loop P18 peptides in human immunode£ciency virus type 1 envelope-immunized individuals. *J Virol* **70**:6741–6750, 1996. (Medline: 96386561).

[Alexander-Miller (1996)] M. A. Alexander-Miller, K. C. Parker, T. Tsukui, C. D. Pendleton, J. E. Coligan, & J. A. Berzofsky. Molecular analysis of presentation by HLA-A2.1 of a promiscuously binding V3 loop peptide from the HIV-1 Envelope protein to human cytotoxic T lymphocytes. *Int Immunol* **8**:641–649, 1996. (Medline: 96324787).

[Brander (1996)] C. Brander, G. Corradin, T. Hasler, & W. Pichler. Peptide immunization in humans: a combined CD8+/CD4+ T cell-targeted vaccine restimulates the memory CD4 T cell response but fails to induce cytotoxic T lymphocytes (CTL). *Clin Exp Immunol* **105**:18–25, 1996. (Medline: 96280772).

[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 (1995)] C. Brander, W. J. Pichler, & G. Corradin. Identi£cation of HIV-protein derived CTL epitopes for their potential use as synthetic vaccine. *Clin Exp Immunol* **101**:107–113, 1995. (Medline: 95347061).

[Brander & Walker(1996)] C. Brander & B. Walker. The HLA-class I restricted CTL response in HIV-1 Infection: Systematic identi£cation of optimal epitopes. *HIV Molecular Immunology Database* pages IV–50 to IV–60, 1996.

[Dadaglio (1991)] G. Dadaglio, A. Leroux, P. Langlade-Demoyen, E. M. Bahraoui, F. Traincard, R. Fisher, & F. Plata. Epitope recognition of conserved HIV envelope sequences by human cytotoxic T lymphocytes. *J Immunol* **147**:2302–2309, 1991. (Medline: 92013025) Notes: Using synthetic peptides, six conserved epitopes on gp120 Env were identi£ed, recognized by polyclonal human CTL in association with HLA-A2 class I. Conserved epitopes: RIQRGPGRAFVTIGK, IIIB; LWVTVYYGVPVWKEATTTLFCA; TTSYTLTSCNTSVITQACPK; SVEINCTRPNNNTRKSI; PEIVTHS; KNCGGEFFYCNS; LPCRIKQFINMWQEVGKAMY; VKIEPLGVAPTKAKRRVVQR. Control: gag, YKRWIILGLNKIVRMYSPT, HLA B27.

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

[Dupuis (1995)] M. Dupuis, S. K. Kundu, & T. C. Merigan. Characterization of HLA-A*0201-restricted cytotoxic T cell epitopes in conserved regions of the HIV type 1 gp160 protein. *J Immunol* **155**:2232–2239, 1995. (Medline: 95363191) Notes: Five HLA-A2 HIV-1 seropositive HIV-1 MN rec gp160 vaccinees had their CTL activity assessed using peptides known to bind with high af£nity to HLA-A*0201. Four of the patients had speci£c CTL activity for a minimum of at least three epitopes, thus the response appears heterogeneous. One of the four peptides was con£rmed to be HLA A2 restricted. Epitopes were highly conserved.

[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).

[Ferris (1999)] R. L. Ferris, C. Hall, N. V. Sipsas, J. T. Safrit, A. Trocha, R. A. Koup, R. P. Johnson, & R. F. Siliciano. Processing of HIV-1 envelope glycoprotein for class I-restricted recognition: dependence on TAP1/2 and mechanisms for cytosolic localization. *J Immunol* **162**:1324–32, 1999. (Medline: 99138809).

[Garboczi (1992)] D. N. Garboczi, D. T. Hung, & D. C. Wiley. HLA-A2-peptide complexes: refolding and crystallization of molecules expressed in Escherichia coli and complexed with single antigenic peptides. *Proc Natl Acad Sci USA* **89**:3429–3433, 1992. (Medline: 92228799).

[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.

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