



gp41 Epitope 1

CONSENSUS-B	RAIEAQQhI	CONSENSUS-C	CONSENSUS-O
Epitope 1	RAIEAQQhI (B51)	C.BI.BU910611	O.CM.ANT70C
CONSENSUS-A	RAIEAQQhI	C.BI.BU910717	O.CM.CM4974
A.KE.K89	-----	C.BI.BU910812	O.CM.MVP5180
A.KE.Q23CXCCG	-----	C.BR.92BR025	O.GA.VI686
A.RW.KIG93	-----	C.BR.BR911513	O.GQ.341HA
A.RW.SF1703	-----	C.BW.BW96BW0502	O.GQ.655HA
A.SE.SOSE7253	-----	C.DJ.DJ259A	O.GQ.HIVU82990
A.SE.TZSE8538	-----	C.DJ.DJ373A	O.GQ.HIVU82991
A.SE.UGSE6594	-----	C.ET.ETH2220	-----
A.SE.UGSE8891	-----	C.IN.11246	CONSENSUS-AE
A.UA.AF082486	-----	C.IN.21068	AE.CF.90CR402
A.UG.92UG037	-----	C.IN.301904	AE.TH.KH03
A.UG.U455	-----	C.IN.301904	AE.TH.KH08
A.ZR.MA246	-----	C.SN.SR364A	AE.TH.TH920149
A.ZR.MC108	-----QV	C.SO.SM145A	AE.TH.93TH253
AG.DJ.DJ263	-----	C.UG.UG268A2	AE.TH.A01021
AG.DJ.DJ264	-----	CONSENSUS-D	AE.TH.CM240
AG.NG.IMG	K-----	D.SN.SR365A2	AE.TH.E11429.A31
		D.TZ.87TZ4632	AE.TH.TH921110
		D.UG.92UG024D	CONSENSUS-CPZ
		D.UG.94UG1141	CPZGAB
		D.UG.C971412	CPZANT
		D.UG.UG266A2	-----
		D.UG.WH015474	-----
		D.ZR.84ZR085	-----
		D.ZR.EI1	-----
		D.ZR.TY1	-----
		D.ZR.NDK	-----
		D.ZR.Z226	-----
		CONSENSUS-F	-----
		F.BR.93BR0201	-----
		F.BR.B2126A	-----
		F.BR.B2163A	-----
		F.FI.FIN6393	-----
		CONSENSUS-G	-----
		G.BE.DRCBL	-----
		G.FI.HH8793	-----
		G.GA.LBV217	-----
		G.SE.SE6165	-----
		CONSENSUS-H	-----
		H.BE.VI991	-----
		H.BE.VI997	-----
		H.CF.90CF056	-----
		CONSENSUS-I	-----
		I.BE.VI991	-----
		I.BE.VI997	-----
		I.CF.90CF056	-----
		CONSENSUS-J	-----
		J.SE.SE91733	-----
		J.SE.SR92809	-----
		CONSENSUS-K	-----
		K.CM.YBF30	-----

gp41 Epitope 3-4



CONSENSUS-B Epitope #	VERYLKDDQQL 3 4	HLA (B14) (B14)	CONSENSUS-C	I-----	CONSENSUS-O	L-TLION----
CONSENSUS-A	A.KE.K89	-----R----	C.BI.BU910611	I-----	O.CM.ANT70C	L-TL-QN----
A.KE.Q23CXCCG	-----R----	C.BI.BU910717	I-----	O.CM.CM4974	O.CM.ANT70C	L-TL-QN----
A.RW.KI693	-----R----	C.BI.BU910812	I-----	O.CM.MVP5180	O.CM.CM4974	L-TLION--R
A.RW.SF1703	-----R----	C.BR.92BR025	I-----R--	O.GA.VI686	O.CM.MVP5180	L-TLION--R
A.SE.SOSE7253	-----R----	C.BR.BR911513	I-----	O.GQ.341HA	O.GA.VI686	L-TLION----
A.SE.TZSE8538	-----R----	C.BW.BW96BW0502	I-----	O.GQ.655HA	O.GQ.341HA	L-TLION----
A.SE.UGSE6594	-----R----	C.DJ.DJ259A	I-----	O.GQ.HIVU82990	O.GQ.655HA	L-TLION----
A.SE.UGSE8891	-----R----	C.DJ.DJ373A	I-----	O.GQ.HIVU82990	O.GQ.HIVU82990	L-TLION----
A.UA.AF082486	-----R----	C.DJ.DJ373A	I-----	O.GQ.HIVU82991	O.GQ.HIVU82991	L-TLION----
A.UG.92UG037	-----R----	C.ET.FTH2220	I-H-R----	CONSENSUS-AE	CONSENSUS-AE	-----KF
A.UG.U455	-----Q----	C.IN.11246	I-----	AE.CF.90CR402	AE.CF.90CR402	-----KF
A.ZR.MA246	-----R----	C.IN.11246	I-----	AE.TH.KH03	AE.TH.KH03	-----KF
A.ZR.MC108	-----R----	C.IN.21068	I-----	AE.TH.KH08	AE.TH.KH08	-----RF
AG.DJ.DJ263	L-S--R----	C.IN.301904	I-----	AE.TH.TH920149	AE.TH.TH920149	-----KF
AG.DJ.DJ264	L--R----	C.SN.SE364A	I-----E--	AE.TH.93TH253	AE.TH.93TH253	-----KF
AG.NG.IBNG	L--R----	C.SO.SM145A	I-----Q--	AE.TH.A01021	AE.TH.A01021	-----KF
AGI.GR.97PVCH	L-S-----	C.UG.UG268A2	I-----	AE.TH.CM240	AE.TH.CM240	-----KF
AGI.GR.97PVMY	L-S--R----	CONSENSUS-D	---?-----	AE.TH.E11429.A31	AE.TH.E11429.A31	-----KF
CONSENSUS-B	-----R----	D.SN.SE365A2	---R----	CONSENSUS-CPZ	CONSENSUS-CPZ	---?--?----?
B.AU.MBC18	-----R----	D.TZ.87TZ4632	---S--R----	CPZGAB	CPZGAB	-----Q--I
B.BE.SIM184	-----R----	D.UG.92UG024D	---S-----	CPZANT	CPZANT	---K--R----
B.CN.RI42	-----R----	D.UG.94UG1141	---S-----			
B.DE.D31	-----R----	D.UG.C971412	---S-----			
B.DE.HAN	-----R----	D.UG.UG266A2	---S-----			
B.FR.HXB2	-----R----	D.UG.WHO15474	---S-----			
B.FR.LAI	-----R----	D.ZR.84ZR085	---Q-----			
B.FR.PIH384	-----Q--RF	D.ZR.ELI	---S-----			
B.GA.OYI	-----R----	D.ZR.TY1	---S-----			
B.GB.CAM1	-----R----	D.ZR.NDK	---R----			
B.JP.ETR	-----R----	D.ZR.Z226	---R----			
B.NL.ACH320A	-----R----	CONSENSUS-E	---?-----			
B.SP.89SP061	-----R----	F.BR.93BR0201	---?-----			
B.TH.TH936705	-----R----	F.BR.B2126A	---Q-----			
B.TT.QZ4589	-----R----	F.BR.B2163A	---Q-----			
B.US.QZ4589	-----R----	F.FI.FIN6393	---R----			
B.US.JRCSP	-----G----	CONSENSUS-F	---R----			
B.US.JRFL	-----G----	G.BE.DRCBL	---R----			
B.US.MN	-----R----	G.FI.HH8793	---R----			
B.US.RF	-----R----	G.GA.LBV217	---Q-----			
B.US.SF2	-----R----	G.SE.SE6165	---R----			
B.US.WEAV160	-----R----	CONSENSUS-G	---R----			
B.ZR.MB314	-----R----	H.BE.VI991	---R----			
		H.BE.VI997	---R----			
		H.CF.90CF056	---R----			
		CONSENSUS-H	---R----			
		J.SE.SE91733	---R----			
		J.SE.SE92809	---R----			
		N.CM.YBF30	I---R--I			

gp41 Epitope 5-10

CONSENSUS-B		RYLKDQGLIG	HLA	CONSENSUS-C		CONSENSUS-O	
Epitope #							
5	RYLRDQQL	(A*2402)	C.BI.BU910611	-----	O.CM.ANT70C	TLIQN-----n	
6	RYLRDQQL	(A*2402)	C.BI.BU910717	-----	O.CM.CM4974	TLIQN--R-N	
7	RYLRDQQLGI	(A*2402)	C.BI.BU910812	-----	O.CM.MVP5180	TLIQN--R-N	
8	RYLRDQQL	(B27)	C.BR.92BR025	-----	O.GA.VI686	TLIQN-----N	
9	RYLRDQQL	(B8)	C.BR.BR911513	-----	O.GQ.341HA	TLIQN-----N	
10	RYLRDQQL	(A24)	C.BW.BW96BW0502	-----	O.GQ.655HA	TLIQN-----N	
CONSENSUS-A			C.DJ.DJ373A	-----	O.GQ.HIVU82990	TLIQN-----N	
	A.KE.K89	-----	C.ET.FTH2220	-H-R-----	O.GQ.HIVU82991	TLIQN-----N	
	A.KE.Q23CXCCG	-----	C.IN.11246	-----	CONSENSUS-AE		
	A.RW.KIG93	-----	C.IN.21066	-----	AE.CF.90CR402	-----	
	A.RW.SF1703	-----	C.IN.301904	-----	AE.TH.KH03	-----	
	A.SE.SOSE7253	-----	C.SN.SR364A	-----	AE.TH.KH08	-----	
	A.SE.TZSE8538	-----	C.SO.SM145A	-----	AE.TH.TH920149	-----	
	A.SE.UGSE8891	-----	C.UG.UG268A2	-----	AE.TH.93TH253	-----	
	A.UA.AF082486	-----	CONSENSUS-D		AE.TH.A01021	-----	
	A.UG.92UG037	-----	D.SN.SR365A2	?-----	AE.TH.CM240	-----	
	A.UG.U455	-----	D.TZ.87TZ4632	-R-----	AE.TH.E11429.A31	-----	
	A.ZR.MA246	-----	D.UG.92UG024D	-R-----	AE.TH.TH921110	-----	
	A.ZR.MC108	-----	D.UG.94UG1141	-R-----	CONSENSUS-CPZ		
			D.UG.C971412	-R-----	CPZGAB	CPZANT	
			D.UG.UG266A2	-Q-----	CONSENSUS-CPZ		
			D.UG.WHO15474	-----	CPZGAB	CPZANT	
			D.ZR.84ZR085	-----	CONSENSUS-CPZ		
			D.ZR.ELI	-----	CPZGAB	CPZANT	
AG.DJ.DJ263	S-R-----		D.ZR.ELI	-----	CPZGAB	CPZANT	
AG.DJ.DJ264	-R-----		D.ZR.TY1	S-----	CPZGAB	CPZANT	
AG.NG.IBNG	-R-----		D.ZR.NDK	-R-----	CPZANT	CPZANT	
			D.ZR.Z226	-----			
AGI.GR.97PVCH	S-----		CONSENSUS-F				
AGI.GR.97PVMY	S-R-----		F.BR.93BR0201	-----			
CONSENSUS-B			F.BR.B2126A	-Q-----			
B.AU.MBC18	-R-----		F.BR.B2163A	-Q-----			
B.BE.S1M184	-----		F.FI.FIN6393	-----			
B.CN.R1A2	-----		CONSENSUS-G				
B.DE.D31	-R-----		G.BE.DRCBL	-----			
B.DE.HAN	-R-----		G.FI.HH8793	-R-----			
B.FR.HXB2	-----		G.GA.LBV217	-Q-----			
B.FR.LAI	-----		G.SE.SE6165	-----			
B.FR.PIH384	-Q-RF-----		CONSENSUS-H				
B.GA.OYT	-----		H.BE.VI991	-----			
B.GB.CAM1	-----		H.BE.VI997	-----			
B.JP.FTR	-----		H.CF.90CF056	-R-----			
B.NL.ACH320A	-M-----		CONSENSUS-I				
B.SP.89SP061	-----		J.SE.SE91733	-----			
B.TH.TH936705	-R-----		J.SE.SR92809	-----			
B.TT.Q24589	-----		CONSENSUS-J				
B.TT.TH936705	-R-----		J.SE.SR91733	-----			
B.US.JRCGF	-M-----		J.SE.SR92809	-----			
B.US.JRFL	-G-----		N.CM.YBF30	-----			
B.US.MN	-----			---R---I-S			
B.US.RF	-R-----						
B.US.SF2	-R-----						
B.US.WEAU160	-----						
B.ZR.MB314	-----						

gp41 Epitope 13

CONSENSUS-B Epitope 13 CONSENSUS-A	WTkIiFlMIv WYKIFIFMI (A*2402)		
A.KE.K89	-----I-		
A.KE.Q23CXCCG	-----I-		
A.RW.KIG93	-----R-		
A.RW.SF1703	-----R-		
A.SE.SOSE7253	-----R-		
A.SE.TZSE8538	-----R-		
A.SE.UGSE6594	-----R-		
A.SE.UGSE8891	-----I-		
A.UA.AF082486	-----I-		
A.UG.92UG037	-----RL-VI-		
A.UG.U455	-----RL-VI-		
A.ZR.MA246	-----RL-VI-		
A.ZR.MC108	-----RL-VI-		
AG.DJ.DJ263	-----		
AG.DJ.DJ264	-----		
AG.NG.IMNG	-----R-		
AGI.GR.97PVCVH	-----		
AGI.GR.97PVMVY	-----		
CONSENSUS-B	-----		
B.AU.MBC18	-----		
B.BE.SIMT84	-----		
B.CN.RL42	-----		
B.DE.D31	-----		
B.DE.HAN	-----L-		
B.FR.HXB2	-----		
B.FR.LAI	-----RL-		
B.FR.PIH384	-----RL-		
B.GA.OYI	-----I-		
B.GB.CAM1	-----I-		
B.JP.ETR	-----		
B.NL.ACH320A	-----		
B.SP.89SP061	-----		
B.TH.TH936705	-----		
B.TT.QZ4589	-----		
B.US.JRC5F	-----		
B.US.JRFL	-----		
B.US.MN	-----R-		
B.US.RF	-----		
B.US.SF2	-----		
B.US.WEAV160	-----		
B.ZR.MB314	-----		
CONSENSUS-C			
C.BI.BU910611	-----		
C.BI.BU910717	-----		
C.BI.BU910812	-----R-		
C.BR.92BR025	-----K-		
C.BR.BR911513	-----		
C.BW.BW96BW0502	-----		
C.DJ.DJ259A	-----		
C.DJ.DJ373A	-----		
C.ET.ETH2220	-----		
C.IN.11246	-----I-		
C.IN.21068	-----I-		
C.IN.301904	-----		
C.SN.SR364A	-----I-		
C.SO.SM145A	-----I-		
C.UG.UG268A2	-----		
CONSENSUS-D			
D.SN.SR365A2	-----V-		
D.TZ.87TZ4632	-----		
D.UG.92UG024D	-----RL-I-		
D.UG.94UG1141	-----		
D.UG.C971412	-----		
D.UG.UG266A2	-----		
D.UG.WH015474	-----		
D.ZR.84ZR085	-----		
D.ZR.ELI	-----I-		
D.ZR.TY1	-----L-		
D.ZR.NDK	-----		
D.ZR.Z226	-----		
CONSENSUS-F			
F.BR.93BR0201	-----		
F.BR.B2126A	-----		
F.BR.B2163A	-----		
F.FI.FIN6393	-----		
CONSENSUS-G			
G.BE.DRCBL	-----R-V-		
G.FI.HH8793	-----		
G.GA.LBV217	-----		
G.SE.SE6165	-----		
CONSENSUS-H			
H.BE.VI991	-----R-		
H.BE.VI997	-----I-		
H.CF.90CF056	-----		
CONSENSUS-J			
J.SE.SE91733	-----I-		
J.SE.SR92809	-----I-		
N.CM.YBF30	-----A-		
CONSENSUS-O			
O.CM.ANT70C	-----A-I-		
O.CM.CM4974	-----A-I-		
O.CM.MVP5180	-----A-I-		
O.GA.VI686	-----MA-I-		
O.GQ.341HA	-----A-I-		
O.GQ.655HA	-----A-I-		
O.GQ.HIVU82990	-----A-I-		
O.GQ.HIVU82991	-----A-I-		
CONSENSUS-AE			
AE.CF.90CF402	-----I-		
AE.TH.KH03	-----		
AE.TH.KH08	-----		
AE.TH.TH920149	-----		
AE.TH.93TH253	-----		
AE.TH.A01021	-----R-I-		
AE.TH.CM240	-----		
AE.TH.E11429.A31	-----		
AE.TH.TH921110	-----A		
CONSENSUS-CPZ			
CPZGAB	-----?--?		
CPZANT	-----L-A-		

CTL

gp41 Epitope 14



CONSENSUS -B
 Epitope 14
CONSENSUS -A
 A. KE. K89
 A. KE. Q23CXCCG
 A. RW. KI693
 A. RW. SF1703
 A. SE. SOSEF7253
 A. SE. TZSE8538
 A. SE. UGSE6594
 A. SE. UGSE8891
 A. VA. AF082486
 A. UG. 92UG037
 A. UG. U455
 A. ZR. MA246
 A. ZR. MC108
 AG. DJ. DJ263
 AG. DJ. DJ264
 AG. NG. IENG
 AGI. GR. 97PVCVH
 AGI. GR. 97PVMY
CONSENSUS -B
 B. AU. MBC18
 B. BE. SIMT84
 B. CN. RL42
 B. DE. D31
 B. DE. HAN
 B. FR. HXB2
 B. FR. LAI
 B. FR. PIH384
 B. GA. OYI
 B. GB. CAM1
 B. JP. ETR
 B. NL. ACH320A
 B. SP. 89SP061
 B. TH. TH936705
 B. TT. Q24589
 B. US. JRC5F
 B. US. JRF1
 B. US. MN
 B. US. RF
 B. US. SF2
 B. US. WEAV160
 B. ZR. MB314
VLSIVNVRQGGVSP1SFQT
VLSIVNVRQGGVSP1SFQT
 (A32)

CONSENSUS -C
 C. BI. BU910611
 C. BI. BU910717
 C. BI. BU910812
 C. BR. 92BR025
 C. BR. BR911513
 C. BW. BW96BW0502
 C. DJ. DJ259A
 C. DJ. DJ373A
 C. ET. ETT2220
 C. IN. 11246
 C. IN. 11068
 C. IN. 301904
 C. SN. SE364A
 C. SO. SML45A
 C. UG. UG268A2
CONSENSUS -D
 D. SN. SE365A2
 D. TZ. 87TZ4632
 D. UG. 92UG024D
 D. UG. 94UG1141
 D. UG. C971412
 D. UG. UG266A2
 D. UG. WHO15474
 D. ZR. 84ZR085
 D. ZR. ELI
 D. ZR. TY1
 D. ZR. NDK
 D. ZR. Z226
CONSENSUS -E
 E. BR. 93BR0201
 E. BR. B2126A
 E. BR. B2163A
 E. FI. FIN6393
CONSENSUS -G
 G. BE. DRGBL
 G. FI. HH8793
 G. GA. LBV217
 G. SE. SE6165
CONSENSUS -H
 H. BE. VI991
 H. BE. VI997
 H. CF. 90CF056
CONSENSUS -I
 I. SE. SE91733
 I. SE. SE92809
 I. CM. YBF30
CONSENSUS -J
 J. SE. SE91733
 J. SE. SE92809
CONSENSUS -K
 K. SN. SE365A2
 K. TZ. 87TZ4632
 K. UG. 92UG024D
 K. UG. 94UG1141
 K. UG. C971412
 K. UG. UG266A2
 K. UG. WHO15474
 K. ZR. 84ZR085
 K. ZR. ELI
 K. ZR. TY1
 K. ZR. NDK
 K. ZR. Z226
CONSENSUS -L
 L. SN. SE365A2
 L. TZ. 87TZ4632
 L. UG. 92UG024D
 L. UG. 94UG1141
 L. UG. C971412
 L. UG. UG266A2
 L. UG. WHO15474
 L. ZR. 84ZR085
 L. ZR. ELI
 L. ZR. TY1
 L. ZR. NDK
 L. ZR. Z226
CONSENSUS -M
 M. BE. VI991
 M. BE. VI997
 M. CF. 90CF056
CONSENSUS -N
 N. SE. SE91733
 N. SE. SE92809
 N. CM. YBF30
CONSENSUS -O
 O. CM. ANT70C
 O. CM. CM4974
 O. CM. MVP5180
 O. GA. VI686
 O. GQ. 341HA
 O. GQ. 655HA
 O. GQ. HIVU82990
 O. GQ. HIVU82991
CONSENSUS -P
 P. CE. 90CE402
 P. TH. KH03
 P. TH. KH08
 P. TH. TH920149
 P. TH. 93TH253
 P. TH. A01021
 P. TH. CM240
 P. TH. E11429. A31
 P. TH. TH921110
CONSENSUS -Q
 Q. GQ. 341HA
 Q. GQ. 655HA
 Q. GQ. HIVU82990
 Q. GQ. HIVU82991
CONSENSUS -R
 R. BE. VI991
 R. BE. VI997
 R. CF. 90CF056
CONSENSUS -S
 S. SE. SE91733
 S. SE. SE92809
CONSENSUS -T
 T. BE. VI991
 T. BE. VI997
 T. CF. 90CF056
CONSENSUS -U
 U. SE. SE91733
 U. SE. SE92809
CONSENSUS -V
 V. BE. VI991
 V. BE. VI997
 V. CF. 90CF056
CONSENSUS -W
 W. SE. SE91733
 W. SE. SE92809
CONSENSUS -X
 X. BE. VI991
 X. BE. VI997
 X. CF. 90CF056
CONSENSUS -Y
 Y. SE. SE91733
 Y. SE. SE92809
CONSENSUS -Z
 Z. BE. VI991
 Z. BE. VI997
 Z. CF. 90CF056

-I-L-----L

-F-----L

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gp41 Epitope 15

CONSENSUS-B Epitope 15 CONSENSUS-A	rlv ^g fla1 RLVNGSIAL (A2)	CONSENSUS-C	CONSENSUS-D	CONSENSUS-E	CONSENSUS-F	CONSENSUS-G	CONSENSUS-H	CONSENSUS-I	CONSENSUS-J	CONSENSUS-K	CONSENSUS-L	CONSENSUS-M	CONSENSUS-N	CONSENSUS-O	CONSENSUS-P	CONSENSUS-Q	CONSENSUS-R	CONSENSUS-S	CONSENSUS-T	CONSENSUS-U	CONSENSUS-V	CONSENSUS-W	CONSENSUS-X	CONSENSUS-Y	CONSENSUS-Z
A.KE.K89	---	C.BI.BU910611	D.SN.SE365A2	---	F.BR.93BR0201	G.BE.DRCBL	H.BE.VI991	J.SE.SE91733	N.CM.YBF30	---	---	---	---	O.CM.ANT70C	PSPQ---	---	---	---	---	---	---	---	---	---	---
A.KE.Q23CXCCG	---	C.BI.BU910717	D.TZ.87TZ4632	---	F.BR.B2126A	G.FI.HH8793	H.BE.VI997	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.CM.CM4974	PWPQ---	---	---	---	---	---	---	---	---	---	---
A.RW.KI693	---	C.BI.BU910812	D.UG.92UG024D	---	F.BR.B2163A	G.GA.LBV217	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.CM.MVP5180	A-PP---	---	---	---	---	---	---	---	---	---	---
A.RW.SF1703	---	C.BR.92BR025	D.UG.C971412	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GA.VI686	PSPQ---	---	---	---	---	---	---	---	---	---	---
A.SE.SOSE7253	---	C.BR.BR911513	D.UG.UG266A2	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.341HA	TSLQ---	---	---	---	---	---	---	---	---	---	---
A.SE.TZSE8538	---	C.BW.BW96BW0502	D.UG.WHO15474	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.655HA	TSLQ---	---	---	---	---	---	---	---	---	---	---
A.UA.AF082486	---	C.DJ.DJ259A	D.ZR.WHO15474	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.HIVU82990	P-OQ---	---	---	---	---	---	---	---	---	---	---
A.UG.92UG037	---	C.DJ.DJ373A	D.ZR.84ZR085	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.HIVU82991	TSLQ---	---	---	---	---	---	---	---	---	---	---
A.UG.U455	---	C.ET.ETH2220	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.HIVU82991	TSLQ---	---	---	---	---	---	---	---	---	---	---
A.ZR.MA246	---	C.IN.11246	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.HIVU82991	TSLQ---	---	---	---	---	---	---	---	---	---	---
A.ZR.MC108	---	C.IN.21068	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.HIVU82991	TSLQ---	---	---	---	---	---	---	---	---	---	---
AG.DJ.DJ263	---	C.IN.301904	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.HIVU82991	TSLQ---	---	---	---	---	---	---	---	---	---	---
AG.DJ.DJ264	---	C.SN.SR364A	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.HIVU82991	TSLQ---	---	---	---	---	---	---	---	---	---	---
AG.NG.IMG	---	C.SO.SM145A	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.HIVU82991	TSLQ---	---	---	---	---	---	---	---	---	---	---
AGI.GR.97PVC	---	C.UG.UG268A2	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	O.GQ.HIVU82991	TSLQ---	---	---	---	---	---	---	---	---	---	---
AGT.GR.97PVMY	---	CONSENSUS-D	D.SN.SE365A2	---	F.BR.93BR0201	G.BE.DRCBL	H.BE.VI991	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-E	PSPQ---	---	---	---	---	---	---	---	---	---	---
CONSENSUS-B	---	D.TZ.87TZ4632	D.TZ.87TZ4632	---	F.BR.B2126A	G.FI.HH8793	H.BE.VI997	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-F	PWPQ---	---	---	---	---	---	---	---	---	---	---
B.AU.MBC18	Q-T--PI	D.UG.92UG024D	D.UG.92UG024D	---	F.BR.B2163A	G.GA.LBV217	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-G	A-PP---	---	---	---	---	---	---	---	---	---	---
B.BE.SIMT84	-T--S	D.UG.C971412	D.UG.C971412	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-H	PSPQ---	---	---	---	---	---	---	---	---	---	---
B.CN.RL42	-K----	D.UG.UG266A2	D.UG.UG266A2	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-I	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.DE.D31	-S----	D.UG.WHO15474	D.UG.WHO15474	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-J	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.DE.HAN	-N-S---	D.ZR.84ZR085	D.ZR.84ZR085	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-K	P-OQ---	---	---	---	---	---	---	---	---	---	---
B.FR.HXB2	-N-S---	D.ZR.ELI	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-L	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.FR.LAI	-N-S---	D.ZR.ELI	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-M	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.FR.PIH384	-AA--V-	D.ZR.ELI	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-N	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.GA.OYI	-D----	CONSENSUS-D	D.SN.SE365A2	---	F.BR.93BR0201	G.BE.DRCBL	H.BE.VI991	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-O	PSPQ---	---	---	---	---	---	---	---	---	---	---
B.GB.CAM1	-T-----	D.TZ.87TZ4632	D.TZ.87TZ4632	---	F.BR.B2126A	G.FI.HH8793	H.BE.VI997	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-P	PWPQ---	---	---	---	---	---	---	---	---	---	---
B.JP.ETR	P-D-L--	D.UG.92UG024D	D.UG.92UG024D	---	F.BR.B2163A	G.GA.LBV217	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-Q	A-PP---	---	---	---	---	---	---	---	---	---	---
B.NL.ACH320A	-N-----	D.UG.C971412	D.UG.C971412	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-R	PSPQ---	---	---	---	---	---	---	---	---	---	---
B.SP.89SP061	Q-D-----	D.UG.UG266A2	D.UG.UG266A2	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-S	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.TH.TH936705	--D-SWT-	D.UG.WHO15474	D.UG.WHO15474	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-T	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.TT.QZ4589	--S-S-I	D.ZR.84ZR085	D.ZR.84ZR085	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-U	P-OQ---	---	---	---	---	---	---	---	---	---	---
B.US.JRCSF	Q-N-----	D.ZR.ELI	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-V	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.US.JRFL	-N-----	D.ZR.ELI	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-W	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.US.MN	-H-----	D.ZR.ELI	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-X	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.US.RF	GA-N---T-	D.ZR.ELI	D.ZR.ELI	---	F.FI.FIN6393	G.SE.SE6165	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-Y	TSLQ---	---	---	---	---	---	---	---	---	---	---
B.US.RF2	-D-----	CONSENSUS-D	D.SN.SE365A2	---	F.BR.93BR0201	G.BE.DRCBL	H.BE.VI991	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-Z	PSPQ---	---	---	---	---	---	---	---	---	---	---
B.US.WEAV160	--D--T-	D.TZ.87TZ4632	D.TZ.87TZ4632	---	F.BR.B2126A	G.FI.HH8793	H.BE.VI997	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-AA	PWPQ---	---	---	---	---	---	---	---	---	---	---
B.ZR.MB314	P--D-L--I	D.UG.92UG024D	D.UG.92UG024D	---	F.BR.B2163A	G.GA.LBV217	H.CF.90CF056	J.SE.SR92809	N.CM.YBF30	---	---	---	---	CONSENSUS-AB	A-PP---	---	---	---	---	---	---	---	---	---	---



gp41 Epitope 21-22

	Consensus	Strain	HLA	Consensus	Strain	Consensus	Strain	Consensus	Strain	Consensus	Strain
CONSENSUS-B Epitope # 21	Gr.....GWEALrK	GRRGWEALrK	HLA (B27) (B27)	CONSENSUS-C	C.BI.BU910611	-??slrGlr-----?	-O.....I-	CONSENSUS-O	O.CM.ANT70C	rLGLWILGQKILr??Cr-I	RGLWILGQKITINVCRI
CONSENSUS-A	A.KE.K89	-HSSLRGLRL--G-		C.BI.BU910717	-HSSLRGLQR--I-	-O.....I-	O.CM.CM4974	SIGLWILGQKTI--CRL	SIGLWILGQKTI--CRL	-LGLWILGQKTI--CRL	RIGLWILGQKITINVCRI
A.RW.KI93	-HSSLKGLRL--G-	C.BI.BU910812	C.BR.92BR025	-HSSLRGLQR--I-	-O.....I-	O.CM.MVP5180	O.GA.VI686	LGLWILGQKITIS-CRI	LGLWILGQKITIS-CRI	-LGLWILGQKTIINVCRI	RIGLWILGQKITINVCRI
A.RW.SF1703	K-SSLRGLRL--G-	C.BR.BR911513	C.BR.BR911513	-SSLRGLQR--I-	-O.....I-	O.GQ.341HA	O.GQ.655HA	O.GQ.HIVU82990	O.GQ.HIVU82990	-IGLWILGQKITIS-CRV	RIGLWILGQKITIDVCR
A.SE.SOSE7253	-HSSLKGLRL--G-	C.BW.BW96BW0502	C.DJ.DJ259A	-O.....T-	-O.....T-	O.GQ.HIVU82991	O.GQ.HIVU82991	RGGLWILGQKITIDVCR	RGGLWILGQKITIDVCR		
A.SE.TZSE8538	-HSSLRGLRL--G-	C.DJ.DJ373A	C.DJ.DJ373A	-O.....T-	-O.....T-			-HSSLKGLRL--G-	-HSSLKGLRL--G-		
A.SE.UGSE6594	-HSSLKGLRL--G-	C.ET.ETH2220	C.ET.ETH2220	-HSSLRGLQR--T-	-HSSLRGLQR--T-			-HSSLQGLRRR--G-	-HSSLQGLRRR--G-		
A.VA.AF082486	-HSSLRGLRL--G-	C.IN.11246	C.IN.11246	-HNSLRGLQR--T-	-HNSLRGLQR--T-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
A.UG.92UG037	-HSSLKGLRL--G-	C.IN.21068	C.IN.21068	-SLRGLQR--T-	-SLRGLQR--T-			-HSSLKGLRL--G-	-HSSLKGLRL--G-		
A.UG.U455	-O.....G-	C.IN.301904	C.IN.301904	-NSLRGLQR--T-	-NSLRGLQR--T-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
A.ZR.MA246	-HSSLKGLRL--G-	C.SN.SE364A	C.SN.SE364A	IO.....I-	IO.....I-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
A.ZR.MC108	-HNSLKGLRL--G-	C.SO.SM145A	C.SO.SM145A	-SSLRELQR--T-	-SSLRELQR--T-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
AG.DJ.DJ263	-HSSLKGLRL--Q-	C.UG.UG268A2	C.UG.UG268A2	-SSLRGLQR--T-	-SSLRGLQR--T-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
AG.DJ.DJ264	-HSSLKGLRL--G-	CONSENSUS-D	D.SN.SE365A2	-O.....?	-O.....?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
AG.NG.ING	-HNSLKGLRL--G-	D.ET.87ET4622	D.ET.87ET4622	-O.....T-	-O.....T-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
AGI.GR.97PVCH	-I.....-GT-	D.UG.92UG024D	D.UG.92UG024D	-O.....I-	-O.....I-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
AGI.GR.97PVMY	-I.....-GT-	D.UG.94UG1141	D.UG.94UG1141	-O.....I-	-O.....I-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
CONSENSUS-B		D.UG.UG266A2	D.UG.UG266A2	-H.....IR-	-H.....IR-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.AU.MBC18	--G.....-I-	D.UG.WHO15474	D.UG.WHO15474	-O.....I-	-O.....I-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.BE.SIMI84	--.....-I-	D.ZR.84ZR085	D.ZR.84ZR085	-O.....I-	-O.....I-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.CN.RI42	--.....-V-R-	D.ZR.ELI	D.ZR.ELI	-O.....I-	-O.....I-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.DE.D31	--.....-V-	D.ZR.JY1	D.ZR.JY1	-O.....I-	-O.....I-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.DE.HAN	--.....-V-	D.ZR.NDK	D.ZR.NDK	-O.....I-	-O.....I-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.FR.HXB2	--.....-V-	D.ZR.Z226	D.ZR.Z226	-O.....I-	-O.....I-			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.FR.LAI	--.....-L-	CONSENSUS-E	F.BR.93BR0201?PGLrK.....??PGLrK.....?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.FR.PIH384	-H.....-L-	CONSENSUS-F	F.BR.B2126ANRGLRR-----LNRGLRR-----L			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.GA.OYI	--.....-V-	CONSENSUS-G	F.BR.B2163ANRGLRR-----LNRGLRR-----L			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.GB.CAMI	--.....-V-	G.BE.DRCBL	G.BE.DRCBLDRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.JP.ETR	--K.....-V-	G.FI.HH8793	G.FI.HH8793DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.NL.ACH320A	--.....-V-	G.GA.LBV217	G.GA.LBV217DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.SP.89SP061	--.....-R-	G.SE.SE6165	G.SE.SE6165DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.TH.TH936705	--.....-R-	CONSENSUS-H	H.BE.VI991DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.TT.OZ4589	--.....-I-	H.BE.VI997	H.BE.VI997DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.US.JRCSF	--.....-V-	H.CF.90CF056	H.CF.90CF056DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.US.JRFL	--.....-V-	CONSENSUS-I	J.SE.SE91733DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.US.RF	--.....-I-	J.SE.SE92809	J.SE.SE92809DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.US.SF2	--.....-I-	CONSENSUS-J	N.CM.YBF30DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.US.WEAV160	--.....-I-	-L-.....-I-	-L-.....-I-DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
B.ZR.MB314	--.....-I-	-L-.....-I-	-L-.....-I-DRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		
		-QSLSRGILQILN-LRTH	-QSLSRGILQILN-LRTHDRGLRR-----?DRGLRR-----?			-HSSLKGLRR--G-	-HSSLKGLRR--G-		



gp41 Epitope 23-24



CONSENSUS-B	slInatAIAV	HLA	CONSENSUS-O	---d?---V---
Epitope #	SLINATDIAV (A2)		O.CM.ANT70C	---DTL-V---
23	LNATDIAV (A2)		O.CM.CM4974	T-FDSI-VS-
24			O.CM.MVP5180	N-DTI-VS-
CONSENSUS-A	n-DtI----		O.GA.VI686	--IDLTL-VT-
A.KE.K89	N-VDTI--V-		O.GQ.341HA	--DTV-V--
A.KE.Q23CXCCG	N-VDTI----		O.GQ.655HA	---DTF-V--
A.RW.KI693	N-VDTI----		O.GQ.HIVU82990	---DTI-V--
A.RW.SF1703	N-FDDT--V-		O.GQ.HIVU82991	--VDTL-V--
A.SE.SOSE7253	N-DTI----			
A.SE.TZSE8538	---DTI----		CONSENSUS-AE	-----d-----
A.SE.UGSE6594	N-DT-----		AE.CF.90CR402	T--D-----T-
A.SE.UGSE8891	N-DT-----		AE.TH.KH03	--D-----
A.UA.AF082486	N-DT-----		AE.TH.KH08	---D-----
A.UG.92UG037	N-IDTI-----		AE.TH.TH920149	--D-A--I
A.UG.U455	N-DT-----		AE.TH.93TH253	--FDL-V-
A.ZR.MA246	T-D-V-V-		AE.TH.A01021	L-----
A.ZR.MC108	N-DT-----		AE.TH.CM240	---D-----
	N-DT-----		AE.TH.E11429.A31	--FD-S---
AG.DJ.DJ263	N-DT-----		AE.TH.TH921110	---D-----
AG.DJ.DJ264	N-DT-----			
AG.NG.IBNG	N-TI-----		CONSENSUS-CPZ	???????????
	N-DT-----		CPZGAB	---D-----
AGI.GR.97PVCH	N-DT-----			
AGI.GR.97PVMY	---DT--V-			
CONSENSUS-B	-----F-----			
B.AU.MBC18	---F-----			
B.BE.SIM184	---T--V-			
B.CN.RI42	G-----			
B.DE.D31	---F-TI---			
B.DE.HAN	-----			
B.FR.HXB2	-----			
B.FR.LAI	-----			
B.FR.PIH384	-----			
B.GA.OYI	---FDTI---			
B.GB.CAM1	-----			
B.JP.ETR	-----			
B.NL.ACH320A	-----			
B.SP.89SP061	---T-----			
B.TH.TH936705	---I-----			
B.TT.QZ4589	-----			
B.US.JRC5F	-----			
B.US.JRFL	-----			
B.US.MN	---T-----			
B.US.RF	---W-----			
B.US.SF2	-----			
B.US.WEAV160	---I--I---			
B.ZR.MB314				
			CONSENSUS-G	n-DTV-----
			G.BE.DRCBL	N-DT-----
			G.FI.HH8793	N-DTI-----
			G.GA.LBV217	N-DTV--T
			G.SE.SE6165	--DTV----
			CONSENSUS-H	?---T-----
			H.BE.VI991	---T-----
			H.BE.VI997	N--T--V-
			H.CF.90CF056	D---T-----
			CONSENSUS-J	---T-----
			J.SE.SE91733	---T-----
			J.SE.SE92809	---T-----
			N.CM.YBF30	----T--V-

HIV CTL Epitope Alignments

gp41 Epitope 27-31



CONSENSUS-B Epitope #		?RAIHIIPRRIRROGIERALI	HLA
27	YRAIRHPRRIRROGLERILL	(B35)	
28	IPRRIRROGL	(B7)	
29	YRAIRHPRRIRROGLERILL	(B8)	
30	RRIRROGLERILL	(A30, B8)	
31	RRIRROGLERILL	(B7)	
CONSENSUS-A		G---N-----F-----	
A.KE.K89	G-----F-----	C.IN.11246	
A.KE.Q23CXCCG	G-----V-----	C.IN.21068	
A.RW.KIG93	G--F-N-----A---I	C.IN.301904	
A.RW.SF1703	G---N-----F---	C.SN.SE364A	
A.SE.SOSE7253	G---N-----F-E--	C.SO.SM145A	
A.SE.TZSE8538	C---N-----V-----	C.UG.UG268A2	
A.SE.UGSE6594	G--F-----F-----		
A.UA.AF082486	G--RN--x----A-K-Q		
A.UG.92UG037	G---N-----F---		
A.UG.U455	G---N-----F---		
A.ZR.MA246	C---N-----F---		
A.ZR.MC108	Y---N-----F----		
AG.DJ.DJ263	G---N-----		
AG.DJ.DJ264	G--RN--V-----		
AG.IMG.IMNG	G--RN-----F---		
AGI.GR.97PVCH	C--RN-----F-K--		
AGI.GR.97PVMY	C---N-----		
CONSENSUS-B		-----	
B.AU.MBCL8	Y-----	F.BR.93BR0201	
B.BE.SIMI84	G--V-----F---	F.BR.B2126A	
B.CN.RI42	Y-----T-----	F.BR.B2163A	
B.DE.D31	W-----V-----	F.FI.FIN6393	
B.DE.HAN	C-----V-----		
B.FR.HXB2	C--R-----I---		
B.FR.LAI	C--R-----I---		
B.FR.PIH384	G---T-----L---		
B.GA.OYI	Y--F-N-----L---		
B.GB.CAM1	C-----L---		
B.JP.ETR	Y-----VK-----		
B.NI.ACH320A	C--V-----V-----		
B.SP.89SP061	C-----Q-----		
B.TH.TH936705	Y-----T----FK---		
B.TT.QZ4589	C-----F-----		
B.US.JRCSF	Y-----T-----		
B.US.JRFL	Y-----T-----		
B.US.MN	G-----T-----		
B.US.RF	L--F-----		
B.US.SF2	Y-----H-----L-		
B.US.WEAU160	C-----L-----		
B.ZR.MB314	C---N--T-----		
CONSENSUS-C		-----?n-----f-A-q	
C.BI.BU910611	G---CS-----F-A-Q	O.CM.ANT70C	
C.BI.BU910717	W--CN--T----F-A-Q	O.CM.CM4974	
C.BI.BU910812	Y---CN-----F-A--	O.CM.MVP5180	
C.BR.92BR025	W--CN-----F-A-Q	O.GQ.VI686	
C.BR.BR911513	W--YN-----F-A-Q	O.GQ.341HA	
C.BW.BW6B0502	C--RN-----F-A-Q	O.GQ.655HA	
C.DJ.DJ259A	W--CN-----F-A-Q	O.GQ.HIVU82990	
C.DJ.DJ373A	W--FCN-----F-A-Q	O.GQ.HIVU82991	
C.ET.ETH2220	W--FCN-----A-Q		
C.IN.11246	C--RN-----A-Q		
C.IN.21068	C--RN-----F-A-Q		
C.IN.301904	C--RN-----F-AV-Q		
C.SN.SE364A	C--SN-----F-A-Q		
C.SO.SM145A	C-GVRN--T----F-A-Q		
C.UG.UG268A2	G-----F-A-Q		
CONSENSUS-D		C-----t-----	
D.SN.SE365A2	C-----T-----		
D.TZ.87TZ4622	V--V-N--T--S---		
D.UG.92UG024D	G---N--T-----L-		
D.UG.94UG1141	V---N--V-----G---		
D.UG.C971412	L---N-----G---		
D.UG.UG266A2	V--N--T--F---		
D.UG.WH015474	C--RN-----		
D.ZR.84ZRO85	CK-V--T-----		
D.ZR.ELI	C--V-N-----S-		
D.ZR.JY1	F--V-----V-----		
D.ZR.NDK	C--NV-----L-		
D.ZR.Z2Z6	C--V--T-----L-		
CONSENSUS-E		G---N--?-----f-----	
F.BR.93BR0201	G---N--?-----f-----		
F.BR.B2126A	G--N--T--F---		
F.BR.B2163A	G--N--T--F---		
F.FI.FIN6393	V--V-N-----RV---I		
CONSENSUS-G		C--?-N--t-----	
G.BE.DRCBL	C--F-N--T-----		
G.FI.HH8793	F--F-N--T-----		
G.GA.LBV217	C--N-----		
G.SE.SE6165	C---N--T-----		
CONSENSUS-H		W-----f--?-	
H.BE.VI991	W-----f--?-		
H.BE.VI997	W--V-----F---		
H.CF.90CF056	W-----F--S-		
CONSENSUS-J		F-----	
J.SE.SE91733	F-----		
J.SE.SE92809	F-----		
N.CM.YBF30	G-G-----I		
CONSENSUS-O		G-g-?n-----i---	
O.CM.ANT70C	G-g-RN-----i---		
O.CM.CM4974	GOG--N-----A--F--		
O.CM.MVP5180	GOGF-----A--I-V		
O.GQ.VI686	G-g-RN--T-----S-		
O.GQ.341HA	G-g-RNV-----I-		
O.GQ.655HA	G-g-NV-----I-		
O.GQ.HIVU82990	G-g-MN-----I-		
O.GQ.HIVU82991	G-E-CNV-----I-		
CONSENSUS-AE		W-----	
AE.CF.90CF402	W-----		
AE.TH.KH03	W--F-----		
AE.TH.KH08	W---I-----Q		
AE.TH.TH920149	W-----V		
AE.TH.93TH253	W-----S-		
AE.TH.A01021	W-----T-		
AE.TH.CM240	W-----		
AE.TH.E11429.A31	W-----I-		
AE.TH.TH921110	W-----		
CONSENSUS-CPZ		--?????????????-----	
CPZGAB	L-I-RN-----		
CPZANT	W-----HGFF--		