

HIV-1/SIVcpz Proteins

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The HIV-1/SIVcpz protein alignments presented here contain the same sequences used in the HIV-1/SIVcpz complete genome alignment. Please refer to the tables on pages 161 and 164 for information about these sequences. Because of the abundance of HIV-1 complete genomes there was no need, and no more space, to include additional sequences in these protein alignments.

Explanation of Symbols in Alignments

Symbol	Meaning
x	nucleotide missing from codon
#	frameshift, or codon contains N or illegal character
*	stop codon
-	domain boundaries
/	protein start point
\	protein end point
∨	splice site or exon join
*	cysteine (in annotation)
^^ [NxS, NxT]	glycosylation site
^*^ [NCS, NCT]	glycosylation site with cysteine
CD4	residue critical for CD4 binding
MHR	major homology region
NLS	nuclear localization signal
phos site	phosphorylation site
PKC	protein kinase C binding
Zn-motif	Zinc finger binding motif
M41L etc.	site of common drug resistance mutations in RT

cyclophilin A binding domain (CyPA)

p17 / p24

Table with 4 columns: Accession ID, Sequence, Alignment, and Position. The table contains multiple rows of protein sequences from various HIV-1 and SIVcpz strains, aligned to a reference sequence. The alignment is shown with dashes and vertical bars indicating gaps and matches. The position column on the right indicates the residue number for each sequence.

HIV-1/SIVcpz proteins

HIV-1/SIVcpz proteins

	cyclophilin A binding domain (CyPA)	major homology region (MHR)	
B.FR.83.HXB2	RVPHPAGFIAPGQMRPRGSDIAGTSTLQEQIGWMT...	NNPPIVGEIYKRWIIILGNKIVRMYSFTSILDRQGPKEFRDYDRFKYLRAEQAQSOEVKNNWTEITLLVQNPDCCKTILKALGPA	340
A1.KE.94.Q23.17	...P...P...G...D...V...K...F...F...T...D...D...A...R...G	...P...D...G...D...V...K...F...F...T...D...D...A...R...G	340
A1.RU.03.03RU20.06.13	...P...P...S...F...D...V...K...F...F...T...D...D...R...S...G	...P...D...S...F...D...V...K...F...F...T...D...D...R...S...G	340
A1.RW.93.93RW037A	...O...P...L...G...D...V...K...F...F...T...D...D...S...R...TG	...O...P...L...G...D...V...K...F...F...T...D...D...S...R...TG	340
A1.SE.94.SE7253	...A...V...P...G...D...V...K...F...F...T...D...D...S...R...AG	...A...V...P...G...D...V...K...F...F...T...D...D...S...R...AG	339
A1.TZ.01.A173	...O...P...I...P...I...Q...G...N...F...A...T...D...G...S...R...SG	...O...P...I...P...I...Q...G...N...F...A...T...D...G...S...R...SG	338
A1.UA.00.98UA0116	...A...Q...F...P...S...D...M...K...K...F...F...T...D...D...A...R...G	...A...Q...F...P...S...D...M...K...K...F...F...T...D...D...A...R...G	339
A1.UG.92.92UG0537	...V...P...A...G...D...M...K...K...F...F...T...D...D...S...R...AG	...V...P...A...G...D...M...K...K...F...F...T...D...D...S...R...AG	340
A1.UG.98.98UG57136	...Q...P...P...G...D...D...K...K...F...F...T...D...D...S...R...AG	...Q...P...P...G...D...D...K...K...F...F...T...D...D...S...R...AG	338
A2.CD.97.97CDKPE4	...P...P...S...S...D...D...K...K...F...F...T...D...D...S...R...AG	...P...P...S...S...D...D...K...K...F...F...T...D...D...S...R...AG	213
A2.CD.97.97CDKSK10	...P...P...S...S...D...D...K...K...F...F...T...D...D...S...R...AG	...P...P...S...S...D...D...K...K...F...F...T...D...D...S...R...AG	0
A2.CD.97.97CDKTB48	...Q...P...P...G...D...D...K...K...F...F...T...D...D...S...R...AG	...Q...P...P...G...D...D...K...K...F...F...T...D...D...S...R...AG	346
A2.CY.94.94CY017_41	...O...P...P...S...D...V...K...F...F...T...D...D...R...S...R...G	...O...P...P...S...D...V...K...F...F...T...D...D...R...S...R...G	336
A.SN.01.DDI579	...P...P...S...V...R...R...F...C...T...D...D...S...R...TG	...P...P...S...V...R...R...F...C...T...D...D...S...R...TG	339
A.SN.01.DDJ369	...P...P...S...V...DM...R...F...C...T...D...D...S...R...TG	...P...P...S...V...DM...R...F...C...T...D...D...S...R...TG	340
A.SN.96.DDJ360	...P...P...S...V...R...R...F...C...T...D...D...S...R...TG	...P...P...S...V...R...R...F...C...T...D...D...S...R...TG	339
A.ZA.04.04ZASK162B1	...P...P...N...D...D...V...V...F...A...G...T...G...G...Q...TG	...P...P...N...D...D...V...V...F...A...G...T...G...G...Q...TG	335
B.AR.00.ARMS008	...V...D...D...S...V...K...K...F...F...T...D...D...H...R...G	...V...D...D...S...V...K...K...F...F...T...D...D...H...R...G	339
B.AU.96.MBCD36	...O...V...K...D...D...K...K...F...F...T...D...D...R...G	...O...V...K...D...D...K...K...F...F...T...D...D...R...G	341
B.CO.01.PCM074	...A...A...S...N...K...K...CT...H...H...R...G	...A...A...S...N...K...K...CT...H...H...R...G	341
B.GA.88.OYI	...L...L...S...S...D...D...K...K...F...F...T...D...D...S...R...G	...L...L...S...S...D...D...K...K...F...F...T...D...D...S...R...G	343
B.NL.00.671.00T36	...L...L...V...N...S...H...I...D...D...I...S...R...G	...L...L...V...N...S...H...I...D...D...I...S...R...G	340
B.RU.04.04RU129005	...L...L...V...N...S...H...I...D...D...I...S...R...G	...L...L...V...N...S...H...I...D...D...I...S...R...G	340
B.TH.90.RK122	...L...L...V...N...S...H...I...D...D...I...S...R...G	...L...L...V...N...S...H...I...D...D...I...S...R...G	340
B.US.90.WEAU160	...L...L...V...N...S...H...I...D...D...I...S...R...G	...L...L...V...N...S...H...I...D...D...I...S...R...G	340
B.US.98.1058.II	...L...L...V...N...S...H...I...D...D...I...S...R...G	...L...L...V...N...S...H...I...D...D...I...S...R...G	338
C.AR.01.ARG4006	...L...L...V...N...A...S...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...N...A...S...D...D...K...K...F...F...T...D...D...R...G	336
C.BR.04.04BR013	...L...L...V...V...G...O...V...K...K...F...F...T...D...D...R...G	...L...L...V...V...G...O...V...K...K...F...F...T...D...D...R...G	338
C.BR.92.BR025_d	...L...L...V...V...V...D...V...K...K...F...F...T...D...D...R...G	...L...L...V...V...V...D...V...K...K...F...F...T...D...D...R...G	337
C.BW.00.00BW07621	...L...L...V...V...A...S...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...A...S...V...D...D...K...K...F...F...T...D...D...R...G	338
C.ET.86.ETH2220	...L...L...V...V...D...D...G...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...D...D...G...V...D...D...K...K...F...F...T...D...D...R...G	337
C.IN.95.95IN21068	...L...L...P...L...L...A...G...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...P...L...L...A...G...V...V...D...D...K...K...F...F...T...D...D...R...G	337
C.IN.99.01IN565_10	...L...L...P...L...L...A...G...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...P...L...L...A...G...V...V...D...D...K...K...F...F...T...D...D...R...G	336
C.KE.00.KER2010	...L...L...NP...A...S...S...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...NP...A...S...S...V...D...D...K...K...F...F...T...D...D...R...G	335
C.TZ.01.BD9_11	...L...L...V...V...MA...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...MA...V...V...D...D...K...K...F...F...T...D...D...R...G	332
C.UY.01.TRA3011	...L...L...V...V...VA...S...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...VA...S...V...D...D...K...K...F...F...T...D...D...R...G	337
C.ZA.04.SK164B1	...L...L...V...L...VA...S...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...L...VA...S...V...D...D...K...K...F...F...T...D...D...R...G	337
C.ZA.05.05ZASK245B1	...L...L...V...L...VA...S...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...L...VA...S...V...D...D...K...K...F...F...T...D...D...R...G	337
C.ZM.02.02ZM115	...L...L...V...V...D...D...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...D...D...S...V...V...D...D...K...K...F...F...T...D...D...R...G	337
C.ZM.96.96ZM651	...L...L...V...V...D...D...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...D...D...S...V...V...D...D...K...K...F...F...T...D...D...R...G	339
D.CD.83.ELI	...L...L...V...V...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	340
D.CD.83.NDK	...L...L...V...V...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	337
D.CM.01.01CM.4412HAL	...L...L...O...V...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...O...V...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	338
D.KE.01.NKU3006	...L...L...I...N...N...K...K...F...F...T...D...D...R...G	...L...L...I...N...N...K...K...F...F...T...D...D...R...G	338
D.TD.99.MN012	...L...L...O...V...D...D...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...O...V...D...D...S...V...V...D...D...K...K...F...F...T...D...D...R...G	340
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D.UG.94.94UG114	...L...L...V...V...L...L...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...L...L...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	340
D.UG.99.99UGD2550	...L...L...Y...L...L...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...Y...L...L...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	338
D.UG.99.99UGK03958	...L...L...Y...L...L...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...Y...L...L...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	336
D.ZA.86.R482	...L...L...V...V...A...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...A...S...S...V...V...D...D...K...K...F...F...T...D...D...R...G	341
F1.BE.93.VI850	...L...L...AP...P...I...G...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...AP...P...I...G...V...D...D...K...K...F...F...T...D...D...R...G	336
F1.BR.89.B2126	...L...L...AQ...P...I...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...AQ...P...I...S...V...V...D...D...K...K...F...F...T...D...D...R...G	336
F1.BR.93.93BR020_1	...L...L...TQ...P...I...G...V...M...D...D...K...K...F...F...T...D...D...R...G	...L...L...TQ...P...I...G...V...M...D...D...K...K...F...F...T...D...D...R...G	336
F1.FI.93.FIN9363_1	...L...L...P...P...Q...S...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...P...P...Q...S...V...D...D...K...K...F...F...T...D...D...R...G	338
F1.FR.96.MP411	...L...L...A...L...Q...S...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...A...L...Q...S...V...D...D...K...K...F...F...T...D...D...R...G	336
F2.CM.02.02CM.0016BBY	...L...L...Q...P...I...A...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...Q...P...I...A...S...V...V...D...D...K...K...F...F...T...D...D...R...G	334
F2.CM.95.MP255	...L...L...Q...P...I...G...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...Q...P...I...G...V...V...D...D...K...K...F...F...T...D...D...R...G	336
F2.CM.95.MP257	...L...L...Q...P...I...G...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...Q...P...I...G...V...V...D...D...K...K...F...F...T...D...D...R...G	340
F2.CM.97.CM53657	...L...L...Q...P...I...N...A...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...Q...P...I...N...A...S...V...V...D...D...K...K...F...F...T...D...D...R...G	334
G.BE.96.DRCHL	...L...L...OQ...I...D...T...A...R...S...V...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...OQ...I...D...T...A...R...S...V...V...D...D...K...K...F...F...T...D...D...R...G	333
G.CM.01.01CM.4049HAN	...L...L...PQ...P...I...R...R...S...D...D...K...K...F...F...T...D...D...R...G	...L...L...PQ...P...I...R...R...S...D...D...K...K...F...F...T...D...D...R...G	338
G.ES.99.X138	...L...L...OQ...P...I...R...R...S...D...D...K...K...F...F...T...D...D...R...G	...L...L...OQ...P...I...R...R...S...D...D...K...K...F...F...T...D...D...R...G	340
G.KE.93.HH8793_12_1	...L...L...PO...P...I...N...R...S...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...PO...P...I...N...R...S...V...D...D...K...K...F...F...T...D...D...R...G	340
G.NG.92.92NG083	...L...L...OQ...P...I...S...R...S...V...D...D...K...K...F...F...T...D...D...R...G	...L...L...OQ...P...I...S...R...S...V...D...D...K...K...F...F...T...D...D...R...G	340
G.SE.93.SE6165	...L...L...OQ...FP...I...S...T...G...F...C...D...D...K...K...F...F...T...D...D...R...G	...L...L...OQ...FP...I...S...T...G...F...C...D...D...K...K...F...F...T...D...D...R...G	340
H.BE.93.VI991	...L...L...P...P...VA...G...D...D...K...K...F...F...T...D...D...R...G	...L...L...P...P...VA...G...D...D...K...K...F...F...T...D...D...R...G	342
H.BE.93.VI997	...L...L...P...P...VA...G...D...D...K...K...F...F...T...D...D...R...G	...L...L...P...P...VA...G...D...D...K...K...F...F...T...D...D...R...G	340
H.CF.90.056	...L...L...P...P...VA...G...D...D...K...K...F...F...T...D...D...R...G	...L...L...P...P...VA...G...D...D...K...K...F...F...T...D...D...R...G	340
J.SE.93.SE7887	...L...L...V...V...G...A...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...G...A...D...D...K...K...F...F...T...D...D...R...G	340
J.SE.94.SE7022	...L...L...V...V...G...A...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...G...A...D...D...K...K...F...F...T...D...D...R...G	340
K.CD.97.EQT811C	...L...L...V...V...G...A...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...G...A...D...D...K...K...F...F...T...D...D...R...G	340
K.CM.96.MP535	...L...L...V...V...G...A...D...D...K...K...F...F...T...D...D...R...G	...L...L...V...V...G...A...D...D...K...K...F...F...T...D...D...R...G	336

Table with 10 columns: Accession ID, p24, p2, p7, p1, p1, p1, p1, p1, p1. Rows list various HIV-1/SIVcpz protein sequences and their alignments.

HIV-1/SIVcpz proteins

HIV-1/SIVcpz proteins

	/ p6	Vpr binding		Vpr binding	/ p6
B.FR.83.HXB2	FLQSR	PEPTA	ESFRSG.VETITPPQK.QE.PID.K	ELY	PLTSLRSLFGNDPSSQ
A1.KE.94.Q23.17	P-N	L	-TCGM-E-VS-L	-OAO	-V-K-L-L
A1.RU.03.03RU20.06_13	P-N	S	-N-GM?E-I-PSL	-OK-R	-SI-K-L
A1.RW.93.93RW037A	P-P	A	-L-GM-E-I-AS	-OK-R	-PTP-AI-K-L
A1.SE.94.SE7253	P-P	A	-L-GM-E-I-AS	-OK-R	-ONS-SV-K-L
A1.TZ.01.A173	P-P	A	-L-GM-EGTASL	-OK-R	-QVP-SV-K-L
A1.UA.00.98UA0116	P-P	S	-D-GR-E-I-P-L	-OK-R	-OHP-SI-K-L
A1.UG.92.92UG0037	P-N	A	-AEIFGMRE-IVS	-ON-R	-DONP-SV-K-L
A1.UG.98.98UG57136	P-N	A	-L-GM-E-I-S	-OK-R	-ONS-SV-K-L
A2.CD.97.97CDKPE4	P-P	A	-D-GM-E	-KN-R	-PHT-AI-K-S-L
A2.CD.97.97CDKS10	P-P	T	-ME-E-I-SSL	-N-R	-PST-AI-K-L
A2.CD.97.97CDKTB48	P-P	A	-NL-M-E-I-SSL	-LET-R	-P-N-AI-K-L
A2.CY.94.94CY017_41	P-P	A	-DLGGM-E-I-SSP	-OK-R	-PP-V-K-L
A.SN.01.DDH579	P-P	A	-LLGR-E-I-SP	-OK-R	-OP-I-K-L
A.SN.01.DDI369	P-P	A	-DLGGM-E-I-SSP	-OK-R	-PP-SV-K-L
A.SN.96.DDJ360	P-N	A	-G-YGM-E-I-S-Q	-K-QT-R	-QP-A-L-P
A.ZA.04.04ZASK162B1	P-N	A	-SF-G-A	-Q	-K-A-K-L
B.AR.00.ARMS008	S	ORL	-E-E-P-C-M-T	-G	-A-A
B.AU.96.MBCD36	N	GA.88.OYI	-GF-E-E-T	-G	-A-A
B.CO.01.PCM074	N	PSQSRPEPTA	-P-E-S-R	-T	-A-K-S
B.GA.88.OYI	N	PPAPSA	-P-E-AA-S	-T	-M-A-K-S
B.NL.00.671.00T36	N	L	-FR-E-S	-S	-A-K-L
B.RU.04.04RU129005	P	US.98.WEAU160	-F-E-S	-S	-A-K-L
B.TH.90.TH12	P	US.98.1058.11	-F-E-S	-S	-A-K-L
B.US.90.WEAU160	P	AR.01.ARG4006	-PE-E-SP	-K-R	-K-S-L
B.US.98.1058.11	P	BR.04.04BR013	-PA-E-SP	-K-R	-K-S-L
C.AR.01.ARG4006	L-N	BR.92.BR025_d	-P-E-SR	-T	-S-L-T
C.BR.04.04BR013	L-N	EW.00.00EW07621	-KEE-E-NTP	-K-R	-K-S-L
C.BR.92.BR025_d	L-N	ET.86.ETH2220	-FE-E-A-SP	-LK-R	-A-K-S-L
C.EW.00.00EW07621	L-N	IN.95.95IN21068	-FE-E-AP	-K-R	-S-L
C.ET.86.ETH2220	L-N	IN.99.01IN565_10	-FE-E-TP	-K-R	-S-L
C.IN.95.95IN21068	L-N	KE.00.KER2010	-FE-E-AJAP	-LKE-R	-K-S-L
C.IN.99.01IN565_10	L-N	TZ.01.BD9_11	-FE-E-AP	-OR-R	-K-S-L
C.KE.00.KER2010	L-N	UY.01.TRA3011	-FE-E-A-SPR	-OK-R	-K-S-L
C.TZ.01.BD9_11	L-N	ZA.04.SK164B1	-FE-E-AP	-L-R	-S-L
C.UY.01.TRA3011	L-N	ZA.05.05ZASK245B1	-FE-E-AP	-G-SK-R	-S-L
C.ZA.04.SK164B1	L-N	ZM.02.02ZM115	-FE-E-TP	-AK	-S-L
C.ZA.05.05ZASK245B1	L-N	ZM.96.96ZM651	-FE-E-AP	-S-R	-S-L
C.ZM.02.02ZM115	L-N	CD.83.ELI	-FE-E-S	-OK	-K-S-L
C.ZM.96.96ZM651	L-N	CD.83.NDK	-GF-E-I-S	-OK	-K-S-L
D.CD.83.ELI	L-N	CM.01.01CM.4412HAL	-GF-E-I-S	-OK	-K-S-L
D.CD.83.NDK	L-N	KE.01.NKU3006	-GF-E-I-S	-OK	-K-S-L
D.CM.01.01CM.4412HAL	L-N	TD.99.MN012	-GF-E-I-S	-OK	-K-S-L
D.KE.01.NKU3006	L-N	UZ.01.A280	-GF-E-I-S	-OK	-K-S-L
D.KE.01.NKU3006	L-N	UG.94.94UG114	-GF-E-I-S	-OK	-K-S-L
D.TD.99.MN012	L-N	UG.99.99UGD2550	-GF-E-I-S	-OK	-K-S-L
D.TZ.01.A280	L-N	UG.99.99UGD2550	-GF-E-I-S	-OK	-K-S-L
D.UG.94.94UG114	L-N	ZA.86.K482	-GF-E-I-S	-OK	-K-S-L
D.UG.99.99UGD2550	L-N	BE.93.VI850	-GFR-E-I-SP	-OK	-K-S-L
D.UG.99.99UGD2550	L-N	BR.89.B2126	-GFR-E-I-SP	-OK	-K-S-L
D.ZA.86.K482	L-N	BR.93.93BR020_1	-P-E-SP	-OK	-K-S-L
F1.BE.93.VI850	L-N	FI.93.FIN9363_1	-LGR-E-V-SPR	-OKE-E	-CO-P-A-K-S
F1.BR.89.B2126	L-N	FR.96.MP411	-GFR-E-I-SP	-OK	-K-S-L
F1.BR.93.93BR020_1	L-N	CM.02.02CM.0016BBY	-GFR-E-I-SP	-OK	-K-S-L
F1.FI.93.FIN9363_1	L-N	CM.95.MP255	-N-GF-EGI	-OKG-E	-OAP-V-K-S
F1.FR.96.MP411	L-N	CM.95.MP257	-GF-E-I-SP	-OK	-K-S-L
F2.CM.02.02CM.0016BBY	L-N	CM.97.CM53657	-GF-E-I-SP	-OK	-K-S-L
F2.CM.95.MP255	L-N	BE.96.DRCBL	-N-GF-E-I-SP	-OKE	-S-K-Q-K
F2.CM.95.MP257	L-N	CM.01.01CM.4049HAN	-GV-E-I-A-SP	-RE	-K-S
F2.CM.97.CM53657	L-N	ES.99.X138	-F-E-I-A-SP	-OKE	-K-S
G.BE.96.DRCBL	L-N	KE.93.HH8793_12_1	-GF-E-I-A-SP	-P	-I-H-A-K-S
G.CM.01.01CM.4049HAN	L-N	NG.92.92NG083	-GF-E-I-A-SP	-KE	-K-S
G.ES.99.X138	L-N	SE.93.SE6165	-LGF-E-I-A-SP	-MKE	-K-S
G.KE.93.HH8793_12_1	L-N	BE.93.VI891	-GF-E-I-SP	-LKE	-Q
G.NG.92.92NG083	L-N	BE.93.VI997	-GF-E-M-SP	-LK	-P-FA-K-S
G.SE.93.SE6165	L-N	CF.90.056	-GF-E-M-SP	-OLK	-P-A-S-L
H.BE.93.VI891	L-N	SE.93.SE7887	-LGL-E-I-PS	-K	-K-S-L
H.BE.93.VI997	L-N	SE.94.SE7022	-LGF-E-I-PS	-K	-K-S-L
H.CF.90.056	L-N	CD.97.EQTB11C	-GF-EKI	-SLR	-MK-Q-QGP-K-S
J.SE.93.SE7887	L-N	ZM.96.MP535	-GF-E-I-SP	-TK	-TK-K-S-L
J.SE.94.SE7022	L-N				
K.CD.97.EQTB11C	L-N				
K.ZM.96.MP535	L-N				

	/ p6	PEPTA	PEPTA	PEPTA	ESFRSG.VETITPPQK.QE.PID.K.ELY.....	PLTSLRSLFGNDPSSQ	Vpr binding
B.FR.83.HXB2							
01 AE.CF.90.90CF402							
01 AE.CN.05.FJ051							
01 AE.HK.x.HK001							
01 AE.JP.93.93JP.NH1							
01 AE.TH.01.01R414I							
01 AE.TH.02.02OUR769I							
01 AE.TH.90.CM240							
02 AG.CM.02.02CM.1669IE							
02 AG.EC.x.EC041							
02 AG.FR.91.DJ264							
02 AG.GH.03.GHNJ196							
02 AG.NG.x.IE8G							
02 AG.SN.98.MP1211							
02 AG.UZ.02.02UZ693							
03 AB.RU.97.KAL153.2							
04 CDX.CV.94.CV032							
05 DF.BE.x.VII1310							
06 CDX.AU.96.BFP90							
07 BC.CN.97.CNS4							
08 BC.CN.97.97CNGX.6F							
09 CDX.GH.96.96GH2911							
10 CD.TZ.96.96TZ.BF061							
11 CDX.GR.x.GR17							
12 BF.AR.99.ARMA159							
13 CDX.CM.96.1849							
14 BG.ES.99.X397							
15 01B.TH.99.99TH.MU2079							
16 AZD.KR.97.97KR004							
18 CDX.CU.99.CU76							
18 CDX.CU.99.CU7							
20 BG.CU.03.CB134							
21 AZD.KE.91.KNH1254							
23 BG.CU.03.CB118							
24 BG.CU.03.CB378							
25 CDX.CM.x.101BA							
28 BF.BR.99.BREPM12609							
29 BF.BR.02.BREPM119							
31 BC.BR.02.110PA							
33_01B.WY.05.05MYKL007_1							
A1C.TZ.02.CO3710							
A1CDGKU.ZA.99.CM4							
A1DHK.NO.97.97NOGLI3							
A1GHU.GA.x.VI354							
A2D.KE.99.KER2003							
AP2.CM.02.02CM.3163MN							
AGU.CM.01.01CM.0989MO							
ARU.CM.01.01CM.1296NG							
BC.MM.99.mIDDU103							
BF1.BR.02.02BR006							
0708.CN.00.HH069							
U.CD.83.83CD003							
U.CD.90.90CD121E12							
U.GR.99.GR303							
U.NL.x.U.NL.95.H10986_D1							
N.CM.02.DJ00131							
N.CM.04.CM.1015_04							
N.CM.04.04CM.1131_03							
N.CM.95.YBF30							
N.CM.97.YBF106							
O.BE.87.AN1770							
O.CM.91.MVPS180							
O.CM.96.96CMABB637							
O.SN.99.SEMP1300							
CPZ.CD.90.ANT							
CPZ.CM.01.SIVcpzCAM13							
CPZ.CM.05.SIVcpzEK505							
CPZ.CM.05.SIVcpzL87							
CPZ.CM.05.SIVcpzMB66							
CPZ.CM.05.SIVcpzMT145							
CPZ.GA.88.GAB1							
CPZ.TZ.01.TAN1							
CPZ.US.85.CPZUS							

HIV-1/SIVcpz proteins

	Gag-Pol TF start	TRANS	PTR	RELOVW GRDNNSPSE .AG.ADR.Q	Gag-Pol TF end	Pol protease start
B.FR.83.HXB2	FFREDL.AFLQ...G.KAREFSSEQ	TRANS	PTR	RELOVW GRDNNSPSE .AG.ADR.Q	Gag-Pol TF end	Pol protease start
A1.KE.94.Q23_17	N-Q	GT	S	D-WDG	TL	V
A1.RU.03.03RU20_06_13	N-Q	R-E-K	S	K-WDE	TS	V
A1.RW.93.93RW037A_1	N-Q	E-K	S	A-WDG	DP	V
A1.SE.94.SE7253	NV	E-K	S	AFWDG	SLPS	V
A1.TZ.01.A173	N-Q	R-E-K-P	S	A-WDG	SLPS	V
A1.UA.00.98UA0116	KN	R-E-K	S	R-WEG	PP	V
A1.UG.92.92UG037	N-Q	R-E-K	S	SRLWDE	SLPS	V
A1.UG.98.98UG57136	N-SQ	E-K	S	AWWDG	LPS	V
A2.CD.97.97CDKFEA4	N-SQ	R-E-K-P	S	G-WNG	AY	V
A2.CD.97.97CDKS10	N-Q	R-E-K	S	NG	LLA	V
A2.CD.97.97CDKTB48	N-Q	R-E-K	S	ENG	LLP	V
A3.CY.94.94CY017_41	N-Q	E-K	S	SPDGR	LLP	V
A.SN.01.DDI579	N-Q	E-K	S	APWEG	PL	V
A.SN.01.DDU369	N-Q	R-E-L	S	SPDGR	TLLP	V
A.SN.96.DDU360	N-Q	E	S	WDG	LFT	V
A.ZA.04.04ZASK162B1	NM	R-P	S	L	G-R-R	S
B.AR.00.ARMS008	KN	R	S	EN-H	S	I
B.AU.96.MBCD36	N-P	E-L	I	G	K	Y
B.CO.01.PCM074	N-P	G-P	ET	RANS	S	I
B.GA.88.OYI	P	E	P	PFSOTRANS	S	I
B.NL.00.671_00T36	P	E	P	TI	P	S
B.RU.04.04RU129005	P	E	P	PTSALS	S	I
B.TH.90.BK132	N-P	D	S	Q	L	DN
B.US.90.WEAU160	V-PK	T	S	L	I	A
B.US.98.1058_11	P	R	S	G	L	T
C.AR.01.ARG4006	N-Q	K-P	P	R	D-PL	TEG
C.BR.04.04BR013	N-P	GE	PT	R	D-PL	TEG
C.BR.92.BR025_d	N-P	E-KS	N	L	D	N
C.BW.00.00BW07621	N-P	E	PP	R	DKPH	E
C.ET.86.ETH2220	T	Q	P	R	S	TF
C.IN.95.95IN21068	N-P	E	PP*	R	D-PS	E
C.IN.99.01IN565_10	N-P	E	P	R	DDPH	E
C.KE.00.KER2010	N-P	E	P	R	DSPC	E
C.TZ.01.BD9_11	N-P	P	A	R	D-PC	E
C.UY.01.TRA37011	N-P	E-K	PP	R	R-G-PL	E
C.ZA.04.SK164B1	N-PE	E	P	R	DDPC	T
C.ZA.05.05ZASK245B1	N-P	E	P	SPANSPTC	R	D-PR
C.ZM.02.02ZM115	N-P	Q	E-G-P	R	PHA	GE
C.ZM.96.96ZM651	N-P	P	A	R	D-PR	VE
D.CD.83.ELI	N-P	G-L-PK	S	PL-K	T	E
D.CD.83.NDK	P	G	S	R	G-PL	T
D.CM.01.01CM_4412HAL	N-Q	L	S	R	R-G-SPL	T
D.KE.01.NKU37006	N-P	G-LP	S	R	G-TLP	T
D.TD.99.MN012	N-Q	E-G-L	S	R	P	T
D.TZ.01.A280	N-P	R-LP	S	D-R	G-KTL	T
D.UG.94.94UG114	N-P	W	TP	D-RIR	G-TS	T
D.UG.99.99UGD23550	N-P	R-LP	S	G	TLP	T
D.UG.99.99UGK09958	N-V-P	T-P-K	S	R	TLP	T
D.ZA.86.R482	T	P	S	RR	G-PL	T
F1.BE.93.VI850	N-Q	E-K-P	S	R	O-RG	PL
F1.BR.89.B2126	N-P	E-K-P	S	R	O-RG	KPL
F1.BR.93.93BR020_1	N-Q	E-KHP	A	V	R	G
F1.FI.93.FIN9363	N-Q	E-K-P*	AS	R	G-PI	E
F1.FR.96.MPA11	N-Q	E-K	A	G	R-O-RGN	PL
F2.CM.02.02CM_0016BBY	N-Q	R-E-W-H	G	G	R-R	R-LP
F2.CM.95.MP255	N-Q	E-K	A	R	R-RG	PLP
F2.CM.95.MP257	NV	E-K	AS	R	R-G	
F2.CM.97.CM53657	N-Q	E-WK	AS	K	R-R	
G.BE.96.DRCHL	N-Q	E	P	R	R-G	
G.CM.01.01CM_4049HAN	N-Q	R-E-L-P	P	RSR	RG	
G.ES.99.X138	N-Q	E	P	R	RG	
G.KE.93.HH8793_12_1	?	E	P	R	R	
G.NG.92.92NG083	N-Q	E-KL-P	D	R	R	
G.SE.93.SE6165	N-Q	E	D-T	KPR	R	
H.BE.93.VI991	N-Q	E	PP-E	R	R	
H.BE.93.VI997	N-Q	R-E-K-P	A	R	R	
H.ICF.90.056	N-Q	R-E-K-P	A	R	R	
J.SE.93.SE7887	N-Q	R-E-L-P	A	PRAR	RG	
J.SE.94.SE7022	N-Q	R-E-P	S	PR	R	
K.CD.97.EQTB11C	V-SQ	R-E-K	S	W	R	
K.CM.96.MP535	N-P	E	S	R	R	

	Gag-Pol TF start	TRANS.	PTR.	RELOVW.GRDNNPSPE..AG.ADR.Q.	Gag-Pol TF end	Pol protease start
B.FR.83.HXB2	FPREDL.AFLQ..G.KAREFSSEQ.	TRANS.	PTR.	RELOVW.GRDNNPSPE..AG.ADR.Q.	Gag-Pol TF end	Pol protease start
01 AE.CF.90.90CF402	N-Q-E-K-P-K	N-N-G-G	N-N-G-G	G-GDG	E-A	S-S-I-V
01 AE.CN.05.FU051	N-Q-GK	N-S-S	N-S-S	K-GNE	T-E	PS-S-LS-V
01 AE.HK.x.HK001	N-Q-E	N-F	N-F	GK-E	F-L	F-L-V
01 AE.JP.93.93JP.NH1	N-Q-R	N-S	N-S	K-GDG	S-LS	S-LS-V
01 AE.TH.01.0UR41A1	N-Q-GK	N-S	N-S	GK-GDG	L-T	F-L-V
01 AE.TH.02.0UR7691	N-Q-G	N-AS	N-AS	K-GDG	L-T	F-L-V
02 AE.TH.90.CM240	N-Q-E	N-AS	N-AS	K-GDG	L-T	F-L-V
02 AG.CM.02.02CM.16691E	N-Q-E-K-P-K	N-S-S	N-S-S	K-GDG	GGRD	NLLTEA
02 AG.EC.x.EC041	N-Q-E-K-P-K	N-S-S	N-S-S	R-NR	G-LL	S-DEG
02 AG.FR.91.DJ264	N-Q-E-K-K	N-S-S	N-S-S	WDG	L	TEG.P
02 AG.GH.03.GHNJ196	N-Q-E-K-K	N-GTI	N-GTI	G-DG	G	SLNP
02 AG.NG.x.IENG	N-Q-E-K-K	N-GTI	N-GTI	WDG	T-L-T	TEG
02 AG.SN.98.MP1211	N-Q-E-K-K	N-GTI	N-GTI	WDG	LLP	TEG
02 AG.UZ.02.02UZ693	N-Q-E-K-K	N-T	N-T	R-GDG	LL-A	EG
03 AB.RU.97.KAL153.2	N-Q-R-E-K	N-A	N-A	K-WDG	RG	PLP
04 CDX.CV.94.CY0332	N-Q-R-E-K	N-A	N-A	GM-REE	RG	LL
05 DF.BE.x.VII1310	N-Q-E-LPP	N-AS	N-AS	RFR	RG	SFLP
06 CDX.AU.96.BFP90	N-Q-E	N-H	N-H	RFR	RG	SFLP
07 BC.CN.97.CM54	N-LP	N-G	N-G	R	PS	TL
08 BC.CN.97.97CNGX.6F	N-Q-E-PP	N-S	N-S	WDE	?LL?	?E.EG
09 CDX.GH.96.96GH2911	N-Q-R-E-LP	N-G-IG	N-G-IG	WDE	?LL?	?E.EG
10 CD.TZ.96.96TZ.BF061	N-Q-R	N-A	N-A	R-R	G-TL	T-E
11 CDX.GR.x.GR17	N-Q-E-PT	N-A	N-A	R-R	G-TL	T-E
12 BF.AR.99.ARMAL159	N-Q-E-K-P	N-AS	N-AS	W-R	RG	LL
13 CDX.CM.96.L1849	N-Q-R-E	N-S	N-S	R-R	RG	SPLP
14 BG.ES.99.X397	N-Q-E	N-A	N-A	G-R	RG	SPLP
15 01B.TH.99.99TH.MU2079	N-Q-E	N-I	N-I	GDG	LLT	LL
16 A2D.KR.97.97KR004	N-P-R-E	N-NT	N-NT	G-WNG	G	PLA
18 CDX.CU.99.CU76	N-Q-E-K-P-K	N-S	N-S	G-G	R	RG
19 CDX.CU.99.CU7	N-Q-E-K-P	N-S	N-S	G-G	R	RG
20 BG.CU.03.CB134	N-P-E-PP	N-C	N-C	R	GN	PL
21 A2D.KE.91.KNH1254	N-P-E-G-L	N-A	N-A	G	RG	SLL
23 BG.CU.03.CB118	N-P-E-G-L	N-A	N-A	R	RG	SLL
24 BG.CU.03.CB378	N-P-E-G-L	N-A	N-A	R	RG	SLL
25 CDX.CM.x.101BA	N-Q-E-KL	N-A-D	N-A-D	G	SPLP	R-EG
28 BF.BR.99.BREPM12609	N-P-E-K-P	N-AS	N-AS	R	RG	PL
29 BF.BR.02.BREPM119	N-P-E-K-P	N-A	N-A	R	RG	PL
31 BC.BR.02.110PA	N-P-E-PP	N-S	N-S	G	R	PL
33_01B.WY.05.05MYKL007_1	N-A-P	N-G-LP	N-G-LP	G	R	PL
A1C.FZ.02.C03710	N-P-E-P	N-S	N-S	R	PH	PH
A1CDGKU.ZA.99.CM4	N-P-R-E-KL	N-S	N-S	R	G	DPPL
A1DHK.NO.97.97NOGL13	N-Q-R	N-L	N-L	WDR	LL	TEG
A1GHU.GA.x.VI354	N-Q-E	N-G-I	N-G-I	R	R	RG
A2D.KE.99.KER2003	N-Q-E-G-L	N-V	N-V	DVR	R	PL
AF2.CM.02.02CM.3163MN	N-P-E-G-KL	N-AS	N-AS	R	R	G
AGU.CM.01.01CM.0989MO	N-Q-E-K	N-A-G	N-A-G	R	R	G
ARJU.CM.01.01CM.1296NG	N-Q-R-E-L	N-I	N-I	R	R	L
BC.CN.96.YNRL9607	N-Q-E-PP	N-S	N-S	G	R	PS
BC.MM.99.mDDU103	N-P-E	N-S	N-S	R	R	PS
BF1.BR.02.02BR006	N-P-E-L	N-T	N-T	R	R	RG
0708.CN.00.HH069	N-P-E-PP	N-AS	N-AS	R	R	RG
U.CD.83.83CD003	N-Q-E	N-S	N-S	R	R	RG
U.CD.90.90CD121E12	N-Q-E	N-S	N-S	R	R	RG
U.GR.99.GR303	N-Q-E	N-D	N-D	R	R	RG
U.NL.x.U.NL.95.H10986_D1	N-Q-R-E-P	N-S	N-S	G	R	RG
N.CM.02.DJ00131	KG-VS	R-ET	Q-PPDNNK	E-H	E-H	EHTG-GE
N.CM.04.04CM.1015_04	KG-VS	R-ET	Q-PPDNNK	E-H	E-H	EHTG-GE
N.CM.04.04CM.1131_03	G-VS	R-ET	L-PPDNN.K	E-H	E-H	EHTG-GE
N.CM.95.YBF30	E-VS	R-ET	KLPPDNN.K	E-H	E-H	EHTG-GE
N.CM.97.YBF106	KG-VS	R-ET	KLPPDNN.K	E-H	E-H	EHTG-GE
O.BE.87.AN170	QI	SGG	H.E	QICA	ET	STPI
O.CM.91.MVPS180	V	SGG	H.E	QICA	ET	STPI
O.CM.96.96CMBAB637	QV	SGG	H.E	QICA	ET	STPI
O.SN.99.SEMP1300	I	SGG	H.E	QICA	ET	STPI
CPZ.CD.90.ANT	TD	PHV	-VOT	-LCA	GGG	SG
CPZ.CM.01.SIVcpzCAML3	G	P	R.E	OICT	Q	D
CPZ.CM.05.SIVcpzEK505	G	S	R.E	K	PPDNN.K	E
CPZ.CM.05.SIVcpzL187	T	P	K	PPDNN.K	E	H
CPZ.CM.05.SIVcpzMB66	T	O	E	P	E	T
CPZ.CM.05.SIVcpzWT145	KK	S	G	E	L	CAAR
CPZ.GA.88.GAB1	R	P	R.E	OICA	Q	EGT
CPZ.TZ.01.TAN1	TH	PLV	VOT	LCA	HPREREGAGDSTDTSG	C
CPZ.US.85.CPZUS	T	VPIVERGIK	ET	LPGK	Q	Q

HIV-1/SIVcpz proteins

HIV-1/SIVcpz proteins

B.FR.83.HXB2	EALLDTGADDTVLEE	MSLPGRWKPKMTGGIGGPFKVRQDYDQILLIETGCHKAIGTIVLVGPTFNWIIIGRNLLLIQIGCTLNFPSPIETI	FWVKKPKGMGDPKVKQMPLEETEEKIKALVELICTEMEEKGEKISKIGPEN	M41L	Protease	Reverse transcriptase	(RT)	209
A1.KE.94.Q23_17	D.IN-K	K	M	T				209
A1.RU.03.03RU20_06_13	D.IN-K	K	M	L				209
A1.RW.93.93RW037A	D.IN-K	R	M	K				209
A1.SE.94.SE7253	D.IN-K	K	M	K				209
A1.TZ.01.A173	D.IN-K	K	M	KR				209
A1.UA.00.98UA0116	D.ID-K	K	I	L				209
A1.UG.92.92UG037	D.IN-K	K	M	L				209
A1.UG.98.98UG57136	D.IN-K	T-K	A	D				210
A2.CD.97.97CDKPE4	D.IN-K	A	KR	M				209
A2.CD.97.97CDKPS10	D.IN-K	A	KR	M				209
A2.CD.97.97CDKTB48	D.IN-K	V	KR	M				202
A2.CY.94.94CY017_41	D.IN-K	A	KR	M				209
A.SN.01.DDH579	D.IN-K	K	M	K				208
A.SN.01.DDU369	D.IN-K	K	M	K				208
A.SN.96.DDU360	D.IN-K	K	M	K				208
A.ZA.04.04ZASK162B1	D.IN-K	K	M	K				208
B.AR.00.ARMS008	ID	TV	Y	K				209
B.AU.96.MBCD36	K	N	V	K				209
B.CO.01.PCM074	ID	E	T	K				210
B.GA.88.OYI	N	N	N	L				209
B.NL.00.671_00T36	D	N	S	T				219
B.RU.04.04RU129005	N	N	V	I				215
B.TH.90.RK132	N	N	V	I				209
B.US.90.WEAU160	D	N	K	V				209
B.US.98.1058_11	N	N	P	N				206
C.AR.01.ARG4006	K	N	VM	K				205
C.BR.04.04BR013	IE	K	I	V				213
C.BR.92.BR025_d	IK	N	K	A				208
C.BW.00.00BW07621	D	IN	K	KR				205
C.ET.86.ETH2220	IN	K	L	KR				216
C.IN.95.95IN21068	V	K	R	K				205
C.IN.99.01IN565_10	LA	K	K	T				205
C.KE.00.KER2010	IN	K	VI	K				211
C.TZ.01.BD9_11	IN	K	R	K				205
C.UY.01.TRA3011	K	N	V	K				205
C.ZA.04.SK164B1	IN	K	K	S				205
C.ZA.05.05ZASK245B1	IN	K	K	L				212
C.ZM.02.02ZM115	K	K	H	PL				210
C.ZM.96.96ZM651	IN	K	E	PM				205
D.CD.83.ELI	N	K	P	Q				208
D.CD.83.NDK	IN	K	Y	M				208
D.CM.01.01CM_4412HAL	D	IN	K	P				210
D.KE.01.NKU3006	ID	K	VD	R				208
D.TD.99.MN012	D	ID	K	V				210
D.TZ.01.A280	IN	K	K	O				210
D.UG.94.94UG114	IN	K	PL	L				210
D.UG.99.99UGD23550	V	K	E	VPV				208
D.UG.99.99UGK03958	V	N	K	V				208
D.ZA.86.86Z82	N	K	PL	I				208
F1.BE.93.VI850	D	IN	K	N				209
F1.BR.89.B2126	D	IN	O	K				209
F1.BR.93.93BR020_1	D	IN	K	N				209
F1.FI.93.FIN9363_1	D	IN	K	K				209
F1.FI.93.FIN9363	D	IN	K	K				209
F1.FR.96.MP411	D	ID	K	I				211
F2.CM.02.02CM_0016BBY	D	IN	S	K				209
F2.CM.95.MP255	D	IN	K	P				209
F2.CM.95.MP257	D	IN	K	VS				209
F2.CM.97.CM53657	D	IN	S	K				209
G.BE.96.DRCHL	ID	K	S	KR				208
G.CM.01.01CM_4049HAN	D	IN	K	I				208
G.ES.99.X138	D	IN	K	L				207
G.KE.93.HH8793_12_1	D	IK	K	L				208
G.NG.92.92NG083	G	IN	K	I				208
G.SE.93.SE6165	D	IN	K	I				206
H.BE.93.VI991	D	IN	K	E				207
H.BE.93.VI997	IN	L	K	I				207
H.CF.90.056	IN	K	E	VA				208
J.SE.93.SE7887	D	ID	R	K				207
J.SE.94.SE7022	D	IN	K	NEVP				207
K.CD.97.EQTB11C	IN	K	Q	V				209
K.CM.96.MP535	IN	K	V	Q				209

M41L

Protease \ / p66, p51 Reverse transcriptase (RT)

B_FR_83_HXB2	EALLDTGADDTVEE	MSLPGRWKPKMIGGIGGFKVRQXDQLLIEICGHKAIGTAVLGGPTVNIIGRLLLQIGCTLNFPIPSIETVPLKPKGMGDKVKQWPLTEKIKALVEICTMEKEGKISKIGPEN	209
01_AE_CF_90_90CF402	D	IN-K-K-M-----D--T--T-K-E--	209
01_AE_CN_05_F0051	D	IN-K-K-M-----D--T--T-K-E--	209
01_AE_HK_x_HK001	D	IN-K-K-M-----D--T--T-K-E--	206
01_AE_JP_93_93JP_NH1	D	IN-K-K-M-----D--T--T-K-E--	207
01_AE_TH_01_0UR4141	D	IN-K-K-M-----D--T--T-K-E--	208
01_AE_TH_02_0UR7691	D	IN-K-K-M-----D--T--T-K-E--	209
01_AE_TH_90_CM240	D	IN-K-K-M-----D--T--T-K-E--	214
02_AG_CM_02_02CM_1669LE	D	IN-K-K-M-----D--T--T-K-E--	209
02_AG_EC_x_EC041	I	K-K-M-----L--T--T-S--	209
02_AG_FR_91_DJ264	I	K-K-M-----L--T--T-S--	209
02_AG_GH_03_GHNU196	KVE	K-K-M-----L--T--T-S--	210
02_AG_NG_x_HNG	D	IN-K-K-M-----D--T--T-A--	210
02_AG_SN_98_MPL1211	D	IN-K-K-M-----D--T--T-A--	209
02_AG_UZ_02_02UZ693	D	ID-K-K-M-----L--H-TD-A--	209
03_AB_RU_97_KAL153_2	D	IN-K-K-M-----T--E--TD--G--	208
04_CPX_CV_94_CV032	D	IN-K-K-M-----L--L--TD--K--	208
05_DF_BE_x_VI1310	D	IN-K-K-M-----L--L--TD--K--	209
06_CPX_AU_96_BFP90	D	IN-K-K-M-----L--L--TD--K--	209
07_BC_CN_97_CN54	G	D-LN-K-K-I-M-----L--L--T--D--	211
08_BC_CN_97_97CNGX_6F	D	LN-K-K-E-P-----L--L--T--D--	205
09_CPX_GH_96_96GH2911	D	LN-K-K-E-P-----L--L--T--D--	208
10_CD_TZ_96_96TZ_BF061	D	IN-K-K-M-----L--L--T--A--	208
11_CPX_GR_x_GR17	N	K-M-----Y--T--K--R--	208
12_BF_AR_99_ARMA159	D	IN-K-K-I-M-----VD--T--	208
13_CPX_CM_96_L849	K	IN-K-K-NMS-E-K-I-M-----L--L--T--	209
14_BG_ES_99_X397	D	IN-K-K-I-M-----L--L--T--K--	216
15_01B_TH_99_99TH_MU2079	P	D-IMP-K-N-P-K-----L--R--	208
16_A2D_KR_97_97KR004	D	IN-K-K-T-EKR-----L--K--E--	208
18_CPX_CU_99_CU76	D	IN-K-K-M-V-L-----L--K--	209
19_CPX_CU_99_CU7	D	IN-K-K-M-KR-----L--K--	207
20_BG_CU_03_CB134	D	IN-K-K-P-Q-----L--D--	203
21_A2D_KE_91_KNH1254	N	K-K-I-M-----L--L--R--	207
23_BG_CU_03_CB118	D	IN-K-K-P-K-----L--L--	205
24_BG_CU_03_CB378	D	IN-K-K-I-M-----L--L--	200
25_CPX_CM_x_101BA	D	IN-K-K-M-S-K-I-M-----L--ND--R--	208
28_BF_BR_99_BREPM12609	D	IN-K-K-D-D-T-----T--	209
29_BF_BR_02_BREPM119	D	IN-K-K-EN-----L--L--E--	209
31_BC_BR_02_L10PA	IE	N-K-N-P-K-----L--L--E--	205
33_01B_WY_05_05WYKL007_1	D	IN-M-M-KR-----L--I--	209
A1C_TZ_02_C03710	IN	-V-K-S-M-L-----L--T--K--T--	206
A1CDGKU_ZA_99_CM4	D	I-K-M-R-----L--TA-E--T--	209
A1DHK_NO_97_97NOGHL3	D	IN-K-K-A-I-M-----L--L--	209
A1DHU_GA_x_V1354	D	IN-L-K-VP-----L--L--Q--R--	208
A2D_KE_99_KER2003	D	IH-K-K-VV-O-T-----L--MD--R--	209
AF2_CM_02_02CM_3163MN	D	IN-K-K-M-----L--L--R--	209
AGU_CM_01_01CM_0989MO	S	IN-K-K-P-Q-L-----L--RI--T--	203
AHJU_CM_01_01CM_1296NG	D	I-K-K-P-K-----L--TA-D--T--	205
BC_CN_96_YNRL9607	VN	K-K-M-L-----L--L--E--	209
BC_MM_99_mIDU103	D	IN-K-K-VP-----L--L--E--	209
BF1_BR_02_02BR006	D	IN-K-K-V-----F--MM-L--L--	208
0708_CN_00_HH069	V	-T-K-E-P-----L--L--T--	205
U_CD_83_83CD003	V	-T-K-KR-----L--L--T--L--	210
U_CD_90_90CD121E12	V	-T-K-KR-----L--L--T--L--	210
U_GD_99_99GD303	G	I-K-R-R-----S--A--I--T--	208
U_NL_x_U_NL_95_H10986_D1	U	NL-x-U-NL-95-H10986-D1	209
N_CM_02_DJ00131	I	IO-E-K-NVT-D-O-R-V-----F--R--A--E--RO--A--O--R--	214
N_CM_04_04CM_1015_04	I	IO-E-K-N-T-D-O-R-V-----F--R--A--E--R--R--	216
N_CM_04_04CM_1131_03	I	IO-E-K-N-T-D-O-R-V-----F--R--A--E--R--R--	216
N_CM_95_YBF30	I	IO-E-K-N-TVD-Q-R-V-----L--K--E--R--R--	216
N_CM_97_YBF106	I	IO-E-K-N-T-D-Q-R-V-----F--R--A--E--R--R--	216
O_BE_87_ANT70	V	NN-IO-E-K-KE-NVTV-E-REVO-----I--GL--AP--SK-E--TA--O--Q--R--	205
O_CM_91_MVP5180	NN	IO-E-K-KE-NVTV-YO-REVO-----L--I--GL--AP--SR-E--TA--O--Q--R--	205
O_CM_96_96CMAB637	V	NN-TO-E-T-GL-GNVTV-E-K-VO-----I--GL--AP--SR-E--TA--O--Q--R--	207
O_SN_99_SEMP1300	V	NN-IO-E-K-T-KE-N-VPV-E-REVL-----I--GL--AP--SK-E--TA--O--Q--R--	205
CPZ_CD_90_ANT	Q	V-G-IH-Q-N-T-S-Q-NKVP-Q-GDRITVIA-----L--N--V--CLL--E--R--SK-E--K--DKL--A--N--R--D--	209
CPZ_CM_01_SIVcpzCAM13	IQD	IO-Q-I-K-NVS-E-K-VO-----L--I--V--S--RI--SA--T--Q--	208
CPZ_CM_05_SIVcpzEX505	G	IO-E-K-K-NVI-O-K-V-----I--O--K--L--T--Q--	215
CPZ_CM_05_SIVcpzL87	D	LE-G-K-N-P-G-K-L-----I--O--R--R--	212
CPZ_CM_05_SIVcpzME66	IE	G-K-NVT-D-KR-V-----I--S--R--R--R--RV--	218
CPZ_CM_05_SIVcpzWT145	I	D-LN-K-S-K-PERV-E-K-ITS-----D--K--F--R--T--K--	202
CPZ_GA_88_GAB1	I	R-IO-L-K-F-NH-E-R-VV-----K--P--V--S--K--E--T--O--	207
CPZ_TZ_01_THAN1	S	FCN-IR-K-Q-T-T-VP-SE-YN-EVQ-GNEKVA-----E--I--I--K--L--V--K--Q--E--T--O--AV--	205
CPZ_US_85_CPZUS	DN	IQIE-T-R-M-K-HVN-E-R-Q-S-----I--I--K--L--S--K--R--R--T--Q--TRV--	211

HIV-1/SIVcpz proteins

HIV-1/SIVcpz proteins

	D67N	K70R	Asp 110 catalytic site	polymerase motif
B.FR.83.HXB2	YINTVPFAIKKDKSTKWRKLVDFRELNKRKTODFWEVQLGHPHAGLKKKSVTVLVDGDAYFVSPVLDLDEDFRKYTAFTIPSSINNETPGIRYQNVLPQGWKSPALFOSSMTKILIEPRFKQNPDIIVIQIMDDLY		H-E-T-V	SK-E-343
A1.KE.94.Q23.17			LK-E-S	LK-E-343
A1.RU.03.03RW020.06.13			L-E-I-S	L-E-I-343
A1.RW.93.93RW037A			LK-E-T	LK-E-I-343
A1.SE.94.SE7253			L-E-I-S	L-E-I-343
A1.TZ.01.A173			S-G-V	SK-E-I-343
A1.UA.00.98UA0116			S-S	SK-E-343
A1.UG.92.92UG037			S-S	SK-E-343
A1.UG.98.98UG57136			S-S	SK-E-343
A2.CD.97.97CDKPE4			S-S	SK-E-343
A2.CD.97.97CDKPS10			S-S	SK-E-343
A2.CD.97.97CDKTB48			S-S	SK-E-343
A2.CY.94.94CY017_41			S-S	SK-E-343
A.SN.01.DDI579			S-S	SK-E-343
A.SN.01.DDU369			S-S	SK-E-343
A.SN.96.DDU360			S-S	SK-E-343
A.ZA.04.04ZASK162B1			S-S	SK-E-343
B.AR.00.ARMS008			S-S	SK-E-343
B.AU.96.MBCD36			S-S	SK-E-343
B.CO.01.PCM074			S-S	SK-E-343
B.GA.88.OYI			S-S	SK-E-343
B.NL.00.671.00T36			S-S	SK-E-343
B.RU.04.04RU129005			S-S	SK-E-343
B.TH.90.RK132			S-S	SK-E-343
B.US.90.WEAU160			S-S	SK-E-343
B.US.98.1058.11			S-S	SK-E-343
C.AR.01.ARG4006			S-S	SK-E-343
C.BR.04.04BR013			S-S	SK-E-343
C.BR.92.BR025_d			S-S	SK-E-343
C.BW.00.00BW07621			S-S	SK-E-343
C.ET.86.ETH2220			S-S	SK-E-343
C.IN.95.95IN21068			S-S	SK-E-343
C.IN.99.01IN565_10			S-S	SK-E-343
C.KE.00.KER2010			S-S	SK-E-343
C.TZ.01.BD9_11			S-S	SK-E-343
C.UY.01.TRA3011			S-S	SK-E-343
C.ZA.04.SK164B1			S-S	SK-E-343
C.ZA.05.05ZASK245B1			S-S	SK-E-343
C.ZM.02.02ZM115			S-S	SK-E-343
C.ZM.96.96ZM651			S-S	SK-E-343
D.CD.83.ELI			S-S	SK-E-343
D.CD.83.NDK			S-S	SK-E-343
D.CM.01.01CM.4412HAL			S-S	SK-E-343
D.KE.01.NKU3006			S-S	SK-E-343
D.TD.99.MN012			S-S	SK-E-343
D.TZ.01.A280			S-S	SK-E-343
D.UG.94.94UG114			S-S	SK-E-343
D.UG.99.99UGD2550			S-S	SK-E-343
D.UG.99.99UGK03958			S-S	SK-E-343
D.ZA.86.K482			S-S	SK-E-343
F1.BE.93.VI850			S-S	SK-E-343
F1.BR.89.B2126			S-S	SK-E-343
F1.BR.93.93BR020_1			S-S	SK-E-343
F1.FI.93.FIN9363_1			S-S	SK-E-343
F1.FR.96.MP411			S-S	SK-E-343
F2.CM.02.02CM.0016BBY			S-S	SK-E-343
F2.CM.95.MP255			S-S	SK-E-343
F2.CM.95.MP257			S-S	SK-E-343
F2.CM.97.CM53657			S-S	SK-E-343
G.BE.96.DRCHL			S-S	SK-E-343
G.CM.01.01CM.4049HAN			S-S	SK-E-343
G.ES.99.X138			S-S	SK-E-343
G.KE.93.HH8793_12_1			S-S	SK-E-343
G.NG.92.92NG083			S-S	SK-E-343
G.SE.93.SE6165			S-S	SK-E-343
H.BE.93.VI991			S-S	SK-E-343
H.BE.93.VI997			S-S	SK-E-343
H.CF.90.056			S-S	SK-E-343
J.SE.93.SE7887			S-S	SK-E-343
J.SE.94.SE7022			S-S	SK-E-343
K.CD.97.EQTB11C			S-S	SK-E-343
K.CM.96.MP535			S-S	SK-E-343

	D67N	K70R	Asp 110 catalytic site	polymerase motif	
B_FR.83_HXB2	PYNTPTVAIKKDKSTKWRKLVDFRELNKRRTODFWEVQLGTFHPAGLKKKSVTVLVDGDAYFVSLDEDFRKYTAFTIPSSINNETPGIRYQNVLPQGWKSGPALFOSSWTKLLEPPFRKQNPDIIVIQIMDDLY				343
01 AE.CF.90.90CF402			G	AR-E	343
01 AE.CN.05.FJ051			V	IK-E	343
01 AE.HK.x.HK001			V	AN-E	340
01 AE.JP.93.93JP.NH1			K	AN-E	341
01 AE.TH.01.01R4141			S	IK-EM	342
01 AE.TH.02.02R7691			L	RK-EM	343
01 AE.TH.90.CM240			S	IK-EM	343
02 AG.CM.02.02CM.16691E			S	IK-EM	348
02 AG.EC.x.EC041			K	TR-E	343
02 AG.FR.91.DJ264			K	AK-E	343
02 AG.GH.03.GHNJ196			K	IK-E	343
02 AG.NG.x.IEING			H	TK-EM	344
02 AG.SN.98.MP1211			K	TK-E	343
02 AG.UZ.02.02UZ693			V	TK-EL	343
03 AB.RU.97.KAL153.2			YK	IK-E	343
04 CPX.CV.94.CY032			O	B-E	343
05 DF.BE.x.VI1310			PE	FK-E	342
06 CPX.AU.96.BFP90			KE	C	343
07 BC.CN.97.CNS4			I	IK-E	345
08 BC.CN.97.97CNGX.6F			I	IK-E	343
09 CPX.GH.96.96GH2911			I	L	339
10 CD.TZ.96.96TZ.BF061			K	IK-E	342
11 CPX.GR.x.GR17			Y	OM	342
12 BF.AR.99.ARMA159			L	T	342
13 CPX.CM.96.1849			S	EV	343
14 BG.ES.99.X397			A	T	350
15 01B.TH.99.99TH.MU2079			K	T-E	342
16 A2D.KR.97.97KR004			S	RK-E	342
18 CPX.CU.99.CU76			V	K-EM	343
19 CPX.CU.99.CU7			M	E-R	343
20 BG.CU.03.CB134			PE	E-E	341
21 A2D.KE.91.KNH1254			S	D	342
23 BG.CU.03.CB118			H	E	337
24 BG.CU.03.CB378			S	E	341
25 CPX.CM.x.101BA			E	EL	339
28 BF.BR.99.BREPM12609			KE	E	334
29 BF.BR.02.BREPM119			R	T-A	342
31 BC.BR.02.110PA			KE	R	343
33_01B.WY.05.05MYKL007_1			K	T	343
			KS	R	339
			G	IK-EM	343
A1C.TZ.02.CO3710			G	AK	340
A1CDGKU.ZA.99.CM4			K	AK-E	343
A1DHK.NO.97.97NOGLL3			A	AK-E	343
A1GHU.GA.x.VI354			Y	EM	342
A2D.KE.99.KER2003			S	EM	342
AP2.CM.02.02CM.3163MN			KE	EM	343
AGU.CM.01.01CM.0989MO			PK	D	341
ARU.CM.01.01CM.1296NG			Y	E	337
BC.CN.96.YNRL9667			K	K-E	339
BC.MM.99.mIDD103			K	C	343
BF1.BR.02.02BR006			E	E	342
0708.CN.00.HH069			K	E	339
U.CD.83.83CD003			N	E	344
U.CD.90.90CD121E12			N	E-A	343
U.GR.99.GR303			K	IK-E	342
U.NL.x.U.NL.95.H10986_D1			PG	Y- AK-EVI	343
N.CM.02.DJ00131			O	KH-E	348
N.CM.04.04CM.1015_04			O	KH-E	350
N.CM.04.04CM.1131_03			O	KH-E	350
N.CM.95.YBF30			O	EK-E	350
N.CM.97.YBF106			O	KH-E	350
O.BE.87.AN1770			G	RD	339
O.CM.91.MVPS180			G	RD	339
O.CM.96.96CMABB637			G	S-EVE	341
O.SN.99.SEMP1300			G	N-E	339
CPZ.CD.90.ANT			I	N-ELE	343
CPZ.CM.01.SIVcpzCAM13			I	A	343
CPZ.CM.05.SIVcpzEK505			I	AK	342
CPZ.CM.05.SIVcpzL87			I	N	346
CPZ.CM.05.SIVcpzMB66			I	N	346
CPZ.CM.05.SIVcpzMT145			I	TKH-E	342
CPZ.GA.88.GAB1			I	EK	341
CPZ.TZ.01.TAN1			I	L	339
CPZ.US.85.CPZUS			I	R	345

HIV-1/SIVcpz proteins

HIV-1/SIVcpz protein alignment: POL

	T215Y	K219Q	
B.FR.83.HXB2	VSDLEIGQHRTKIEELRQHLRGLITTPDKKQKPEPFLWMGYELHPDKWTQPIVLPEKSDWTWVNDIQKLVGKLNWASQIYPIGIVKRVQLCKLRGTALTEVPLPTEEALELAENRELLKPEVHGVYDPS		477
A1.KE.94.Q23.17	-----A-----A-----S-----I-----E-----K-----A-----A-----D-----V-----		477
A1.RU.03.03RU020.06.13	-----A-----S-----F-----M-----D-----M-----D-----A-----A-----D-----V-----		477
A1.RW.93.93RW037A	-----A-----D-----A-----S-----F-----E-----E-----A-----K-----R-----A-----D-----V-----		477
A1.SE.94.SE7253	-----N-----K-----F-----D-----E-----M-----D-----A-----K-----A-----D-----V-----		477
A1.TZ.01.A173	-----G-----A-----S-----F-----M-----D-----A-----K-----A-----D-----V-----		477
A1.UA.00.98UA0116	-----A-----V-----A-----A-----F-----F-----Q-----N-----A-----K-----R-----A-----D-----V-----		477
A1.UG.98.98UG0537	-----A-----A-----A-----A-----F-----F-----K-----R-----A-----K-----R-----A-----D-----V-----		477
A1.UG.98.98UG57136	-----A-----A-----A-----A-----F-----F-----K-----R-----A-----K-----R-----A-----D-----V-----		477
A2.CD.97.97CDKPE4	-----A-----A-----A-----A-----F-----F-----K-----R-----A-----K-----R-----A-----D-----V-----		469
A2.CD.97.97CDKS10	-----S-----V-----A-----A-----K-----K-----A-----K-----A-----D-----V-----		470
A2.CD.97.97CDKTIB48	-----N-----S-----V-----A-----A-----K-----K-----A-----K-----A-----D-----V-----		477
A2.CY.94.94CY017_41	-----A-----A-----A-----A-----K-----K-----O-----D-----A-----K-----A-----D-----V-----		476
A.SN.01.DDI579	-----A-----S-----N-----01-----D-----D-----U-----J-----3-----6-----A-----K-----R-----A-----D-----V-----		476
A.SN.01.DDU369	-----A-----S-----N-----96-----D-----D-----U-----J-----3-----6-----A-----K-----R-----A-----D-----V-----		476
A.ZA.04.04ZASK162B1	-----E-----K-----F-----F-----M-----M-----N-----N-----Y-----A-----R-----K-----A-----V-----		477
B.AR.00.ARMS008	-----E-----K-----F-----F-----M-----M-----N-----N-----Y-----A-----R-----K-----A-----V-----		477
B.AU.96.MBCD36	-----E-----K-----F-----F-----M-----M-----N-----N-----Y-----A-----R-----K-----A-----V-----		477
B.CO.01.PCM074	-----E-----K-----F-----F-----M-----M-----N-----N-----Y-----A-----R-----K-----A-----V-----		478
B.GA.88.OYI	-----M-----R-----K-----F-----D-----H-----I-----S-----K-----K-----O-----I-----V-----		477
B.NL.00.67L.00T36	-----M-----R-----K-----F-----D-----H-----I-----S-----K-----K-----O-----I-----V-----		487
B.RU.04.04RU129005	-----M-----R-----K-----F-----D-----H-----I-----S-----K-----K-----O-----I-----V-----		483
B.TH.90.RK132	-----K-----F-----F-----F-----D-----E-----K-----K-----A-----K-----H-----A-----H-----		477
B.US.90.WEAU160	-----K-----F-----F-----F-----D-----E-----K-----K-----A-----K-----H-----A-----H-----		474
B.US.98.1058.II	-----A-----K-----E-----K-----F-----I-----O-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		473
C.AR.01.ARG4006	-----A-----K-----E-----K-----F-----I-----O-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		473
C.BR.04.04BR013	-----A-----K-----E-----K-----F-----I-----O-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		481
C.BR.92.BR025_d	-----V-----R-----K-----K-----F-----Q-----ED-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		476
C.BW.00.00BW07621	-----A-----P-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		473
C.ET.86.ETH2220	-----A-----K-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		484
C.IN.95.95IN21068	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		473
C.IN.99.01IN565_10	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		473
C.KY.01.KER2010	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		473
C.TZ.01.BD9_11	-----A-----V-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		479
C.UY.01.TRA3011	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		473
C.ZA.04.SK164B1	-----M-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		473
C.ZA.05.05ZASK245B1	-----M-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		480
C.ZM.02.02ZM115	-----M-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		478
C.ZM.96.96ZM651	-----K-----E-----E-----K-----F-----R-----S-----K-----E-----N-----N-----E-----R-----		473
D.CD.83.ELI	-----K-----E-----E-----K-----F-----R-----S-----K-----E-----N-----N-----E-----R-----		476
D.CD.83.NDK	-----A-----K-----E-----K-----F-----T-----E-----T-----E-----K-----A-----A-----I-----K-----K-----		476
D.CM.01.01CM.4412HAL	-----O-----E-----K-----F-----S-----I-----HOE-----S-----K-----K-----R-----A-----R-----T-----		478
D.KE.01.NKU3006	-----I-----G-----K-----F-----Y-----H-----E-----E-----K-----K-----A-----K-----R-----T-----		478
D.TD.99.MN012	-----I-----V-----G-----K-----F-----Y-----H-----E-----E-----K-----K-----A-----K-----R-----T-----		478
D.TZ.01.A280	-----V-----G-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		478
D.UG.94.94UG114	-----V-----G-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		476
D.UG.99.99UGD2550	-----V-----G-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		476
D.UG.99.99UGK03958	-----V-----G-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		476
D.ZA.86.R482	-----E-----H-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477
F1.BE.93.VI850	-----L-----M-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477
F1.BR.89.B2126	-----L-----M-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477
F1.BR.93.93BR020_1	-----L-----M-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477
F1.FI.93.FIN9363	-----L-----M-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477
F1.FR.96.MP411	-----L-----M-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		479
F2.CM.02.02CM.0016BBY	-----L-----M-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477
F2.CM.95.MP255	-----L-----M-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477
F2.CM.95.MP257	-----L-----M-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477
F2.CM.97.CM53657	-----L-----M-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477
G.BE.96.DRCL	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		474
G.CM.01.01CM.4049HAN	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		476
G.ES.99.X138	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		475
G.KE.93.HH8793_12_1	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		476
G.NG.92.92NG083	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		476
G.SE.93.SE6165	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		474
H.BE.93.VI891	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		475
H.BE.93.VI997	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		475
H.CF.90.056	-----A-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		476
J.SE.93.SE7887	-----E-----R-----K-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		475
J.SE.94.SE7022	-----E-----R-----K-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		475
K.CD.97.EQTB11C	-----P-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477
K.CM.96.MP535	-----P-----A-----E-----K-----F-----Q-----O-----D-----A-----K-----R-----A-----D-----V-----		477

T215Y K219Q

B_FR.83_HXB2	VSDLEIGQHRTKIEELRQHLLRWGLITTPDKKHOKEPFFLWMGYELHPDKWTQPIVLPKDSWTVNDIQKLVGKLNWASQIYPIKVRQICKLRGTKALTEVILPITEAELEAENRELLKPEVHGVIYDPS	477
01 AE.CF.90.90CF402	V-D-A-S-F-R-A-A-DIVT	477
01 AE.CN.05.FJ051	I-A-S-F-E-R-K-A-RIK	477
01 AE.HK.x.HK001	I-A-S-F-E-R-E-A-IK	474
01 AE.JP.93.93JP.NH1	R-I-A-S-F-E-R-E-A-IK	475
01 AE.TH.01.OUR41I	A-S-F-E-R-E-A-K	476
01 AE.TH.02.OUR769I	A-S-F-E-R-E-A-K	477
01 AE.TH.90.CM240	A-S-F-E-R-E-A-K	482
02 AG.CM.02.02CM.16691E	A-E-F-F-Q-N-A-K-A-DIVT	477
02 AG.EC.x.EC041	R-A-V-E-K-F-Q-A-K-A-DWVI	477
02 AG.FR.91.DJ264	A-E-K-F-Q-A-K-A-DIV	477
02 AG.GH.03.GHNJ196	A-E-K-F-Q-A-K-A-DIV	478
02 AG.NG.x.IBNG	A-E-K-F-Q-A-K-A-DIV	477
02 AG.SN.98.MP1211	A-E-K-F-Q-A-K-A-DIV	477
02 AG.UZ.02.02UZ693	A-E-K-F-Q-A-K-A-DIV	477
03 AB.RU.97.KAL153_2	A-E-K-F-Q-A-K-A-DIV	477
04 CPX.CV.94.CV032	A-E-K-F-Q-A-K-A-DIV	476
05 DF.BE.x.VI1310	A-E-K-F-Q-A-K-A-DIV	477
06 CPX.AU.96.BFP90	A-E-K-F-Q-A-K-A-DIV	479
07 BC.CN.97.CNS4	A-E-K-F-Q-A-K-A-DIV	477
08 BC.CN.97.97CNGX_6F	A-E-K-F-Q-A-K-A-DIV	473
09 CPX.GH.96.96GH2911	A-E-K-F-Q-A-K-A-DIV	476
10 CD.TZ.96.96TZ_BF061	A-E-K-F-Q-A-K-A-DIV	476
11 CPX.GR.x.GR17	A-E-K-F-Q-A-K-A-DIV	476
12 BF.AR.99.ARMA159	A-E-K-F-Q-A-K-A-DIV	477
13 CPX.CM.96.1849	A-E-K-F-Q-A-K-A-DIV	484
14 BG.ES.99.X397	A-E-K-F-Q-A-K-A-DIV	476
15 01B.TH.99.99TH_MU2079	A-E-K-F-Q-A-K-A-DIV	477
16 A2D.KR.97.97KR004	A-E-K-F-Q-A-K-A-DIV	475
18 CPX.CU.99.CU76	A-E-K-F-Q-A-K-A-DIV	476
19 CPX.CU.99.CU77	A-E-K-F-Q-A-K-A-DIV	471
20 BG.CU.03.CB134	A-E-K-F-Q-A-K-A-DIV	475
21 A2D.KR.91.KNH1254	A-E-K-F-Q-A-K-A-DIV	473
23 BG.CU.03.CB118	A-E-K-F-Q-A-K-A-DIV	468
24 BG.CU.03.CB378	A-E-K-F-Q-A-K-A-DIV	477
25 CPX.CM.x.101BA	A-E-K-F-Q-A-K-A-DIV	477
28 BF.BR.99.BREPM12609	A-E-K-F-Q-A-K-A-DIV	473
29 BF.BR.02.BREPM119	A-E-K-F-Q-A-K-A-DIV	473
31 BC.BR.02.110PA	A-E-K-F-Q-A-K-A-DIV	477
33_01B.WY.05.05MYKL007_1	A-E-K-F-Q-A-K-A-DIV	477
A1C.TZ.02.CO3710	A-E-K-F-Q-A-K-A-DIV	474
A1CDGKU.ZA.99.CM4	A-E-K-F-Q-A-K-A-DIV	477
A1DHK.NO.97.97NOGLI3	A-E-K-F-Q-A-K-A-DIV	477
A1GHU.GA.x.VI354	A-E-K-F-Q-A-K-A-DIV	476
A2D.KR.99.KER2003	A-E-K-F-Q-A-K-A-DIV	476
AP2.CM.02.02CM.3163MN	A-E-K-F-Q-A-K-A-DIV	475
AGU.CM.01.01CM_0989MO	A-E-K-F-Q-A-K-A-DIV	471
ARUTU.CM.01.01CM_1296NG	A-E-K-F-Q-A-K-A-DIV	473
BC.CN.96.YNRL9667	A-E-K-F-Q-A-K-A-DIV	476
BC.MM.99.mIDDU103	A-E-K-F-Q-A-K-A-DIV	473
BF1.BR.02.02BR006	A-E-K-F-Q-A-K-A-DIV	473
0708.CN.00.HH069	A-E-K-F-Q-A-K-A-DIV	477
U.CD.83.83CD003	A-E-K-F-Q-A-K-A-DIV	477
U.CD.90.90CD121E12	A-E-K-F-Q-A-K-A-DIV	476
U.GR.99.GR303	A-E-K-F-Q-A-K-A-DIV	477
U.NL.x.U.NL_95_H10986_D1	A-E-K-F-Q-A-K-A-DIV	477
N.CM.02.DJ00131	A-E-K-F-Q-A-K-A-DIV	482
N.CM.04.04CM.1015_04	A-E-K-F-Q-A-K-A-DIV	484
N.CM.04.04CM.1131_03	A-E-K-F-Q-A-K-A-DIV	484
N.CM.95.YBF30	A-E-K-F-Q-A-K-A-DIV	484
N.CM.97.YBF106	A-E-K-F-Q-A-K-A-DIV	484
O.BE.87.AN170	A-E-K-F-Q-A-K-A-DIV	473
O.CM.91.MVPS180	A-E-K-F-Q-A-K-A-DIV	475
O.CM.96.96CMABB637	A-E-K-F-Q-A-K-A-DIV	473
O.SN.99.SEM1300	A-E-K-F-Q-A-K-A-DIV	477
CPZ.CD.90.ANT	A-E-K-F-Q-A-K-A-DIV	476
CPZ.CM.01.SIVcpzCAM13	A-E-K-F-Q-A-K-A-DIV	480
CPZ.CM.05.SIVcpzEK505	A-E-K-F-Q-A-K-A-DIV	480
CPZ.CM.05.SIVcpzILB7	A-E-K-F-Q-A-K-A-DIV	476
CPZ.CM.05.SIVcpzMB66	A-E-K-F-Q-A-K-A-DIV	475
CPZ.CM.05.SIVcpzMT145	A-E-K-F-Q-A-K-A-DIV	473
CPZ.GA.88.GAB1	A-E-K-F-Q-A-K-A-DIV	473
CPZ.TZ.01.TAN1	A-E-K-F-Q-A-K-A-DIV	479
CPZ.US.85.CPZUS	A-E-K-F-Q-A-K-A-DIV	479

HIV-1/SIVcpz proteins

HIV-1/SIVcpz proteins

B.FR.83.HXB2	KDLIAELIQGQGGQWYQIQYQEPFKNLTGKVARMRGHTNDYKQLTEAVYKQITTSIVLWGK.TPKFKLPIQKQETWETWTEYMQATWIPWEPVNTPLVKLWYQLKXKPIVGAETFFVVDGAANRETKLGA	p51_end \\ Rnase H_start	610
A1.KE.94.Q23_17	D---D---F---K-S---R-A-V---VVM---D---MD---L---D---A---		610
A1.RU.03.03RU20_06_13	V---D---D---KKS---AV---VA---I---KKS---R---A---M---I---		610
A1.RW.93.93RW037A_1	V---D---D---K-S---A-V---VVM---R---R---MD---D---I---R---		610
A1.SE.94.SE7253	LD---D---K-S---R-A-V---VVM---D---MD---D---A---D---R---		610
A1.TZ.01.A173	V---D---D---K-S---A-V---VVM---D---MD---D---I---D---R---		610
A1.UA.00.98UA0116	V---D---D---KKS---AV---G-I---R---A---M---I---T---		610
A1.UG.92.92UG037	D---I---K-S---A-V---VVM---D---MD---D---A---D---A---		610
A1.UG.98.98UG57136	D---D---KKS---A-V---VAM---R---D---MD---D---E-V---		610
A2.CD.97.97CDKFE4	D---D---KKS---A-I---R---D---MD---D---E-V---		610
A2.CD.97.97CDK510	S---S---KKS---A---R---D---MD---D---E-V---		610
A2.CD.97.97CDKTB48	D---D---KKS---A---R---D---MD---D---E-V---		610
A2.CY.94.94CY0117_41	A---S---KKS---A---R---D---MD---D---E-V---		610
A.SN.01.DDI579	N---D---K-S---R-V-V---VVM---D---MD---D---I---R---		609
A.SN.01.DDU369	V---D---K-S---R-V-V---VVM---D---MD---D---I---R---		609
A.SN.96.DDU360	D---D---KKS---R-V-V---VVM---D---MD---D---I---R---		609
A.ZA.04.04ZASK162B1	D---D---KKS---R-V-V---VVM---D---MD---D---I---R---		609
B.AR.00.ARMS008	V---V---DN---A---R---A---M---I---R---A---M---I---		610
B.AU.96.MBCD36	V---V---FT---A---K---A---K---K---I---N---N---VK---		610
B.CO.01.PCM074	V---V---P---I---S---R---S---S---*---S---I---		611
B.GA.88.OYI	V---L---K-V---A---Q---O---A---A---D---D---I---		610
B.NL.00.671_00T36	K---T---R---V---?---I---A---A---D---D---I---		620
B.TH.90.BK132	L---V---V---A---A---A---A---A---A---A---A---		616
B.US.90.WEAU160	L---V---V---A---A---A---A---A---A---A---A---		610
B.US.98.1058_11	L---V---V---A---A---A---A---A---A---A---A---		610
C.AR.01.ARG4006	E---K-T---R---AO---I---R---S---D---D---T---M---		606
C.BR.04.04BR013	D---ED---K-T---R---AO---I---R---S---D---D---P---		614
C.BR.92.BR025_d	N---ND---K-T---R---AL---I---R---A---D---*---I---M---		609
C.BW.00.00BW07621	D---D---ND---K-T---R---SR---D---D---D---L---V---D---I---		606
C.ET.86.ETH2220	ND---F-F---F-KRGT---AV---AL---R---A---D---A---V---I---		617
C.IN.95.95IN21068	D---D---K-T---R---A---AL---R---R---D---A---V---I---		606
C.IN.99.01INS65_10	L---HD---K-T---R---A---AL---R---R---D---A---V---I---		606
C.KE.00.KER2010	HD---K-T---R---A---AV---R---R---D---A---V---I---		606
C.TZ.01.BD9_11	HD---K-T---R---A---AV---R---R---D---A---V---I---		612
C.UY.01.TRA3011	D---TK---T---R---AL---I---R---A---D---A---M---M---		606
C.ZA.04.SK164B1	ND---K-T---R---AL---I---R---A---D---A---E---S---K---		606
C.ZA.05.05ZASK245B1	D---D---KR---T---R---A---T---AK---I---D---A---V---I---		613
C.ZM.02.02ZM115	DD---KRKA---AO---AO---I---R---D---A---V---SK---K---		611
C.ZM.96.96ZM651	HD---K-T---I---R---I---R---L---L---D---A---V---		606
D.CD.83.ELI	H---H---A---R---S---R---R---R---A---A---I---		609
D.CD.83.NDK	L---D---T---S---A---A---A---A---I---I---I---		609
D.CM.01.01CM_4412HAL	V---D---W---S---A---A---A---DA---M---I---S---D---		611
D.KE.01.NKU3006	D---D---KL---AQ---C---R---R---AQ---C---I---S---		609
D.TD.99.MN012	V---S---SW---AL---A---M---R---R---A---M---I---S---		611
D.TZ.01.A280	E---K-T---K-T---AL---G---I---R---A---R---R---		611
D.UG.94.94UG114	D---D---K-T---AO---C---R---R---A---C---I---R---		611
D.UG.99.99UGD23550	D---D---OY---K-T---AO---C---P---R---D---L---S---I---		609
D.UG.99.99UGK03958	D---D---OY---K-T---AO---C---R---R---D---L---S---R---		609
D.ZA.86.R482	N---I---A---A---G---R---R---R---I---R---T---R-Q---		609
F1.BE.93.VI850	D---N---KV---S---AL---RS---L---D---D---D---S---K---		611
F1.BR.89.B2126	H---K---S---K---L---L---D---D---L---D---K---K---		610
F1.BR.93.93BR020_1	H---K---S---K---L---L---D---D---L---D---K---K---		610
F1.FI.93.FIN9363_1	PKL---R---K---S---SL---D---R---L---D---D---L---D---S---K---		610
F1.FR.96.MPA11	L---D---KT---S---I-E-D---VAR-C---S---R---A---D---S---K---		612
F2.CM.02.02CM_0016BBY	HD---HR---KR---S---V---A---G---V---R---R---T---I---S---I---		610
F2.CM.95.MP255	HD---H---RKS---V---VA---G---V---R---R---I---T---A---		610
F2.CM.95.MP257	HD---H---RKS---V---VA---G---V---R---R---I---T---A---		610
F2.CM.97.CM53657	V---HD---H---R---S---V---A---G---V---R---R---I---T---A---		610
G.BE.96.DRCBL	V---V---Y---KGS---V---A---G---I---I---K---V---V---Y---		607
G.CM.01.01CM_4049HAN	E---V---LD---Y---KGS---V---A---I---I---R---V---Y---		609
G.ES.99.X138	E---V---LD---Y---KGS---V---A---I---I---R---V---Y---		608
G.KE.93.HH8793_12_1	E---V---E---Y---KRGT---V---A---A---I---R---R---T---A---Y---		609
G.NG.92.92NG083	E---V---PD---Y---KGS---V---A---G---I---R---R---T---P---Y---		609
G.SE.93.SE6165	E---V---LD---Y---KGS---V---A---A---I---R---R---T---P---Y---		607
H.BE.93.VI991	E---PD---K-S---V---A---A---H---H---H---H---H---M---		608
H.BE.93.VI997	PD---K-N-S---I---R---A---A---H---H---H---H---H---I---		608
H.C.F.90.056	R---R---K-T---I---I---R---S---H---H---H---H---H---Y-I		609
J.SE.93.SE7887	E---V---LD---KR-S---A-V---AL-A---R---R---D---D---M---S---T---		608
J.SE.94.SE7022	RE---V---LD---KR-S---SOV---AL-A---R---R---D---D---M---S---T---		608
K.CD.97.EQTb11C	H---H---Y---I---S---V---VAM---G---R---R---G---G---Q---		610
K.CM.96.MP535	ND---H---H---Y---I---S---V---A---G---R---R---H---K---R---		610

B.FR.83.HXB2	KDLIAELIQGGQWYQIYQEPFKNLKTKGVARMRGHTNDYKQLTEAVYKQITTSIVLWGK.TPKFKLPIQKQETWETWTEYMQATWIPEWEPVNTPLVKLWYQLEKPIVGAETFFYVDGAARRETKLQKA	p51_end	\\	Rnase H_start
01 AE.CF.90.90CF402	V-D-K-S-R-A-V-VA	R-R-R-M	D-M	S-Q
01 AE.CN.05.FJ051	D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
01 AE.HK.x.HK001	D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
01 AE.JP.93.93JP.NH1	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
01 AE.TH.01.OUP4141	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
01 AE.TH.02.OUP7691	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
02 AE.TH.90.CM240	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
02 AG.CM.02.02CM.16691E	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
02 AG.EC.x.EC041	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
02 AG.FR.91.DJ264	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
02 AG.GH.03.GHNJ196	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
02 AG.NG.x.IENG	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
02 AG.SN.98.MPI211	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
02 AG.UZ.02.02UZ693	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
03 AB.RU.97.KAL153_2	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
04 CDX.CV.94.CY032	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
05 DF.BE.x.VII1310	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
06 CDX.AU.96.BFP90	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
07 BC.CN.97.CM54	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
08 BC.CN.97.97CNGX.6F	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
09 CDX.GH.96.96GH2911	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
10 CD.TZ.96.96TZ.BF061	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
11 CDX.GR.x.GR17	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
12 BF.AR.99.ARMA159	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
13 CDX.CM.96.1849	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
14 BG.ES.99.X397	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
15 01B.TH.99.99TH.MU2079	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
16 A2D.KR.97.97KR004	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
18 CDX.CU.99.CU76	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
19 CDX.CU.99.CU7	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
20 BG.CU.03.CB134	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
21 A2D.KE.91.KNH1254	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
23 BG.CU.03.CB118	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
24 BG.CU.03.CB378	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
25 CDX.CM.x.101BA	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
28 BF.BR.99.BREPM12609	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
29 BF.BR.02.BREPM119	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
31 BC.BR.02.110PA	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
33_01B.MY.05.05MYKL007_1	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
A1C.TZ.02.CO3710	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
A1CDGKU.ZA.99.CM4	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
A1DHK.NO.97.97NOGLI3	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
A1GHU.GA.x.VI354	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
A2D.KE.99.KER2003	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
AF2.CM.02.02CM.3163MN	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
AGU.CM.01.01CM.0989MO	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
ARJUTU.CM.01.01CM.1296NG	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
BC.CN.96.YNRL9607	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
BC.MM.99.mDDU1003	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
BF1.BR.02.02BR006	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
0708.CN.00.HH069	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
U.CD.83.83CD003	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
U.CD.90.90CD121E12	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
U.GR.99.GR303	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
U.NL.x.U.NL.95.H10986_D1	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
N.CM.02.DJ00131	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
N.CM.04.04CM.1015_04	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
N.CM.04.04CM.1131_03	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
N.CM.95.YBF30	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
N.CM.97.YBF106	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
O.BE.87.ANI770	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
O.CM.91.MVPS180	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
O.CM.96.96CMAB637	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
O.SN.99.SEMP1300	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
CPZ.CD.90.ANT	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
CPZ.CM.01.SIVcpzCAM13	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
CPZ.CM.05.SIVcpzEK505	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
CPZ.CM.05.SIVcpzLI17	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
CPZ.CM.05.SIVcpzMB66	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
CPZ.CM.05.SIVcpzMT145	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
CPZ.GA.88.GAB1	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
CPZ.TZ.01.TAN1	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S
CPZ.US.85.CPZUS	V-V-D-K-S-R-A-V-A	R-R-R-M	D-L	S-S

HIV-1/SIVcpz proteins

B.FR.83.HXB2	GYVWNRGRQKVVTLTDTTNRQTEIQAIYIALQDGLSEVWVTDVSDYALGIIQAPDQSESELVNQIIEQLIKKIKKYLAWVFAHKIGI GENEQVDKLSVAGRKKVFLDGDIDKQAD.EHEKXVHSWRAMASDFNL	666 RT and p15 Rnaase H end \ / p31 Integrase start	743
A1.KE.94.Q23.17	H-H-S-E-H-H-S-K-I-K-E-D-S-S-K-E-R-S-E-R-T		743
A1.RU.03.03RU20.06.13	H-H-S-E-H-H-S-R-I-K-E-R-S-S-K-E-R-S-E-R-T		743
A1.RW.93.93RW037A.13	H-H-S-E-H-H-S-SA-H-R-N-K-G-D-S-S-K-E-R-S-E-R-T		743
A1.SE.94.SE7253	H-H-S-E-H-H-S-I-K-G-D-S-S-K-E-R-S-E-R-T		743
A1.TZ.01.A173	H-H-S-E-H-H-S-R-D-I-K-E-D-S-S-K-E-R-S-E-R-T		743
A1.UA.00.98UA0116	H-H-S-E-H-H-S-I-K-E-R-S-S-K-E-R-S-E-R-T		743
A1.UG.92.92UG037	H-H-S-E-H-H-SG-K-E-D-S-S-K-E-R-S-E-R-T		743
A1.UG.98.98UG57136	H-H-S-E-H-H-S-K-D-I-L-K-E-D-S-S-I-E-R-S-E-R-T		743
A2.CD.97.97CDKFE4	H-H-S-E-H-H-S-K-E-R-S-S-K-E-R-S-E-R-T		743
A2.CD.97.97CDK510	H-H-S-E-H-H-S-K-E-R-S-S-K-E-R-S-E-R-T		743
A2.CD.97.97CDKTB48	H-H-S-E-H-H-S-K-E-R-S-S-K-E-R-S-E-R-T		743
A2.CY.94.94CY017.41	H-H-S-E-H-H-S-ER-I-K-E-R-S-S-K-E-R-S-E-R-T		743
A.SN.01.DDI579	H-H-S-E-H-H-S-S-ME-S-S-K-E-R-S-E-R-T		743
A.SN.01.DDU369	H-H-S-E-H-H-S-R-I-K-E-R-S-S-K-E-R-S-E-R-T		743
A.SN.96.DDU360	H-H-S-E-H-H-S-SK-I-K-E-R-S-S-K-E-R-S-E-R-T		743
A.ZA.04.04ZASK162B1	H-H-S-E-H-H-S-P-R-A-I-K-E-R-S-S-R-E-D-T		743
B.AR.00.ARMS008	D-P-K-H-K-K-I-K-E-R-S-S-K-E-R-S-E-R-T		743
B.AU.96.MBCD36	H-H-S-E-H-H-S-K-I-K-E-R-S-S-K-E-R-S-E-R-T		743
B.CO.01.PCM074	D-S-H-H-S-S-K-E-R-S-S-K-E-R-S-E-R-T		743
B.GA.88.OYI	D-S-H-H-S-S-K-E-R-S-S-K-E-R-S-E-R-T		743
B.NL.00.671.00T36	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
B.RU.04.04RU129005	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
B.TH.90.BK132	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
B.US.90.WEAU160	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
B.US.98.1058.11	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.AR.01.ARG4006	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.BR.04.04BR013	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.BR.92.R025.d	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.BW.00.00BW07621	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.ET.86.ETH2220	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.IN.95.95IN21068	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.IN.99.01IN565.10	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.KE.00.KER2010	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.TZ.01.BD9.11	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.UY.01.TRA3011	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.ZA.04.SK164B1	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.ZA.05.05ZASK245B1	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.ZM.02.02ZM115	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
C.ZM.96.96ZM651	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
D.CD.83.ELI	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
D.CD.83.NDK	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
D.CM.01.01CM.4412HAL	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
D.KE.01.NKU3006	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
D.TD.99.MN012	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
D.TZ.01.A280	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
D.UG.94.94UG114	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
D.UG.99.99UGD23550	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
D.UG.99.99UGK03958	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
D.ZA.86.R482	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
F1.BE.93.VI850	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
F1.BR.89.B2126	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
F1.BR.93.93BR020.1	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
F1.FI.93.FIN9363	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
F1.FR.96.MP411	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
F2.CM.02.02CM.0016BBY	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
F2.CM.95.MP255	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
F2.CM.95.MP257	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
F2.CM.97.CM53657	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
G.BE.96.DRCLB	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
G.CM.01.01CM.4049HAN	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
G.ES.99.X138	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
G.KE.93.HH8793.12.1	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
G.NG.92.92NG083	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
G.SE.93.SE6165	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
H.BE.93.VI991	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
H.BE.93.VI997	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
H.CF.90.056	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
J.SE.93.SE7887	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
J.SE.94.SE7022	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
K.CD.97.EQTB11C	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743
K.CM.96.MP535	H-H-S-E-H-H-S-IPIK-H-K-S-S-T-T-R-E-E		743

p66 RT and p15 RNase H end \ / p31 Integrase start

GYVTRGRQKVVTLTDITNQTEIQAIYIALQALDSGLEWVITDSQYALGIIQAPDQSESELVNIQIIEQLIKKEKYLAWFAHKIGENQVQKLSVAGIRKVLFLDGDKQAD.EHEKXHSNWRAMASDFNL	743
B.FR.83.HXB2	743
01 AE.CF.90.90CF402	743
01 AE.CN.05.FU051	743
01 AE.HK.x.HK001	743
01 AE.JP.93.93JP.NH1	740
01 AE.TH.01.OUR4141	741
01 AE.TH.02.OUR7691	742
01 AE.TH.90.CM240	743
02 AG.CM.02.02CM.16691E	748
02 AG.EC.x.EC041	743
02 AG.FR.91.DJ264	743
02 AG.GH.03.GHNJ196	743
02 AG.NG.x.IENG	744
02 AG.SN.98.MP1211	743
02 AG.UZ.02.02UZ693	743
03 AB.RU.97.KAL153.2	743
04 CPX.CV.94.CY0332	743
05 DF.BE.x.VII1310	742
06 CPX.AU.96.BFP90	743
07 BC.CN.97.CM54	745
08 BC.CN.97.97CNGX.6F	743
09 CPX.GH.96.96GH2911	739
10 CD.TZ.96.96TZ.BF061	742
11 CPX.GR.x.GR17	742
12 BF.AR.99.ARMA159	742
13 CPX.CM.96.1849	743
14 BG.ES.99.X397	750
15 01B.TH.99.99TH.MU2079	742
16 A2D.KR.97.97KR004	743
18 CPX.CU.99.CU76	741
19 CPX.CU.99.CU7	742
20 BG.CU.03.CB134	737
21 A2D.KE.91.KNH1254	741
23 BG.CU.03.CB118	741
24 BG.CU.03.CB378	734
25 CPX.CM.x.101BA	742
28 BF.BR.99.BREPM12609	743
29 BF.BR.02.BREPM119	743
31 BC.BR.02.110PA	739
33_01B.WY.05.05MYKL007_1	743
A1C.TZ.02.CO3710	740
A1CDGKU.ZA.99.CM4	743
A1DHK.NO.97.97NOGLI3	743
A1GHU.GA.x.VI354	742
A2D.XE.99.KER2003	742
AP2.CM.02.02CM.3163MN	743
AGU.CM.01.01CM.0989MO	741
ARJU.CM.01.01CM.1296NG	737
BC.CN.96.YNRL9607	739
BC.MM.99.middul03	743
BF1.BR.02.02BR006	742
0708.CN.00.HH069	739
U.CD.83.83CD003	744
U.CD.90.90CD121E12	743
U.GR.99.GR303	741
U.NL.x.U.NL.95.H10986_D1	743
N.CM.02.DJ00131	748
N.CM.04.CM.1015_04	750
N.CM.04.04CM.1131_03	750
N.CM.95.YBF30	750
N.CM.97.YBF106	750
O.BE.87.AN170	739
O.CM.91.MVPS180	739
O.CM.96.96CMWAB637	741
O.SN.99.SEMP1300	739
CPZ.CD.90.ANT	743
CPZ.CM.01.SIVcpzCAM13	742
CPZ.CM.05.SIVcpzEK505	749
CPZ.CM.05.SIVcpzL187	746
CPZ.CM.05.SIVcpzMB66	742
CPZ.CM.05.SIVcpzWT145	741
CPZ.GA.88.GAB1	739
CPZ.TZ.01.TZAN1	745
CPZ.US.85.CPZUS	745

HIV-1/SIVcpz proteins

B.FR.83.HXB2	PPVKAKEIVASCDK_CQLKGEAMHGQVDCSPGIWQLDCTHLEGGKIVLVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPKVTHHTDNGSNFTGATVRAACWAGIK_QEFGIPYNPQSQGVVBSMNKELKK	875
A1.KE.94.Q23_17	IVVSSAKNQNQ	875
A1.RU.03.03RU20_06_13	IVSSAKNQNQ	875
A1.RW.93.93RW037A	IVSSAKNQNQ	875
A1.SE.94.SE7253	IVSSAKNQNQ	875
A1.TZ.01.A173	IVSSAKNQNQ	875
A1.UA.00.98UA0116	IVSSAKNQNQ	875
A1.UG.92.92UG037	IVSSAKNQNQ	875
A1.UG.98.98UG57136	IVSSAKNQNQ	875
A2.CD.97.97CDKFE4	IVSSAKNQNQ	875
A2.CD.97.97CDKS10	IVSSAKNQNQ	875
A2.CD.97.97CDKTB48	IVSSAKNQNQ	875
A2.CY.94.94CY0117_41	IVSSAKNQNQ	875
A1.SN.01.DDI579	IVSSAKNQNQ	875
A1.SN.01.DDJ369	IVSSAKNQNQ	875
A1.SN.96.DDJ360	IVSSAKNQNQ	875
A.ZA.04.04ZASK162B1	IVSSAKNQNQ	875
B.AR.00.ARMS008	IVSSAKNQNQ	875
B.AU.96.MBCD36	IVSSAKNQNQ	875
B.CO.01.PCM074	IVSSAKNQNQ	875
B.GA.88.OYI	IVSSAKNQNQ	875
B.NL.00.671_00T36	IVSSAKNQNQ	875
B.RU.04.04RU129005	IVSSAKNQNQ	875
B.TH.90.BK132	IVSSAKNQNQ	875
B.US.90.WEAU160	IVSSAKNQNQ	875
B.US.98.1058_11	IVSSAKNQNQ	875
C.AR.01.ARG4006	IVSSAKNQNQ	875
C.BR.04.04BR013	IVSSAKNQNQ	875
C.BR.92.BR025_d	IVSSAKNQNQ	875
C.BW.00.00BW07621	IVSSAKNQNQ	875
C.ET.86.ETH2220	IVSSAKNQNQ	875
C.IN.95.95IN21068	IVSSAKNQNQ	875
C.IN.99.01INS65_10	IVSSAKNQNQ	875
C.KE.00.KER2010	IVSSAKNQNQ	875
C.TZ.01.BD9_11	IVSSAKNQNQ	875
C.UY.01.TRA3011	IVSSAKNQNQ	875
C.ZA.04.SK164B1	IVSSAKNQNQ	875
C.ZA.05.05ZASK245B1	IVSSAKNQNQ	875
C.ZM.02.02ZM115	IVSSAKNQNQ	875
C.ZM.96.96ZM651	IVSSAKNQNQ	875
D.CD.83.ELI	IVSSAKNQNQ	874
D.CD.83.NDK	IVSSAKNQNQ	874
D.CM.01.01CM_4412HAL	IVSSAKNQNQ	876
D.KE.01.NK03006	IVSSAKNQNQ	874
D.TD.99.MN012	IVSSAKNQNQ	876
D.TZ.01.A280	IVSSAKNQNQ	876
D.UG.94.94UG114	IVSSAKNQNQ	876
D.UG.99.99UGD23550	IVSSAKNQNQ	874
D.UG.99.99UGK0958	IVSSAKNQNQ	874
D.ZA.86.R482	IVSSAKNQNQ	874
F1.BE.93.VI850	IVSSAKNQNQ	876
F1.BR.89.B2126	IVSSAKNQNQ	875
F1.BR.93.93BR020_1	IVSSAKNQNQ	875
F1.FI.93.FIN9363_1	IVSSAKNQNQ	877
F1.FR.96.MP411	IVSSAKNQNQ	875
F2.CM.02.02CM_0016BBY	IVSSAKNQNQ	875
F2.CM.95.MP255	IVSSAKNQNQ	875
F2.CM.95.MP257	IVSSAKNQNQ	875
F2.CM.97.CM53657	IVSSAKNQNQ	875
G.BE.96.DRCBL	IVSSAKNQNQ	872
G.CM.01.01CM_4049HAN	IVSSAKNQNQ	874
G.ES.99.X138	IVSSAKNQNQ	873
G.KE.93.HH8793_12_1	IVSSAKNQNQ	874
G.NG.92.92NG0083	IVSSAKNQNQ	872
G.SE.93.SE6165	IVSSAKNQNQ	873
H.BE.93.VI991	IVSSAKNQNQ	873
H.BE.93.VI997	IVSSAKNQNQ	873
H.CF.90.056	IVSSAKNQNQ	874
J.SE.93.SE7887	IVSSAKNQNQ	873
J.SE.94.SE7022	IVSSAKNQNQ	873
K.CD.97.EQTB11C	IVSSAKNQNQ	876
K.CM.96.MP535	IVSSAKNQNQ	875

B.FR.83.HXB2	PPVAKIEIVASCDK.CQLKGEAMHQVDCSPGIWQIDCTHLEGKVIILVAVHVASGYIEAEVIPAETGQETAYFLKLKAGWPVKTIHTDNGSNFTGATVRAACWAGTK.QEFGIPYNPQSGVGVESMNKELKK	875
01 AE.CF.90.90CF402	RV-S-A-K-NVQ	875
01 AE.CN.05.FJ051	V-S-A-K-DVR	875
01 AE.HK.x.HK001	V-S-A-K-NVR	875
01 AE.JP.93.93JP.NH1	V-S-A-K-NVR	872
01 AE.TH.01.OUR4141	V-S-A-K-NVR	873
01 AE.TH.02.OUR7691	V-S-AMK-DVH	874
01 AE.TH.90.CM240	V-S-A-K-NV-	875
02 AG.CM.02.02CM_16691E	V-S-A-K-NVQ	880
02 AG.EC.x.EC041	V-S-A-K-NVT	875
02 AG.FR.91.DJ264	V-S-A-K-NVT	875
02 AG.GH.03.GHNU196	RV-S-A-K-NVT	875
02 AG.NG.x.IBNG	V-S-A-K-DV-	876
02 AG.SN.98.MP1211	V-S-A-K-NVT	875
02 AG.UZ.02.02UZ693	KMAS-VV-S-A-K-KVT?-L-?	876
03 AB.RU.97.KAL153_2	V-S-A-K-NVT	875
04 CPX.CV.94.CV032	V-S-A-K-NVT	875
05 DF.BE.x.VI11310	M-A-P-S-A-K-D-N	874
06 CPX.AU.96.BFP90	M-P-SGA-K-O	875
07 BC.CN.97.CN54	V-S-A-K-N-T	877
08 BC.CN.97.97CNGX_6F	V-S-A-K-N-T	875
09 CPX.GH.96.96GH2911	V-S-A-K-NVT	871
10 CD.TZ.96.96TZ_BF061	V-S-A-K-NVT	874
11 CPX.GR.x.GR17	VV-S-A-K-NVT	874
12 BF.AR.99.ARMA159	V-SNA-K-Q	874
13 CPX.CM.96.11849	P-IS-M-K-Q	875
14 BG.ES.99.X397	V-S-A-K-N-T	862
15 01B.TH.99.99TH_MU2079	V-S-A-K-N-T	874
16 A2D.KR.97.97KR004	V-S-AMK-NVR-WD	875
18 CPX.CU.99.CU76	V-P-IS-P-K-VQ	875
19 CPX.CU.99.CU7	V-P-S-A-K-N-T	873
20 BG.CU.03.CB134	V-S-A-K-NVT	874
21 A2D.RE.91.KNH1254	V-S-A-K-N-T	869
23 BG.CU.03.CB118	WI-V-P-IS-P-K-N-T	873
24 BG.CU.03.CB378	V-P-IS-A-K-D-T	871
25 CPX.CM.x.101BA	V-P-IS-A-K-D-T	866
28 BF.BR.99.BREPM12609	V-SNA-K-E	874
29 BF.BR.02.BREPM119	V-SNA-K-E	875
31 BC.BR.02.110PA	K-V-I-L-G-I-R-P-ISTA-K	875
33 01B.WY.05.05MYKL007_1	I-RV-I-SN-K-Q	871
A1C.TZ.02.C03710	I-A-N-RV-I-S-A-K-NVQ	875
A1CDGKU.ZA.99.CM4	I-V-S-A-K-Q	872
A1DHK.NO.97.97NOGLI3	I-V-S-A-K-N	875
A1GHU.GA.x.VI354	I-V-IS-A-K-D	875
A2D.KE.99.KER2003	I-V-T-S-A-K-NVT	874
AF2.CM.02.02CM_3163MN	I-V-P-IS-A-K	874
AHTU.CM.01.01CM_0989MO	I-V-S-A-K-D-Q	875
AHTU.CM.01.01CM_1296NG	I-V-P-S-A-K-N-T	873
BC.CN.96.YNRL9607	I-M-S-A-K-DVQ	869
BC.MM.99.mIDU103	I-R-SNS-K	871
BFI.BR.02.02BR006	I-R-SNA-K	875
0708.CN.00.HH069	I-SI-K	874
U.CD.83.83CD003	I-V-S-A-K-Q	871
U.CD.90.90CD121E12	TV-S-A-K-Q	876
U.GR.99.GR303	T-S-A-K-Q	875
U.NL.x.U.NL.95.H10986_D1	AG.IR-P-N-V-S-AMK-NVT-S	873
N.CM.02.DJ00131	I-N-M-I-A-YI-V-P-S-A-K	875
N.CM.04.04CM_1015_04	I-N-V-L-J-V-P-S-K-N-T	860
N.CM.04.04CM_1131_03	I-N-V-L-L-I-V-P-S-K-S	862
N.CM.95.YBF30	I-N-V-L-L-I-V-P-S-K-N	882
N.CM.97.YBF106	I-N-V-L-L-I-V-P-IS-K	882
O.BE.87.ANT70	I-P-HI-I-EV-I-M-I-I-F	871
O.CM.91.MVPS180	I-P-HI-T-Y-E-M-I-I-DF	871
O.CM.96.96CMWAB637	I-P-HI-I-Y-EV-I-I-F	873
O.SN.99.SEMP13000	I-N-P-HI-I-Y-EV-I-I-F	871
CPZ.CD.90.ANT	I-Q-HV-R-L-V-T-M-I-I-S-F-MAD-KS	875
CPZ.CM.01.SIVcpzCAM13	I-N-V-L-L-I-I-S-VL-T-SNA-K-N-O-K	874
CPZ.CM.05.SIVcpzE505	I-I-TN-V-I-I-L-M	881
CPZ.CM.05.SIVcpzL87	I-I-I-M	878
CPZ.CM.05.SIVcpzMB66	I-I-I-M	878
CPZ.CM.05.SIVcpzWT145	I-I-I-M	874
CPZ.GA.88.GAB1	I-Q-H-V-I-I	873
CPZ.TZ.01.TAN1	I-Q-P-HI-I-Y-E-I-I-F	871
CPZ.US.85.CPZUS	I-P-I-I-L-I	877



HIV-1/SIVcpz proteins

HIV-1/SIVcpz protein alignment: POL

B.FR.83.HXB2	I I G V P D Q A E H L K T A V Q M A V F T H N P K R K G G I G G Y S A G E R I V D I I A T D I Q T K E L Q K I T K I Q N F R Y V R S R N P L M K G P A K L L W K G E G A V V I Q D N S D I K V V P R R K A K I R D Y G K M A G D D C V A S R Q E D	1003
A1.KE.94.Q23.17	E-----I-----H-----D-----F-----G-----	1003
A1.RU.03.03RU20.06.13	E-----E-----P-----D-----I-----N-----	1002
A1.RW.93.93RW037A	A-----I-----I-----H-----K-----D-----V-----G-----	1003
A1.SE.94.SE7253	E-----E-----I-----K-----D-----I-----N-----L-----G-----	1003
A1.TZ.01.A173	E-----E-----I-----D-----I-----G-----	1003
A1.UA.00.98UA0116	E-----E-----I-----I-----K-----C-----D-----I-----N-----V-----K-----G-----	1003
A1.UG.92.92UG037	E-----E-----I-----S-----L-----D-----V-----I-----	1004
A1.UG.98.98UG57136	I-----I-----I-----D-----I-----C-----	1003
A2.CD.97.97CDKFE4	I-----I-----H-----H-----L-----M-----*-----E-----D-----I-----G-----	995
A2.CD.97.97CDKS10	I-----I-----R-----R-----D-----I-----G-----	997
A2.CY.94.94CY017.41	E-----E-----I-----I-----D-----I-----G-----	1003
A.SN.01.DDI579	E-----E-----I-----Q-----I-----D-----I-----G-----	1002
A.SN.01.DDJ369	E-----E-----I-----I-----D-----I-----G-----	1002
A.SN.96.DDJ360	E-----E-----I-----I-----D-----I-----G-----	1002
A.ZA.04.04ZASK162B1	I-----I-----D-----S-----V-----R-----E-----	1002
B.AR.00.ARMS008	I-----I-----D-----N-----E-----	1003
B.AU.96.MBCD36	I-----I-----D-----D-----V-----	1003
B.CO.01.PCM074	K-----K-----I-----S-----E-----E-----K-----N-----G-----	1004
B.GA.88.OYI	E-----E-----E-----	1003
B.NL.00.671.00T36	E-----E-----I-----E-----D-----I-----V-----	1013
B.RU.04.04RU129005	I-----I-----O-----D-----E-----D-----V-----	1009
B.TH.90.BK132	E-----E-----D-----E-----D-----	1003
B.US.90.WEAU160	E-----E-----I-----Q-----D-----D-----K-----M-----	1003
B.US.98.1058.11	E-----E-----I-----R-----D-----D-----V-----	1000
C.AR.01.ARG4006	I-----I-----I-----L-----D-----I-----K-----A-----	999
C.BR.04.04BR013	I-----I-----I-----L-----D-----I-----V-----K-----A-----N-----	1007
C.BR.92.BR025.d	I-----I-----M-----M-----D-----I-----L-----V-----K-----A-----M-----	1002
C.BW.00.00BW07621	R-----R-----R-----I-----O-----I-----I-----K-----A-----G-----	999
C.ET.86.ETH2220	E-----E-----R-----N-----L-----D-----I-----A-----G-----	1010
C.IN.95.95IN21068	I-----I-----I-----V-----D-----I-----K-----A-----G-----	999
C.IN.99.01INS65.10	I-----I-----I-----I-----D-----I-----N-----E-----K-----A-----G-----	999
C.KE.00.KER2010	I-----I-----R-----I-----Q-----D-----I-----K-----A-----G-----	999
C.TZ.01.BD9.11	I-----I-----R-----R-----I-----Q-----D-----I-----K-----A-----G-----	999
C.UY.01.TRA3011	I-----I-----L-----L-----D-----I-----V-----K-----A-----M-----N-----	1005
C.ZA.04.SK164B1	I-----I-----L-----L-----D-----I-----V-----K-----A-----M-----N-----	999
C.ZA.05.05ZASK245B1	I-----I-----L-----L-----D-----I-----V-----K-----A-----M-----D-----	999
C.ZM.02.02ZM115	E-----E-----I-----I-----D-----I-----G-----	1006
C.ZM.96.96ZM651	E-----E-----I-----I-----D-----I-----G-----	1004
D.CD.83.ELI	I-----I-----R-----I-----N-----K-----D-----I-----A-----G-----	999
D.CD.83.NDK	I-----I-----R-----I-----D-----I-----K-----A-----G-----	1002
D.CM.01.01CM.4412HAL	I-----I-----R-----I-----D-----I-----V-----	1002
D.KE.01.NKU3006	I-----I-----S-----H-----I-----D-----I-----V-----	1004
D.TD.99.MN012	I-----I-----R-----I-----D-----I-----E-----E-----	1002
D.TZ.01.A280	I-----I-----S-----L-----T-----D-----I-----H-----V-----K-----G-----	1004
D.UG.94.94UG114	E-----E-----I-----I-----D-----V-----E-----V-----	1004
D.UG.99.99UGD23550	E-----E-----I-----I-----D-----V-----E-----V-----	1004
D.UG.99.99UGK0958	E-----E-----I-----I-----D-----I-----V-----	1002
D.ZA.86.R482	I-----I-----L-----H-----L-----S-----Y-----T-----A-----S-----V-----T-----V-----I-----G-----	1002
F1.BE.93.VI850	I-----I-----S-----R-----V-----E-----I-----V-----G-----	1004
F1.BR.89.B2126	I-----I-----S-----S-----R-----V-----E-----I-----V-----G-----	1004
F1.BR.93.93BR020.1	I-----I-----R-----I-----R-----D-----V-----E-----E-----G-----	1003
F1.FI.93.FIN9363	I-----I-----R-----I-----R-----D-----V-----E-----E-----G-----	1003
F1.FR.96.MP411	I-----I-----S-----R-----I-----I-----V-----E-----E-----G-----	1003
F2.CM.02.02CM.0016BBY	I-----I-----S-----R-----I-----I-----S-----F-----D-----I-----N-----E-----D-----I-----G-----	1005
F2.CM.95.MP255	I-----I-----F-----F-----D-----V-----N-----E-----D-----I-----G-----	1003
F2.CM.95.MP257	I-----I-----S-----S-----R-----D-----V-----N-----E-----D-----I-----G-----	1003
F2.CM.97.CM53657	I-----I-----F-----F-----D-----I-----I-----N-----E-----D-----I-----G-----	1003
G.BE.96.DRCBL	I-----I-----S-----S-----R-----D-----I-----N-----E-----D-----I-----G-----	1000
G.CM.01.01CM.4049HAN	I-----I-----S-----S-----R-----D-----I-----N-----E-----D-----I-----G-----	1002
G.ES.99.X138	I-----I-----S-----A-----D-----I-----N-----E-----D-----I-----G-----	1001
G.KE.93.HH8793.12.1	I-----I-----S-----I-----Q-----F-----D-----I-----N-----E-----D-----I-----G-----	1002
G.NG.92.92NG083	I-----I-----S-----I-----D-----I-----N-----E-----D-----I-----G-----	1002
G.SE.93.SE6165	I-----I-----S-----I-----D-----V-----N-----E-----D-----I-----G-----	1000
H.BE.93.VI991	R-----R-----I-----P-----S-----O-----K-----E-----E-----G-----	1001
H.BE.93.VI997	R-----R-----I-----S-----N-----K-----E-----E-----G-----	1001
H.CF.90.056	I-----I-----S-----N-----K-----E-----E-----G-----	1002
J.SE.93.SE7887	I-----I-----R-----R-----D-----I-----P-----E-----E-----G-----	1001
J.SE.94.SE7022	I-----I-----I-----D-----I-----E-----E-----G-----	1001
K.CD.97.EQTB11C	I-----I-----I-----D-----I-----E-----E-----G-----	1003
K.CM.96.MP535	I-----I-----L-----N-----K-----E-----E-----G-----	1003

B.FR.83.HXB2
 01 AE.CF.90.90CF402
 01 AE.CN.05.FJ051
 01 AE.HK.x.HK001
 01 AE.JP.93.93JP.NH1
 01 AE.TH.01.OUR4141
 01 AE.TH.02.OUR7691
 01 AE.TH.90.CM240
 02 AG.CM.02.02CM.16691E
 02 AG.EC.x.EC041
 02 AG.FR.91.DJ264
 02 AG.GH.03.GHNJ196
 02 AG.NG.x.IBNG
 02 AG.SN.98.MP1211
 02 AG.UZ.02.02UZ693
 03 AB.RU.97.KAL153.2
 04 CPX.CV.94.CY032
 05 DF.BE.x.VI11310
 06 CPX.AU.96.BFP90
 07 BC.CN.97.CN54
 08 BC.CN.97.97CNGX.6F
 09 CPX.GH.96.96GH2911
 10 CD.TZ.96.96TZ.BF061
 11 CPX.GR.x.GR17
 12 BF.AR.99.ARMAL159
 13 CPX.CM.96.1849
 14 BG.ES.99.X397
 15 01B.TH.99.99TH.MU2079
 16 A2D.KR.97.97KR004
 18 CPX.CU.99.CU76
 19 CPX.CU.99.CU7
 20 BG.CU.03.CB134
 21 A2D.KR.91.KNH1254
 23 BG.CU.03.CB118
 24 BG.CU.03.CB378
 25 CPX.CM.x.101BA
 28 BF.BR.99.BREPM12609
 29 BF.BR.02.BREPM119
 31 BC.BR.02.110PA
 33 01B.WY.05.05MYKL007_1
 A1C.TZ.02.C03710
 A1CDGKU.ZA.99.CM4
 A1DHK.NO.97.97NOGLI3
 A1GHU.GA.x.VI354
 A2D.KE.99.KER2003
 AF2.CM.02.02CM.3163MN
 AGU.CM.01.01CM.0989MO
 AHJU.CM.01.01CM.1296NG
 BC.CN.96.YNRL9607
 BC.MM.99.mINDU103
 BF1.BR.02.02BR006
 0708.CN.00.HH069
 U.CD.83.83CD003
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125 N-N E-K-KK-Y O-K O-K O-H H-ORR I-V-R O-A
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125 QV-MI L-T IFTTKCKD-K TDT-KRAG-I T-ERSK-VLH-AC-P H-IGL QGT-I-T-TR-TAAG-V-O-I
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HIV-1/SIVcpz proteins

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 -Q--KV-V-S--RSR--E-A--R-ENP--C
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 -RV--O--T--VA--T--K-V-G--R--R--C
 -QV-R--N-P--K-Q-T--T--VA--R--R--R--C
 -Q--D--T--R--RR--Q-V--T--E--C
 -O--D--T--K--R--Q-V--RD--E--C
 -R--T-Q--T--A--T--V--Q-V--S-Q--C
 -R--C--T--VA-R--RP--V--K-V--Q--C

HIV-1/SIVcpz proteins

Table with columns for protein names (e.g., B.FR.83.HXB2, A1.KE.94.Q23.17), alignment positions (101-101), and amino acid sequences. The sequences are aligned in columns, with gaps represented by dashes. The table is organized into three main sections: intramolecular disulfide bonding, nuclear localization signal, and exon 1/exon 2.

	intra	disulfide	nuclear	localization	signal	exon 1	exon 2	
	molecul	bonding	bonding	signal	signal	exon 1	exon 2	
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01 AE.HK.x.HK001	N	N	N	N	N	N	N	N
01 AE.JP.93.93JP.NH1	N	N	N	N	N	N	N	N
01 AE.TH.01.00R4141	N	N	N	N	N	N	N	N
01 AE.TH.02.00R7691	N	N	N	N	N	N	N	N
01 AE.TH.00.CM240	N	N	N	N	N	N	N	N
02 AG.CM.02.02CM.1669LE	N	N	N	N	N	N	N	N
02 AG.EC.x.EC041	N	N	N	N	N	N	N	N
02 AG.FR.91.DJ264	N	N	N	N	N	N	N	N
02 AG.GH.03.GHJ196	N	N	N	N	N	N	N	N
02 AG.NG.x.IBNG	N	N	N	N	N	N	N	N
02 AG.SN.98.MP1211	N	N	N	N	N	N	N	N
02 AG.UZ.02.02UZ693	N	N	N	N	N	N	N	N
03 AB.RU.97.KAL153.2	N	N	N	N	N	N	N	N
04 CPX.CV.94.CV032	N	N	N	N	N	N	N	N
05 DF.BE.x.VI1310	N	N	N	N	N	N	N	N
06 CPX.AU.96.BFP90	N	N	N	N	N	N	N	N
07 BC.CN.97.CM54	N	N	N	N	N	N	N	N
08 BC.CN.97.197CNGX.6F	N	N	N	N	N	N	N	N
09 CPX.GH.96.96GH2911	N	N	N	N	N	N	N	N
10 CD.TZ.96.96TZ.BF061	N	N	N	N	N	N	N	N
11 CPX.GR.x.GR17	N	N	N	N	N	N	N	N
12 BF.AR.99.ARMA159	N	N	N	N	N	N	N	N
13 CPX.CM.96.1849	N	N	N	N	N	N	N	N
14 BG.ES.99.X397	N	N	N	N	N	N	N	N
15 01B.TH.99.99TH.MD2079	N	N	N	N	N	N	N	N
16 AZD.KR.97.97KR004	N	N	N	N	N	N	N	N
18 CPX.CU.99.CU76	N	N	N	N	N	N	N	N
19 CPX.CU.99.CU7	N	N	N	N	N	N	N	N
20 BG.CU.03.CB134	N	N	N	N	N	N	N	N
21 AZD.KB.91.KNH1254	N	N	N	N	N	N	N	N
23 BG.CU.03.CB118	N	N	N	N	N	N	N	N
24 BG.CU.03.CB378	N	N	N	N	N	N	N	N
25 CPX.CM.x.101BA	N	N	N	N	N	N	N	N
28 BF.BR.99.BREPM12609	N	N	N	N	N	N	N	N
29 BF.BR.02.BREPM119	N	N	N	N	N	N	N	N
31 BC.BR.02.101PA	N	N	N	N	N	N	N	N
33_01B.WY.05.05WYKL007_1	N	N	N	N	N	N	N	N
A1C.TZ.02.CO3710	N	N	N	N	N	N	N	N
A1CDGKU.ZA.99.CM4	N	N	N	N	N	N	N	N
A1DCK.NO.97.N04	N	N	N	N	N	N	N	N
A1DCK.NO.97.97N04	N	N	N	N	N	N	N	N
A1GHU.GA.x.VI354	N	N	N	N	N	N	N	N
A2D.XE.99.KBR2003	N	N	N	N	N	N	N	N
AFU.CM.02.02CM.3163MN	N	N	N	N	N	N	N	N
AGU.CM.01.01CM.0998MO	N	N	N	N	N	N	N	N
ARU.CM.01.01CM.1296NG	N	N	N	N	N	N	N	N
BC.MM.99.mIDU103	N	N	N	N	N	N	N	N
BF1.BR.02.02BR006	N	N	N	N	N	N	N	N
0708.CN.00.HH069	N	N	N	N	N	N	N	N
U.CD.83.83CD003	N	N	N	N	N	N	N	N
U.CD.90.90CD121E12	N	N	N	N	N	N	N	N
U.GR.99.GR303	N	N	N	N	N	N	N	N
U.NL.x.U.NL.95.H10986_D1	N	N	N	N	N	N	N	N
N.CM.02.DJ00131	N	N	N	N	N	N	N	N
N.CM.04.04CM.1015_04	N	N	N	N	N	N	N	N
N.CM.04.04CM.1131_03	N	N	N	N	N	N	N	N
N.CM.95.YBF30	N	N	N	N	N	N	N	N
N.CM.97.YBF106	N	N	N	N	N	N	N	N
O.BE.87.ANT70	N	N	N	N	N	N	N	N
O.CM.91.MVPS180	N	N	N	N	N	N	N	N
O.CM.96.96CMBAB637	N	N	N	N	N	N	N	N
O.SN.99.SEMP1300	N	N	N	N	N	N	N	N
CPZ.CD.90.ANT	N	N	N	N	N	N	N	N
CPZ.CM.01.SIVcpzCAM13	N	N	N	N	N	N	N	N
CPZ.CM.05.SIVcpzEK505	N	N	N	N	N	N	N	N
CPZ.CM.05.SIVcpzL87	N	N	N	N	N	N	N	N
CPZ.CM.05.SIVcpzMB66	N	N	N	N	N	N	N	N
CPZ.CM.05.SIVcpzMT145	N	N	N	N	N	N	N	N
CPZ.GA.88.GAB1	N	N	N	N	N	N	N	N
CPZ.TZ.01.TAN1	N	N	N	N	N	N	N	N
CPZ.US.85.CPZUS	N	N	N	N	N	N	N	N

HIV-1/SIVcpz proteins

HIV-1/SIVcpz proteins

HIV-1/SIVcpz protein alignment: REV

high affinity binding site

Leu-rich effector domain

Sequence alignment of HIV-1/SIVcpz proteins showing domains: high affinity binding site, Leu-rich effector domain, and high affinity binding site. Includes accession numbers and residue positions.

Table with columns for accession numbers (e.g., B.FR.83.HXB2, O1.AE.CF.90.90CF402), protein names (e.g., MAGRSGSDSEE, ST.D.L.LAA.T.I), and amino acid sequences. The sequences are aligned across multiple rows, with gaps represented by dashes. The table is organized into vertical columns corresponding to the sequence positions.

HIV-1/SIVcpz proteins

HIV-1/SIVcpz proteins

	transmembrane domain	alpha helix	phos	phos	alpha helix	cytoplasmic domain	
B.FR.83.HXB2IPIVAIV.AL.VVA.IIIAIVVMSVITIEYRKLKIQ...RKI.....DRUIDRLEIARAEDSGN.ESEG.....EISAU.VEM.....GVEMGH.....HAPWVDV.....DLDLDL	82
A1.KE.94.Q23.17	LE-S---G-I-L-L-A-T-G-K-RK-	E-IR---D-TE-L-T-I.....	D-D	YDLG-DNI-I-	81
A1.RU.03.03R020.06_13	LE-Y-I---FV---T-G-L-K-	E-IR---D-TE-L-T-M.....	V-N	YDLG-DNN-N-	81
A1.FW.93.93RW037A	LE-C-A-G---L-L-L-T-G-K-L-K-	N-IR---D-PTN-L-K.....	N	YDLG-DNN-N-	81
A1.SE.94.SE7255	ST-W-I-G-I-L-L-L-T-G-K-L-K-	K-VE-IR---D-DTN-LA-I.....	N	YDLG-DNN-N-	82
A1.TZ.01.A173	LE-W---G---L-V-T-G-KK-L-K-	E-IR---D-TE-L-L.....	N	YDLG-DNN-N-	81
A1.UA.00.98UA0116	LE-Y---G---FV---T-G-L-K-	E-IR---D-RE-L-T-M.....	V-N	YLL-DNN-N-	81
A1.UG.92.92UG037	LE-C-V-G---L-L-L-T-G-K-L-K-	V-IR---D-RE-L-L.....	D-D	YDLG-DNN-N-	81
A1.UG.98.98UG57136	LQ-C-A-G---L-L-L-T-G-IRLRK-K	E-IR---D-DT-LAK.....	N	YDLGGDIN-N-	81
A2.CD.97.97CDKFE4	LA-L-S-G---L-L-L-T-T-G-ORKE	K-IS---D-TE-L-T-M.....	GV-ILFF	75
A2.CD.97.97CDKS10	LE-A---G---L-A-T-T-F-RE	W-Q-IS---D-DT-L.....	N	LNFG-ANN-N-	81
A2.CD.97.97CDKTB48	LA-L-S-G---S-L-L-TV-F-K-KK-	W-LE-IS---D-TE-L-KW.....	G-N	LNFG-ANN-N-	81
A2.CY.94.94CY0117_41	LV-L-I-G---L-L-L-T-T-F-K-KK-	W-K-IS---D-TE-L-T.....	V-D	LDV-DNN-N-	81
A2.SN.01.DDI579	LE-W-I-G---L-L-L-T-T-G-K-V-K-KR-	E-IR---D-TE-L-T.....	V-D	NI-IDNN-N-	81
A.SN.01.DDI369	LE-C-I-G---I-V-L-T-T-G-K-LRK-	E-IR---D-TE-L-T.....	V-D	NI-IDNN-N-	81
A.SN.96.DDI360	LGWV---G-I-L-L-L-TL-G-K-V-K-KR-	E-IR---D-TE-L-T.....	V-D	DI-NDN-N-	81
A.ZA.04.04ZASK162B1	LE-C-A-G---L-L-L-T-G---L	K-IT---D-TE-L-T.....	D-N	YDLG-DNNWNW	81
B.AR.00.ARMS008	LT-A---A-V-T-LL---SI-I	A-V---DQE-LA---G-GHHAF			89
B.AU.96.MBCD36	LO---A-A-T-F-R	IR---D-DOE-L-T.....	DV	NIN	81
B.CO.01.PCM074	LV-L---A-L-F-RK-	IR---DHE-L-L.....	D	NI	81
B.GA.88.OYI	LO-L---V-T-LL	IR---DOE-L.....	M		81
B.NL.00.671.00T36	LT---A---L-I-T-L	IR---DOE-L.....	N		81
B.RU.04.04RU129005	LE-L---G---L-L-L-L	IR---DOE-L.....	L	IN**	81
B.TH.90.BK132	LO-LG---G---L-L-L-L	IR---DOE-L.....	I		81
B.US.90.WEAU160	LY-L---A-L-L-L-K	KI---IR---DOE-L.....	YAH	NI	84
B.US.98.1058.11	LY-LG---L-L-L-L-K	KI---IR---DOE-L.....	YAH	NI	84
C.AR.01.ARG4006	?DYRLIG-G---I-L-L-I-T-AY-LV	KR---W-E-IR---D-TE-L-ETM	D	LRLH-L?	81
C.AR.04.04BR013	LTVRVDRILG-V---I-L-LV-L-I-T-AY-LV	KR---W-E-IR---D-TE-L-ETM	D	N	86
C.BR.92.BR025_d	LIGRIDYRLG-V---I-L-V-I-T-AY-LV	R---W-VK-IR---G-DTE-L-ETM	D	LRL-LGN	86
C.BW.00.00BW07621	LLAAVDYRIVG-V---F-I-L-L-T-AY-L-L	K---R---K-IR---D-DHE-L-TM	D	LRL-L-ANGG	86
C.EI.86.EI82220	LDYKLGVG---I-L-L-T-Y-LVQ	W-K-IR---D-TE-L-TM	D	LRL-L-N	82
C.IN.99.95IN21068	LDYKLGVG---I-L-L-T-Y-FLV	W-K-IR---D-TE-L-TM	D	LRL-L-N	82
C.IN.99.01IN565_10	LLARVDYRILG-V---I-L-L-T-T-Y-L	W-E-IR---D-TE-L-ATM	D	LRL-L-N	86
C.KE.00.KER2010	LEARDYRILG-V---L-L-L-T-AY-L-L-K	W-E-IR---D-TE-L-ATM	D	LRL-L-N	86
C.TZ.01.BD9_11	LEARDYRILG-V---L-L-L-T-AY-L-L-K	W-E-IR---D-TE-L-ATM	D	LRL-L-N	86
C.UY.01.TRA3011	FIEKIDYRILG-V---I-L-S-V-I-T-Y-LV	R---W-V-IR---DIE-L-ETM	D	LGLL-L-NGG	86
C.ZA.04.SK164B1	FLARVDYR-GVG---I-L-L-L-I-T-Y-LV	NK---IRD-E---DIE-L-ATM	D	LRL-L-DNNN	86
C.ZA.05.05ZASK245B1	FLARVDYR-GVG---I-L-L-L-I-T-Y-LV	W-E-IR---D-TE-L-ANM	G	LRL-L-A	86
C.ZM.02.02ZM115	LLARVDYR-GVG---I-L-L-L-I-T-Y-LV	W-VN-IR---D-TE-L-TM	D	LRL-L-AN	86
C.ZM.96.96ZM651	LLARVNYR-GVG---I-L-L-L-T-AY-L	W-K-IR---D-TE-L-ATM	D	LRL-L-N	86
D.CD.83.ELI	LV-I-A---L-L-L-T-F-R-KK-R	C-L---IT---DREKL-K	I		81
D.CD.83.NDK	LV-I-A---L-L-L-T-F-R-K	C-L---IR---DRE-L-K	K		81
D.CM.01.01CM_4412HAL	LEILAIVA---A-L-L-L-V-T-Y-KK-O	IR---D-DRE-L-T-M	AD		82
D.CM.01.NK03006	LA-L---G-I-L-L-V-T-Y-CKRVO-K	IR---D-DRE-L-T-M	AD		81
D.TD.99.MN012	LV-L---T-L-L-I-T-Y-R-KK	Y---IR---D-TE-L-T-M	P	AD	82
D.TZ.01.A280	LE-T-A---I-S-L-L-T-Y-R-KK	K---W-IR---D-TE-L-T	N		81
D.UG.94.94UG114	LE-L---L-L-L-T-F-CK-IR	W---IR---DKE-L	D	A	81
D.UG.99.99UGD23550	LV-L---L-L-L-T-LF-CK-LKG	KR---W-IR---DTE-L	P		89
D.UG.99.99UGK09958	LV-L---L-L-L-T-LF-C-RKKE	W-IR---DRE-L-K	I		81
D.ZA.86.R482	LQ-LS-L---A-L---YT-F-F-K-K-T	C---IR---DRE-L-K	G		81
F1.BE.93.VI850	LLAIG-A---I-L-L-T-Y-K-LV	NK-YK-IR---DAE-LA-G	P	FI-G-INNN	81
F1.BR.89.B2126	FLAIS-T---I-L-L-T-AY-K-LV	N-YE-IR---DAE-LA-G	P	FI-G-INN	81
F1.BR.93.93BR020_1	LLAIG-A---I-L-L-T-AY-K-LV	N-YK-IS---DAE-LA-G	V-P	FI-G-INNN	81
F1.FI.93.FIN9363	LLAIT---F-I-L-L-V-T-F-K-LV	N-YI-IR---DAE-LA-G	K-P	FI-G-INNN	81
F1.FR.96.MP411	LYVIS---F-I-L-L-T-F-K-LV	N-YE-IR---DAE-LA-G	S	FI-SG-INNN	81
F2.CM.02.02CM_0016BBY	LI-LV---F-I-L-L-T-Y-K-Q	KR---N-YE-IR---DAE-LA-G	V-L	FI-GMINNN	81
F2.CM.95.MP255	LLA-G-S---I-L-L-T-I-YL-K-L	KR---N-YE-IR---DAE-LA-G	V-P	FI-G-INNN	81
F2.CM.95.MP257	SLV-G-S---Y-I-V-L-I-T-Y-K-L	KR---N-YE-IR---DAE-LA-G	V-P	LI-G-INNN	81
F2.CM.97.CM53657	LLTI---Y-I-L-L-I-T-Y-K-L	KR---NK-YK-IR---DAE-LA-G	P	FI-G-INNN	81
G.BE.96.DRCBL	LE-S---G-I-S-A-T-F-RK	KR---EK-L-IR---DTE-LAT-M	L-D	FD-VGNN	81
G.CM.01.01CM_4049HAN	LE-A---G-I-F-A-I-T-F-RK	K---K-LE-IR---DTE-LA-M	R	FD-VGNN	81
G.ES.99.X138	LE-A---G-I-G-A-I-T-F-Q-KE-RK	K---Q-L-IR---DTE-LAT	D	FD-IGNN	81
G.KE.93.HH8793_12_1	LE-S---G-I-F-A-I-T-LVQ-E-RK	V---I-IR---DRE-LAT-M	D	FD-VGNN	81
G.NG.92.92NG083	LE-S?---G-I-F-A-TI-F-RK	K---F-A-IR---DTE-LAT-M	D	FD-VGNN	78
G.SE.93.SE6165	LV-L---G-I-F-A-T-F-F-E-RK	K---R---GK-L-IR---D-TE-LVT	D	FD-VGNNN	81
H.BE.93.VI991	LGIG-G---I-F---T-AY-L?K	E-IR---D-TE-L-K		LNIGY-A	80
H.BE.93.VI997	IGIG-G---I-F---T-Y-LVK	K---Q-I-G		LNIGY-A	77
H.CF.90.056	LGIG-G---T-F-VI-T-Y-K-LV	K---I-G	M	LNIGY-A	80
J.SE.93.SE7887	LO-A---F-I---FL-GM-T-Y-K-L	K---N-IR---D-TE-LAD		DL-N-N	81
J.SE.94.SE7022	LO---I---I---FFL-C-T-Y-K-L	K---N-IR---D-DT-LAE		DL-N-N	81
K.CD.97.EQB11C	Lt-G-I---A-L-L-I-T-AYL	NW-F-IR---DTE-LA-G	T	LILG-INNN	80
K.CM.96.MP535	LA-S---L-L-I-T-Y-LVK	K---N-IR---DAE-LADI-G	L	LILGNINN	80

transmembrane domain -||- cytoplasmic domain -|

Table with 4 columns: Accession ID, Transmembrane domain, Cytoplasmic domain, and Residue number. The table contains a detailed amino acid sequence alignment for HIV-1/SIVcpz VPU proteins, including sequences from B.FR.83.HXB2 to CPZ.U.85.CPZUS.

HIV-1/SIVcpz proteins

HIV-1/SIVcpz
proteins

	signal peptide	gp120		*	*	***						
B.FR.83.HXB2	MRVKE...KYQHL.WRW	...GWRWGT	...MLLGLML.IC	...SAT.E	...KL.WVTYVYGVVWKEATITLFCASDAKAYDTEVHNWATHACVPTDPPQEVVLVNVTEFNPKWKNMVDQMHE	106						
A1.KE.94.Q23.17	...MGIORNC	...L	...I	...TII.F	...V	...N	...RD.D	...E.K	...IH.D	...K	...N	...T
A1.RU.03.03RU20.06.13	...KA.GMORN	...M	...I	...FW?II.M	...K.A	...N	...RD.E	...K	...IA.E	...K	...D	...OT
A1.RW.93.93RW037A	...MGTMORNC	...N	...I	...III	...V	...N	...D.E	...N	...H.E	...E	...N	...T
A1.SE.94.SE7253	...MGTMORNC	...L	...II	...I	...TA.D	...N	...D.E	...Q	...K	...M	...E	...S
A1.TZ.01.A173	...GIORNS	...F.L	...I	...LII	...A.A.D	...N	...D.E	...A	...H.E	...E	...N	...T
A1.UA.00.98UA0116	...KARGORNC	...M	...I	...FW?II.M	...K.A	...N	...RD.E	...K	...D	...I	...E	...QT
A1.UG.92.92UG037	...MGLERN	...PCW	...I	...I	...NTA	...N	...D.N	...K	...S	...L	...K	...N
A1.UG.98.98UG57136	...MGLORNC	...N	...I	...VIL	...A	...N	...RD.E	...S	...M	...E	...K	...T
A2.CD.97.97CDK510	...MGFTQS	...N	...I	...LI	...K	...A	...D.E	...D	...E	...A	...K	...N
A2.CD.97.97CDKTB48	...T.MGFORNC	...KW	...E	...I	...LVF	...I	...M	...K	...A	...K	...D	...N
A3.CY.94.94CY017.41	...MGFORN	...L	...G	...I	...LI	...I	...M	...K	...D	...I	...N	...Q
A.SN.01.DDI579	...M.MGIORN	...LP	...M	...I	...IS	...C	...II	...Q	...LD	...E	...N	...T
A.SN.01.DDU369	...T.MGIORNC	...TPW	...I	...I	...IF	...LII	...K	...K	...D	...E	...N	...T
A.SN.96.DDU360	...M.MGIORN	...LP	...I	...I	...MI	...N	...D.E	...O	...LD	...E	...N	...T
A.ZA.04.04ZASK162B1	...M.TORN	...PRW	...I	...I	...II	...G	...D.D	...SK	...MN	...E	...K	...G
B.AR.00.ARMS008	...A.IRRNW	...G	...GTMILL	...Y	...A	...NNNTN	...R	...K	...D	...IN	...P	...N
B.AU.96.MBCD36	...T.M	...TRKN	...R	...I	...EED	...W	...R	...A	...S	...IA	...E	...H
B.CO.01.PCM074	...GIMRNC	...R	...*	...I	...N	...N	...R	...A	...K	...H	...L	...E
B.GA.88.OYI	...TARGTRKN	...R	...I	...I	...A	...N	...R	...A	...D	...N	...N	...O
B.NL.00.671.00T36	...K	...GTRKN	...R	...I	...T	...N	...R	...K	...L	...E	...N	...N
B.RU.04.04RU129005	...A	...GTRKN	...R	...I	...S	...A	...O	...R	...LN	...A	...N	...T
B.TH.90.BK132	...TRKNC	...L	...I	...I	...S	...A	...N	...A	...T	...N	...A	...T
B.US.90.WEAU160	...K	...I	...I	...I	...S	...A	...N	...A	...T	...N	...A	...T
B.US.98.1058.11	...GIRKNC	...S	...I	...I	...I	...R	...A	...N	...E	...A	...E	...N
C.AR.01.ARG4006	...A	...GIORNC	...KW	...I	...I	...LGFC	...N	...V	...G	...N	...K	...Q
C.BR.04.04BR013	...G	...TORNC	...KW	...I	...I	...LGFW	...FL	...N	...V	...G	...N	...Q
C.BR.92.BR025.d	...EGTORNC	...OM	...I	...VI	...LGFW	...V	...Y	...N	...V	...I	...G	...Q
C.BW.00.00BW07621	...K	...MGIORNC	...OM	...I	...I	...LGFW	...N	...M	...G	...N	...R	...Q
C.ET.86.ETH2220	...RGLLRN	...OM	...I	...V	...LGFW	...N	...N	...N	...D	...SP	...S	...Q
C.IN.95.95IN21068	...RGLLRN	...OM	...I	...I	...LGFW	...N	...N	...K	...K	...LL	...D	...D
C.IN.99.01IN565.10	...RGLORNC	...OM	...I	...I	...LGFW	...N	...N	...K	...K	...LL	...D	...D
C.KZ.01.BD9.11	...RGRSRNW	...OM	...M	...S	...LGFW	...NS	...R	...N	...R	...KAP	...I	...D
C.UY.01.TRA3011	...RGLORNC	...KW	...I	...I	...LGFW	...NS	...R	...N	...R	...KAP	...I	...D
C.ZA.04.SK164B1	...RGLLRN	...TW.G	...I	...I	...LGFW	...L	...RGE	...NS	...T	...K	...S	...D
C.ZA.05.05ZASK245B1	...T	...MPTRN	...ROW	...I	...I	...LGFW	...Y	...N	...V	...G	...N	...D
C.ZM.96.96ZM651	...R	...ILRNW	...RW	...T	...I	...LGFW	...N	...N	...S	...EK	...I	...D
D.CD.83.ELI	...ARGIERNC	...NW	...K	...I	...I	...T	...N	...S	...E	...A	...I	...N
D.CD.83.NDK	...AR	...KERN	...C	...I	...T	...A	...D	...D	...I	...E	...K	...N
D.KE.01.01CM.4412HAL	...MGLERN	...S	...K	...I	...LMTY	...A	...G	...N	...I	...D	...L	...N
D.KE.01.NKU3006	...TGPERN	...N	...K	...I	...L	...LMTY	...A	...G	...N	...I	...D	...N
D.TZ.99.MN012	...RGLERN	...N	...K	...L	...LMTY	...A	...D	...O	...I	...S	...E	...K
D.TZ.01.A280	...M	...TORN	...N	...I	...W	...TY	...VA	...O	...I	...R	...N	...N
D.UG.94.94UG114	...R	...TKRN	...K	...I	...V	...G	...S	...N	...K	...A	...I	...N
D.UG.99.99UGD23550	...R	...GTRKN	...K	...I	...GTMILL	...L	...SAIGD	...G	...N	...K	...E	...N
D.UG.99.99UGK03958	...R	...IERN	...S	...I	...I	...TY	...KVA	...G	...E	...K	...A	...Y
D.ZA.86.R482	...ARGIERNC	...N	...K	...I	...I	...TY	...A	...G	...N	...R	...K	...Y
F1.BE.93.VI850	...RGMORNC	...G	...K	...L	...LF	...I	...N	...A	...D	...N	...N	...D
F1.BR.89.B2126	...RGMORNC	...G	...K	...L	...LF	...I	...N	...N	...N	...E	...R	...D
F1.BR.93.93BR020.1	...RGMORNC	...G	...K	...L	...LF	...I	...N	...A	...N	...S	...E	...D
F1.FI.93.FIN9363	...RGMORNC	...G	...K	...L	...LF	...I	...N	...K	...A	...D	...N	...T
F1.FR.96.MPA11	...RVMORNC	...G	...K	...L	...LF	...I	...N	...N	...N	...S	...E	...K
F2.CM.02.02CM.0016B5Y	...RGMORNC	...G	...K	...F	...LF	...I	...N	...A	...D	...N	...N	...D
F2.CM.95.MP255	...R	...MORNC	...G	...L	...LF	...I	...N	...AN	...D	...D	...P	...D
F2.CM.95.MP257	...R	...MORNC	...G	...L	...LF	...I	...N	...A	...D	...N	...N	...D
F2.CM.97.CM53657	...R	...MORNC	...G	...L	...LF	...I	...N	...N	...A	...D	...N	...D
G.BE.96.DRCL	...G	...IORNC	...N	...I	...LI	...LVI	...A	...ED	...NAP	...HS	...S	...N
G.CM.01.01CM.4049HAN	...RGLORNC	...P	...K	...I	...LI	...LVI	...N	...S	...N	...N	...N	...Q
G.ES.99.X138	...G	...GLERN	...N	...I	...LI	...LVI	...N	...S	...N	...N	...N	...D
G.KE.93.HH8793.12.1	...G	...GLERN	...N	...I	...LI	...LVI	...N	...S	...N	...N	...N	...D
G.NG.92.92NG5083	...G	...GLERN	...N	...I	...LI	...LVI	...N	...S	...N	...N	...N	...D
G.SE.93.SE6165	...TGFORNC	...*	...K	...I	...LI	...LVI	...N	...S	...N	...N	...N	...D
H.BE.93.VI991	...T	...M	...TORN	...PS	...I	...L	...L	...V	...G	...N	...R	...T
H.BE.93.VI997	...T	...MR	...N	...PQM	...G	...I	...L	...Y	...A	...G	...N	...T
H.C.F.90.056	...T	...M	...TORN	...PS	...I	...L	...L	...A	...Q	...N	...K	...I
J.SE.93.SE7887	...T	...M	...TOTSMLS	...L	...IF	...N	...R	...D	...K	...K	...S	...D
J.SE.94.SE7022	...AR	...IORNC	...G	...K	...R	...I	...I	...N	...N	...N	...N	...D
K.CD.97.EQTB11C	...RGMORNC	...T	...G	...N	...I	...LF	...I	...I	...A	...N	...N	...T
K.CM.96.MP535	...RGMORNC	...T	...G	...N	...I	...LF	...I	...I	...NA	...D	...N	...T

Table with 4 columns: Accession ID, Signal peptide, gp120, and Amino acid sequence. The table lists various HIV-1 and SIVcpz strains and their corresponding protein sequences, with a signal peptide asterisk and gp120 label above the sequences.

Accession	Sequence
B_FR.83_HXB2	DIISLWQSLKPCVKLTPLCVLSKCTDKLTKDNTV.....
01 AE.CF.90.90CF402	V-...T-H-KASFTNA-...SDR-KMEDAVR-...MT-ELQD-K-EVH-L-...TS-VVO-SSVQ-...NNNNNGTSGNNSHKFR-IH-...K-...
01 AE.CM.05.FJ051	V-...T-N-NAAVNSK-...SITV-NNTVGNITDDV-...T-...MT-EL-D-K-A-V-L-R-LV-...N-E-R-IN-...K-...
01 AE.HK.x.HK001	V-...T-N-NAAVNSK-...SITV-NNTVGNITDDV-...T-...MT-EL-D-K-A-V-L-R-LV-...N-E-R-IN-...K-...
01 AE.JP.93.93JP.NH1	V-...T-N-NAAVNSK-...SITV-NNTVGNITDDV-...T-...MT-EL-D-K-A-V-L-R-LV-...N-E-R-IN-...K-...
01 AE.TH.01.01R4141	V-...T-N-KLEVK-I-...TVKVPVIGNITD-VR-...T-...MT-EL-D-K-V-V-L-...VO-GD-...KNNNSDI-R-IN-...K-...
01 AE.TH.02.02OUR7691	V-...T-N-NANLTVG-...STMTEASIGNITD-VR-...T-...MT-EL-D-K-VH-L-R-...VO-E-...KKTSSSE-R-IN-...K-...
02 AG.CM.02.02CM.16691E	V-...T-N-NANLTVG-...STMTEASIGNITD-VR-...T-...MT-EL-D-K-VH-L-R-...VO-E-...KKTSSSE-R-IN-...K-...
07 BC.CN.97.CNS4	V-...T-N-IPYISIDDM-...R-V-...T-...TT-EL-D-RR-...L-RH-VWEMEG-...NESR-I-...T-...
02 AG.EC.x.EC041	V-...T-N-ONVT-I-EE-...MRE-...MT-EL-D-K-VS-L-R-...VVQ-NE-...SSNSQ-R-IN-...A-...
02 AG.FR.91.DJ264	V-...T-D-VNYSNSGI-...VKSISRDMQ-...MT-EL-D-K-OVS-L-R-...VVQ-NE-...SSNSQ-R-IN-...A-...
02 AG.GH.03.GHNJ196	V-...T-D-HSPT-SEEN-...KIGNIS-EMQ-...T-EL-D-NR-MH-L-RQ-V-MNESL-...VSIINTNS-DQ-R-IN-...TV-...
02 AG.NG.x.IE8G	V-...T-D-HNPN-SYEN-...NLITSDMN-...T-EV-D-KK-MH-L-R-...VVQ-NE-...NNGSQ-R-IN-...A-...
02 AG.SN.98.MU1211	V-...T-D-HNYNTR-N-...SK-N-P-A-...T-VVQ-DRK-MS-L-I-V-K-...NA-Y-R-IN-...A-...
02 AG.UZ.02.02UZ693	V-...T-D-H-Y-SNVSD-...P-A-...T-VVQ-DRK-MS-L-I-V-K-...NA-Y-R-IN-...A-...
04 AB.RU.97.KAL153_2	V-...T-N-N-KEVTS-...TMTSIIKMM-M-...T-DL-D-K-K-L-...RI-V-NA-...RYPINGSNPNNS-EB-M-IN-...A-T-K-...
05 DF.BE.x.VI1310	V-...T-N-TFT-INAATINS-...NGTVI-EG-...D-T-E-D-K-K-L-...RI-V-NA-...RYPINGSNPNNS-EB-M-IN-...A-T-K-...
06 CPX.AU.96.BEP90	V-...T-N-P-ANSTA-...NSTVN-TFLKE-T-AVQ-...MT-EVND-KL-VH-L-RP-V-SS-...DSSNS-R-IN-...T-K-...
07 BC.CN.97.CNS4	V-...T-E-RNVSNS-D-...T-N-PAIENK-...LGNNSTNLTGNN-ILVDDISK-...T-E-D-TK-...L-RP-V-GD-...DSSNS-R-IN-...T-K-...
08 BC.CN.97.97CNGX_6F	V-...T-E-RNVSNS-D-...TYHETIHESVK-M-...AT-VV-DRK-TV-L-R-...V-LTK-...KNYSENSEY-R-IN-...A-...
09 CPX.GH.96.96GH2911	V-...T-D-HRVN-SKPN-...TTSDESEVRMQ-...T-EL-D-H-V-SL-RS-VS-NA-...ENSGENSEY-R-IN-...A-...
10 CD.TZ.96.96TZ_BF061	V-...G-I-N-NGINATND-...VGDPRMT-...TT-EYKD-KK-L-...VVQ-GD-...SN-R-IN-...A-...
11 CPX.GR.x.GR17	V-...E-A-N-A-...RDNAID-...T-...ELED-KK-R-L-R-...VVQ-ND-...SSNIGQ-R-IN-...V-AVK-...
12 BF.AR.99.ARMA159	V-...T-N-SVANATA-N-...ATANGQNTLEB-P-A-Q-...MT-E-D-QL-VH-L-R-...V-G-...GSET-R-IN-...T-*
13 CPX.CM.96.1849	V-...I-S-T-N-NNITS-SSI-...NST-OGRE-...Y-MT-GVDRR-V-SL-RV-E-EG-...NSNSGSSSB-R-I-...K-...
14 BG.ES.99.X397	V-...E-T-N-PNTTS-N-...ATNTIN-SLEM-...M-...T-L-D-IK-...L-S-VEA-...NR-R-...I-...
15 01B.TH.99.99TH_MU2079	V-...T-N-NRTI-G-...T-...T-...D-L-S-VEA-...NR-R-...I-...
16 A2D.KR.97.97KR004	V-...T-N-SRV-TISS-...TOSPSNNTM-...EIT-EL-D-K-VQ-L-E-VOLNS-...SDSNDTLNQ-R-IH-D-T-...
18 CPX.CU.99.CU76	V-...E-T-N-NVNYSG-N-...TYA-N-SL-...ATR-M-...F-T-EV-E-OKO-L-? -VS-VG-...?NSNSYD-R-IN-...V-T-K-...
19 CPX.CU.99.CU76	V-...T-D-...HM-...MT-EL-D-K-QI-SL-...V-GD-...ENN-...I-IN-...A-...
20 BG.CU.03.CB134	V-...T-N-SVT-NCTK-...EGNNTVDNCAD-...T-E-D-K-KO-...L-OR-...VQ-SG-...ENN-...R-IN-...V-T-K-...
21 AD.KR.91.KNH1254	V-...T-N-AGTSELV-...STNSV-TNSSTL-...AAGMO-...VT-VV-D-KO-...L-RP-V-...ENN-...R-IN-...V-T-K-...
23 BG.CU.03.CB118	V-...E-T-N-KVDCB-RN-...CTTTGTVNSAD-...T-E-D-SK-...L-M-DK-...NNSKNYSD-R-IN-...V-T-K-...
24 BG.CU.03.CB378	V-...E-T-N-NQTK-...NCTEE-NSTVNC-...T-ELQD-KK-...L-I-V-N-...SSNNNSYD-R-IN-...V-T-K-...
25 CPX.CM.x.101BA	V-...E-I-Q-T-N-VT-NCNRRINNSNC-...SHSINSTEKNTNLIANGCOR-...T-ELKD-KK-...L-VV-ED-...GNSND-R-IN-...A-K-...
28 BF.BR.99.BREPM12609	V-...E-I-Q-T-N-NNVTV-MN-...AINTVNSVFEAME-M-...VT-GD-M-...L-VV-A-...NA-T-IN-...A-...
29 BF.BR.02.BREPM119	V-...O-T-N-S-G-N-...M-...DWGR-...M-...T-DL-D-K-V-...VT-G-...N-R-I-...L-...
31 BC.BR.02.110PA	V-...*T-N-S-AISNA-KTNAN-...QTNAOT-NNSST-DM-...MT-EL-D-IR-VH-L-R-...V-LNE-...NNSSGD-R-IN-...A-...
33_01B.WY.05.05MYK1007_1	V-...I-H-NANLTV-...RQTWAPSLLENVTE-S-...TT-EL-D-K-V-L-...VS-GG-...NKSNSSE-R-IN-...K-...
A1C.TZ.02.C03710	V-...T-D-HYNVTVI-...NEM-...Y-VT-V-D-R-RV-SL-...VVQ-EN-...KNSNGSQ-R-IN-...A-...
A1CDGKU.ZA.99.CM4	V-...T-N-SNVNVS-G-...NTSS-K-A-...AT-E-N-RK-V-L-...V-LKD-...NSN-S-I-IN-...A-...
A1DHK.GA.97.97NOGLI3	V-...T-N-PA-H-D-...TNNIS-OPSOA-...VT-A-Q-VH-L-R-LVS-...NDDN-O-R-IN-...A-...
A1GHU.GA.x.VI354	V-...QI-T-N-SKINIIN-S-...TDKANVTNDA-MR-...T-E-DRKK-...L-H-LV-...T-...E-KTFI-IH-...T-...
A2D.KR.99.KER2003	V-...T-N-N-OVRNSG-...TON-NOYDM-...T-VV-D-RKOV-...L-V-V-N-...DDNT-ST-R-IN-...A-...
AF2.CM.02.02CM.3163MN	V-...T-N-KANFTSKD-...DPTKAN-PTQDNDMDR-...T-EL-D-KK-V-SL-...TVE-K-...DSNN-O-R-IN-...A-...
AGU.CM.01.01CM_0989MO	V-...E-T-N-K-NVTS-...NT-NNTSVV-Q-...T-EV-D-RQO-...L-MVO-ND-...DNN-ST-R-IN-...V-T-K-...
ARU.CM.01.01CM_1296NG	V-...T-N-VDTMRTN-...ANANIS-I-TEV-Q-...VT-LLAK-KK-Q-...L-...V-EE-...GNDPNTAVN-R-IN-...A-...
BC.MM.99.mIDU103	V-...I-T-E-RNVS-NG-V-...TY-KYVESK-...AT-EL-DRK-TV-L-...V-LNE-...KNSSENSEH-R-IN-...A-...
BF1.BR.02.02BR006	V-...T-N-NLNGA-SNSTS-...NSNKREGMRNSKIVE-MR-...T-GT-...D-L-...VV-...NV-RMINR-...K-...
0708.CN.00.HH069	V-...T-N-N-NITN-...NSSD-NTINWEKV-E-MTI-...VT-G-GN-K-...L-D-VVAVE-...GNA-M-RH-...K-...
U.CD.83.83CD003	V-...F-T-N-I-V-S-N-...TYNETYND-...AT-LLTRKNTV-...L-R-V-L-DEN-...SGKNSSESSEY-R-IN-...A-...
U.CD.90.90CD121E12	V-...SS-T-N-VGTNNTA-...NT-EAT-T-...KVP-ELKD-TEVHTL-...VV-LNV-...TNNSSISST-R-IN-...T-...
U.GR.99.GR303	V-...T-N-KNPSCVALN-...C-NVATDMR-...M-Y-MT-EM-D-K-V-SL-...R-VVOMGS-...TNSSYGT-R-IN-...T-...
U.NL.x.U.NL_95.H01986_D1	V-...E-T-N-VT-R-S-...GNNATVR-...L-...T-VLOD-KR-...L-RF-VV-LNS-...DNNSSNYSB-R-IN-...I-T-K-...
N.CM.02.DJ00131	V-...T-MN-SNSGNRT-...DEKPKGNTDL-ARRM-...T-E-HD-KKQA-SL-...VE-VV-LND-...GNNST-R-IN-...TAV-...
N.CM.04.04CM.1015_04	V-...E-T-MH-NSNGNE-...VDN-ELDIGYKM-...VT-ERKD-KKLA-SL-...AE-VVQLNE-...SDSTNQT-R-I-K-TSV-...
N.CM.04.04CM.1131_03	V-...E-T-MH-NSNGNE-...VGN-TLDIGYKOM-...VT-FREDRK-A-SL-...TE-VVQLND-...SDS-SNT-T-IN-K-TV-...
N.CM.95.YBF30	V-...E-T-ML-N-SYGERN-...NT-MTTRPDIGYKOM-...AT-ELTD-KKQV-SL-...VE-VV-NA-...YKNT-R-IN-...TAV-...
N.CM.97.YBF106	V-...E-T-ML-NNSNGNSAG-...NSTTNRTEDL-DRQM-...T-E-DRKKOV-SL-...VE-VV-KD-...GT-NNT-R-IN-...TAV-...
O.BE.87.AN770	V-...-OM-F-OME-NIAGT-E-...M-1KMN-GYNCPT-...PSTTSTVTKPTTP-VDGKLOE-N-O-GEKD-K-...MK-I-...G-LMKOD-...NNE-NC-Y-WH-...TT-...
O.CM.91.MVPS180	V-...E-M-F-OMN-V-OTNKT-...LLNETIN-MR-...VT-VLTD-KEQK-L-...VS-LSKVND-...TSSTNKNSKM-T-N-SIT-...
O.CM.96.96CMBAB637	V-...-OM-F-OMN-VNAT-S-...NTPRT-FATPTPG-ENMK-K-E-VT-LLK-KE-Q-L-...VS-LTKVNE-...SETGNTEPI-T-IN-SIT-K-...
O.SN.99.SEMP1300	V-...E-T-M-F-OMN-VNDE-S-...VKNDTSSGEM-K-E-VT-VLKD-KE-Q-L-...VS-LMKVNE-...NND-M-T-IN-SIT-K-...
CPZ.CD.90.ANT	V-...-M2Q-FQ-H-...M-1KMN-GYNCPT-...PSTTSTVTKPTTP-VDGKLOE-N-O-GEKD-K-...MK-I-...G-LMKOD-...NNE-NC-Y-WH-...TT-...
CPZ.CM.01.SIVcpzCAM13	V-...-S-T-M-SVTRONS-SNSN-...NNPTLK-NT-...KNQTVLQOM-...T-...TT-EL-D-KKQV-SL-...VD-LQSLGS-...GTGDT-TMIN-...TA-...
CPZ.CM.05.SIVcpzK505	V-...-E-T-S-SWRVSN-S-...VNTQNVQOM-...VT-EL-D-KKQV-SL-...MG--L-T-...NNSGNSNSQ-R-IN-...TAV-...
CPZ.CM.05.SIVcpzL87	V-...-VN-V-I-T-N-SIP-F-NSS-...INSNETM-...TT-EL-D-KKQV-SL-...VD-LQ-LQ-NK-...T-E-IN-...TA-...
CPZ.CM.05.SIVcpzMB66	V-...E-T-N-SLF-CLKEN-...GNTNCTVQISTGND-FANNIIVGIDMY-...AT-EL-DRKKQV-SL-...RQ-LE-LEG-...NKPPEGKVAL-R-YN-TAM-...
CPZ.CM.05.SIVcpzMT145	V-...T-T-NNPT-TSC-...NSTDRDL-DMR-...VT-EL-D-KKQV-SL-...VE-TA-G-...NST-R-IN-...TA-...
CPZ.GA.88.GAB1	V-...T-Q-SKANFSQAK-...NLTKQSSPPL-M-...T-Q-SKANFSQAK-...VT-EL-D-KKQV-SL-...VE-VNVLG-...ENNT-R-LIN-...TA-...
CPZ.TZ.01.TAN1	V-...L-FQ-F-F-1KMT-TMT-T-K-...TLNSATTLTPTVLSLSPNV-VV-...OT-FD-D-KKQI-SL-...RE-VKE-G-...NNN-Y-HN-...TA-...
CPZ.US.85.CPZUS	V-...I-TMT-LNPDNSSA-...VNTTDDIMR-...T-EL-D-KKQV-SL-...VD-LAH-N-...NT-R-IN-...TA-...

HIV-1/SIVcpz proteins

Accession	Sequence	Accession	Sequence	Accession	Sequence	Accession	Sequence
B.FR.83.HXB2	ACPKVSFEPIDPHYCAPAGFALLKCNKFTNGTGCPTNSTVQCTHGIRPVPVSTQLLNGSLAEE...	V3 loop	...NNNTRKRIRIQGPGRAVFT...IG...				
01 AE.CF.90.90CF402	D-D-N-D-N-K-S-K-S-A-A		H-K-I-FKKV-ISA-I-V-H-T-N				
01 AE.CN.05.FJ051	T-VV-D-N-K-S-A-A		H-R-T-S-T-I-OL-YR-T-E				
01 AE.HK.x.HK001	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
01 AE.JP.93.93JP.NH1	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
01 AE.TH.01.OUR4141	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
01 AE.TH.02.OUR7691	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
02 AG.CM.02.02CM.16691E	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
02 AG.EC.x.EC041	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
02 AG.FR.91.DJ264	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
02 AG.GH.03.GHNJ196	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
02 AG.NG.x.IBNG	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
02 AG.SN.98.MP1211	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
02 AG.UZ.02.02UZ693	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
03 AB.RU.97.KAL153.2	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
04 CPX.CV.94.CV032	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
05 DF.BE.x.VI1310	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
06 CPX.AU.96.BEP90	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
07 BC.CN.97.CNS4	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
08 BC.CN.97.97CNGX.6F	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
09 CPX.GH.96.96GH2911	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
10 CD.TZ.96.96TZ.BF061	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
11 CPX.GR.x.GR17	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
12 BF.AR.99.ARMA159	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
13 CPX.CM.96.1849	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
14 BG.ES.99.X397	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
15 01B.TH.99.99TH.MU2079	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
16 A2D.KR.97.97KR004	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
18 CPX.CU.99.CU76	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
20 BG.CU.03.CB134	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
21 A2D.KR.91.KNH1254	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
23 BG.CU.03.CB118	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
24 BG.CU.03.CB378	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
25 CPX.CM.x.101BA	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
28 BF.BR.99.BREPM12609	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
29 BF.BR.02.BREPM119	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
31 BC.BR.02.110PA	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
33_01B.WY.05.05MYK1007_1	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
A1C.TZ.02.CO3710	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
A1CDGKU.ZA.99.CM4	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
A1DHU.NO.97.97NOGL13	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
A1GHU.GA.x.VI354	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
A2D.KR.99.KER2003	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
AF2.CM.02.02CM.3163MN	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
AGU.CM.01.01CM.0989MO	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
ARU.CM.01.01CM.1296NG	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
BC.MM.99.mIDU103	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
BF1.BR.02.02BR006	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
0708.CN.00.HH069	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
U.CD.83.83CD003	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
U.CD.90.90CD121E12	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
U.GR.99.GR303	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
U.NL.x.U.NL.95.H10986_D1	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
N.CM.02.DJ00131	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
N.CM.04.04CM.1015_04	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
N.CM.04.04CM.1131_03	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
N.CM.95.YBF30	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
N.CM.97.YBF106	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
O.BE.87.AN770	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
O.CM.91.MVPS180	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
O.CM.96.96CMWAB637	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
O.SN.99.SEMP1300	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
CPZ.CD.90.ANT	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
CPZ.CM.01.SIVcpzCAM13	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
CPZ.CM.05.SIVcpzEK505	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
CPZ.CM.05.SIVcpzL87	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
CPZ.CM.05.SIVcpzMB66	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
CPZ.CM.05.SIVcpzMT145	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
CPZ.GA.88.GAB1	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
CPZ.TZ.01.TFAN1	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				
CPZ.US.85.CPZUS	T-VV-D-N-K-S-A-A		S-TS-T-I-OL-YR-T-E				

HIV-1/SIVcpz proteins

	V3 loop	V4 loop	CD4	CD4		
B_FR.83_HXB2	..K.I.G.N.MRQAHCNISRAKWNITKQIASKLR..EQFG...N.....NKKTIIF..KQS..SGCDPEIVTHSFGCG.EFFYNSTQIFN.....STW.....FNSTWSTEGSNTEGSD.TIIT.LPC	..I.N..D.I.K.Y.E-NKT-KE-VTR-..HL-..G-..TM-S-..RP-..TM-H-R-R-..T-A-..T-N-..ING-MOEV-GTN-G-N-..				
01 AE.CF.90_90CF402	..I.N..D.I.K.Y.E-NKT-KE-VTR-..HL-..G-..TM-S-..RP-..TM-H-R-R-..T-A-..T-N-..ING-MOEV-GTN-G-N-..					
01 AE.CN.05_HU001	..I.N..D.I.K.Y.E-NKT-HE-VVG-..H-..N-..K-..TN-R-..OPH-..L-TM-H-R-..T-N-..N-..NGTMEG-GTDNG-..I-..					
01 AE.HK.x.FK051	..I.N..D.I.K.Y.E-NKT-HE-VVG-..H-..N-..K-..TN-R-..OPH-..L-TM-H-R-..T-N-..N-..NGTMEG-GTDNG-..I-..					
01 AE.JP.93_93JP_NH1	..I.N..D.I.K.Y.E-NKT-KE-VTE-..K-..H-N-..K-..TN-R-..OPH-..L-TM-H-R-..T-N-..D-..S-..NTTIT-R-NRS.NFI-..					
01 AE.TH.01_01RA41I1	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
01 AE.TH.02_02OUR7691	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
02 AG.CM.02_02CM240	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
02 AG.CM.02_02CM16691E	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
07 BC.EC.x.EC041	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
02 AG.EC.x.EC041	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
02 AG.FR.91_DJ264	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
02 AG.GH.03_GHNJ196	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
02 AG.NG.x.IEING	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
02 AG.SG.98_MP1211	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
02 AG.UZ.02_02UZ693	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
04 AB.RU.97_KAL153_2	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
03 CPX.CV.94_CV0332	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
05 DF.BE.x.VI1310	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
06 CPX.AU.96_BFP90	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
07 BC.CN.97_CNS4	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
08 BC.CN.97_97CNGX_6F	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
09 CPX.GH.96_96GH2911	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
10 CD.TZ.96_96TZ_BF061	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
11 CPX.GR.x.GR17	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
12 BF.AR.99_ARMAL159	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
13 CPX.CM.96_1849	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
14 BG.ES.99_X397	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
15 01B.TH.99_99TH_MU2079	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
16 A2D.KR.97_97KR004	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
18 CPX.CU.99_CU76	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
19 CPX.CU.99_CU77	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
20 BG.CO.03_CB134	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
21 A2D.KE.91_KNH1254	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
23 BG.CO.03_CB118	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
24 BG.CO.03_CB378	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
25 CPX.CO.x.101BA	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
28 BF.BR.99_BREPML12609	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
29 BF.BR.02_BREPML19	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
31 BC.BR.02_110PA	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
33_01B.WY.05_05MYK1007_1	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
A1C.TZ.02_C03710	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
A1C.DGU.ZA.99_CM4	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
A1D.HU.NO.97_97NOGL13	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
A1G.HU.GA.x.VI354	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
A2D.KE.99_KER2003	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
AP2.CM.02_02CM_3163MN	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
AGU.CM.01_01CM_0989MO	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
ARU.CM.01_01CM_1296NG	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
BC.MM.99_m1DU103	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
BF1.BR.02_02BR006	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
0708.CN.00_HH069	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
U.CD.83_83CD003	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
U.CD.90_90CD121E12	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
U.GR.99_GR303	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
U.NL.x.U.NL_95_H10986_D1	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
N.CM.02_DJ00131	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
N.CM.04_C01015_04	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
N.CM.04_04CM_1131_03	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
N.CM.95_YBF30	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
N.CM.97_YBF106	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
O.BE.81_AN170	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
O.BE.97_MVPS180	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
O.CM.96_96CMBAB637	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
O.SN.99_SEMP1300	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
CPZ.CD.90_ANT	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
CPZ.CM.01_SIVcpzCAM13	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
CPZ.CM.05_SIVcpzK505	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
CPZ.CM.05_SIVcpzL87	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
CPZ.CM.05_SIVcpzMB66	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
CPZ.CM.05_SIVcpzMT145	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
CPZ.GA.88_GAB1	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
CPZ.HZ.01_TAN1	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					
CPZ.US.85_CPZUS	..I.N..D.I.K.Y.E-NKT-..E-..V-G-..H-..K-..GTEK-..V-..OPP-..L-TM-H-R-..T-K-..N-C-..MENE-SKGC-NDNNG-..					

HIV-1/SIVcpz proteins

	CD4	CD4 binding	* ^^^	- ^^^ V5 -	gp120 \ / gp41	fusion peptide	
B.FR.83.HXB2	RIKQIINM.WQ.KVGMAYAPPISQIRCSNITGLLITRDGG.....	NSNNESEIFRPPG.GDMRDNRSELYKVKVVKIEPIGVAPTAKRRVV.....	QREKR.A.VG.IGALFL.GFLGAA.GST				
A1.KE.94.Q23.17	RA-Q	P-V-K-E	..KD-VN-T	E	R	E	V
A1.RU.03.03RU20.06_13	R-O	K-S-E	..GTT-?S-T	I	N	R	E
A1.RW.93.93RW037A	RA-Q	E-V	..VN-IVN-T	R	N	E	I
A1.SE.94.SE7253	RA-Q	I-E	..VV-STN-T	N	K	R	I
A1.TZ.01.A173	RA-Q	I-E	..RN-SIN-T	R	R	E	I
A1.UA.00.98UA0116	R-Q	E-N-E	..SGA-SK-TY-I	N	I	E	A
A1.UG.92.92UG037	R-Q	Q-V-K-E	..VNSSD-T	R	R	E	A
A1.UG.92.98UG057136	Q-Q	V-M-K	..GNSSP-T	R	R	E	V
A2.CD.97.97CDK510	VD	A-V-Y-T	..S-TN	I	SR	E	V
A2.CD.97.97CDKTB48	R-R	A-V-K-T	..MI	R	R	E	V
A3.CY.94.94CY017_41	R-R	A-I-K-T	..II	R	R	E	V
A.SN.01.DDI579	R-Q	Q-V-N-T	..DMSSTN-T	N	K	R	V
A.SN.01.DDU369	R-Q	V-K-V	..L-SSP-T	N	K	R	V
A.SN.96.DDU360	R-VH	Q-V-N-T	..DN-STD-K	R	R	E	V
A.ZA.04.04ZASK162B1	L-R	R-Q	..LELN-TNN-T	I	R	E	V
B.AR.00.ARCMS008	R	E	..G-TSRDN-T	V	I	E	V
B.AU.96.MBCD36	R	I-N-T	..L-SDN-T	E	E	I	M
B.CO.01.PCM074	E	R-I-N-T	..T-TNN-T	E	R	E	M
B.GA.88.OYI	V	E	..K-TT-GI	A	Q	R	M
B.NL.00.671.00T36	R	E	..GGE-ST	R	R	E	M
B.RU.04.04RU129005	Q	R-S	..AN-STT-V	?			M
B.TH.90.BK132	E	G-T	..NO-GT-T	N	K	E	V
B.US.90.WEAU160	R	E	..SSEE-OT	N	K	E	V
B.US.98.1058.11	E	R	..KN-GT-GT-V	N	K	E	V
C.AR.01.ARG4006	E	R-M-T-R	..T-GT-NT	E	N	I	V
C.BR.04.04BR013	K	VR	..VK-M-T-R	E	K	I	V
C.BR.92.BR025_d	G	R	..TGMHDT	E	E	K	V
C.BW.00.00BW07621	G	R	..A-N-I-K	E	E	K	V
C.ET.86.ETH2220	G	R	..E-I-M-R	A	KPHPTK	E	V
C.IN.95.95IN21068	E	R	..E-K-T-R	V	EDKNNIET-KT	E	V
C.IN.99.01IN565_10	E	R	..A-N-T-K	I	V	KTKD-DT	V
C.KE.00.KER2010	R	R	..A-N-T-T-K	Q	T	KT-T	V
C.TZ.01.BD9_11	G	R	..N-A-N-T-K	V		TD-T-T	V
C.UY.01.TRA3011	V	G	..R-A-N-T-K	V		TD-T-T	V
C.ZA.04.SK164B1	K	R	..A-N-T-R	N	K	E	V
C.ZA.05.05ZASK245B1	E	R	..A-N-T-N-S	V	NNNDTG-DT	E	V
C.ZM.02.02ZM115	G	Q	..A-N-T-E	V	..NTSTE	E	V
C.ZM.96.96ZM651	R	E	..A-N-T-K	E	K	I	V
D.CD.83.ELI	K	VA	..GR-I	E	R-N-A-K-D	V	V
D.CD.83.NDK	V	L	..ERN-L	I	IN-STN-T		V
D.CM.01.01CM.4412HAL	G	R	..E-L-K	K	..AN-SSH-TI		V
D.KE.01.NK03006	E	R	..E-L-K	..TSDSA-T			V
D.TD.99.MN012	G	R	..R-A-N-L-V	S	NNNA-AS-S		V
D.TZ.01.A280	E	R	..A-L-T	N	VN-SRE		V
D.UG.94.94UG114	E	R	..E-F-N	A	AINSSON-T		V
D.UG.99.99UGD23550	G	R	..A	A-N-SQ-T			V
D.UG.99.99UGK09958	G	R	..E-L-Q	A	AINDSQ-T		V
D.ZA.86.R482	R	Y	..Q-TL	F	..NESNN-T		V
F1.BE.93.VI850	V	G	..R-TS	A-N-T-N	..NESNI-T	E	V
F1.BR.89.B2126	R	V	..E-R	A-E-N-T-N	..ONS-OT-T	E	V
F1.BR.93.93BR020_1	K	FV	..E-R	N-A-N-T-N	..L-STN-T	E	V
F1.FR.96.MPA411	K	Q	..G-Q	A-A-N-T-N-T	..OSN-SD-T	E	V
F2.CM.02.02CM.0016BBY	V	V	..R-R	A-K-Q-N	..QS-DT-RT-T	E	V
F2.CM.95.MP255	R	FV	..RI-R	E-E-Q-T	..SKA-NID-L-I	E	V
F2.CM.95.MP257	V	R	..Q	A-K-Q-N	..KIDDK-L-I	R	V
F2.CM.97.CM53657	R	V	..R-R	A-A-Q-N-S	..EG--TL	Q	V
G.BE.96.DRCLB	K	VR	..R-Q	A-N-T-R	..KN-TNNDTL	Q	V
G.CM.01.01CM.4049HAN	K	VR	..R-Q	A-N-T-K	..DN-ST	T	V
G.ES.99.X138	G	ES	..99.X	A-N-T-K	..NTRD-T	E	V
G.KE.93.HH8793_12_1	K	VR	..R-Q	S	..RDT-GT	A	V
G.NG.92.92NG6083	K	VR	..Q	L-ANLV-K	..NA-NAS-T-T	A	V
G.SE.93.SE6165	K	VR	..R-Q	A-N-E-N-S	..N-NDSTE-T	E	V
H.BE.93.VI991	K	V	..R-Q	R-N-T-I	..NNNNTNTS	T	V
H.BE.93.VI997	V	R	..R-Q	K-S-T-V	..N-TNNVT	E	V
H.CF.90.056	V	R	..R-Q	Q-N-M-V	..KG-DNYT	E	V
J.SE.93.SE7887	K	VR	..RT-Q	I	..NRNG-E-GT-T	T	V
J.SE.94.SE7022	K	VR	..RT-Q	I	..NRNG-E-GT-T	T	V
K.CD.97.EQTB11C			..Q	I	..ND-NTRTE-T		V
K.CM.96.MP535			..I	A-S-N	..N-THN-T		V

	CD4	CD4 binding	* ^^^	- ^^^ V5 -	gp120 \ / gp41	fusion peptide		
B.FR.83.HXB2	RIKQIINM.WQ.KVGMAYAPPISQIRCSNITGLLITRDGG	I	INO-OT-KN-T	NRK	Q	I	R	QREKR.A.VG.IGALFL.GFLGAA.GST
01 AE.CF.90.90CF402	V	EV-N-V	EV-N-V	EV-N-V	EV-N-V	EV-N-V	EV-N-V	
01 AE.CN.05.FJ051	E	S-N-V	S-N-V	S-N-V	S-N-V	S-N-V	S-N-V	
01 AE.HK.X.HK001	ET	R-S-O-V	R-S-O-V	R-S-O-V	R-S-O-V	R-S-O-V	R-S-O-V	
01 AE.JP.93.93JP.NH1	GA	K-S-N-V	K-S-N-V	K-S-N-V	K-S-N-V	K-S-N-V	K-S-N-V	
01 AE.JH.01.01JH4141	E	R-D-V	R-D-V	R-D-V	R-D-V	R-D-V	R-D-V	
01 AE.TH.02.02THR7691	K	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
01 AE.TH.90.CM240	K	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
02 AG.CM.02.02CM.16691E	L	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
02 AG.EC.X.EC041	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
02 AG.FR.91.DJ264	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
02 AG.GH.03.GHNJ196	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
02 AG.NG.X.IE8G	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
02 AG.SZ.02.02UZ693	K	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
03 AB.RU.97.KAL153.2	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
04 CDX.CV.94.CY0332	L	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
05 DF.BE.X.VI1310	K	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
07 BC.CN.97.CNS4	K	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
08 BC.CN.97.97CNGX.6F	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
09 BC.GH.96.96GH2911	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
10 CD.TZ.96.96TZ.BF061	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
11 CDX.GR.X.GR17	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
12 BF.AR.99.ARMA159	K	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
13 CDX.CM.96.1849	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
14 BG.ES.99.X397	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
15 01B.TH.99.99TH.MU2079	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
16 A2D.KR.97.97KR004	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
18 CDX.CV.99.CU76	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
19 CDX.CV.99.CU7	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
20 BG.CU.03.CB134	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
21 A2D.KE.91.KNH1254	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
23 BG.CU.03.CB118	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
24 BG.CU.03.CB378	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
25 CDX.CM.X.101BA	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
28 BF.BR.99.BREPM12609	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
29 BF.BR.02.BREPM119	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
31 BC.BR.02.110PA	G	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
33_01B.WY.05.05MYKL007_1	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
A1C.TZ.02.C03710	K	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
A1CDGKU.ZA.99.CM4	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
A1DHK.NO.97.97NOGLI3	K	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
A1GHU.GA.X.VI354	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
A2D.KE.99.KER2003	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
AP2.CM.02.02CM.3163MN	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
AGU.CM.01.01CM.0989MO	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
ARU.CM.01.01CM.1296NG	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
BC.CN.96.YNRL9667	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
BC.MM.99.mIDDU103	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
BF1.BR.02.02BR006	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
0708.CN.00.HH069	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
U.CD.83.83CD003	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
U.CD.90.90CD121E12	V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
U.GR.99.GR303	Q	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
U.NL.X.U.NL.95.H10986_D1	Y	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
N.CM.02.DJ00131	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
N.CM.04.04CM.1015_04	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
N.CM.04.04CM.1131_03	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
N.CM.95.YBF30	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
N.CM.97.YBF106	R	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
O.BE.87.AN1770	K	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
O.CM.91.MVPS180	O	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
O.CM.96.96CMBAB637	O	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
O.SN.99.SEMP1300	O	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
CPZ.CD.90.ANT	CPZ	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
CPZ.CM.01.SIVcpzCAM13	CPZ	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
CPZ.CM.05.SIVcpzEK505	CPZ	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
CPZ.CM.05.SIVcpzL87	CPZ	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
CPZ.CM.05.SIVcpzMB66	CPZ	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
CPZ.CM.05.SIVcpzMT145	CPZ	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
CPZ.CM.88.GAB1	CPZ	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
CPZ.TZ.01.TAN1	CPZ	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	
CPZ.US.85.CPZUS	CPZ	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	R-N-V	

HIV-1/SIVcpz proteins

B.FR.83.HXB2	DLLLIVT...RIVELLGR.....RGWEALKYWNW.LLQYWSQEL.KNSAVSLL...NATAIYAAGTDRVTEVQACRAIRHPRRIRQGLERILL	*	856
01 AE.CF.90.90CF402	-FI-AA...T-H.SSLQGLR-R-G-LG-S-V...RI-IT...D-T-GW...I-R-W-L...A		871
01 AE.CN.05.FJ051	-FIS-AA...T-H.SSLKGLR-G-LG-L-I...DT-GW...A-RW-FL...A-Q		855
01 AE.HK.x.HK001	-FI-AA...T-H.SSLKGLR-G-LG-L-I...DT-GW...A-RW-L...T-V		859
01 AE.JP.93.93JP.NH1	-FI-AA...T-H.SSLKGLR-G-LG-L-I...DT-GW...A-RW-L...A-V		857
01 AE.TH.01.0UR4141	-FI-AA...T-H.SSLKGLR-G-LG-L-I...DT-GW...A-RW-L...A		861
01 AE.TH.02.0UR7691	-FI-AA...T-H.SSLKGLR-G-LG-L-I...DT-GW...A-RW-L...A		861
01 AE.TH.90.CM240	-FI-AA...T-H.SSLKGLR-G-LG-L-I...DT-GW...A-RW-L...A		857
02 AG.CM.02.02CM_16691E	-FV-A...T-H.SSLKGLR...LG-S-S-G...IN...DTI...N...IG-R-G-VLN...V		847
02 AG.EC.x.EC041	-FV-A...T-H.SSLKGLR...LG-S-S-G...IN...DTI...N...IG-R-G-VLN...V		849
02 AG.FR.91.DJ264	-FV-AV...A-H.SSLKGLR...LG-T-G...IN...DTI...NW...IG-RVG...N-V		855
02 AG.GH.03.GHNJ196	-FV-A...T-H.SSLKGLR...LG-T-G...R...DTI...NW...IG-RIA-CN...A-I		859
02 AG.NG.x.IENG	-FI-AA...T-H.NCLKGLR-G-L-LS-V...IN...DTI...V-NW...A-IG-RVG...F-A		854
02 AG.SN.98.MP1211	-FV-AA...T-H.SSLKGLR...HL-S-C...IN...DT...H.SSLKGLR...I-RTG-CN...A-Q		861
03 AB.UZ.02.02UZ693	-FA-AA...TA-O.SSLKGLR...L-T-C...IN...DTI...S-IN...IG-RF-M-N...A-KA-Q		849
03 AB.UZ.97.KAL153_2	-AA...T...I...L-S-P-G...R...T...V...A...R...C...LN...A		840
04 CPX.CV.94.CY032	-T-V...T...I...L-S-P-G...R...T...V...A...R...C...LN...A		856
05 DF.BE.x.VII1310	-T-V...T...I...L-S-P-G...R...T...V...A...R...C...LN...A		861
06 CPX.AU.96.BFP90	-FG-AA...T-I...NSLRGLQ...I-LG-IC-G...O-I-F...D-A-NW...A-RIP-FLNV...F-A		859
07 BC.CN.97.CM54	-FT-VAA...V...NSLRGLQ...LGS-V-G...K-TI-V...DTI...I-L-L-YS...F-AA-Q		859
08 BC.CN.97.97CNGX_6F	-FI-LFA...G...NSLRGLQ...LGS-V-G...K-TI-V...DTI...I-L-L-YS...F-AA-Q		864
09 CPX.GH.96.96GHZ911	-FI-AA...T-I-H...V-QI-LG-A-G...I...DTI...E-GW...I-R-V-LN-T...A		842
10 CD.TZ.96.96TZ_BF061	-I-A...M...I...L...S...I...DTI...E-GW...I-R-V-LN-T...A		840
11 CPX.GR.x.GR17	-FI-AA...T...S-LG-A-G...S...I...DTI...E-GW...I-R-V-LN-T...A		844
12 BF.AR.99.ARMAL159	-V...T...H.SSLKGLR...R-L-V-GR-I-IT...DS...I-L-AL-RIG-VINA-V...A		843
13 CPX.CM.96.1849	-FI-A...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A-Q		867
14 BG.ES.99.X397	-VS-A...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A		865
15 01B.TH.99.99TH_MU2079	-W-AA...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A		854
16 A2D.KR.97.97KR004	-CIS-AA...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A		862
18 CPX.CU.99.CU76	-W-AA...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A		866
19 CPX.CU.99.CU7	-FTS-AA...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A		803
20 BG.CU.03.CB134	-I-V...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A		853
21 A2D.KE.91.KNH1254	-AA...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A		862
22 BG.CU.03.CB118	-AA...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A		855
24 BG.CU.03.CB378	-FI-AA...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A		864
25 CPX.CM.x.101BA	-FI-AA...T...H.SSLKGLR...G-L-L-G...IN...DTV...I-NW...A-RVG-LN-V...F-A		874
28 BF.BR.99.BREPM12609	-T...T-G...I...LKS-V-GL-K-I...DTI...I-NW...A-RVG-LN-V...F-A		868
29 BF.BR.02.BREPM119	-I-AA...A...K...GLRQ...I-LG-S-GL-I-I...DTI...I-NW...A-RVG-LN-V...F-A		869
31 BC.BR.02.110PA	-I-AA...A...K...GLRQ...I-LG-S-GL-I-I...DTI...I-NW...A-RVG-LN-V...F-A		867
33_01B.WY.05.05MYKL007_1	-I-AA...A...K...GLRQ...I-LG-S-GL-I-I...DTI...I-NW...A-RVG-LN-V...F-A		857
A1C.FZ.02.CO3710	-FI-AA...T...H.SSLKGLR...G-L-L-V-GR-I-IN-F...DTI...I-NW...A-RVG-LN-V...F-A		857
A1CDGKU.ZA.99.CM4	-SI-A...L-H...I-L-S...IN-F...DTI...I-NW...A-RVG-LN-V...F-A		856
A1DHK.NO.97.97NOGL13	-LA...T-T-S...K...L-G...L-G...IN...DTI...I-NW...A-RVG-LN-V...F-A		847
A1GHU.GA.x.VI354	-A...T...K...L-G...L-G...IN...DTI...I-NW...A-RVG-LN-V...F-A		846
A2D.KE.99.KER2003	-I-AG...E-G...L-GR-R-N-Y...I-RR...LN...F-A		852
AF2.CM.02.02CM_3163MN	-FI-AA...D...RGLKG-V-L-A-GR-I-I...DTV...I-NW...A-RVG-LN-V...F-A		854
AFU.CM.01.01CM_0989MO	-FI-AA...T-I-H...V-QI-LG-L-L-G-I...DTV...I-NW...A-RVG-LN-V...F-A		857
AHJU.CM.01.01CM_1296NG	-FI-AA...T-DI-H...V-QI-LG-L-L-G-I...DTI...I-NW...A-RVG-LN-V...F-A		853
BC.CN.96.YNRL9607	-A...I...R...I...V...DTI...I-NW...A-RVG-LN-V...F-A		846
BC.MW.99.MDDU1003	-A...I...R...I...V...DTI...I-NW...A-RVG-LN-V...F-A		863
BF1.BR.02.02BR006	-S...V...NSLRGLQ...LGS-V-GL...K-TI-V...DTI...I-NW...A-RVG-LN-V...F-A		852
0708.CN.00.HH069	-FI-VAA...V...NSLRGLQ...LGS-V-GL...K-TI-V...DTI...I-NW...A-RVG-LN-V...F-A		863
U.CD.83.83CD003	-I-V...KGLR...L-G-VL-G...I...DTI...I-NW...A-RVG-LN-V...F-A		847
U.CD.90.90CD121E12	-FIS-A...KGLR...L-G-VL-G...I...DTI...I-NW...A-RVG-LN-V...F-A		845
U.GR.99.GR303	-FI-AA...T-I-T...?G-OT-LGE-SVI-V...QK-T...DI...V-GW...TG-RIG-L...F-A		860
U.NL.x.U.NL.95.H10986_D1	-V...L...RGLRGS...L-S-V...IN...DTI...I-NW...A-RVG-LN-V...F-A		861
N.CM.02.DJ00131	-S-LQ...TL...SLRGLQLN-LRRL-G-IIA-GK...D-I...DTI...I-NW...A-RVG-LN-V...F-A		842
N.CM.04.04CM_1015_04	-TQ...TL-I-Q...SLRGLQLN-LR-RL-G-I-A-GK...D-I...DTI...I-NW...A-RVG-LN-V...F-A		833
N.CM.04.04CM_1131_03	-?Q...TL-Q...SLRGLQLN-LR-RL-G-I-A-GK...D-I...DTI...I-NW...A-RVG-LN-V...F-A		855
N.CM.95.YBF30	-S...IR...TL...QSLRGLQLN-LRTHL-G-I-A-GK...RD-I...DTI...I-NW...A-RVG-LN-V...F-A		852
N.CM.97.YBF106	-S...IR...TL-I...QSLRGLQLN-LRRL-G-IIA-GK...D-I...DTI...I-NW...A-RVG-LN-V...F-A		839
O.BE.87.AN170	N-ASGTQ...KVISY-RL.GLWILGOKLIVCRICAA.VT...L-Q-T...DTL-V-NW-GI-AGI-RIGTG-N...S		859
O.CM.91.MVPS180	N-ISGRH...LIDY-L.GLWILGOKTI-CRUCGA.VM...L-TN...DTI-VS-NW-GI-LGL-RIGGFL...A--V		872
O.CM.96.96CMBAB637	S-ASGRH...NVTSY-L.GLWILGOKTI-CRUCGA.VM...L-QK-T-V...DTI-GNW-SI-LGI-RIG-G-LN...F-C		876
O.SN.99.SEMP1300	N-ASGHQ...TVISH-L.GLWILGOKTI-CRUCIA.VI...L-Q-T...DTL-V-NW-GI-LGL-RIG-G-LN...A		868
CPZ_CD_90_ANT	TC-NLW...AVLOH-C...ITPRLCNHLEN-SPTL-TII...RTEILKNI...DRL-W-G-K-SILLAL-TIV-I-EV...IA-N		858
CPZ.CM.01.SIVcpzCAM13	S-C-S-LR...QL-K-O.LIINILRLIQ-K-TLLRG...I-GR-RT-T...D-G...I-PA-IVP-I-CN...T		864
CPZ.CM.05.SIVcpzEK505	-V-AR...TL-IV-Q.YTLKGLRV-L-LQG-I-GK...I-IN...DT...I-L-RIG-G-L...A		845
CPZ.CM.05.SIVcpzL87	-L...TL-V-Q.YTLKGLR-R-IHHRG-I-G...T-I...DT...I-IA-RFG-G-LN...F-A		880
CPZ.CM.05.SIVcpzMB66	-CASLW...LL-I-Q.YSLRVOQITG-HOHRG-T-TT-I...DT...G...IL-ATRLG-L...A		855
CPZ.CM.05.SIVcpzWT145	S-ACN-WRQKLTGH-IL.HSLRLL...R-CHLGG...I-I...DT...I-FA-VTL-I-N...A		871
CPZ.GA.88.GAB1	NFTW-LN.ISLQALKQ-IISALSHIVHRTIIVGVR.OIIE-SNTYASLR...IQADRL-NPTGWW-LI-G-VIA-G-N...LA-N		871
CPZ.TZ.01.TAN1	-LR...-T-QI-Q-NINKGQLLN-LRARC-G-VIA-AR...-V-T...DT...L-TRRLFLG-I...S		836

HIV-1/SIVcpz proteins

HIV-1/SIVcpz proteins

	R105	and	D123 essential for dimerization	normal Nef end				
B.FR.83.HXB2	HQRRQDIIDLWIYHTQGYF	PD	QNYTPGP	GWRYPDITGWCXKIVPVEPDK	IEE	ANKGENTS	LLHPSVLSHGMDDDPEREVLWEKFDLSRLAFHHVARELHPFYFKNC
A1.KE.94.Q23.17	Y-RK-E-V-V	-	T-F-F	F-D-E-V-K	-	TE-N	ICO	E-K-K-LK-R-WY
A1.RU.03.03R020.06.13	Y-KK-E-V-V	-	I-F-F	D-EE-V	-	TE-N	ICO	E-K-M-K-H-LK-R-WY
A1.RW.93.93R0037A	Y-RK-E-V-V	-	I-F-F	D-GE-V-R	-	TE-N	ICO	DD-O-K-M-H-Y-FY
A1.SE.94.SE7253	Y-R-E-V-V	-	I-F-F	D-E-V-Q	-	E-N	MCO	E-K-T-R-LR-R-Q-M-FY
A1.TZ.01.A173	Y-R-E-V-V	-	I-F-F	D-EE-V-K	-	TE-N	ICO	D-T-R-T-K-LK-I-DY
A1.UA.00.98UA0116	Y-KK-E-V-V	-	I-F-F	D-TE-V	-	TE-N	ICO	E-K-M-K-LT-R-FY
A1.UG.92.92UG0537	Y-KK-E-V-V	-	I-F-F	D-E-E-V	-	TE-N	ICO	E-K-T-R-K-S-KV-K-FY
A1.UG.98.98UG57136	Y-R-E-V-V	-	T-F-F	D-E-V-K	-	TE-N	ICO	E-T-I-K-H-LK-I-Q-FY
A2.CD.97.97CDKPE4	Y-K-E-V-V	-	-
A2.CD.97.97CDKKS10	Y-K-E-V-V	-	-
A2.CD.97.97CDKTB48	Y-K-E-V-V	-	A-F-F	D-SE-V	-	TE-N	ICO	AE-K-K-LR-L-Q-FY
A2.CY.94.94CY0117_41	Y-K-M-V-V	-	I-F-F	SE-V	-	TE-N	ICO	V-R-R-R-R-Y
A.SN.01.DD1579	Y-O-V-V	-	T-F-F	DOAE-V	-	TTG-N	CO	V-T-G-M-K-LK-T-M-FY
A.SN.01.DD15369	Y-O-V-V	-	T-F-F	DOAA-V	-	TTG-N	ICO	E-K-M-K-LK-I-O-FY
A.SN.96.DD4360	Y-RK-E-V-V	-	T-F-F	QAE-V-Q	-	DTQ-N	ICO	I-Q-K-M-K-LK-L-M-FY
A.SA.04.04ZASK162B1	Y-RK-E-V-V	-	T-F-F	QEQ-V	-	TA-N	M	E-G-M-K-M-K-Y
B.AR.00.ARMS008	Y-RK-E-V-V	-	-
B.AU.96.MBCD36	Y-RK-E-V-V	-	-
B.CO.01.PCM074	Y-K-E-V-V	-	-
B.GA.88.OY1	Y-K-E-V-V	-	-
B.NL.00.671.00T36	Y-K-E-V-V	-	-
B.RU.04.04RU129005	Y-O-V-V	-	-
B.TH.90.RK132	Y-O-V-V	-	-
B.US.90.WEAU160	Y-K-E-V-V	-	-
B.US.98.1059.11	Y-Q-E-V-V	-	-
C.AR.01.ARG4006	Y-O-K-E-V-V	-	-
C.BR.04.04BR013	Y-KK-E-V-V	-	-
C.BR.92.BR025.d	Y-KK-E-V-V	-	-
C.BW.00.00BW07621	Y-TK-KE-V-V	-	-
C.ET.86.ETH2220	Y-KK-E-V-V	-	-
C.IN.95.95IN21068	Y-KK-E-V-V	-	-
C.IE.99.01IN565.10	Y-KK-E-V-V	-	-
C.KE.00.KER2010	Y-KK-E-V-V	-	-
C.TZ.01.BD9.11	Y-KK-E-V-V	-	-
C.UY.01.TRA3011	Y-K-E-V-V	-	-
C.ZA.04.SK164B1	W-KO-R-E-V-V	-	-
C.ZA.05.05ZASK245B1	Y-KO-E-V-V	-	-
C.KM.02.02KM115	Y-KO-E-V-V	-	-
C.ZM.96.96ZM651	Y-KK-E-V-V	-	-
D.CD.83.ELI	W-KK-E-V-V	-	-
D.ED.83.NDK	W-KK-E-V-V	-	-
D.CM.01.01CM.4412HAL	Y-K-E-V-V	-	-
D.KE.01.NKU3006	W-KK-E-V-V	-	-
D.TD.99.MN012	W-TD.99.MN012	-	-
D.TZ.01.A280	W-PK-E-V-V	-	-
D.UG.94.94UG114	W-PK-E-V-V	-	-
D.UG.99.99UGD23550	W-PK-E-V-V	-	-
D.UG.99.99UGK03958	W-PK-E-V-V	-	-
D.ZA.86.R482	W-KE-E-V-V	-	-
F1.BE.93.VI850	Y-KK-G-T-V	-	-
F1.BR.89.B2126	Y-KK-E-V-V	-	-
F1.BR.93.93BR020.1	Y-K-E-V-V	-	-
F1.FI.93.FIN9363	Y-KK-E-V-V	-	-
F1.FR.96.MP411	Y-KK-E-V-V	-	-
F2.CM.02.02CM.0016BBY	Y-KK-E-V-V	-	-
F2.CM.95.MP255	Y-KK-E-V-V	-	-
F2.CM.95.MP257	Y-KK-E-V-V	-	-
F2.CM.97.CM53657	Y-K-E-V-V	-	-
G.BE.96.DRCL	Y-KK-E-V-V	-	-
G.CM.01.01CM.4049HAN	Y-KQ-E-V-V	-	-
G.ES.99.X138	Y-KK-E-V-V	-	-
G.KE.93.HH8793.12_1	Y-KK-E-V-V	-	-
G.NG.92.92NG083	Y-KK-E-V-V	-	-
G.SE.93.SE6165	Y-KK-E-V-V	-	-
H.BE.93.VI891	Y-KK-E-V-V	-	-
H.BE.93.VI997	Y-KK-E-V-V	-	-
H.CF.90.056	Y-KQ-E-V-V	-	-
J.SE.93.SE7887	Y-KK-E-V-V	-	-
J.SE.94.SE7022	Y-KK-E-V-V	-	-
K.CD.97.EQT811C	Y-K-E-V-V	-	-
K.CM.96.MP535	Y-KK-E-V-V	-	-

