Sequences in the *Pol* Alignment

COMMON NAME	LOCUS	ACC #	FIRST AUTHOR	REFERENCE
SUBTYPE A:				
U455	HIVU455	M62320	Oram,J.D.	ARHR 6, 1073 (1990)
IBNG	HIVIBNG	L39106	Howard,R.M.	ARHR 10: 1755 (1994)
SUBTYPE B:				
SF2	HIVSF2	K02007	Sanchez-Pescador,R.	Science 227, 484 (1985)
LAI	HIVLAI	K02013	Wain-Hobson,S.	Cell 40, 9 (1985)
HXB2R	HIVHXB2R	K03455	Starcich,B.	Science 227, 538 (1985)
NL43	HIVNL43	M19921	Buckler,C.E.	JVI 59: 284 (1986)
NY5CG	HIVNY5CG	M38431	Theodore,T.	PNAS 83: 5038 (1986)
LW123	HIVLW123	U12055	Reitz,M.	ARHR 10, 1143 (1994)
MN	HIVMN	M17449	Gurgo,C.	Virol. 164, 531 (1988)
JRCSF	HIVJRCSF	M38429	Koyanagi,S.	Science 236: 819 (1987)
JRFL	HIVJRFL	M74978	O'Brien,W.A.	Nature 348, 69 (1990)
OYI	HIVOYI	M26727	Wain-Hobson,S.	AIDS 3: 707 (1989)
CAM1	HIVCAM1	D10112	McIntosh,A.	Unpublished (1991)
HAN	HIVHAN	U43141	Sauermann,U.	ARHR 6, 813 (1990)
D31	HIVD31	U43096	Dietrich,U.	Unpublished (1992)
RF	HIVRF	M17451	Starcich,B.R.	Cell 45, 637 (1986)
YU2	HIVYU2	M93258	Li,Y.	JVI 65, 3973 (1991)
BCSG3C	HIVBCSG3C	L02317	Ghosh,S.K.	Virol. 194, 858 (1993)
P896	HIVP896	M96155	Collman,R.	JVI 66, 7517 (1992)
RET7	HIVRET7	Z31355	Gurusinghe,A.	Unpublished (1994)
VE1RT	HIVVE1RT	U16765	Quinones-Mateu,M.E.	Unpublished (1995)
VE2RT	HIVVE2RT	U16767	Quinones-Mateu,M.E.	Unpublished (1995)
VE3RT	HIVVE3RT	U16769	Quinones-Mateu,M.E.	Unpublished (1995)
VE4RT	HIVVE4RT	U16771	Quinones-Mateu,M.E.	Unpublished (1995)
VE5RT	HIVVE5RT	U16773	Quinones-Mateu,M.E.	Unpublished (1995)
VE6RT	HIVVE6RT	U16775	Quinones-Mateu,M.E.	Unpublished (1995)
VE7RT	HIVVE7RT	U16777	Quinones-Mateu,M.E.	Unpublished (1995)
VE8RT	HIVVE8RT	U16779	Quinones-Mateu,M.E.	Unpublished (1995)
HX330BC	HIVHX330BC	U28653	Tachedjian,G.	Virol. In Press (1996)
HX660BC	HIVHX660BC	U28647	Tachedjian,G.	Virol. In Press (1996)
HXBCRT	HIVHXBCRT	U28646	Tachedjian,G.	Virol. In Press (1996)
PD165BC	HIVPD165BC	U28649	Tachedjian,G.	Virol. In Press (1996)
PD330BC	HIVPD330BC	U28650	Tachedjian,G.	Virol. In Press (1996)
PD495BC	HIVPD495BC	U28651	Tachedjian,G.	Virol. In Press (1996)
PD660BC	HIVPD660BC	U28652	Tachedjian,G.	Virol. In Press (1996)
PDBCRT	HIVPDBCRT	U28648	Tachedjian,G.	Virol. In Press (1996)
3202A12	HIV3202A12	U34603	Guillon,C.	ARHR 11, 1537 (1995)
3202A21	HIV3202A21	U34604	Guillon,C.	ARHR 11, 1537 (1995)
MANC	HIVMANC	U23487	Zhu,T.	Nature 3745, 503 (1995)
WEAU160	HIVWEAU160	U21135	Ghosh,S.	Unpublished (1995)

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SUBTYPE D:				
ELI	HIVELI	K03454	Alizon,M.	Cell 46, 63 (1986)
Z2Z6	HIVZ2Z6	M22639	Theodore,T.	Unpublished (1988)
NDK	HIVNDK	M27323	Spire,B.	Gene 81, 275 (1989)
SUBTYPE O:				
ANT70C	HIVANT70C	L20587	Vanden Haesevelde,M.	JVI 68, 1586 (1994)
MVP5180	HIVMVP5180	L20571	Gurtler,L.G.	JVI 68, 1581 (1994)
SUBTYPE U:				
MAL	HIVMAL	K03456	Alizon,M.	Cell 46, 63 (1986)
CPZ:				
CPZGAB	SIVCPZGAB	X52154	Huet,T.	Nature 345, 356 (1990)
CPZANT	SIVCPZANT	U42720	Vanden Hasesevelde	Virol. In Press (1996)

Subtypes C and E-H are not currently represented in POL. The sequence MAL could not easily be assigned to any of the three POL subtypes, A, B, and D.

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CONSENSUS-A   FFRE.NLAFQQGEAR?F............SSE..QT??NS?TSR?LWDGG?D??.L?...???G?E?..Q     35
U455          ----.----------E-............---..--RA--P---N-----K-D..-P...CET-A-R..-     48
IBNG          ----.----------K-............---..--GT--S---E-----R-TS.-S....TA-T-G..-     48

CONSENSUS-B   FFRE.dLafpqGkAref???????????sSe..QtRaNSptrrElqVwgrdnnSlS????EAGadr..Q     49
SF2           ----.----L-------............---..----------------GE-----...-------..-     49
LAI           ----.----L-------SSEQTRANSPTI---..------------------------...-------..-     61
HXB2R         ----.----L-------............---..---------------------P-...-------..-     49
NL43          ----.------------............---..------------------------...-------..-     49
NY5CG         ----.------------............---..------------------------...-------..-     49
LW123         ----.----L-------............---..---------------------P-...-------..-     49
MN            ----.----L----.--............---..-N--------------------EAGE---D--..-     52
JRCSF         ----.----L-------...........P--..------------------S----EAGA------..-     53
JRFL          ----.----L-------............---..---------K--------S----...-------..-     49
OYI           ----.------------............---..--------S---R--------P-...-------..-     49
CAM1          ----.N------E----............---..----------------E-----...-------..-     49
HAN           ----.-------E--K-............---..----------------S.-S---...-------..-     48
D31           ----.----L-------............--A..------------------S----...-------..-     49
RF            ----.N----------L............---..------------------.----...---E--..-     48
YU2           ----.----------K-............---..-------I---R---R-------...-------..-     49
BCSG3C        ----.------------............---..------S---------G----P-...----G-..-     49
P896          ----.N-----------............---..----------------G------...-------..-     49
3202A12       ----.------------............---..------------------------...----EG..-     49
3202A21       ----.------------............---..-------------------------...----EG..-     49
MANC          ----.---L--------............---..---------G-----------C-...---T--..-     49
WEAU160       ----.--V--K------............---..---T----------Q--------...----N-..-     49

CONSENSUS-D   FFRE.dLAFPQGKAGEl............Sse..QTRANSPTSRELRVWGrD.NPLS....eTGAER..Q     48
ELI           ----.N-----------...........-PK..------------------.----....K------..-     48
Z2Z6          ----.------------............---..------------------.----...-------..-     48
NDK           ----.-----------F...........---..----------------G-.----...-------..-     48

CONSENSUS-O   FFR?.?LASGGHEARQL............CAE..TS?PISPT?.....GGGSE.....GT?ES??E?G??     35
ANT70         ---Q.I-----------...........---..--T-----D....-----------..--G--GT-R-PE     45
MVP5180       ---E.V-----------...........---..--V-----N....-----------..--R--ES-G-SG     45

CONSENSUS-U   FFRE.NLAFPQGKAREF............PSE..QTRANSPTSRELRVWGGDK.TLS....ETGAER..Q     48
MAL           ----.------------............---..------------------.----...-------..-     48

CONSENSUS-CPZ FFRE??????????R?L............CAE??????N??T?R?L??????????....?????????     13
CPZGAB        ----.RLAFPQREA-Q-............----..QNRT-GP-D-E-WVPGGRE........EPGEERGRE     47
CPZANT        ----TDPHVVGVQT-E-............---GGSSGA-SS-H-D-SGGAQEDSEGS............Q     46
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                     protease
                       \/          <- gag cds end
CONSENSUS-A   G?..??SF?FPQITLWQRPLVTV?I?GQLIEALLDTGADDTVLEDINLPGKWKPK?IGGIGGFIKVRQYD     96
U455          -...TD--S--------------K-G----------------------------I--------------    115
IBNG          -A..IS--N--------------R-E----------------------------M--------------    116

CONSENSUS-B   G...tVSfsfPQiTLWQRPlVTikigGQLKEALLDTGADDTVleeMnLPgrWKPKMIGGIGGFIKVrQYd    116
SF2           -...----N--------------R-------------------------K-------------------    116
LAI           -...----N-------------------------------------S-----------------------    128
HXB2R         -...----N---V---------------------------------S-----------------------    116
NL43          -...-------------------------------------------------------------G---    116
NY5CG         -...-----------------------------------------------------------------    116
LW123         -...----N-------------------------------------S-----------------------    116
MN            -...P--------------I-----------------------G-----R--------------------    119
JRCSF         -...I---N-----------------------------------D-D-----------------------    120
JRFL          -...N---N-----------------------------------D-D-----------------------    116
OYI           -...----NL---------I------------------------------------------------    116
CAM1          -...-----------------------------------------------------------------    116
HAN           -...---L-L--------------------------------V---S-----------------------    115
D31           -...-------------------------------------------S-----------------------    116
RF            -...---------------I--V---------------------------K-------------------    115
YU2           -...-----------------------------------------------------------------    116
BCSG3C        -...N--L--------------------------------------------------------------    116
P896          -...---L----------------V------------------D-S----------------------E    116
3202A12       -...---L-L------------------------------------------------------------    116
3202A21       -...---L-L------------------------------------------------------------    116
MANC          -...---L----T---------------------------------------------------------    116
WEAU160       -...A---N----------------E------------------D-----K-------------------    116

CONSENSUS-D   G...TVSFnfPQITLWQRPLVtIKIGGQLKEALLDTGADDTVLEEmNLPGKWKPKMIGGIGGFIKVRQYD    115
ELI           -...-----------------A-----------------------------------------------    115
Z2Z6          -...-----C------------------------------------------------------------    115
NDK           -...----S-------------------------------------I-----------------------    115

CONSENSUS-O   R...A???CLPQIPLWDRPIVTA?VGGHLCE?LLDTGADDTVLNNIQLEG?W?PKMIGGIGGFIKVKEY?     94
ANT70         -...-LSV---------------R-------V------------------K-K----------------D    112
MVP5180       -...-VPI---------------K-------A------------------R-T----------------N    112

CONSENSUS-U   G...IVSFSFPQITLWQRPVVTVRVGGQLKEALLDTGADDTVLEEINLPGKWKPKMIGGIGGFIKVRQYD    115
MAL           -...-----------------------------------------------------------------    115

CONSENSUS-CPZ ??????S???P?I?LWQRP???V???GQ?C?ALLDTGADDTV?E?I?LQG?WKPK?IGGIGGFI?V?Q??     55
CPZGAB        Q...SI-TNL-Q-T-----LIP-KVE--L-E-----------I-R-Q---L----M--------K-K-FD    114
CPZANT        GGGGTT-LVF-E-P-----MME-LIQ--K-Q-----------V-G-H---N----T--------S-Q-YN    116
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                                          protease \/ p66, p51
CONSENSUS-A   QILIEICGKK?IGTVLVGPTPVNIIGRNMLTQIGCTLNFPISPIETVPVKLKP?MDGPKVKQWPLTEEKI    164
U455          ----------T-------------------------------------------E----------------    185
IBNG          ----------A-------------------------------------------G----------------    186

CONSENSUS-B   QilieICGHKAiGTVLVGPTPVNIIGRNLLTQiGCTLNFPISPIETVPVKLKPGMDGPKVKQWPLTEEKI    186
SF2           --PV--------------------------------------------------------------------    186
LAI           ------------------------------------------------------------------------    198
HXB2R         ------------------------------------------------------------------------    186
NL43          ------------------------------------------------------------------------    186
NY5CG         ------------------------------------------------------------------------    186
LW123         ------------------------------------------------------------------------    186
MN            --T-G---------------------------L-------------------------------------    189
JRCSF         --P-D------V------------------------------------------------------------    190
JRFL          ------------------------------------------------------------------------    186
OYI           --------------------------------L-------------------------------------    186
CAM1          --P---------------------------------------------------------------------    186
HAN           ---V--------------------------------------------------------------------    185
D31           ------------------------------------------------------------------------    186
RF            ------------------------------------------------------------------------    185
YU2           --P---------------------------------------------------------------------    186
BCSG3C        --P---------------------------------------------------------------------    186
P896          --D--------K------------------------------------------------------------    186
RET7                                                  --------------------------------     31
VE1RT                                                 --------------------------------     31
VE2RT                                                 --------------------------------     31
VE3RT                                                 --------------------------------     31
VE4RT                                                 --------------------------------     31
VE5RT                                                 --------------------------------     31
VE6RT                                                 --------------------------------     31
VE7RT                                                 --------------------------------     31
VE8RT                                                 --------------------------------     31
HX330BC                                               --------------------------------     31
HX660BC                                               --------------------------------     31
HXBCRT                                                --------------------------------     31
PD165BC                                               --------------------------------     31
PD330BC                                               --------------------------------     31
PD495BC                                               --------------------------------     31
PD660BC                                               --------------------------------     31
PDBCRT                                                --------------------------------     31
3202A12       --A---------------------------------------------------------------------    186
3202A21       --P---------------------------------------------------------------------    186
MANC          ------------------------------------------------------------------------    186
WEAU160       -VP----------------------------------------------------------------------    186

CONSENSUS-D   QIlIEICG?KAiGTVLVGPTPVNIIGRNLLTQIGCTLNFPISPIETVPVKLKPGMDGPKVKQWPLTEEKI    184
ELI           --P-----Q---------------------------------------------------------------    185
Z2Z6          --------H---------------------------------------------------------------    185
NDK           --------Y--M------------------------------------------------------------    185

CONSENSUS-O   NVTVE??G?EVQGTVLVGPTPVNI?GRNILTGLGCTLNFPISPIAPVPVKLKPGMDGPKVKQWPLS?EKI    159
ANT70         -----IE-R---------------I-----------------------------------------K---    182
MVP5180       -----VQ-K---------------L-----------------------------------------R---    182

CONSENSUS-U   QILIEICGKKAIGTILVGPTPVNIIGRNMLTQIGCTLNFPISPIETVPVKLKPGMDGPRVKQWPLTEEKI    185
MAL           ------------------------------------------------------------------------    185

CONSENSUS-CPZ ?V?I?I??R?V??TVL?GP?PVNIIGRN?L??LGCTL?FPIS??ETVPVKLK?GMDGP?VKQWPLS?EKI    106
CPZGAB        N-H-E-EG-K-VG---V--T--------I-TQ-----V----SI--------P-----K-------A---    184
CPZANT        K-P-Q-GD-T-LA---L--N--------V-CL-----N----KV--------E-----R-------K---    186
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                        | M41L               D67N |  | K70R
CONSENSUS-A   KALT?IC?EMEKEGKISKIGPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPH?AGLK    231
U455          ----E--N-------------------------------------------------------T----    255
IBNG          ----D--T-------------------------------------------------------P----    256

CONSENSUS-B   KaLvEICTemEKEGKISKiGPENPYNTPvFAIKKKDSTKWRKLVDFRELNkrTQDFweVQlGIPHPaGlK    256
SF2           ----------------------------------------------------------------------    256
LAI           ----------------------------------------------------------------------    268
HXB2R         ----------------------------------------------------------------------    256
NL43          ----------------------------------------------------------------------    256
NY5CG         ----------------------------------------------------------------------    256
LW123         ----------------------------------------------------------------------    256
MN            ---I-----------------------------------------------K------------------    259
JRCSF         ----------------------------------------------------R-------------------    260
JRFL          ----------------------------------------------------K------------------    256
OYI           -V-I--------------V-------------------------------------------------    256
CAM1          ----------------------------------------------------------------------    256
HAN           ---I------------------------------------------------------------------    255
D31           ----------------------------------------------------------------------    256
RF            ----------------------------------------------------------------------    255
YU2           ----------------------------------------------------------------------    256
BCSG3C        ----------------------------------------------------------------------    256
P896          ----------------------------------------------------------------------    256
RET7          ------------------------------------------------------S-------------    101
VE1RT         ---T----K-------------------I--------------------------------------V-    101
VE2RT         ---------L------------------------------------------------------------    101
VE3RT         ----------------------------------------------------------------------    101
VE4RT         ---I-----L-----------------------------------------K------------------    101
VE5RT         ----------------------------------------------------------------------    101
VE6RT         ----------------------------------------------------------------------    101
VE7RT         ----------------------------------------------------------------------    101
VE8RT         ----------------------------------------------------------------------    101
HX330BC       ----------------------------------------------------------------------    101
HX660BC       ----------------------------------------------------------------------    101
HXBCRT        ----------------------------------------------------------------------    101
PD165BC       ------------------------------------------------------------I---------    101
PD330BC       ------------------------------------------------------------K------------    101
PD495BC       ------------------------------------------------------------K------------    101
PD660BC       ------------------------------------------------------------K------------    101
PDBCRT        ----------------------------------------------------------------------    101
3202A12       ----------------------------------------------------------------------    256
3202A21       ----------------------------------------------------------------------    256
MANC          ----------------------------------------------------------------------    256
WEAU160       ------------------------------------------------------------------S---    256

CONSENSUS-D   KALTEICTeMEKEGKISRiGPENPYNTPIFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLK    254
ELI           --------D-------------------------------------------------------------    255
Z2Z6          ------------------V---------------------------------------------------    255
NDK           ----------------------------------------------------------------------    255

CONSENSUS-O   EALTAICQEMEQEGKISRIGPENPYNTPIFAIKKKD?TKWRKLVDFRELNKRTQ?FWEVQLGIPHPGGLK    227
ANT70         -------------------------------------G-----------------E---------------    252
MVP5180       -------------------------------------S-----------------D---------------    252

CONSENSUS-U   KALTEICKDMEKEGKILKIGPENPYNTPVFAIKKKDSTKWRKLVNFRELNKRTQDFWEVQLGIPHPAGLK    255
MAL           ----------------------------------------------------------------------    255

CONSENSUS-CPZ ?AL?EIC???E?E?KIS?IGP?NPYNTPIFAIKKKD??KWRKLVDFRELNKRTQDFWE?QLGIPHPAGLK    164
CPZGAB        K--T---QEM-K-G---K---E--------------ST--------------------V-----------    254
CPZANT        E--K---DKL-A-N---R---D--------------TS--------------------I-----------    256
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CONSENSUS-A   KKKSVTVLDVGDAYFSVPLD??FRKYTAFTIPS?NNETPG?RYQYNVLPQGWKGSP?IFQ?SMTKILEPF    295
U455          --------------------ES-----------I------V---------------S---S---------    325
IBNG          --------------------KD-----------V------I---------------A---A---------    326

CONSENSUS-B   kkKSvTvLDVGDaYFSVPLdkdFRKYTaFTIPSiNNEtPgiRYQYNVLPQGWKGsPAIfQsSMtkILEPF    326
SF2           ------------------------------------------------------------------------    326
LAI           --------------------E-----------------------------------------------------    338
HXB2R         --------------------E-----------------------------------------------------    326
NL43          Q-------------------------------------------------------------C---------    326
NY5CG         Q-------------------------------------------------------------C---------    326
LW123         --------------------E-----------------------------------------------------    326
MN            ------------------------------------------------------------------------    329
JRCSF         ------------------------------------------------------------------------    330
JRFL          -R----------------------------------------------------------------------    326
OYI           ------------------------------------------------------------------------    326
CAM1          ---------------------------------T--------------------------------------    326
HAN           ------------------------------------------------------------------------    325
D31           --------------------E-------------------V------------------------------    326
RF            ---------------------E-----------------R------------------------------    325
YU2           -------------------HE-------------------T-----------------------T-----    326
BCSG3C        ------------R-----------------------------------------------------------    326
P896          --------------------E---------------------------------------------------    326
RET7          -------------------H-------------T-----------------------------I------    171
VE1RT         ---------------------------------V--------------------------------------    171
VE2RT         ---------------------------------V-------------------------C---------    171
VE3RT         ------------------------------------------------------------------------    171
VE4RT         ---------------------------------T--------------------------------------    171
VE5RT         ---------------------E--------------------------------------C---------    171
VE6RT         ---------------------E------------------V-----------------S-C---------    171
VE7RT         --------------------EG----------------------------------------------------    171
VE8RT         --------------------E-------------T--------------------------------------    171
HX330BC       --------------------E--------------------------------A---------------    171
HX660BC       --------------------E--------------------------------A---------------    171
HXBCRT        -R------------------E-----------------------------------------------------    171
PD165BC       --------------------ES----------------------------------------------------    171
PD330BC       --------------------ES----------------------------------------------------    171
PD495BC       --------------------ES----------------------------------------------------    171
PD660BC       --------------------ES----------------------------------------------------    171
PDBCRT        --------------------ES----------------------------------------------------    171
3202A12       ---------------------------------V-------------------------C---------    326
3202A21       ----G-A--------------------------V--------------------------C---------    326
MANC          -------------------YE------V---------A--V-----------------------------    326
WEAU160       --------------------E-----------------------------------------------------    326

CONSENSUS-D   KKKSVTVLDVGDAYFSVPLDeDFRKYTAFTIpSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPF    324
ELI           --------------------------------S-------------------------------------    325
Z2Z6          --------------------K-----------------------------------------------------    325
NDK           ------------------------------------------------------------------------    325

CONSENSUS-O   Q?QSVTVLDVGDAYFSCPLDPDFRKYTAFTIPSVNNETPG?RYQYNVLPQGWKGSPAIFQSSMTKILDPF    295
ANT70         -K--------------------------------------I-----------------------------    322
MVP5180       -R--------------------------------------V-----------------------------    322

CONSENSUS-U   KKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPF    325
MAL           ------------------------------------------------------------------------    325

CONSENSUS-CPZ ?KKSVTVLDVGDAYFS?PLD?DFRKYTAFTIPS?NNETPG?RY?YNVLPQGWKGSP?IFQ?SMTKIL?PF    225
CPZGAB        K---------------C---K------------I------V--Q------------S---S------E--    324
CPZANT        Q---------------I---Q------------V------I--C------------A---A------A--    326
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HIV1 POL

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                    polymerase motif
                          /<-->/                    T215Y |   | K219Q
CONSENSUS-A   R???P?IVIYQYMDDLYVGSDLEIGQHRAKIEELR?HLL?WGF?TPDKKHQKEPPFLWMGYELHPDKWTV    358
U455          -SQH-D-----------------------------A---S---I---------------------------    395
IBNG          -TKN-E-----------------------------G---K---T---------------------------    396

CONSENSUS-B   rKQNPdivIYQYMDDLYVGSDLEIgQHRtKIEeLRqhLLrwGftTPDKKHQKePPFLWMGYELHPDKWTV    396
SF2           ----------------------------------------------------------------------    396
LAI           -------------------------------------------L---------------------------    408
HXB2R         -------------------------------------------L---------------------------    396
NL43          ----------------------------------------------------------------------    396
NY5CG         ----------------------------------------------------------------------    396
LW123         -------------------------------------------L---------------------------    396
MN            ----------------------------A------R-----------------------------------    399
JRCSF         -------I--------------------------------K-----------------------------    400
JRFL          -------I--------------------A-------------------------------------------    396
OYI           ----------------------------------------------------------------------    396
CAM1          -------------------------------------------L---------------------------    396
HAN           ------------------------E--------------K-----------------------------    395
D31           ----------------------------------------------------------------------    396
RF            K----E----------------------I------E---K-----------------------------    395
YU2           ------L---------------------------------------------------------------    396
BCSG3C        ----------------------------------------------------------------------    396
P896          ---------------------------A---D------K-----------------------------    396
RET7          -----E----------------------A----------K-----------------------------    241
VE1RT         ------------------------E---------------G---------------------------    241
VE2RT         ---------------------------------------K---Y---------------------------    241
VE3RT         -----------------------------------G---K--L---------------------------    241
VE4RT         ----------------------------------------------------------------------    241
VE5RT         -----G------------------------------E---------------------------------    241
VE6RT         -------D--------------------------------K-----------------------------    241
VE7RT         ---------------------------------------K-----------------------------    241
VE8RT         -----G-----------------------------E---------------------------------    241
HX330BC       K---------------------------------------------------------------------    241
HX660BC       K---------------------------------------------------------------------    241
HXBCRT        -------------------------------------------L---------------------------    241
PD165BC       ---------------------------------------K-----------------------------    241
PD330BC       ---------------------------------------K-----------------------------    241
PD495BC       -------G--------------------------------K-----------------------------    241
PD660BC       -------G--------------------------------K-----------------------------    241
PDBCRT        ---------------------------------------K-----------------------------    241
3202A12       ----------------------------------------------------------------------    396
3202A21       ----------------------------------------------------------------------    396
MANC          ------V----------------------------Y--K-----------------------------    396
WEAU160       ----------------------------------------------------D-----------------    396

CONSENSUS-D   RKQNPEiVIYQYMDDLYVGSDLEIGQHRTKIEeLREHLLRWGFTtPDKKHQKEPPFLWMGYELHPDKWTV    394
ELI           ------M-------------------------K-----------R-------------------------    395
Z2Z6          ----------------------------------------------------------------------    395
NDK           ----------------------------------------------------------------------    395

CONSENSUS-O   R??NPE?EI?QY?DDLYVGSDLPL?EHRKR?ELLREHLYQWGFTTPDKKHQKEPPFLWMGYELHPDKWTV    358
ANT70         -RD---L--C--M-----------T-----I---------------------------------------    392
MVP5180       -KS---V--Y--I-----------A-----V---------------------------------------    392

CONSENSUS-U   RTKNPEIVIYQYMDDLYVGSDLEIGQHRTKIEELREHLLKWGFTTPDKKHQKEPPFLWMGYELHPDKWTV    395
MAL           ----------------------------------------------------------------------    395

CONSENSUS-CPZ R?K?P???IYQYMDDLYVGSD?EI??HR???E?LRQHL??WG??TPDKKHQKEPPF?WMGYELHPDKWTV    278
CPZGAB        -E-N-DIT-------------L--DQ--KKV-E-----LK--FT------------L--------------    394
CPZANT        -D-Y-AVE-------------M--TA--EMI-K-----QV--LE------------Q-------------    396
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CONSENSUS-A   QP??LPEKDSWTVNDIQKLVGKLNWASQIYAGIK?KQLC?LLRGAKALTDIV?LTEEAELELAENREI..    421
U455          --IQ-----------------------------V----K------------T---------------..    463
IBNG          --VE-----------------------------I----R------------A---------------..    464

CONSENSUS-B   QPIvLPEkdsWTVNDIqKLVGKLNWASQIYaGIkVkqLCkLLrgtKALTEviplTeEAELELAENREI..    464
SF2           ---M-------------------------------------------------------------..    464
LAI           ------------------------------P----R--------------------------------..    476
HXB2R         ------------------------------P----R--------------------------------..    464
NL43          -----------------------------------R---------------V----------------..    464
NY5CG         -----------------------------------R--------I------V----------------..    464
LW123         ------------------------------P----R--------------------------------..    464
MN            ------------------------------------------------------------------..    467
JRCSF         -------------------------------------------------------K------------..    468
JRFL          ------------------------------------------------------------------..    464
OYI           ---M--------------------------------N-------------------------------..    464
CAM1          ---M-----------------------------------------------V----------------..    464
HAN           ---------------------------------------------P----------K------------..    463
D31           ---T-------------------------------R--------A----------K------------..    464
RF            ----------------------------------------------------VQ--K------------..    463
YU2           -----------------------------------R--------------------------------..    464
BCSG3C        ------------------------------S--------------------VT----------------..    464
P896          ----------------------------------------------------V----------------..    464
RET7          ---------------------------------------------P------V---K------------..    309
VE1RT         ---M----E---------------------------------------------------------..    309
VE2RT         ------------------------------------------------------------------..    309
VE3RT         ----------------H-------------P--------R------------A--K------------..    309
VE4RT         --------E---------------------P--------------------S---------------..    309
VE5RT         ---I-------------------------P-------------A-----------------------..    309
VE6RT         -------E----------------------P-----------WAA------V----------------..    309
VE7RT         ------------------------------------------------------------------..    309
VE8RT         ---E-------------------------------R--------------------------------..    309
HX330BC       ------------------------------P----R--------------------------------..    309
HX660BC       ---------R--------------------P----R--------------------------------..    309
HXBCRT        ------------------------------P--R-R--------------------------------..    309
PD165BC       ---M--------------------------------------------------------------..    309
PD330BC       ---M--------------------------------------------------------------..    309
PD495BC       ---M--------------------------------------------------------------..    309
PD660BC       ---M--------------------------------------------------------------..    309
PDBCRT        ---M--------------------------------------------------------------..    309
3202A12       ---M-------------------------------R--------------------------------..    464
3202A21       -----------------------------------RH-------------------------------..    464
MANC          ---T-------------------------P-------------A----------K------------..    464
WEAU160       ---K----E-----------------------------------------I--I---------------..    464

CONSENSUS-D   QsIkLPEKESWTVNDIQkLVgkLNWASQIYpGIKVrQLCKLLRGTKALTEViPLTEEAELELAENREI..    462
ELI           -----------------N--ER-------------------------------------------..    463
Z2Z6          ------------------------------------------------------------------..    463
NDK           -P-N-------------------------A----K---------------V----------------..    463

CONSENSUS-O   Q?IQLP?K?VWTVNDIQKL?GKLNWASQIYQGIRV?ELCKLIRGTKSLTEVVPLS?EAELELEENRE?..    419
ANT70         -S----N-D----------I---------------R-------------------R-----------R..    460
MVP5180       -P----D-E----------V---------------K-------------------K-----------K..    460

CONSENSUS-U   QPIQLPDKESWTVNDIQKLVGKLNWASQIYPGIKVKQLCKLLRGAKALTDIVPLTAEAELELAENREI..    463
MAL           ------------------------------------------------------------------..    463

CONSENSUS-CPZ Q?I?LPE???WTVNDIQKL?GKLNWASQIYPGIK?KQLC?LIRG?K?LTD?V??T?EAELEL?EN??I??    329
CPZGAB        -P-Q---KEV---------I--------------I----K----T-K---V-PL-P------A--RE-..    462
CPZANT        -K-K---PDD---------V--------------T----R----V-S---R-QM-R------E--KQ-xx    466
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HIV1 POL

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CONSENSUS-A   .LK?PVHGVYYDP?KDLVAE?QKQGQDQWTYQIYQEPFKNLKTGKYA?KRSAHTNDVKQLTEVVQKV??E    484
U455          .--D---------S------I--------------------------R-------------------ST-    532
IBNG          .--E---------T------L--------------------------K-------------------AM-    533

CONSENSUS-B   .LKePVHgvYyDPsKdLiaEiQKQGqgQWTYQIyQEPfknLkTgKYarmrGaHTNDvkQLtEAVQKiatE    533
SF2           .------E---------V-----------------------------------------------VS--    533
LAI           .---------------------------------------------T------------------T--    545
HXB2R         .-----------------------------------------------------------------T--    533
NL43          .-----------------------------------------------K--------------------    533
NY5CG         .-----------------------------------------------K--------------------    533
LW123         .-------------------------------------------------T---------------T--    533
MN            .-------------------V-------------------------------------------------    536
JRCSF         .-----------------V--------------F--------------T-------------------N-    537
JRFL          .-------------------L------------------I--------T-------------------N-    533
OYI           .----------------V--L-----------------------------------------------TQ-    533
CAM1          .-------------------L--------------------------K---T------------------    533
HAN           .---------C------V-------E-----------------------------I-------------    532
D31           .-----------------------------------------------------------------T--    533
RF            .----------------------------------------------------------------V---    532
YU2           .-----------------------------------------------T---------------------    533
BCSG3C        .-----------------------------------------A----T------------------T--    533
P896          .------------T------L----------------Y-------------------------------    533
RET7          .-----------------------------------------------------------------T--    378
VE1RT         .------------------------D----------------------T--T------------------    378
VE2RT         .------------T-------------------------------------T------------------    378
VE3RT         .-------------------------------------------------V-----R--V------TI-    378
VE4RT         .----------------------------------------------------------------V---    378
VE5RT         .--------------------------D---------------------T---------------------    378
VE6RT         .-------------------V----E--------------------T-S--T------------------    378
VE7RT         .------------T------------------------------------------------------    378
VE8RT         .------------T---V-------H--------------------------------------V---    378
HX330BC       .-----------------------------------------------------------------T--    378
HX660BC       .-----------------------------------------------------------------T--    378
HXBCRT        .-----------------------------------R-------------------------T--    378
PD165BC       .----------------V--L----------------------------K------------------I-    378
PD330BC       .----------------V--L----------------------------K------------------I-    378
PD495BC       .----------------V--L----------------------------K------------------I-    378
PD660BC       .----------------V--L----------------------------K------------------I-    378
PDBCRT        .----------------V--L----------------------------K------------------I-    378
3202A12       .-------A--------V-------------------------------------------------Q-    533
3202A21       .--------------E--------------------------------------------------T--    533
MANC          .--V-------------T--------------------RS-------K---T--------------VT--    533
WEAU160       .-------------------L----------------------------V------------------T--    533

CONSENSUS-D   .LKEPVHGVYYDPSKDLIAEiQKQGhGQWTYQIYQEPFKNLKTGKYARmRGAHTNDVKQLaEaVQkIsTE    531
ELI           .-----------------------------------------------------------------R----    532
Z2Z6          .-----------------------------------------------------------------V-------    532
NDK           .-------------------L----D----------------------T-----------T------A--    532

CONSENSUS-O   .LK?PVHGVYYQPDKDLWV?IQK?G??QWTYQ?YQ?EHKNLKTGKY?RQKASHTNDIRQLAEV?QKVSQE    479
ANT70         .--Q---------------N---Q-GE-----I--E----------T----------------I------    529
MVP5180       .--E---------------S---H-EG-----V--D----------A----------------V------    529

CONSENSUS-U   .LKEPVHGVYYDPSKDLIAEIQKQGQGQWTYQIYQEQYKNLKTGKYARIKSAHTNDVKQLTEAVQKIAQE    532
MAL           .------------------------------------------------------------------------    532

CONSENSUS-CPZ ???????G?YY?P???L?A?IQKQG??QWTYQI?Q???K?LK?GKYAR????HTN??RQLA??VQKI??E    367
CPZGAB        .VSTPVH-V--D-DKE-I-E-----NC------F-EPH-N--T-----QRSA---DI----EA----AT-    531
CPZANT        xLQQKIE-Y--Q-GLP-K-T-----SG------Y-NEG-L--A-----PTGT---EV----GV----GL-    536
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                                                                p51 \/
CONSENSUS-A   SIVIWGK?PKFRLPIQ?ETWE?WWMEYWQATWIPEWEFVNTPPLVKLWYQLEKDPI?GAETFYVDGAANR    550
U455          -------I--------K----A-----------------------------------A--------------    602
IBNG          -------T--------R----T-----------------------------------V--------------    603

CONSENSUS-B   sIvIWGKtPKFklpIQKETWe?WWteYwqATWIPEWEfVNTPPLVKLWYQLEkePivGaetFYVDGAAnr    602
SF2           -------I-------------A--M---------------------------------------------    603
LAI           ---------------------T-----------------------------------------------S-    615
HXB2R         ---------------------T-----------------------------------------------    603
NL43          ---------------------A-----------------------------------I-------------    603
NY5CG         ---------------------A-----------------------------------I-------------    603
LW123         ---------------------T-----------------------------------------------    603
MN            -----------R---------T-----T$--------V-------------------------------    605
JRCSF         -------I-------------T-----------------------------------------------    607
JRFL          -------I-------------T-----------------------------------------------    603
OYI           ---------------------A------------------------------D----------------    603
CAM1          --------------------DA--ID---------------------------------------------    603
HAN           G----------R---------A-----------------------------------------------    602
D31           ---------------------A------------------------------T-----------------    603
RF            ---------------------A-----------------------------------I-------------    602
YU2           ---------------------T-----------------------------------I-------------    603
BCSG3C        C-I--------R---------T-----------------------------------E-------------    603
P896          -----------N.X-------A---D-------------------------------------------    602
RET7          -------I-------------T--------------------------------SR-$N1             437
VE1RT         G--------------------T------------------------------D----------------    448
VE2RT         ---------------------T-----------------------------------------------    448
VE3RT         -----------R---------T-----------------------------------------------    448
VE4RT         -----------R---------A-----------------------------------V-----------    448
VE5RT         ---------------------T-----------------------------------I-----------S-    448
VE6RT         ---------------------T-----------------------------------I-----------S-    448
VE7RT         -----------R---------T-----------------------------------A-------------    448
VE8RT         -------I-------------A--M---------------------------------------------    448
HX330BC       ---------------------T-----------------------------------------------S-    448
HX660BC       ---------------------T-----------------------------------------------S-    448
HXBCRT        ---------------------T-----------------------------------------------    448
PD165BC       -----------R---------A--M---------------------------------------------    448
PD330BC       -----------R---------A--M---------------------------------------------    448
PD495BC       -----------R---------A--M---------------------------------------------    448
PD660BC       -----------R---------A--M---------------------------------------------    448
PDBCRT        -----------R---------A--M---------------------------------------------    448
3202A12       ---------------------A-----------------------------------------------    603
3202A21       ---------------------A-----------------------------------------------    603
MANC          --I----I-------------DA----------------------------------------------    603
WEAU160       ---------------------T-----------------------------------------------K    603

CONSENSUS-D   SIVIWGkTPKFrLPIQKETWETWW?EYWQATWIPEWEFVNTPPLVKLWYQLEKEPIIGAETFYVDGAANR    600
ELI           ------R-----------------A-------------------------------------------    602
Z2Z6          ------------------------V-------------------------------------------    602
NDK           -----------K------------I-------------------------------------------    602

CONSENSUS-O   ?I?IWGKLPKF?LPVTRETWETWWA?YWQATWIPEWEFVSTPPLIKLWY?LE?EPI?GAET?YVDGAANR    541
ANT70         S-I--------K-------------D-----------------------R--S---M----Y--------    599
MVP5180       A-V--------R-------------E-----------------------Q--T---V----F--------    599

CONSENSUS-U   SIVIWGKTPKFRLPIQKETWEAWWTEYWQATWIPEWEFVNTPPLVKLWYQLETEPIVGAETFYVDGAANR    602
MAL           ----------------------------------------------------------------------    602

CONSENSUS-CPZ SIVIWG??PKF?LP???E?W?AWW??YWQATWIPEWEF?NTPPL??LWY?L???PIP???T?YVDGAANR    416
CPZGAB        ------KT---R--VQK-S-E---AE------------I-----VK---S-ETE---TTD-Y--------    601
CPZANT        ------EV---Q--ITR-T-D---SD------------V-----IR---N-LAD---EAE-F--------    606
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HIV1 POL

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CONSENSUS-A   ETK?GKAGYVTDRGRQKVVSLTETTNQKTELHAIHLALQDSGSEVNIVTDSQYALGIIQAQPDRSESE?V    618
U455          ---L-------------------------------------------------------------I-    672
IBNG          ---I-------------------------------------------------------------L-    673

CONSENSUS-B   eTklGkAGYVTdrGRQkVvsltdTTNQkTeLqAIhLALQDSGlEVNIVtDSQYAlGIIQAQPDkSESElV    672
SF2           --------------------IA--------------------------------------------    673
LAI           -----------N-------T-----------------------------------------------    685
HXB2R         -----------N-------T--------------Y----------------------------Q------    673
NL43          --------------------P-----------------------------------------------    673
NY5CG         --------------------P-----------------------------------------------    673
LW123         -----------NK------P--N-----------Y-----------------------------------    673
MN            ---K-------N-----------------------------------------------------------    675
JRCSF         -----------S-----------------------------------------------------------    677
JRFL          -----------N-----------------------------------------------------------    673
OYI           ----------------------------------------------------------------------    673
CAM1          --R----------------P--------------Y-----------------------------------    673
HAN           ---------------------N----------------------------------------------    672
D31           ------------------------------------------------S-----I---------------    673
RF            ----------------------------------------------------------------------    672
YU2           -----------NK---------------------Y----------------------------R------    673
BCSG3C        -----------NK------T-----------E--------------------------------------    673
P896          D--S-----------------A----------------------------------------------    672
VE1RT         --------------------V--------K------------S---------------------------    518
VE2RT         ---S-------NK---------------------Y----------------------------------    518
VE3RT         -------------------------------------------------------------I------    518
VE4RT         -----------N--------IA--------------------P--------------------------I-    518
VE5RT         --------------------P-----------------------------------------------    518
VE6RT         ------------K-------I-----------------------------------------------    518
VE7RT         -----R-----NK------T-------R--------------S-------------------------I-    518
VE8RT         --------------------------------Q-----------------------------------I-    518
HX330BC       -----------N-------T-----------------------------------------------    518
HX660BC       -----------N-------T-----------------------------------------------    518
HXBCRT        -----------N-------T--------------Y----------------------------Q------    518
PD165BC       ------------K-------I-----------------------------------------------    518
PD330BC       ------------K-------I-----------------------------------------------    518
PD495BC       ------------K-------I-----------------------------------------------    518
PD660BC       ------------K-------I-----------------------------------------------    518
PDBCRT        ------------K-------I-----------------------------------------------    518
3202A12       ---------------------N------------N----------------------------------    673
3202A21       ---------------------N------------N----------------------------------    673
MANC          ------------------I-----------------------------S---------------------    673
WEAU160       -----------N----R-----------------------------------------------Q------    673

CONSENSUS-D   ETKLGKAGYVTDRGRQKVVPfTDTTNQKTELQAINLALQDSGLEVNIVTDSQYALGIIQAQPDKSESELV    670
ELI           --------------------L-----------------------------------------------    672
Z2Z6          ----------------------------------------------------------------------    672
NDK           ----------------------------------------------------------------------    672

CONSENSUS-O   ?TKLGKAGYVTEQGKQ?IIKL?ETTNQKAELMA?L?ALQDSKE?VNIVTDSQY?LG?ISSQPTQS?SPIV    602
ANT70         E---------------K----D-----------I-L-------T---------A--V--------E----    669
MVP5180       N---------------N----E-----------V-I-------Q---------V--I--------D----    669

CONSENSUS-U   ETKKGKAGYVTDRGRQKVVSLTETTNQKTELQAIHLALQDSGSEVNIVTDSQYALGIIQAQPDKSESEIV    672
MAL           ----------------------------------------------------------------------    672

CONSENSUS-CPZ ????GKAGYVTD?G??????L??TTNQQAEL?A?L?AL?DS???VNIVTDSQY?LG??Q??PD?SES?LV    459
CPZGAB        ETKT--------K-KQKIIS-EN--------K-L-L--Q--DQQ---------V--II-SQ--H---E--    671
CPZANT        NSQL--------R-RSRVKH-QK--------Q-I-M--E--TGP---------A--VL-GT--Q---P--    676
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CONSENSUS-A   NQIIEKLI?K?KVYLSWVPAHKGIGGNEQVDKLVS?GIRKVLFLDGIDKAQE?HE?YH?NW?AMASDFNL    681
U455          --------E-E------------------------S----------------D--K--C--R--------    742
IBNG          --------K-D------------------------N----------------E--R--S--K--------    743

CONSENSUS-B   sQIIEqLIKKEKVYLaWVPAHKGIGGNEQVDkLVSaGiRkvLfldgidkAQeeHEKYHsNWrAMAsDFNL    742
SF2           ------------------------------------------N-------------------------    743
LAI           N--------------------------------------------------D------------------    755
HXB2R         N--------------------------------------------------D------------------    743
NL43          ------------------------------G-------------------------------------    743
NY5CG         ------------------------------------------------------------------------    743
LW123         N---------------------------------------I----------D------------------    743
MN            ----------------------------------------------------D-----------------    745
JRCSF         ----------------------------------------------------D-----------------    747
JRFL          ----------------------------------------------------D--------K--------    743
OYI           ------------------------------------------------------------------------    743
CAM1          -----E-----------------------------------------------------------------    743
HAN           ----------------------------------------------------D------------N----    742
D31           ---------------T------------------------------------D------------------    743
RF            ------------------------------R---T---------------D------------------    742
YU2           ------------------------------------------------------------------------    743
BCSG3C        --------------------------------------V-------------------------------    743
P896          ------------------------------------------------------------T-----------    742
VE1RT         -----E-------------------------------------SGRHR$                        565
VE2RT         N-----------------------------------------R--SGRHR$                        565
VE3RT         N----------------------------------T------SGRHR$                        565
VE4RT         N--------------------------------------I-SGRHR$                        565
VE5RT         -----------------------------------S------SGRHR$                        565
VE6RT         ------------------------------------------SGRHR$                        565
VE7RT         ---------------------------------------I-SGRHR$                        565
VE8RT         -----------------------------------T---R--SGRHR$                        565
HX330BC       ------------------------------------------------                        566
HX660BC       ------------------------------------------------                        566
HXBCRT        N-----------------------------------------------                        566
PD165BC       ------------------------------------------RWNR$                        565
PD330BC       ------------------------------------------RWNR$                        565
PD495BC       ------------------------------------------RWNR$                        565
PD660BC       ------------------------------------------RWNR$                        565
PDBCRT        ------------------------------------------RWNR$                        565
3202A12       ------------------------------------------------------------------------    743
3202A21       ------------------------------------------------------------------------    743
MANC          ------------------------------------------------------------------------    743
WEAU160       -----------------------------------S----------------------------------    743

CONSENSUS-D   sQIIEQLIKKEKVYLAWVPAHKGIGGNEQVDKLVSQGIRKVLFLDGIDKAQEEHEKYHNNWRAMASDFNL    740
ELI           N-----------------------------------------------------------------------    742
Z2Z6          ------------------------------------------------------------------------    742
NDK           ------------------------------------------------------------------------    742

CONSENSUS-O   QQIIEELTKKE?VYLTWVPAHKGIGGNEKIDKLVSKDIRRVLFLEGIDQAQEDHEKYHSNW?ALAS?FGL    669
ANT70         -----------Q-----------------------------------------------K----E---    739
MVP5180       -----------R-----------------------------------------------R----D---    739

CONSENSUS-U   NQIIEQLIQKDKVYLSWVPAHKGIGGNEQVDKLVSSGIRKVLFLDGIDKAQEEHEKYHSNWRAMASDFNL    742
MAL           ------------------------------------------------------------------------    742

CONSENSUS-CPZ ??II??LIK?E?IYLSWVPAHKGIGGNEQVDKLVS?GIR?VLFL?GID?AQE?H??YHSNW???A???NL    510
CPZGAB        NQ--EE---K-K-----------------------A---K----D---R---E-ER-----KAM-SDF--    741
CPZANT        EE--QK---R-Q-----------------------Q---Q----E---K---D-DK-----RSL-DEY--    746
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HIV1 POL

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CONSENSUS-A   PP?VAKEIVASC?KCQ?KGEAMHGQVDC?PGIWQLDCTHLEGK?ILVAVHVASGYIEAEVIPAETGQETA    746
U455          --V---------N---L-----------S--------------V--------------------------    812
IBNG          --I---------D---M-----------G--------------I--------------------------    813

CONSENSUS-B   PPvVAKEIVASCdKCQLKGEAMHGQVDCSPGIWQLDCTHLEGKvILVAVHVASGYIEAEVIPaETGQETA    812
SF2           ------------------------------------------I--------------------------    813
LAI           ------------------------------------------------------------------------    825
HXB2R         ------------------------------------------------------------------------    813
NL43          ------------------------------------------------------------------------    813
NY5CG         ------------------------------------------------------------------------    813
LW123         ------------------------------------------------------------------------    813
MN            --I---------------------------------------------------------------------    815
JRCSF         --I---------------------------------------------I--------------------------    817
JRFL          ------------------------------------------------I--------------------------    813
OYI           ------------------------------------------------I--------------------------    813
CAM1          ------------------------------------------------------------------------    813
HAN           ------------------------------------------------I------------------V-------    812
D31           ------------------------------------------------------------------------    813
RF            ------------------------------------------------I--------------------------    812
YU2           ------------------------------------------------------------------------    813
BCSG3C        ------------------------------------------------I--------------------------    813
P896          ------------N-----------------------------------------------------------    812
3202A12       ------------------------------------------------I--------------------------    813
3202A21       ------------------------------------------------I--------------------------    813
MANC          ------------------------------------------------------------------------    813
WEAU160       ------------------------------------------------I--------------------------    813

CONSENSUS-D   PPVVAKEIVASCDKCQLKGEAMHGQVDCSPGIWQLDCTHLEGKVILVAVHVASGYIEAEVIPAETGQETA    810
ELI           ------------------------------------------------------------------------    812
Z2Z6          ------------------------------------------------------------------------    812
NDK           ------------------------------------------------------------------------    812

CONSENSUS-O   PP?VAKEIIASCPKCHIKGEA?HGQVD?SPE?WQ?DCTH?EGKIIIVAVHVAS?FIEAEVIPAETGQETA    732
ANT70         --V------------------I-----C---V--I----M-------------G----------------    809
MVP5180       --I------------------T-----Y---I--M----L-------------D----------------    809

CONSENSUS-U   PPIVAKEIVASCDKCQLKGEAMHGQVDCSPGIWQLDCTHLEGKIIIVAVHVASGYIEAEVIPAETGQETA    812
MAL           ------------------------------------------------------------------------    812

CONSENSUS-CPZ PPIVAKEI?A?CDKC?VKGEA?HGQVDCSPGIWQVDCTHLEGKVIIVAVHV?SG?IEAEV???ETG??TA    569
CPZGAB        --------V-H----Q-----M-----------------------------A--Y-----IPA---QE--    811
CPZANT        --------I-Q----H-----R-----------------------------S--F-----MAD---KS--    816
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CONSENSUS-A   YFILKLAGRWPVKVIHTDNGSNFTSAAVKA?CWWAN??QEFGIPYNPQSQGVVESMNKELKKIIGQVR?Q    812
U455          ------------------------------V-----IQ------------------------------E-    882
IBNG          ------------------------------A-----VT------------------------------D-    883

CONSENSUS-B   YFlLKLAGRWPVktiHTDNGsNFtstTVkAACWWaGiKQEFGIPYNPQSQGVvESMNkeLKkIIGQVRDQ    882
SF2           ------------------------------------------------------------N------------    883
LAI           ------------------------------------------------------------------------    895
HXB2R         ------------------------GA--R-----------------------------------------    883
NL43          --------------V-------------------------------------I-----------------    883
NY5CG         --------------V-------------------------------------I-----------------    883
LW123         -------------------------A----------------------------------------------    883
MN            --------------------P-------------T-----------------I-----------------    885
JRCSF         ------------T-----------------------------------------------------------    887
JRFL          ------------------------------------------------------------------------    883
OYI           --I-----------------------------------------------------------N------------    883
CAM1          --------------------G--I--------------------------------N------------    883
HAN           --------------V-----P---------------------------------------------------    882
D31           --I-----------------------------------V-----------------------------------    883
RF            --I----------V-----------------------------------------Q--Q--------    882
YU2           ------------T------------A----------------------------------------------    883
BCSG3C        ------------------------------------------------------------------------    883
P896          ------------------------------------------------------------------------    882
3202A12       --I---------T------------A----------------------------------------------    883
3202A21       --I---------T------------A----------------------------------------------    883
MANC          ------------T-----------------------------------------------------------    883
WEAU160       --I-----------------------------------------------------I-----------------    883

CONSENSUS-D   YFlLKLAGRWPVKvVHTDNGSNFTSAaVKAACWWAGIKQEFGIPYNPQSQGVVESMNKELKKIIGQVRDQ    880
ELI           ------------------------------------------------------------------------    882
Z2Z6          --I----------I------------------------------------------------------------    882
NDK           --------------------------T---------------------------------------------    882

CONSENSUS-O   YFLLKLAARWPVKVIHTDNGPNFTS??MKAACWW??IQHEFGIPYNPQSQGVVEAMNKELKSIIQQVRDQ    798
ANT70         -------------------------TT-------AN-----------------------------------    879
MVP5180       -------------------------AA-------TG-----------------------------------    879

CONSENSUS-U   YFILKLAGRWPVKVVHTDNGSNFTSAAVKAACWWANIKQEFGIPYNPQSQGVVESMNKELKKIIGQVREQ    882
MAL           ------------------------------------------------------------------------    882

CONSENSUS-CPZ YFLLKLA?RWPVKTIHTDNG?NFTSAAVKAACWWA?I?QEFGIPYNPQSQGVVES?NK?LK?IIGQ?RDQ    631
CPZGAB        -------G------------P--------------D-K-----------------L--E--K----V---    881
CPZANT        -------S------------A--------------N-Q-----------------M--Q--Q----I---    886
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HIV1 POL

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CONSENSUS-A   AEHLKTAVQMAVFIHNFKRKGGIGGYSAGERIIDIIA?DIQTKELQKQI?KIQNFRVYYRDSRDPIWKGP    880
U455          --------------------------------------T-----------S--------------------    952
IBNG          --------------------------------------S-----------I--------------------    953

CONSENSUS-B   AEHLKtAVQMAVFIHNFKRKGGIGGYSAGeRIvdIIAtDIQtkeLQKQITKIQNFRVYYRDsrdPlWKGp    952
SF2           ------------------------------------------------------------NK-------    953
LAI           ----------------------------------------------------------------------    965
HXB2R         -------------------------------------------------------------N------    953
NL43          ------------------------------------------------------------------V----    953
NY5CG         ----------------------------------------I-----------------------V----    953
LW123         -------------------------------------------------------------N------    953
MN            -----R---------------------------G-----------------------------------    955
JRCSF         --------------------------------I----------------------------N---I----    957
JRFL          ------------------------------------------------------------E------    953
OYI           ------------------------------------------------------------E------    953
CAM1          --------------------------------I-----------------------------------    953
HAN           ------------------------------------------------------------E-F----    952
D31           ----------------------------------------------------------------------    953
RF            -------------------------------------------------------------------H    952
YU2           ----------------------------------------------------------------------    953
BCSG3C        ------------------------------------------------------------NK-------    953
P896          --------------------------------------S-------------------------------    952
3202A12       ----------------------------------------------------------------------    953
3202A21       ----------------------------------------------------------------------    953
MANC          ----------------------------G--------------------------------N------    953
WEAU160       --------------------------------I---------QQ--------------------------    953

CONSENSUS-D   AEHLKTAVQMAVFIHNFKRkgGIGGYSAGERIIDIIATDIQTkELQKQIiKIQNFRVYYRDSRDPIWKGP    950
ELI           -------------------RR-------------------------------------------------    952
Z2Z6          ------------------------------------------------T--------------------    952
NDK           -----------------------------------------R--------------------------    952

CONSENSUS-O   AEHL?TAVQMAVFVHNFKRKGGIGGYTAGER?IDILASQIQTTELQKQILK?NNFRVYYRDSRDPIWKGP    865
ANT70         ----R--------------------------I-------------------1                    930
MVP5180       ----K--------------------------L-------------------I------------------    949

CONSENSUS-U   AEHLKTAVQMAVFIHNFKRKGGIGGYSAGERIIDMIATDIQTKELQKQITKIQNFRVYYRDNRDPIWKGP    952
MAL           ----------------------------------------------------------------------    952

CONSENSUS-CPZ AE?LKTAV?MAV?IHNFKRKGGIGGYT?G?RI?DI?ATDIQT??LQ?QILK?Q?FRV?YRDSRDP?WKGP    687
CPZGAB        --H-----Q---F--------------A-E--I--I------SE--K----V-K---Y-------I----    951
CPZANT        --Q-----V---H--------------P-Q--L--L------TQ--N----I-Q---H-------V----    956
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                                      vif cds ->
CONSENSUS-A   AKLLWKGEGAVVIQDNSDIKVVPRRKAKIIRDYGKQMAGDDC?AGRQDED      929
U455          ------------------------------------------M-------     1002
IBNG          ------------------------------------------V-------     1003

CONSENSUS-B   AKLLWKGEGAVVIQDNsdIKVVPRRKaKiIRDYGKQmagDDCVAsRQDED     1002
SF2           --------------------------------------------------     1003
LAI           --------------------------------------------------     1015
HXB2R         --------------------------------------------------     1003
NL43          --------------------------------------------------     1003
NY5CG         --------------------------------------------------     1003
LW123         --------------------------------------------------     1003
MN            ----------------N-----------V-------T-------------     1005
JRCSF         --------------------------V-----------------------     1007
JRFL          --------------------------V-----------------------     1003
OYI           --------------------------------------------------     1003
CAM1          --------------------------------------------------     1003
HAN           --------------------------------------GS-----------     1002
D31           -----------------E--------------------------G-----     1003
RF            --------------------------------------------------     1002
YU2           ---------------------------------------------G-----     1003
BCSG3C        --------------------------------------------------     1003
P896          --------------------------------------------------     1002
3202A12       --------------------------------------------------     1003
3202A21       --------------------------------------------------     1003
MANC          -----------------E--------V-----------------G-----     1003
WEAU160       --------------------------------------------------     1003

CONSENSUS-D   AKLLWKGEGAVVIQDnSDIKVVPRRKVKIIRDYGKQMAGDDCVASRQDED     1000
ELI           ---------------K----------------------------------     1002
Z2Z6          --------------------------------------------------     1002
NDK           --------------------------------------------------     1002

CONSENSUS-O   AQLLWKGEGAVVIQDKGDIKVVPRRKAKIIRDYGKQMAGTDSMANRQTESESMEQPGEIP      925
MVP5180       ------------------------------------------------------------     1009

CONSENSUS-U   AKLLWKGEGAVVIQDNSDIKVVPRRKAKIIRDYGKQMAGDDCVAGGQDEDKHGTAW     1008
MAL           -------------------------------------------------------     1008

CONSENSUS-CPZ A?LLWKGEGAVVIQDQGELKVVPRRKAKIIRDYGKQMAGDDCVASRQNEDKHGTAW      742
CPZGAB        -T-----------------------------------------------------     1007
CPZANT        -Q-----------                                              969
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HIV1 POL CONSENSUS

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CONSENSUS-A   FFRE.NLAFQQGEAR?F............SSE..QT??NS?TSR?LWDGG?D??.L?...???G?E?..Q     35
CONSENSUS-B   ----.d---p--k--e-???????????---..--Ra--p-r-E-qVw-r-nnS-S???-EA-adr..-     49
CONSENSUS-D   ----.d---P--K-GEl.............---..--RA--P---E-RVW-r-.NP-S....eT-A-R..-     48
CONSENSUS-O   ---?.?--SGGH---QL............CA-..TS-PI-P-?......--GSE.....GT-ES?---G??     35
CONSENSUS-U   ----.----P--K--E-............P--..--RA--P---E-RVW-G-K.T-S....ET-A-R..-     48
CONSENSUS-CPZ ----??????????--L............CA-????---?--?---????-?--??-.....--?-?-???     13

                     protease
                       \/          <- gag cds end
CONSENSUS-A   G?..??SF?FPQITLWQRPLVTV?I?GQLIEALLDTGADDTVLEDINLPGKWKPK?IGGIGGFIKVRQYD     96
CONSENSUS-B   -...tV--s--------------ik-g---K--------------eM----r----M--------------    116
CONSENSUS-D   -...TV--n--------------IK-G---K--------------Em---------M--------------    115
CONSENSUS-O   R...A-??CL---P--D--I--A-VG-H-C-?-----------NN-Q-E-?-?--M----------KE-?     94
CONSENSUS-U   -...IV--S----------V---RVG---K--------------E----------M--------------    115
CONSENSUS-CPZ ?-??---?-?-?-?-----???--?---?C?-----------?-?-?-Q-?-------------?-?-??     55

                                          protease \/ p66, p51
CONSENSUS-A   QILIEICGKK?IGTVLVGPTPVNIIGRNMLTQIGCTLNFPISPIETVPVKLKP?MDGPKVKQWPLTEEKI    164
CONSENSUS-B   --------H-A-----------------L------------------------G----------------    186
CONSENSUS-D   --------?-A-----------------L------------------------G----------------    184
CONSENSUS-O   NVTV-??-?EVQ------------?---I--GL------------AP-------G-----------S?---    159
CONSENSUS-U   ----------A---I-------------------------------------G----R-----------    185
CONSENSUS-CPZ ?V?-?-??R?V??---?--?--------?-??L----?----??--------?G----?------S?---    106

                       | M41L                D67N |  | K70R
CONSENSUS-A   KALT?IC?EMEKEGKISKIGPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPH?AGLK    231
CONSENSUS-B   ---vE--T-------------------------------------------------------P----    256
CONSENSUS-D   ----E--T---------R----------I-----------------------------------P----    254
CONSENSUS-O   E---A--Q---Q-----R----------I-------?----------------?----------PG---    227
CONSENSUS-U   ----E--KD-------L---------------------------N--------------------P----    255
CONSENSUS-CPZ ?--?E---??-?-?---?---?------I-------??--------------------?------P----    164

CONSENSUS-A   KKKSVTVLDVGDAYFSVPLD??FRKYTAFTIPS?NNETPG?RYQYNVLPQGWKGSP?IFQ?SMTKILEPF    295
CONSENSUS-B   --------------------kd-----------i------i---------------A---s---------    326
CONSENSUS-D   --------------------eD-----------I------I---------------A---S---------    324
CONSENSUS-O   Q?Q-------------C---PD-----------V----------------------A---S------D--    295
CONSENSUS-U   --------------------ED-----------I------I---------------A---S---------    325
CONSENSUS-CPZ ?---------------?----D----------------------?------------------------?--    225

                  polymerase motif
                       /<-->/                     T215Y |   | K219Q
CONSENSUS-A   R???P?IVIYQYMDDLYVGSDLEIGQHRAKIEELR?HLL?WGF?TPDKKHQKEPPFLWMGYELHPDKWTV    358
CONSENSUS-B   -KQN-d----------------------t------q---r---t--------------------------    396
CONSENSUS-D   -KQN-E----------------------T------E---R---T--------------------------    394
CONSENSUS-O   ---N-E?E-?--?---------PL?E--KR?-L--E--YQ---T--------------------------    358
CONSENSUS-U   -TKN-E----------------------T------E---K---T--------------------------    395
CONSENSUS-CPZ --K---??-------------?--??--???-?--Q--?---?-------------?-------------    278

CONSENSUS-A   QP??LPEKDSWTVNDIQKLVGKLNWASQIYAGIK?KQLC?LLRGAKALTDIV?LTEEAELELAENREI..    421
CONSENSUS-B   --Iv------------------------------V----k----t----Evip---------------..    464
CONSENSUS-D   -sIk----E---------------------p---Vr---K----T----EViP---------------..    462
CONSENSUS-O   -?IQ--?-?V---------?----------Q--RV?E--K-I--T-S--EV-P-S?------E----?..    419
CONSENSUS-U   --IQ--D-E-----------------------P---V----K------------P--A------------..    463
CONSENSUS-CPZ -?I----???---------?----------P----------I--?-?---?--?-?------?--??-??    329

CONSENSUS-A   .LK?PVHGVYYDP?KDLVAE?QKQGQDQWTYQIYQEPFKNLKTGKYA?KRSAHTNDVKQLTEVVQKV??E    484
CONSENSUS-B   .--e---------s---i--i-----g--------------------rm-G-----------A---iat-    533
CONSENSUS-D   .--E---------S---I--i----hG--------------------Rm-G---------a-a---IsT-    531
CONSENSUS-O   .----------Q-D---WV?I--?-??-----?--?EH--------?RQKAS----IR--A--?---SQ-    479
CONSENSUS-U   .--E---------S---I--I-----G---------QY---------RIK------------A---IAQ-    532
CONSENSUS-CPZ ???-???-?--?--??-?-?I----??------?-???-?--?----R????---??R--A??---I---    367

                                                                          p51 \/
CONSENSUS-A   SIVIWGK?PKFRLPIQ?ETWE?WWMEYWQATWIPEWEFVNTPPLVKLWYQLEKDPI?GAETFYVDGAANR    550
CONSENSUS-B   -------t---k----K-------t----------------------------e--v-------------    602
CONSENSUS-D   -------T--------K----T--?-----------------------------E--I-------------    600
CONSENSUS-O   ?-?----L---?--VTR----T--A?-------------S----I----?--?E-------?--------    541
CONSENSUS-U   -------T--------K----A--T---------------------------TE--V-------------    602
CONSENSUS-CPZ ------?----?--??--?-?A--??------------?-----??---?-???--P???-?--------    416

CONSENSUS-A   ETK?GKAGYVTDRGRQKVVSLTETTNQKTELHAIHLALQDSGSEVNIVTDSQYALGIIQAQPDRSESE?V    618
CONSENSUS-B   ---l-----------------d--------q----------l--------------------k----l-    672
CONSENSUS-D   ---L----------------Pf-D--------Q--N-------L--------------------K----L-    670
CONSENSUS-O   ?--L-------EQ-K-?IIK-?------A--M-?L?-----KE?---------?--?-SS--TQ-?-PI-    602
CONSENSUS-U   ---K---------------------------Q------------------------------K----I-    672
CONSENSUS-CPZ ???---------?-??????-??----QA--?-?L?--?--???---------?--??-??--?---?L-    459

CONSENSUS-A   NQIIEKLI?K?KVYLSWVPAHKGIGGNEQVDKLVS?GIRKVLFLDGIDKAQE?HE?YH?NW?AMASDFNL    681
CONSENSUS-B   s----q--K-E----a------------------a----------------e--K--s--r---------    742
CONSENSUS-D   s----Q--K-E----A------------------Q----------------E--K--N--R---------    740
CONSENSUS-O   Q----E-TK-E?---T------------KI-----KD--R----E---Q---D--K--S----L--?-G-    669
CONSENSUS-U   -----Q--Q-D-----------------------S----------------E--K--S--R---------    742
CONSENSUS-CPZ ??--??--K?E?I---------------------------?----?---?-----?---S---??-???--    510
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CONSENSUS-A   PP?VAKEIVASC?KCQ?KGEAMHGQVDC?PGIWQLDCTHLEGK?ILVAVHVASGYIEAEVIPAETGQETA    746
CONSENSUS-B   --v---------d---L-----------S--------------v--------------------------    812
CONSENSUS-D   --V---------D---L-----------S--------------V--------------------------    810
CONSENSUS-O   --------I---P--HI----?-----?S-E?--?----?---I-I-------?F---------------    732
CONSENSUS-U   --I---------D---L-----------S--------------I-I------------------------    812
CONSENSUS-CPZ --I-----?-?-D--?V----?------S-----V--------V-I-----?--?-----???---??--    569

CONSENSUS-A   YFILKLAGRWPVKVIHTDNGSNFTSAAVKA?CWWAN??QEFGIPYNPQSQGVVESMNKELKKIIGQVR?Q    812
CONSENSUS-B   --l----------t-----------tT---A----GiK------------------------------D-    882
CONSENSUS-D   --l-----------V---------------A----GIK------------------------------D-    880
CONSENSUS-O   --L----A------------P----??M--A---??IQH---------------A------S--Q---D-    798
CONSENSUS-U   --------------V---------------A-----IK------------------------------E-    882
CONSENSUS-CPZ --L----?-----T------?---------A----?I------------------?--?--?----?-D-    631

CONSENSUS-A   AEHLKTAVQMAVFIHNFKRKGGIGGYSAGERIIDIIA?DIQTKELQKQI?KIQNFRVYYRDSRDPIWKGP    880
CONSENSUS-B   ---------------------------------v----t-----------T---------------l----    952
CONSENSUS-D   -------------------------------------T-----------i--------------------    950
CONSENSUS-O   ----?--------V------------T----?---L-SQ---T------L-?N-----------------    865
CONSENSUS-U   -----------------------------------M--T-----------T-----------N--------    952
CONSENSUS-CPZ --?-----?---?-------------T?-?--?--?-T----??--?--L-?-?---?-------?----    687

                                     vif cds ->
CONSENSUS-A   AKLLWKGEGAVVIQDNSDIKVVPRRKAKIIRDYGKQMAGDDC?AGRQDED                       929
CONSENSUS-B   ------------------------------------------V-s-----                      1002
CONSENSUS-D   --------------------------V---------------V-S-----                      1000
CONSENSUS-O   -Q--------------KG----------------------T-SM-N--T-SESMEQPGEIP             925
CONSENSUS-U   ------------------------------------------V--G----KHGTAW                 1008
CONSENSUS-CPZ -?-------------QGEL-----------------------V-S--N--KHGTAW                 742
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