

Protein Alignment Summary Table (Vpu)

Name	Accession No.	Region	First Author	Reference
CONSENSUS-A				
U455	M62320	complete genome	Oram, J.D.	ARHR 6 (9), 1073–1078 (1990)
UG273A	L22957	env, tat, vpu, rev, and nef	Louwagie, J.J.	J. Virol. 69 (1), 263–271 (1995)
UG275A	L22951	env, tat, vpu, rev, and nef	Louwagie, J.J.	J. Virol. 69 (1), 263–271 (1995)
92RW009	U88823	complete genome	Gao, F.	Unpublished;
92UG037	U51190	complete genome	Gao, F.	J. Virol. 70 (3), 1651–1657 (1996)
CONSENSUS-B				
SF2	K02007	complete genome	Sanchez-Pescador, R.	(in) Weiss, R.L., Teich, N., Varmus, H. and Coffin, J. (Eds.), <i>RNA Tumor Viruses</i> , Second Edition, 2, Vol. 2:1124–1141, Cold Spring Harbor Laboratory, Cold Spring Harbor (1985)
CONSENSUS-C				
HXB2	K03455 M38432	complete genome	Rosen, C.A.	Cell 41, 813–823 (1985)
LAI	K02013	complete genome	Wain-Hobson, S.	Cell 40, 9–17 (1985)
MN	M17449	complete genome	Gurgo, C.	Virology 164, 531–536 (1988)
NL43	M19921	complete genome	Adachi, A.	J. Virol. 59, 284–291 (1986)
JRC5F	M38429	complete genome	Koyanagi, S.	Science 236, 819 (1987)
JRFL	U63632	complete genome	O'Brien, W.A.	Nature 348, 69 (1990)
P896	U39362	complete genome	Collman, R.	J. Virol. 66, 7517 (1992)
WEAU160	U21135	complete genome	Ghosh, S.K.	Unpublished (1995)
92US657.1	U04908	tat, rev, env and partial vpr, nef	Gao, F.	J. Virol. 70 (3), 1651–1657 (1996)
HNN008	Z68505	vpu	Kuiken, C.L.	J. Gen. Virol. 77: 783–792 (1996)
JGV86	Z68602	vpu	Kuiken, C.L.	J. Gen. Virol. 77: 783–792 (1996)
JGV90	Z68607	vpu	Kuiken, C.L.	J. Gen. Virol. 77: 783–792 (1996)
JGV97	Z68614	vpu	Kuiken, C.L.	J. Gen. Virol. 77: 783–792 (1996)
CONSENSUS-D				
ETH2220	U46016	complete genome	Salminen, M.O.	ARHR 12(14), 1329–1339 (1996)
92BR025	U52953	complete genome	Gao, F.	J. Virol. 70 (3), 1651–1667 (1996)
CONSENSUS-E				
Z2Z6	M22639	complete genome	Theodore, T.	Unpublished (1988)

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Z6	K03458	pol, vif, vpr, tat, rev, vpu, env, nef, 3' LTR	Srinivasan, A.	Gene 52, 71–82 (1987)
NDK	M27323	complete genome	Spire, B.	Gene 81, 275–284 (1989)
TZ012	U12407	envelope V1-V3 vpu partial	Siwka, W.	ARHR 10 (12), 1753–1754 (1994)
TZ064	U12413	envelope V1-V3 vpu partial	Siwka, W.	ARHR 10 (12), 1753–1754 (1994)
TZ030	U12411	envelope V1-V3 vpu partial	Siwka, W.	ARHR 10 (12), 1753–1754 (1994)
TZ017	U12409	envelope V1-V3 vpu partial	Siwka, W.	ARHR 10 (12), 1753–1754 (1994)
MAL	K03456	complete genome	Alizon, M.	Cell 46, 63–74 (1986)
84ZR085	U88822	complete genome	Gao, F.	Unpublished
94UG1141	U88824	complete genome	Gao, F.	Unpublished
CONSENSUS-E				
CM240X	L14572	V3 region, envelope tat nef rev vpu	Mascola, J.J.	J. Infect. Dis. 169, 48–54 (1993)
93TH253	U51189	complete genome	Gao, F.	J. Virol. 70 (3), 1651–1657 (1996)
CONSENSUS-F				
BZ126A	L22082	env tat rev nef vpu	Louwagie, J.	ARHR 10 (5), 561–567 (1994)
BZ163A	L22085	env tat rev nef vpu	Louwagie, J.	ARHR 10, 561 (1994)
93BR029.4	AF005495	complete genome	Gao, F.	Unpublished
93BR020.1	AF005494	complete genome	Gao, F.	Unpublished
U40561	AF005496	complete genome	Gao, F.	Unpublished
CONSENSUS-G				
92NG083.2	U88826	complete genome	Gao, F.	Unpublished (1997)
92NG003.1	U88825	complete genome	Gao, F.	Unpublished (1997)
CONSENSUS-O				
ANT70C	L20587	complete genome	Vanden Haesevelde, M.	J. Virol. 68 (3), 1586–1596 (1994)
MVP5180	L20571	complete genome	Gurtler, L.	J. Virol. 68, 1581–1585 (1994)
CONSENSUS-CPZ				
CPZGAB	X52154	complete genome	Huet, T.	Nature 345 (6273), 356–359 (1990)
CPZANT	U42720	gag, pol, vif, vpr, tat, rev, vpu, partial env	Vanden Haesevelde, C.	Virology 221, 346 (1996)

	transmembrane domain \ cytoplasmic domain	alpha helix	env cds -> phos	phos alpha helix				
WEAU160	MOSL.....QIIAIVLVVAGIATVWVSIVILVEKRIILRGR.....KIDRLI	IDRIRDRV	EDSGNESEGOEE	LSAL.....VEM	GHHAPWIDDD	L	81
CONSENSUS-A	-E-C---G-I-L-L-L---T-G---K-l-k-?k-.....?????	81
U455	-E-W-TG-I-L-L-L---T-G---\$K-NC\$SK-K\$TGHIL-.....E-NNYDLGVDNN-NYDLGVDNN-	81	
UG273A	-N-C-G-I-L-L-L---T-G---D-K-L-K--E-E-A-T-A-NYNLGFDDN-NYNLGFDDN-	81	
UG275	-SP-PPL-H-C-G---L-L-L---T-G---KRL-K--K-SE-DTD-K-K-NYDLG-ANN-	84	
AC_92RW009	-T.....E-Y---I-L-V---TLAG---K-L-K--KK-E-KID-K-GV-NYDLG-VNN-	80	
92UG037	-L.....E-C-V-G---L-L-L---T-G---K-L-K--V-E-DR-L-DYDLG-DNN-	80	
CONSENSUS-B?--?--?--??????	80	
SF2S-VA---T---#EEK-LV-	80	
HXB2	-T-PI.....P-V---I---LIE-EISAVEMGV-	82	
LAI	-P-I.....A---I---LIE-EISAVEMGV-N-	81	
MN	-P.....V-A---I---SE-EVSVEMGD-V-N-	80	
NI43	-P-I.....IV---I---LIE-EVSVEMGL-N-	81	
JRCG3F	-P.....Y---I---K-E-RLN-N-	81	
JRFL	-L.....A---I---F-EEAR-L-V-	80	
P896F-L---T-F-#EDDV-	80	
92US657-L-xF-LEDV-	79	
HN0008V-xxxxxD-V-	79	
JGV90	-P.....x---V-L---T-x--N-IE-T--D--VN-MM	79	
JGV97	-P.....T.....VA---L---L-N-SE-xxM	79	
CONSENSUS-C	-??-??2DVR??-?I-L-?-?-T-AY-L?R-??k-?E?TM	64	
ETH2220	-VD-LAKVDYRLV--FI-L-L-?-?-T-AY-LR?k-?E?TM	86	
92BR025	-LE-IGRIDYR-GVG-I-L-V-I-T-AY-LVR-WVK-KE-G-T-ETM	86	
CONSENSUS-D	-P.....V.....lT-E-C-?k-wE-?V-??	78	
Z226	-PS.....-I-A---A---T-F-R-K-CIEK-K-	81	
Z6	-R-P.....-I-A---A---T-F-R-K-CIE#R-	81	
NDK	-P.....V-I-A---I---T-Y-R-K-CEER	81	
TZ012	-P.....V-I-A---I---T-Y-R-K-CEER	81	
TZ064	-I-P.....V---V-A-L---T-ICKRLKWN-E-R-	81	
TZ030	-P.....V---V-A-L---T-ICKRLKWN-E-R-	81	
TZ017	-P.....V---V-A-L---T-ICKRLKWN-E-R-	80	
AD_MAL	-I-P.....V---TL---T-F-I-RETK-	81	
84ZR085-L-L---T-F-R-KWE-EK-	81	
94TG1141	-P.....E---G-L-L---T-F-CK-LRWEK-	80	
CONSENSUS-E	??P.....E-S---G-?-L-L---T-A?kE?TD?	74	
CM240X	ITP.....E-S---G-I-L-L---T-AFKEETD	81	
93TH253	NAP.....E-S---G-L-L-L---T-AFKEETDK	81	
CONSENSUS-F	S???.LANS?T-I-L-L---T-?YLNYE??	73	
B2126A	-SYF.....LAIS-T-I-L---T-AYLNYEG	81	
B2163A	-SD.....LAISVT-I-L---T-YNYEEG	81	
BF_93BR029	..SY.....LVIGLA-IA-L---T-AYELVNYK-EA	80	
93BR0201	..SN.....LAIG-A-I-L---T-AYK-LVNYK-SEA	80	
90CR056	..YI.....GL-G-G---TF---VI---T-YCK-LVKEG	79	
CONSENSUS-G	..?.....E-?P?P?P-?-?-A-?-?-??P?P?P-?-?E???	54	
AG_92NG003	..A.....E-S---I-F-A-TI---FRKKEM	76	
AG_92NG003	..A.....E-A---AG---A-A---TSR#E?M	72	
CONSENSUS-O	..H??.?L-?I?SALP??-NV?P-?.F??.L-?Y-?-??QDR?P?E-LERLR?EIRD-DY-N?EE?Q?EVM?-?SH-F?N-M.FE??	59	
ANT10	..HHR.....DL---LISALP-NVTL-G-F-L-?Y-EKEQDRKERE-LERLR?EIRD-DY-N-EE-Q?EVM-LSH-F?N-M.FE.P	85	
MV95180	..HOE.....NL---LISALP-NVTL-L-FN.L-I-Y-VKQDRROE-LERLRKEIRD-DY-N-EE-Q?EVM-LSH-F?N-M.FE.P	85	
CONSENSUS-CPZ	..TL.....VG-VLI---GLIANN-CI-GYIIKWG-RYK-HLETEENLTL-EN-EE-R-EQ-IHNYNHNHFM-M.F	23	
CPZGAB	..CPZANT.....FEV-FL-FSIVL.WI-CIPI-YKLKIYKQ-QIDNKN-QRI-EVLSRLSID-AIEED-EADTY	88	
CPZANTTMIYIGS-FAN-V.YREGDE	83	

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