

---



---

**HMMER Sequences in the Vpu Alignment**


---

A_U455	HIVU455	M62320	Oram,J.D.	ARHR 6, 1073 (1990)
B_SF2	HIVSF2	K02007	Sanchez-Pescador,R.	Science 227, 484 (1985)
D_ELI	HIVELI	K03454	Alizon,M.	Cell 46, 63 (1986)
F_BZ163A	HIV1BZ163A	L22085	Louwagie,J.J.	ARHR 10, 561 (1994)
O_ANT70C	HIVANT70C	L20587	Vanden Haesevelde,M.	JVI 68, 1586 (1994)
O_MVP5180	HIVMVP5180	L20571	Gurtler,L.G.	JVI 68, 1581 (1994)
CPZGAB	SIVCPZGAB	X52154	Huet,T.	Nature 345, 356 (1990)
CPZANT	SIVCPZANT	U42720	Vanden Haesevelde,M.	Virology 221, 346 (1996)

---



---

## HIV1 VPU

The following alignment and most likely sequence were generated using the HMMER program as described in Part III. For simplicity, only representative HIV1s are shown. Two sites of phosphorylation are indicated. One conserved, gapless block was found using the BLOCKMAKER and Motif (or Gibbs) program, which is shown by shading. The "Cobbler" sequence from the Motif analysis follows this alignment. For further information about the VpU protein, see the section by K. Strebel in Part III of this compendium.

```

env cds ->
phos | |phos
most-likely MQPLQILAIIVALVVALIIAIVVWTIVFI...EYRKILR...QRKIDRL.IDRIRERA..EDS.GNES.EGDQE 62
A_U455      -T--E-W--TG-I----L-----G-...-$K-NC$$S..KK-$TG#.LN-----..----.D--T- 59
B_SF2       --S-----S---VA-----L-...-----#-----K-.....K-..... 61
D_ELI       ---G-I--A-----I-L-----R-KK...--R--C-.L---T-----R- 62
F_BZ163A    -SD-LAISVT--I-----Y-...--L-...--N-.YEG-----A- 62
O_ANT70     -HHRDL---IIISAL-F-NVIL-GFILRKYL-QKEQD-K..E-E-LER.LR---IR..D--.DY--.N-EE- 66
O_MVP5180   -HQENL--LI--SALCL-NVLI-LFNLRIYLVQ--QD-R..EQE-LER.LR--K-IR..D--DY--N-EE-Q 67
CPZGAB      -TL-VG-VL.I--GLIAWN-CI-GYIIKW..G--RYK-HRLETE-E--.NLIL-----N-EE- 65
CPZANT      -TNIFEY-F.....-AFS--L-I-CIPILYKLY--YK...-QQ--NKRQ--I-VLSRRL-IDSAL.-E-E- 63

most-likely .E.LSALVEM.GHHAPWDVD...DL 81
A_U455      .-.-L----.-NYDLGVDN...N- 78
B_SF2       .-.-L-----L----- 80
D_ELI       .K.-K-----I-..... 81
F_BZ163A    .-.A--G--.-PFI-G-IV...N- 81
O_ANT70     Q-.VMD--LSH-FDN-MFEP..... 85
O_MVP5180   .-.VME-IHSH-FAN-MFEL..... 85
CPZGAB      .-R-EQ-IHN.YN-NNHFANPMF-- 88
CPZANT      .A.DTYYLGS.-FAN-VYREG..-E 83

```

\*\*COBBLER sequence from MOTIF\*\*

```

>VPU A_U455, with embedded consensus blocks
mtpleiwaitglivalilailvvtivgiekknkskktglnRIREVAEDSGNESNGDEEE
lsl1lvemgnydlgvdn1

```

HIV1 VPU CONSENSUS

	env cds ->	
	phos	phos
CONSENSUS-A	mtPL???eIcAIvGLiVALILAIvVWTIVgI.eyKkllkqr.....Kidrl?ikRIRERA.EDSgNES	57
CONSENSUS-B	-qs-...q-?---a-v--a-i-----f-?--r-i-R--.....?-----d-----	56
CONSENSUS-D	-Q--...v-l---A-v---i-----f-.crr-kr--.....-w-.d-----?	57
CONSENSUS-F	-S??...LAIS?TA-----I-----?Y-.-R---R--.....-N--.YE?--?--	51
CONSENSUS-O	-H??...?LL-?I??SAL??INV??-?.F?..LR?Y-?--?QDR?E?E-LER.LR--?-IR.D--DY--	42
CONSENSUS-U	-Q--...T-T-----V--F-A-----S--Y-.-R-IR--K......LD-----	57
CONSENSUS-CPZ	--??...????L?????W?-CI???I????-?YK????.....?????-?.?I?????..?????-	14
CONSENSUS-A	?GDT?E.L?kL...VEM.GnydlgvdnNL\$	78
CONSENSUS-B	e--qe-.-sa-????--?-H?apwdvdD--	79
CONSENSUS-D	E--rE-.-sa-.....-HhAPwd?Ddm-	80
CONSENSUS-F	E--AE-.-A?-....G--.-PFIP-DI?---	73
CONSENSUS-O	N?EE-QEVM?-....??SH-F?NPM.FE??	59
CONSENSUS-U	D---E-.-ST-....M--.-YEYILDND---	81
CONSENSUS-CPZ	-?EE--??-?????????FANP?..????DE	23