



SURE v1.0 amino acid sequence unanimity alignments for HIV-1 Vif protein (created Jun 23, 2015; reformatted Nov 19, 2018, v6)  
Viral and Human Genomics Laboratory, Facultad de Medicina UASLP (<http://midasmap.uaslp.mx/suretool/>).  
Ave. Venustiano Carranza #2405 Col. Filtrros Lomas CP 78210 San Luis Potosí, SLP, Mexico

	1	10	20	30	40	50	60	70	80	90	100	110
HXB2	MENRWQVMIV	WQVDRMRIRT	WKSLVKHHMY	VSGKARGWFY	RHHYESPHPR	ISSEVHIPLG	D...ARLVITTYW	GLHTGERDWH	LGQGVSIWR	KKRYSTQVDP	ELADQLIHL	Y
MX033			N-G-D	R-R-K	M-K	ISSEVHIPLG	.NT--IVK	--D--	H--	--RK-N-I	D--K	
MX050			K-N-I	I-K-K-V	K	INT-	--K-V	E		K-NRK	I-NM	
MX066			N-Y	C-K-V	TN	V--	...K-K	E	A	D-S	IL	D
MX071				I-K-K-I	K	DC-N-K	...K			K-E	S-I	G
MX071_2	R		IH	--K-K-I	K	DCTN-K	...K			K-TE	S	G
MX078			N	IH	I-K-K-V	K	IN	--K-L-K	E	A-K	--G	S
MX077			N	Y-IH	I-K-K-I	K	TN	...VK	E	A	N	A
MX081				D	--K-K-Y	R	T	...K		A	N	N
MX086			SK	IH	I-K-K-S	N		...K-K			ES	GI
MX089			K	N	--K-TEK	V	NN	T	G	H	QR	K
MX091			A	N	--K	H-K	V	...I	N		R	DI
MX101	V			I-K-K-S	K	TN	...E-I	S			RX	
MX109		I		I-K-K-D	D	TN-K	--K-R				K	H
MX110			SK	IH	I-K-K-S	N		...K-K			ES	GI
MX110_2	L		SK	IH	I-K-K-S	N		...K-K			ES	GI
MX111			A	H	R-K-KE	S	A-S-K	V--C		S	EK	DT
MX112					I-K-K-S		TN	...K-R			ERS	H
MX118			I		N-K-K	Y	D	...K		A	R	S
MX119			S		I-R-K-V		TN	...A			G	N
MX122			N	Y-H	I-R-PKK	P	T	...NI-V			G	D
MX123				Y	I--K-L	P	I	...V				I
MX125			A	H	R-K-KE	S	A-S-K	V--C		S	EK	DT
MX131			A	N	--K-K-L		A	V--			G	N
MX133			N	Y-IH	M-K-TKK	V	T	...E-V			G	N
MX158			N	N	--K-KR	V	HN	...DK			GS	I
MX160				IH	I-K-KR	S	NN-Q	C	...K		E-K	AT
MX166			A		M-K-KK	V	NT-K	...D-GV			Q	R
MX168			N		--K-Q		T-K	...M			R	EH
MX172			N	Y	I-K-K		NI	...GK-VI			A	N
MX176		A		H	K--KK	Q	NI	K--M	G...S		T	GT
MX186			N	C	I--I	I-K-K	HQ-H	M--G	...K-GV		R	R
MX190			N		I-K-K		TI-K	...T-V			R	T
MX196				H	--KR	I	K	TN	...K		R	N
MX207			N	Y	I-K-K		TN	...G			R	N
MX207_2			N	Y	I-K-K		TN	...G			R	N
MX230			K	N	ITK--N	V	Q-TN	...K-VA	Q		E	I
MX313			Y	H	I-K-K		Q-T	K	...GKADK	V	QRK	I
MX324					I--K-I		TN	...I	E...D		R	R
MX327			N		N-K-K		TI-K	...K-VI			R	T
MX350					T-K-K-S		NT	...K			R	R
MX350_2					N-K-K-S		T	...T-AV			R	R
MX350_3					T-K-K-S		NT	...E	E...K		R	T
MX351	A		KA	NR	I-K-TK	V	K	NAN	V--A-V		RS	R
MX354					--K-KR	C	K	TN	...K-R		ERS	D
MX355					I-K-GKR	S	K	TN	...K-R		ERS	D
MX370			I		I-K-K-V		K	TN	...DK-V		S	N
MX375				D	I-K-K	C	K	TN	...K-I		ERS	N
MX376			H		K-I	TK-V	K	SN	...E	E...V	RT	I
MX381					I-K-K		K	TN	...V		G	N
MX381_2			N	Y	I-K-K		K	TN	...E		R	G
MX385				Y	C-R-TKK		T	K	...E-V		R	N
MX385_2				Y	C-R-KK		T	K	...E-V		R	N
MX390					--K-VKE	V	T		...V		R	N
MX399			N		--E-KK	V	HN	T	...EK		G	N
MX399_2			N		--K-KK	V	HN	T	...EE		G	N
MX401			N		R--KK	C	K	TN	...IE	K...K	REG	N
MX403	A				I--KR	C	K	TN	...IE	K...K	REG	N
MX409			N		I-K-K	C	K	TN	...K-K		ERS	D
MX450			K		I-K-K	S	K	TN	...K-I-R		ERS	I
MX463			K	I	I-K-K	L		YH	--D	.SK	S	
MX464			K		IH	I-K-K	X				V	
MX469	K		K		I-K-K	V	K	TAN	V--	...T-V	A	
MX470			A	H	--KK	S	K	NT	--T	...K	N	
MX473					--K-K		K	DI-K	--R	G...V	G	N
MX474			R	H	I-Y	I--KK	S	NNN	V--	E...T-V	N	A
MX540		A		N	--K-S		K	I	--I	...I	E	N
MX542			N		I-K--I		K		V--	...K-VK	H	
MX546			N		I-K-K	I	K	HAN	V--	...T-V	A	
MX554					I-K-K	C	K	TN	...K-I		A	
Cons_D					--K-K	L	K	DC-K	--K	E...VK	R	
MX141		V		N	--K-KR	A	K		E...K-K		RS	N
MX210				H	--K-K		K	T	...K-V		R	
MX352			K	H	I-K-K	V	N		G	...K-K	K	E
MX395			N	G	I-K-K	V				E...T-K	K	E
MX396			N		I-K-K	V				E...VK	K	E
Cons_A			N		--K-KD		K	R	K	V--	VR	L
Cons_G			N		--K-K		K	R	K	V--	VR	L
MX384			N		--K-Q		K	R	K	V--	VR	L
MX384_2			N		--K-Q		K	R	K	V--	VR	L
MX384_3			N		--K-Q		K	R	K	V--	VR	L





## Key to annotations

The following Vif protein motifs descriptions are based on criteria established by Bell *et al*, 2007.

- Tryptophans ( $W^5$ ,  $W^{11}$ ,  $W^{21}$ ,  $W^{38}$  &  $W^{79}$ ) involved in APOBEC3G recognition and suppression are shown in cyan highlight).
- APOBEC3 binding motifs are shown in dark blue highlight; the C-terminal APOBEC3F-binding motif ( $^{171}EDRWN^{175}$ ) is not highlighted for simplicity.
- The  $^{88}EW^{89}$  motif located in central hydrophilic region known to be involved in enhancing steady state expression is shown in yellow highlight and red font.
- The nuclear localization inhibitory signal ( $^{90}RLRR^{93}$ ) is shown in red highlight. Sequences not having the consensus RLRR motif but having residues with conservative physicochemical properties are also shown in highlight.
- The  $^{95}ST^{96}$  CKII and p44/42 Mitogen-Activated Protein Kinase (MAPK) phosphorylation sites are shown in magenta highlighting. Residues other than ST that can also be phosphorylated are also shown in highlight.
- In any case, clinical isolate or subtype consensus sequences not having the aforementioned functional sites or motifs are shown without highlight in the corresponding region (i.e.  $W^{11}$  which in MX071\_2 is represented by an  $R^{11}$ ).
- The zinc-binding motif ( $H^{108}C^{114}C^{133}H^{139}$ ) is shown in black highlight and white font.
- Viral BC Box ( $^{144}SLQYLALAALITPK.K^{158}$ ) is shown in green highlight and based on the criteria suggested by Bizinoto *et al*, 2013.
- The protease processing site ( $L^{150}$ ) is also shown in black highlight.
- Threonine phosphorylation sites ( $T^{155}$  and  $T^{170}$ ) are shown in yellow highlight.
- The Cullin-binding box ( $^{159}KPPLPSVTKLTEDR^{173}$ ) is shown in grey highlight.

## References

*Molecular characterization of the HIV type 1 subtype C accessory genes vif, vpr, and vpu.* Bell CM, Connell BJ, Capovilla A, Venter WD, Stevens WS, Papathanasopoulos MA. AIDS Res Hum Retroviruses. 2007 Feb;23(2):322-30.

*Codon pairs of the HIV-1 vif gene correlate with CD4+ T cell count.* Bizinoto MC, Yabe S, Leal É, Kishino H, Martins Lde O, de Lima ML, Morais ER, Diaz RS, Janini LM. BMC Infect Dis. 2013 Apr 11;13:173.