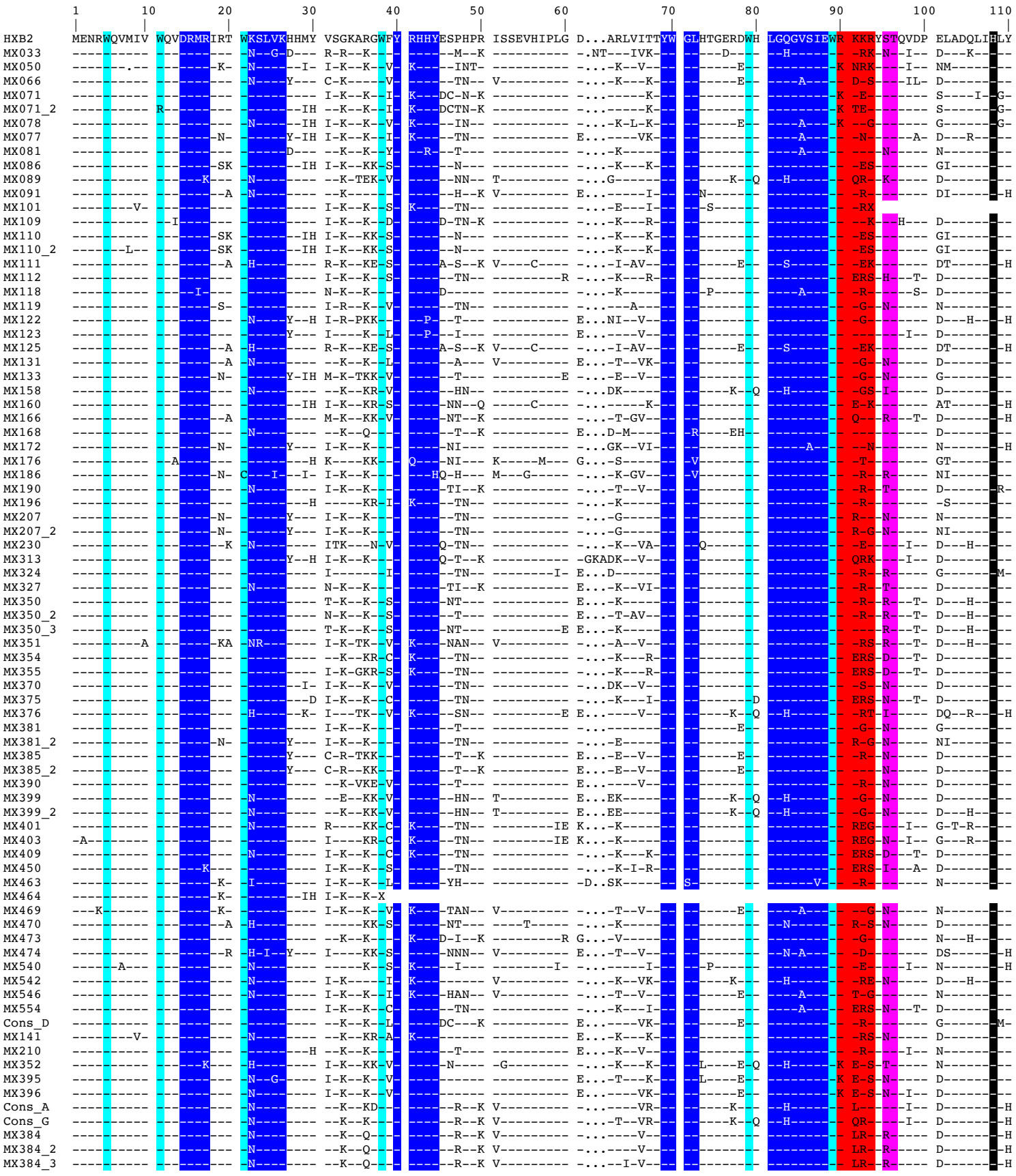
SURe v1.0 amino acid sequence unanimity alignments for HIV-1 Vif protein (created Jun 23, 2015; reformatted Nov 19, 2018, v6)
Viral and Human Genomics Laboratory, Facultad de Medicina UASLP (http://midasmap.uaslp.mx/suretool/).
Ave. Venustiano Carranza #2405 Col. Filtros Lomas CP 78210 San Luis Potosí,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



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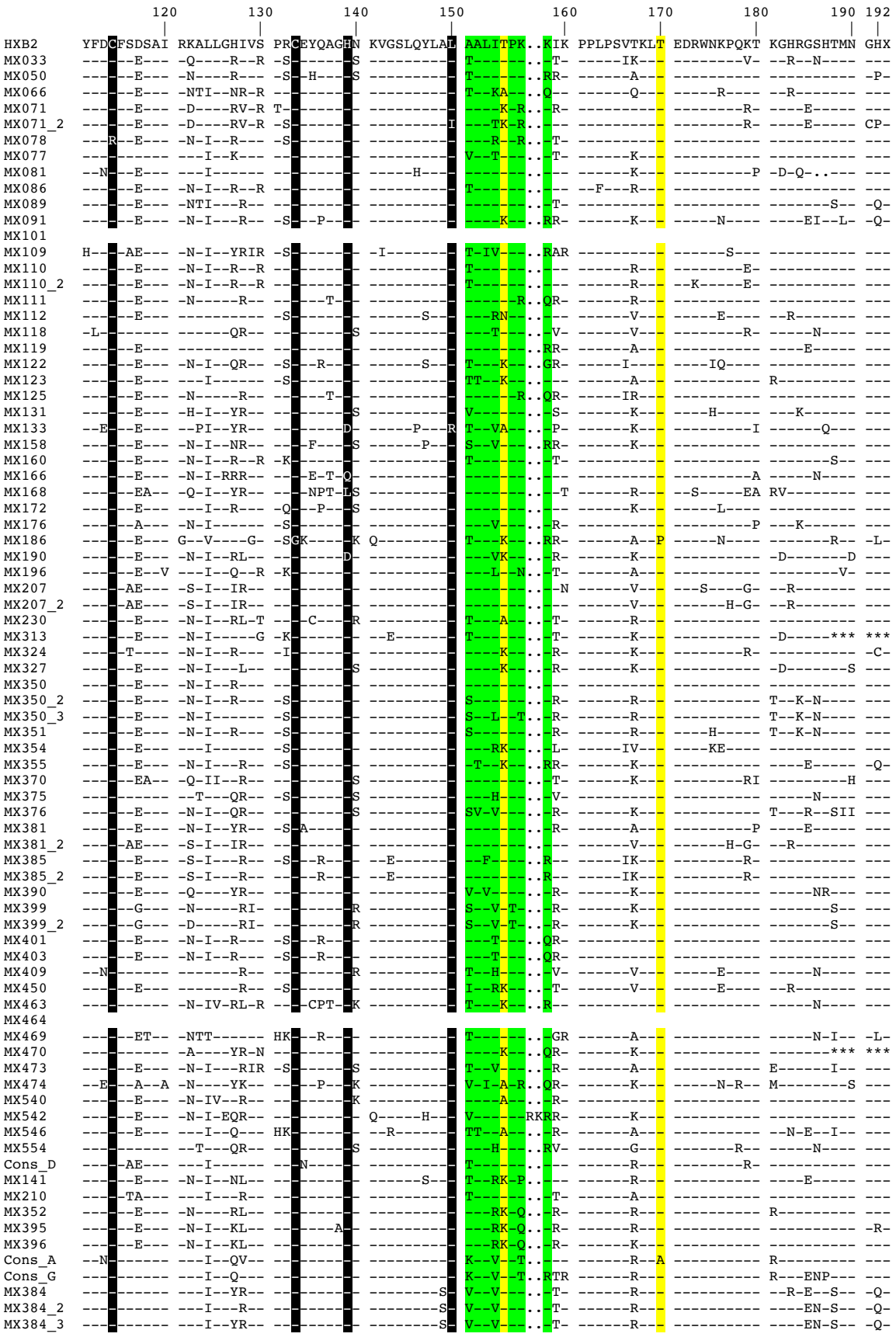

Key to annotations

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 aslo 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.