

Positive and Negative Regulatory Elements in the HIV-1 5'UTR Control Specific **Recognition by Gag**

Background

- Human Immunodeficiency Virus type 1 (HIV-1) is responsible for the development of Acquired Immunodeficiency Syndrome (AIDS).
- Approximately 37 million people are currently infected by the HIV-1 worldwide (WHO).

World Map of HIV-1 Prevalence Global HIV Prevalence = 0.8%





Figure from Laskey, S. B., & Siliciano, R.F. (2014)



Figure from Lu, K. et. al. (2011)

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Figure from El-Wahab, E. W. et. al. (2014)

Recent studies from the Marquet Lab suggest that regions upstream of Psi in the 5'UTR inhibit high affinity Gag binding, allowing for preferential packaging of genomic RNA over viral spliced RNAs.



Figure adapted from El-Wahab, E. W. et. al. (2014)

Figures from Webb, J. A. et. al. (2013)

• $\mathbf{K}_{d(1M)}$: Describes the nonelectrostatic (specific) component of binding.

• Z_{eff}: Reflects the number of charges mediating the protein-RNA interaction.





Gag∆p6		
RNA Variant (20.5 nM)	K _{d(1M)}	Z _{eff}
TARpolyA	5.60 (± 6.45) x 10 ⁻¹	10 (± 1.0)
Psi-2	3.59 (± 1.56) x 10 ⁻⁵	5.4 (± 0.5)
356mer	1.63 (± 1.64) x 10 ⁻³	8.1 (± 1.0)
400mer	1.51 (± 0.49) x 10 ⁻⁵	2.3 (± 0.3)
Psi+	1.34 (± 0.74) x 10 ⁻⁴	4.7 (± 1.1)
228mer	5.15 (± 5.32) x 10 ⁻³	7.6 (± 1.0)
Omega	4.14 (± 3.01) x 10 ⁻⁵	2.7 (± 0.7)

• The negative region present in the HIV 356mer diminishes Psi-like binding. The positive region in addition to the negative region in the HIV 400mer restores Psi-like binding.

• Psi+ interacts similar to Psi-2 suggesting that the positive region does not increase binding specificity by itself.

Native-PAGE Assesses RNA Conformation



Future Work

- Optimize native gel conditions for HIV 400mer and 356mer. Run native gels on all of the experimental constructs to study how RNA conformation changes in the presence and absence of Omega.
- Probe the secondary structure of the HIV 400mer using selective 2'-hydroxyl acylation and primer extension (SHAPE).