Supplemental Material to:

Jeffrey D. Levengood, Michele Tolbert, Mei-Ling Li,
Blanton S. Tolbert

High affinity interaction of hnRNP A1 with conserved RNA structural elements is required for translation and replication of enterovirus 71

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Figure S1. ^{1}H-^{1}H NOESY spectra showing the imino NOEs of (A) $\mathrm{SLII}^{\Delta\mathrm{BL}}$, (B) $\mathrm{SLII}^{\Delta\mathrm{LS}\Delta\mathrm{BL}}$, (C) $\mathrm{SLII}^{\mathrm{GNRA}}$, and (D) $\mathrm{SLII}^{\mathrm{CCC}}$ collected at 298K. Note well-defined NOE cross peaks are observed for the tandem A139:U163/A140:U162 base pairs in $\mathrm{SLII}^{\Delta\mathrm{BL}}$ and for the C147:G154 closing pair in $\mathrm{SLII}^{\mathrm{GNRA}}$. NOE evidence for the formation of the aforementioned base pairs are either missing or weak in spectra collected for wild-type SLII^{2231}.

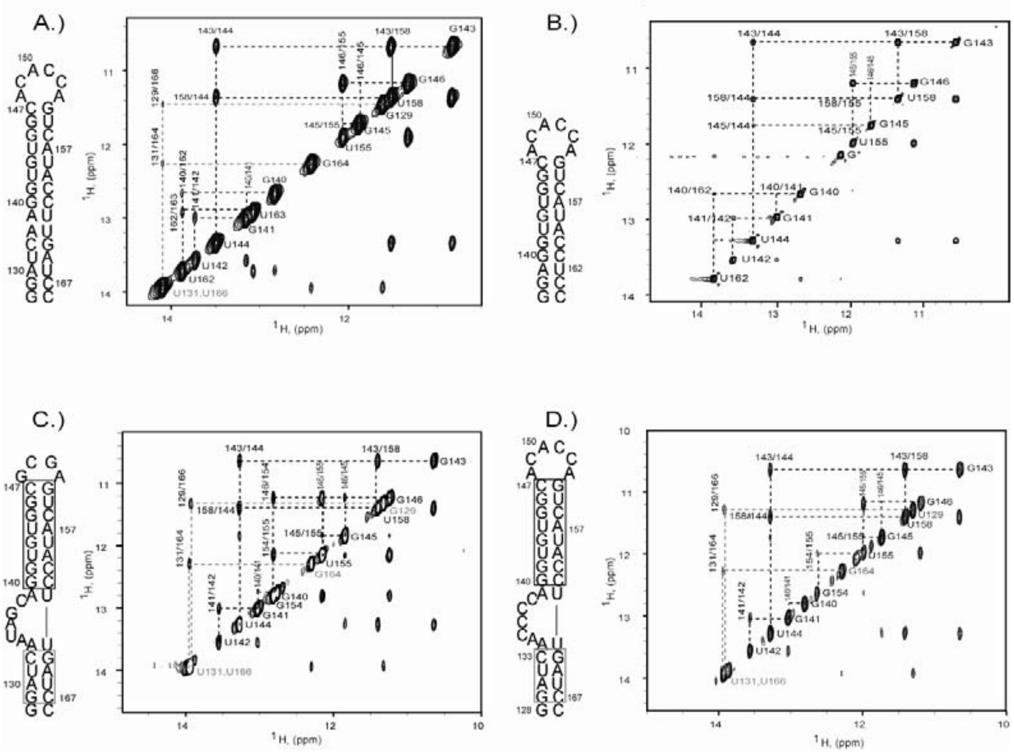


Figure S2. Reverse calorimetric titration of SLII^{2231} into UP1 (298K). The titration was performed under identical solution conditions and injection schedule as reported in methods. Upper panel shows the raw thermogram resulting from titration of 45 µM SLII^{2231} into 2.0 µM UP1. Lower panel shows processed data fit to a one-site binding isotherm along with the converged fitting parameters. Note the upper limit of the K_d (78.1 nM) from this fit is consistent with the average values of K_{d1} and K_{d2} (~89 nM) obtained from the forward titration.

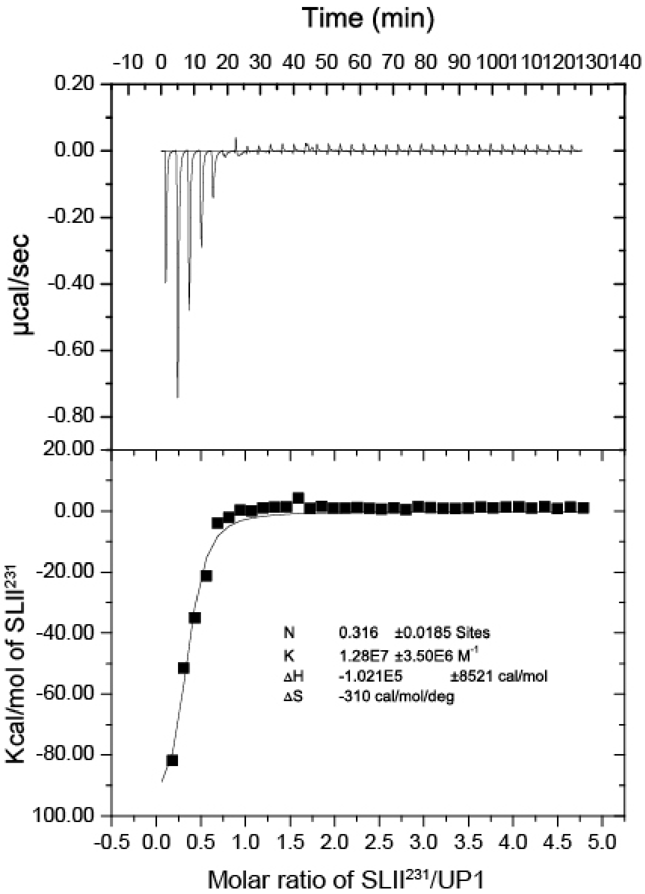
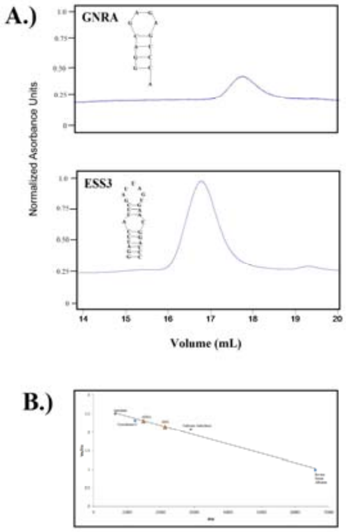


Figure S3. Calibration standards for Superdex 200 10/300 GL size exclusion column. Chromatographic trace of (A) a GNRA tetraloop RNA construct and the HIV ESS3 stem loop. (B) Calibration curve of the 200 10/300 column using Sigma Gel Filtration Molecular Weight Markers (MW-GF-70). Both the GNRA and HIV ESS3 stem loops elute earlier than expected based on their theoretical molecular weights.



GenBank accession codes of EV71 strains used in the alignments.

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