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Supplemental Material to:

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Supplementary material

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Figure S1. Binding of TIA-1 RRM3 to one of the "good RNA targets". *Left.*- Averaged chemical-shifts changes of RRM3 upon addition of GCUCC to a protein:RNA ratio of 1:1.5. *Middle.*- Ribbon mapping of $\Delta\delta_{avg}$. Residues with $0.013 \leq \Delta\delta_{avg} \leq 0.02$ ppm are yellow and those with $\Delta\delta_{avg} > 0.02$ are in orange. Prolines and not assigned residues are in grey whereas those non perturbed residues are colored in blue. *Right.*- TIA-1 RRM3 surface with the same orientation and color code as *Middle*. Note that G273 and T276 residues are colored in red because of their NH amide signals are broadening beyond the detection limit. The white asterisk (*) indicates that W272 corresponds to the N^{ε} nucleus in the indole ring. The structure representations were created with Chimera software[1] using the file generated from chemical shifts assignments of RRM3 domain (BMRB accession number 18829) at the CS23D2.0 web server.[2]

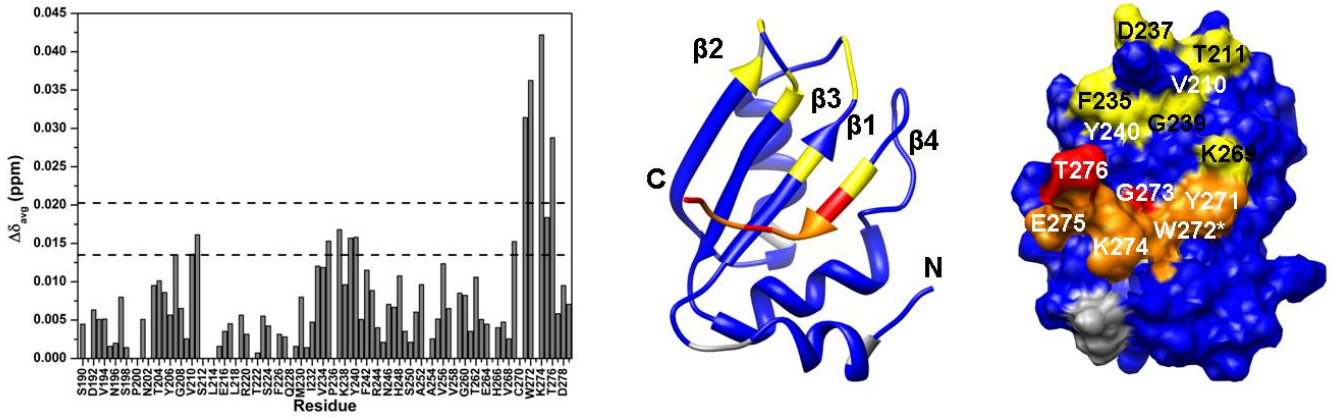
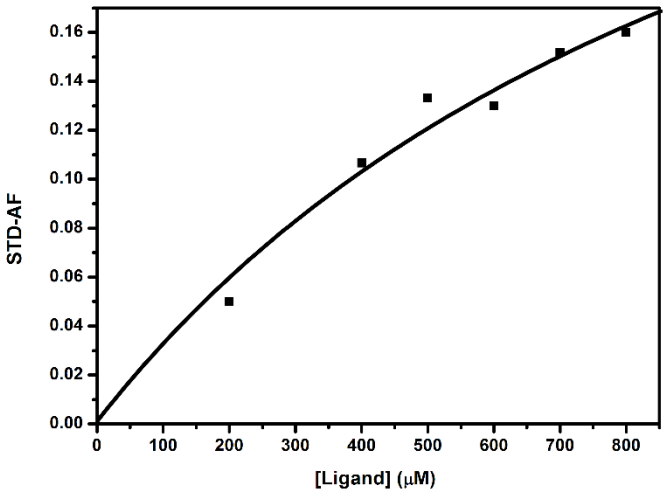


Figure S2. Binding isotherms from STD-AF values during the titration of RRM3 with the ACCCC and GCUCC oligos

ACCCC

$K_D = 1100 \pm 480$ μM



GCUCC

$K_D = 155 \pm 41$ μM

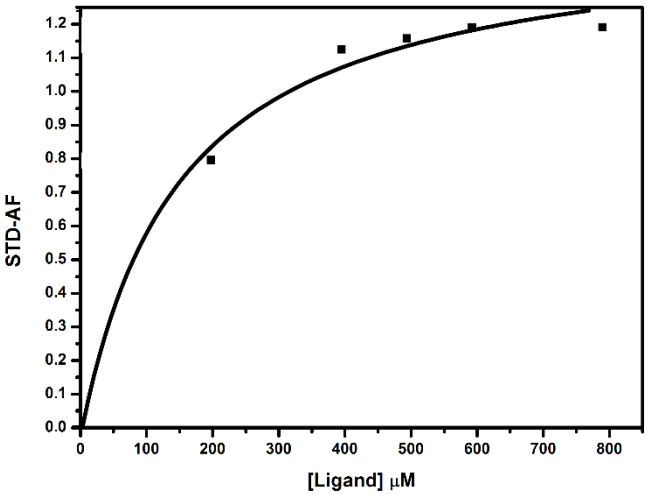
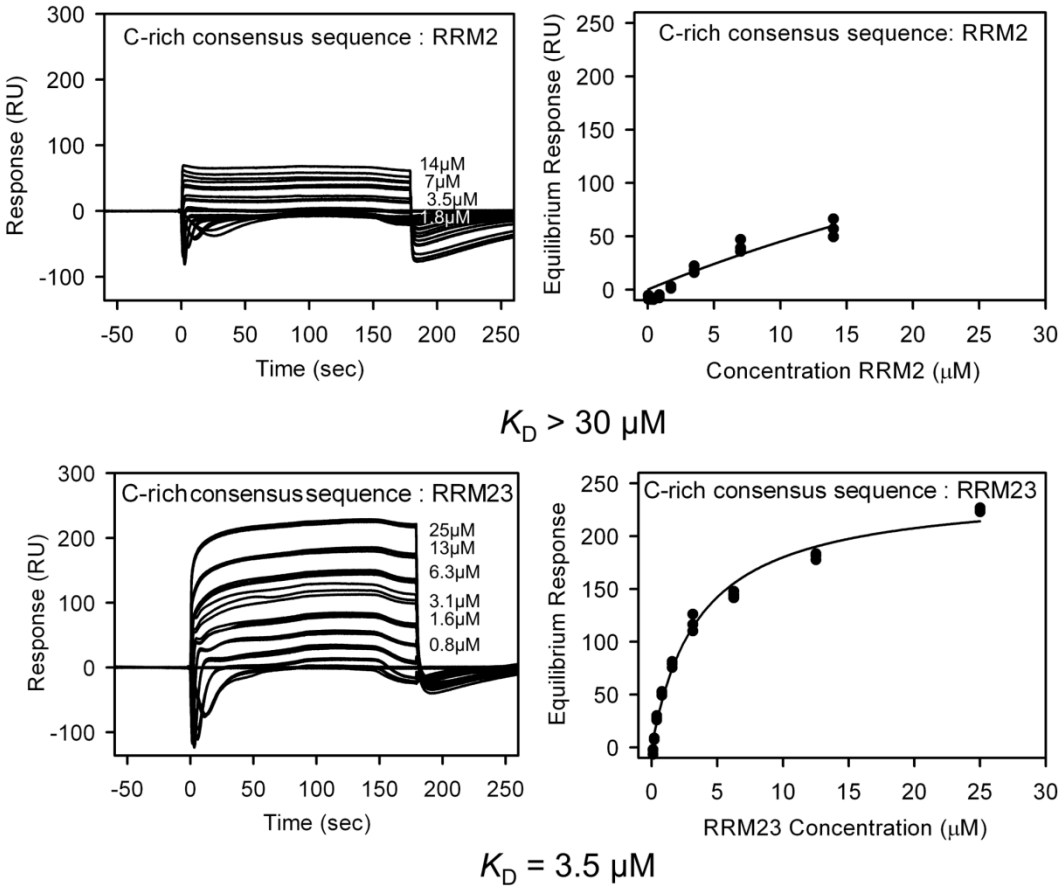


Figure S3. SPR Analysis of the interactions of different TIA-1 constructs with 5´ UUGCCACCUCCUGCUCCUGCCCAGA 3´ RNA. The binding of TIA-1 RRM2 (top) and TIA-1 RRM23 (bottom) to the RNA sequence is shown. RNA, biotinylated at the 5'-end, were captured on SA coated sensor chips in parallel. Each protein was injected across the four flow cells (blank cell and a cell for the RNA sequence) at a range of concentrations and in triplicate. Injections were performed for 180 seconds (association phase), followed by a 360-second flow of running buffer to assess dissociation. The data were used to construct binding curves for K_D determination or approximation (where steady state binding was not achieved).



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