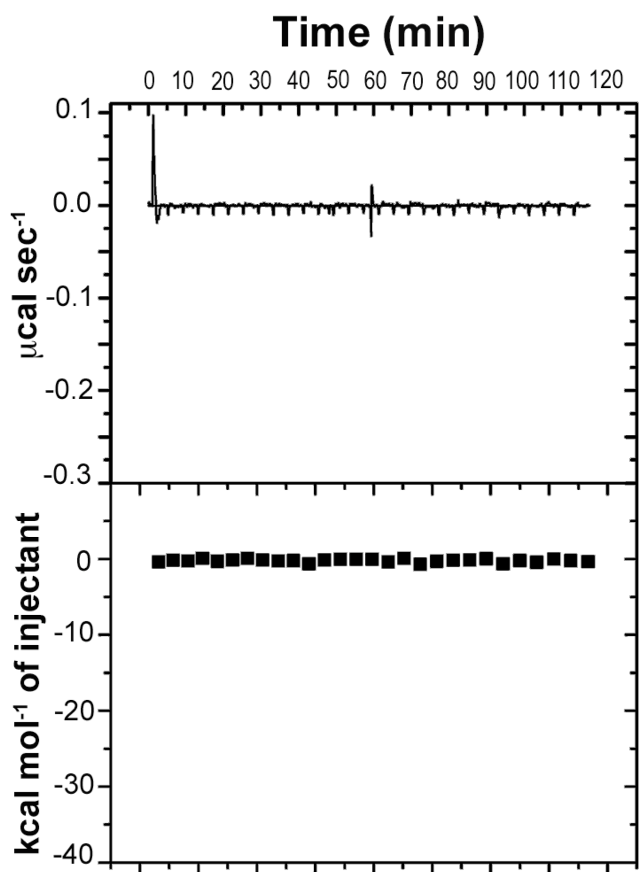
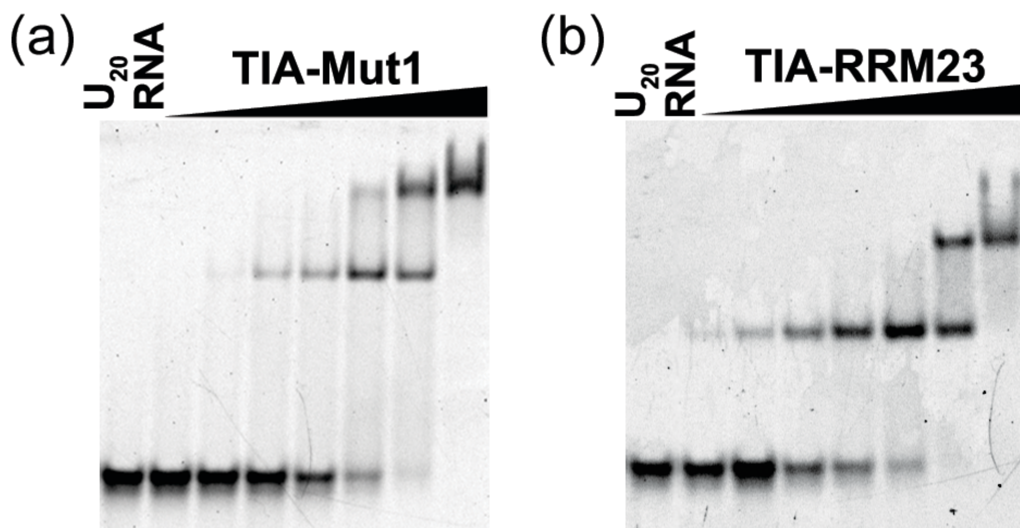
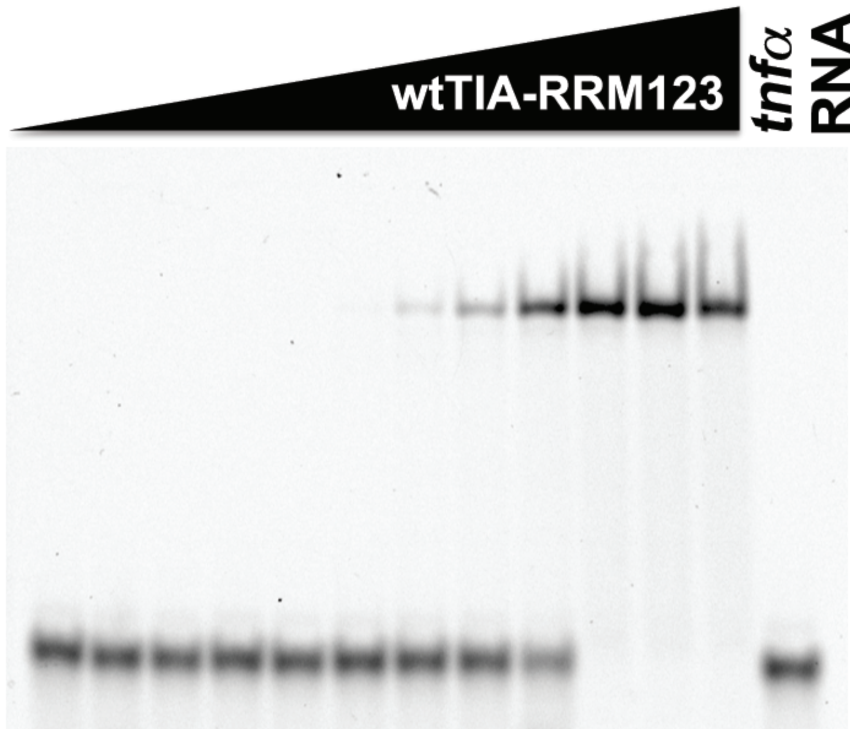
Supplementary Figure S1. Titration of wtTIA-RRM123 (70 μM) into buffer.



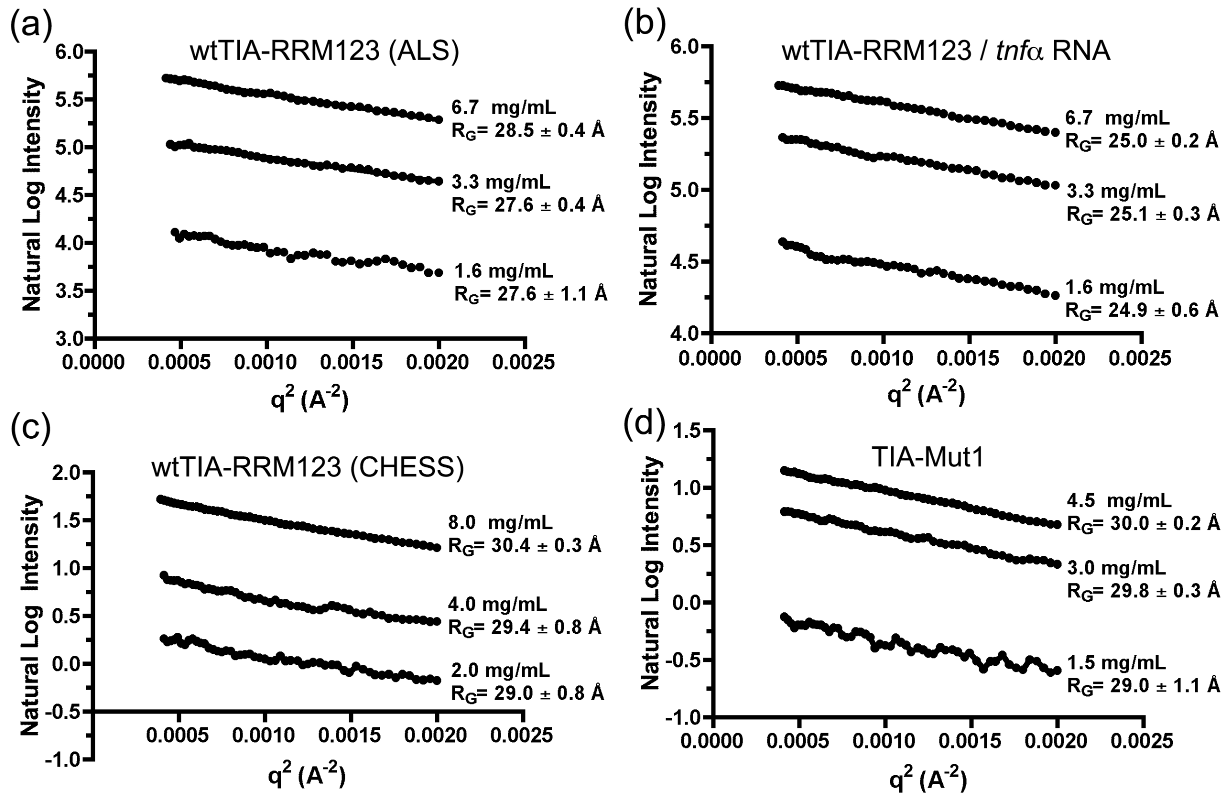
Supplementary Figure S2. Qualitative electrophoretic mobility shift assays confirm formation of two complexes during titration of (a) TIA-Mut1 or (b) TIA-RRM23 into fluorescein-labeled U_{20} RNA (2.5 μM). The final protein concentrations were 0.3, 0.5, 0.9, 1.4, 2.2, 3.5 and 5.6 μM for TIA-Mut1, or 0.3, 0.5, 0.8, 1.3, 2.0, 3.3, and 5.3 μM for TIA-RRM23.



Supplementary Figure S3. Qualitative electrophoretic mobility shift assay demonstrating a single complex between wtTIA-RRM123 and the *tnfα* RNA oligonucleotide (5'-UUAUUUAUUUA-3') used for SAXS data collection. The fluorescein-labeled RNA (2.5 μM final concentration) was detected by emission at 520 nm. The final protein concentrations were 0.002, 0.005, 0.013, 0.03, 0.07, 0.16, 0.37, 0.86, 2.0, 4.7, 10.9, and 25.3 μM.



Supplementary Figure S4. Guinier plots of (a) wtTIA-RRM123 (Advanced Light Source), (b) wtTIA-RRM123 / *tnf-α* RNA, (c) wtTIA-RRM123 (Cornell High Energy Synchrotron Source), and (c) TIA-Mut1 are linear with R_G values among the concentration series that match within measurement error.



Supplementary Figure S5. Kratky plots (a) or pairwise distance distribution functions (b) of wtTIA-RRM123 SAXS data collected either at the Advanced Light Source (ALS) or Cornell High Energy Synchrotron Source (CHESS).