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Supplemental Information

Interpreting the Dynamics of Binding Interactions of snRNA and U1A Using a Coarse-Grained Model

Zhongjie Han, Qi Shao, Weikang Gong, Shihao Wang, Jiguo Su, Chunhua Li, and Yang Zhang

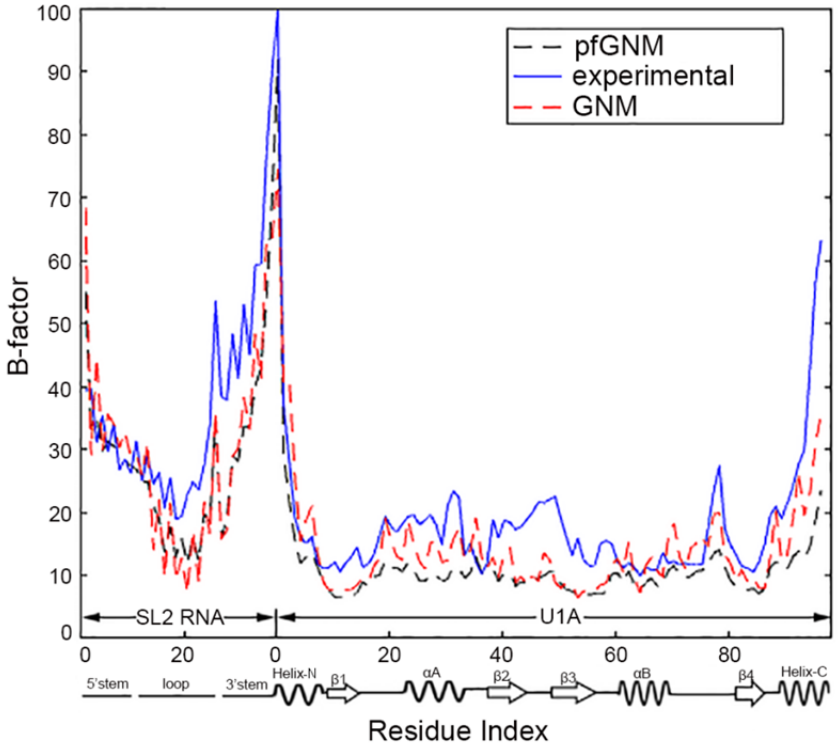

FIGURE S1. Comparison between the experimental (blue line) and computed B-factors of P, O4' and C_α atoms of U1A-RNA complex. Red and black lines represent the results obtained from the conventional GNM and pfGNM models, respectively.

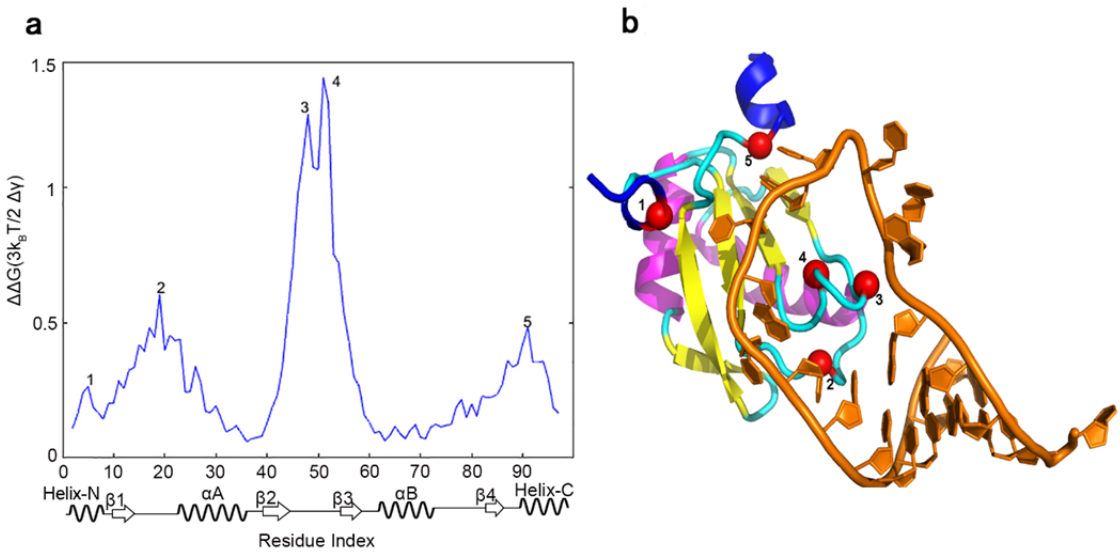

FIGURE S2. Identified functionally key residue clusters with pfGNM-based thermodynamic method. (a) Binding free energy changes ΔΔG in response to residual mutations. The clusters of key residues with relatively high ΔΔG values are marked by the numbers 1-5. (b) Locations of the central residues for the 5 clusters of key residues.

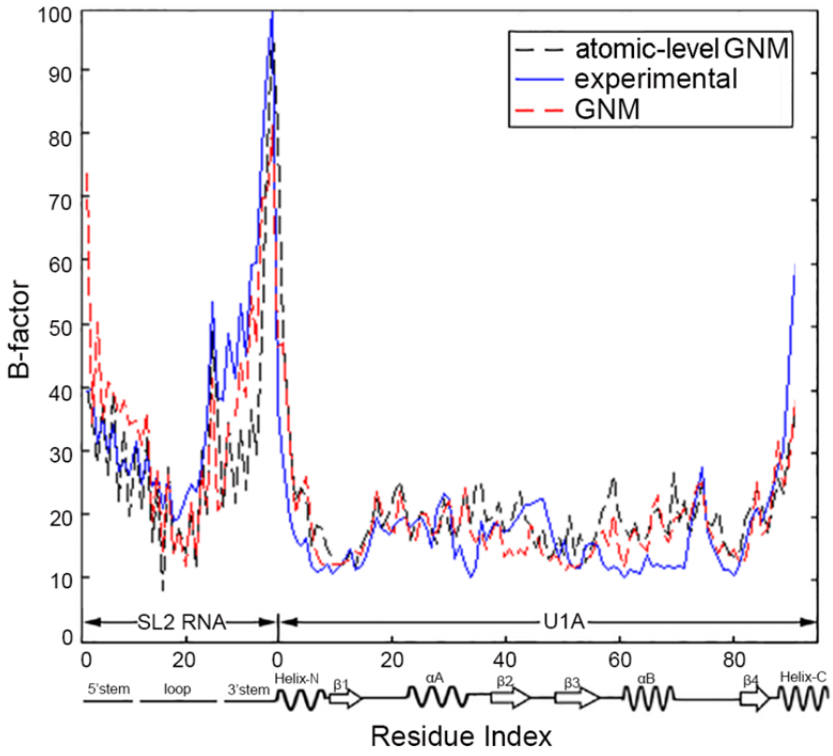

FIGURE S3. Comparison between the experimental (blue line) and computed B-factors of P, O4' and C_α atoms of U1A-RNA complex. Red and black lines represent the results obtained from the conventional residue-level GNM and atomic-level GNM models, respectively.

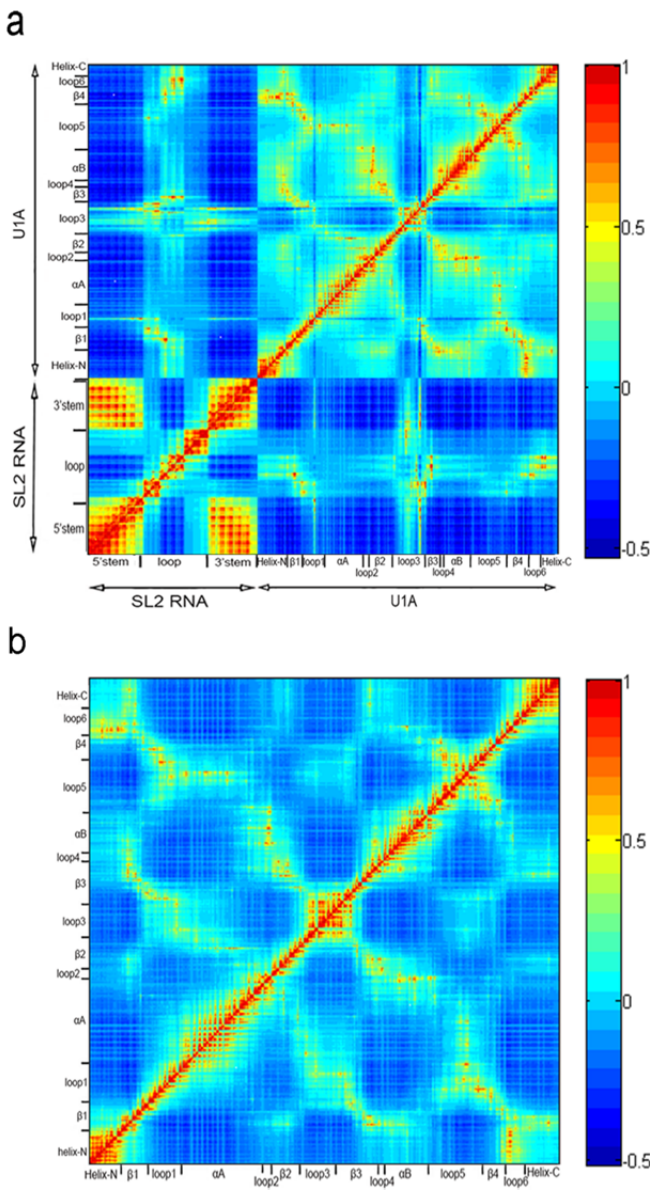

FIGURE S4. Fluctuation cross-correlation calculated by the atomic-level GNM using the dominant ninety-three low frequency modes contributing 50% and 52% to atomic fluctuations for U1A-RNA complex (a) and protein U1A (b). As shown in the color bar, the blue regions in the figure indicate negative correlation and the red regions present positive correlation.

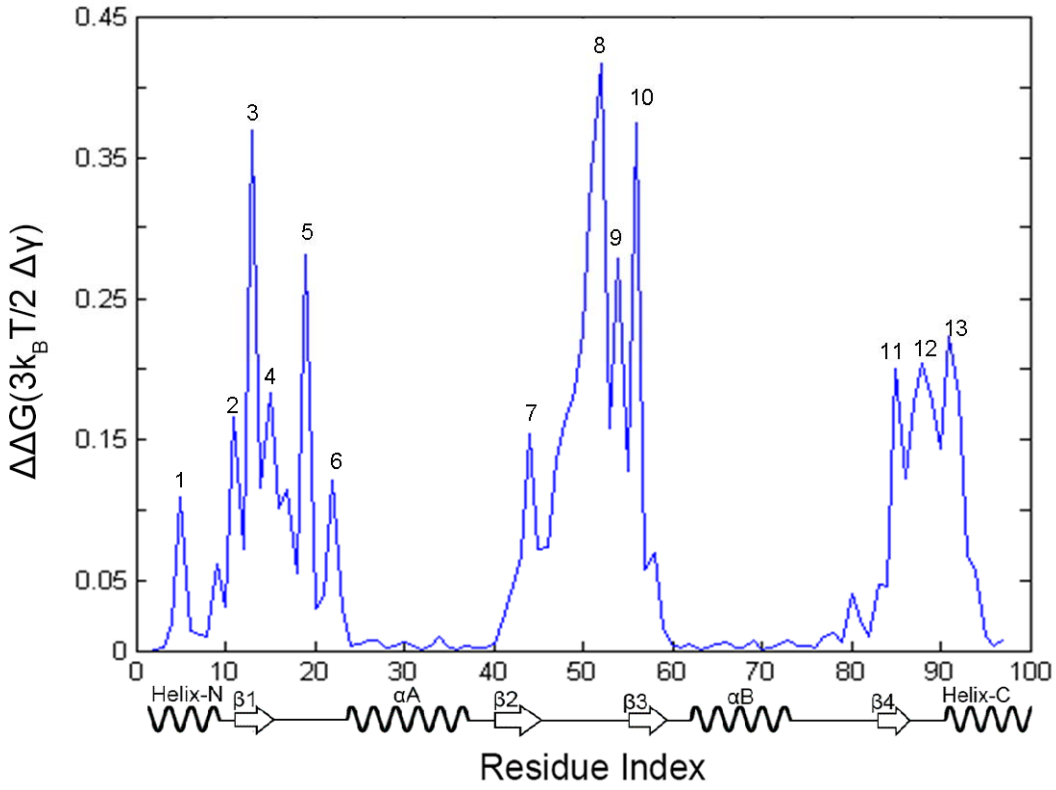

FIGURE S5. Identified functionally key residue clusters with the atomic-level GNM-based thermodynamic method. The clusters of key residues with relatively high ΔΔG values are marked by the numbers 1-13.

Normal mode analysis

Normal mode analysis is performed on protein U1A with and without RNA binding respectively. The program Gromacs (version 4.5.4, double precision) with the Amber03 force field is used. The calculation of the vibrational spectrum is preceded by an energy minimization. A shift function with cutoff at 10 Å is used for the electrostatics and van der Waals interactions. Initial optimization is done with a steepest descent algorithm and finally using low-memory Broyden-Fletcher-Goldfarb Shanno (L-BFGS) quasi-Newtonian optimization to a maximal absolute gradient of 1.78×10^{-9} kJ/(mol·nm) and 9.94×10^{-10} kJ/(mol·nm) for protein U1A with and without RNA binding respectively. After energy minimization, the root-mean-square deviations of molecule backbone with respect to the initial structures are 0.67 and 0.90 Å, respectively. Subsequently the Hessian matrix is calculated, which is the matrix of second derivatives of the potential energy with respect to the mass-weighted atomic coordinates. Diagonalization of this matrix yields the eigenvalues λ and eigenvectors u_k (the normal modes), which include the six spurious translations and rotations at zero energy.

The mean-square fluctuation of the ith atom, ΔR_i, can be calculated from the eigenvectors and eigenvalues:

$$\left\langle \Delta R_{\mathrm{i}} \cdot \Delta R_{\mathrm{i}} \right\rangle = \frac{k_B T}{m_i} \sum_{k=7}^{3N-6} \lambda_{\mathrm{k}}^{-1} \left[u_{\mathrm{k}} \right]_i^2$$

The fluctuation cross-correlation between the ith and jth atoms is given by:

$$\left\langle \Delta R_{\mathrm{i}} \cdot \Delta R_{\mathrm{j}} \right\rangle = \frac{k_B T}{\sqrt{m_i}\sqrt{m_j}} \sum_{k=7}^{3N-6} \lambda_k^{-1} \left[u_k \right]_i \left[u_k \right]_j$$

where m_i and m_j are the masses of the ith and jth atoms.

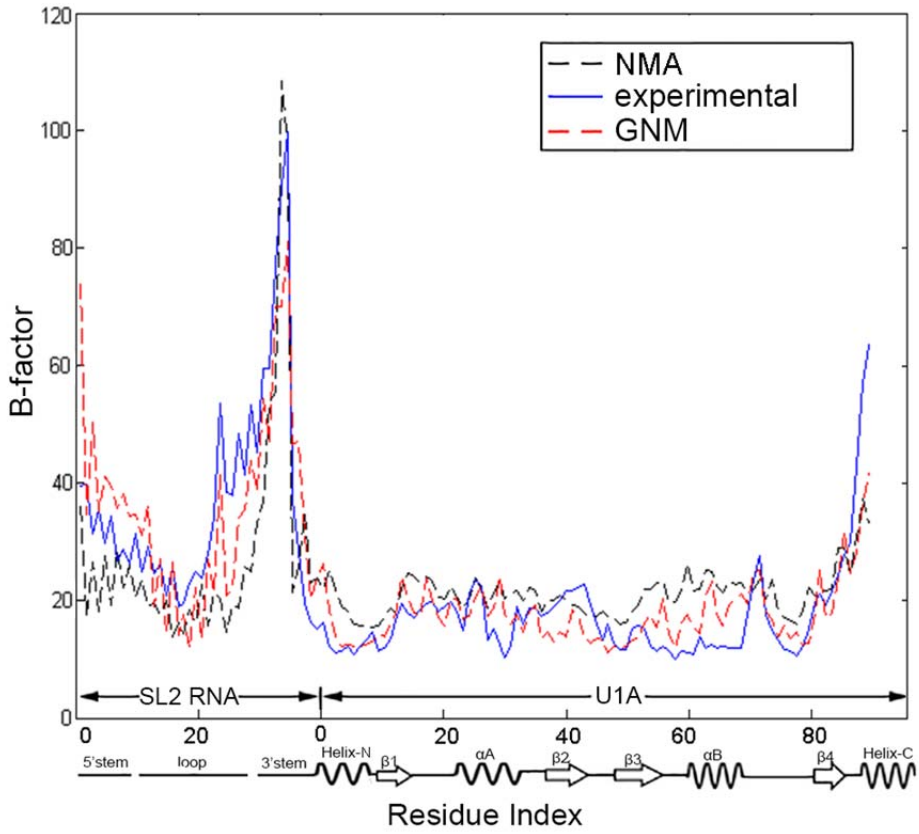

FIGURE S6. Comparison between the experimental (blue line) and computed B-factors of P, O4' and C_α atoms of U1A-RNA complex. Red and black lines represent the results obtained from the conventional GNM and NMA models, respectively.

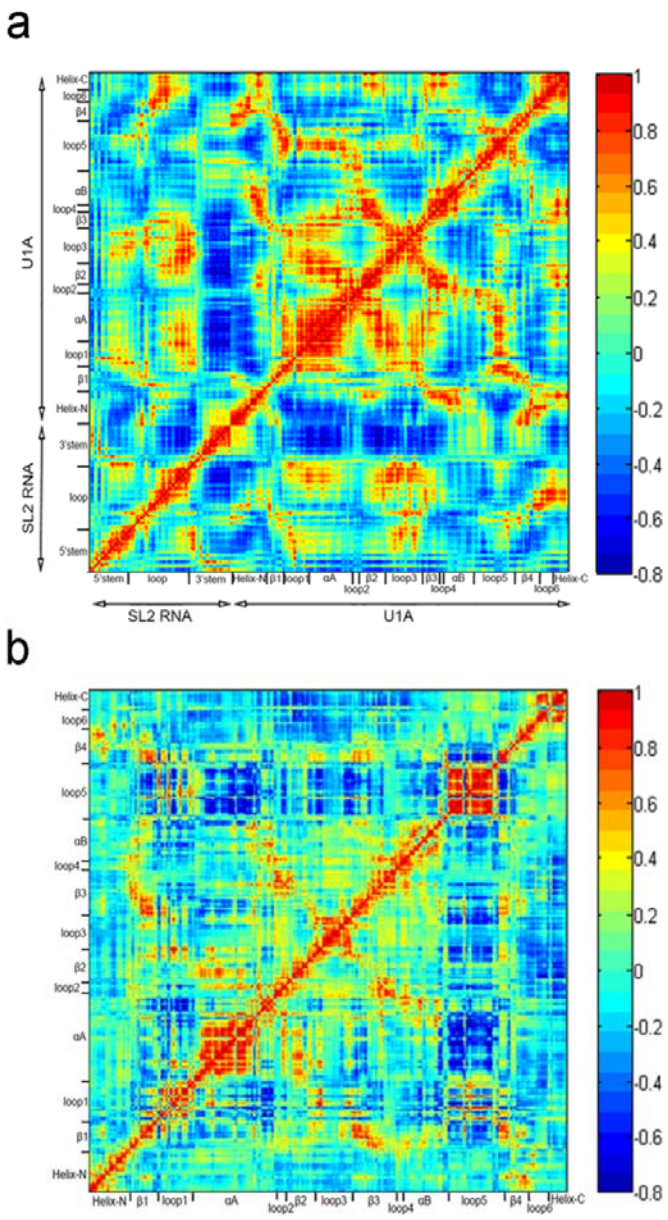

FIGURE S7. Fluctuation cross-correlation calculated by NMA using the dominant fifteen low frequency modes contributing 71% and 53% to atomic fluctuations for U1A-RNA complex (a) and protein U1A (b). As shown in the color bar, the blue regions in the figure indicate negative correlation and the red regions present positive correlation.

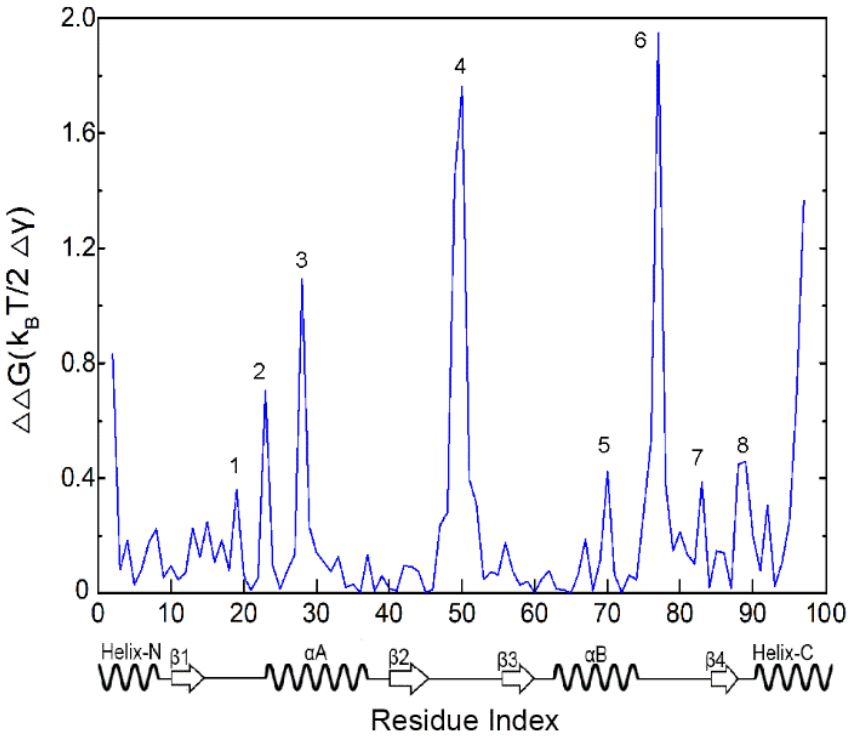

FIGURE S8. Identified functionally key residue clusters with the NMA-based thermodynamic method. The clusters of key residues with relatively high ΔΔG values are marked by the numbers 1-8.