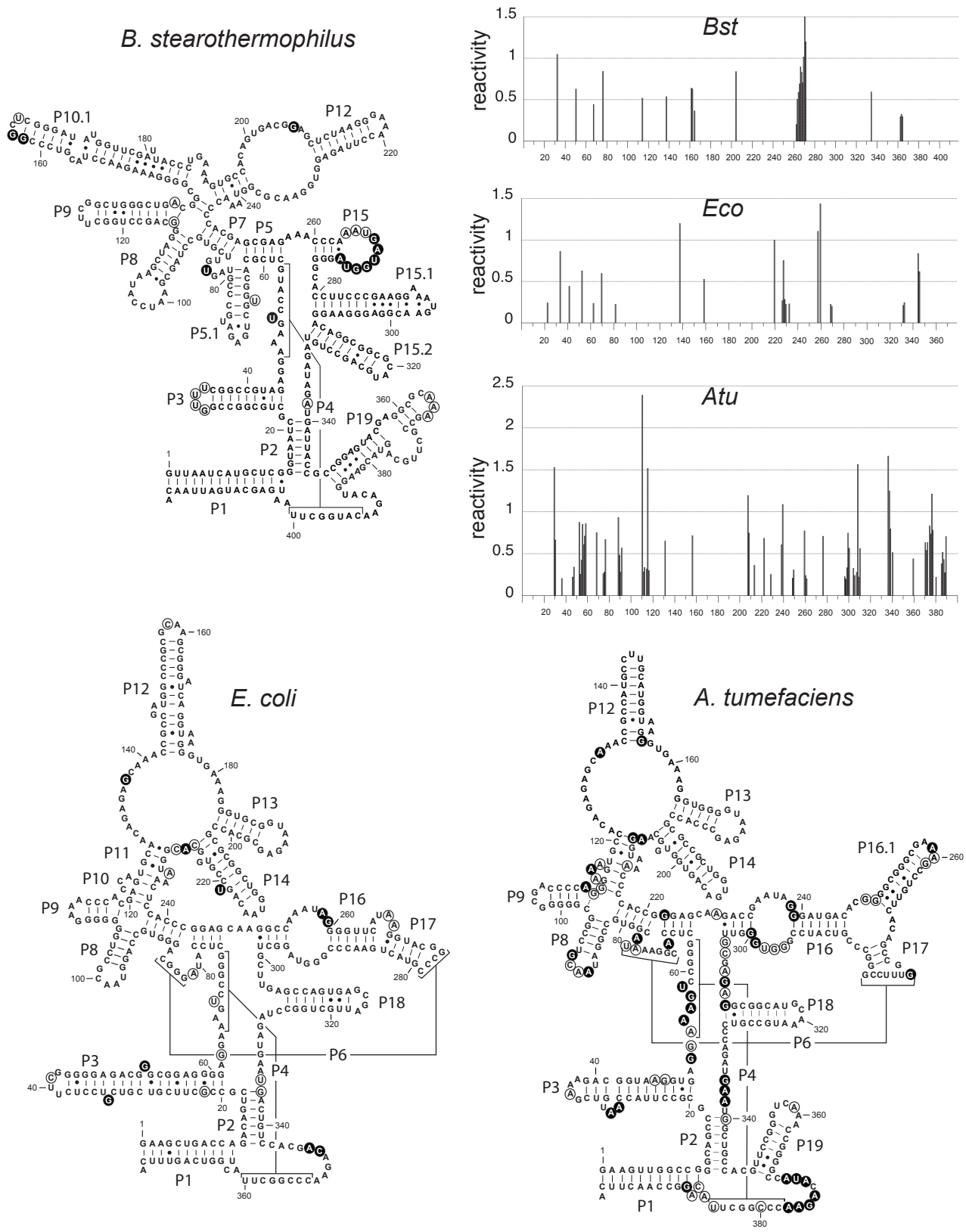
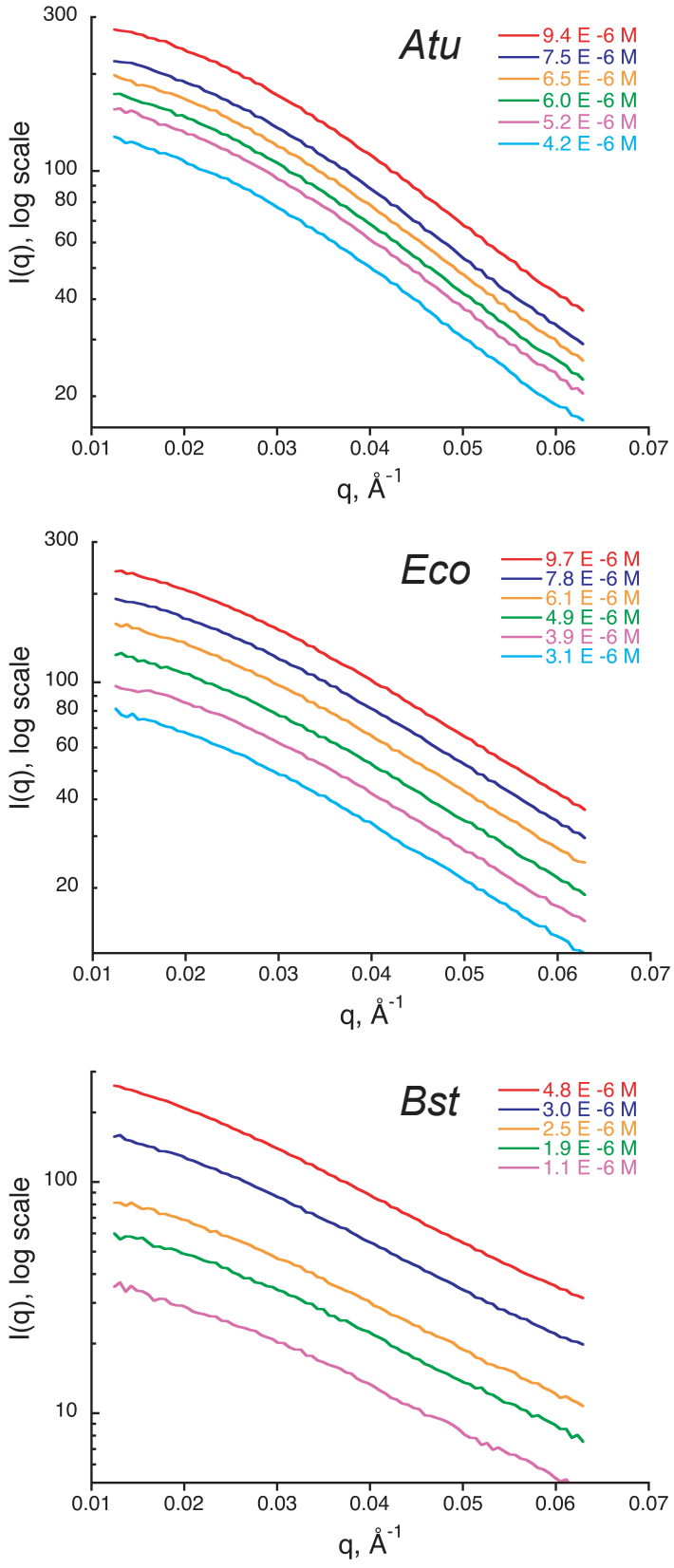
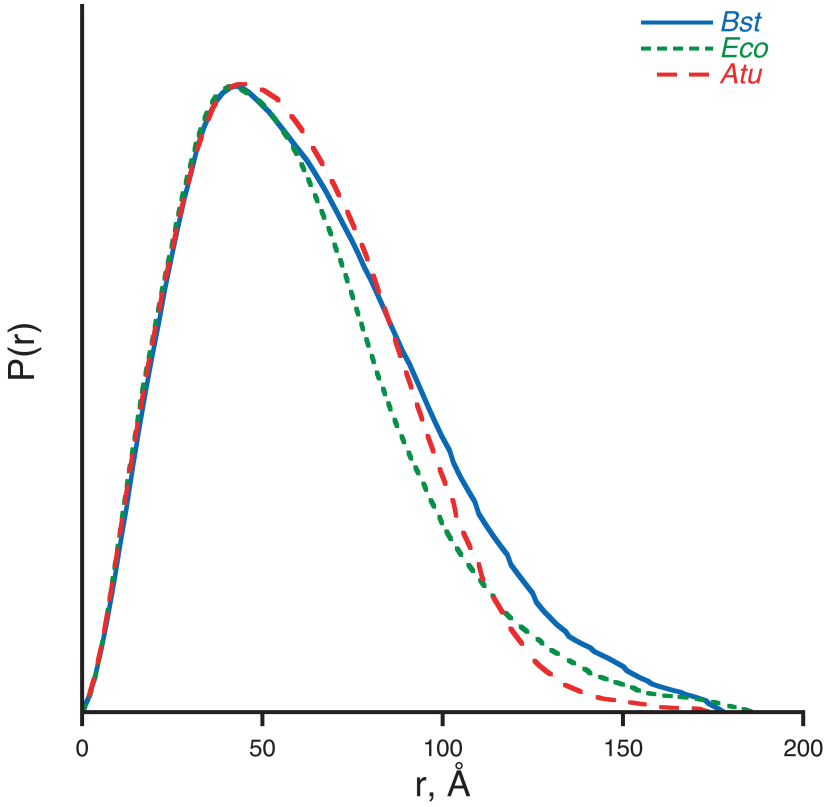


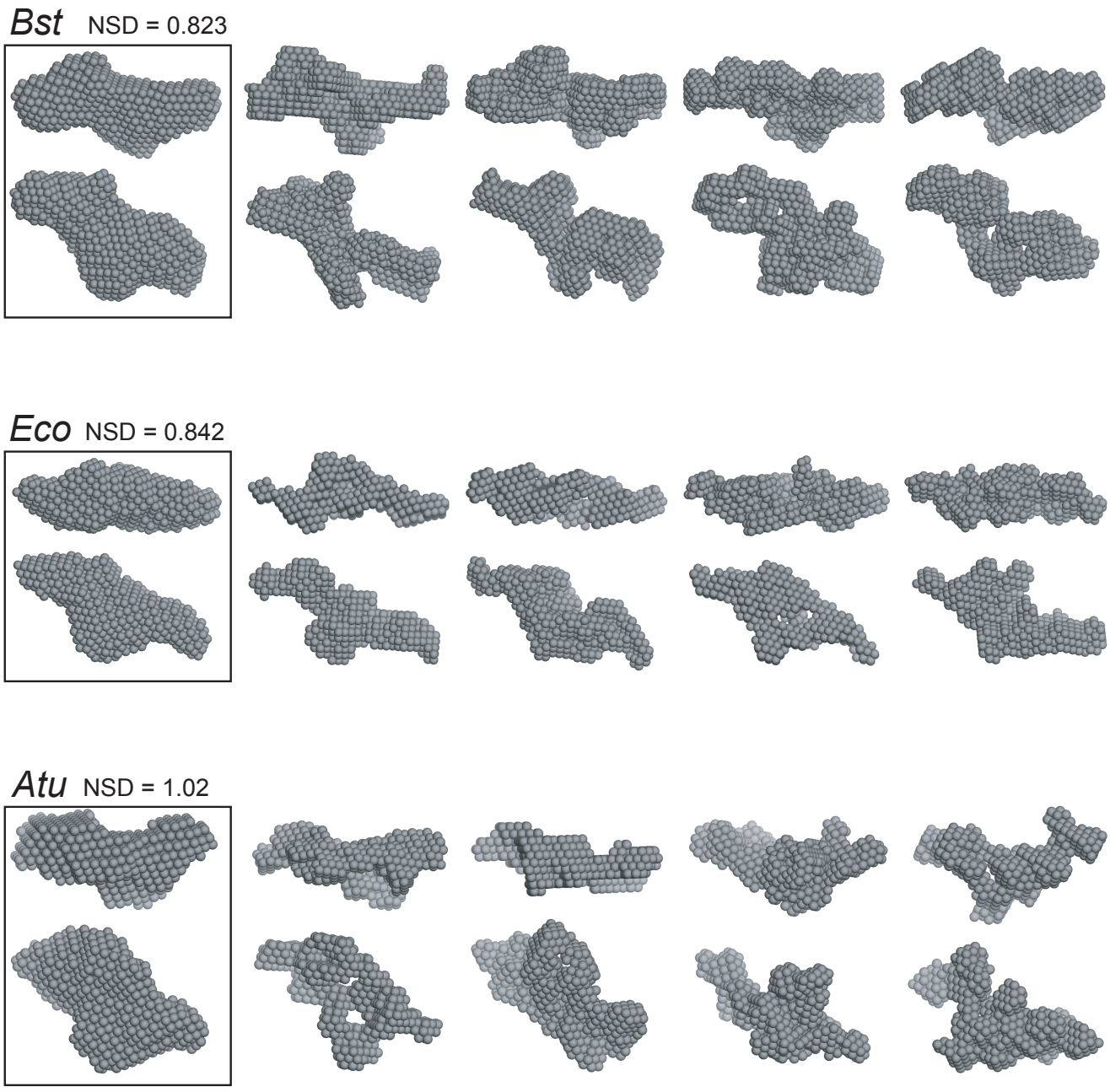
SUPPLEMENTARY FIGURE 1. SHAPE analysis of the quality of RNA samples prepared by HS native method. SHAPE analysis of RNA samples was performed as described in Materials and Methods; reactivity to NMIA was calculated as described by Mortimer and Weeks (2009) and plotted versus nucleotide number. Nucleotides with reactivity below 0.2 were omitted for clarity. Structural distribution of the reactive nucleotides is analyzed in the context of secondary structures, with open circles labeling nucleotides with reactivity between 0.2 and 0.5 and closed circles representing reactivity above 0.5.



SUPPLEMENTARY FIGURE 2. Concentration dependence of the scattered intensity for each RNA sample prepared by HS native method.



SUPPLEMENTARY FIGURE 3. P(r) distributions calculated for each RNA from experimental SAXS data.



SUPPLEMENTARY FIGURE 4. *Ab initio* modeling of scattering envelopes. For each RNA, ten independent *ab initio* reconstructions of scattering envelope were generated with DAMMIF and superimposed with DAMSEL and DAMSUP with NSD values as indicated. Four individual reconstructions are shown for each RNA in two different orientations. All 10 superimposed models in each case were averaged and filtered with DAMAVER and DAMFILT to generate the reconstructions shown in the boxes on the left.