Mining for recurrent long-range interactions in RNA structures reveals embedded hierarchies in network families

Supplementary Material

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1 Overview of the method

Figure S1: Overview of the method. (1) Extraction of the secondary structures from the crystallized tertiary structures. (2) All interaction graphs are extracted from the derived secondary structures. (3) The maximal interaction networks are extracted. (4) The recurrent interaction networks are clustered and gathered in a fully organized and searchable website.
Figure S2: RMSD between the elements of the A-minor Type I/II RIN. Each plot is normalized to have an area of 1. The blue parts only consists of the elements that have a GNRA stem loop, the green part of all the others. The orange position is the nucleotide involved in a single cSS long-range interaction as shown in Fig. 6a.
3 Interaction Network

Figure S3: Figure2 bottom right in full page. The details of an interaction network.
4 The trans-Watson-Crick/Hoogsteen mesh

Figure S4: A major cluster of the trans-Watson-Crick-Hoogsteen mesh is based on a triple base pair between conserved residues in the core of tRNA structure.