Abundance of pseudoknots in the RNA world[1] DANIEL AAL-BERTS, EVAN MILLER, Williams College — The pseudoknot fold is often seen in auto-catalytic RNA and in viruses. A recent polymer physics model and statistical-mechanical theory predicts relative probabilities of different pseudoknot folds consonant with a database of known folds. Now we extend that theory for a preliminary estimate of the abundance of pseudoknot folds in RNA sequences, finding approximately 1 per 40,000 nucleotides. This theoretical probability density compares favorably to what we infer from structure databases and has implications for genome organization, RNA folding algorithms, and the RNA World.

Daniel Aalberts
Williams College

Date submitted: 12 Jan 2006   Electronic form version 1.4