This chart shows the prediction accuracy for comparative, canonical base-pairs of a given contact distance for 23S rRNA grouped by phylogeny. RNA Contact Distance is defined as the number of nucleotides intervening between the 5' and 3' halves of a base-pair. Folding parameters for Mfold 3.1 were window size (W)=1, max suboptimals (MAX)=750, and percent suboptimality (P)=5%.