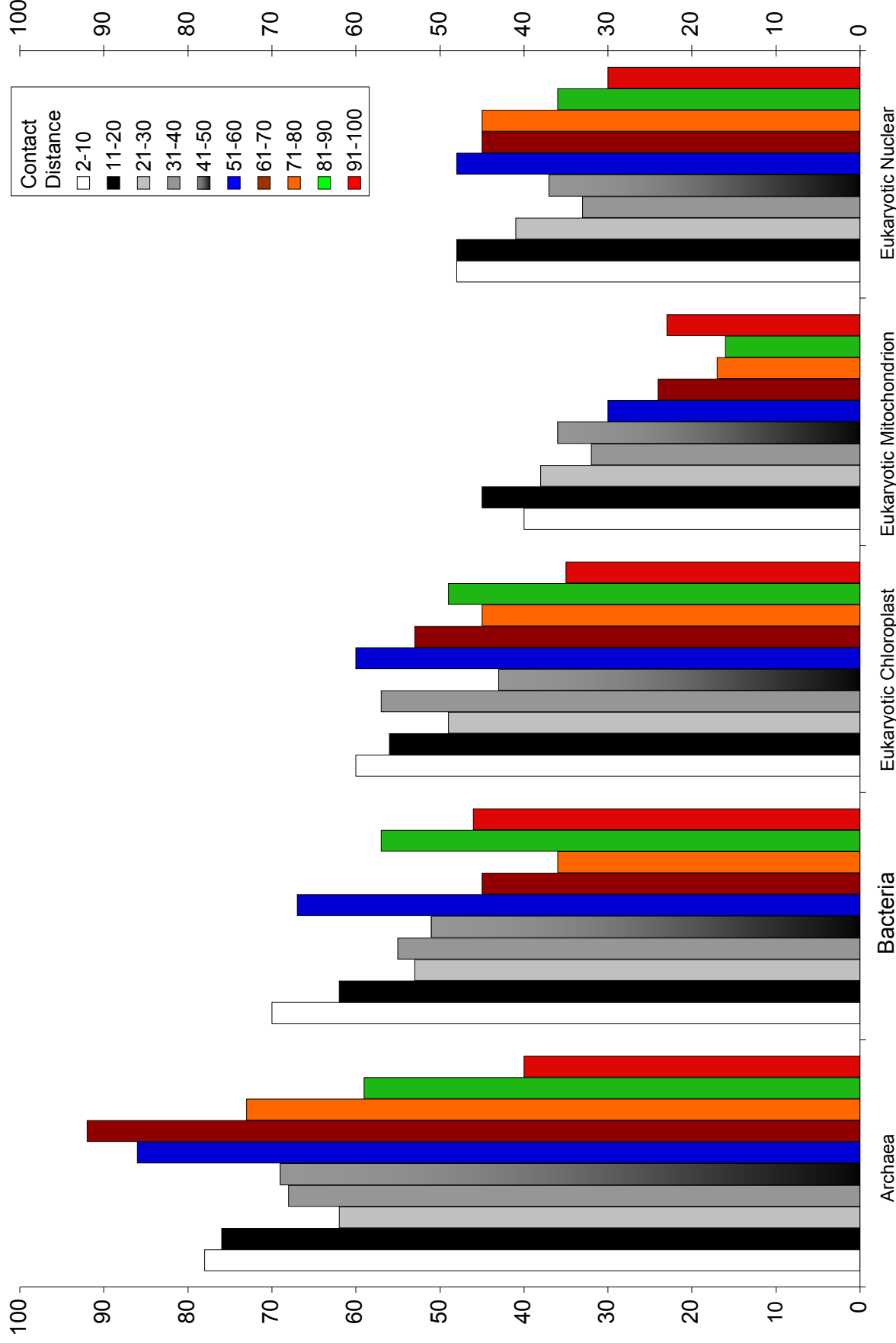


% of Comparative, Canonical Base-pairs with a Given Contact Distance Predicted Correctly

Accuracy of Base-pair Prediction by MFold w/EFN2 as a Function of RNA Contact Distance and Phylogeny for 16S rRNA



This chart shows the prediction accuracy for comparative, canonical base-pairs with a contact distance less than 100 for 16S rRNAs, 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 suboptimal (MAX)=750, percent suboptimality (P)=5%, and efn2 re-evaluation and re-ordering of the predicted folds.

% of Comparative, Canonical Base-pairs with a Given Contact Distance Predicted Correctly