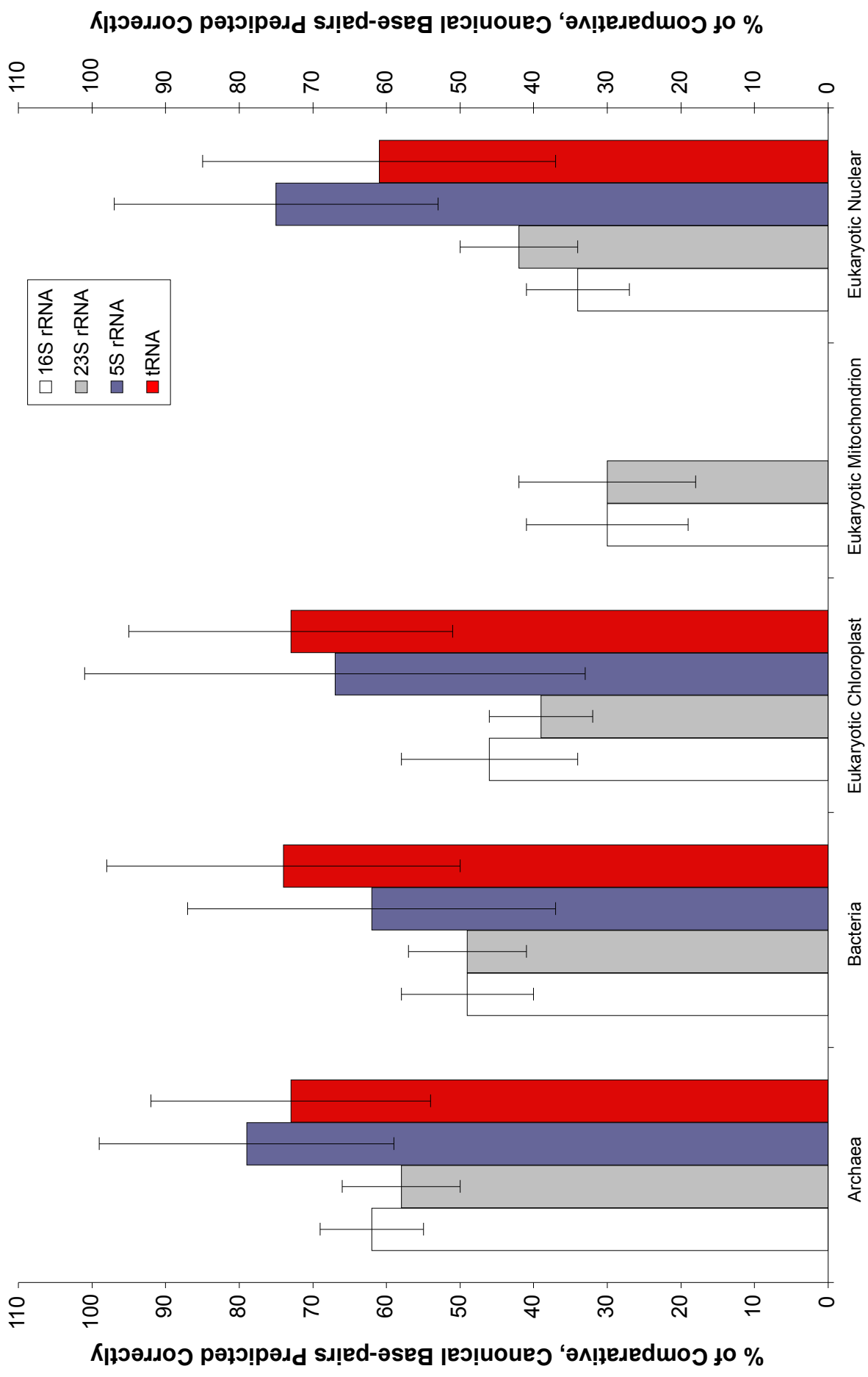


Accuracy of MFold w/EFN2 for RNA Secondary Structure Prediction



Accuracy of MFold 3.1 grouped by Phylogeny and RNA Type. Black bars represent the standard deviation of mean average accuracy. 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.