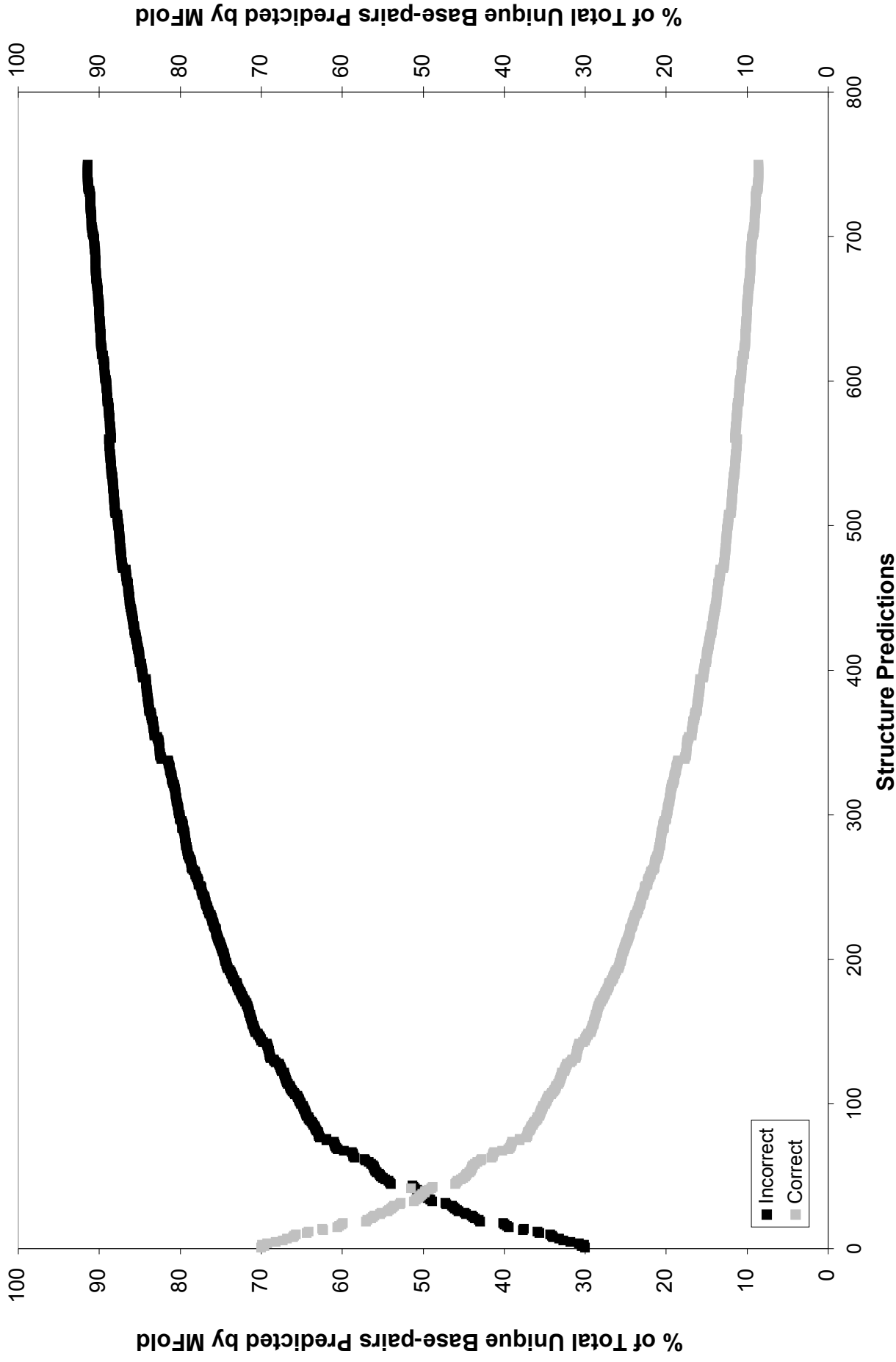


Cumulative Unique Correctly and Incorrectly Predicted Base-Pairs for the Suboptimal Population of 16S rRNA *H. Volcanii* with Mfold 3.1 and EFN2



The cumulative percentage of unique base-pairs from the suboptimal population of 750 structure predictions for the 16S rRNA *H. volcanii* is observed. All base-pairs in the first (i.e optimal) structure prediction are considered unique. For subsequent structure predictions, the number of additional unique base-pairs observed is added to the running total and the cumulative percentage correct and incorrect is determined. Folding parameters for Mfold 3.1 were window size (W)=1, max suboptimals (MAX)=750, percent suboptimality (P)=5% and efn2 re-evaluation and re-ordering of predicted folds.