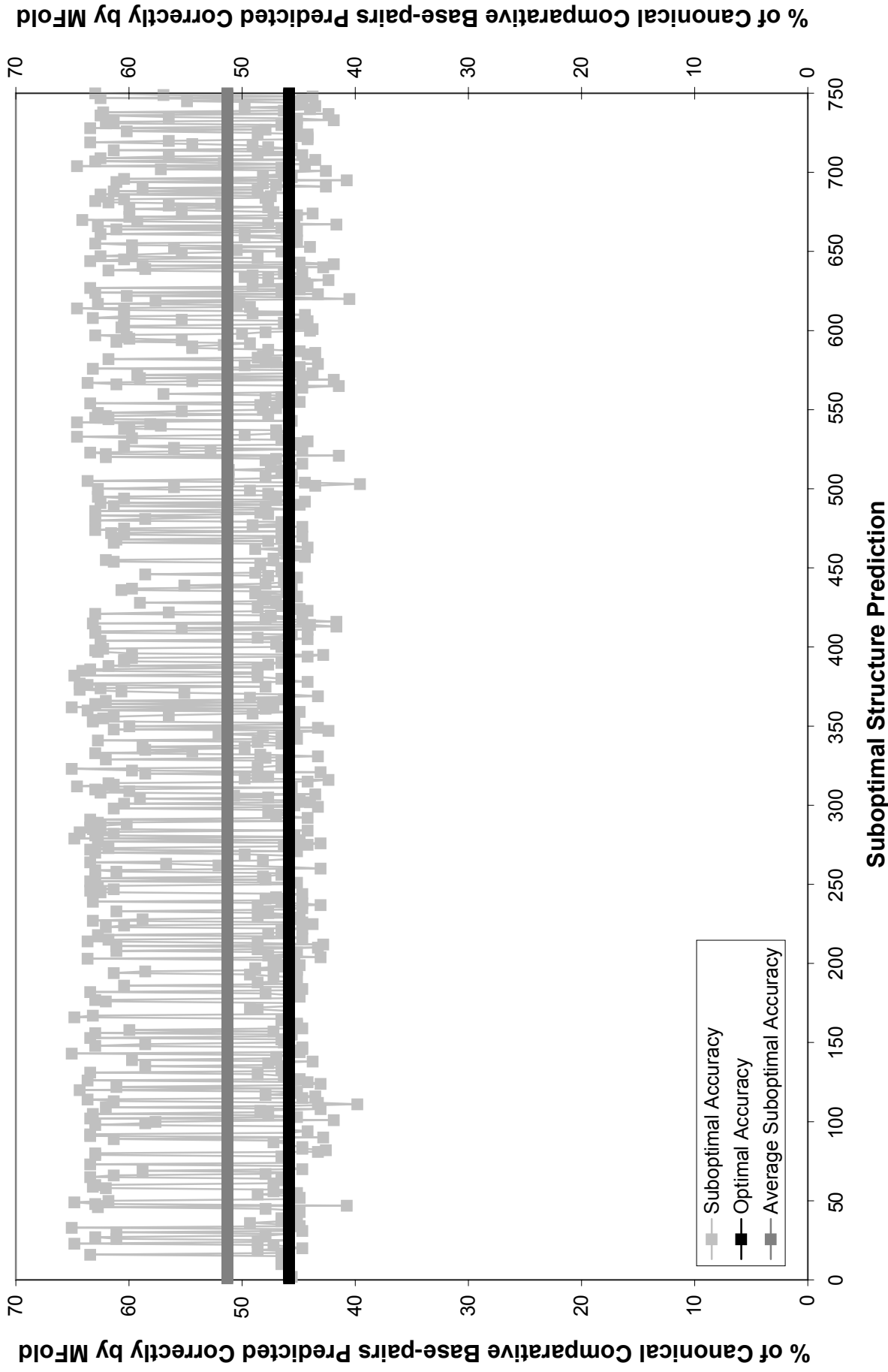


Accuracy of Individual Structure Predictions within the Suboptimal Population of the 16S rRNA *Methanospirillum Hungatei* with Mfold 3.1



The accuracy of each structure prediction within the population of 750 structure predictions for the 16S rRNA *Methanospirillum Hungatei* is observed. The solid black line represents the accuracy of the optimum or minimum free energy structure prediction. The dark gray line represents the average accuracy for a structure prediction within the suboptimal population. Suboptimal structure predictions are ordered by increasing free energy (suboptimal 50 has a lower free energy than suboptimal 51). Folding parameters for Mfold 3.1 were window size (W)=1, max suboptimals (MAX)=750, and percent suboptimality (P)=5%.