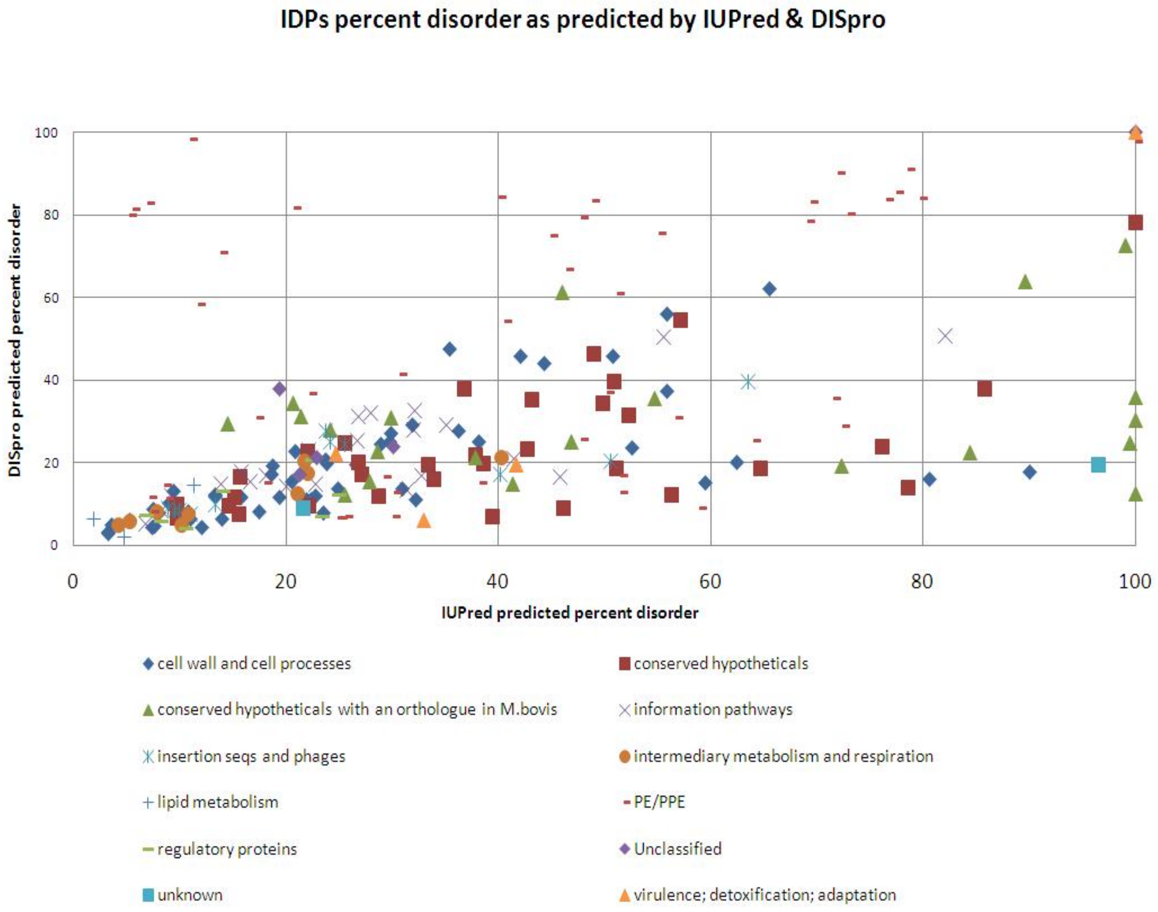

Fig. S1. Scatter plot depicting the percent of disorder predicted in a protein by both the algorithms – IUPred on the *x*-axis and DISpro on the *y*-axis. The data points are further classified on the basis of functional classes.

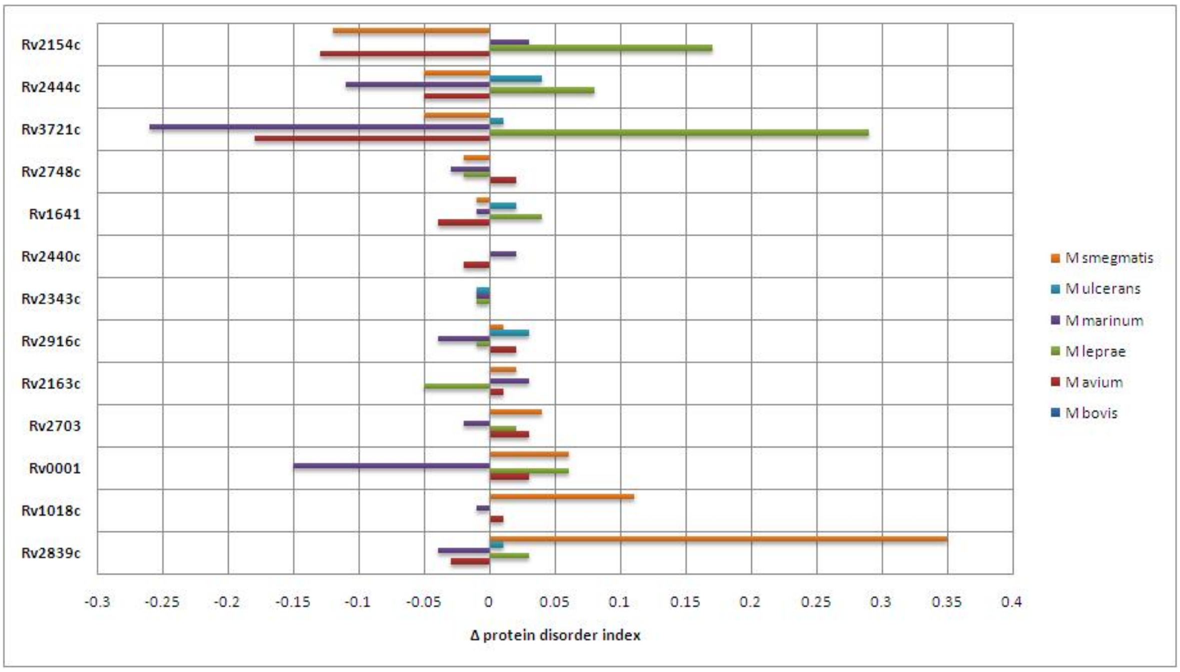

Fig. S2. Extent of sequence conservation of IDRs across six other mycobacterial species. The *x*-axis depicts the difference in the protein disorder index between *M. tuberculosis* and other related species. The thirteen potential drug targets are shown on the *y*-axis.