



Supplementary Figure S9. Distribution of 424 missense mutations that map to a 3D structure into different classes with the two FoldX thresholds separately represented. The results of FoldX predictions are shown for 99% confidence predictions (2 STDEV =1.6 kcal/mol, and for 95% confidence predictions (1 STDEV = 0.8 kcal/mol). The different groups (1a_domain, 1b_actSite, 2_inhibitoryProtein, and 3_folding) follow the classification as shown in main figure 3. The label '99' and '95' indicate the different confidence thresholds of FoldX energies.