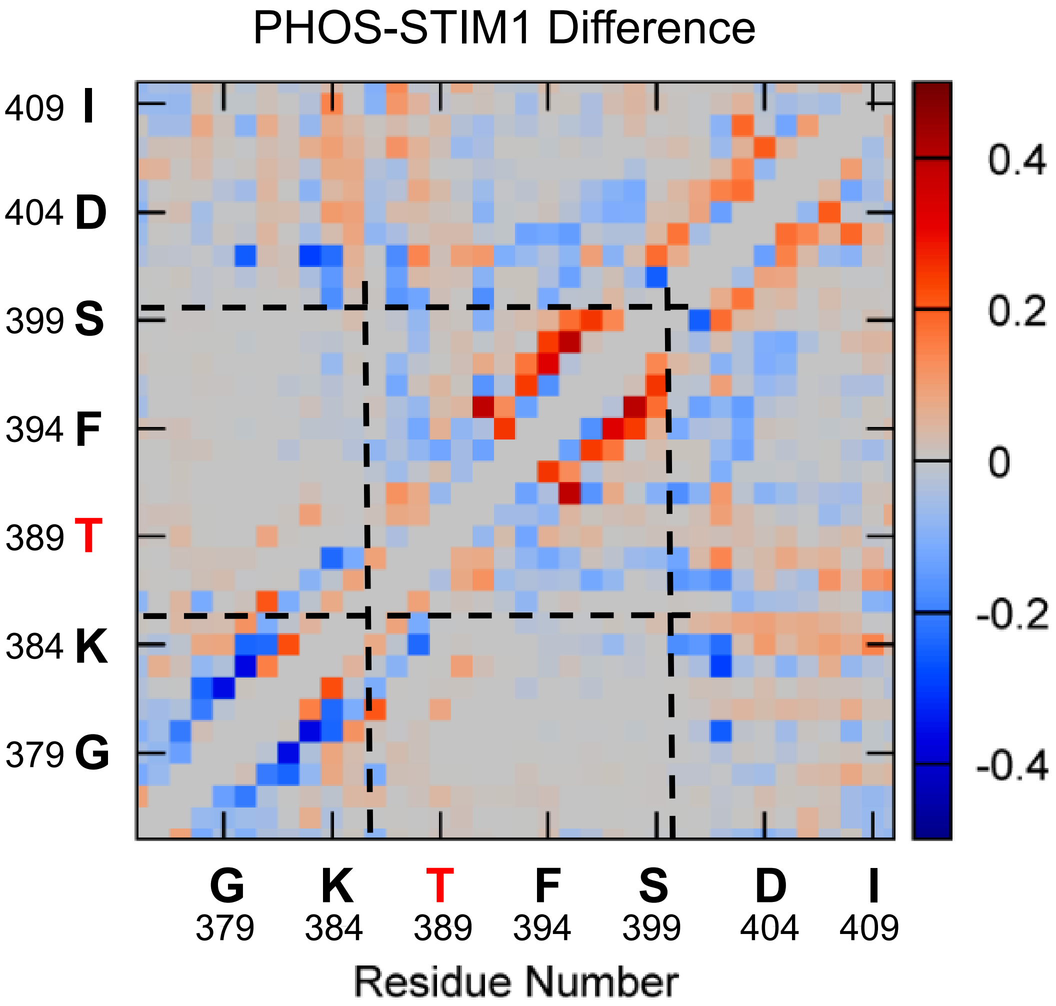
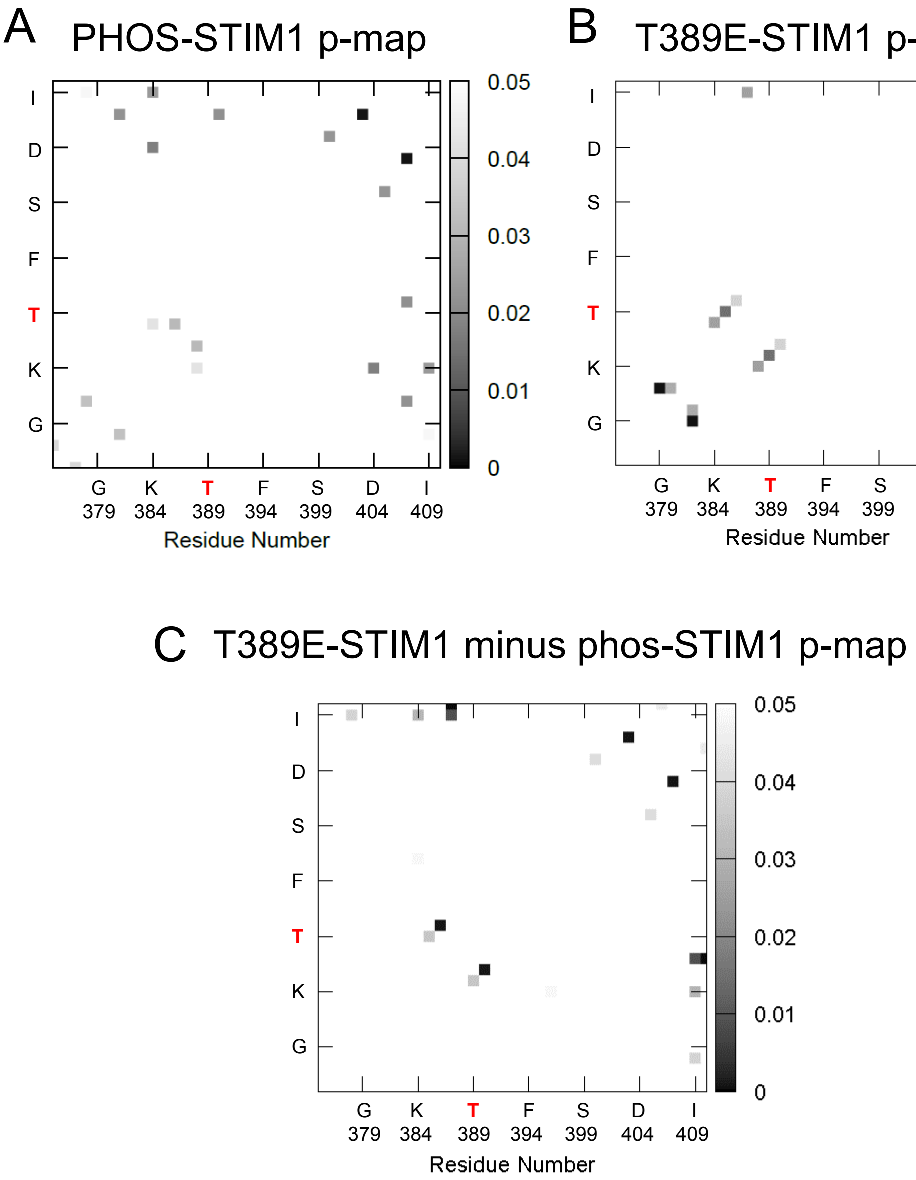
Supplemental Fig. S1



Supplemental Figure S1. Full difference contact map comparing phos-STIM1 to wild-type-STIM1. This is the same data as in Figure 7A, but showing all contacts instead of just the region of encompassing residues 386-399, shown in Fig. 7.

Supplemental Fig. S2



Supplemental Figure S2. **Representative P-value maps for side-chain contact probabilities.** This heat map shows the probability that the differences seen between the probabilities of sidechain-sidechain contacts for two different proteins would happen at random (p-value), if the actual structure ensemble was the same. Each simulation is treated as a single measurement of probability, and the p-value was calculated using the Welch t-test (which does not assume the variances of the two populations are equal).