Feature	Minimum Value	Boundary 1	Boundary 2	Boundary 3	Maximum Value
ln(HHSearch e-value)	-100	-92.1	-62.44	-20.99	-0.01
Average BLOSUM Score	-4	-1.5	-0.5	1.5	11.0
Average Burial in Template Structure	2.0	9.5	11.0	12.5	20.5
Average Distance to Alignment Gap	1	8.5	14.0	22.0	180.0

Supporting Table S1: Summary statistics for feature variables. Each aligned residue pair was annotated with the four statistics listed above using the approach outlined in *Methods*. In order to calculate the single-feature deviation estimates shown in **Figure 1**, each variable was divided into four quantiles of equal size using the boundaries listed above.