

Supplemental Material for

Effective Inter-Residue Contact Definitions for Accurate Protein Fold Recognition

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Figure S1

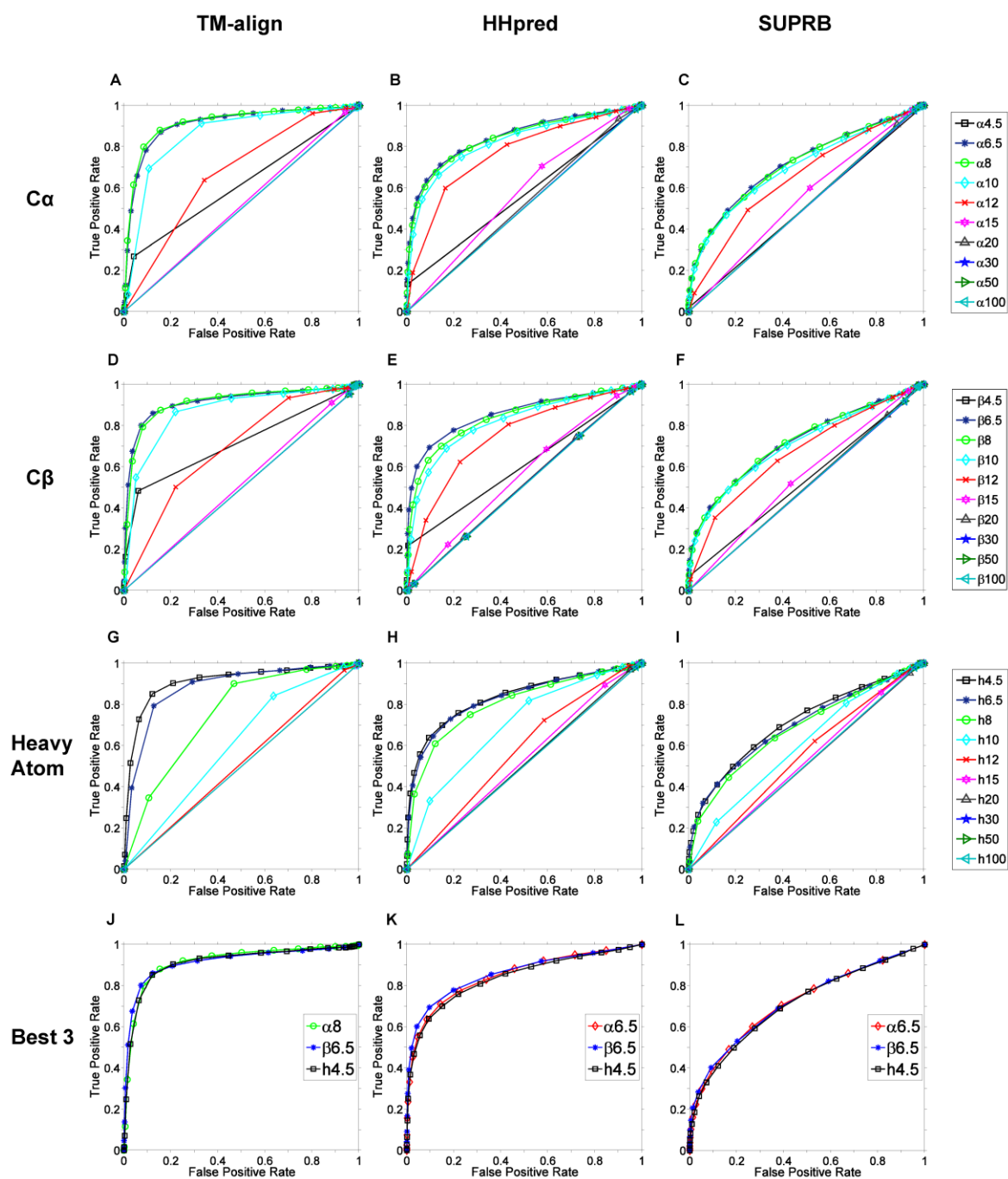


Figure 1. ROC curves of structure pair retrieval on the superfamily dataset. To determine corresponding residues in protein pairs, TM-align (the left column), HHpred (the middle column), and SUPRB (the right column) were used. Three different bases for residue contact definitions are used, the $C\alpha$ - $C\alpha$ (the first row), the $C\beta$ - $C\beta$ distance (the second row), and the heavy atom distance (the third row). The panels are ordered in the same way as in Figure 1.