



**Figure S3. Hit Rates of DockRank and other scoring schemes on the ZDock3-BM3 decoy set.** The Hit Rates of the top 1000 ranked conformations selected by DockRank (red, using predicted interface residues from a partner-specific predictor, PS-HomPPI) are compared with two energy-based scoring functions, IRAD (black) and ZRank (yellow), and with variants of DockRank using interface residues predicted by three state-of-the-art non partner-specific protein interface residue predictors: NPS-HomPPI (pink), PrISE (green), and meta-PPISP (blue). Hit Rates of DockRank's scoring function supplied with partner-specific actual interface residues (stem dashed line) are plotted to define the upper bound of Hit Rates of DockRank's scoring function. Studied here are 67 docking cases that have at least one hit ( $I-RMSD \leq 2.5 \text{ \AA}$ ) and for which PS-HomPPI is able to predict the interface residues between the receptor and the ligand.