

Supplemental Material for
CMsearch: simultaneous exploration of protein sequence
space and structure space improves not only protein
homology detection but also protein structure prediction

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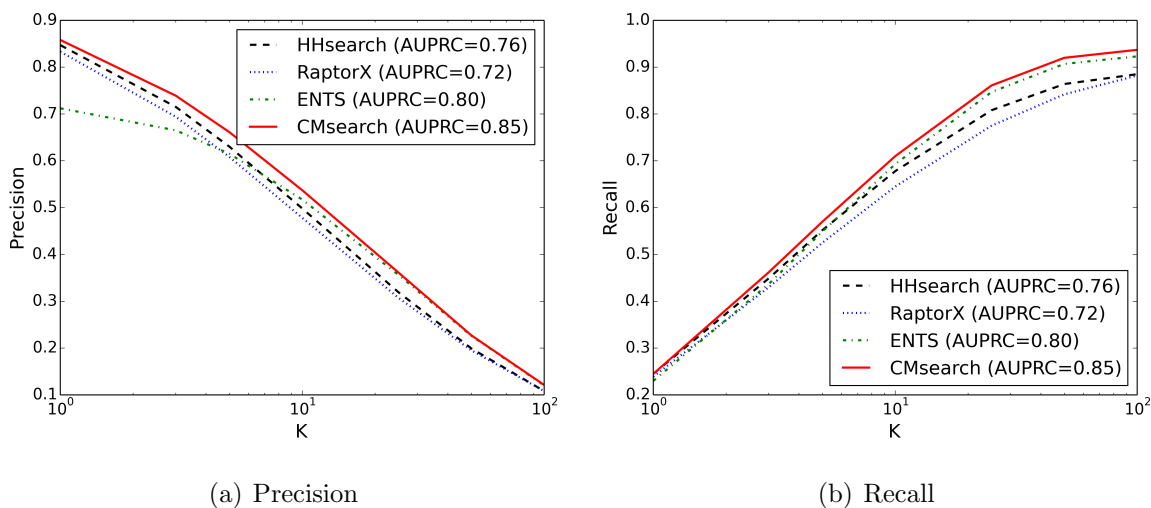


Figure S1: Precision and recall of homology detection when different numbers of top predictions are considered by HHsearch, RaptorX, ENTS, and CMsearch (with HHsearch as the sequence similarity metric) on the PDB30 dataset: for $K = 10$, the precision for the four methods is 0.50, 0.48, 0.52, and 0.54, respectively; and the recall of the four methods is 0.68, 0.65, 0.69, and 0.71, respectively.