

Supporting online material
for:
Title
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Fig. 1_Appendix

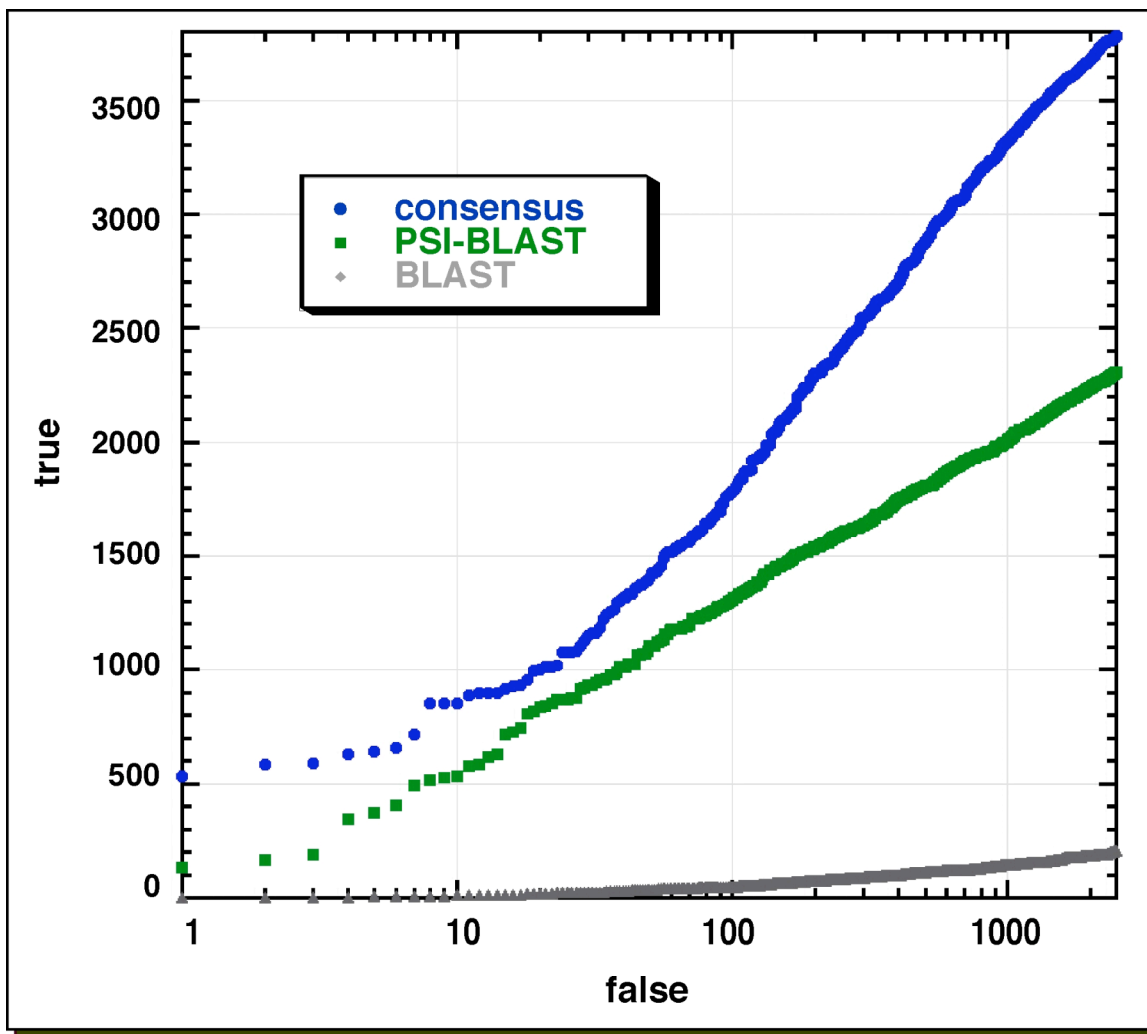


Fig. A1: **Consensus sequences increase number of true hits at any error rate.** We sorted Max-BLAST and PSI-BLAST alignments by e-value. The scores were generated by aligning a set of 2476 query proteins against each other. True positive pairs belonged to the same SCOP superfamily while false positive ones had different SCOP folds (see Methods). The logarithm scale of the horizontal axis clearly shows that consensus alignments improve performance at any error rate.