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Histograms summarizing the occurrences of Pfam-A functional domains in the human (blue) and MTB (red) proteomes. Nearly 30 % of the proteins in both species have been assigned more than one domain.

Figure S2:

Pair-wise comparisons between MTB proteins and their putative orthologs listed in the Integr8 (upper figure), eggNOG (lower left) and KEGG Orthology/KO (lower right) databases. Note the relatively smaller number of orthologs assigned by Integr8.

Figure S3:

Using the interolog approach to extend the limited set of DDI templates provided by PDB. Evolutionarily conserved PPIs (involving orthologs) are assumed to share a common underlying pattern of domain-domain interactions. This allows interacting domains to be inferred for PPIs for which structure information is not directly available (here, A'-B').

Figure S4:

Diversity in terms of length and sequence composition across the polypeptide sequences assigned to the Ulp1 protease family C-terminal catalytic domain (PF02902). The scatter plot follows from all-vs-all pairwise sequence alignment using the Smith-Waterman method. Pairs coming from the same proteome (blue) or from different proteomes (cyan) have been assigned different colors.

Figure S5:

Statistical over-representation of interacting Pfam domain pairs (from iPfam/3DID) in a PPI network for co-localized, coexpressed cytosolic proteins in *E. coli*. Several domain pairs do not show significant association with the PPI set. The darker horizontal line represents the p-value < 0.05 threshold.

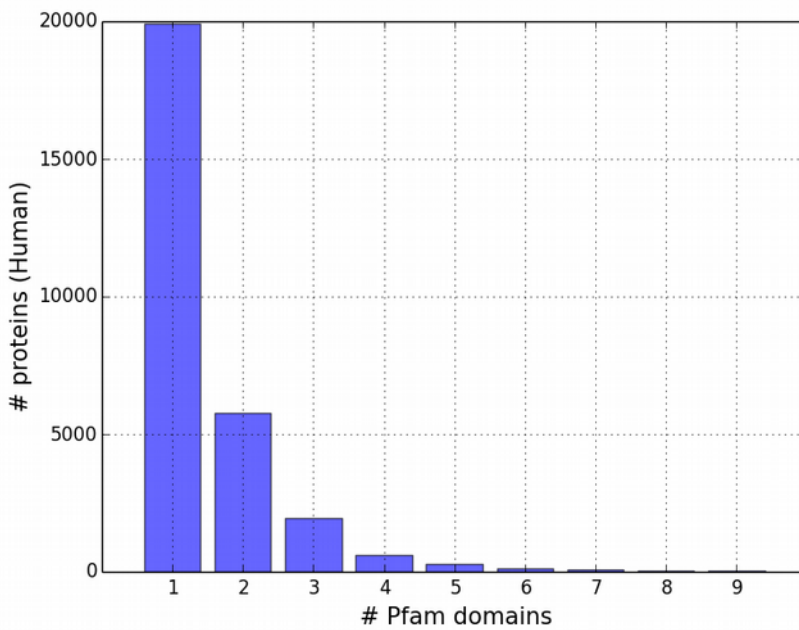
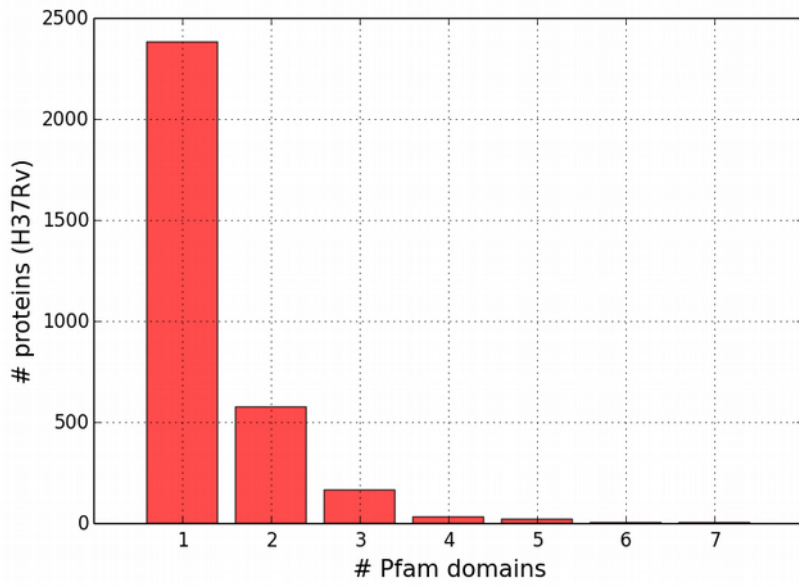


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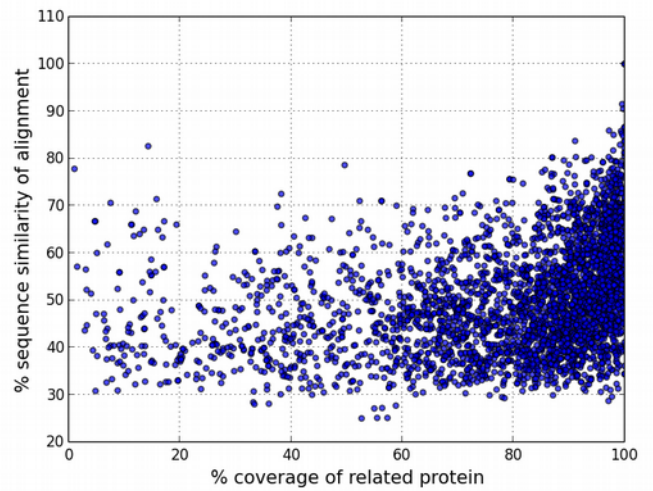
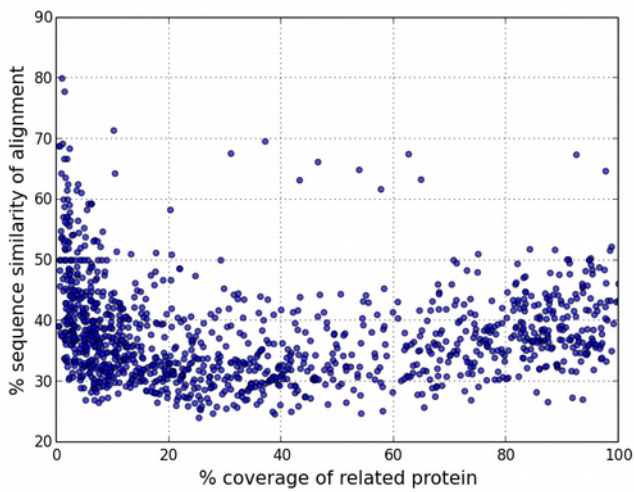
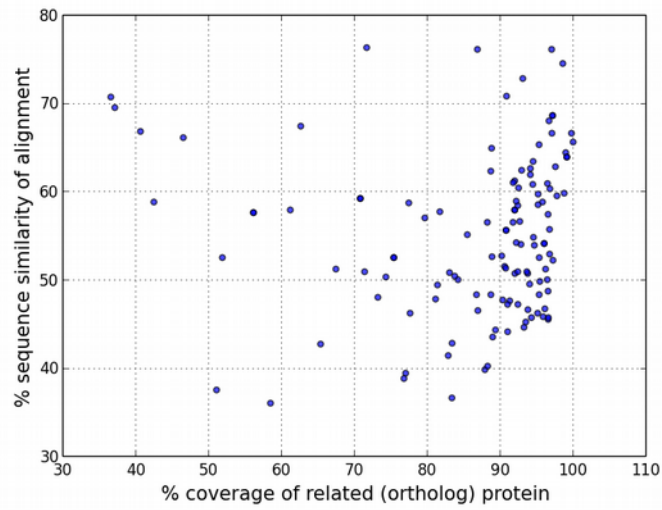


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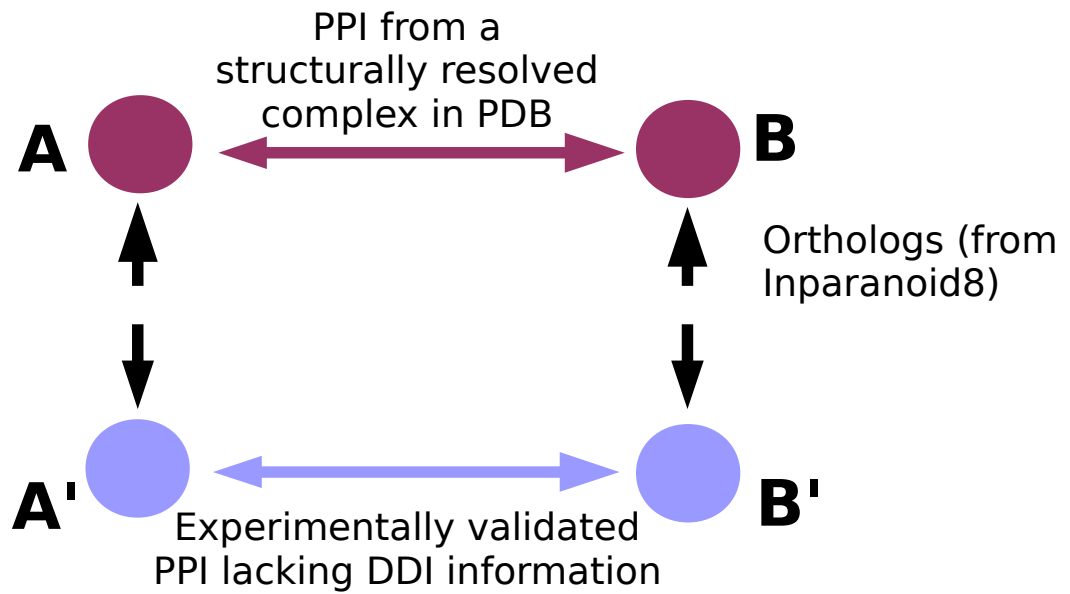


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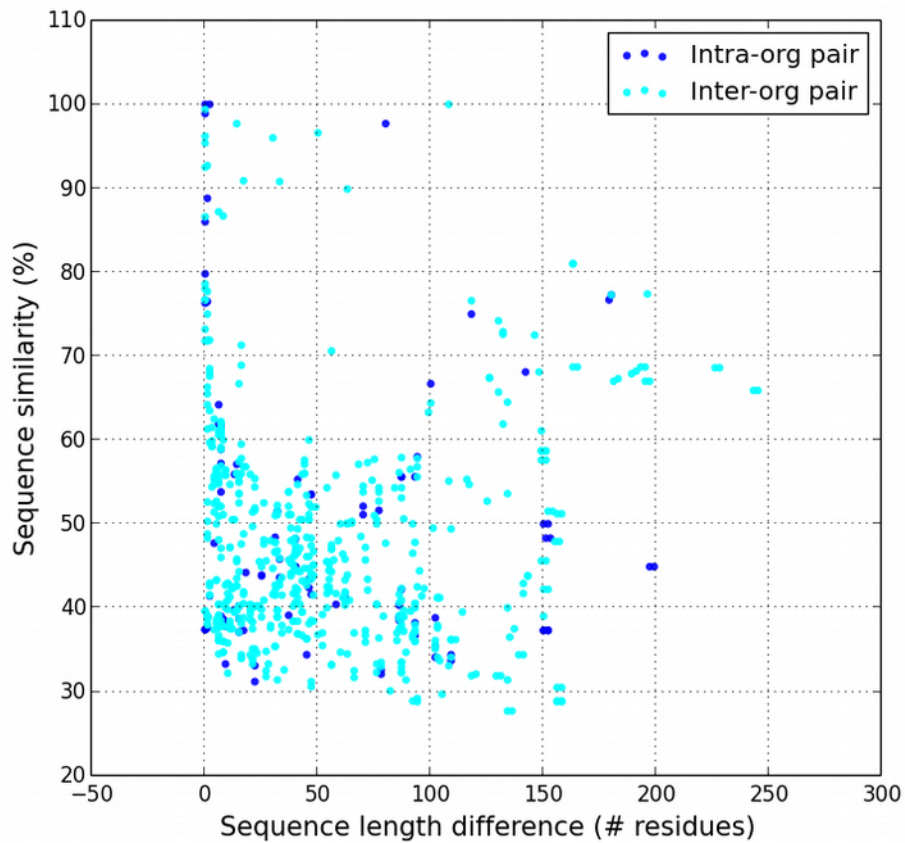


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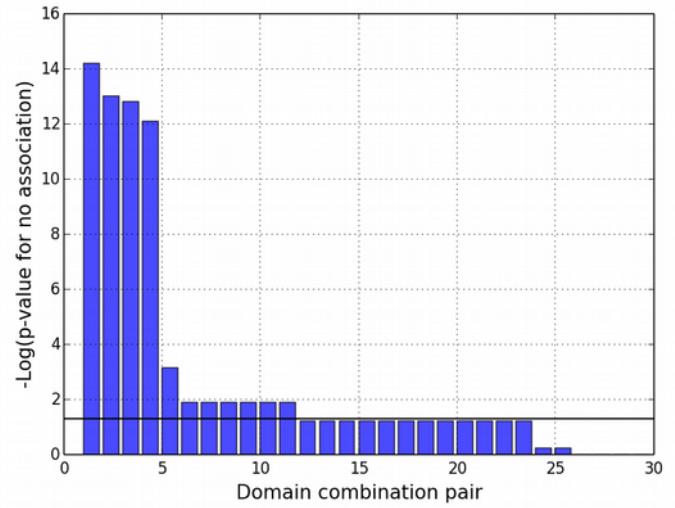
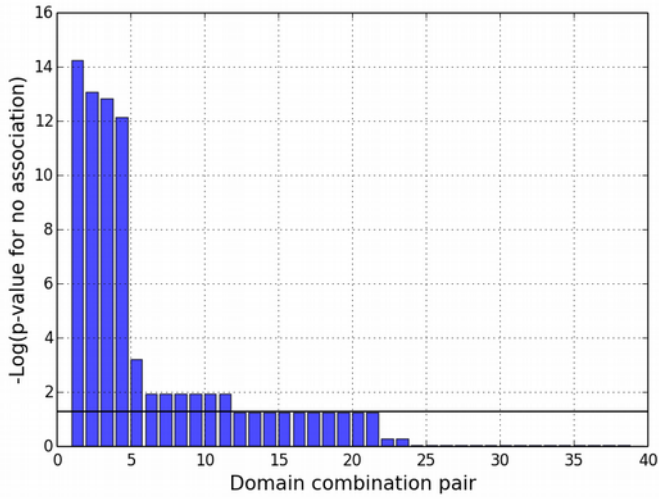


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