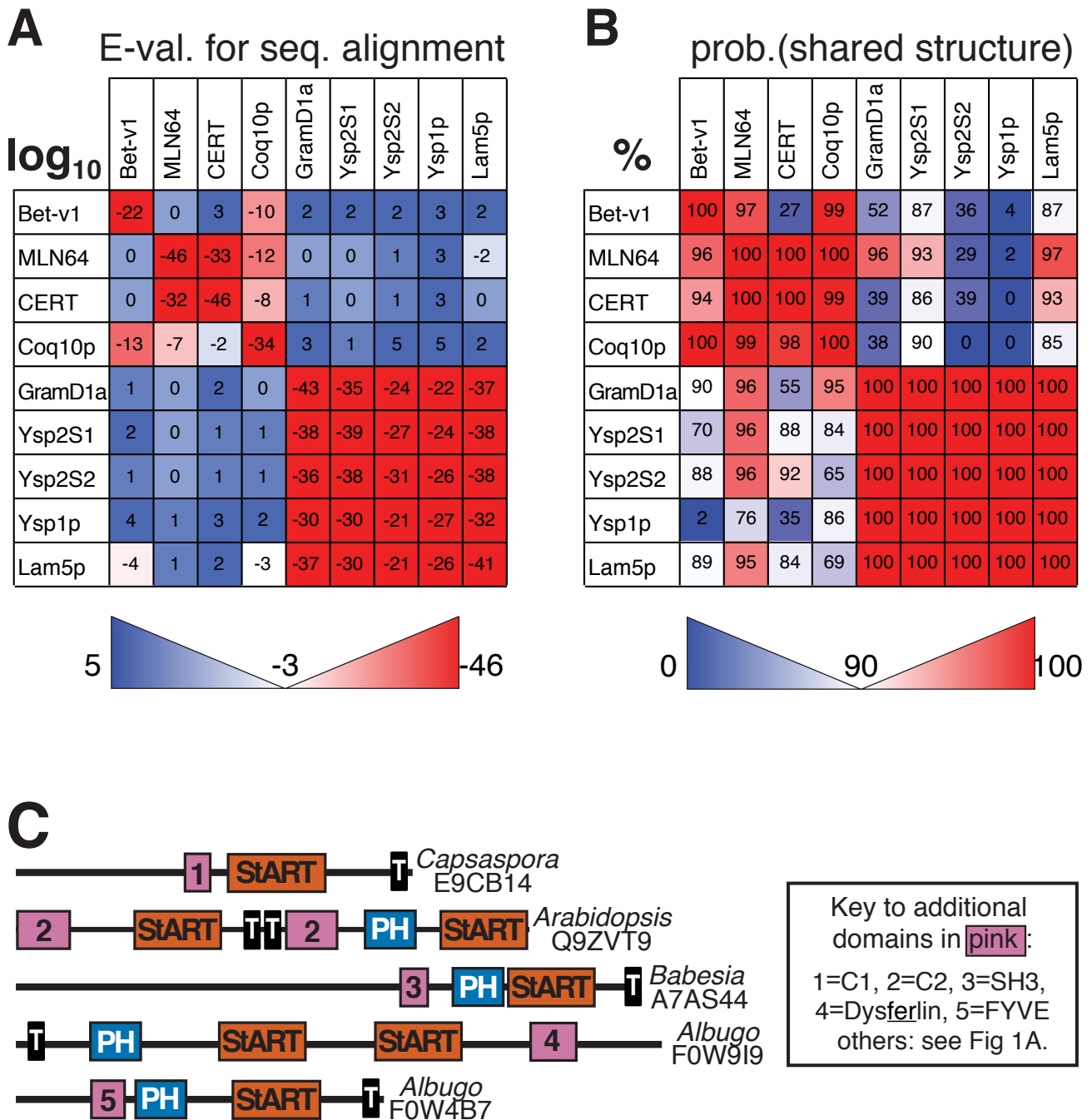


# Figure 1 - Figure Supplement 2



**Figure 1–Figure Supplement 2: Relationships of StART-like domains**

**A.** Each row shows E-values of sequence alignments obtained with the HMM alignment tool HHblits (Remmert *et al.*, 2012). Each row was seeded with the sequence indicated on the left, and the strength of hit to each target is expressed as  $\log_{10}$ . **B.** As A, but reporting HHpred results. Values indicate the probabilities of sharing the same structure (%). For both A. and B. squares are colored to indicate if the hit is above (red) or below (blue) the thresholds for significance: 90% in A, -3 ( $=\log_{10} 0.001$ ) in B. HHpred is more sensitive than HHblits, identifying many more links between known StARTdomains and new StART-like proteins. **C.** Selected proteins with StART-like domains show a diverse range of accessory domains. Despite variation in the positioning of TMD(s), most of each protein is in the cytoplasm. Accessory domains (pink) are typically implicated in membrane targeting (see key).