



FIGURE 27.34. Phylogenomics-based prediction of gene function. The figure illustrates the process for two examples: (1) Choose the gene of interest; (2) identify homologs; (3) build a multiple sequence alignment for the homologs; (4) calculate a gene tree representing all the homologs; (5) overlay that function onto the tree when a gene's function is known; (6) use character state reconstruction methods to infer the functions of uncharacterized genes. The *bottom panel* shows the actual evolutionary history for each example. (Modified from Eisen J.A. *Genome Res.* **8**: 163–167, Fig. 1, © 1998 CSHLP.)