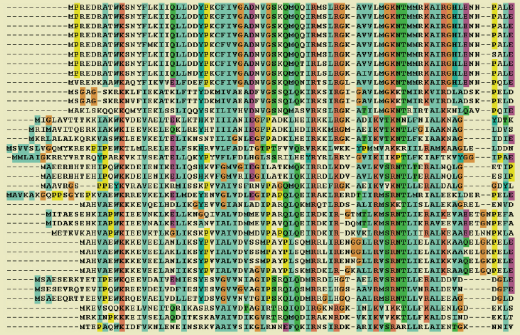
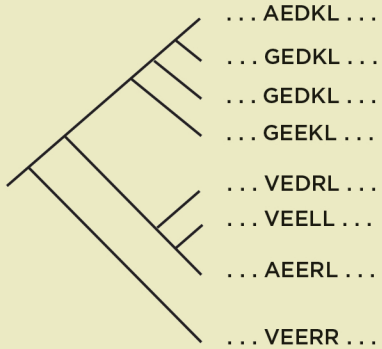
HOW TO RESURRECT A PROTEIN

Ancestral sequence reconstruction relies on phylogeny and statistics to infer the most likely amino acid sequence for an ancient protein.

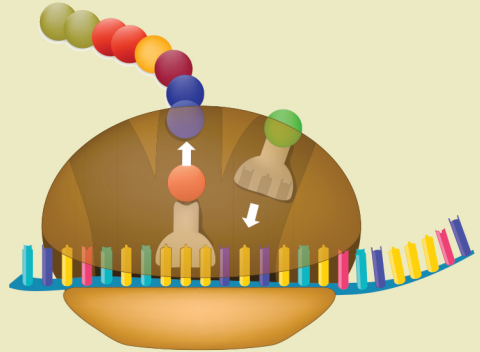


SEQUENCE ALIGNMENT: Scientists collect sequences from databanks of the modern versions of the protein of interest from different organisms.



TREE BUILDING: Computer algorithms construct a phylogenetic tree for the proteins. (*Curr Opin Struct Biol*, 38:37–43, 2016).

ANCESTRAL RECONSTRUCTION: The programs can then infer the sequences that likely existed at nodes of the tree, before the modern species evolved.



LABORATORY TESTS: Finally, the scientists order synthetic DNA and generate those proteins in the lab to use for experiments.