Branches of the TGF-β superfamily phylogenetic tree represent the divergence of each family member from a hypothetical common ancestor. The branch length reflects the number of amino acid changes between each protein and the common ancestor.

The mature domains of each molecule were aligned using ClustalW [1]. The alignment was then processed with ProtTest and Neighbor using the PhyML/PAUP*tree [2]. The tree used as the basis for the third diagram was created using TreeView [3]. The branches of the phylogenetic tree represent divergence of each family from a common ancestor. The branch lengths reflect the number of amino acid changes between each protein and the hypothetical ancestor, and simply have no real time dimension to them.