

Phylogenetic tree of Cytosolic Cysteine Synthase (CysS) proteins. The tree is rooted at the top with A01MSA022 and branches downwards. Each node is labeled with a protein ID and its taxonomic classification. The tree shows a clear division into two main groups: the alpha-CysS group (top half) and the beta-CysS group (bottom half). The alpha-CysS group includes proteins from various Gram-negative and Gram-positive bacteria, such as Burkholderia, Pseudomonas, and Rhodococcus. The beta-CysS group is more diverse, including proteins from Gram-negative bacteria like Burkholderia and Rhodococcus, as well as Gram-positive bacteria like Bacillus, Streptomyces, and Clostridium. The tree also shows several uncharacterized proteins and proteins with unknown functions. The scale bar at the bottom indicates a distance of 0.1 substitutions per site. The tree is a maximum likelihood tree based on a concatenated alignment of the CysS protein sequences. The bootstrap values are shown at the nodes. The tree is a good representation of the evolutionary relationships between the different CysS proteins.