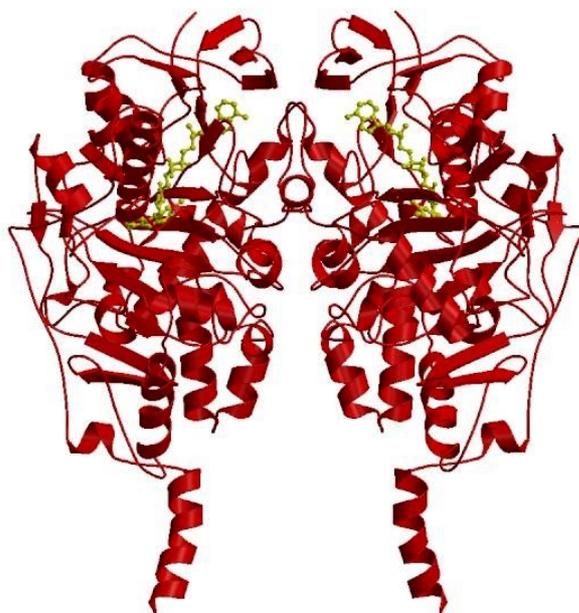


Both A and B forms of MAO are membrane bound proteins localized to the outer membrane of the mitochondrion. A prominent structural feature is related to the 60-residue C-terminal tail. This region forms an extended segment that traverses the protein surface and then folds into an α -helix. This helix protrudes from the basal face of the structure with its axis approximately parallel to the molecular twofold axis in an orientation suited to anchor the protein to the outer mitochondrial membrane. In addition to this transmembrane helix, two apolar loops located at different positions in the sequence form two hydrophobic patches on the protein surface which are probably involved in membrane binding. This is one of the very few known structures of a monotonically inserted membrane protein to be completed revealing a different method of insertion than that of other monotonically inserted proteins, such as prostaglandin synthases and hopene-squalene cyclase. It may be similar to that for insertion of mammalian P450 reductases, but those structures were obtained after removal of their hydrophobic tails, whereas the MAO-B structure is for intact, full-length protein.



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