Conversion of methane to methanol through multi-component

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Methanotrophs consume methane as their sole carbon source and play an essential role in the global carbon cycle by limiting its atmospheric content. These bacteria oxidize methane to methanol using soluble methane monooxygenases having hydroxylase, regulatory, and reductase protein components. Until now, the catalytic mechanism has remained ambiguous due to a lack of atomic-level information about component interactions. We have recently reported the 2.9 Å resolution crystal structure of soluble methane monooxygenase hydroxylase (MMOH) in complex with its regulatory component (MMOB) from Methylococcus capsulatus (Bath). MMOB docks in a canyon formed at the $\alpha_2\beta_2$ interface of the $\alpha_2\beta_2\gamma_2$ MMOH dimer, and its unstructured N-terminus forms a ring-like structure on the MMOH α-subunit. These interactions control O_2, methane, and proton access to the catalytic diiron center at the active site by altering the internal architecture of the α-subunits and effect conformational changes at key active site residues involved in methane oxidation.