

showing a dodecamer³¹ or a tetradecamer²⁷, and these studies also differ on other aspects of the global architecture. In an effort to characterize the architectures and oligomeric states of Vps4 further, we have determined two new crystal structures of the *S. cerevisiae* Vps4 core enzyme, performed analytical ultracentrifugation analyses that define the oligomeric state of the inactive Vps4 complex, and carried out extensive mutagenesis aimed at discriminating between different Vps4 assembly models and identifying residues that perform key functions in the active and inactive states.