The oligomerization state of SKD1 is regulated by ATP

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Yeast *vps* mutants have been isolated by their vacuolar morphologies which differ significantly from that of the wild-type. Among them, class E *vps* mutants possess an exaggerated form of a pre-vacuolar endosome-like compartment. Recently, an ESCRT (endosomal sorting complex required for transport) model is proposed for MVB (multivesicular body) sorting by the class E Vps proteins in yeast. SKD1 (suppressor of K^+ transport growth defect 1), which belongs to the AAA (ATPases associated with diverse cellular activities) type ATPase family, is identified as a mouse homologue of class E Vps protein, Vps4. SKD1 interacts with several ESCRT proteins and plays an important role in the MVB vesicle formation.

It has been reported that AAA family proteins alter their oligomerization states between monomer and hexamer depending on ATP hydrolysis. We overproduced and purified recombinant mouse SKD1 protein and found that SKD1 shows two different oligomerization states in solution by size exclusion chromatography and small angle X-ray scattering. To elucidate the molecular mechanism of SKD1 in detail, X-ray crystallographic study of SKD1 has been performed. At present, the resolution is up to 3.5 Å and an AAA motif (α/β and α subdomains), a β-domain and a C-terminal α-helical region could be identified. (N-terminal region is disordered and not defined). Based on the current structure and the solution experiments, we will discuss the relationship between the crystal structure and the oligomerization state regulated by ATP.