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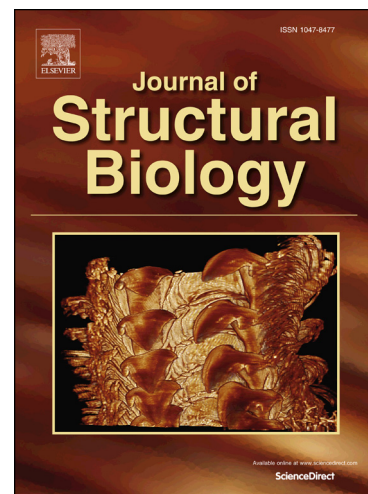
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Cryo-EM analysis of a domain antibody bound rotary ATPase complex

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Abstract

The bacterial A/V-type ATPase/synthase rotary motor couples ATP hydrolysis/synthesis with proton translocation across biological membranes. The A/V-type ATPase/synthase from *Thermus thermophilus* has been extensively studied both structurally and functionally for many years. Here we provide an 8.7 Å resolution cryo-electron microscopy 3D reconstruction of this complex bound to single-domain antibody fragments, small monomeric antibodies containing just the variable heavy domain. Docking of known structures into the density revealed the molecular orientation of the domain antibodies, suggesting that structure determination of co-domain antibody:protein complexes could be a useful avenue for unstable or smaller proteins. Although previous studies suggested that the presence of fluoroaluminate in this complex could change the rotary state of this enzyme, we observed no gross structural rearrangements under these conditions.

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