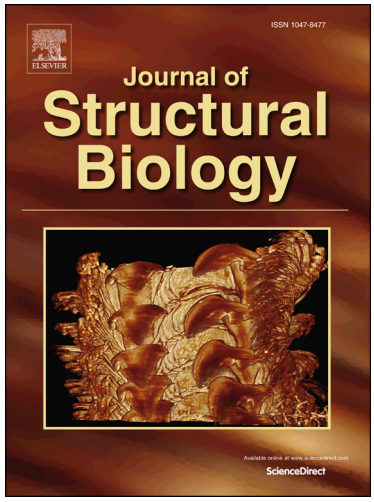

Technical Note

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

Roberta B Davies, Callum Smits, Andrew SW Wong, Daniela Stock, Mary Christie, Sara Sandin, Alastair G Stewart

PII: S1047-8477(17)30013-8
DOI: http://dx.doi.org/10.1016/j.jsb.2017.01.002
Reference: YJSBI 7020

To appear in: *Journal of Structural Biology*

Received Date: 31 October 2016
Revised Date: 16 January 2017
Accepted Date: 17 January 2017

Please cite this article as: Davies, R.B., Smits, C., SW Wong, A., Stock, D., Christie, M., Sandin, S., Stewart, A.G., Cryo-EM analysis of a domain antibody bound rotary ATPase complex, *Journal of Structural Biology* (2017), doi: http://dx.doi.org/10.1016/j.jsb.2017.01.002

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

Roberta B Davies[1,2], Callum Smits[1], Andrew SW Wong[3], Daniela Stock[1,4], Mary Christie[1,4], Sara Sandin[3,5] and Alastair G Stewart[1,4]

[1]Molecular, Structural and Computational Biology Division, The Victor Chang Cardiac Research Institute, Darlinghurst, NSW 2010, Australia.
[2]Current address: School of Physics, The University of New South Wales, NSW 2052, Australia.
[3]NTU Institute of Structural Biology, Nanyang Technological University, 636921, Singapore.
[4]Faculty of Medicine, The University of New South Wales, Sydney, NSW 2052, Australia.
[5]School of Biological Sciences, Nanyang Technological University, 637551, Singapore.

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.