Subunit Interactions at the V_1-V_o Interface in the Yeast Vacuolar ATPase

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Supplementary Information

A

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aNT (S.c.)   MAEKEEAIFRSAEMALVQFYIPQEISRDSAYTLGQLGLVQFRDLNSKVRAFQRTF---VN  57
INT (M.r.)   -------------MEKLIVAGPKRLARELLAELQKAGVVHIDPLRPDELGEYRLSPTEEA  47
                          N-half proximal lobe

                                                       aNT(104-372)
aNT (S.c.)   EIRRLDNVERQYRYFYSLLKKHDIKLYEGDTDKYLDGSGELYVPPSGSVIDDYVRNASYL  117
INT (M.r.)   ELKRWEAVVSQAEQSLTVVGLATVPS----------------SKPFTGSLEEAEAVLRPV  91

aNT (S.c.)   EERLIQMEDATDQIEVQKNDLEQYRFILQSGDEFFLKGDNTDSTSYMDEDMIDANGENIA  177
INT (M.r.)   ASRAEVLGKERAALEEEIQTIELFGKAAEKLAALA------------HG----------  128
                   N- half coiled coil

aNT (S.c.)   AAIGASVNYVTGVIARDKV-ATLEQILWRVLRGNLFFKTVEIEQPVYDVKTREYKHKNAF  236
INT (M.r.)   LDESPRLGVIPFLVAKPEELEAVRKALQEALADRFVLEAEPLEN-----------Q-LAA  176
                                  distal lobe

aNT (S.c.)   IVFSHGDLIIKRIRKIAESLDANLYDVDSSNEGRSQ--QLAKVNKNLSDLYTVLKTTSTT  294
INT (M.r.)   LVVVKRS-ELEAARSSLSRLGLAELRFPGAYGAMPLGKAAARMKERARLAPEELVGIREE  235
                                              C-half coiled coil

aNT (S.c.)   LESELYAIAKELDSWFQDVTREKAIFEILNKSNYDTNRKILIAEGWIPRDELATLQARLG  354
INT (M.r.)   VARLSRESGEALIALWTRAKDEVARYKAVADMA--AGKYGAALMGWVPQKAKGKVEEALG  293
                                                   C-half proximal lobe

aNT (S.c.)   EMIARLGIDVPSIIQVLDTNHTPPTFHRTNKFTAGFQSICDCYGIAQYREIN         406
INT (M.r.)   RLR--------DQIVY                                             301
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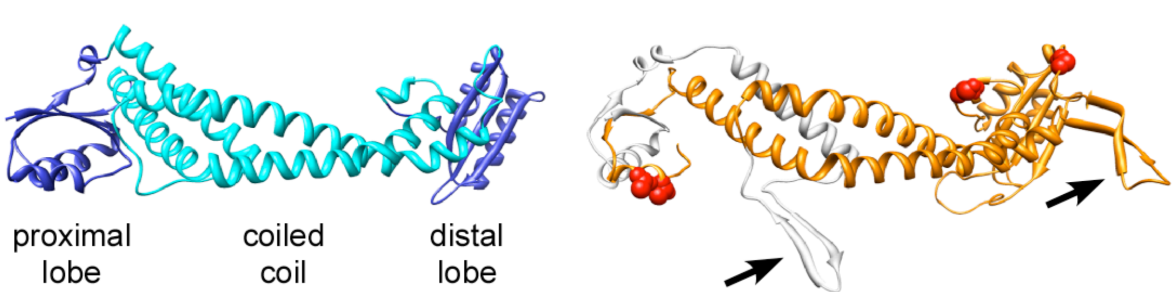
B



I_{NT} (M. ruber; 3rrk.pdb)

a_{NT} (yeast, swissmodel)

Figure S1: *A*, Primary sequence alignment of the N-terminal domains of *S. cerevisiae* Vph1p (1-406) and *M. ruber* subunit I(1-301). Secondary structure is shaded in blue and pink for β structure and α helix, respectively. *B*, Vph1p primary sequence (1-357) threaded into the *M. ruber* I_{NT} crystal structure (3rrk) using Swiss-Model (swissmodel.expasy.org). Left, ribbon representation of *M. ruber* I_{NT} crystal structure with proximal and distal lobes colored in dark blue and the coiled coil domain in cyan. Right, model of Vph1p(1-357). Arrows point to Vph1p sequence elements not present in the *M. ruber* I_{NT} domain. The sites from which photo crosslinks to subunits EG was observed are in red spacefill. The Vph1p construct analyzed here is highlighted in orange.