NIH Research Resource Center and Regional Consortium for Cryo-EM at SLAC

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The molecular mechanism of transmembrane proton translocation in rotary motor ATPases is not fully understood. Here we report the 3.5 Å resolution cryo-EM structure of lipid nanodisc-reconstituted Vo proton channel of the yeast vacuolar H^+-ATPase (V-ATPase), captured in a physiologically relevant autoinhibited state. The atomic model provides details of the residues at the interface of the proteolipid (***c***-) ring and the transmembrane portion of subunit ***a*** that form the proton pathway. Together with previous mutagenesis studies, we propose a chemical basis for transmembrane proton transport.