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**A Preliminary Model of Major Vault Protein.** Daniel H. Anderson<sup>1</sup>, Valerie A. Kickhoefer<sup>2</sup>, Stuart A. Sievers<sup>3</sup>, Leonard H. Rome<sup>2</sup>, David Eisenberg<sup>1,2</sup>, <sup>1</sup>HHMI at UCLA, <sup>2</sup>Dept. of Biol. Chem. at UCLA Medical School, <sup>3</sup>Dept. of Chem. and Biochem, UCLA.

Vaults are the largest known ribonucleoprotein structures. The vault is 405Åx405Åx680Å and is among the largest objects to have crystallized. The vault capsule is built from 96 copies of the 95.8kDa major vault protein, with 24- and 48-fold symmetry. Although the resolution is only about 9Å, the symmetry-averaged electron density could be parsed to build a model. Atom placement was not possible at this resolution, but it was possible to deduce what structural elements could result in each region of density. Sequence analysis assisted model-building. A preliminary model was built mostly by a “stream-pool” algorithm. A “stream” of density connected to its context at its ends could be assigned helical structure. A flat “pool” of density could be assigned 2-, 3-, or 4-strand beta-sheets, depending on whether its connections were on the same or opposite edges of the “pool.” A perfect chain trace would contain 873 residues with correctly assigned sequence. This first model (the “connectivity diagram”) contains 668 residues, mostly poly-alanine. Although the model contains obvious flaws, it does indicate zones of structure stabilization, and is an important step towards the goal of engineering the vault nanocapsule.