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Crystallization and Preliminary Phasing of Recombinant Vaults. Daniel H.Anderson¹, V.A.Kickhoefer², S.Raval-Fernandes², L.H.Rome², D.Eisenberg^{1,2}. ¹HHMI at UCLA, ²Dept. of Biological Chemistry, David Geffen School of Medicine at UCLA.

Vaults are the largest known ribonucleoprotein structures, hollow capsules built from 96 copies of Major Vault Protein (MVP), fewer copies of two other proteins and a small RNA. The mass of a rat liver vault is 13 million Daltons, with dimensions about 750x450x450Å³ (internal volume is about 50 million Å³). Despite the massive cost to the cell of building vaults, their biological role is still speculative. Extending the cryo-EM vault structure *via* crystallography to derive a chain trace would be of great value to allow modification of the vault structure, and possibly to indicate function.

The best crystals thus far contain empty vaults built from a cysteine-tag construct of MVP, diffracting to about 8Å resolution. The crystal parameters are: C2 symmetry, a=631Å, b=465Å, c=585Å, β=123.8°.

Molecular replacement (MR) using a cryo-EM half-vault search model recovers the whole-vault shape in the crystal symmetry. Solvent flattening improved the initial MR phases. Depending on the level of non-equivalence we find, non-crystallographic symmetry averaging could range from 8- to 48-fold.

Reference: L.B.Kong, A.C.Siva, L.H.Rome, P.L.Stewart (1999) *Structure*, 7, 371-379.
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