**Figure S5. Manual molecular replacement.** Automated molecular replacement did not accurately place the vault 2-fold at a crystal 2-fold (compare Supporting Figs. S4, S6). The vault cryo-EM electron density is shown in cross-section. (a) The half-vault density was scaled smaller by 0.96. The center point of the whole vault was translated to (0,0,0) (black dot), placing the high-symmetry vault axis on the orthogonal Z axis. (b) The density was rotated -13.7° around the Y axis to position the density in the crystal coordinate system. (The crystal β angle is 123.8° between the X and Z axes.) The crystal 2-fold along Y (perpendicular to the black dot at (0,0,0)) generated the whole vault (see Fig. S6). The density rotation program thinned the vault shell. Thickness and isotropic shrinkage of the vault were adjusted to pack the cell (see Methods and Text S7). The two figure components were made at the same scale with CCP4 program MAPSLICER [1], then combined and labeled with Photoshop.
