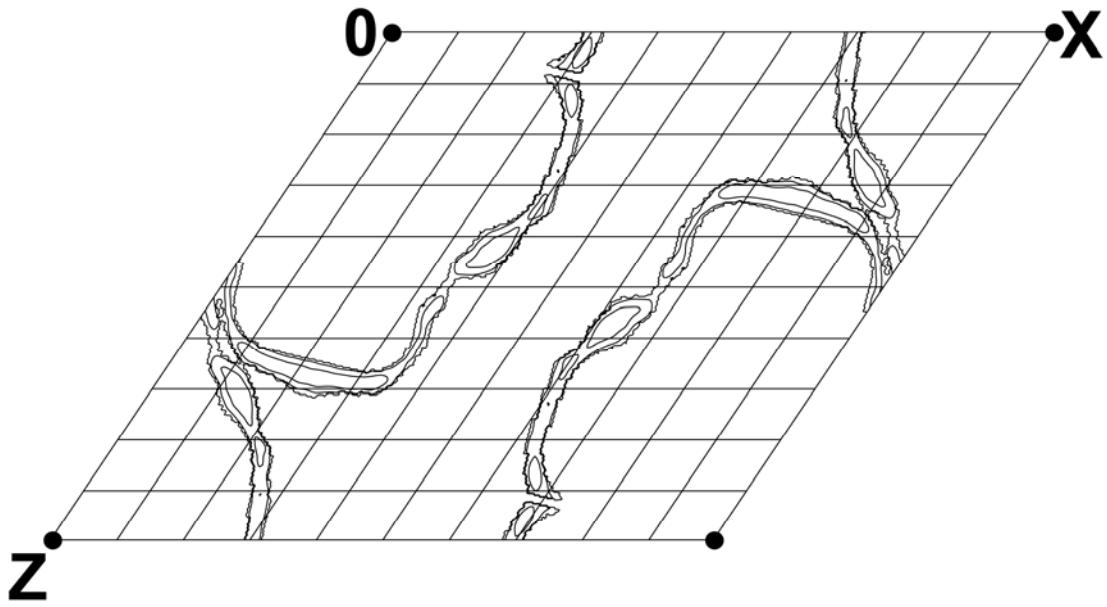
Figure S6. Initial half-vault phasing model manually placed at (0,0,0). The half-vault electron density from cryo-EM was placed relative to the crystal axes as shown in Fig. S5, simplifying the NCS operators (compare to Fig. S4). The crystal 2-folds along **Y** (perpendicular to the page at the black dots) generated the whole vaults. The density rotation programs (MAPMASK and MAPROT [1]) deleted surface voxels. Consequently, there was no phasing model for the N-termini, and in this section the cap and shoulder just touch. To make this figure, the map was sectioned at **Y** = 0 (with MAPSLICER [1]). Vaults above and below (translated by variants of the centering operation **(X+1/2, Y+1/2, Z)**) pack snugly against this layer.

1. CCP4 (1994) The CCP4 suite: programs for protein crystallography. Acta Crystallogr D Biol Crystallogr 50: 760-763.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