Group II intron

15297 micrographs were collected from which 4155270 particles were extracted. 2D classification produced crisp classes of particles from which 881868 particles were used for 3D volume reconstruction. The final map (2.8 A resolution) improves previously available crystallographic data providing new insights into this important and pharmacologically relevant ribozyme. Future work will focus on understanding its mechanism of folding, catalysis and small molecule recognition in more detail.