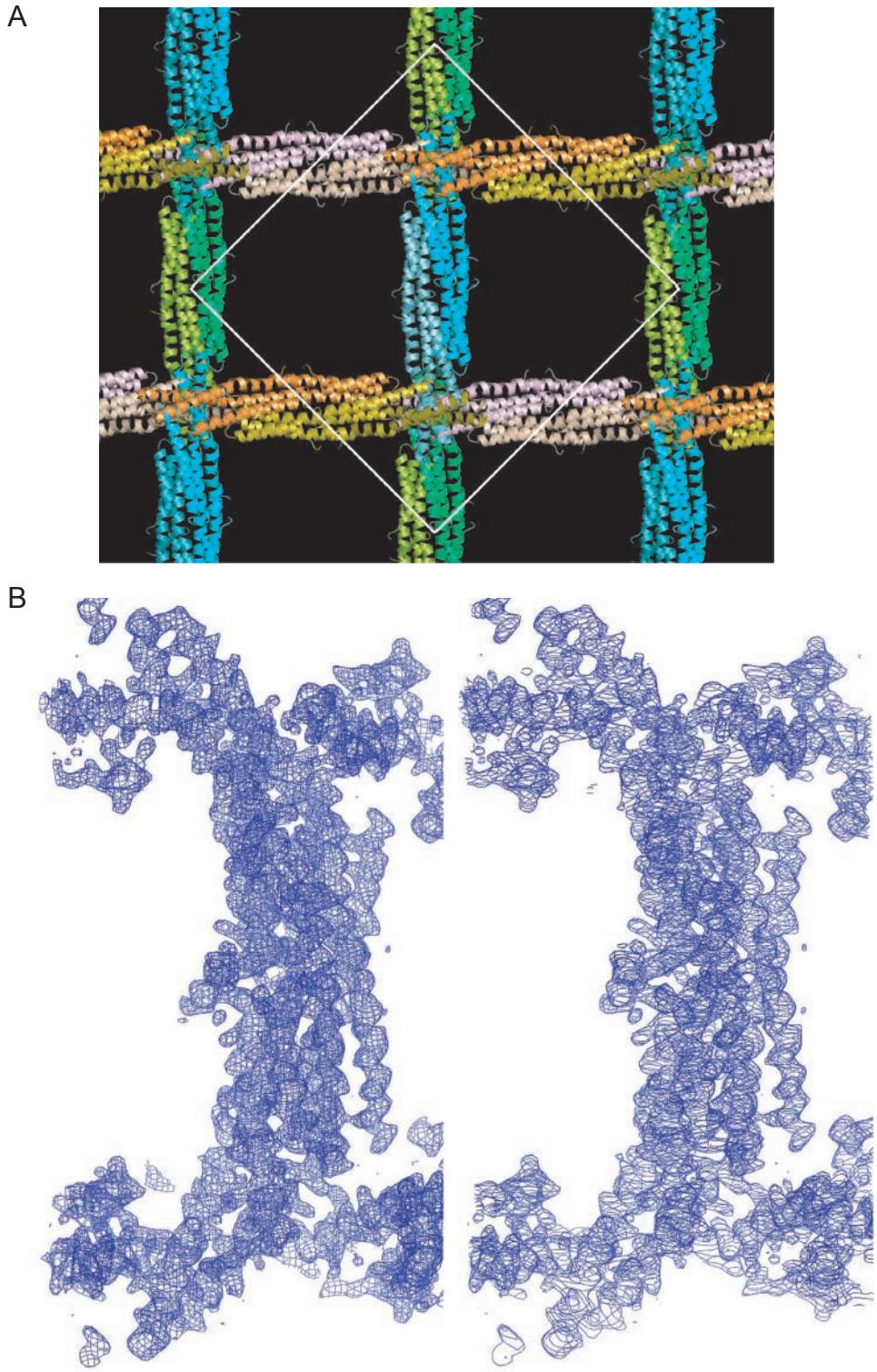
Supplementary Figure 1



Supplementary Figure 1. Crystal packing and experimental density map of the wild-type endophilin A1 BAR domain. (A) The crystal belongs to the space group $I\,4_1$ and shows a high solvent content of 83%. Two polypeptide chains in the dimer are related by the crystallographic two-fold rotational symmetry. Elongated crescent-shaped proteins are packed into a meshwork that allows macro molecules to penetrate into the crystal. This packing is stable at least from pH 5.4 to 9.5. The ΔApp mutant showed almost identical crystal packing. (B) Stereoviews of the experimental electron-density map contoured at 1.2 σ covering an entire endophilin A1 BAR dimer. The map was calculated at 3.2 Å resolution with density modified MAD phases by RESOLVE.