

ABCB10A (4AYX) Materials & Methods

Construct details and protein purification are identical to a previous SGC structure PDB ID [4AYT](#)

Crystallization: Crystals were grown in sitting drops at 20°C. Rod-shaped crystals appeared after 1-2 weeks. Two variants of this trigonal crystal form were observed differing by approximately 5 Å in their ab unit cell dimensions (forms A or B).

Rod Form B: Drops comprising 100nl protein solution (8mg/ml; ABCB10A DDM/CDL/AMP-PCP) and 100nl of reservoir solution (0.1 M NaCl, 50mM NDSB-256, 0.1 M glycine pH 9.5, 30-36% (v/v) PEG300) were equilibrated against 20% of the same reservoir solution.

Crystal plates were transferred to 6°C prior to directly flash cooling crystals in liquid nitrogen.

Data Collection:

Resolution: 2.9 Å

Data were collected at 100°K using a 10x10µm beamsizes on I24 microfocus beamline (Diamond Light Source, UK). Data collection was restricted to either end of the rod-shaped crystals due to internal disorder.

Data were collected to 2.9 Å using a single 10µmx10µm crystal volume.

Structure Solution: The structure was solved by molecular replacement using the related rod form A structure - PDB ID 4AYT. Refinement was carried out with BUSTER using LSSR restraints to the better resolved rod form A (4AYT) structure.