

ABCB10A (3ZDQ) 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.

Drops comprising 100nl protein solution (8mg/ml; ABCB10A purified in a buffer containing 0.02% DDM, 0.01%CDL, 0.2M NaCl, 0.5mM TCEP, 0.5mM MgCl₂, 20mM HEPES pH7.5) and 100nl of reservoir solution (0.1 M NaCl, 0.1 M glycine pH 9.25, 30-36% (v/v) PEG300) were equilibrated against 20μl of the same reservoir solution.

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

Data Collection:

Resolution: 2.85Å

Data were collected at 100°K using a 10x10um 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.

The final dataset were collected to 2.85Å using two 10μmx10μm crystal volumes located at either end of the crystal.

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 rod form A (4AYT) structure.