Supplementary Figure 1: Transmembrane profile of the PrMATE1 using TMHMM software.
Supplementary Figure 2: Structural superposition of PrMATE1 model and the template MATE transporter of *Vibrio cholerae* (PDB: 3MKT). (Left) side view; (Right) axial view. The template is displayed in red, the modelled PrMATE1 in blue.
Supplementary Figure 3: Protein-ligand interaction mode by docking studies. A) PrMATE1 protein with different conformers of catechin as ligand in side view and axial view. B) PrMATE1-mutant protein with a catechin as ligand in side view and axial view. For catechin, a coloured gradient is used: blue for the most favourable energy, red for the least favourable one.
Supplementary Figure 4: Protein-ligand interaction mode by docking studies. A) PrMATE1 protein with different conformers of cyanidin 3’-O-glucoside as ligand in side view and axial view. B) PrMATE1-mutant protein with a cyanidin 3’-O-glucoside as ligand in side view and axial view. For cyanidin 3’-O-glucoside, a coloured gradient is used: blue for the most favourable energy, red for the least favourable one.
Supplementary Figure 5: Protein-ligand interaction mode by docking studies. A) PrMATE1 protein with different conformers of epicatechin 3’-O-glucoside as ligand in side view and axial view. B) PrMATE1-mutant protein with a epicatechin 3’-O-glucoside as ligand in side view and axial view. For epicatechin 3’-O-glucoside, a coloured gradient is used: blue for the most favourable energy, red for the least favourable one.
Supplementary Figure 6: Structural superposition of native PrMATE1 model and PrMATE1-mutant model. (A) Side view, (B) axial view, and (C) a detailed view of the recognition site after structural superposition that shows five residues mutated. In orange the PrMATE1-mutant, and grey shows the native PrMATE1 structural model.
Supplementary Table 1. Validation of PrMATE1 protein structures using PROCHECK program (Ramachandran plot)

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a Most favourable region;  b Additional allowed regions;  c Generously allowed regions;  d Disallowed regions.