to the SMR are small in terms of their primary structural features, ranging between 100 and 200 amino acid residues in their polypeptide chains (Grinius and Goldberg 1994). Consequently, the relatively short polypeptides possessed by transporters of the SMR family leave room for only approximately four transmembrane segments to be present per polypeptide, requiring that these monomer polypeptides assemble into larger multimers in order to form complete structural configurations that accommodate solute transport across the membrane (Paulsen et al. 1996; Nara et al. 2007; Bay et al. 2008). Topological studies have indicated that the SMR transporters consist of either homooligomers or heterooligomers, depending on the nature of the particular transport system of interest (Nara et al. 2007; Kolbusz et al. 2010; Stockbridge et al. 2013). Interestingly, certain members of the SMR family have been implicated to assemble into a multipartite complex involving OmpW, an outer membrane protein in *E. coli* (Beketskaia et al. 2014). Extensive effort has been directed upon the SMR efflux pumps from a structure–function perspective (Wong et al. 2014; Padariya et al. 2015; Qazi et al. 2015), substrate-binding site analyses (Bay and Turner 2009; Wong et al. 2014; Banigan et al. 2015; Padariya et al. 2015; Dastvan et al. 2016), mechanistic studies of substrate translocation (Schuldiner 2009; Wong et al. 2014), effects of membrane lipid composition on transport activities (Bay and Turner 2013; Mors et al. 2013), and in terms of transport modulation (Ovchinnikov et al. 2018). One of the best studied transporters of the SMR family is EmrE, from *E. coli* (Schuldiner 2009; Padariya et al. 2015; Qazi et al. 2015; Dastvan et al. 2016; Ovchinnikov et al. 2018). As such, EmrE is an excellent model system for efflux inhibitor studies (Nasie et al. 2012; Dutta et al. 2014; Ovchinnikov et al. 2018).

8.1.2.5 PACE Family of Drug Transporters

Transporters of the PACE family represent a recent development in solute transport biology (Hassan et al. 2015, 2018). A key member of the PACE family to emerge, AceI, had originated from *A. baumannii*, which has been demonstrated to confer multidrug resistance in host cells (Hassan et al. 2013). Homologues of AceI and belonging to the PACE family have been located in a variety of bacterial species (Hassan et al. 2013, 2015). Interestingly, it was reported that chlorhexidine, a known substrate for AceI, enhanced the expression of the *aceI* gene and that exposure to the inducer provided increased levels of resistance to chlorhexidine in *Acinetobacter baylyi* host cells (Fuangthong et al. 2011). It is anticipated that as newer investigations are reported for members of the PACE family of drug transporters, these transporter systems will become increasingly important both at the biomedical science research and at clinical medicine levels.