transporters harbor at least two or more sets each of 6-helical hydrophobic membrane spanning domains and two highly conserved intracellularly located hydrophilic nucleotide-binding domains (Nikaido and Hall 1998). Other elements of the ABC drug transporters include an ATP signature structural motif, conserved Walker A and Walker B sequence and structural motifs, and loop structures, denoted as Q, D, and H loops (Altenberg 2004).

8.1.1.2 Bacterial ABC Drug Transporters

Several key bacterial pathogens possess ABC drug transporters. The *Staphylococcus aureus* bacteria, serious clinical pathogens in their own right, harbor several known ABC transporters. One of these, Sav1866, confers resistance to vinblastine, tetraphenylphosphonium, Hoechst 33342, and ethidium bromide and has had its crystal structure determined to a 3 Å resolution (Dawson and Locher 2006). Another drug efflux system of the ABC transporter type, Isa(E), bestows resistance to lincosamides, streptogramin A, and the pleuromutilins in both methicillin-susceptible and methicillin-resistant strains of *S. aureus* (Wendlandt et al. 2013). The cholera-causing *Vibrio cholerae* bacteria express the ABC efflux pump called VcaM, which transports doxorubicin, daunomycin, and fluoroquinolones, such as norfloxacin and ciprofloxacin, conferring resistance to these agents (Huda et al. 2003b; Lu et al. 2018). In *Escherichia coli*, one example of an intensively studied ABC transporter is the MacB pump, which transports primarily members of the macrolide class of antimicrobial agents (Kobayashi et al. 2001). Interestingly, MacB associates with an accessory secondary active transporter, called MacA, a peripheral membrane associated protein of the membrane fusion superfamily, and TolC, an outer membrane protein, all of which come together to confer bacterial drug resistance (Kobayashi et al. 2001; Lin et al. 2009). A similar tripartite ABC drug transporter system also resides in key *Salmonella enterica* bacteria, although this particular system is less well understood (Bogomolnaya et al. 2013). In the respiratory pathogen *Streptococcus pneumoniae*, an ABC drug exporter system called PatAB was discovered to confer resistance against fluoroquinolone agents (Baylay et al. 2015). Another tripartite ABC drug efflux system, FuaABC, was found in the pathogen *Stenotrophomonas maltophilia*, and its transport system was demonstrated to provide resistance against fusaric acid (Hu et al. 2012). The causative agent of tuberculosis, *Mycobacterium tuberculosis*, was found to contain an ABC transporter, called Rv1218c, which confers resistance to a variety of antimicrobials, like the pyridones, pyrroles, biaryl-piperazines, and bisanilino-pyrimidines (Balganesh et al. 2010; Wang et al. 2013). These ABC transporters and others will undoubtedly continue to be important model systems for investigations of solute transport involving antimicrobial agents not only in bacterial microorganisms but also in conferring resistance to anticancer chemotherapeutics in human medicine (Li et al. 2016).