simulation needed to cover the timescale of conformational changes of peptides in the presence of membrane (order of several microseconds) is often bottleneck for efficient design of novel peptides using this approach. Therefore, in this section, some alternative methods to AMP design are considered.

As the structural diversity of AMPs with their conformational flexibility prevents the straightforward establishment of structure–activity relationships, testing a set of peptides with random sequences can provide a basis for developing a QSAR model by the amino acid composition of the most active peptides. Such a model created by using artificial neural networks enabled a development of quantitative and predictive *in silico* models of antibiotic activity that successfully predicted the activity of 100 000 virtual peptides (Cherkasov et al. 2009). The inclusion of the genetic algorithm heuristic search method improved further the identification of additional active peptides with greater efficiency, which was confirmed by *in vitro* testing of most promising candidates against several resistant bacterial strains (Fjell et al. 2011).

The use of machine learning approaches can be utilized to develop predictive models based on the results of short molecular dynamics simulations of AMPs (100 ns). The predicted 3D structures of AMPs extracted from the molecular dynamics simulation trajectories were used to calculate their 3D descriptors used to build random forest (RF) and support vector machine (SVM) models. These models were used to design novel AMPs, with proven antibacterial activities in *in vitro* experiments against several strains of bacteria (Liu et al. 2018).

The analysis of the sequence of AMPs is less demanding on computational resources. The arrangement and frequencies of amino acid residues in known AMP sequences carry information on the propensity of residue combinations to form particular structures. While the sequences can be used as strings in the development of predictive SVM models (Meher et al. 2017; Bhadra et al. 2018), it would be beneficial to understand the underlying principles and relationships behind particular arrangements of amino acids and their activities. A long short-term memory (LSTM) language model was developed that correctly deciphered the underlying grammar of AMP sequences. The application of this model has resulted in a lead molecule with potential to inhibit methicillin-resistant and carbapenem-resistant clinical isolates *in vitro* and *in vivo* activity (Nagarajan et al. 2018).

It is apparent that the further work on the design of novel peptides should encompass the prediction of their primary and tertiary structure. Therefore, as much the structural information available in the Protein Data Bank is needed, the information available in the AMP database (APD) (Wang et al. 2016), the collection of sequences and structures of antimicrobial peptides (CAMP) (Waghu et al. 2016), and the database of biofilm-active antimicrobial peptides (BaAMPs) (Di Luca et al. 2015) should be equally utilized.