analysis of such large and complex data sets increasingly requires the use of artificial intelligence methods to ensure the best outcome of the rational design of therapeutic agents.

13.3 Identification of Novel Targets and Novel Mechanisms of Action

A recent analysis of FDA-approved drugs indicates that only 198 biomolecules from various pathogens are targeted by antibiotics for the use in humans (Santos et al. 2016). This limited number of bacterial targets in combination with the significant decrease in number of approved antibiotics (Kinch et al. 2014; Kinch and Griesenauer 2018) that either belong to the previously known class or do act on known target class (Coussens et al. 2018) signifies the need to design molecules that would bypass resistance mechanisms by acting on novel bacterial targets. It is believed that such novel antibiotics would, therefore, reduce the likelihood of cross-resistance through the existing resistance mechanisms as they would inherently have a possibly different mode of action (Chopra et al. 2002). Furthermore, identifying novel targets in the bacterial resistant strains would be essential to address the issues related to failed treatments of infections by these pathogens.

The application of genome sequencing techniques can be used not only for the detection of pathogens and monitoring the spread of infection (Punina et al. 2015), but also it can reveal the capacity of pathogens to encode proteins, which potentially serve as targets for antibiotics. In combination with information that can be obtained from metabolomic, proteomic, and transcriptomic techniques, whole genome sequencing can identify those proteins that are essential for the pathogen survival (Fields et al. 2017) and possibly orthologue to those found in human. Identification of such proteins, especially those that do not belong to known classes of drug targets, would ensure that any novel antibiotic developed would have minimal side effects.

Genome sequence of multiple strains of *Staphylococcus aureus* revealed a core genome comprising 1441 genes with 239 genes conserved in all *S. aureus* strains. Interestingly, 94 of these genes are experimentally found to be essential for *Escherichia coli*, providing opportunities for developing inhibitors of proteins encoded by these genes as potential antibiotics (Bosi et al. 2016). A genome-wide protein interaction network, interactome, can further improve the understanding of essential biochemical pathways in bacteria and support identification of pathogen-specific proteins as putative drug targets. A protein interaction network built between proteins of a selected *S. aureus* strain, MRSA252, enabled identification of pyruvate kinase as an essential hub protein in MRSA interactome. The significant divergence of MRSA and human