Genes capable of conferring resistance to clinically used antibiotics have been found in many different natural environments. However, a concise overview of the resistance genes found in common human bacterial pathogens is lacking, which complicates risk ranking of environmental reservoirs. Here, we present an analysis of potential antibiotic resistance genes in the 17 most common bacterial pathogens isolated from humans. We analyzed more than 20,000 bacterial genomes and defined a clinical resistome as the set of resistance genes found across these genomes. Using this database, we uncovered the co-occurrence frequencies of the resistance gene clusters within each species enabling identification of co-dissemination and co-selection patterns. The resistance genes identified in this study represent the subset of the environmental resistome that is clinically relevant and the dataset and approach provides a baseline for further investigations into the abundance of clinically relevant resistance genes across different environments. To facilitate an easy overview the data is presented at the species level at www.resistome.biosustain.dtu.dk.