Background and importance Antimicrobial resistance (AMR) is one of the most important global threats and antibiotic (mis)use is one of the main drivers behind it. Previously we identified suboptimal antibiotic use at our emergency department. International antibiotic guidelines for specific conditions cannot be adopted without the knowledge of local epidemiology and resistance, these are the essential first steps to develop an empirical antibiotic protocol.

Aim and objectives To identify predominant isolates, clinical specimens and reveal resistance patterns of bacterial isolates.

Materials and methods The study was performed at the emergency department of the University of Szeged. All positive microbiological isolates were retrieved for a five-year period. Non-bacterial isolates, contaminants and duplicate isolates were screened and excluded. Bacterial identification was performed using MALDI-TOF MS. Antibiotic susceptibility-testing and interpretation of drug resistance were based on ESCMID/EUCAST standards.

Results Finally, 6885 bacterial isolates were recovered of which nearly two-thirds (n=4502 isolates) were Gram-negative species. Blood culture (35.6%), urinary samples (urinary catheter-23.1%, midstream urine-12.1% or deep wound or abscess samples (14.0%) were the most frequent clinical specimens. The Escherichia genus (n=2194) was the most frequent Gram-negative isolate (with one exception E. coli), followed by members of the Klebsiella genus (n=664, most frequently K. pneumoniae) and the Proteus spp. (n=526, most frequently P. mirabilis). Staphylococcus aureus (n=561), Enterococcus spp. (n=471) and Streptococcus pneumoniae (n=431) were the most frequent Gram-positive isolates. The top three Gram-positive and Gram-negative isolates were responsible for nearly 75% -75% of the corresponding clinical isolates. The ciprofloxacin resistance was above 30% for E.coli and K.pneumoniae and were above 40% for P. mirabilis. On the other hand E.coli was susceptible in acceptable rate (below 20%) for many beta-lactams. For gram positives vancomycin resistant E. faecium (VRE) was detected in 33.3%, while methicillin resistant S. aureus (MRSA) was detected in 16.1%.

Conclusion and relevance The most frequent bacteria and current resistance patterns were identified. Some of the revealed resistance patterns (e.g. high fluoroquinolone resistance among Gram-negative bacteria) may pose therapeutic challenges. The results of this survey will guide the development of our local antibiotic guideline.