Here is a short abstract of Dipannita's PhD thesis work:

Rise in multidrug resistant and highly virulent bacterial pathogens makes it imperative to not only monitor the spread of these pathogenic bacteria carrying classical resistance and virulence markers, but also makes it essential to explore non-classical mechanisms that confer higher survival advantage leading to increased pathogenic potential. Here, we investigated the prevalence of multidrug resistance conferring antimicrobial resistance genes (ARGs) in community-acquired paediatric UTIs and found that CTX-M-type extended-spectrum beta-lactamases (ESBLs) are the most common ARGs in our communities, which mirrors the global shift to CTX-M-type ESBL from TEM- and SHV-type ESBLs. We also found the high-risk clonal group, ST131, to be the most common causative pathogen of paediatric UTIs.

Next, we investigated how triclosan, a common household biocide, affects the chromosome structure of E. coli. We mapped the structural landscape of wild-type and Δdcm E. coli chromosomes under triclosan stress using Hi-C to identify triclosan-induced chromosomal interaction domains (CIDs). Two CIDs were common to the wild-type and Δdcm E. coli, including a CID with a common boundary at fabI gene, which encodes the triclosan target. All mutations and structural variants under triclosan stress were observed within or in close proximity to triclosan-induced CIDs. Absence of Dcm methylation impacts both short- and long-range interactions in triclosan stress. Single-base resolution methylome maps reveal hypermethylation of adenines (in wild-type and Δdcm) and cytosines (in wild-type) in the two common triclosan-induced CIDs. Furthermore, global gene expression profiling identified enrichment of highly expressed genes within the two common CIDs.

Lastly, we also explored epigenetic signatures associated with the recently emergent hypervirulent K. pneumoniae (hvKp). The hvKp pathotype has overall higher levels of adenine and cytosine methylation compared to its classical counterpart. Virulence genes are hypermethylated compared to other genes in hvKp. Furthermore, we found several differentially methylated genes (DMGs) in hvKp, including an efflux pump associated with multidrug resistance and biofilm formation, and functional classification of these DMGs showed that most are involved in inorganic ion transport and metabolism. Overall, our findings indicate that it is crucial to examine both classical and non-classical mechanisms regulating bacterial physiology and pathogenesis, as this can lead to the discovery of novel drug targets, diagnostic markers or improved strategies for treating bacterial infections.