evotec

#RESEARCHNEVERSTOPS

EvostrAIn™

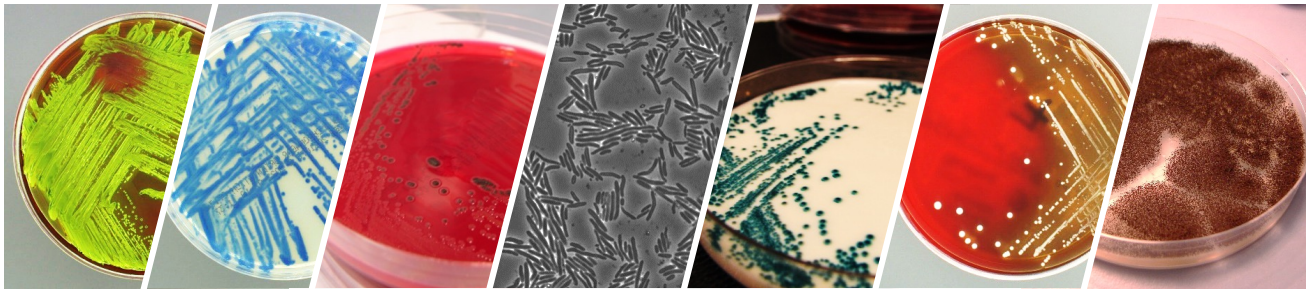
- EvostrAIn™ is a comprehensive collection of geographically diverse human pathogenic bacteria and fungi. The collection includes reference strains and clinical isolates including the ESKAPE pathogens, strains from the WHO priority pathogen lists and CDC antibiotic resistance threats reports. Currently the collection has over 10,000 isolates and is constantly being updated
- The collection is highly characterised and in many cases, strains are fully sequenced with defined mechanisms of resistance. This enables the strains to be used to de-risk cross-resistance towards known targets. TPP focused panels can be used at any stage of the projects, from hit identification to profiling of lead compounds and candidates, both *in vitro* and *in vivo*
- Many strains and isolates are validated in *in vivo* models of infection allowing rapid progress and continuity from *in vitro* to *in vivo* models of disease

Areas of expertise

Antimicrobial resistance

Bacterial, fungal and viral pathogens

In vitro, *in vivo* and Hollow Fibre Infection Models



Strain Characterisation

The EvostrAIn™ collection of isolates has broad geographical, temporal, genotypic and phenotypic diversity. Isolates are characterised using a combination of:

- Whole-genome sequencing
- Biochemical testing using the Vitek 2 Compact and standard laboratory techniques
- Antimicrobial susceptibility testing using both CLSI and EUCAST guidelines as well as bespoke methods developed in conjunction with clients and collaborators

These methods allow not only species and strain identification but also:

- Detection of the presence (or absence) of resistance and virulence factors
- Antimicrobial susceptibility profiling
- Multilocus sequence typing (MLST) and for some species *in silico* serotyping
- Comparative bioinformatics and genomics
- Metabolic pathways characterisation
- Plasmid identification
- Pangenomic analysis (prevalence of a specific gene or mutation within the collection)
- Phylogenetic analysis (comparison of genomes to known data)
- Genome-wide association studies (GWAS)

This level of characterisation allows us to provide highly bespoke optimised panels of organisms to drive our partners antimicrobial drug discovery program forwards, or select relevant strains to address specific questions. These bespoke panels can be used for:

- Antimicrobial susceptibility testing to industry standards, including combination testing
- Biofilm formation and eradication
- Frequency of resistance
- Mechanism of action / resistance
- *In vitro* PK-PD assays including killing kinetics, post-antibiotic effect (PAE), and the Hollow Fibre Infection Model
- *In vivo* PK/PD models

Selected examples of species available (many more available on request)

Gram negative bacteria

- *Escherichia coli*
- *Klebsiella pneumoniae*
- *Acinetobacter baumannii*
- *Pseudomonas aeruginosa*
- *Neisseria gonorrhoeae* and *N. meningitidis*
- *Mycoplasma*
- *Chlamydia*

Gram positive bacteria

- *S. aureus* (MSSA, MRSA and VRSA)
- *Enterococci* (including VRE)
- *Streptococci* (including *S. pyogenes* and S. *pneumoniae*)
- *Lactobacilli*

Anaerobes

- *Clostridioides difficile*
- *Clostridium perfringens*
- *Bacteroides fragilis*
- *Faecalibacterium prausnitzii*
- *Akkermansia muciniphila*
- *Bifidobacterium longum*
- *Alistipes finegoldii*
- *Fusobacterium nucleatum*

Fungi

- *Candida spp.* (Including *C. auris, C. albicans and C. tropicalis*)
- *Cryptococcus neoformans*
- *Aspergillus spp.* (including *A. fumigatus* and *A. flavus*)
- *Dermatophytes* (*Epidermophyton floccosum, Trichophyton rubrum* and *T. mentagrophytes*)

Mycobacteria

- *Mycobacterium tuberculosis*
- *Non-tuberculosis mycobacteria*