

Functional Genomics for Infectious Disease

- Pathogen functional genomics analyses for unbiased, multidimensional small molecule effect characterisation (RNA-, DNA-seq analyses to characterise pathogen genome and transcriptome)
 - Genome assembly and annotation with a focus on resistance and virulence (Illumina, ONT, hybrid)
 - Short- (SNP, short indels) and long-range (insertion, deletion, inversion, translocation, duplication) variant analysis associated with resistance (Illumina, ONT)
 - Bacterial genome wide association study (GWAS)
 - Transcriptome analysis (RNAseq) and functional interpretation
 - Bacterial population sequencing and variant characterisation (PoolSeq)
 - Molecular phylogeny
 - Network analysis (enrichment analysis, pathway mapping)
- Custom bioinformatics analyses using Artificial Intelligence (AI)

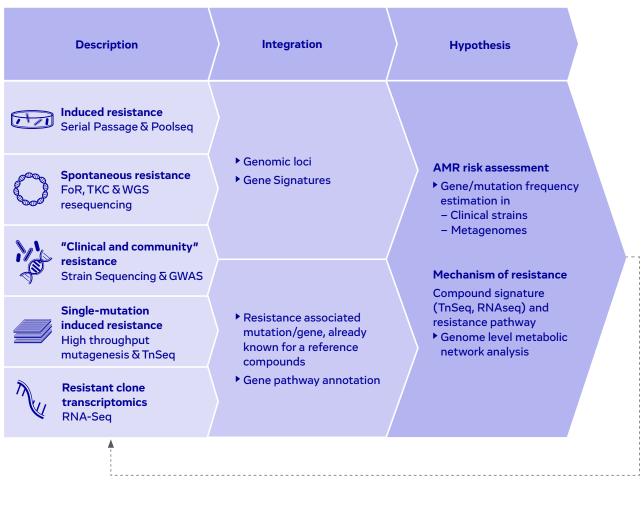
	Target ID & Screening	Hit-to-Lead	Lead Optimisation	Late Lead Optimisation	IND and Clinical studies
Genomics WGS, Pool-seq		Target ID & MoR			MoR
Transposon Sequencing	Target ID	Target ID, MoR & MoA		Translation In vitro / In vivo)
Transcript- omics (dual-) RNA-seq	Target ID	MoR & MoA		Translation In vitro / In vivo	<i>In silico</i> toxicity prediction

Pathogen and host response multi-omics analyses



- Genomics database of EvoStrain[™], Evotec's large and rapidly evolving collection of phenotypically characterised strains
- ► EvoStrain[™] genomics toolbox to design *in silico* optimised screening panels according to Target Product Profile (TPP)

- In silico strain typing, pangenome analysis, plasmid identification, target comparative genomics/protein analysis
- Saturated transposon library sequencing for MoA, MoR and translational model assessment, using essential gene and differential fitness analyses
- Genome scale metabolic model analysis for omics data integration identifying MoA and MoR to de-risk programs
- BSL2/3, NGS, phenomics and bioinformatics 'under the same roof'



From genome-wide data to hypothesis