

# COMBINE Preclinical Bacterial Repository

## Bacterial Identification

Bacterial Strain	DSMZ ID	Historical ID
<i>Pseudomonas aeruginosa</i>	DSM 116114	PA.88276

The bacterial species has been confirmed by 16S rDNA gene sequencing.

## Bacterial Isolation

Country	Institution	Date	Source
UK	North Bristol NHS Trust	22/11/2019	Blood Culture

## Antimicrobial resistance

Meropenem	Levofloxacin
Not resistant	Not resistant

*In vitro* antimicrobial resistance has been determined following EUCAST guidelines.

## Intended use

The [COMBINE<sup>1</sup>](#) Preclinical Bacterial Strain Repository contains Gram-negative bacterial strains shown to be reproducibly virulent in the COMBINE murine pneumonia models. The COMBINE protocol was developed

together with stakeholders from academia, industry and regulatory experts to standardise and refine antimicrobial efficacy models. Key information were published in a summary report ([Arrazuria et al., 2022](#))<sup>2</sup>.

## *In Vivo* Virulence

*In vivo* virulence was assessed in CD-1 mice rendered neutropenic by intraperitoneal administration of 150 mg/kg and 100 mg/kg cyclophosphamide on days -4 and -1 pre infection, respectively. Following intranasal inoculated with approximately  $1-2 \times 10^8$  CFU, strains were considered virulent when the following criteria were met:

- Baseline bacterial burden of 6-7 log<sub>10</sub> CFU/lung 2 h post infection;
- At least 1 log<sub>10</sub> increase in CFU/lung relative to baseline at the humane or experimental endpoint ( $\leq 26$  h);
- Endpoint being reached between 12 h and 26 h post infection.

*In vivo* virulence has been confirmed in two independent laboratories following the COMBINE protocol.

## Acquisition

Strains of the COMBINE Preclinical Bacterial Repository are made available via the German Collection of Microorganisms and Cell Cultures (DSMZ).  
<https://www.dsmz.de/collection/catalogue/details/culture/DSM-116114>

## Contact

Inquiries may be addressed to [IMI-COMBINE@pei.de](mailto:IMI-COMBINE@pei.de).

<sup>1</sup> <https://amr-accelerator.eu/project/combine/>

<sup>2</sup> Arrazuria et al., Front Microbiol, 2022, doi 10.3389/fmicb.2022.988725