

EURGen_C26-23 is an **OXA-484-producing *Escherichia coli*** strain from Denmark

Sequence type:

ST471 (Pasteur)

ST410 (Achtman)

Resistance genes and mutations¹:

Antimicrobial agent	Resistance gene	Reported gene with mutation or insertion and reported change
Carbapenems	<i>bla</i> _{OXA-484}	Not detected
Third generation cephalosporins	<i>bla</i> _{CMY-42}	Not detected
Other beta-lactams	<i>bla</i> _{TEM-1}	<i>ftsI</i> insertion YRIN_N337N
Colistin	Not detected	Not detected
Fluoroquinolones	<i>qnrS1</i>	<i>gyrA</i> _D87N, <i>gyrA</i> _S83L, <i>parC</i> _S80I, <i>parE</i> _S458A
Aminoglycosides	<i>aac(3)-IId</i> , <i>aadA5</i> , <i>aph(3'')-Ib</i> , <i>aph(6)-Id</i>	Not detected
Tetracyclines	<i>tet</i> (B)	Not detected
Trimethoprim	<i>dfrA17</i>	Not detected
Sulphonamide	<i>sul2</i>	Not detected
Fosfomycin	Not detected	Not detected

¹Detected using AMRFinder 4.2.7 and ResFinder 4.7.2 (database 2.6.0)

Phenotype:

Antimicrobial agent	Reference MIC (mg/ml)	Reference inhibition zone (mm) ²	Interpretation ³
Piperacillin-tazobactam	>64	6	R
Cefiderocol	ND	13-18	R
Cefotaxime	>8	6	R
Ceftazidime	>16	6	R
Ceftazidime-avibactam	8	13-14	S ⁴
Ceftolozane-tazobactam	>16	6	R
Ertapenem	>2	12-16	R
Imipenem	1-2	19-23	S ⁵
Imipenem-relebactam	0.5-2	23-25	S
Meropenem	1	22-24	S ⁴
Meropenem-vaborbactam	0.5-1	20-23	S
Aztreonam	>16	6	R
Aztreonam-avibactam	>16	16-18	R
Ciprofloxacin	>4	6	R
Levofloxacin	>4	6	R
Amikacin	1-2	20-23	S
Gentamicin	>16	6	R
Tobramycin	8	11-13	R
Tigecycline	0.125	20-22	S
Colistin	0.25-0.5	-	S
Trimethoprim-sulfamethoxazole	>16	6	R
Fosfomycin	0.5	25-28	S

ND: not determined

²Using EUCAST disk diffusion methodology (https://www.eucast.org/ast_of_bacteria/disk_diffusion_methodology)

³SIR-categorization according to The European Committee on Antimicrobial Susceptibility Testing. Breakpoint tables for interpretation of MICs and zone diameters. Version 16.1, 2026. <https://www.eucast.org>.

⁴ Inhibition zones are close to the breakpoint, increasing the risk of erroneous SIR categorisation.

⁵ MICs and inhibition zones are close to the breakpoint, increasing the risk of erroneous SIR categorisation.