

1 Table S1. PLZ Challenge Set Characterized Strains Listing

Strain	Organism	Genotype beta-lactams (<i>genes</i> identified by WGS)	Genotype aminoglycosides (PROTEINS and <i>genes</i> identified by WGS)	Beta-lactam and aminoglycoside [GEN, TOB, NET, AMI only]	BMD PLZ MIC (µg/mL)
1	<i>Citrobacter koseri</i>	<i>bla</i> _{TEM-110} <i>bla</i> _{MAL-CKO Like}	AAC(3)-IIa APH(3'')-Ib APH(6)-Id ANT(3'')-Ia	Acquired Pase Aminoglycoside resistant (AME*)	2
2	<i>Citrobacter koseri</i>	<i>bla</i> _{TEM-3} <i>bla</i> _{MAL-CKO Like}	AAC(6')-Ib like ANT(3'')-Ia	ESBL Aminoglycoside resistant (AME)	0.25
3	<i>Klebsiella aerogenes</i>	<i>bla</i> _{TEM-1}	AAC(3)-IIa AAC(6')-Ib like ANT(3'')-Ia APH(3'')-Ib APH(6)-Id	Carbapenem Resistant (impermeability) Aminoglycoside Resistant (AME)	0.5
4	<i>Enterobacter cloacae</i>	<i>bla</i> _{MIR}	None	Carbapenem Resistant (impermeability) Aminoglycoside wild	0.25
5	<i>Escherichia coli</i>	<i>bla</i> _{TEM-2}	APH(3')-Ib	Acquired Pase Aminoglycoside wild	0.25
6	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{TEM-11} <i>bla</i> _{SHV-83}	AAC(3)-IIa ANT(3'')-Ia	ESBL and/or SHV hyperproduction Aminoglycoside Resistant (AME)	0.25
7	<i>Escherichia coli</i>	<i>bla</i> _{TEM-21}	AAC(3)-IIa AAC(6')-Ib like	ESBL Aminoglycoside Resistant (AME)	1
8	<i>Escherichia coli</i>	<i>bla</i> _{TEM-29} <i>bla</i> _{CTX-M}	AAC(3)-IIa ANT(3'')-Ia APH(3'')-Ib APH(6)-Id	ESBL Aminoglycoside Resistant (AME)	0.5
9	<i>Klebsiella aerogenes</i>	<i>bla</i> _{TEM-24} <i>bla</i> _{AMPC}	AAC(6')-Ib like ANT(3'')-Ia	ESBL Aminoglycoside Resistant (AME)	1
10	<i>Citrobacter freundii</i>	<i>bla</i> _{CMY-2 like} <i>bla</i> _{TEM-3} <i>bla</i> _{OXA-10 like}	AAC(3)-IIa AAC(6')-Ib like AAC(6')-If ANT(3'')-Ia	ESBL Aminoglycoside Resistant (AME)	0.5
11	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SHV (multiple alleles including one for an ESBL)} <i>bla</i> _{KPC} <i>bla</i> _{OXA-9 Like} <i>bla</i> _{FOX} <i>bla</i> _{CARB-1 like}	AAC(3)-IVa AAC(6')-Ib like ANT(2'')-Ia ANT(3'')-Ia APH(3')-Ia APH(4)-Ia	ESBL + Acquired Case + Carbapenemase (KPC) Aminoglycoside Resistant (AME)	0.25
12	<i>Citrobacter freundii</i>	<i>bla</i> _{CMY-2 like}	None	High level Case Aminoglycoside wild	1

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13	<i>Escherichia coli</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{KPC} <i>bla</i> _{OXA-1} like	AAC(6')-IIc ANT(3'')-Ia APH(3'')-Ib APH(6)-Id	Carbapenemase (KPC) Aminoglycoside Resistant (AME)	2
14	<i>Enterobacter cloacae</i>	<i>bla</i> _{VIM}	AAC(6')-II ANT(3'')-Ia APH(3')-Ia APH(3'')-Ib APH(6)-Id	Carbapenemase (MBL) Aminoglycoside Resistant (AME)	0.5
15	<i>Enterobacter cloacae</i>	<i>bla</i> _{IMP} <i>bla</i> _{ACT}	AAC(6')-Ib like	Carbapenemase (MBL) Aminoglycoside Resistant (AME)	0.25
16	<i>Serratia marcescens</i>	<i>bla</i> _{VIM} <i>bla</i> _{SEC}	AAC(6')-Ic AAC(6')-II ANT(3'')-Ia	Carbapenemase (MBL) Aminoglycoside Resistant (AME)	1
17	<i>Serratia marcescens</i>	<i>bla</i> _{IMP} <i>bla</i> _{OXA-1} like <i>bla</i> _{SEC}	AAC(6')-Ic	Carbapenemase (MBL) Aminoglycoside Resistant (AME)	1
18	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SHV} (multiple alleles including one for an ESBL) <i>bla</i> _{VIM} <i>bla</i> _{MOX}	AAC(6')-II AAC(6')-I _p ANT(3'')-Ia APH(2'')-IIa APH(3')-Ia APH(3'')-Ib APH(6)-Id	ESBL + Acquired Case + Carbapenemase (MBL) Aminoglycoside Resistant (AME)	0.5
19	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{shv} (multiple alleles including one for an ESBL) <i>bla</i> _{KPC} <i>bla</i> _{OXA-9} like	AAC(6')-Ib like ANT(3'')-Ia	ESBL + Carbapenemase (KPC) Aminoglycoside Resistant (AME)	0.25
20	<i>Citrobacter freundii</i>	<i>bla</i> _{CMY-2} like <i>bla</i> _{NDM} <i>bla</i> _{OXA-10} like truncated <i>bla</i> _{CTX-M}	AAC(3)-IIa AAC(6')-Ib like truncated ANT(2'')-Ia ANT(3'')-Ia	ESBL + Carbapenemase (MBL) Aminoglycoside Resistant (AME)	0.5
21	<i>Citrobacter freundii</i>	<i>bla</i> _{TEM-2} <i>bla</i> _{CMY-2} like	AAC(3)-IIa ANT(3'')-Ia	Acquired Pase Aminoglycoside Resistant (AME)	0.25
22	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SHV-1} <i>bla</i> _{OXA-48}	None	Carbapenemase (OXA-48) Aminoglycoside wild	0.25
23	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{CTX-M} <i>bla</i> _{SHV-11} <i>bla</i> _{NDM} <i>bla</i> _{OXA-1} like	AAC(3)-IIa AAC(6')-Ib like truncated AAC(6')-Ib-cr truncated ANT(3'')-Ia	ESBL + Carbapenemase (MBL) Aminoglycoside Resistant (AME)	0.25

Strain	Organism	Genotype beta-lactams (<i>genes</i> identified by WGS)	Genotype aminoglycosides (PROTEINS and <i>genes</i> identified by WGS)	Beta-lactam and aminoglycoside [GEN, TOB, NET, AMI only]	BMD PLZ MIC (µg/mL)
24	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{CTX-M} <i>bla</i> _{TEM} truncated <i>bla</i> _{SHV} truncated <i>bla</i> _{NDM} <i>bla</i> _{OXA-1} like <i>bla</i> _{OXA-9} like <i>bla</i> _{DHA} truncated	AAC(3)-IIa AAC(6')-Ib like truncated APH(3'')-Ib APH(6)-Id <i>armA</i>	ESBL + Carbapenemase (MBL) Aminoglycoside Resistant (AME and RNA methylase <i>armA</i>)	>256
25	<i>Providencia stuartii</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{NDM} <i>bla</i> _{VEB} <i>bla</i> _{CMY-2} like	AAC(2')-Ia APH(3')-Ia APH(3'')-VI APH(3'')-Ib APH(6)-Id ? ANT(3'')-Ia <i>rmtC</i>	ESBL + Acquired Case +Carbapenemase (MBL) Aminoglycoside Resistant (AME and RNA methylase <i>rmtC</i>)	256
26	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{CTX-M} <i>bla</i> _{TEM-1} <i>bla</i> _{SHV-11} <i>bla</i> _{OXA-181} <i>bla</i> _{OXA-1} like	AAC(3)-IIa AAC(6')-Ib like truncated AAC(6')-Ib-cr truncated ANT(3'')-Ia APH(3'')-Ia APH(3'')-Ib APH(6)-Id <i>rmtF</i>	ESBL + Carbapenemase (OXA-181) Aminoglycoside resistant (AME and RNA methylase <i>rmtF</i>)	>256
27	<i>Escherichia coli</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{CTX-M}	APH(3'')-Ib APH(6)-Id ANT(3'')-Ia <i>rmtB</i>	ESBL Aminoglycoside resistant (RNA methylase <i>rmtB</i>)	>256
28	<i>Escherichia coli</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{NDM} <i>bla</i> _{VEB} <i>bla</i> _{OXA-9} like	AAC(6')-Ib like truncated APH(3'')-Ib APH(6)-Id ANT(2'')-Ia ANT(3'')-Ia <i>armA</i>	ESBL + Carbapenemase (MBL) Aminoglycoside resistant (AME and RNA methylase <i>armA</i>)	>256
29	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{CTX-M} <i>bla</i> _{TEM-1} <i>bla</i> _{SHV-1} <i>bla</i> _{OXA-48} <i>bla</i> _{OXA-1} like	AAC(3)-IIa AAC(6')-Ib-cr APH(3')-Ia APH(3'')-Ib APH(6)-Id	ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME)	0.25
30	<i>Escherichia coli</i>	<i>bla</i> _{CTX-M} <i>bla</i> _{TEM-1} <i>bla</i> _{OXA-48}	AAC(3)-IIa ANT(3'')-Ia APH(3'')-Ib APH(6)-Id	ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME)	0.5
31	<i>Citrobacter koseri</i>	<i>bla</i> _{MAL-CKO} Like	None	Pase Aminoglycoside wild	0.25
32	<i>Klebsiella oxytoca</i>	<i>bla</i> _{OXY}	APH(3')-Ia truncated	Beta lactam and Aminoglycoside wild	0.5

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33	<i>Klebsiella oxytoca</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{OXA-2 Like} truncated <i>bla</i> _{OXY}	AAC(6')-IIc ANT(2'')-Ia truncated APH(3'')-Ia APH(3'')-Ib APH(6)-Id	Carbapenem Resistant (impermeability) Aminoglycoside Resistant (AME)	1
34	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SHV-12} <i>bla</i> _{OXA-48} <i>bla</i> _{OXA-1 like}	AAC(3)-IIa AAC(6')-Ib-cr ANT(3'')-Ia	ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME)	0.5
35	<i>Klebsiella oxytoca</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{KPC} <i>bla</i> _{OXA-9 like} <i>bla</i> _{OXY}	AAC(6')-Ib like ANT(3'')-Ia APH(3'')-Ia truncated APH(3'')-Ib APH(6)-Id truncated	Carbapenemase (KPC) Aminoglycoside Resistant (AME)	0.5
36	<i>Klebsiella oxytoca</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{KPC} <i>bla</i> _{OXA-9 like} <i>bla</i> _{OXY}	AAC(6')-Ib like ANT(3'')-Ia APH(3'')-Ia truncated APH(3'')-Ib APH(6)-Id truncated	Carbapenemase (KPC) Aminoglycoside Resistant (AME)	0.25
37	<i>Klebsiella oxytoca</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{KPC} <i>bla</i> _{OXA-9 like} <i>bla</i> _{OXY}	AAC(6')-Ib like ANT(3'')-Ia APH(3'')-Ia truncated APH(3'')-Ib APH(6)-Id truncated	Carbapenemase (KPC) Aminoglycoside Resistant (AME)	0.25
38	<i>Klebsiella oxytoca</i>	<i>bla</i> _{OXY}	None	High level natural Pase (K1) Aminoglycoside wild	0.25
39	<i>Enterobacter cloacae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{CTX-M} <i>bla</i> _{OXA-48} <i>bla</i> _{OXA-1 like} <i>bla</i> _{ACT}	AAC(3)-IIa AAC(6')-Ib-cr ANT(3'')-Ia APH(3'')-Ib truncated APH(6)-Id	ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME)	0.25
40	<i>Enterobacter cloacae</i>	<i>bla</i> _{SHV-12} <i>bla</i> _{VIM} <i>bla</i> _{ACT}	AAC(6')-Ib like ANT(3'')-Ia	ESBL + Carbapenemase (MBL) Aminoglycoside Resistant (AME)	0.25
41	<i>Escherichia coli</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{CTX-M} <i>bla</i> _{NDM} <i>bla</i> _{OXA-1 like} <i>bla</i> _{OXA-9 like} <i>bla</i> _{DHA} truncated	AAC(3)-IIa AAC(6')-Ib like truncated AAC(6')-Ib-cr truncated ANT(3'')-Ia <i>armA</i>	ESBL + Carbapenemase (MBL) Aminoglycoside resistant (AME and RNA methylase <i>armA</i>)	>256
42	<i>Klebsiella aerogenes</i>	<i>bla</i> _{TEM-24}	AAC(6')-Ib like truncated ANT(3'')-Ia	ESBL Aminoglycoside Resistant (AME)	0.5
43	<i>Enterobacter cloacae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SHV-12} <i>bla</i> _{ACT}	AAC(6')-Ib like AAC(6')-IIc ANT(3'')-Ia APH(3'')-Ib APH(6)-Id	ESBL Aminoglycoside Resistant (AME)	0.5

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44	<i>Enterobacter cloacae</i>	<i>bla</i> _{CTX-M} <i>bla</i> _{OXA-1} like <i>bla</i> _{ACT}	AAC(3)-IIa AAC(6')-Ib-cr ANT(3'')-Ia APH(3'')-Ib APH(6)-Id	ESBL Aminoglycoside Resistant (AME)	0.5
45	<i>Enterobacter cloacae</i>	<i>bla</i> _{CTX-M} <i>bla</i> _{SHV-12} <i>bla</i> _{ACT}	AAC(6')-Ib like ANT(2'')-Ia ANT(3'')-Ia	ESBL Aminoglycoside Resistant (AME)	0.25
46	<i>Enterobacter cloacae</i>	<i>bla</i> _{ACT}	None	High Level Case Aminoglycoside wild	0.5
47	<i>Enterobacter cloacae</i>	<i>bla</i> _{ACT}	None	Beta lactam and Aminoglycoside wild	0.5
48	<i>Providencia stuartii</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SCO} <i>bla</i> _{ACC}	AAC(2')-Ia APH(3'')-Ia APH(3'')-Ib APH(6)-Id ANT(3'')-Ia	Undetermined for beta-lactams Aminoglycoside wild	1
49	<i>Citrobacter freundii</i>	<i>bla</i> _{CMY-2} like	None	High Level Case Aminoglycoside wild	0.5
50	<i>Klebsiella aerogenes</i>	None	None	High Level Case Aminoglycoside wild	0.5
51	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SHV-11} <i>bla</i> _{CTX-M} <i>bla</i> _{OXA-1} like <i>bla</i> _{OXA-48}	AAC(3)-IIa AAC(6')-Ib-cr	ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME)	8
52	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SHV-11} <i>bla</i> _{CTX-M} <i>bla</i> _{OXA-1} like <i>bla</i> _{OXA-48}	AAC(3)-IIa AAC(6')-Ib-cr	ESBL + Carbapenemase (OXA-48) Aminoglycoside Resistant (AME)	16
53	<i>Proteus mirabilis</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SHV-12}	APH(3'')-Ia APH(3'')-Ib APH(6)-Id ANT(3'')-Ia	ESBL Aminoglycoside wild	32
54	<i>Klebsiella aerogenes</i>	None	None	Undetermined	8
55	<i>Morganella morganii</i>	<i>bla</i> _{DHA}	None	Undetermined	16
56	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SHV-11} <i>bla</i> _{KPC} <i>bla</i> _{OXA-9} like	AAC(6')-Ib like APH(3'')-Ib APH(6)-Id ANT(3'')-Ia	Carbapenemase (KPC) Aminoglycoside Resistant (AME)	2
57	<i>Klebsiella aerogenes</i>	<i>bla</i> _{SHV-12}	AAC(6')-Ib like AAC(6')-IIc ANT(3'')-Ia	ESBL + Carbapenem Resistant (impermeability) Aminoglycoside Resistant (AME)	1

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58	<i>Citrobacter freundii</i>	<i>bla</i> _{CMY-2} like	None	Beta lactam and Aminoglycoside wild	0.5
59	<i>Morganella morganii</i>	<i>bla</i> _{DHA}	None	High Level Case Aminoglycoside wild	8
60	<i>Morganella morganii</i>	<i>bla</i> _{DHA}	None	Beta lactam and Aminoglycoside wild	2
61	<i>Proteus mirabilis</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{CMY-2} like <i>bla</i> _{OXA-2} like	AAC(3)-IIa AAC(6')-Ib like ANT(3'')-Ia	ESBL + Acquired Case Aminoglycoside Resistant (AME)	8
62	<i>Proteus vulgaris</i> group	None	None	Acquired Pase Aminoglycoside wild	4
63	<i>Serratia marcescens</i>	None	AAC(6')-Ic	Undetermined for beta-lactams Aminoglycoside Resistant (AME)	1
64	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{SHV} (<i>multiple alleles including one for an ESBL</i>) <i>bla</i> _{OXA-10} like	APH(3'')-Ib APH(6)-Id truncated ANT(3'')-Ia truncated	ESBL + Carbapenem Resistant (impermeability) Aminoglycoside undetermined	8
65	<i>Serratia marcescens</i>	<i>bla</i> _{SEC}	None	Beta lactam and Aminoglycoside wild	1
66	<i>Proteus vulgaris</i> group	None	None	Acquired Pase or wild (cefuroximase) Aminoglycoside wild	4
67	<i>Proteus vulgaris</i> group	None	None	Acquired Pase Aminoglycoside wild	2
68	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{SHV} (<i>multiple alleles including one for an ESBL</i>) <i>bla</i> _{VEB} <i>bla</i> _{OXA-10} like	AAC(6')-Ib like APH(3')-Ia APH(3'')-Ib APH(6)-Id ANT(2'')-Ia ANT(3'')-Ia <i>rmtB</i>	ESBL Aminoglycoside Resistant (AME and RNA methylase <i>rmtB</i>)	>256
69	<i>Escherichia coli</i>	<i>bla</i> _{TEM-1}	APH(3'')-Ib APH(6)-Id	Acquired Pase Aminoglycoside undetermined	4
70	<i>Proteus vulgaris</i> group	None	None	Undetermined	2
71	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{SHV-11}	None	Acquired Pase Aminoglycoside undetermined	4
72	<i>Proteus mirabilis</i>	<i>bla</i> _{TEM-1}	APH(3')-Ia APH(3'')-Ib APH(6)-Id ANT(3'')-Ia	Acquired Pase Aminoglycoside wild	4

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73	<i>Klebsiella oxytoca</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{OXY}	ANT(3'')-Ia	High level Natural Pase (K1) Aminoglycoside undetermined	2
74	<i>Proteus vulgaris</i> group	None	None	High level cefuroxime Aminoglycoside wild	4
75	<i>Escherichia coli</i>	<i>bla</i> _{TEM-1}	None	Acquired Pase Aminoglycoside undetermined	4
76	<i>Proteus mirabilis</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{CARB-1 like}	AAC(3)-Id APH(3')-Ia APH(3'')-Ib APH(6)-Id ANT(3'')-Ia	Inhibitor resistant Pase Aminoglycoside Resistant (AME)	2
77	<i>Klebsiella pneumoniae</i>	<i>bla</i> _{SHV-1} <i>bla</i> _{KPC}	<i>armA</i>	Carbapenemase (KPC) Aminoglycoside Resistant (RNA methylase <i>armA</i>)	>256
78	<i>Escherichia coli</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{CTX-M} <i>bla</i> _{OXA-1 like}	AAC(3)-IIa AAC(6')-Ib-cr ANT(3'')-Ia <i>rmtB</i>	ESBL Aminoglycoside Resistant (AME and RNA methylase <i>rmtB</i>)	>256
79	<i>Escherichia coli</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{CTX-M}	AAC(3)-IIa APH(3')-IIa ANT(3'')-Ia <i>rmtB</i>	ESBL Aminoglycoside Resistant (AME and RNA methylase <i>rmtB</i>)	>256
80	<i>Escherichia coli</i>	<i>bla</i> _{TEM-1} <i>bla</i> _{CTX-M}	AAC(3)-IIa	ESBL Aminoglycoside Resistant (AME)	1

2 *AME = Aminoglycoside Modifying Enzymes

3 Pase = penicillinase

4 Case = cephalosporinase