

Isolate	Bacterial species	Mutation targeted gene	Associated protein information	Mutation	Mutation type	Colistin MIC	Chlrohexidine MIC	Oxetidine MIC	Cefotaxime MIC	Ciprofloxacin MIC	AMX	AMXCLAV	TK	TCCLAV	PIPTAZ	PIP	TEM	FOX	CTX	AZT	CAZ	FEP	IMP	ERT	GEN	NET	TOB	AMK	NAL	OPX	CIP	SXT	POS
<i>Enterobacter cloacae</i> wild type	<i>E. cloacae</i>	/	/	/	/	0.125	10	2.5	0.0125	0.016	9	9	30	33	28	26	31	7	29	38	28	35	31	32	22	28	23	24	25	35	40	30	21
COL-M1	<i>E. cloacae</i>	- / → Gene_01288	NA /Hypothetical protein 85% homologous to YnfG	G→T	intogenic	32	40	2.5	0.023	0.012	8	8	26	26	24	23	25	6	24	34	24	30	24	27	23	23	21	22	24	33	38	28	19
CHX-M1	<i>E. cloacae</i>	hamA ← mptA → hamC ← hml →	Outer membrane protein assembly factor HamA MltA interacting protein Outer membrane protein assembly factor HamC TerR/AcrR family transcriptional regulator family	Δ1 bp T→A A→C C→T	deletion Y2108 *94E P66L	8	160	2.5	0.5	0.064	8	8	27	27	19	24	20	6	23	37	26	29	29	31	26	29	26	26	23	31	38	28	20
CHX-M2	<i>E. cloacae</i>	asd → / → glfB	Aspartate-semialdehyde dehydrogenase/1,4-alpha-glucan branching enzyme	G→T	intogenic	8	160	2.5	0.5	0.125	8	8	26	28	20	23	22	6	24	36	27	32	28	28	26	30	26	25	22	31	37	26	20
		hml →	TerR/AcrR family transcriptional regulator family	G→A	G187R																												
OCT-M1	<i>E. cloacae</i>	Gene_02347 → nasD ← / ← tsgA	Putative membrane protein with AamA-like domain, 65% identity with YnfP from <i>Escherichia coli</i> K-12 Nitrite reductase [NAD(P)H] transmembrane transporter	G→A C→A	G1114R	0.125	20	5.0	0.25	0.047	6	6	29	28	24	24	23	10	27	38	29	34	30	35	25	29	26	26	15	30	38	24	21
OCT-M2	<i>E. cloacae</i>	ompX	Outer membrane Protein X precursor	A→G	L14P	0.125	20	2.5	0.25	0.047	6	6	25	25	21	21	23	6	24	35	26	34	30	35	25	25	24	25	15	28	31	25	20
<i>Escherichia coli</i> wt	<i>E. coli</i>	/	/	/	/	0.125	0.625	2.5	0.032	0.008	25	27	30	35	29	27	23	27	36	40	33	38	37	37	27	29	26	29	25	39	40	32	33
CHX-M3	<i>E. coli</i>	mptA →	MltA interacting protein	A→G	intogenic	0.125	2.5	1.25	0.032	0.008	24	30	29	34	27	23	21	29	38	40	32	38	37	31	28	29	27	29	32	40	40	40	31
CHX-M4	<i>E. coli</i>	yybB →	putative transporter YybB	A→C	K123T	<0.1	1.25	1.25	0.032	0.0016	24	28	31	34	29	29	22	29	35	40	32	38	32	40	31	40	36	40	31	40	40	40	29
<i>Klebsiella oxytoca</i> wt	<i>K. oxytoca</i>	/	/	/	/	0.125	9	1.7	0.016	0.016	6	34	13	35	31	19	30	32	37	40	36	39	40	40	28	26	29	30	29	37	40	34	21
COL-M2	<i>K. oxytoca</i>	phoQ ← ls ← lptD ←	Sensor protein PhoQ Transketolase LPS assembly protein LptD	A→C C→G T→G	M293R D174H T672P	96	20	2.5	0.016	0.012	6	29	6	30	20	17	26	22	33	38	30	37	36	28	26	30	29	29	22	32	39	30	21
COL-M3	<i>K. oxytoca</i>	phoQ ←	Sensor protein PhoQ	C→A	K354N	128	16.7	2.0	0.032	0.012	6	36	6	40	29	19	29	36	36	40	37	38	36	38	26	27	27	23	30	40	40	32	22
CHX-M5	<i>K. oxytoca</i>	phoQ ← lpxJ ← mvaA ←	Sensor protein PhoQ Lpx penase Molybdopterin molybdenumtransferase	T→G C→T T→A	K64Q G383D K340M	0.125	27.5	2.3	0.016	0.016	6	36	6	40	29	19	29	36	36	40	37	38	36	38	26	27	27	23	30	40	40	32	22
CHX-M6	<i>K. oxytoca</i>	Gene_3346 → / -	Stress induced protein with GalB superfamily domain / -	C→A	intogenic	26.7	40	2.5	0.094	0.094	6	35	6	33	30	19	30	30	37	40	35	38	40	37	29	28	29	31	31	38	40	40	22
OCT-M3	<i>K. oxytoca</i>	hml3R1_1	TerR/AcrR family transcriptional regulator family	+ C	insertion	0.125	16	4.2	0.094	0.094	6	35	6	33	30	19	30	30	37	40	35	38	40	37	29	28	29	31	31	38	40	40	22
<i>Klebsiella pneumoniae</i> wt	<i>K. pneumoniae</i>	/	/	/	/	0.25	10	1.25	0.032	0.032	6	29	10	30	26	19	28	27	33	37	31	35	33	34	28	30	25	25	25	35	40	36	18
COL-M4	<i>K. pneumoniae</i>	rhlB_2 →	Sensor protein RaiB	C→A	D122E	256	10	1.25	0.032	0.016	6	27	6	24	19	18	18	14	30	40	26	32	38	36	29	31	29	29	18	28	36	26	22
COL-M5	<i>K. pneumoniae</i>	rhlB_2 → lptD ←	Sensor protein RaiB LPS assembly protein LptD	C→T T→G	P131L T491P	256	10	1.25	0.032	0.016	6	25	6	23	16	16	15	16	30	37	24	33	37	36	28	30	28	17	26	34	24	20	
CHX-M7	<i>K. pneumoniae</i>	smaA ← malt_2 →	Methyl viologen resistance protein SmvA HTH-type transcriptional regulator MatT	C→A G→A	intogenic E159K	0.25	40	1.25	0.032	0.016	6	29	10	30	26	19	28	27	33	37	31	35	33	34	28	30	25	25	25	35	40	36	18
CHX-M8	<i>K. pneumoniae</i>	uvrA ← smaA ← ramR ←	UDP-glucose: undecaprenyl phosphate glucose-1-phosphate transferase Methyl viologen resistance protein SmvA TerR/AcrR family transcriptional regulator family	(A)5 → 6 C→T G→A	insertion A368T Q122*	0.25	20	1.25	0.032	0.016	6	29	10	30	26	19	28	27	33	37	31	35	33	34	28	30	25	25	25	35	40	36	18
OCT-M4	<i>K. pneumoniae</i>	Gene_04779 ←	Putative membrane protein with AamA-like domain, 72% identity with YnfP from <i>Escherichia coli</i> K-12	C→T	W495*	0.25	10	2.5	0.25	0.125	6	29	10	30	26	19	28	27	33	37	31	35	33	34	28	30	25	25	25	35	40	36	18
OCT-M5	<i>K. pneumoniae</i>	smaA ← ramR ←	Methyl viologen resistance protein SmvA TerR/AcrR family transcriptional regulator family	G→A Δ1bp	A474V deletion	0.25	20	2.5	0.38	0.125	6	29	10	30	26	19	28	27	33	37	31	35	33	34	28	30	25	25	25	35	40	36	18