

Table S6 - Antibiotic resistance genes in *K. pneumoniae* KP6870155 predicted by CARD

RGI_ Criteria	gene	ARO_Term	SNP	location	Resistance_Mechanis m	AMR_Gene_ Family	Drug_Class	%ID_ Matching Region	%Length_ Reference Sequence	Detection_ Criteria
Strict	<i>baeR</i>	baeR		chromosome	antibiotic efflux	resistance-no	aminoglycosid	92.47	100	protein homolo
Perfect	<i>bla_1</i>	SHV-1		chromosome	antibiotic inactivation	SHV beta-lacti	carbapenem, c	100	100	protein homolo
Perfect	<i>bla_2</i>	SHV-2A		pKP0155_3	antibiotic inactivation	SHV beta-lacti	carbapenem, c	100	100	protein homolo
Strict	<i>ftsI_2</i>	Haemophilus D350N		chromosome	antibiotic target alterati	Penicillin-bind	cephalosporin, 52.37	96.39	96.39	protein variant i
Strict	<i>ampH</i>	Escherichia coli amp		chromosome	antibiotic inactivation	ampC-type be	cephalosporin, 85.45	100.26	100.26	protein homolo
Strict	<i>tuf1_1</i>	Escherichia c R234F		chromosome	antibiotic target alterati	elfamycin resi	elfamycin anti	97.97	96.33	protein variant i
Strict	<i>tuf1_1</i>	Escherichia c R234F		chromosome	antibiotic target alterati	elfamycin resi	elfamycin anti	97.97	96.33	protein variant i
Strict	<i>mprA</i>	emrR		chromosome	antibiotic efflux	major facilitat	fluoroquinolon	92.57	100	protein homolo
Strict	<i>marR</i>	Escherichia coli mar		chromosome	antibiotic target alterati	resistance-no	fluoroquinolon	84.03	100	protein overexp
Perfect	<i>bepF</i>	oqxA		chromosome	antibiotic efflux	resistance-no	fluoroquinolon	100	100	protein homolo
Strict	<i>marA</i>	marA		chromosome	antibiotic efflux, reduce	resistance-no	fluoroquinolon	92.74	97.64	protein homolo
Strict	<i>oqx25</i>	adeF		chromosome	antibiotic efflux	resistance-no	fluoroquinolon	60.96	99.15	protein homolo
Strict	<i>oqx25</i>	adeF		chromosome	antibiotic efflux	resistance-no	fluoroquinolon	41.71	97.92	protein homolo
Strict	<i>fosA</i>	FosA6		chromosome	antibiotic inactivation	fosfomycin thi	fosfomycin	97.12	100	protein homolo
Strict		Escherichia c E350Q		chromosome	antibiotic target alterati	antibiotic-resi	fosfomycin	95.03	100	protein variant i
Perfect	<i>mdtI</i>	Klebsiella pneumoni		chromosome	antibiotic efflux	major facilitat	macrolide anti	100	100	protein homolo
Strict	<i>mdtJ</i>	Klebsiella pneumoni		chromosome	antibiotic efflux	major facilitat	macrolide anti	99.17	100	protein homolo
Strict	<i>emrB</i>	Klebsiella pneumoni		chromosome	antibiotic efflux	major facilitat	macrolide anti	93.95	100	protein homolo
Strict	<i>emrA_1</i>	Klebsiella pneumoni		chromosome	antibiotic efflux	major facilitat	macrolide anti	99.74	100	protein homolo
Strict	<i>hns</i>	H-NS		chromosome	antibiotic efflux	major facilitat	macrolide anti	94.07	98.54	protein homolo
Strict	<i>crp</i>	CRP		chromosome	antibiotic efflux	resistance-no	macrolide anti	99.05	100	protein homolo
Strict	<i>ompN_2</i>	Klebsiella pneumoni		chromosome	reduced permeability to	General Bacte	monobactam, 99.2	100	100	protein homolo
Strict	<i>msbA_1</i>	msbA		chromosome	antibiotic efflux	ATP-binding c	nitroimidazole	92.78	100	protein homolo
	<i>cat3*</i>			chromosome						
	<i>arsH*</i>			pKP0155_2						
	<i>arsC_2*</i>			pKP0155_2						
	<i>arsB_2*</i>			pKP0155_2						

<i>arsR2</i> *	pKP0155_2	
<i>folP_1</i> *	pKP0155_2	sulfonamide
<i>folP_2</i> *	chromosome	sulfonamide
<i>ant1</i> *	pKP0155_2	aminoglycoside
<i>emrE</i> *	pKP0155_2	

*resistance associated genes within KP6870155 not identified by CARD

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