

Practice #1: ResFinder + PointFinder

SRR27241771 (Genes)

Resistance gene	Identity	Alignment Length/Gene Length	Coverage	Position in reference	Contig	Position in contig	Phenotype	Accession no.
aac(6')-laa	99.54	438/438	100	1..438	SRR27241771_12/1	52440..52877	Amikacin, Tobramycin	NC_003197
aadA16	99.65	846/846	100	1..846	SRR27241771_27/1	78..923	Spectinomycin, Streptomycin	EU675686
blaTEM-1B	100	861/861	100	1..861	SRR27241771_37/1	534..1394	Amoxicillin, Ampicillin, Cephalothin, Piperacillin, Ticarcillin	AY458016
mph(A)	100	906/906	100	1..906	SRR27241771_47/1	4965..5870	Erythromycin, Azithromycin, Spiramycin, Telithromycin	D16251
floR	98.19	1214/1215	99.9177	1..1214	SRR27241771_105/1	3191..4404	Chloramphenicol, Florfenicol	AF118107
qnrB6	100	645/645	100	1..645	SRR27241771_117/1	192..836	Ciprofloxacin	EF523819
ARR-3	100	453/453	100	1..453	SRR27241771_27/1	3636..4088	Rifampicin	JF806499
sul1	100	840/840	100	1..840	SRR27241771_53/1	4..843	Sulfamethoxazole	U12338
tet(B)	100	1206/1206	100	1..1206	SRR27241771_72/1	1421..2626	Doxycycline, Tetracycline, Minocycline	AP000342
dfrA27	100	474/474	100	1..474	SRR27241771_27/1	1104..1577	Trimethoprim	FJ459817

SRR27241771 (Point mutations)

Mutation	Nucleotide change	Amino acid change	Resistance	PMID

SRR27241772 (Genes)

Resistance gene	Identity	Alignment Length/Gene Length	Coverage	Position in reference	Contig	Position in contig	Phenotype	Accession no.
aph(6)-Id	99.88	837/837	100	1..837	SRR27241772_44/1	7618..8454	Streptomycin	M28829
aph(3'')-Ib	100	804/804	100	1..804	SRR27241772_44/1	8454..9257	Streptomycin	AF321551
aac(6')-Iaa	98.63	438/438	100	1..438	SRR27241772_51/1	48278..48715	Amikacin, Tobramycin	NC_003197
aph(3')-Ia	100	816/816	100	1..816	SRR27241772_68/1	115..930	Unknown Aminoglycoside, Kanamycin, Kanamycin, Neomycin, Neomycin, Kanamycin, Lividomycin, Paromomycin, Ribostamycin	V00359
aadA2	100	564/792	71.212121	229..792	SRR27241772_100/1	1..564	Spectinomycin, Streptomycin	JQ364967
aadA2	100	564/819	68.864469	256..819	SRR27241772_100/1	1..564	Spectinomycin, Streptomycin	NC_010870
aadA1	100	792/792	100	1..792	SRR27241772_113/1	1556..2347	Spectinomycin, Streptomycin	JQ414041
blaCTX-M-15	100	876/876	100	1..876	SRR27241772_63/1	254..1129	Amoxicillin, Ampicillin, Aztreonam, Cefepime, Cefotaxime, Ceftazidime, Ceftriaxone, Piperacillin, Ticarcillin	AY044436
mph(A)	99.5	604/921	65.472313	319..921	SRR27241772_100/1	7203..7806	Erythromycin, Azithromycin, Spiramycin, Telithromycin	U36578
floR	98.19	1214/1215	99.917695	1..1214	SRR27241772_44/1	3269..4482	Chloramphenicol, Florfenicol	AF118107
cmIA1	99.92	1260/1260	100	1..1260	SRR27241772_113/1	204..1463	Chloramphenicol	M64556
sul2	99.88	816/816	100	1..816	SRR27241772_44/1	9318..10133	Sulfamethoxazole	AY034138
sul1	100	840/840	100	1..840	SRR27241772_100/1	1069..1908	Sulfamethoxazole	U12338
sul3	100	792/792	100	1..792	SRR27241772_113/1	4029..4820	Sulfamethoxazole	AJ459418
tet(A)	99.92	1275/1275	100	1..1275	SRR27241772_44/1	5083..6357	Doxycycline, Tetracycline	AF534183
dfrA12	100	498/498	100	1..498	SRR27241772_7/1	614..1111	Trimethoprim	AM040708

SRR27241772 (Point mutations)

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83F	TCC -> TTC	S -> F	Nalidixic Acid, Ciprofloxacin	10471553
gyrA p.D87G	GAC -> GGC	D -> G	Nalidixic Acid, Ciprofloxacin	11283069
parC p.T57S	ACC -> AGC	T -> S	Nalidixic Acid, Ciprofloxacin	15388468
parC p.S80I	AGC -> ATC	S -> I	Nalidixic Acid, Ciprofloxacin	15388468

Practice #2: AMR FinderPlus

SRR27241771 (Genes and point mutations)

Contig id	Start	Stop	Strand	Gene symbol	Scope	Element type	Class	Method	% Coverage of reference sequence	% Identity to reference sequence
SRR27241771_101/1	3911	4144	-	merE	plus	STRESS	MERCURY	BLASTX	100	96.15
SRR27241771_101/1	4144	4506	-	merD	plus	STRESS	MERCURY	BLASTX	100	90.08
SRR27241771_101/1	4527	6209	-	merA	plus	STRESS	MERCURY	BLASTX	100	93.23
SRR27241771_101/1	6995	7339	-	merT	plus	STRESS	MERCURY	BLASTX	99.14	99.13
SRR27241771_101/1	7429	7854	+	merR	plus	STRESS	MERCURY	BLASTX	98.61	92.96
SRR27241771_105/1	3191	4402	+	floR	core	AMR	PHENICOL	EXACTX	100	100
SRR27241771_113/1	47515	49704	+	sinH	plus	VIRULENCE	NA	EXACTX	100	100
SRR27241771_117/1	192	833	+	qnrB6	core	AMR	QUINOLONE	ALLELEX	100	100
SRR27241771_15/1	19613	20143	-	sodC1	plus	VIRULENCE	NA	BLASTX	100	99.44
SRR27241771_27/1	81	923	-	aadA16	core	AMR	AMINOGLYCOSIDE	EXACTX	100	100
SRR27241771_27/1	1107	1577	-	dfrA27	core	AMR	TRIMETHOPRIM	EXACTX	100	100
SRR27241771_27/1	3639	4088	-	arr-3	core	AMR	RIFAMYCIN	EXACTX	100	100
SRR27241771_37/1	537	1394	-	blaTEM-1	core	AMR	BETA-LACTAM	ALLELEX	100	100
SRR27241771_42/1	18124	18699	-	terD	plus	STRESS	TELLURIUM	BLASTX	100	95.31
SRR27241771_42/1	18751	19788	-	terC	plus	STRESS	TELLURIUM	BLASTX	100	90.46
SRR27241771_42/1	19814	20266	-	terB	plus	STRESS	TELLURIUM	BLASTX	100	90.73
SRR27241771_42/1	21449	22027	-	terZ	plus	STRESS	TELLURIUM	EXACTX	100	100
SRR27241771_42/1	28598	29062	+	terW	plus	STRESS	TELLURIUM	EXACTX	100	100
SRR27241771_47/1	4968	5870	-	mph(A)	core	AMR	MACROLIDE	EXACTX	100	100
SRR27241771_53/1	7	843	-	sul1	core	AMR	SULFONAMIDE	EXACTX	100	100
SRR27241771_53/1	840	1184	-	qacEdelta1	core	STRESS	QUATERNARY AMMONIUM	ALLELEX	100	100
SRR27241771_63/1	23575	24036	-	golS	plus	STRESS	GOLD	EXACTX	100	100
SRR27241771_63/1	24051	26336	-	golT	plus	STRESS	COPPER/GOLD	BLASTX	100	99.74
SRR27241771_63/1	26613	27836	+	mdsA	plus	AMR	EFFLUX	BLASTX	100	98.04
SRR27241771_63/1	27836	31000	+	mdsB	plus	AMR	EFFLUX	EXACTX	100	100
SRR27241771_69/1	11799	12980	-	emrD	plus	AMR	EFFLUX	BLASTX	100	92.64
SRR27241771_72/1	1424	2626	-	tet(B)	core	AMR	TETRACYCLINE	EXACTX	100	100

SRR27241772 (Genes and point mutations)

Contig id	Start	Stop	Strand	Gene symbol	Scope	Element type	Class	Method	% Coverage of reference sequence	% Identity to reference sequence
SRR27241772_100/1	1	561	+	aadA2	core	AMR	AMINOGLYCOSIDE	PARTIAL_CONTIG_ENDX	71.1	100
SRR27241772_100/1	728	1072	+	qacEdelta1	core	STRESS	QUATERNARY AMMONIUM	ALLELEX	100	100
SRR27241772_100/1	1069	1905	+	sul1	core	AMR	SULFONAMIDE	EXACTX	100	100
SRR27241772_100/1	7222	7806	-	mph(A)	core	AMR	MACROLIDE	PARTIAL_CONTIG_ENDX	64.78	100
SRR27241772_101/1	85573	87762	+	sinH	plus	VIRULENCE	NA	BLASTX	100	98.77
SRR27241772_106/1	12719	13900	-	emrD	plus	AMR	EFFLUX	BLASTX	100	92.89
SRR27241772_107/1	5690	5803	+	astA	plus	VIRULENCE	NA	BLASTX	100	97.37
SRR27241772_109/1	9063	11108	+	ireA	plus	VIRULENCE	NA	BLASTX	100	99.85
SRR27241772_113/1	204	1460	+	cmIA1	core	AMR	PHENICOL	EXACTX	100	100
SRR27241772_113/1	1556	2344	+	aadA1	core	AMR	AMINOGLYCOSIDE	EXACTX	100	100
SRR27241772_113/1	2517	2846	+	qacL	core	STRESS	QUATERNARY AMMONIUM	EXACTX	100	100
SRR27241772_113/1	4032	4820	-	sul3	core	AMR	SULFONAMIDE	EXACTX	100	100
SRR27241772_21/1	6553	7014	-	golS	plus	STRESS	GOLD	BLASTX	100	99.35
SRR27241772_21/1	7029	9314	-	golT	plus	STRESS	COPPER/GOLD	BLASTX	100	99.48
SRR27241772_21/1	9591	10814	+	mdsA	plus	AMR	EFFLUX	BLASTX	100	98.28
SRR27241772_21/1	10814	13978	+	mdsB	plus	AMR	EFFLUX	BLASTX	100	99.53
SRR27241772_44/1	3269	4480	+	floR	core	AMR	PHENICOL	BLASTX	100	99.75
SRR27241772_44/1	5086	6282	-	tet(A)	core	AMR	TETRACYCLINE	BLASTX	100	99.75
SRR27241772_44/1	7624	8454	-	aph(6)-ld	core	AMR	AMINOGLYCOSIDE	BLASTX	99.64	100
SRR27241772_44/1	8457	9257	-	aph(3'')-lb	core	AMR	AMINOGLYCOSIDE	EXACTX	100	100
SRR27241772_44/1	9321	10133	-	sul2	core	AMR	SULFONAMIDE	EXACTX	100	100
SRR27241772_47/1	171835	174468	+	gyrA_D87G	core	AMR	QUINOLONE/TRICLOSAN	POINTX	100	99.77
SRR27241772_47/1	171835	174468	+	gyrA_S83F	core	AMR	QUINOLONE/TRICLOSAN	POINTX	100	99.77
SRR27241772_53/1	45066	47321	-	parC_S80I	core	AMR	QUINOLONE	POINTX	100	99.6
SRR27241772_63/1	254	1126	+	blaCTX-M-15	core	AMR	BETA-LACTAM	ALLELEX	100	100
SRR27241772_68/1	118	930	-	aph(3')-la	core	AMR	AMINOGLYCOSIDE	EXACTX	100	100
SRR27241772_7/1	617	1111	-	dfrA12	core	AMR	TRIMETHOPRIM	EXACTX	100	100