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ResFinder-3.2 Server - Results

Input Files: *E005.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Rifampicin						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Glycopeptide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Tetracycline						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
tet(A)	99.92	1200 / 1200	NXLF01000051.1 Escherichia coli strain ST-131:E005 NODE_51_length_7793_cov_38.7485_ID_101, whole genome shotgun sequence	4150..5349	Tetracycline resistance	AJ517790

Colistin						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Macrolide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
mdf(A)	97.81	1233 / 1233	NXLF01000012.1 Escherichia coli strain ST-131:E005 NODE_12_length_151655_cov_50.7131_ID_23, whole genome shotgun sequence	50536..51768	Warning: gene is missing from Notes file. Please inform curator.	Y08743
mph(A)	99.89	906 / 906	NXLF01000052.1 Escherichia coli strain ST-131:E005 NODE_52_length_7696_cov_47.1951_ID_103, whole genome shotgun sequence	6624..7528	Macrolide resistance	D16251

Phenicol						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
catB3	100	442 / 633	NXLF01000074.1 Escherichia coli strain ST-131:E005 NODE_74_length_2383_cov_117.947_ID_147, whole genome shotgun sequence	99..540	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXLF01000074.1 Escherichia coli strain ST-131:E005 NODE_74_length_2383_cov_117.947_ID_147, whole genome shotgun sequence	99..540	Phenicol resistance	U13880

Beta-lactam						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**

blaCTX-M-15	100	876 / 876	NXLF01000067.1 Escherichia coli strain ST-131:E005 NODE_67_length_2972_cov_216.032_ID_133, whole genome shotgun sequence	1706..2581	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaOXA-1	100	831 / 831	NXLF01000074.1 Escherichia coli strain ST-131:E005 NODE_74_length_2383_cov_117.947_ID_147, whole genome shotgun sequence	678..1508	Beta-lactam resistance	HQ170510
blaTEM-1B	100	861 / 861	NXLF01000050.1 Escherichia coli strain ST-131:E005 NODE_50_length_8371_cov_133.702_ID_99, whole genome shotgun sequence	236..1096	Beta-lactam resistance Alternate name; RblaTEM-1	AY458016

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(3)-IIa	99.77	861 / 861	NXLF01000068.1 Escherichia coli strain ST-131:E005 NODE_68_length_2797_cov_68.1042_ID_135, whole genome shotgun sequence	1795..2655	Aminoglycoside resistance	X51534
aac(3)-IId	99.83	583 / 861	NXLF01000097.1 Escherichia coli strain ST-131:E005 NODE_97_length_848_cov_153.244_ID_193, whole genome shotgun sequence	266..848	Aminoglycoside resistance	EU022314
aac(6')-Ib-cr	100	600 / 600	NXLF01000074.1 Escherichia coli strain ST-131:E005 NODE_74_length_2383_cov_117.947_ID_147, whole genome shotgun sequence	1639..2238	Fluoroquinolone and aminoglycoside resistance	DQ303918

aadA5	100	789 / 789	NXLF01000070.1 Escherichia coli strain ST-131:E005 NODE_70_length_2654_cov_68.6297_ID_139, whole genome shotgun sequence	263..1051	Aminoglycoside resistance	AF137361
aph(3'')-Ib	100	804 / 804	NXLF01000051.1 Escherichia coli strain ST-131:E005 NODE_51_length_7793_cov_38.7485_ID_101, whole genome shotgun sequence	1457..2260	Aminoglycoside resistance Alternate name; aph(3'')-Ib	AF321551
aph(6)-Id	100	831 / 831	NXLF01000051.1 Escherichia coli strain ST-131:E005 NODE_51_length_7793_cov_38.7485_ID_101, whole genome shotgun sequence	2266..3096	Aminoglycoside resistance Alternate name; aph(6)-Id	CP000971

Fusidicacid

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Fosfomycin

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Nitroimidazole

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Sulphonamide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
sul1	100	840 / 840	NXLF01000052.1 Escherichia coli strain ST-131:E005	474..1313	Sulphonamide	U12338

			NODE_52_length_7696_cov_47.1951_ID_103, whole genome shotgun sequence		resistance	
sul2	100	816 / 816	NXLF01000051.1 Escherichia coli strain ST-131:E005 NODE_51_length_7793_cov_38.7485_ID_101, whole genome shotgun sequence	581..1396	Sulphonamide resistance	AY034138

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
dfrA17	100	474 / 474	NXLF01000070.1 Escherichia coli strain ST-131:E005 NODE_70_length_2654_cov_68.6297_ID_139, whole genome shotgun sequence	1182..1655	Trimethoprim resistance	FJ460238

Oxazolidinone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXLF01000074.1 Escherichia coli strain ST-131:E005 NODE_74_length_2383_cov_117.947_ID_147, whole genome shotgun sequence	1639..2238	Fluoroquinolone and aminoglycoside resistance	DQ303918

extended output

Selected %ID threshold: ***90 %***

Selected minimum length: ***60 %***

Results as text

Hit in genome sequences

Resistance gene sequences

Results as tabseperated file

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

16S_rrsC
No known mutations found in 16S_rrsC

gyrB
No known mutations found in gyrB

16S_rrsB
No known mutations found in 16S_rrsB

16S_rrsH
No known mutations found in 16S_rrsH

ampC
No known mutations found in ampC

parE				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

23S
No known mutations found in 23S

pmrB
No known mutations found in pmrB

pmrA
No known mutations found in pmrA

gyrA				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

rpoB
No known mutations found in rpoB

parC				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

folP
No known mutations found in folP

Download the result table

Download the result table

CITATIONS

For publication of results, please cite:

- Identification of acquired antimicrobial resistance genes. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. J Antimicrob Chemother. 2012 Jul 10. PMID: 22782487 doi: 10.1093/jac/dks261

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ResFinder-3.2 Server - Results

Input Files: *E003.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Macrolide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
mdf(A)	99.92	1233 / 1233	NXIZ01000009.1 Escherichia coli strain E003 NODE_9_length_143897_cov_47.6126, whole genome shotgun sequence	12037..13269	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(B)	100	1206 /	NXIZ01000110.1 Escherichia coli strain E003	517..1722	Tetracycline	AF326777

		1206	NODE_110_length_2799_cov_25.8559, whole genome shotgun sequence		resistance	

Nitroimidazole

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Fosfomycin

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aadA5	100	789 / 789	NXIZ01000073.1 Escherichia coli strain E003 NODE_73_length_11594_cov_47.2424, whole genome shotgun sequence	7638..8426	Aminoglycoside resistance	AF137361
aph(3'')-Ib	100	804 / 804	NXIZ01000099.1 Escherichia coli strain E003 NODE_99_length_4640_cov_45.1682, whole genome shotgun sequence	972..1775	Aminoglycoside resistance Alternate name; aph(3'')-Ib	AF321551
aph(6)-Id	100	837 / 837	NXIZ01000099.1 Escherichia coli strain E003 NODE_99_length_4640_cov_45.1682, whole genome shotgun sequence	136..972	Aminoglycoside resistance Alternate name; aph(6)-Id	M28829

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number

No hit found

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCMY-2	100	1146 / 1146	NXIZ01000036.1 Escherichia coli strain E003 NODE_36_length_35478_cov_71.7592, whole genome shotgun sequence	9202..10347	Beta-lactam resistance	X91840

Rifampicin

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
dfrA17	100	474 / 474	NXIZ01000073.1 Escherichia coli strain E003 NODE_73_length_11594_cov_47.2424, whole genome shotgun sequence	7034..7507	Trimethoprim resistance	FJ460238

Phenicol

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
catA1	99.85	660 / 660	NXIZ01000073.1 Escherichia coli strain E003 NODE_73_length_11594_cov_47.2424, whole genome shotgun sequence	351..1010	Phenicol resistance	V00622

Sulphonamide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
sul1	100	840 / 840	NXIZ01000073.1 Escherichia coli strain E003 NODE_73_length_11594_cov_47.2424, whole genome shotgun sequence	8973..9812	Sulphonamide resistance	U12338
sul2	100	816 / 816	NXIZ01000099.1 Escherichia coli strain E003 NODE_99_length_4640_cov_45.1682, whole genome shotgun sequence	1836..2651	Sulphonamide resistance	HQ840942

Colistin						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Glycopeptide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

extended output

Selected %ID threshold: *90 %*

Selected minimum length: *60 %*

Results as text

Hit in genome sequences

Resistance gene sequences

Results as tabseperated file

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

folP

No mutations found in folP

pmrA

No mutations found in pmrA

16S_rrsH

No known mutations found in 16S_rrsH

rpoB

No mutations found in rpoB

pmrB

No mutations found in pmrB

parC

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parC p.A56T	GCC → ACC	A → T	Nalidixic acid,Ciprofloxacin	12654733
parC p.S80I	AGC → ATC	S → I	Nalidixic acid,Ciprofloxacin	8851598

16S_rrsC

No known mutations found in 16S_rrsC

16S_rrsB

No mutations found in 16S_rrsB

ampC

No mutations found in ampC

gyrA				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

23S
No known mutations found in 23S

parE
No mutations found in parE

gyrB
No known mutations found in gyrB

Download the result table

Download the result table

CITATIONS

For publication of results, please cite:

- Identification of acquired antimicrobial resistance genes. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. J Antimicrob Chemother. 2012 Jul 10. PMID: 22782487 doi: 10.1093/jac/dks261

ResFinder-3.2 Server - Results

Input Files: *E009.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(3)-IIa	99.12	794 / 861	NXLH01000079.1 Escherichia coli strain ST-131:E009 NODE_79_length_2003_cov_64.7426_ID_157, whole genome shotgun sequence	1..794	Aminoglycoside resistance	L22613
aac(3)-IId	99.12	794 / 861	NXLH01000079.1 Escherichia coli strain ST-131:E009 NODE_79_length_2003_cov_64.7426_ID_157, whole genome shotgun sequence	1..794	Aminoglycoside resistance	EU022314
aac(6')-Ib-cr	100	600 / 600	NXLH01000074.1 Escherichia coli strain ST-131:E009 NODE_74_length_2383_cov_57.8052_ID_147, whole genome shotgun sequence	1639..2238	Fluoroquinolone and aminoglycoside resistance	DQ303918
aadA5	100	789 / 789	NXLH01000070.1 Escherichia coli strain ST-131:E009 NODE_70_length_2653_cov_37.9824_ID_139, whole genome shotgun sequence	263..1051	Aminoglycoside resistance	AF137361
aph(3'')-Ib	100	804 / 804	NXLH01000052.1 Escherichia coli strain ST-131:E009 NODE_52_length_7789_cov_17.7293_ID_103, whole genome shotgun sequence	1456..2259	Aminoglycoside resistance Alternate name; aph(3'')-Ib	AF321551
aph(6)-Id	100	831 / 831	NXLH01000052.1 Escherichia coli strain ST-131:E009 NODE_52_length_7789_c	2265..3095	Aminoglycoside resistance	CP000971

			ov_17.7293_ID_103, whole genome shotgun sequence		Alternate name; aph(6)-Id	

Colistin						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Nitroimidazole						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Glycopeptide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Sulphonamide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
sul1	100	840 / 840	NXLH01000057.1 Escherichia coli strain ST-131:E009 NODE_57_length_6124_cov_27.371_ID_113, whole genome shotgun sequence	474..1313	Sulphonamide resistance	U12338
sul2	99.88	816 / 816	NXLH01000052.1 Escherichia coli strain ST-131:E009 NODE_52_length_7789_cov_17.7293_ID_103, whole genome shotgun sequence	581..1395	Sulphonamide resistance	AY034138

Rifampicin						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Phenicol

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
catB3	100	442 / 633	NXLH01000074.1 Escherichia coli strain ST-131:E009 NODE_74_length_2383_cov_57.8052_ID_147, whole genome shotgun sequence	99..540	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXLH01000074.1 Escherichia coli strain ST-131:E009 NODE_74_length_2383_cov_57.8052_ID_147, whole genome shotgun sequence	99..540	Phenicol resistance	U13880

Fusidicacid

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	99.92	1200 / 1200	NXLH01000052.1 Escherichia coli strain ST-131:E009 NODE_52_length_7789_cov_17.7293_ID_103, whole genome shotgun sequence	4147..5346	Tetracycline resistance	AJ517790

Oxazolidinone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-15	100	876 / 876	NXLH01000068.1 Escherichia coli strain ST-131:E009	1706..2581	Beta-lactam	AY044436

			NODE_68_length_2972_cov_109.368_ID_135, whole genome shotgun sequence		resistance Alternate name; UOE-1	
blaOXA-1	100	831 / 831	NXLH01000074.1 Escherichia coli strain ST-131:E009 NODE_74_length_2383_cov_57.8052_ID_147, whole genome shotgun sequence	678..1508	Beta-lactam resistance	HQ170510
blaTEM-1B	100	861 / 861	NXLH01000051.1 Escherichia coli strain ST-131:E009 NODE_51_length_8371_cov_78.5783_ID_101, whole genome shotgun sequence	236..1096	Beta-lactam resistance Alternate name; RblaTEM-1	AY458016

Macrolide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
mdf(A)	97.81	1233 / 1233	NXLH01000001.1 Escherichia coli strain ST-131:E009 NODE_1_length_609707_cov_28.8805_ID_1, whole genome shotgun sequence	422292..423524	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number

dfrA17	100	474 / 474	NXLH01000070.1 Escherichia coli strain ST-131:E009 NODE_70_length_2653_cov_37.9824_ID_139, whole genome shotgun sequence	1182..1655	Trimethoprim resistance	FJ460238

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXLH01000074.1 Escherichia coli strain ST-131:E009 NODE_74_length_2383_cov_57.8052_ID_147, whole genome shotgun sequence	1639..2238	Fluoroquinolone and aminoglycoside resistance	DQ303918

Fosfomycin

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

extended output

Selected %ID threshold: *90 %*

Selected minimum length: *60 %*

Results as text

Hit in genome sequences

Resistance gene sequences

Results as tabseperated file

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

16S_rrsC
No known mutations found in 16S_rrsC

pmrB
No known mutations found in pmrB

parC

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

gyrB
No known mutations found in gyrB

pmrA
No known mutations found in pmrA

parE

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

gyrA

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

folP

No known mutations found in folP

23S

No known mutations found in 23S

rpoB

No known mutations found in rpoB

16S_rrsH

No known mutations found in 16S_rrsH

ampC

No known mutations found in ampC

16S_rrsB

No known mutations found in 16S_rrsB

Download the result table

Download the result table

CITATIONS

For publication of results, please cite:

- Identification of acquired antimicrobial resistance genes. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. J Antimicrob Chemother. 2012 Jul 10. PMID: 22782487 doi: 10.1093/jac/dks261

Center for Genomic Epidemiology compare

ResFinder-3.2 Server - Results

Input Files: *E011.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Nitroimidazole						
Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Fusidicacid						
Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Rifampicin						
Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Beta-lactam						
Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-15	100	876 / 876	NXKR01000088.1 Escherichia coli strain ST-131:E011 NODE_88_length_3369_cov_145.789, whole genome shotgun sequence	1894..2769	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaOXA-1	100	831 / 831	NXKR01000103.1 Escherichia coli strain ST-131:E011 NODE_103_length_2484_cov_65.9737, whole genome shotgun sequence	729..1559	Beta-lactam resistance	HQ170510

Glycopeptide						

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Trimethoprim						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
dfrA14	100	474 / 474	NXKR01000046.1 Escherichia coli strain ST-131:E011 NODE_46_length_21384_cov_30.9932, whole genome shotgun sequence	10903..11376	Trimethoprim resistance	AF393510
dfrA17	100	474 / 474	NXKR01000063.1 Escherichia coli strain ST-131:E011 NODE_63_length_10755_cov_77.7079, whole genome shotgun sequence	1543..2016	Trimethoprim resistance	FJ460238

Aminoglycoside						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
aac(3)-IIa	99.77	861 / 861	NXKR01000096.1 Escherichia coli strain ST-131:E011 NODE_96_length_2804_cov_41.0062, whole genome shotgun sequence	99..959	Aminoglycoside resistance	X51534
aac(6')-Ib-cr	100	600 / 600	NXKR01000103.1 Escherichia coli strain ST-131:E011 NODE_103_length_2484_cov_65.9737, whole genome shotgun sequence	1690..2289	Fluoroquinolone and aminoglycoside resistance	DQ303918
aadA5	100	789 / 789	NXKR01000063.1 Escherichia coli strain ST-131:E011 NODE_63_length_10755_cov_77.7079, whole	2147..2935	Aminoglycoside resistance	AF137361

			genome shotgun sequence			
aph(3")-Ib	99.81	529 / 804	NXKR01000046.1 Escherichia coli strain ST-131:E011 NODE_46_length_21384_cov_30.9932, whole genome shotgun sequence	11396..11923	Aminoglycoside resistance Alternate name; aph(3")-Ib	[AF321551]()
aph(6)-Id	100	837 / 837	NXKR01000046.1 Escherichia coli strain ST-131:E011 NODE_46_length_21384_cov_30.9932, whole genome shotgun sequence	9717..10553	Aminoglycoside resistance Alternate name; aph(6)-Id	[M28829]()

Macrolide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
mdf(A)	97.81	1233 / 1233	NXKR01000012.1 Escherichia coli strain ST-131:E011 NODE_12_length_165049_cov_25.0754, whole genome shotgun sequence	64137..65369	Warning: gene is missing from Notes file. Please inform curator.	[Y08743]()
mph(A)	100	906 / 906	NXKR01000063.1 Escherichia coli strain ST-131:E011 NODE_63_length_10755_cov_77.7079, whole genome shotgun sequence	9632..10537	Macrolide resistance	[D16251]()

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXKR01000103.1 Escherichia coli strain ST-131:E011 NODE_103_length_2484_cov_65.9737, whole genome shotgun sequence	1690..2289	Fluoroquinolone and aminoglycoside resistance	DQ303918

Phenicol						
Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
catB3	100	442 / 633	NXKR01000103.1 Escherichia coli strain ST-131:E011 NODE_103_length_2484_cov_65.9737, whole genome shotgun sequence	150..591	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXKR01000103.1 Escherichia coli strain ST-131:E011 NODE_103_length_2484_cov_65.9737, whole genome shotgun sequence	150..591	Phenicol resistance	U13880

Sulphonamide						
Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
sul1	99.88	840 / 840	NXKR01000063.1 Escherichia coli strain ST-131:E011 NODE_63_length_10755_cov_77.7079, whole genome shotgun sequence	3482..4321	Sulphonamide resistance	U12338
sul2	100	816 / 816	NXKR01000046.1 Escherichia coli strain ST-131:E011 NODE_46_length_21384_cov_30.9932, whole genome shotgun sequence	11984..12799	Sulphonamide resistance	AY034138

Colistin						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Oxazolidinone						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Fosfomycin						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

extended output

Selected %ID threshold: *90 %*

Selected minimum length: *60 %*

Results as text

Hit in genome sequences

Resistance gene sequences

Results as tabseperated file

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

16S_rrsH
No known mutations found in 16S_rrsH

folP
No known mutations found in folP

pmrB
No known mutations found in pmrB

rpoB
No known mutations found in rpoB

parE

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

gyrA

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

parC

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

pmrA
No known mutations found in pmrA

ampC
No known mutations found in ampC

16S_rrsC
No known mutations found in 16S_rrsC

gyrB
No known mutations found in gyrB

23S
No known mutations found in 23S

16S_rrsB
No known mutations found in 16S_rrsB

Download the result table

Download the result table

CITATIONS

For publication of results, please cite:

- Identification of acquired antimicrobial resistance genes.
  Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV.
  J Antimicrob Chemother. 2012 Jul 10.
  PMID: 22782487 doi: 10.1093/jac/dks261

Center for Genomic Epidemiology

ResFinder-3.2 Server - Results

Input Files: *E019.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Trimethoprim						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
dfrA17	100	474 / 474	NXLG01000064.1 Escherichia coli strain ST-617:E019 NODE_64_length_10136_cov_53.4991_ID_127, whole genome shotgun sequence	975..1448	Trimethoprim resistance	FJ460238

Sulphonamide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
sul1	100	840 / 840	NXLG01000064.1 Escherichia coli strain ST-617:E019 NODE_64_length_10136_cov_53.4991_ID_127, whole genome shotgun sequence	2914..3753	Sulphonamide resistance	U12338
sul2	100	816 / 816	NXLG01000074.1 Escherichia coli strain ST-617:E019 NODE_74_length_6277_cov_243.491_ID_147, whole genome shotgun sequence	4027..4842	Sulphonamide resistance	AY034138

Aminoglycoside						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
aac(3)-IId	99.88	861 / 861	NXLG01000087.1 Escherichia coli strain ST-617:E019 NODE_87_length_3875_cov_69.9187_ID_173, whole genome shotgun sequence	2730..3590	Aminoglycoside resistance	EU022314

aac(6')-Ib-cr	100	600 / 600	NXLG01000097.1 Escherichia coli strain ST-617:E019 NODE_97_length_2384_cov_121.065_ID_193, whole genome shotgun sequence	146..745	Fluoroquinolone and aminoglycoside resistance	DQ303918
aadA5	100	789 / 789	NXLG01000064.1 Escherichia coli strain ST-617:E019 NODE_64_length_10136_cov_53.4991_ID_127, whole genome shotgun sequence	1579..2367	Aminoglycoside resistance	AF137361
aph(3")-Ib	100	801 / 804	NXLG01000074.1 Escherichia coli strain ST-617:E019 NODE_74_length_6277_cov_243.491_ID_147, whole genome shotgun sequence	4906..5706	Aminoglycoside resistance Alternate name; aph(3")-Ib	AF321551
aph(6)-Id	100	572 / 837	NXLG01000074.1 Escherichia coli strain ST-617:E019 NODE_74_length_6277_cov_243.491_ID_147, whole genome shotgun sequence	5706..6277	Aminoglycoside resistance Alternate name; aph(6)-Id	18676889
aph(6)-Id	100	572 / 837	NXLG01000074.1 Escherichia coli strain ST-617:E019 NODE_74_length_6277_cov_243.491_ID_147, whole genome shotgun sequence	5706..6277	Aminoglycoside resistance Alternate name; aph(6)-Id	AF024602
aph(6)-Id	100	572 / 837	NXLG01000074.1 Escherichia coli strain ST-617:E019 NODE_74_length_6277_cov_243.491_ID_147, whole genome shotgun sequence	5706..6277	Aminoglycoside resistance Alternate name; aph(6)-Id	M28829

Glycopeptide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXLG01000097.1 Escherichia coli strain ST-617:E019 NODE_97_length_2384_cov_121.065_ID_193, whole genome shotgun sequence	146..745	Fluoroquinolone and aminoglycoside resistance	DQ303918

Fusidicacid

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(B)	100	1206 / 1206	NXLG01000077.1 Escherichia coli strain ST-617:E019 NODE_77_length_5283_cov_179.57_ID_153, whole genome shotgun sequence	2453..3658	Tetracycline resistance	AF326777

Nitroimidazole

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-15	100	876 / 876	NXLG01000076.1 Escherichia coli strain ST-617:E019 NODE_76_length_5583_cov	2737..3612	Beta-lactam resistance	AY044436

			_98.5852_ID_151, whole genome shotgun sequence		Alternate name; UOE-1	
blaOXA-1	100	831 / 831	NXLG01000097.1 Escherichia coli strain ST-617:E019 NODE_97_length_2384_cov_121.065_ID_193, whole genome shotgun sequence	876..1706	Beta-lactam resistance	HQ170510

Macrolide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
mdf(A)	99.92	1233 / 1233	NXLG01000003.1 Escherichia coli strain ST-617:E019 NODE_3_length_235313_cov_66.8949_ID_5, whole genome shotgun sequence	145428..146660	Warning: gene is missing from Notes file. Please inform curator.	Y08743
mph(A)	100	906 / 906	NXLG01000064.1 Escherichia coli strain ST-617:E019 NODE_64_length_10136_cov_53.4991_ID_127, whole genome shotgun sequence	9063..9968	Macrolide resistance	D16251

Phenicol

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
catA1	99.75	407 / 660	NXLG01000079.1 Escherichia coli strain ST-617:E019 NODE_79_length_4792_cov_68.2312_ID_157, whole genome shotgun sequence	4260..4666	Phenicol resistance	V00622

catB3	100	442 / 633	NXLG01000097.1 Escherichia coli strain ST-617:E019 NODE_97_length_2384_cov_121.065_ID_193, whole genome shotgun sequence	1844..2285	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXLG01000097.1 Escherichia coli strain ST-617:E019 NODE_97_length_2384_cov_121.065_ID_193, whole genome shotgun sequence	1844..2285	Phenicol resistance	U13880

extended output

cfdz

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

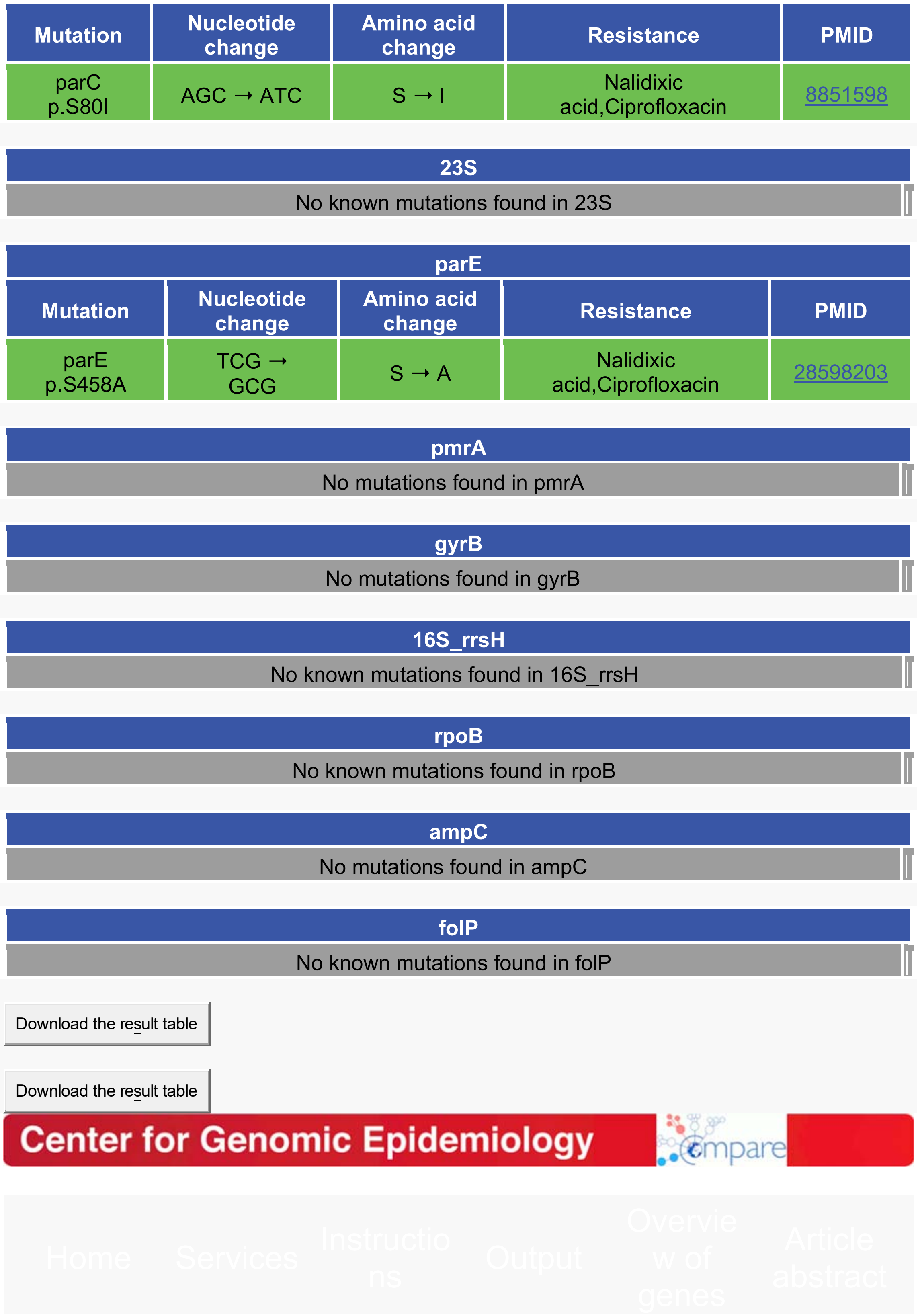
pmrB
No mutations found in pmrB

16S_rrsB
No mutations found in 16S_rrsB

16S_rrsC
No known mutations found in 16S_rrsC

gyrA				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

parC



Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parC p.S80I	AGC → ATC	S → I	Nalidixic acid,Ciprofloxacin	8851598

23S

No known mutations found in 23S

parE

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parE p.S458A	TCG → GCG	S → A	Nalidixic acid,Ciprofloxacin	28598203

pmrA

No mutations found in pmrA

gyrB

No mutations found in gyrB

16S_rrsH

No known mutations found in 16S_rrsH

rpoB

No known mutations found in rpoB

ampC

No mutations found in ampC

folP

No known mutations found in folP

ResFinder-3.2 Server - Results

Input Files: *E020.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Phenicol						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
catA1	99.75	407 / 660	NXJB01000089.1 Escherichia coli strain ST-617:E020 NODE_89_length_4719_cov_55.4455, whole genome shotgun sequence	4260..4666	Phenicol resistance	V00622
catB3	100	442 / 633	NXJB01000105.1 Escherichia coli strain ST-617:E020 NODE_105_length_2484_cov_111.431, whole genome shotgun sequence	150..591	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXJB01000105.1 Escherichia coli strain ST-617:E020 NODE_105_length_2484_cov_111.431, whole genome shotgun sequence	150..591	Phenicol resistance	U13880

Macrolide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
mdf(A)	99.92	1233 / 1233	NXJB01000001.1 Escherichia coli strain ST-617:E020 NODE_1_length_354459_cov_47.0873, whole genome shotgun sequence	208609..209841	Warning: gene is missing from Notes file. Pleas	Y08743

					e inform curator.	
mph(A)	100	906 / 906	NXJB01000069.1 Escherichia coli strain ST-617:E020 NODE_69_length_11231_cov_61.9453, whole genome shotgun sequence	10108..11013	Macrolide resistance	D16251

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(3)-IId	99.88	861 / 861	NXJB01000097.1 Escherichia coli strain ST-617:E020 NODE_97_length_3830_cov_65.1862, whole genome shotgun sequence	2729..3589	Aminoglycoside resistance	EU022314
aac(6')-Ib-cr	100	600 / 600	NXJB01000105.1 Escherichia coli strain ST-617:E020 NODE_105_length_2484_cov_111.431, whole genome shotgun sequence	1690..2289	Fluoroquinolone and aminoglycoside resistance	DQ303918
aadA5	100	789 / 789	NXJB01000069.1 Escherichia coli strain ST-617:E020 NODE_69_length_11231_cov_61.9453, whole genome shotgun sequence	2624..3412	Aminoglycoside resistance	AF137361
aph(3'')-Ib	99.88	801 / 804	NXJB01000082.1 Escherichia coli strain ST-617:E020 NODE_82_length_6231_cov_208.46, whole genome shotgun sequence	2299..3098	Aminoglycoside resistance Alternate name; aph(3'')-Ib	AF321551
aph(6)-Id	100	837 / 837	NXJB01000082.1 Escherichia coli strain ST-617:E020 NODE_82_length_6231_cov_208.46, whole	3098..3934	Aminoglycoside resistance Alternate	M28829

			genome shotgun sequence		name; aph(6)-Id	

Beta-lactam						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
blaCTX-M-15	100	876 / 876	NXJB01000084.1 Escherichia coli strain ST-617:E020 NODE_84_length_5632_cov_81.2413, whole genome shotgun sequence	2736..3611	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaOXA-1	100	831 / 831	NXJB01000105.1 Escherichia coli strain ST-617:E020 NODE_105_length_2484_cov_111.431, whole genome shotgun sequence	729..1559	Beta-lactam resistance	HQ170510
blaTEM-1B	100	861 / 861	NXJB01000083.1 Escherichia coli strain ST-617:E020 NODE_83_length_5883_cov_100.728, whole genome shotgun sequence	277..1137	Beta-lactam resistance Alternate name; RblaTEM-1	AY458016

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
sul1	100	840 / 840	NXJB01000069.1 Escherichia coli strain ST-617:E020 NODE_69_length_11231_cov_61.9453, whole genome shotgun sequence	3959..4798	Sulphonamide resistance	U12338

sul2	100	816 / 816	NXJB01000082.1 Escherichia coli strain ST-617:E020 NODE_82_length_6231_cov_208.46, whole genome shotgun sequence	1420..2235	Sulphonamide resistance	AY034138

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(B)	100	1206 / 1206	NXJB01000088.1 Escherichia coli strain ST-617:E020 NODE_88_length_5017_cov_114.011, whole genome shotgun sequence	2231..3436	Tetracycline resistance	AF326777

Nitroimidazole

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
dfrA17	100	474 / 474	NXJB01000069.1 Escherichia coli strain ST-617:E020 NODE_69_length_11231_cov_61.9453, whole genome shotgun sequence	2020..2493	Trimethoprim resistance	FJ460238

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXJB01000105.1 Escherichia coli strain ST-617:E020	1690..2289	Fluoroquinolone and	DQ303918

			NODE_105_length_2484_cov_111.431, whole genome shotgun sequence		aminoglycoside resistance	

extended output

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

gyrA

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

23S

No known mutations found in 23S

gyrB

No mutations found in gyrB

parE

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parE p.S458A	TCG → GCG	S → A	Nalidixic acid,Ciprofloxacin	28598203

16S_rrsC

No known mutations found in 16S_rrsC

pmrA

No mutations found in pmrA

parC				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
parC p.S80I	AGC → ATC	S → I	Nalidixic acid,Ciprofloxacin	8851598

16S_rrsB
No mutations found in 16S_rrsB

16S_rrsH
No known mutations found in 16S_rrsH

ampC
No mutations found in ampC

folP
No known mutations found in folP

rpoB
No mutations found in rpoB

pmrB
No mutations found in pmrB

Download the result table

Download the result table

Center for Genomic Epidemiology compare

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ResFinder-3.2 Server - Results

Input Files: *E021.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Phenicol						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
catB3	100	442 / 633	NXIO01000090.1 Escherichia coli strain ST-131:E021 NODE_90_length_2384_cov_153.732_ID_179, whole genome shotgun sequence	100..541	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXIO01000090.1 Escherichia coli strain ST-131:E021 NODE_90_length_2384_cov_153.732_ID_179, whole genome shotgun sequence	100..541	Phenicol resistance	U13880

Macrolide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
mdf(A)	97.81	1233 / 1233	NXIO01000012.1 Escherichia coli strain ST-131:E021 NODE_12_length_166728_cov_101.803_ID_23, whole genome shotgun sequence	99763..100995	Warning: gene is missing from Notes file. Please inform curator.	Y08743
mph(A)	100	906 / 906	NXIO01000056.1 Escherichia coli strain ST-131:E021 NODE_56_length_9965_cov_136.992_ID_111, whole genome shotgun sequence	8893..9798	Macrolide resistance	D16251

Sulphonamide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
sul1	100	840 / 840	NXIO01000056.1 Escherichia coli strain ST-131:E021 NODE_56_length_9965_cov_136.992_ID_111, whole genome shotgun sequence	2743..3582	Sulphonamide resistance	U12338
sul2	100	816 / 816	NXIO01000062.1 Escherichia coli strain ST-131:E021 NODE_62_length_6854_cov_124.933_ID_123, whole genome shotgun sequence	580..1395	Sulphonamide resistance	AY034138

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXIO01000090.1 Escherichia coli strain ST-131:E021 NODE_90_length_2384_cov_153.732_ID_179, whole genome shotgun sequence	1640..2239	Fluoroquinolone and aminoglycoside resistance	DQ303918

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	100	1200 / 1200	NXIO01000062.1 Escherichia coli strain ST-131:E021 NODE_62_length_6854_cov_124.933_ID_123, whole genome shotgun sequence	4149..5348	Tetracycline resistance	AJ517790

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number

dfrA17	100	474 / 474	NXIO01000056.1 Escherichia coli strain ST-131:E021 NODE_56_length_9965_cov_136.992_ID_111, whole genome shotgun sequence	804..1277	Trimethoprim resistance	FJ460238

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-15	100	876 / 876	NXIO01000082.1 Escherichia coli strain ST-131:E021 NODE_82_length_3051_cov_427.082_ID_163, whole genome shotgun sequence	471..1346	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaOXA-1	100	831 / 831	NXIO01000090.1 Escherichia coli strain ST-131:E021 NODE_90_length_2384_cov_153.732_ID_179, whole genome shotgun sequence	679..1509	Beta-lactam resistance	HQ170510

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(3)-IIa	99.77	861 / 861	NXIO01000084.1 Escherichia coli strain ST-131:E021 NODE_84_length_2798_cov_179.104_ID_167, whole genome shotgun sequence	143..1003	Aminoglycoside resistance	X51534
aac(6')-Ib-cr	100	600 / 600	NXIO01000090.1 Escherichia coli strain ST-131:E021 NODE_90_length_2384_cov_153.732_ID_179, whole genome shotgun sequence	1640..2239	Fluoroquinolone and aminoglycoside resistance	DQ303918
aadA5	100	789 /	NXIO01000056.1 Escherichia coli strain ST-131:E021	1408..2196	Aminoglycoside	AF137361

		789	NODE_56_length_9965_cov_136.992_ID_111, whole genome shotgun sequence		resistance	
aph(3'')-Ib	100	804 / 804	NXIO01000062.1 Escherichia coli strain ST-131:E021 NODE_62_length_6854_cov_124.933_ID_123, whole genome shotgun sequence	1456..2259	Aminoglycoside resistance Alternate name; aph(3'')-Ib	AF321551
aph(6)-Id	100	831 / 831	NXIO01000062.1 Escherichia coli strain ST-131:E021 NODE_62_length_6854_cov_124.933_ID_123, whole genome shotgun sequence	2265..3095	Aminoglycoside resistance Alternate name; aph(6)-Id	CP000971

extended output

Show Point mutation results

Chromosomal point mutations - Results

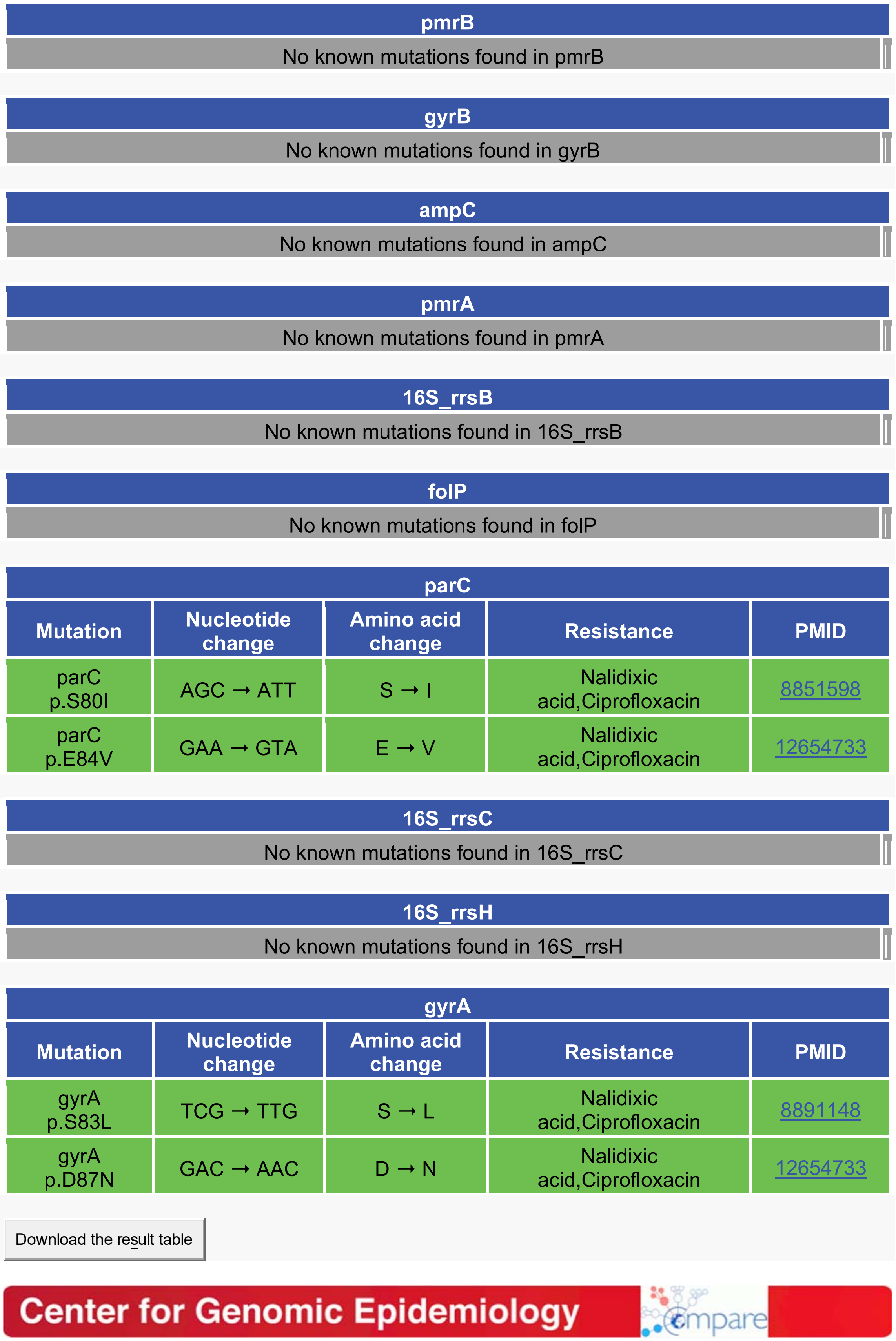
Species: ***escherichia_coli***

Known Mutations

rpoB
No mutations found in rpoB

parE				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

23S
No known mutations found in 23S



pmrB

No known mutations found in pmrB

gyrB

No known mutations found in gyrB

ampC

No known mutations found in ampC

pmrA

No known mutations found in pmrA

16S_rrsB

No known mutations found in 16S_rrsB

folP

No known mutations found in folP

parC

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

16S_rrsC

No known mutations found in 16S_rrsC

16S_rrsH

No known mutations found in 16S_rrsH

gyrA

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

ResFinder-3.2 Server - Results

Input Files: *E035.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-15	100	876 / 876	NXJC01000041.1 Escherichia coli strain ST-998:E035 contig_41, whole genome shotgun sequence	3828..4703	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaTEM-1B	100	861 / 861	NXJC01000041.1 Escherichia coli strain ST-998:E035 contig_41, whole genome shotgun sequence	146..1006	Beta-lactam resistance Alternate name; RblaTEM-1	AY458016

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aadA1	100	792 / 792	NXJC01000036.1 Escherichia coli strain ST-998:E035 contig_36, whole genome shotgun sequence	7763..8554	Aminoglycoside resistance	JX185132

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
dfrA1	99.79	474 / 474	NXJC01000036.1 Escherichia coli strain ST-998:E035 contig_36, whole genome shotgun sequence	8647..9120	Trimethoprim resistance	AF203818
dfrA1	99.79	474 / 474	NXJC01000036.1 Escherichia coli strain ST-998:E035 contig_36, whole genome shotgun sequence	8647..9120	Trimethoprim resistance	AJ238350
dfrA1	99.79	474 / 474	NXJC01000036.1 Escherichia coli strain ST-998:E035 contig_36, whole genome shotgun sequence	8647..9120	Trimethoprim resistance	X00926

Colistin

Sulphonamide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
sul1	100	840 / 840	NXJC01000036.1 Escherichia coli strain ST-998:E035 contig_36, whole genome shotgun sequence	6419..7258	Sulphonamide resistance	U12338

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number

tet(B)	100	1206 / 1206	NXJC01000130.1 Escherichia coli strain ST-998:E035 contig_130, whole genome shotgun sequence	1229..2434	Tetracycline resistance	AF326777

Macrolide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
mdf(A)	97.97	1233 / 1233	NXJC01000042.1 Escherichia coli strain ST-998:E035 contig_42, whole genome shotgun sequence	4454..5686	Warning: gene is missing from Notes file. Please inform curator.	Y08743

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ResFinder-3.2 Server - Results

Input Files: *E040.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Sulphonamide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
sul2	100	816 / 816	NXIP01000084.1 Escherichia coli strain ST-95:E040 NODE_84_length_2903_cov_70.7707_ID_167, whole genome shotgun sequence	128..943	Sulphonamide resistance	HQ840942
sul3	100	792 / 792	NXIP01000083.1 Escherichia coli strain ST-95:E040 NODE_83_length_2935_cov_77.4944_ID_165, whole genome shotgun sequence	1971..2762	Sulphonamide resistance	AJ459418

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
dfrA5	100	474 / 474	NXIP01000119.1 Escherichia coli strain ST-95:E040 NODE_119_length_887_cov_179.188_ID_237, whole genome shotgun sequence	199..672	Trimethoprim resistance	X12868

Phenicol

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
cmlA1	99.92	1260 / 1260	NXIP01000055.1 Escherichia coli strain ST-95:E040 NODE_55_length_10536_cov_146.169_ID_109, whole genome shotgun sequence	2599..3858	Phenicol resistance	M64556

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number

blaCTX-M-14	100	876 / 876	NXIP01000107.1 Escherichia coli strain ST-95:E040 NODE_107_length_1376_cov_92.8724_ID_213, whole genome shotgun sequence	349..1224	Beta-lactam resistance Amino acid sequences of CTX-M-14 and CTX-M-18 are identical	AF252622
blaTEM-1B	100	861 / 861	NXIP01000089.1 Escherichia coli strain ST-95:E040 NODE_89_length_2114_cov_129.714_ID_177, whole genome shotgun sequence	634..1494	Beta-lactam resistance Alternate name; RblaTEM-1	AY458016

Macrolide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
mdf(A)	97.81	1233 / 1233	NXIP01000004.1 Escherichia coli strain ST-95:E040 NODE_4_length_311653_cov_117.437_ID_7, whole genome shotgun sequence	250787..252019	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Aminoglycoside

Resistance gene	Identity	Query / Templ	Contig	Position in contig	Predicted phenotype	Accession number

		ate length				
aadA1	100	792 / 792	NXIP01000055.1 Escherichia coli strain ST-95:E040 NODE_55_length_10536_cov_146.169_ID_109, whole genome shotgun sequence	1715..2506	Aminoglycoside resistance	JQ414041
aadA2b	99.87	780 / 780	NXIP01000055.1 Escherichia coli strain ST-95:E040 NODE_55_length_10536_cov_146.169_ID_109, whole genome shotgun sequence	4120..4899	Warning: gene is missing from Notes file. Please inform curator.	D43625
aph(3")-Ib	100	803 / 804	NXIP01000099.1 Escherichia coli strain ST-95:E040 NODE_99_length_1680_cov_321.589_ID_197, whole genome shotgun sequence	845..1647	Aminoglycoside resistance Alternate name; aph(3")-Ib	AF024602
aph(3")-Ib	99.88	804 / 804	NXIP01000099.1 Escherichia coli strain ST-95:E040 NODE_99_length_1680_cov_321.589_ID_197, whole genome shotgun sequence	845..1648	Aminoglycoside resistance Alternate name; aph(3")-Ib	AF313472
aph(3")-Ib	99.88	804 / 804	NXIP01000099.1 Escherichia coli strain ST-95:E040 NODE_99_length_1680_cov_321.589_ID_197, whole genome shotgun sequence	845..1648	Aminoglycoside resistance Alternate name; aph(3")-Ib	AF321550
aph(3")-Ib	99.88	804 / 804	NXIP01000099.1 Escherichia coli strain ST-95:E040 NODE_99_length_1680_cov_321.589_ID_197, whole genome shotgun sequence	845..1648	Aminoglycoside resistance Alternate name; aph(3")-Ib	AF321551
aph(3')-IIa	100	795 / 795	NXIP01000086.1 Escherichia coli strain ST-95:E040 NODE_86_length_2695_co	1559..2353	Aminoglycoside resistance	V00618

			v_148.314_ID_171, whole genome shotgun sequence			
aph(6)-Id	100	837 / 837	NXIP01000099.1 Escherichia coli strain ST-95:E040 NODE_99_length_1680_cov_321.589_ID_197, whole genome shotgun sequence	9..845	Aminoglycoside resistance Alternate name; aph(6)-Id	M28829

Fosfomycin						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
fosA3	100	417 / 417	NXIP01000091.1 Escherichia coli strain ST-95:E040 NODE_91_length_2094_cov_141.083_ID_181, whole genome shotgun sequence	1321..1737	Fosfomycin resistance	AB522970

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

gyrB
No known mutations found in gyrB

16S_rrsC
No known mutations found in 16S_rrsC

parC
No known mutations found in parC

gyrA

No known mutations found in gyrA

rpoB

No mutations found in rpoB

16S_rrsH

No known mutations found in 16S_rrsH

pmrB

No known mutations found in pmrB

pmrA

No known mutations found in pmrA

folP

No known mutations found in folP

ampC

No known mutations found in ampC

23S

No known mutations found in 23S

parE

No known mutations found in parE

16S_rrsB

No known mutations found in 16S_rrsB

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ResFinder-3.2 Server - Results

Input Files: *E053.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Sulphonamide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
sul1	100	761 / 828	NXIR01000080.1 Escherichia coli strain ST-73:E053 NODE_80_length_4325_cov_65.4411_ID_159, whole genome shotgun sequence	3466..4226	Sulphonamide resistance	AY522923
sul1	100	761 / 840	NXIR01000080.1 Escherichia coli strain ST-73:E053 NODE_80_length_4325_cov_65.4411_ID_159, whole genome shotgun sequence	3466..4226	Sulphonamide resistance	X15024
sul2	100	816 / 816	NXIR01000077.1 Escherichia coli strain ST-73:E053 NODE_77_length_4582_cov_62.3674_ID_153, whole genome shotgun sequence	1808..2623	Sulphonamide resistance	HQ840942

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	100	1200 /	NXIR01000045.1 Escherichia coli strain ST-73:E053	2181..3380	Tetracycline	AJ517790

		1200	NODE_45_length_11767_cov_106.183_ID_89, whole genome shotgun sequence		resistance	

Aminoglycoside						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
aac(3)-IIa	99.77	861 / 861	NXIR01000093.1 Escherichia coli strain ST-73:E053 NODE_93_length_2841_cov_190.367_ID_185, whole genome shotgun sequence	186..1046	Aminoglycoside resistance	X51534
aac(6')-Ib-cr	100	600 / 600	NXIR01000103.1 Escherichia coli strain ST-73:E053 NODE_103_length_2384_cov_166.905_ID_205, whole genome shotgun sequence	1640..2239	Fluoroquinolone and aminoglycoside resistance	DQ303918
aph(3'')-Ib	100	804 / 804	NXIR01000077.1 Escherichia coli strain ST-73:E053 NODE_77_length_4582_cov_62.3674_ID_153, whole genome shotgun sequence	944..1747	Aminoglycoside resistance Alternate name; aph(3'')-Ib	AF321551
aph(3')-Ia	100	816 / 816	NXIR01000137.1 Escherichia coli strain ST-73:E053 NODE_137_length_1281_cov_123.984_ID_273, whole genome shotgun sequence	230..1045	Aminoglycoside resistance	V00359
aph(6)-Id	100	837 / 837	NXIR01000077.1 Escherichia coli strain ST-73:E053 NODE_77_length_4582_cov_62.3674_ID_153, whole genome shotgun sequence	108..944	Aminoglycoside resistance Alternate name; aph(6)-Id	M28829

Quinolone						
Resistance gene	**Identity**	**Query / Templ**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**

		ate length				
aac(6')-Ib-cr	100	600 / 600	NXIR01000103.1 Escherichia coli strain ST-73:E053 NODE_103_length_2384_cov_166.905_ID_205, whole genome shotgun sequence	1640..2239	Fluoroquinolone and aminoglycoside resistance	DQ303918

Phenicol

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
catA1	99.85	660 / 660	NXIR01000110.1 Escherichia coli strain ST-73:E053 NODE_110_length_2220_cov_68.7492_ID_219, whole genome shotgun sequence	1239..1898	Phenicol resistance	V00622
catB3	100	442 / 633	NXIR01000103.1 Escherichia coli strain ST-73:E053 NODE_103_length_2384_cov_166.905_ID_205, whole genome shotgun sequence	100..541	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXIR01000103.1 Escherichia coli strain ST-73:E053 NODE_103_length_2384_cov_166.905_ID_205, whole genome shotgun sequence	100..541	Phenicol resistance	U13880

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
dfrA7	100	474 / 474	NXIR01000080.1 Escherichia coli strain ST-73:E053 NODE_80_length_4325_cov_65.4411_ID_159, whole genome shotgun sequence	2422..2895	Trimethoprim resistance	AB161450

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-15	100	876 / 876	NXIR01000060.1 Escherichia coli strain ST-73:E053 NODE_60_length_6894_cov_156.76_ID_119, whole genome shotgun sequence	2780..3655	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaOXA-1	100	831 / 831	NXIR01000103.1 Escherichia coli strain ST-73:E053 NODE_103_length_2384_cov_166.905_ID_205, whole genome shotgun sequence	679..1509	Beta-lactam resistance	HQ170510

Macrolide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
mdf(A)	98.13	1233 / 1233	NXIR01000004.1 Escherichia coli strain ST-73:E053 NODE_4_length_296822_cov_91.0986_ID_7, whole genome shotgun sequence	194825..196057	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

gyrA
No known mutations found in gyrA

parE
No known mutations found in parE

pmrA
No known mutations found in pmrA

16S_rrsC
No known mutations found in 16S_rrsC

23S
No known mutations found in 23S

folP
No mutations found in folP

16S_rrsB
No known mutations found in 16S_rrsB

rpoB
No mutations found in rpoB

parC
No known mutations found in parC

gyrB
No known mutations found in gyrB

pmrB
No known mutations found in pmrB

ampC
No mutations found in ampC

16S_rrsH

No known mutations found in 16S_rrsH

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ResFinder-3.2 Server - Results

Input Files: *E056.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Phenicol

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
catB3	100	442 / 633	NXJD01000102.1 Escherichia coli strain ST-131:E056 NODE_102_length_2296_cov_37.5359, whole genome shotgun sequence	56..497	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXJD01000102.1 Escherichia coli strain ST-131:E056 NODE_102_length_2296_cov_37.5359, whole genome shotgun sequence	56..497	Phenicol resistance	U13880

Macrolide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
mdf(A)	97.81	1233 /	NXJD01000011.1 Escherichia coli strain ST-	55638..56870	Warning:	Y08743

		1233	131:E056 NODE_11_length_156556_cov_39.1534, whole genome shotgun sequence		gene is missing from Notes file. Please inform curator.	

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	100	1200 / 1200	NXJD01000053.1 Escherichia coli strain ST-131:E056 NODE_53_length_10102_cov_31.5745, whole genome shotgun sequence	7999..9198	Tetracycline resistance	AJ517790

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(3)-IIa	99.77	861 / 861	NXJD01000097.1 Escherichia coli strain ST-131:E056 NODE_97_length_2753_cov_40.0626, whole genome shotgun sequence	142..1002	Aminoglycoside resistance	X51534
aac(6')-Ib-cr	100	600 / 600	NXJD01000102.1 Escherichia coli strain ST-131:E056 NODE_102_length_2296_cov_37.5359, whole genome shotgun sequence	1596..2195	Fluoroquinolone and aminoglycoside resistance	DQ303918

Beta-lactam						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
blaCTX-M-15	100	876 / 876	NXJD01000084.1 Escherichia coli strain ST-131:E056 NODE_84_length_4202_cov_36.3012, whole genome shotgun sequence	1981..2856	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaOXA-1	100	831 / 831	NXJD01000102.1 Escherichia coli strain ST-131:E056 NODE_102_length_2296_cov_37.5359, whole genome shotgun sequence	635..1465	Beta-lactam resistance	HQ170510

Quinolone						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
aac(6')-Ib-cr	100	600 / 600	NXJD01000102.1 Escherichia coli strain ST-131:E056 NODE_102_length_2296_cov_37.5359, whole genome shotgun sequence	1596..2195	Fluoroquinolone and aminoglycoside resistance	DQ303918

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

23S
No known mutations found in 23S

16S_rrsC

No known mutations found in 16S_rrsC

ampC

No known mutations found in ampC

parE

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

gyrA

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

gyrB

No known mutations found in gyrB

pmrB

No known mutations found in pmrB

folP

No known mutations found in folP

16S_rrsB

No known mutations found in 16S_rrsB

parC

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

16S_rrsH

No known mutations found in 16S_rrsH

rpoB

No mutations found in rpoB

pmrA
No known mutations found in pmrA

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ResFinder-3.2 Server - Results

Input Files: *E058.fasta*

Show Acquired antimicrobial resistance results

Macrolide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
mdf(A)	97.81	1233 / 1233	NXLI01000005.1 Escherichia coli strain ST-131:E058 NODE_5_length_284479_cov_58.0191_ID_9, whole genome shotgun sequence	172769..174001	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Colistin

Phenicol						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
catB3	100	442 / 633	NXLI01000066.1 Escherichia coli strain ST-131:E058 NODE_66_length_2384_cov	100..541	Phenicol resistance	AJ009818

			_63.1182_ID_131, whole genome shotgun sequence			
catB3	100	442 / 633	NXLI01000066.1 Escherichia coli strain ST-131:E058 NODE_66_length_2384_cov_63.1182_ID_131, whole genome shotgun sequence	100..541	Phenicol resistance	U13880

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXLI01000066.1 Escherichia coli strain ST-131:E058 NODE_66_length_2384_cov_63.1182_ID_131, whole genome shotgun sequence	1640..2239	Fluoroquinolone and aminoglycoside resistance	DQ303918

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-15	100	876 / 876	NXLI01000051.1 Escherichia coli strain ST-131:E058 NODE_51_length_4247_cov_68.2392_ID_101, whole genome shotgun sequence	1391..2266	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaOXA-1	100	831 / 831	NXLI01000066.1 Escherichia coli strain ST-131:E058 NODE_66_length_2384_cov_63.1182_ID_131, whole genome shotgun sequence	679..1509	Beta-lactam resistance	HQ170510

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number

aac(3)-IIa	99.77	861 / 861	NXLI01000061.1 Escherichia coli strain ST-131:E058 NODE_61_length_2798_cov_34.0133_ID_121, whole genome shotgun sequence	1796..2656	Aminoglycoside resistance	X51534
aac(6')-Ib-cr	100	600 / 600	NXLI01000066.1 Escherichia coli strain ST-131:E058 NODE_66_length_2384_cov_63.1182_ID_131, whole genome shotgun sequence	1640..2239	Fluoroquinolone and aminoglycoside resistance	DQ303918

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	100	1200 / 1200	NXLI01000042.1 Escherichia coli strain ST-131:E058 NODE_42_length_9712_cov_37.4924_ID_83, whole genome shotgun sequence	8043..9242	Tetracycline resistance	AJ517790

extended output

Selected %ID threshold: *90 %*

Selected minimum length: *60 %*

Results as text

Hit in genome sequences

Resistance gene sequences

Results as tabseperated file

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

parC				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

ampC
No known mutations found in ampC

rpoB
No mutations found in rpoB

parE				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

23S
No known mutations found in 23S

16S_rrsC
No known mutations found in 16S_rrsC

16S_rrsH
No known mutations found in 16S_rrsH

folP
No known mutations found in folP

gyrB

No known mutations found in gyrB

pmrB

No known mutations found in pmrB

gyrA

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

16S_rrsB

No known mutations found in 16S_rrsB

pmrA

No known mutations found in pmrA

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ResFinder-3.2 Server - Results

Input Files: *E057.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	100	1200 / 1200	NXIS01000072.1 Escherichia coli strain ST-665:E057 NODE_72_length_4135_cov_69.8994_ID_143, whole genome shotgun sequence	1784..2983	Tetracycline resistance	AJ517790

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCMY-2	100	1146 / 1146	NXIS01000018.1 Escherichia coli strain ST-665:E057 NODE_18_length_94138_cov_167.593_ID_35, whole genome shotgun sequence	79152..80297	Beta-lactam resistance	X91840

Macrolide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
mdf(A)	99.59	1233 / 1233	NXIS01000014.1 Escherichia coli strain ST-665:E057 NODE_14_length_109477_cov_121.047_ID_27, whole genome shotgun sequence	46470..47702	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Show Point mutation results

Chromosomal point mutations - Results

Species: *escherichia_coli*

Known Mutations

pmrA

No mutations found in pmrA

rpoB

No mutations found in rpoB

23S

No known mutations found in 23S

ampC

No mutations found in ampC

16S_rrsH

No known mutations found in 16S_rrsH

parC

No known mutations found in parC

16S_rrsC

No known mutations found in 16S_rrsC

pmrB

No mutations found in pmrB

gyrA

No mutations found in gyrA

parE

No mutations found in parE

16S_rrsB

No known mutations found in 16S_rrsB

folP
No known mutations found in folP

gyrB
No mutations found in gyrB

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ResFinder-3.2 Server - Results

Input Files: *E060.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Fosfomycin						
Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Macrolide						
Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number

mdf(A)	97.81	1233 / 1233	NXLJ01000005.1 Escherichia coli strain ST-131:E060 NODE_5_length_252029_cov_54.9786_ID_9, whole genome shotgun sequence	186274..187506	Warning: gene is missing from Notes file. Please inform curator.	Y08743
mph(A)	100	906 / 906	NXLJ01000043.1 Escherichia coli strain ST-131:E060 NODE_43_length_11279_cov_42.2442_ID_85, whole genome shotgun sequence	10206..11111	Macrolide resistance	D16251

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXLJ01000070.1 Escherichia coli strain ST-131:E060 NODE_70_length_2384_cov_47.1151_ID_139, whole genome shotgun sequence	1640..2239	Fluoroquinolone and aminoglycoside resistance	DQ303918

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
dfrA17	100	474 / 474	NXLJ01000043.1 Escherichia coli strain ST-131:E060 NODE_43_length_11279_cov_42.2442_ID_85, whole genome shotgun sequence	2117..2590	Trimethoprim resistance	FJ460238

Sulphonamide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
sul1	100	840 / 840	NXLJ01000043.1 Escherichia coli strain ST-131:E060 NODE_43_length_11279_cov_42.2442_ID_85, whole genome shotgun sequence	4056..4895	Sulphonamide resistance	U12338
sul2	100	816 / 816	NXLJ01000052.1 Escherichia coli strain ST-131:E060 NODE_52_length_6299_cov_188.108_ID_103, whole genome shotgun sequence	4049..4864	Sulphonamide resistance	AY034138

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(3)-IIa	99.77	861 / 861	NXLJ01000066.1 Escherichia coli strain ST-131:E060 NODE_66_length_2798_cov_32.7429_ID_131, whole genome shotgun sequence	1796..2656	Aminoglycoside resistance	X51534
aac(6')-Ib-cr	100	600 / 600	NXLJ01000070.1 Escherichia coli strain ST-131:E060 NODE_70_length_2384_cov_47.1151_ID_139, whole genome shotgun sequence	1640..2239	Fluoroquinolone and aminoglycoside resistance	DQ303918
aadA5	100	789 / 789	NXLJ01000043.1 Escherichia coli strain ST-131:E060 NODE_43_length_11279_cov_42.2442_ID_85, whole genome shotgun sequence	2721..3509	Aminoglycoside resistance	AF137361
aph(3'')-Ib	100	804 / 804	NXLJ01000052.1 Escherichia coli strain ST-131:E060 NODE_52_length_6299_cov_188.108_ID_103, whole genome shotgun sequence	4925..5728	Aminoglycoside resistance Alternate name;	AF321551

					aph(3")-Ib	
aph(6)-Id	100	572 / 837	NXLJ01000052.1 Escherichia coli strain ST-131:E060 NODE_52_length_6299_cov_188.108_ID_103, whole genome shotgun sequence	5728..6299	Aminoglycoside resistance Alternate name; aph(6)-Id	18676889
aph(6)-Id	100	572 / 837	NXLJ01000052.1 Escherichia coli strain ST-131:E060 NODE_52_length_6299_cov_188.108_ID_103, whole genome shotgun sequence	5728..6299	Aminoglycoside resistance Alternate name; aph(6)-Id	AF024602
aph(6)-Id	100	572 / 837	NXLJ01000052.1 Escherichia coli strain ST-131:E060 NODE_52_length_6299_cov_188.108_ID_103, whole genome shotgun sequence	5728..6299	Aminoglycoside resistance Alternate name; aph(6)-Id	M28829

Phenicol						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
catB3	100	442 / 633	NXLJ01000070.1 Escherichia coli strain ST-131:E060 NODE_70_length_2384_cov_47.1151_ID_139, whole genome shotgun sequence	100..541	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXLJ01000070.1 Escherichia coli strain ST-131:E060 NODE_70_length_2384_cov_47.1151_ID_139, whole genome shotgun sequence	100..541	Phenicol resistance	U13880

Beta-lactam						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
blaCTX-M-15	100	876 / 876	NXLJ01000039.1 Escherichia coli strain ST-131:E060 NODE_39_length_14861_c	11250..12125	Beta-lactam resistance	AY044436

			ov_59.0868_ID_77, whole genome shotgun sequence		Alternate name; UOE-1	
blaOXA-1	100	831 / 831	NXLJ01000070.1 Escherichia coli strain ST-131:E060 NODE_70_length_2384_cov_47.1151_ID_139, whole genome shotgun sequence	679..1509	Beta-lactam resistance	HQ170510
blaTEM-1B	100	861 / 861	NXLJ01000026.1 Escherichia coli strain ST-131:E060 NODE_26_length_42878_cov_83.7678_ID_51, whole genome shotgun sequence	40380..41240	Beta-lactam resistance Alternate name; RblaTEM-1	AY458016

Tetracycline						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
tet(A)	100	1200 / 1200	NXLJ01000014.1 Escherichia coli strain ST-131:E060 NODE_14_length_148691_cov_49.7764_ID_27, whole genome shotgun sequence	146782..147981	Tetracycline resistance	AJ517790

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

rpoB

No mutations found in rpoB

pmrB

No known mutations found in pmrB

pmrA

No known mutations found in pmrA

gyrB

No known mutations found in gyrB

23S

No known mutations found in 23S

folP

No known mutations found in folP

parE

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

16S_rrsC

No known mutations found in 16S_rrsC

gyrA

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

16S_rrsB

No known mutations found in 16S_rrsB

16S_rrsH

No known mutations found in 16S_rrsH

parC

Mutation	Nucleotide change	Amino acid change	Resistance	PMID

parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

ampC
No known mutations found in ampC

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ResFinder-3.2 Server - Results

Input Files: *E062.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Quinolone						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
aac(6')-Ib-cr	100	600 / 600	NXJE01000083.1 Escherichia coli strain ST-131:E062 NODE_83_length_2296_cov_34.0013, whole genome shotgun sequence	1596..2195	Fluoroquinolone and aminoglycoside resistance	DQ303918

Phenicol

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
catB3	100	442 / 633	NXJE01000083.1 Escherichia coli strain ST-131:E062 NODE_83_length_2296_cov_34.0013, whole genome shotgun sequence	56..497	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXJE01000083.1 Escherichia coli strain ST-131:E062 NODE_83_length_2296_cov_34.0013, whole genome shotgun sequence	56..497	Phenicol resistance	U13880

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXJE01000083.1 Escherichia coli strain ST-131:E062 NODE_83_length_2296_cov_34.0013, whole genome shotgun sequence	1596..2195	Fluoroquinolone and aminoglycoside resistance	DQ303918

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	100	1200 / 1200	NXJE01000052.1 Escherichia coli strain ST-131:E062 NODE_52_length_10140_cov_30.8601, whole genome shotgun sequence	943..2142	Tetracycline resistance	AJ517790

Macrolide

Resistance gene	Identity	Query / Templ	Contig	Position in contig	Predicted phenotype	Accession number

		ate length				
mdf(A)	97.81	1233 / 1233	NXJE01000010.1 Escherichia coli strain ST-131:E062 NODE_10_length_165057_cov_34.0438, whole genome shotgun sequence	64141..65373	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-15	100	876 / 876	NXJE01000070.1 Escherichia coli strain ST-131:E062 NODE_70_length_4202_cov_38.387, whole genome shotgun sequence	1981..2856	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaOXA-1	100	831 / 831	NXJE01000083.1 Escherichia coli strain ST-131:E062 NODE_83_length_2296_cov_34.0013, whole genome shotgun sequence	635..1465	Beta-lactam resistance	HQ170510

Colistin

Show Point mutation results

Chromosomal point mutations - Results

Species: *escherichia_coli*

Known Mutations

parE				
Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

16S_rrsC
No known mutations found in 16S_rrsC

16S_rrsB
No known mutations found in 16S_rrsB

folP
No known mutations found in folP

pmrA
No known mutations found in pmrA

ampC
No known mutations found in ampC

parC				
Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

pmrB
No known mutations found in pmrB

gyrA				
Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

23S
No known mutations found in 23S

gyrB
No known mutations found in gyrB

rpoB
No mutations found in rpoB

16S_rrsH
No known mutations found in 16S_rrsH

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Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Fusidicacid						
Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Trimethoprim						
Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Nitroimidazole

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXJE01000083.1 Escherichia coli strain ST-131:E062 NODE_83_length_2296_cov_34.0013, whole genome shotgun sequence	1596..2195	Fluoroquinolone and aminoglycoside resistance	DQ303918

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXJE01000083.1 Escherichia coli strain ST-131:E062 NODE_83_length_2296_cov_34.0013, whole genome shotgun sequence	1596..2195	Fluoroquinolone and aminoglycoside resistance	DQ303918

Oxazolidinone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Phenicol

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
catB3	100	442 / 633	NXJE01000083.1 Escherichia coli strain ST-131:E062 NODE_83_length_2296_c	56..497	Phenicol resistance	AJ009818

			ov_34.0013, whole genome shotgun sequence			
catB3	100	442 / 633	NXJE01000083.1 Escherichia coli strain ST-131:E062 NODE_83_length_2296_cov_34.0013, whole genome shotgun sequence	56..497	Phenicol resistance	U13880

Glycopeptide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	100	1200 / 1200	NXJE01000052.1 Escherichia coli strain ST-131:E062 NODE_52_length_10140_cov_30.8601, whole genome shotgun sequence	943..2142	Tetracycline resistance	AJ517790

Macrolide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
mdf(A)	97.81	1233 / 1233	NXJE01000010.1 Escherichia coli strain ST-131:E062 NODE_10_length_165057_cov_34.0438, whole genome shotgun sequence	64141..65373	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Colistin

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Beta-lactam						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
blaCTX-M-15	100	876 / 876	NXJE01000070.1 Escherichia coli strain ST-131:E062 NODE_70_length_4202_cov_38.387, whole genome shotgun sequence	1981..2856	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaOXA-1	100	831 / 831	NXJE01000083.1 Escherichia coli strain ST-131:E062 NODE_83_length_2296_cov_34.0013, whole genome shotgun sequence	635..1465	Beta-lactam resistance	HQ170510

Fosfomycin						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Sulphonamide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

Rifampicin						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
No hit found						

extended output

Selected %ID threshold: *90 %*

Selected minimum length: *60 %*

Results as text

Hit in genome sequences

Resistance gene sequences

Results as tabseperated file

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

pmrB

No known mutations found in pmrB

16S_rrsB

No known mutations found in 16S_rrsB

gyrA

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

16S_rrsH

No known mutations found in 16S_rrsH

folP

No known mutations found in folP

16S_rrsC

No known mutations found in 16S_rrsC

pmrA

No known mutations found in pmrA

parE

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

parC

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

23S

No known mutations found in 23S

gyrB

No known mutations found in gyrB

ampC

No known mutations found in ampC

rpoB

No mutations found in rpoB

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Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Rifampicin

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
ARR-2	100	453 / 453	NXKS01000052.1 Escherichia coli strain ST-410:K011 NODE_52_length_16301_cov_51.8803_ID_103, whole genome shotgun sequence	1068..1520	Rifampicin resistance	HQ141279

Quinolone

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aac(6')-Ib-cr	100	600 / 600	NXKS01000086.1 Escherichia coli strain ST-410:K011 NODE_86_length_2381_cov_148.955_ID_171, whole genome shotgun sequence	1640..2239	Fluoroquinolone and aminoglycoside resistance	DQ303918

Phenicol

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
catB3	100	442 / 633	NXKS01000086.1 Escherichia coli strain ST-410:K011 NODE_86_length_2381_cov_148.955_ID_171, whole genome shotgun sequence	100..541	Phenicol resistance	AJ009818
catB3	100	442 / 633	NXKS01000086.1 Escherichia coli strain ST-410:K011 NODE_86_length_2381_cov_148.955_ID_171, whole genome shotgun sequence	100..541	Phenicol resistance	U13880
cmlA1	99.68	1260 / 1260	NXKS01000052.1 Escherichia coli strain ST-410:K011 NODE_52_length_16301_cov_51.8803_ID_103, whole genome shotgun sequence	1841..3100	Phenicol resistance	M64556
floR	98.35	1214 / 1215	NXKS01000071.1 Escherichia coli strain ST-410:K011 NODE_71_length_6114_cov_21.4545_ID_141, whole genome shotgun sequence	4475..5688	Phenicol resistance	AF118107

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
dfrA23	100	561 / 561	NXKS01000052.1 Escherichia coli strain ST-410:K011 NODE_52_length_16301_cov_51.8803_ID_103, whole genome shotgun sequence	9415..9975	Trimethoprim resistance	AJ746361

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number

blaCTX-M-15	100	876 / 876	NXKS01000078.1 Escherichia coli strain ST-410:K011 NODE_78_length_4254_cov_145.597_ID_155, whole genome shotgun sequence	644..1519	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaOXA-1	100	831 / 831	NXKS01000086.1 Escherichia coli strain ST-410:K011 NODE_86_length_2381_cov_148.955_ID_171, whole genome shotgun sequence	679..1509	Beta-lactam resistance	HQ170510
blaOXA-10	100	801 / 801	NXKS01000052.1 Escherichia coli strain ST-410:K011 NODE_52_length_16301_cov_51.8803_ID_103, whole genome shotgun sequence	3365..4165	Beta-lactam resistance Alternate name; PSE-2	J03427

Macrolide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
mdf(A)	98.78	1233 / 1233	NXKS01000010.1 Escherichia coli strain ST-410:K011 NODE_10_length_140324_cov_46.8878_ID_19, whole genome shotgun sequence	63075..64307	Warning: gene is missing from Notes file. Please inform curator.	Y08743
mph (A)	100	906 / 906	NXKS01000076.1 Escherichia coli strain ST-410:K011 NODE_76_length_4337_cov	3264..4169	Macrolide resistance	D16251

			_42.5559_ID_151, whole genome shotgun sequence			

Sulphonamide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
sul1	100	840 / 840	NXKS01000052.1 Escherichia coli strain ST-410:K011 NODE_52_length_16301_cov_51.8803_ID_103, whole genome shotgun sequence	5438..6277	Sulphonamide resistance	U12338
sul2	100	816 / 816	NXKS01000019.1 Escherichia coli strain ST-410:K011 NODE_19_length_88471_cov_71.4106_ID_37, whole genome shotgun sequence	2070..2885	Sulphonamide resistance	AY034138

Aminoglycoside						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
aac(3)-IIa	99.77	861 / 861	NXKS01000084.1 Escherichia coli strain ST-410:K011 NODE_84_length_2798_cov_154.955_ID_167, whole genome shotgun sequence	1796..2656	Aminoglycoside resistance	X51534
aac(6')-Ib-cr	100	600 / 600	NXKS01000086.1 Escherichia coli strain ST-410:K011 NODE_86_length_2381_cov_148.955_ID_171, whole genome shotgun sequence	1640..2239	Fluoroquinolone and aminoglycoside resistance	DQ303918
aadA1	99.75	792 / 792	NXKS01000052.1 Escherichia coli strain ST-410:K011 NODE_52_length_16301_cov_51.8803_ID_103, whole genome shotgun sequence	4182..4973	Aminoglycoside resistance	JQ414041
aadA1	99.75	792 /	NXKS01000052.1 Escherichia coli strain ST-410:K011	4182..4973	Aminoglycoside	JX185132

		792	NODE_52_length_16301_cov_51.8803_ID_103, whole genome shotgun sequence		resistance	
aph(3")-Ib	100	804 / 804	NXKS01000019.1 Escherichia coli strain ST-410:K011 NODE_19_length_88471_cov_71.4106_ID_37, whole genome shotgun sequence	1206..2009	Aminoglycoside resistance Alternate name; aph(3")-Ib	AF321551
aph(6)-Id	100	837 / 837	NXKS01000019.1 Escherichia coli strain ST-410:K011 NODE_19_length_88471_cov_71.4106_ID_37, whole genome shotgun sequence	370..1206	Aminoglycoside resistance Alternate name; aph(6)-Id	M28829

Tetracycline						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
tet(A)	100	1200 / 1200	NXKS01000080.1 Escherichia coli strain ST-410:K011 NODE_80_length_3950_cov_38.9055_ID_159, whole genome shotgun sequence	1784..2983	Tetracycline resistance	AJ517790

extended output

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

gyrA				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

parC				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
parC p.S80I	AGC → ATC	S → I	Nalidixic acid,Ciprofloxacin	8851598

16S_rrsB
No known mutations found in 16S_rrsB

pmrB
No known mutations found in pmrB

23S
No known mutations found in 23S

rpoB
No known mutations found in rpoB

ampC
No mutations found in ampC

folP
No mutations found in folP

16S_rrsC
No known mutations found in 16S_rrsC

pmrA
No known mutations found in pmrA

parE				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
parE p.S458A	TCG → GCG	S → A	Nalidixic acid,Ciprofloxacin	28598203

gyrB
No mutations found in gyrB

16S_rrsH
No known mutations found in 16S_rrsH

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ResFinder-3.2 Server - Results

Input Files: *E063.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Sulphonamide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
sul2	100	816 / 816	NXIT01000025.1 Escherichia coli strain ST-131:E063 NODE_25_length_87986_cov_109.647_ID_49, whole genome shotgun sequence	12934..13749	Sulphonamide resistance	AY034138

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aph(3")-Ib	100	529 / 804	NXIT01000025.1 Escherichia coli strain ST-131:E063 NODE_25_length_87986_cov_109.647_ID_49, whole genome shotgun sequence	12345..12873	Aminoglycoside resistance Alternate name; aph(3")-Ib	AF321551
aph(6)-Id	100	837 / 837	NXIT01000025.1 Escherichia coli strain ST-131:E063 NODE_25_length_87986_cov_109.647_ID_49, whole genome shotgun sequence	10666..11502	Aminoglycoside resistance Alternate name; aph(6)-Id	M28829

Macrolide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
mdf(A)	97.73	1233 / 1233	NXIT01000013.1 Escherichia coli strain ST-131:E063 NODE_13_length_151395_cov_99.5836_ID_25, whole genome shotgun sequence	99762..100994	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number

blaCTX-M-15	100	876 / 876	NXIT01000025.1 Escherichia coli strain ST-131:E063 NODE_25_length_87986_cov_109.647_ID_49, whole genome shotgun sequence	25943..26818	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaTEM-1B	100	861 / 861	NXIT01000025.1 Escherichia coli strain ST-131:E063 NODE_25_length_87986_cov_109.647_ID_49, whole genome shotgun sequence	22261..23121	Beta-lactam resistance Alternate name; RblaTEM-1	AY458016

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
dfrA14	100	474 / 474	NXIT01000025.1 Escherichia coli strain ST-131:E063 NODE_25_length_87986_cov_109.647_ID_49, whole genome shotgun sequence	11852..12325	Trimethoprim resistance	AF393510

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	100	1200 / 1200	NXIT01000072.1 Escherichia coli strain ST-131:E063 NODE_72_length_5248_cov_66.1651_ID_143, whole genome shotgun sequence	1784..2983	Tetracycline resistance	AJ517790

Show Point mutation results

Chromosomal point mutations - Results

Species: *escherichia_coli*

Known Mutations

pmrA
No known mutations found in pmrA

16S_rrsH
No known mutations found in 16S_rrsH

folP
No known mutations found in folP

parE				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

pmrB
No known mutations found in pmrB

16S_rrsB
No known mutations found in 16S_rrsB

rpoB
No known mutations found in rpoB

ampC
No known mutations found in ampC

23S
No known mutations found in 23S

parC				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**

parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

16S_rrsC
No known mutations found in 16S_rrsC

gyrB
No known mutations found in gyrB

gyrA				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

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ResFinder-3.2 Server - Results

Input Files: *K091.fasta*

Show Acquired antimicrobial resistance results

No hit found

Sulphonamide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
sul1	100	840 / 840	NXKQ01000037.1 Escherichia coli strain K091 NODE_37_length_11029_cov_64.2095, whole genome shotgun sequence	3643..4482	Sulphonamide resistance	U12338

Macrolide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
mdf(A)	97.97	1233 / 1233	NXKQ01000001.1 Escherichia coli strain K091 NODE_1_length_967759_cov_49.018, whole genome shotgun sequence	344618..345850	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Tetracycline						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
tet(B)	100	1206 / 1206	NXKQ01000054.1 Escherichia coli strain K091 NODE_54_length_2847_cov_75.404, whole genome shotgun sequence	1264..2469	Tetracycline resistance	AF326777

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aadA1	100	792 / 792	NXKQ01000037.1 Escherichia coli strain K091 NODE_37_length_11029_cov_64.2095, whole genome shotgun sequence	2347..3138	Aminoglycoside resistance	JX185132

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-15	100	876 / 876	NXKQ01000041.1 Escherichia coli strain K091 NODE_41_length_8179_cov_80.6043, whole genome shotgun sequence	3863..4738	Beta-lactam resistance Alternate name; UOE-1	AY044436
blaTEM-1B	100	861 / 861	NXKQ01000041.1 Escherichia coli strain K091 NODE_41_length_8179_cov_80.6043, whole genome shotgun sequence	181..1041	Beta-lactam resistance Alternate name; RblaTEM-1	AY458016

Trimethoprim

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
dfrA1	99.79	474 / 474	NXKQ01000037.1 Escherichia coli strain K091 NODE_37_length_11029_cov_64.2095, whole genome shotgun sequence	1781..2254	Trimethoprim resistance	AF203818
dfrA1	99.79	474 / 474	NXKQ01000037.1 Escherichia coli strain K091	1781..2254	Trimethoprim	AJ238350

			NODE_37_length_11029_cov_64.2095, whole genome shotgun sequence		resistance	
dfrA1	99.79	474 / 474	NXKQ01000037.1 Escherichia coli strain K091 NODE_37_length_11029_cov_64.2095, whole genome shotgun sequence	1781..2254	Trimethoprim resistance	X00926

Show Point mutation results

Chromosomal point mutation - Results

Species: *escherichia_coli*

Known Mutations

gyrA
No known mutations found in gyrA

gyrB
No known mutations found in gyrB

16S_rrsC
No known mutations found in 16S_rrsC

16S_rrsH
No known mutations found in 16S_rrsH

pmrA
No known mutations found in pmrA

folP
No known mutations found in folP

parC
No known mutations found in parC

parE
No known mutations found in parE

ampC
No mutations found in ampC

23S
No known mutations found in 23S

pmrB
No known mutations found in pmrB

rpoB
No mutations found in rpoB

16S_rrsB
No known mutations found in 16S_rrsB

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ResFinder-3.2 Server - Results

Input Files: *K075.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Macrolide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**

mdf(A)	98.3	1233 / 1233	NXKJ01000001.1 Escherichia coli strain ST-648:K075 NODE_1_length_423633_cov_194.917, whole genome shotgun sequence	107394..108626	Warning: gene is missing from Notes file. Please inform curator.	Y08743

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-14	100	876 / 876	NXKJ01000143.1 Escherichia coli strain ST-648:K075 NODE_143_length_1484_cov_445.971, whole genome shotgun sequence	106..981	Beta-lactam resistance Amino acid sequences of CTX-M-14 and CTX-M-18 are identical	AF252622

Sulphonamide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
sul3	100	792 / 792	NXKJ01000111.1 Escherichia coli strain ST-648:K075 NODE_111_length_2847_cov_292.201, whole genome shotgun sequence	1927..2718	Sulphonamide resistance	AJ459418

Phenicol

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
cmlA1	99.92	1260 / 1260	NXKJ01000078.1 Escherichia coli strain ST-648:K075 NODE_78_length_7787_cov_385.817, whole genome shotgun sequence	3779..5038	Phenicol resistance	M64556

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	100	1200 / 1200	NXKJ01000096.1 Escherichia coli strain ST-648:K075 NODE_96_length_3812_cov_207.436, whole genome shotgun sequence	1504..2703	Tetracycline resistance	AJ517790

Fosfomycin

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
fosA3	100	417 / 417	NXKJ01000122.1 Escherichia coli strain ST-648:K075 NODE_122_length_2202_cov_421.231, whole genome shotgun sequence	311..727	Fosfomycin resistance	AB522970

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aadA1	100	792 / 792	NXKJ01000078.1 Escherichia coli strain ST-648:K075 NODE_78_length_7787_cov_385.817, whole genome shotgun sequence	5131..5922	Aminoglycoside resistance	JQ414041

aadA2b	99.87	780 / 780	NXKJ01000078.1 Escherichia coli strain ST-648:K075 NODE_78_length_7787_cov_385.817, whole genome shotgun sequence	2738..3517	Warning: gene is missing from Notes file. Please inform curator.	D43625
aph(3'')-Ib	100	803 / 804	NXKJ01000083.1 Escherichia coli strain ST-648:K075 NODE_83_length_7307_cov_314.041, whole genome shotgun sequence	1143..1945	Aminoglycoside resistance Alternate name; aph(3'')-Ib	AF024602
aph(3'')-Ib	99.88	804 / 804	NXKJ01000083.1 Escherichia coli strain ST-648:K075 NODE_83_length_7307_cov_314.041, whole genome shotgun sequence	1142..1945	Aminoglycoside resistance Alternate name; aph(3'')-Ib	AF313472
aph(3'')-Ib	99.88	804 / 804	NXKJ01000083.1 Escherichia coli strain ST-648:K075 NODE_83_length_7307_cov_314.041, whole genome shotgun sequence	1142..1945	Aminoglycoside resistance Alternate name; aph(3'')-Ib	AF321550
aph(3'')-Ib	99.88	804 / 804	NXKJ01000083.1 Escherichia coli strain ST-648:K075 NODE_83_length_7307_cov_314.041, whole genome shotgun sequence	1142..1945	Aminoglycoside resistance Alternate name; aph(3'')-Ib	AF321551
aph(3')-IIa	100	795 / 795	NXKJ01000094.1 Escherichia coli strain ST-648:K075 NODE_94_length_4203_cov_289.913, whole genome shotgun sequence	298..1092	Aminoglycoside resistance	V00618
aph(6)-Id	100	837 / 837	NXKJ01000083.1 Escherichia coli strain ST-648:K075 NODE_83_length_7307_cov_314.041, whole	1945..2781	Aminoglycoside resistance Alternate	M28829

			genome shotgun sequence		name; aph(6)-Id	

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

16S_rrsC

No known mutations found in 16S_rrsC

rpoB

No mutations found in rpoB

folP

No mutations found in folP

ampC

No known mutations found in ampC

parE

No known mutations found in parE

16S_rrsB

No known mutations found in 16S_rrsB

pmrB

No known mutations found in pmrB

parC

No known mutations found in parC

16S_rrsH

No known mutations found in 16S_rrsH

gyrB

No known mutations found in gyrB

gyrA				
Mutation	**Nucleotide change**	**Amino acid change**	**Resistance**	**PMID**
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148

pmrA
No mutations found in pmrA

23S
No known mutations found in 23S

Download the result table

Contact: Vibeke Dybdahl Hammer, Telephone: +45 3588 6420, E-mail: vdha@food.dtu.dk

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ResFinder-3.2 Server - Results

Input Files: *E013.fasta*

Show Acquired antimicrobial resistance results

Acquired antimicrobial resistance gene - Results

Trimethoprim

Macrolide						
Resistance gene	**Identity**	**Query / Template length**	**Contig**	**Position in contig**	**Predicted phenotype**	**Accession number**
mdf(A)	97.81	1233 / 1233	NXIN01000013.1 Escherichia coli strain ST-131:E013 NODE_13_length_151384_cov_116.767_ID_25, whole genome shotgun sequence	50388..51620	Warning: gene is missing from	Y08743

					Notes file. Please inform curator.	

Aminoglycoside

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
aph(3")-Ib	100	804 / 804	NXIN01000060.1 Escherichia coli strain ST-131:E013 NODE_60_length_5812_cov_101.321_ID_119, whole genome shotgun sequence	3553..4356	Aminoglycoside resistance Alternate name; aph(3")-Ib	[AF321551]
aph(6)-Id	100	831 / 831	NXIN01000060.1 Escherichia coli strain ST-131:E013 NODE_60_length_5812_cov_101.321_ID_119, whole genome shotgun sequence	2717..3547	Aminoglycoside resistance Alternate name; aph(6)-Id	[CP000971]

Tetracycline

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
tet(A)	100	1200 / 1200	NXIN01000060.1 Escherichia coli strain ST-131:E013 NODE_60_length_5812_cov_101.321_ID_119, whole genome shotgun sequence	464..1663	Tetracycline resistance	[AJ517790]

Sulphonamide

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number

sul2	100	816 / 816	NXIN01000060.1 Escherichia coli strain ST-131:E013 NODE_60_length_5812_cov_101.321_ID_119, whole genome shotgun sequence	4417..5232	Sulphonamide resistance	AY034138

Beta-lactam

Resistance gene	Identity	Query / Template length	Contig	Position in contig	Predicted phenotype	Accession number
blaCTX-M-27	100	876 / 876	NXIN01000079.1 Escherichia coli strain ST-131:E013 NODE_79_length_1717_cov_92.1156_ID_157, whole genome shotgun sequence	493..1368	Beta-lactam resistance	AY156923

extended output

Show Point mutation results

Chromosomal point mutations - Results

Species: ***escherichia_coli***

Known Mutations

16S_rrsC

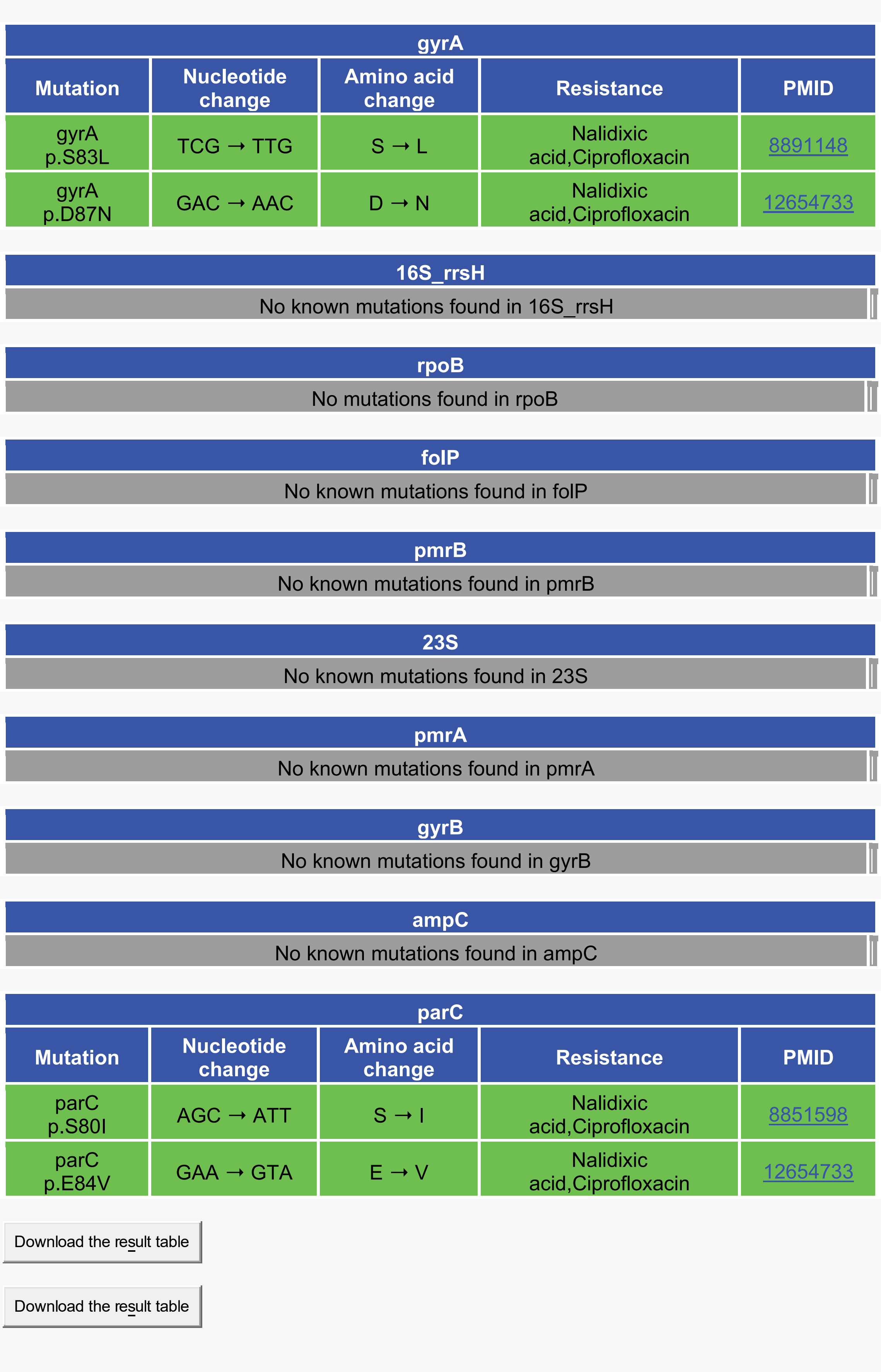
No known mutations found in 16S_rrsC

parE

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parE p.I529L	ATT → CTT	I → L	Nalidixic acid,Ciprofloxacin	14506034

16S_rrsB

No known mutations found in 16S_rrsB



gyrA

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83L	TCG → TTG	S → L	Nalidixic acid,Ciprofloxacin	8891148
gyrA p.D87N	GAC → AAC	D → N	Nalidixic acid,Ciprofloxacin	12654733

16S_rrsH

No known mutations found in 16S_rrsH

rpoB

No mutations found in rpoB

folP

No known mutations found in folP

pmrB

No known mutations found in pmrB

23S

No known mutations found in 23S

pmrA

No known mutations found in pmrA

gyrB

No known mutations found in gyrB

ampC

No known mutations found in ampC

parC

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
parC p.S80I	AGC → ATT	S → I	Nalidixic acid,Ciprofloxacin	8851598
parC p.E84V	GAA → GTA	E → V	Nalidixic acid,Ciprofloxacin	12654733

CITATIONS

For publication of results, please cite:

- Identification of acquired antimicrobial resistance genes.
  Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV.
  J Antimicrob Chemother. 2012 Jul 10.
  PMID: 22782487 doi: 10.1093/jac/dks261