致病菌耐药毒力测试报告

卫生健康委员会专用

流程：高通量双端测序致病菌耐药毒力分析流程

分析流程版本：v1.0.0

各文库情况展示

文库编号	原始下机序列数量	过滤后序列数量	过滤后序列比例(%)	耐药基因检出数量	毒力基因检出数量
DRR102537	1392636	1372138	98.5281	48	29
DRR129836	1990138	1749351	87.9010	54	30
DRR154108	669251	665238	99.4004	54	35

耐药基因展示

Show 1,000 entries Search:

gene	DRR102537文库	DRR129836文库	DRR154108文库	DRR216764文库	ERR016870文库
aadA-	/	m	m	/	m
aadA2	/	/	/	/	m
acrA_2	m	m	m	m	/
acrB	m	m	m	m	/
acrD	m	m	m	m	/
AcrE	/	/	m	m	/
AcrF	m	m	m	m	/
AcrS	m	m	m	m	/
APH_3____Ib	/	/	/	m	m
APH_3___Ia	/	/	/	/	m
APH_6__Id	/	/	/	m	/
bacA	m	m	m	m	/
catII_from_Escherichia	/	/	/	/	m
cmlA-	/	/	/	/	m
cpxA	m	m	m	m	/
CRP	m	m	m	m	/
cyaA_1	/	m	m	m	/
dfrA1	/	m	/	/	/

dfrA12	/	/	/	/	m
EC_13+	m	m	m	m	/
emrA	m	m	m	m	/
emrE_1	/	/	/	m	/
emrK	m	m	m	m	/
emrR	m	m	m	m	/
emrY	m	m	m	m	/
eptA	m	/	m	m	/
Escherichia_coli_23S	m	m	m	/	m
Escherichia_coli_AcrAB_TolC_1	m	m	m	m	/
Escherichia_coli_EF_Tu	m	/	/	/	/
Escherichia_coli_GlpT	m	m	m	m	/
Escherichia_coli_LamB	m	m	m	m	/
evgA	m	m	m	m	/
evgS	m	m	m	m	/
gadW	/	m	/	m	/
gadX	m	m	m	m	/
golS	/	/	/	/	m
gyrA_8	/	/	/	/	m
H_NS	m	m	m	m	/
kdpE	m	m	m	m	/
Klebsiella_pneumoniae_KpnH+	m	m	m	m	/
leuO	m	m	m	m	/
marA	m	m	m	m	/
mdfA	m	m	m	m	/
mdsA	/	/	/	/	m
mdsC	/	/	/	/	m
mdtA	m	m	m	m	/
mdtB	m	m	m	m	/
mdtC	m	m	m	m	/

mdtE	m	m	m	m	/
mdtF	m	m	m	m	/
mdtG	m	m	m	m	/
mdtH	m	m	m	m	/
MdtK	/	/	/	/	m
mdtM	/	m	m	m	/
mdtN	m	/	m	m	/
mdtO	m	/	m	m	/
mdtP	m	/	m	m	/
mipA	m	m	m	m	/
mlaD	m	m	m	m	/
mlaF	m	m	m	m	/
mphA	/	m	/	/	/
Mrx	/	m	/	/	/
msbA	m	m	m	m	/
OXA_-_10	/	m	/	/	/
Plasmid_encoded_cat__pp_cat_+	/	m	/	/	/
PmrF	m	m	m	m	/
porin_OmpC	m	m	m	m	/
qacE-	/	/	m	/	m
rrsB+	m	/	m	m	m
SAT_2	/	m	/	/	/
sdiA	/	/	/	/	m
sul1	/	/	m	/	m
sul2	/	/	/	m	/
sul3	/	/	/	/	m
TEM_-	/	m	/	/	m
tet_B_	/	m	/	/	/
TolC	m	m	m	m	/
ugd	/	/	m	/	/
uhpA	m	m	m	m	/
YojI	m	m	m	m	/

Showing 1 to 80 of 80 entries

耐药基因注释

Show 1,000 entries Search:

序号	基因名称	详细解释
1	AAC_6__I-_3	b"AAC(6')-Iy is a chromosomal-encoded aminoglycoside acetyltransferase in S. enteritidis and S. enterica. Regulatory mutation required to increase expression of this chromosomally-encoded gene for resistance. In the specific system, aminoglycoside resistance was due to a transcriptional fusion secondary to a chromosomal deletion in which the downstream aac(6')-Iy gene was placed under the control of the upstream nmpC promoter.";AAC(6')-Iy
2	AAC_6__Ib7	b"AAC(6')-Ib7 is a plasmid-encoded aminoglycoside acetyltransferase in E. cloacae and C. freundii.";AAC(6')-Ib7; AAC(6')-Ib7;b"AAC(6')-Ib7 is a plasmid-encoded aminoglycoside acetyltransferase in E. cloacae and C. freundii."
3	APH_3__Ia	APH(3')-Ia;b"APH(3')-Ia is a transposon-encoded aminoglycoside phosphotransferase in E. coli and S. enterica. It is identical at the protein sequence to APH(3')-Ic, an aminoglycoside phosphotransferase encoded by plasmids, transposons and genomic islands in K. pneumoniae, A. baumannii, S. marcescens, Corynebacterium spp., Photobacterium spp. and Citrobacter spp."
4	APH_3__Ib	APH(3'')-Ib;b"APH(3'')-Ib is an aminoglycoside phosphotransferase encoded by plasmids, transposons, integrative conjugative elements and chromosomes in Enterobacteriaceae and Pseudomonas spp."; b"APH(3'')-Ib is an aminoglycoside phosphotransferase encoded by plasmids, transposons, integrative conjugative elements and chromosomes in Enterobacteriaceae and Pseudomonas spp.";APH(3'')-Ib
5	APH_6__Id	b'APH(6)-Id is an aminoglycoside phosphotransferase encoded by plasmids, integrative conjugative elements and chromosomal genomic islands in K. pneumoniae, Salmonella spp., E. coli, Shigella flexneri, Providencia alcalifaciens, Pseudomonas spp., V. cholerae, Edwardsiella tarda, Pasteurella multocida and Aeromonas bestiarum.';APH(6)-Id; APH(6)-Id;b'APH(6)-Id is an aminoglycoside phosphotransferase encoded by plasmids, integrative conjugative elements and chromosomal genomic islands in K. pneumoniae, Salmonella spp., E. coli, Shigella flexneri, Providencia alcalifaciens, Pseudomonas spp., V. cholerae, Edwardsiella tarda, Pasteurella multocida and Aeromonas bestiarum.'
6	AcrE	b'AcrE is a membrane fusion protein, similar to AcrA.';AcrE; AcrE;b'AcrE is a membrane fusion protein, similar to AcrA.'
7	AcrF	AcrF;b'AcrF is a inner membrane transporter, similar to AcrB.'; b'AcrF is a inner membrane transporter, similar to AcrB.';AcrF
8	AcrS	b'AcrS is a repressor of the AcrAB efflux complex and is associated with the expression of AcrEF. AcrS is believed to regulate a switch between AcrAB and AcrEF efflux.';AcrS; AcrS;b'AcrS is a repressor of the AcrAB efflux complex and is associated with the expression of AcrEF. AcrS is believed to regulate a switch between AcrAB and AcrEF efflux.'
9	CRP	b'CRP is a global regulator that represses MdtEF multidrug efflux pump expression.';CRP; CRP;b'CRP is a global regulator that represses MdtEF multidrug efflux pump expression.'
10	EC_13+	b'EC-18 is a EC beta-lactamase.';EC-18; b'A class C ampC beta-lactamase (cephalosporinase) enzyme described in Escherichia coli shown clinically to confer resistance to penicillin-like and cephalosporin-class antibiotics.';Escherichia coli ampC beta-lactamase

11	Escherichia_coli_23S	Escherichia coli 23S rRNA with mutation conferring resistance to oxazolidinone antibiotics
12	Escherichia_coli_AcrAB_TolC	Escherichia coli AcrAB-TolC with AcrR mutation conferring resistance to ciprofloxacin, tetracycline, and ceftazidime
13	Escherichia_coli_AcrAB_TolC_1	Escherichia coli AcrAB-TolC with MarR mutations conferring resistance to ciprofloxacin and tetracycline
14	Escherichia_coli_EF_Tu	Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin; Escherichia coli EF-Tu mutants conferring resistance to Enacyloxin IIa
15	Escherichia_coli_GlpT	Escherichia coli GlpT with mutation conferring resistance to fosfomycin
16	Escherichia_coli_LamB	Escherichia coli LamB;b'LamB is a negative regulator for antibiotic resistance, it serves as a porin to influx antibiotic. When down-regulated, it increases resistance to chlortetracycline, ciprofloxacin, balofloxacin and nalidixic acid. It also interacts with Odp1, an energy metabolic enzyme, creating a complex that decreases in antibiotic-resistant strains.'; b'LamB is a negative regulator for antibiotic resistance, it serves as a porin to influx antibiotic. When down-regulated, it increases resistance to chlortetracycline, ciprofloxacin, balofloxacin and nalidixic acid. It also interacts with Odp1, an energy metabolic enzyme, creating a complex that decreases in antibiotic-resistant strains.';Escherichia coli LamB
17	Escherichia_coli_PtsI	Escherichia coli PtsI with mutation conferring resistance to fosfomycin
18	Escherichia_coli_UhpT	Escherichia coli UhpT with mutation conferring resistance to fosfomycin
19	H_NS	b'H-NS is a histone-like protein involved in global gene regulation in Gram-negative bacteria. It is a repressor of the membrane fusion protein genes acrE, mdtE, and emrK as well as nearby genes of many RND-type multidrug exporters.';H-NS; H-NS;b'H-NS is a histone-like protein involved in global gene regulation in Gram-negative bacteria. It is a repressor of the membrane fusion protein genes acrE, mdtE, and emrK as well as nearby genes of many RND-type multidrug exporters.'
20	Klebsiella_pneumoniae_KpnH+	b'emrB is a translocase in the emrB -TolC efflux protein in E. coli. It recognizes substrates including carbonyl cyanide m-chlorophenylhydrazone (CCCP), nalidixic acid, and thioloactomycin.';emrB
21	Klebsiella_pneumoniae_PBP3	Klebsiella pneumoniae PBP3 mutants conferring resistance to ceftazidime-avibactam
22	MdtK	MdtK;b'A multidrug and toxic compound extrusions (MATE) transporter conferring resistance to norfloxacin, doxorubicin and acriflavine.'
23	Mrx	Mrx;b'Mrx is part of the macrolide inactivation gene cluster in Aeromonas hydrophila.'
	OXA_-	

24	_10	OXA-1;b'OXA-1 is a beta-lactamase found in E. coli.'
25	Pasteurella_multocida_16S	Pasteurella multocida 16S rRNA mutation conferring resistance to spectinomycin
26	Plasmid_encoded_cat__pp_cat_+	catA1;b'catA1 (formerly in CARD as catI) is a chromosome and transposon-encoded variant of the cat gene found in Escherichia coli and Acinetobacter baumannii.'
27	PmrF	b'PmrF is required for the synthesis and transfer of 4-amino-4-deoxy-L-arabinose (Ara4N) to Lipid A, which allows gram-negative bacteria to resist the antimicrobial activity of cationic antimicrobial peptides and antibiotics such as polymyxin. pmrF corresponds to 1 locus in Pseudomonas aeruginosa PAO1 and 1 locus in Pseudomonas aeruginosa LESB58.';PmrF; PmrF;b'PmrF is required for the synthesis and transfer of 4-amino-4-deoxy-L-arabinose (Ara4N) to Lipid A, which allows gram-negative bacteria to resist the antimicrobial activity of cationic antimicrobial peptides and antibiotics such as polymyxin. pmrF corresponds to 1 locus in Pseudomonas aeruginosa PAO1 and 1 locus in Pseudomonas aeruginosa LESB58.'
28	SAT_2	SAT-2;b'SAT-2 is a plasmid-mediated streptothricin acetyltransferase, which confers resistance to streptothricin, a nucleoside antibiotic. Originally described from an E. coli plasmid sequence by Heim et al., 1989.'
29	TEM_-	b'TEM-95 is a broad-spectrum beta-lactamase found in E. coli.';TEM-95; TEM-95;b'TEM-95 is a broad-spectrum beta-lactamase found in E. coli.'
30	Thermus_thermophilus_23s	Thermus thermophilus 23s rRNA conferring resistance to pleuromutilin antibiotics
31	TolC	TolC;b'TolC is a protein subunit of many multidrug efflux complexes in Gram negative bacteria. It is an outer membrane efflux protein and is constitutively open. Regulation of efflux activity is often at its periplasmic entrance by other components of the efflux complex.'
32	YojI	YojI;b'YojI mediates resistance to the peptide antibiotic microcin J25 when it is expressed from a multicopy vector. YojI is capable of pumping out microcin molecules. The outer membrane protein TolC in addition to YojI is required for export of microcin J25 out of the cell. Microcin J25 is thus the first known substrate for YojI.'; b'YojI mediates resistance to the peptide antibiotic microcin J25 when it is expressed from a multicopy vector. YojI is capable of pumping out microcin molecules. The outer membrane protein TolC in addition to YojI is required for export of microcin J25 out of the cell. Microcin J25 is thus the first known substrate for YojI.';YojI
33	aadA-	aadA;b"ANT(3'')-Ia is an aminoglycoside nucleotidyltransferase gene encoded by plasmids, transposons, integrons in Enterobacteriaceae, A. baumannii, P. aeruginosa and Vibrio cholerae."; b'aadA3 is an aminoglycoside nucleotidyltransferase gene encoded by plasmids, transposons and integrons in E. coli.';aadA3
34	aadA13	b'aadA13 is an aminoglycoside nucleotidyltransferase gene encoded by plasmids and integrons in Pseudomonas rettgeri, P. aeruginosa, Y. enterocolitica and E. coli.';aadA13
35	aadA2	b'aadA2 is an aminoglycoside nucleotidyltransferase gene encoded by plasmids and integrons in K. pneumoniae, Salmonella spp., Corynebacterium glutamicum, C. freundii and Aeromonas spp.';aadA2
36	acrA_1	b'AcrA is a subunit of the AcrAB-TolC multidrug efflux system in E. cloacae.';Enterobacter cloacae acrA

37	acrA_2	b'AcrA is a subunit of the AcrAB-TolC multidrug efflux system found in E. coli.';Escherichia coli acrA; Escherichia coli acrA;b'AcrA is a subunit of the AcrAB-TolC multidrug efflux system found in E. coli.'
38	acrB	b'Protein subunit of AcrA-AcrB-TolC multidrug efflux complex. AcrB functions as a herterotrimer which forms the inner membrane component and is primarily responsible for substrate recognition and energy transduction by acting as a drug/proton antiporter.';acrB; acrB;b'Protein subunit of AcrA-AcrB-TolC multidrug efflux complex. AcrB functions as a herterotrimer which forms the inner membrane component and is primarily responsible for substrate recognition and energy transduction by acting as a drug/proton antiporter.'
39	acrD	acrD;b'AcrD is an aminoglycoside efflux pump expressed in E. coli. Its expression can be induced by indole, and is regulated by baeRS and cpxAR.'; b'AcrD is an aminoglycoside efflux pump expressed in E. coli. Its expression can be induced by indole, and is regulated by baeRS and cpxAR.';acrD
40	bacA	bacA;b'The bacA gene product (BacA) recycles undecaprenyl pyrophosphate during cell wall biosynthesis which confers resistance to bacitracin.'; b'The bacA gene product (BacA) recycles undecaprenyl pyrophosphate during cell wall biosynthesis which confers resistance to bacitracin.';bacA
41	catII_from_Escherichia	b'catII is a chloramphenicol acetyltransferase. This particular catII is found in E.coli K-12. Confers resistance to chloramphenicol.';catII from Escherichia coli K-12
42	cmlA-	b'cmlA1 is a plasmid or transposon-encoded chloramphenicol exporter that is found in Pseudomonas aeruginosa and Klebsiella pneumoniae.';cmlA1
43	cpxA	b'CpxA is a membrane-localized sensor kinase that is activated by envelope stress. It starts a kinase cascade that activates CpxR, which promotes efflux complex expression.';cpxA
44	cyaA_1	b'CyaA (adenylate cyclase) is involved with the synthesis of cyclic AMP which regulates the fosfomycin transporter glpT. As a result, mutations to cyaA confer resistance to fosfomycin.';Escherichia coli cyaA with mutation conferring resistance to fosfomycin; Escherichia coli cyaA with mutation conferring resistance to fosfomycin;b'CyaA (adenylate cyclase) is involved with the synthesis of cyclic AMP which regulates the fosfomycin transporter glpT. As a result, mutations to cyaA confer resistance to fosfomycin.'
45	dfrA1	dfrA1;b'dfrA1 is an integron-encoded dihydrofolate reductase.'
46	dfrA12	dfrA12;b'dfrA12 is an integron-encoded dihydrofolate reductase found in Vibrio cholerae.'
47	emrA	emrA;b'EmrA is a membrane fusion protein, providing an efflux pathway with EmrB and TolC between the inner and outer membranes of E. coli, a Gram-negative bacterium.'
48	emrE_1	Escherichia coli emrE;b'Member of the small MDR (multidrug resistance) family of transporters; in Escherichia coli this protein provides resistance against a number of positively charged compounds including ethidium bromide and erythromycin; proton-dependent secondary transporter which exchanges protons for compound translocation.'
49	emrK	emrK;b'emrK is a membrane fusion protein that is a homolog of EmrA. Together with the inner membrane transporter EmrY and the outer membrane channel TolC, it mediates multidrug efflux.'; b'emrK is a membrane fusion protein that is a homolog of EmrA. Together with the inner membrane transporter EmrY and the outer membrane channel TolC, it mediates multidrug efflux.';emrK
50	emrR	emrR;b'EmrR is a negative regulator for the EmrAB-TolC multidrug efflux pump in E. coli. Mutations lead to EmrAB-TolC overexpression.'; b'EmrR is a negative regulator for the EmrAB-TolC multidrug efflux pump in E. coli. Mutations lead to EmrAB-TolC overexpression.';emrR
51	emrY	b'emrY is a multidrug transport that moves substrates across the inner membrane of the Gram-negative E. coli. It is a homolog of emrB.';emrY; emrY;b'emrY is a multidrug transport that

		moves substrates across the inner membrane of the Gram-negative E. coli. It is a homolog of emrB.'
52	eptA	eptA;b'PmrC mediates the modification of Lipid A by the addition of 4-amino-4-deoxy-L-arabinose (L-Ara4N) and phosphoethanolamine, resulting in a less negative cell membrane and decreased binding of polymyxin B.'; b'PmrC mediates the modification of Lipid A by the addition of 4-amino-4-deoxy-L-arabinose (L-Ara4N) and phosphoethanolamine, resulting in a less negative cell membrane and decreased binding of polymyxin B.';eptA
53	evgA	evgA;b'EvgA, when phosphorylated, is a positive regulator for efflux protein complexes emrKY and mdtEF. While usually phosphorylated in a EvgS dependent manner, it can be phosphorylated in the absence of EvgS when overexpressed.'; b'EvgA, when phosphorylated, is a positive regulator for efflux protein complexes emrKY and mdtEF. While usually phosphorylated in a EvgS dependent manner, it can be phosphorylated in the absence of EvgS when overexpressed.';evgA
54	evgS	evgS;b'EvgS is a sensor protein that phosphorylates the regulatory protein EvgA. evgS corresponds to 1 locus in Pseudomonas aeruginosa PAO1 and 1 locus in Pseudomonas aeruginosa LESB58.'
55	fabG	Escherichia coli fabG mutations conferring resistance to triclosan
56	fabI	Escherichia coli fabI mutations conferring resistance to isoniazid and triclosan
57	folP_2	Escherichia coli folP with mutation conferring resistance to sulfonamides
58	folP_3	Salmonella gallinarum folP with mutation conferring resistance to sulfonamides
59	gadW	gadW;b'GadW is an AraC-family regulator that promotes mdtEF expression to confer multidrug resistance. GadW inhibits GadX-dependent activation. GadW clearly represses gadX and, in situations where GadX is missing, activates gadA and gadBC.'
60	gadX	gadX;b'GadX is an AraC-family regulator that promotes mdtEF expression to confer multidrug resistance.'; b'GadX is an AraC-family regulator that promotes mdtEF expression to confer multidrug resistance.';gadX
61	golS	b'GolS is a regulator activated by the presence of golD, and promotes the expression of the MdsABC efflux pump.';golS
62	gyrA_8	Salmonella isangi gyrA conferring resistance to fluoroquinolones
63	gyrA_9	Escherichia coli gyrA with mutation conferring resistance to triclosan
64	gyrB_1	Escherichia coli gyrB conferring resistance to aminocoumarin
65	gyrB_3	Salmonella isangi gyrB conferring resistance to fluoroquinolones
66	kdpE	b'kdpE is a transcriptional activator that is part of the two-component system KdpD/KdpE that is studied for its regulatory role in potassium transport and has been identified as an adaptive regulator involved in the virulence and intracellular survival of pathogenic bacteria. kdpE regulates a range of virulence loci through direct promoter binding.';kdpE; kdpE;b'kdpE is a transcriptional activator that is part of the two-component system KdpD/KdpE that is studied for its regulatory role in potassium transport and has been identified as an adaptive regulator involved in the virulence and intracellular survival of pathogenic bacteria. kdpE regulates a range of virulence loci through direct promoter binding.'
67	leuO	leuO;b'leuO, a LysR family transcription factor, exists in a wide variety of bacteria of the family Enterobacteriaceae and is involved in the regulation of as yet unidentified genes affecting the stress response and pathogenesis expression. LeuO is also an activator of the MdtNOP efflux pump.'; b'leuO, a LysR family transcription factor, exists in a wide variety of bacteria of the family Enterobacteriaceae and is involved in the regulation of as yet unidentified genes affecting the stress response and pathogenesis expression. LeuO is also an activator of the MdtNOP efflux pump.';leuO

68	marA	b'In the presence of antibiotic stress, E. coli overexpresses the global activator protein MarA, which besides inducing MDR efflux pump AcrAB, also down- regulates synthesis of the porin OmpF.';marA; marA;b'In the presence of antibiotic stress, E. coli overexpresses the global activator protein MarA, which besides inducing MDR efflux pump AcrAB, also down- regulates synthesis of the porin OmpF.'
69	mdfA	Escherichia coli mdfA;b'Multidrug efflux pump in E. coli. This multidrug efflux system was originally identified as the Cmr/CmlA chloramphenicol exporter.'; b'Multidrug efflux pump in E. coli. This multidrug efflux system was originally identified as the Cmr/CmlA chloramphenicol exporter.';Escherichia coli mdfA
70	mdsA	mdsA;b'MdsA is the membrane fusion protein of the multidrug and metal efflux complex MdsABC.'
71	mdsB	mdsB;b'MdsB is the inner membrane transporter of the multidrug and metal efflux complex MdsABC. mdsB corresponds to 1 locus in Pseudomonas aeruginosa PAO1 (gene name: mexQ) and 2 loci in Pseudomonas aeruginosa LESB58.'
72	mdsC	b'MdsC is the outer membrane channel of the multidrug and metal efflux complex MdsABC.';mdsC
73	mdtA	mdtA;b'MdtA is the membrane fusion protein of the multidrug efflux complex mdtABC.'; b'MdtA is the membrane fusion protein of the multidrug efflux complex mdtABC.';mdtA
74	mdtB	mdtB;b'MdtB is a transporter that forms a heteromultimer complex with MdtC to form a multidrug transporter. MdtBC is part of the MdtABC-TolC efflux complex.'; b'MdtB is a transporter that forms a heteromultimer complex with MdtC to form a multidrug transporter. MdtBC is part of the MdtABC-TolC efflux complex.';mdtB
75	mdtC	b'MdtC is a transporter that forms a heteromultimer complex with MdtB to form a multidrug transporter. MdtBC is part of the MdtABC-TolC efflux complex. In the absence of MdtB, MdtC can form a homomultimer complex that results in a functioning efflux complex with a narrower drug specificity. mdtC corresponds to 3 loci in Pseudomonas aeruginosa PAO1 (gene name: muxC/muxB) and 3 loci in Pseudomonas aeruginosa LESB58.';mdtC
76	mdtE	b'MdtE is the membrane fusion protein of the MdtEF multidrug efflux complex. It shares 70% sequence similarity with AcrA.';mdtE; mdtE;b'MdtE is the membrane fusion protein of the MdtEF multidrug efflux complex. It shares 70% sequence similarity with AcrA.'
77	mdtF	mdtF;b'MdtF is the multidrug inner membrane transporter for the MdtEF-TolC efflux complex.'
78	mdtG	mdtG;b'The MdtG protein, also named YceE, appears to be a member of the major facilitator superfamily of transporters, and it has been reported, when overexpressed, to increase fosfomycin and deoxycholate resistances. mdtG is a member of the marA-soxS-rob regulon.'
79	mdtH	mdtH;b'Multidrug resistance protein MdtH.'; b'Multidrug resistance protein MdtH.';mdtH
80	mdtM	b'Multidrug resistance protein MdtM.';mdtM; mdtM;b'Multidrug resistance protein MdtM.'
81	mdtN	b'Multidrug resistance efflux pump. Could be involved in resistance to puromycin, acriflavine and tetraphenylarsonium chloride.';mdtN
82	mdtO	mdtO;b'Multidrug resistance efflux pump. Could be involved in resistance to puromycin, acriflavine and tetraphenylarsonium chloride.'; b'Multidrug resistance efflux pump. Could be involved in resistance to puromycin, acriflavine and tetraphenylarsonium chloride.';mdtO
83	mdtP	mdtP;b'Multidrug resistance efflux pump. Could be involved in resistance to puromycin, acriflavine and tetraphenylarsonium chloride.'; b'Multidrug resistance efflux pump. Could be involved in resistance to puromycin, acriflavine and tetraphenylarsonium chloride.';mdtP
84	mef_B_	b'mef(B) is a macrolide efflux gene located in the vicinity of sul3 in Escherichia coli. There is also a mefB found in Streptococcus agalactiae that confers resistance to macrolides.';mef(B)

85	mipA	b'MltA-interacting protein (mipA), is an antibiotic resistance-related outer membrane protein. Deletion of mipA increases kanamycin, nalidixic acid and streptomycin resistance.';Escherichia coli mipA
86	mlaD	mlaD;b'mlaD from the mla system is a gene proposed to play a part in the transport of phospholipids to the outer membrane. Insertions in mlaD are shown to confer resistance to linezolid.'; b'mlaD from the mla system is a gene proposed to play a part in the transport of phospholipids to the outer membrane. Insertions in mlaD are shown to confer resistance to linezolid.';mlaD
87	mlaF	b'mlaF from the mla system is a gene proposed to play a part in the transport of phospholipids to the outer membrane. Insertions in mlaF are shown to confer resistance to linezolid.';mlaF; mlaF;b'mlaF from the mla system is a gene proposed to play a part in the transport of phospholipids to the outer membrane. Insertions in mlaF are shown to confer resistance to linezolid.'
88	mphA	b"The mphA gene encodes for resistance enzyme MPH(2')-I which preferentially inactivate 14-membered macrolides (e.g.erythromycin, telithromycin, roxithromycin) over 16-membered macrolides (e.g.tylosin, spiramycin). It phosphorylates macrolides at 2'-OH hydroxyl of desosamine sugar of macrolides in a GTP-dependent manner.";mphA
89	msbA	b'MsbA is a multidrug resistance transporter homolog from E. coli and belongs to a superfamily of transporters that contain an adenosine triphosphate (ATP) binding cassette (ABC) which is also called a nucleotide-binding domain (NBD). MsbA is a member of the MDR-ABC transporter group by sequence homology. MsbA transports lipid A, a major component of the bacterial outer cell membrane, and is the only bacterial ABC transporter that is essential for cell viability.';msbA; msbA;b'MsbA is a multidrug resistance transporter homolog from E. coli and belongs to a superfamily of transporters that contain an adenosine triphosphate (ATP) binding cassette (ABC) which is also called a nucleotide-binding domain (NBD). MsbA is a member of the MDR-ABC transporter group by sequence homology. MsbA transports lipid A, a major component of the bacterial outer cell membrane, and is the only bacterial ABC transporter that is essential for cell viability.'
90	murA_2	Escherichia coli murA with mutation conferring resistance to fosfomycin
91	nfsA	Escherichia coli nfsA mutations conferring resistance to nitrofurantoin
92	ompF	Escherichia coli ompF with mutation conferring resistance to beta-lactam antibiotics
93	parC_3	Shigella flexneri parC conferring resistance to fluoroquinolones; Escherichia coli parC conferring resistance to fluoroquinolones
94	parC_4	Salmonella enterica parC conferring resistance to fluoroquinolones
95	parE_1	Escherichia coli parE conferring resistance to fluoroquinolones
96	parE_2	Salmonella serovars parE conferring resistance to fluoroquinolones
97	porin_OmpC	b'In the presence of antibiotic stress, there is a coupled down-regulation of the porin OmpC with the OmpF. Mutants both lacking both OmpC and OmpF proteins are resistant to cephaloridine and cefazolin. Analyses of genes involved in the increased resistance to tetracycline suggest that the up-regulation of efflux pump genes is accompanied by a decrease of OmpF and OmpC synthesis. Homologs of OmpC have been identified in Escherichia coli, Salmonella enterica, Klebsiella aerogenes and Serratia marcescens.';porin OmpC; porin OmpC;b'In the presence of antibiotic stress, there is a coupled down-regulation of the porin OmpC with the OmpF. Mutants both lacking both OmpC and OmpF proteins are resistant to cephaloridine and cefazolin. Analyses of genes involved in the increased resistance to tetracycline suggest that the up-regulation of efflux pump genes is accompanied by a decrease of OmpF and OmpC synthesis. Homologs of OmpC have been identified in Escherichia coli, Salmonella enterica, Klebsiella aerogenes and Serratia marcescens.'
		b"QacEdelta1 is a resistance gene conferring resistance to antiseptics. It is different from QacE

98	qacE-	only at the 3'-terminus.";qacEdelta1; qacEdelta1;b"QacEdelta1 is a resistance gene conferring resistance to antiseptics. It is different from QacE only at the 3'-terminus."
99	ramR	Salmonella enterica ramR mutants
100	rpoB_1	Escherichia coli rpoB mutants conferring resistance to rifampicin
101	rrsB+	Escherichia coli 16S rRNA (rrsB) mutation conferring resistance to tetracycline; Salmonella enterica 16S rRNA (rrsD) mutation conferring resistance to spectinomycin
102	sdiA	b"SdiA is a cell division regulator that is also a positive regulator of AcrAB only when it's expressed from a plasmid. When the sdiA gene is on the chromosome, it has no effect on expression of acrAB.";sdiA
103	soxR_1	Escherichia coli soxR with mutation conferring antibiotic resistance
104	soxR_2	Salmonella enterica soxR with mutation conferring antibiotic resistance
105	soxS	Salmonella serovars soxS with mutation conferring antibiotic resistance
106	soxS_1	Escherichia coli soxS with mutation conferring antibiotic resistance
107	sul1	b'Sul1 is a sulfonamide resistant dihydropteroate synthase of Gram-negative bacteria. It is linked to other resistance genes of class 1 integrons.';sul1
108	sul2	b'Sul2 is a sulfonamide resistant dihydropteroate synthase of Gram-negative bacteria, usually found on small plasmids.';sul2
109	sul3	b'Sul3 is a sulfonamide resistant dihydropteroate synthase similar to Sul1 and Sul2. Its resistance gene was found encoded in E. coli plasmid DNA of sulfonamide resistant isolates.';sul3
110	tetR	tetR
111	tet_A_	b'TetA is a tetracycline efflux pump found in many species of Gram-negative bacteria.';tet(A)
112	tet_B_	b'Tet(B) is a tetracycline efflux protein expressed in many Gram-negative bacteria. It confers resistance to tetracycline, doxycycline, and minocycline, but not tigecycline.';tet(B)
113	ugd	ugd;b'PmrE is required for the synthesis and transfer of 4-amino-4-deoxy-L-arabinose (Ara4N) to Lipid A, which allows gram-negative bacteria to resist the antimicrobial activity of cationic antimicrobial peptides and antibiotics such as polymyxin.'
114	uhpA	Escherichia coli uhpA with mutation conferring resistance to fosfomycin;b'uhpA is a positive activator of the fosfomycin importer uhpT, thus mutations to uhpA confer fosfomycin resistance by reducing uhpT expression. Both knockout and amino acid substitution mutations have been found that confer resistance, with the Protein Knockout model describing the large, knockout mutations causing loss of function of the gene, and the Protein Variant model describing the amino acid substitutions.'; b'uhpA is a positive activator of the fosfomycin importer uhpT, thus mutations to uhpA confer fosfomycin resistance by reducing uhpT expression. Both knockout and amino acid substitution mutations have been found that confer resistance, with the Protein Knockout model describing the large, knockout mutations causing loss of function of the gene, and the Protein Variant model describing the amino acid substitutions.';Escherichia coli uhpA with mutation conferring resistance to fosfomycin

毒力基因展示

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Search:

gene	DRR102537_setB文库	DRR102537文库	DRR129836文库	DRR152857_subreads文库	DRR154108文库
ACE_T6SS	m	/	/	/	/
AcrAB	m	m	m	m	m
Adhesive_fimbriae	m	m	/	m	m
Aerobactin	/	/	m	/	m
Agf	m	m	m	m	m
AIDA-I	m	/	/	/	/
Alginate	m	/	m	m	/
Allantion_utilization	m	m	m	m	m
Alpha-Hemolysin	/	/	/	/	m
Antigen_43,AIDA-I_type	m	/	/	/	/
AslA	m	m	m	m	m
Cah,AIDA-I_type	m	/	/	/	/
Capsule	m	m	m	m	/
CDT	/	/	/	/	m
ClyA	m	/	/	/	/
CNF-1	/	/	/	/	m
Colicin_E1	m	/	/	/	/
Contact-dependent_inhibition_CDI_system	m	/	/	/	/
Curli_fibers	m	m	m	m	m
E.coli_laminin-binding_fimbriae_(ELF)	m	/	/	/	/
EaeH	m	/	/	/	/
EAST1	m	m	/	/	m
ECP	m	m	/	m	m
EF-Tu	m	/	/	/	/
EhaB,AIDA-I_type	m	/	/	/	/

EHS	m	/	/	/	/
Ent	m	m	m	m	m
Enterobactin	m	m	m	m	m
Enterobactin_synthesis_and_transport	m	/	/	/	/
Eps_T2SS	m	m	m	/	m
ETT2	m	/	/	/	/
EVP_(E._tarda_virulent_protein)	m	/	/	/	/
Exe_T2SS	m	m	m	/	m
F1C_fimbriae	/	/	/	/	m
F9_fimbriae	m	/	/	/	/
FdeC	m	m	/	m	m
Flagella	m	m	m	m	m
Fur	m	m	m	m	m
Gsp	m	/	/	/	/
Hemolysin/cytolysin_A	m	/	/	/	/
Hemolysin_HlyA	m	/	/	/	/
Hemorrhagic_E.coli_pilus_(HCP)	m	/	/	/	/
Ibes	m	m	m	m	m
Intimin	/	/	m	/	/
Isocitrate_lyase	/	/	/	m	/
Lateral_flagella	m	m	/	/	m
Ler	/	/	m	/	/
LOS	/	/	/	m	/
LPS	m	m	m	m	m
Nitrate_reductase	m	/	/	m	/
O-antigen	/	/	/	m	/
OmpA	m	m	m	m	m
OmpD	m	/	/	/	/
P_fimbriae	/	/	/	/	m
Peritrichous_fla	m	/	/	/	/

gella					
Pet	/	/	m	/	/
PhoPQ	/	/	/	m	/
PmrAB	/	/	/	m	/
Polar_flagella	m	m	/	/	m
Pyoverdine	m	/	/	m	/
RcsAB	m	m	m	m	m
RpoS	m	m	m	m	m
S_fimbriae	/	/	/	/	m
Sat	/	/	m	/	/
SCI-I_T6SS	m	/	/	/	/
SigA	m	/	m	m	/
Stc	m	/	/	/	/
Stg_fimbriae	m	/	/	/	/
Streptococcal_plasmin_receptor/GAPDH	m	/	/	/	/
T2SS	m	m	m	m	m
T6SS	m	m	m	m	m
T6SS-II	m	/	/	/	/
Tia/Hek	m	/	/	/	/
TraJ	m	m	/	/	/
TTSS	/	/	m	/	m
TTSS_secreted_effectors	m	m	m	m	m
Type_1_fimbriae	m	m	m	m	m
Type_I_fimbriae	m	m	m	m	m
UpaG_adhesin,trimeric_AT	m	/	/	/	/
Vanchrobactin	m	/	/	/	/
Ybt	/	/	/	m	/
Yersiniabactin	/	/	/	m	/
Z1307	m	/	/	/	/

毒力基因注释

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VF数据库编号	基因名称	功能	机制
VF0044	LOS	Major immunogen; LOS phosphorylcholine (ChoP) may influence invasion via interaction with PAF receptor and stimulates of inflammatory signals; LPS phase variation is characterized by the spontaneous loss and gain of oligosaccharide structures present in the outer core. the phase variable expression of LPS biosynthesis genes promotes evasion of antigen-specific host immune defences and allow colonization of different host microenvironments	Lic1(lic1A-lic1D) responsible for the addition of phosphorylcholine to LPS. lic1A mediates phase variation (tetranucleotide repeat region); phase-variable gene lic3A encodes an alpha-2,3-sialyltransferase that is responsible for the addition of Neu5Ac to terminal lactose in the LPS, LPS sialylation has been shown to be important for resistance to the killing effectors of normal human serum
VF0085	LPS	Mediates biological effects including resistance to serum killing and phagocytosis; the binding to normal CFTR (cystic fibrosis transmembrane conductance regulator) and invasion of host cells may make a contribution to virulence in the human eye; internalization by binding to normal CFTR protein expressed by airway epithelial cells followed by desquamation of bacteria-laden epithelial cells, constitutes a host defense mechanism. If this mechanism fails to function properly, abnormally high bacterial carriage would promote the establishment of chronic bacterial infection	Binding interaction occurs between the first extracellular loop of CFTR (predicted to be in amino acids 108-117 of the mature protein) and the complete outer portion of the core polysaccharide of the LPS
VF0091	Alginate	Allows the bacteria form biofilm; contributes to the persistence of the bacteria in the CF lung: act as an adhesin, preventing the bacteria from being expelled from the lung, and alginate slime layer makes it more difficult for phagocytes to ingest and kill the bacteria	/
VF0094	Pyoverdine	Effective at acquiring iron from transferrin and lactoferrin; cytotoxic due to its ability to stimulating the production of reactive oxygen species	Pvd is a fluorescent dihydroxyquinoline derivative connected to a small peptide and contains hydroxamate and catecholate residues to chelate ferric ion, Fe (III). Pvd chelates Fe (III) in a 1:1 stoichiometry with high affinity (stability constant, 10**32); FpvA is the specific receptor for Fe(III)-pyoverdin
VF0102	Type_1_fimbriae	The adhesin FimH mediates T3SS1-independent uptake in murine DCs.	/
VF0103	Agf	Aids in attachment to the villi of enterocytes, also cause the bacteria to become attached to each other	/
			PhoQ contains distinct binding sites for Mg2+ and Ca2+, and is maximally repressed in the

VF0111	PhoPQ	Activated by low divalent cations magnesium and calcium levels; control expression of more than 40 genes; required for intracellular survival, cationic antimicrobial peptides (CAMPs) resistance, stimulation of cytokine secretion	presence of both cations. PhoP-PO4 activates expression of pags (for PhoP-activated genes), including cation transporter, outer membrane proteins, nonspecific acid phosphatase, enzymes important for LPS modification, and pmrAB (a second two-component system that are activated in response to mildly acidic environment. PmrAB leads to an increased substitution of phosphates with 4-amino-4-deoxy-L-arabinose in both the core oligosaccharide and the lipid A components of LPS, these cations stabilize the outer membrane by neutralizing the negative charge of phosphate groups, PmrAB induced modification of LPS composition may be vital to maintenance of outer membrane integrity); represses transcription of prgs (for PhoP-repressed genes) required for epithelial cell invasion, including hilA, prgHIJKorgA operon; regulate acid tolerance response (ATR)
VF0112	RpoS	Necessary for sustaining a log-phase acid tolerance response (ATR), induction a stationary-phase acid survival system, production of thin aggregative fimbriae and expression of spv gene during stationary phase	/
VF0113	Fur	Repress the expression of iron-regulated genes; also required for acid-induced activation of atr genes	/
VF0119	SigA	Cytopathic protease involved in intestinal fluid accumulation	Serine protease; cytopathic activity is due to its ability to degrade the cytoskeletal protein, alpha-fodrin
VF0123	Aerobactin	Iron uptake, critical for intracellular growth	Aerobactin biosynthesis is driven by enzymes encoded by the iucABCD genes. IutA is the outer membrane receptor required for ferri-aerobactin uptake.
VF0136	Yersiniabactin	FyuA/Psn-Irp system uses yersiniabactin, a siderophore that can remove iron from a number of mammalian proteins, due to its extremely high affinity for ferric iron	YbtA is an AraC-like regulator required for transcription of fyuA/psn, irp2 and ybtP, also downregulate its own transcription; In the presence of iron, Fur, a cytosolic protein that on binding ferrous iron changes conformation and binds DNA at a specific site called a Fur box, thus preventing transcription, downregulates transcription of fyuA/psn, irp2 and other iron-regulated genes
VF0172	TTSS	Injects Tir and other effector molecules directly into the host cell. Effector molecules activate cell-signaling pathways, causing alterations in the host cell cytoskeleton and resulting in the depolymerization of actin and the loss of microvilli	/
		Binding of intimin to Tir triggers dramatic intracellular changes including reorganization of cytoskeletal proteins, actin polymerization	

VF0177	Intimin	at the site of intimate bacterial contact, and formation of a characteristic attaching and effacing (A/E) lesion; alternative intimin receptor may be beta1-integrin, but intimin-beta1-integrin association is not essential for EPEC adhesin; Another intimin binding protein recently identified as nucleolin	/
VF0185	CDT	Involving chromatin disruption, which leads to G2/M-phase growth arrest of the target cell and ultimately cell death	/
VF0188	EAST1	Activates guanylate cyclase resulting in ion secretion	/
VF0189	Ler	Activates the LEE2, LEE3, tir, and orf19 promoters; required for LEE4 expression; not activates the LEE1 promoter; controls genes located outside the LEE, such as espC and genes encoding several morphologically distinct types of fimbriae	Acts as an anti-repressor protein that overcomes the H-NS-mediated silencing on the LEE2/LEE3 promoter region
VF0191	TTSS	Injects Tir and other effector molecules directly into the host cell. Effector molecules activate cell-signaling pathways, causing alterations in the host cell cytoskeleton and resulting in the depolymerization of actin and the loss of microvilli	/
VF0192	Ler	Activates the LEE2, LEE3, tir, and orf19 promoters; required for LEE4 expression; not activates the LEE1 promoter; controls genes located outside the LEE, such as espC and genes encoding several morphologically distinct types of fimbriae	Acts as an anti-repressor protein that overcomes the H-NS-mediated silencing on the LEE2/LEE3 promoter region
VF0202	Intimin	Binding of intimin to Tir triggers dramatic intracellular changes including reorganization of cytoskeletal proteins, actin polymerization at the site of intimate bacterial contact, and formation of a characteristic attaching and effacing (A/E) lesion; alternative intimin receptor may be beta1-integrin, but intimin-beta1-integrin association is not essential for EHEC adhesin; Another intimin binding protein recently identified as nucleolin	/
VF0213	Adhesive_fimbriae	Adhesin, receptor is the oligosaccharide components of glycolipids and glycoproteins	/
VF0216	EAST1	Activates guanylate cyclase resulting in ion secretion	/
VF0217	Pet	Serine protease, leading to cytoskeletal changes and epithelial-cell rounding by cleavage of the cytoskeletal protein spectrin	/
		PapG mediates binding to the alpha-D-galactopyranosyl-(1-4)-beta-D-galactopyranoside (Galalpha(1,4)Gal) moiety	

VF0220	P_fimbriae	present in a globoseries of glycolipids found on host cells lining the upper urinary tract and erythrocytes; three adhesin variants of PapG-G-I, G-II, G-III recognize three different but related Galalpha(1,4)Gal receptors; PapG-mediated interactions with its Galalpha(1,4)Gal-containing glycolipid receptor can activate specific responses in the bacteria and in the epithelial cell that promote virulence: activating the UPEC iron-acquisition system and triggering the intracellular release from receptor glycolipids of ceramide, an important second messenger that can activate cytokine production, through the activation of serine/threonine protein kinases and phosphatase	/
VF0221	Type_1_fimbriae	Makes an important contribution to colonization of the bladder	FimH is the adhesin protein binding to mannose-containing glycoprotein receptors, known as uroplakins, which are located on the luminal surface of the bladder epithelial cells. This binding is followed by invasion of uroepithelia cells
VF0222	S_fimbriae	S fimbriae binds to receptors containing sialic acid sugar moieties, the sialic acid residues are presented on UP3, one of four integral membrane uroplakin proteins	/
VF0224	F1C_fimbriae	Adhesin	Binds of to the GalNAcbeta1-4Galbeta sequence of glycolipids, i.e., asialo-GM1 and asialo-GM2 with high affinity; An additional binding to carbohydrate structures GlcNAcbeta1-3Galbeta, Galbeta1-4Glc, Gal, and Glc of glycolipids may indicate functional low-affinity receptor sites
VF0225	Alpha-Hemolysin	Cytotoxic to many types of cells: erythrocytes, granulocytes, monocytes, endothelial cells and renal epithelial cells; stimulating the release of IL-1beta and TNF	HlyA frist binds a receptor on the cell surface, a beta2-integrin in leukocytes or glycophorin in red blood cells, then becomes inserted in the cell membrane. Calcium binding to the glycine-rich repeats is essential for membrane lysis
VF0226	CNF-1	Induces the formation of actin stress fibers and membrane ruffling, necrosis	CNF1 is internalized via receptor-mediated endocytosis upon binding to a cell surface receptor: 37-kDa laminin receptor precursor (LRP); Binding of the toxin to its cell surface receptor allows CNF1 entry into endocytic vesicles. The toxin utilizes the acidic conditions found in endosomes to inject its catalytic domain inside the cytosol; activates Rho GTPases by deamidation of glutamine 63 of RhoA, or glutamine 61 in Rac1 and Cdc42 into glutamic acid. The glutamine residue is essential for GTP hydrolysis, and its modification results in constitutively activated Rho GTPases by arresting the Rho GTPases cycle between the GDP-bound inactive and GTP-bound active forms

VF0228	Enterobactin	Iron uptake: the siderophore enterobactin imported through the FepA receptor and the FepBCDG system	/
VF0229	Aerobactin	Iron uptake	/
VF0231	Sat	A vacuolating cytotoxin expressed by UPEC, elicits defined damage to kidney epithelium during upper urinary tract infection and thus contributes to pathogenesis of urinary tract infection	/
VF0236	OmpA	Contributes to brain microvascular endothelial cells (BMECs) invasion via a ligand-receptor interaction. Interaction of OmpA with its receptor induces actin condensation at the binding site. The actin reorganization induced by E. coli depends on activation of several host proteins involved in signaling, including focal adhesion kinase, PI3-kinase, PKC-alpha, and caveolin-1; OmpA also binds to C4b-binding protein, to avoid complement-mediated attack	Binds to a 95-kDa HBMEC receptor, Ecgp, for E. coli invasion. OmpA-Ecgp interaction occurs via GlcNAc1,4-GlcNAc epitopes as well as the protein backbone of the receptor. The presence of Ecgp on human brain microvascular endothelial cell, but not on non-brain endothelial cells. Ecgp is a gp96 (a cell surface glycoprotein related to heat shock proteins) homologue.
VF0237	Ibes	Contributes to brain microvascular endothelial cells (BMECs) invasion via a ligand-receptor interaction	Unknown; the roles of Ibe proteins in E. coli K1 invasion of BMECs were verified by deletion and complementation experiments
VF0238	AslA	Contributes to brain microvascular endothelial cells (BMECs) invasion	Unknown; the roles of AslA proteins in E. coli K1 invasion of BMECs were verified by deletion and complementation experiments
VF0240	CNF-1	Induces the formation of actin stress fibers and membrane ruffling, necrosis	CNF1 is internalized via receptor-mediated endocytosis upon binding to a cell surface receptor: 37-kDa laminin receptor precursor (LRP); Binding of the toxin to its cell surface receptor allows CNF1 entry into endocytic vesicles. The toxin utilizes the acidic conditions found in endosomes to inject its catalytic domain inside the cytosol; The C-terminal domain activates Rho GTPases by deamidation of glutamine 63 of RhoA, or glutamine 61 in Rac1 and Cdc42 into glutamic acid. The glutamine residue is essential for GTP hydrolysis, and its modification results in constitutively activated Rho GTPases by arresting the Rho GTPases cycle between the GDP-bound inactive and GTP-bound active forms
VF0241	TraJ	Contributes to the ability of E. coli K1 to invade the central nervous system and cause meningitis in the neonatal rat; TraJ contributes to the early systemic dissemination of E. coli K1 in the oral infection process is via specific TraJ-dependent bacterial interactions with macrophages. TraJ enables the bacteria to be taken up efficiently by macrophages. In the early steps of	/

		dissemination, the intracellular environment of the phagocytes provides a protective or safe site from the initial host inflammatory defense mechanisms	
VF0253	Isocitrate_lyase	Required for persistent infection	Isocitrate lyase is the initial enzyme in the glyoxylate shunt, a secondary metabolic pathway that allows bacteria to utilize fatty acids as carbon and energy sources when the availability of primary carbon sources is limiting; Isocitrate lyase, in combination with malate synthase, catalyzes the conversion of isocitrate to malate, a reaction that allows maintenance of the TCA cycle and synthesize carbohydrates from fatty acids
VF0257	SigA	Sigma A interacts with a transcriptional activator WhiB3 to allow the expression of genes necessary for virulence	/
VF0273	Flagella	Swimming motility; play a role in biofilm formation and other pathogenic adaptations	/
VF0302	Nitrate_reductase	Nitrate respiration helps the bacteria to survive in O2-depleted areas of inflammatory or necrotic tissue	/
VF0333	T2SS	Still unknown.	/
VF0392	O-antigen	LPS O antigen mutants were severely impaired in their ability to colonize the Peyer's patches and did not colonize spleen and liver. The absence of O antigen in the outer membrane affects the expression of other Yersinia virulence factors.	/
VF0394	Flagella	Required for efficient cellular invasion; YplA, a phospholipase is secreted by this type III flagellum secretion system. YplA is required for survival of Y. enterocolitica in the Peyer's patches and for stimulation of the acute inflammatory response of the host to the infection; contributed to the initiation of biofilm formation	/
VF0404	ECP	ECP, composed of a 21-kDa pilin subunit EspA, is a pilus-adherence factor that is crucial to the virulence of E. coli O157 in humans, and is also carried by commensal strains of E. coli.; It is suggested that pathogenic E. coli strains may use ECP to mimic commensal E. coli and provide themselves with an ecological advantage for host colonization and evasion of the immune system.	/
VF0430	Flagella	Polar flagella required for motility and macrophage invasion	/
VF0473	Polar_flagella	Necessary for motility, adhesion and invasion; glycosylation of the flagellin may play a role in	/

		provoking a proinflammatory response	
VF0474	Lateral_flagella	Inducible lateral peritrichous flagellar system is responsible for movement across solid surfaces or through viscous environments known as swarming motility; glycosylation of the lateral flagellin is essential for swarming motility over surfaces	/
VF0478	Exe_T2SS	Essential for secretion of many virulence factors, such as aerolysin, proteases, haemolysin and DNase	/
VF0506	FdeC	Binding to epithelial cells and collagen I, II, V, VI; aggregation; kidney and bladder colonization	/
VF0519	Flagella	Contributes to the virulence of pathogenic Vibrio through adhesion or biofilm formation	The flagellar regulatory system positively mediates the transcription of diguanylate cyclase CdgD which results in the transcription of a hemagglutinin that enhances intestinal colonization; c-di-GMP directly bound to YcgR interacts with components of the flagellar motor to disrupt flagellar rotation, thereby leading to decreased motility and inducing the biofilm formation
VF0560	Capsule	Assisting in evading the host immune system by protecting bacteria from opsonophagocytosis and serum killing	/
VF0561	LPS	Resistant to serum complement; also play a role in protecting bacteria from antimicrobial peptides, including polymyxin antibiotics	/
VF0562	Ent	May be necessary for penetration to deeper tissues	/
VF0564	Ybt	The phenolate siderophore Ybt contributes to evasion of the activity of lipocalin2 in the lung a host factor which neutralizes enterobactin-based iron acquisition	/
VF0565	Aerobactin	Citrate-hydroxamate siderophore aerobactin is needed for successful infection by hypervirulent K. pneumoniae in pneumonic infections	/
VF0566	Type_I_fimbriae	Adhering to human mucosal or epithelial surfaces	/
VF0568	AcrAB	May mediate resistance against host-derived antimicrobial peptides; associated with antibiotic resistance	/
VF0571	RcsAB	RcsB combined with the unstable auxiliary regulator RcsA to bind to an RcsAB box in the promoter region to upregulate the cps genes expression	/
			Allantoin is a metabolic intermediate of

VF0572	Allantion_utilization	Providing a nitrogen source to increase virulence in K. pneumoniae at certain sites of infection	purine degradation by various organisms including microbes and has been identified as a source of nitrogen in various bacterial species and as both a nitrogen source and a carbon source in K. pneumoniae.
VF0579	T6SS	Plays a role in interbacterial competition and host colonization	T6SS encoded by chromosome in S. sonnei gives S. sonnei an advantage in a niche-specific enviroment over E. coli, S. flexneri and other closely related species. T6SS predominate S. sonnei colonization in host and help it during interbacterial competition.
VF0613	Eps_T2SS	V. cholerae causes diarrhea by T2SS-dependent secretion of cholera toxin; V. cholerae exports, via the T2SS, other extracellular factors, including chitinases, proteases, DNase, and pilin, which aid in its ability to successfully occupy diverse ecological niches; Eps T2SS also secretes the three proteins RbmA, RbmC, and Bap1, which are necessary for robust, shear-resistant biofilm formation	/
VF0646	Hemolysin_HlyA	Unknown	Unknown
VF0692	Brucebactin	Unknown	Unknown
VF0783	T6SS-II	Unknown	Unknown
VF0785	Pul	Unknown	Unknown
VF0877	EF-Tu	Unknown	Unknown
VF0923	Yersiniabactin	Unknown	Unknown
VF0955	Stc	Unknown	Unknown
VF0967	Peritrichous_flagella	Unknown	Unknown
VF0969	OmpD	Unknown	Unknown
VF0975	T6SS	Unknown	Unknown
VF0976	ClyA	Unknown	Unknown
VF0977	ClyA	Unknown	Unknown
		IcsB (Nepsilon-fatty acyltransferase. Disruption of the actin cytoskeleton in eukaryotes; evasion of autophagy.); IpaA (Recruit focal adhesion protein vinculin to promote actin depolymerization at the site of entry.); IpaB (Caspase-1 binding proteins. Counteracts exfoliation by binding directly to Mad2L2 to release its inhibitory effect on the anaphase-promoting complex/cyclosome, thereby causing a delayed mitotic progression	

VF0978	TTSS_secreted_effectors	or cell cycle arrest at the G2/M phase and favouring bacterial multiplication; activates Caspase-1 and induces cell death; interacts with CD44 on the epithelial cell membrane and stimulates bacterial basolateral invasion.); IpaC (Binds the host cell-adhesion protein beta-catenin and facilitates efficient protrusion formation.); IpaH (Possible E3 ubiquitin ligase. Suppresses inflammatory response.); IpaH (Possible E3 ubiquitin ligase. Suppresses inflammatory response.); IpaH (Possible E3 ubiquitin ligase. Suppresses inflammatory response.); IpaH (Possible E3 ubiquitin ligase. Suppresses inflammatory response.); IpaH (Possible E3 ubiquitin ligase. Suppresses inflammatory response.); IpaH0722 (E3 ubiquitin ligase. Dampens the inflammatory response by inhibiting the PKC-mediated activation of NF-kappaB by ubiquitinating TRAF2.); IpaH1.4 (E3 ubiquitin ligase. Suppresses inflammatory response.); IpaH2.5 (E3 ubiquitin ligase. Suppresses inflammatory response.); IpaH4.5 (E3 ubiquitin ligase. Ubiquitinates the p65 subunit of NF-kappaB to modulate host inflammatory response.); IpaH7.8 (E3 ubiquitin ligase. Induction of pyroptosis by ubiquitylating and promoting proteasome degradation.); IpaH9.8 (E3 ubiquitin ligase. Binds to a splicing factor U2AF35 to modulate host immune responses; targets NEMO/Ikkgamma to dampen the host NF-kappaB-mediated inflammatory response; targets guanylate-binding protein GBP1 by LRR domain leads to their proteasomal degradation.); IpaJ (Cysteine protease. Cleaves an array of N-myristoylated proteins involved in cellular growth, signal transduction, autophagasome maturation and organelle function.); IpgB1 (GEF. Plays a pivotal role in producing membrane ruffles by exploiting the RhoG-ELMO-Dock180 pathway to stimulate Rac1 activity.); IpgB2 (RhoA-GEF. Induces stress fiber formation.); IpgD (Phosphoinositide 4-phosphatase. Hydrolyses phosphatidylinositol (4,5)- bisphosphate, contributes to the disruption of cortical actin structures required for efficient bacterial uptake.); OspB (Interacts directly with the scaffolding protein IQGAP1 to activate mTORC1 and promote mTORC1-dependent cell proliferaction.); OspC1 (Inhibition of apoptosis by preventing caspase-8 activity.); OspC2; OspC3 (ADP-riboxanase. Inhibition of pyroptosis by inhibiting caspase-4 activation.); OspC4; OspD1 (Anti-activator for MxiE.); OspD2 (Inhibition of necrosis.); OspD3/senA (Protease. Inhibition of necroptosis by degrading RIPK1 and RIPK3.); OspE1	/

		(Counteracts exofoliation by interacting with integrin-liked kinase to stabilize focal adhesions and block cell detachment, thereby favouring bacterial dissemination within epithelial tissue.); OspE2 (Counteracts exofoliation by interacting with integrin-liked kinase to stabilize focal adhesions and block cell detachment, thereby favouring bacterial dissemination within epithelial tissue.); OspF (Phosphothreonine lyase. Acts as a lyase that irreversibly dephosphorylates mitogenactivated protein kinases (MAPK) in the nucleus of the host cell to suppress innate immune response; interacts with retinoblastoma protein to recruit factors such as histone deacetylase, which downregulate IL-8 production via chromatin remodelling.); OspG (Protein kinase. Binds to ubiquitin-conjugating enzyme UbcH5 to antagonize degradation of inhibitor IkappaBalpha by blocking its ubiquitinylation, thus suppresses innate immune response.); OspI (Glutamine deamidase. Inhibits the E2 ubiquitin-conjugating activity leading to the suppression of TRAF6-dependent inflammatory signaling.); VirA (TBC-like GTPase-activating protein. VirA activates calpain protease by directly binding the calpain inhibitor calpastatin; hydrolyzes GTP to block Rab1 signaling so as to disrupt ER-to Golgi trafficking.); OspZ (S-adenosyl-L-methionine-dependent methyltransferase. Binds to TAB3 to decreased IL-8 transcription through modification of TAB3.)	
VF0984	Enterobactin_synthesis_and_transport	Unknown	Unknown
VF0988	ClyA	Unknown	Unknown
VF1042	Streptococcal_plasmin_receptor/GAPDH	Unknown	Unknown
VF1109	Tia/Hek	Unknown	Unknown
		Cif (Deamidase. Induces cytopathic effects of actin stress fiber formation and cell cycle arrest.); EspB (Pore formation, actin disruption, microvilli effacement, anti-phagocytosis.); EspF (Inducing degradation of the aniapoptic protein AbcF2, tight junction disruption, microvilli effacement and elongation, mitochondrial dysfunction, N-WASP activation, SGLT-1 inactivation,	

VF1110	TTSS_secreted_effectors	pedestal maturation, inhibition of NHE3 activity, membrane remodelling; targets and disrupts the nucleolus late in infection, which is temporally controlled by host mitochondria.); EspFu/tccP (Inducing degradation of the aniapoptic protein AbcF2, tight junction disruption, microvilli effacement and elongation, mitochondrial dysfunction, N-WASP activation, SGLT-1 inactivation, pedestal maturation, inhibition of NHE3 activity, membrane remodelling; targets and disrupts the nucleolus late in infection, which is temporally controlled by host mitochondria.); EspG (TBC-like GTPase activating protein. Efficiently catalyzes GTP hydrolysis in Rab1 to disrupt of Rab1-mediated ER-to-Golgi trafficking.); EspH (First bacterial effector acting directly on RhoGEFs, EspH directly binds to the DH-PH domain in RhoGEFs to disrupt RhoGEF-Rho signaling; critical for inhibiting macrophage phagocytosis.); EspJ (Inhibit both IgG- and complement receptor-mediated phagocytosis.); EspK; EspL1; EspL2 (Cysteine protease. Bounds F-actin-aggregating annexin 2 directly to increase annexin 2's ability to aggregate Tir-induced F-actin; block necroptosis and in flammation.); EspL4; EspM1 (GEF. Activates the RhoA signaling pathway and induce the formation of stress fibres; inhibit pedestal formation and induce tight junction mislocalization.); EspM2 (GEF. Activates the RhoA signaling pathway and induce the formation of stress fibres; inhibit pedestal formation and induce tight junction mislocalization.); EspN; EspO1-1; EspO1-2; EspR1; EspR3; EspR4; EspT (GEF. Activates Rac1 and Cdc42 leading to formation of membrane ruffles and lamellipodia; induces membrane ruffles to facilitate bacterial invasion into non-phagocytic cells in a process involving Rac1 and Wave2.); EspW; EspX1; EspX2; EspX4; EspX5; EspX6; EspX7/nleL (E3 ubiquitin ligase, HECT-like. Modulates pedestal formation.); EspY1; EspY2; EspY3; EspY4; EspY5; Map (GEF. Mimics the host Dbl and catalyses the exchange of GDP for GTP in Cdc42, involved in effacement, SGLT1 inhibition, formation of filopodia and disruption of mitochondrial function.); NleA/espI (Disruption of tight junctions by inhibition of host cell protein trafficking through COPII-dependent pathways.); NleB1 (Blocks translocation of the p65 and to the host cell nucleus to inhibit NF-kappaB pathway, but NleE and NleB act at different points in the NF-kappaB signaling pathway.); NleB2 (May also have anti-inflammatory activity.); NleC (Metalloprotease. Zn-	/

		dependent endopeptidases that specifically clip and inactivate RelA (p65), thus blocking NF-kappaB pathway.); NleD (Metalloprotease. Zn-dependent endopeptidases that specifically clip and inactivate JNK and p38, thus blocking AP-1 pathway.); NleE (PMN tran-epithelial migration; blocks translocation of the p65 to the host cell nucleus by preventing IkappaB degradation to inhibit NF-kappaB pathway.); NleF; NleG-1; NleG2-2; NleG2-3; NleG2-4; NleG5-1; NleG5-2; NleG6-1; NleG6-2; NleG6-3; NleG7 (U-box type E3 ubiquitin ligases.); NleG8-2; NleH1 (Ser/Thr protein kinase. Binds directly to a subunit of NF-kappaB, the ribosomal protein S3 (RPS3), reducing the nuclear abundance of RPS3 to dampen host transcriptional outputs; interact with Bax inhibitor-1 to block apoptosis.); NleH2 (Putative kinase. Attenuates NF-kappaB pathway.); SepZ/espZ (EspZ interacts with CD98 in host cell membranes to promote host cell survival, therefore provide the pathogen with valuable time to colonize efficiently prior to dissemination.); TccP2; Tir (Mimics host immunoreceptor tyrosine-based inhibition motifs (ITIMs), also see helicobacter CagA. EHEC Tir lacks the Nck binding site. Conserved NPY (Asn-Pro-Tyr) motif recruits the adaptor protein IRTKS and/or IRSp53. IRTKS/IRSp53 link Tir and TccP/EspFu, which in turn activates N-WASP; Receptor for intimin; effacement; SGLT1 inhibition; recruits SHIP2 to control actin-pedestal morphology; maintains the integrity of the epithelium by keeping the destructive activity of EspG and EspG2 in check.)	
		EspF (Inducing degradation of the aniapoptic protein AbcF2, tight junction disruption, microvilli effacement and elongation, mitochondrial dysfunction, N-WASP activation, SGLT-1 inactivation, pedestal maturation, inhibition of NHE3 activity, membrane remodelling; targets and disrupts the nucleolus late in infection, which is temporally controlled by host mitochondria.); EspFu/tccP (Inducing degradation of the aniapoptic protein AbcF2, tight junction disruption, microvilli effacement and elongation, mitochondrial dysfunction, N-WASP activation, SGLT-1 inactivation, pedestal maturation, inhibition of NHE3 activity, membrane remodelling; targets and disrupts the nucleolus late in infection, which is temporally controlled by host mitochondria.); EspG (TBC-like GTPase activating protein. Efficiently catalyzes GTP hydrolysis in Rab1 to disrupt of Rab1-mediated ER-to-Golgi trafficking.); EspH (First	

VF1111	TTSS_secreted_effectors	bacterial effector acting directly on RhoGEFs, EspH directly binds to the DH-PH domain in RhoGEFs to disrupt RhoGEF-Rho signaling; critical for inhibiting macrophage phagocytosis.); EspJ (Inhibit both IgG- and complement receptor-mediated phagocytosis.); EspL1; EspL2 (Cysteine protease. Bounds F-actin-aggregating annexin 2 directly to increase annexin 2's ability to aggregate Tir-induced F-actin; block necroptosis and in flammation.); EspM1 (GEF. Activates the RhoA signaling pathway and induce the formation of stress fibres; inhibit pedestal formation and induce tight junction mislocalization.); EspM2 (GEF. Activates the RhoA signaling pathway and induce the formation of stress fibres; inhibit pedestal formation and induce tight junction mislocalization.); EspO1-1; EspR1; EspR3; EspR4; EspV (Inducing radical morphological changes in host cells.); EspW; EspX1; EspX2; EspX4; EspX5; EspX6; EspY1; EspY2; EspY3; EspY4; Map (GEF. Mimics the host Dbl and catalyses the exchange of GDP for GTP in Cdc42, involved in effacement, SGLT1 inhibition, formation of filopodia and disruption of mitochondrial function.); NleA/espI (Disruption of tight junctions by inhibition of host cell protein trafficking through COPII-dependent pathways.); NleB2 (May also have anti-inflammatory activity.); NleB2-2; NleC (Metalloprotease. Zn-dependent endopeptidases that specifically clip and inactivate RelA (p65), thus blocking NF-kappaB pathway.); NleD (Metalloprotease. Zn-dependent endopeptidases that specifically clip and inactivate JNK and p38, thus blocking AP-1 pathway.); NleE (PMN tran-epithelial migration; blocks translocation of the p65 to the host cell nucleus by preventing IkappaB degradation to inhibit NF-kappaB pathway.); NleF; NleG-1; NleG-2; NleG-3; NleG2-2; NleG2-4; NleG5-1; NleG6-1; NleG7 (U-box type E3 ubiquitin ligases.); NleG8-2; NleH1 (Ser/Thr protein kinase. Binds directly to a subunit of NF-kappaB, the ribosomal protein S3 (RPS3), reducing the nuclear abundance of RPS3 to dampen host transcriptional outputs; interact with Bax inhibitor-1 to block apoptosis.); NleH2 (Putative kinase. Attenuates NF-kappaB pathway.); SepZ/espZ (EspZ interacts with CD98 in host cell membranes to promote host cell survival, therefore provide the pathogen with valuable time to colonize efficiently prior to dissemination.); Tir (Mimics host immunoreceptor tyrosine-based inhibition motifs (ITIMs), also see helicobacter CagA. EHEC Tir lacks the Nck binding site.	/

		Conserved NPY (Asn-Pro-Tyr) motif recruits the adaptor protein IRTKS and/or IRSp53. IRTKS/IRSp53 link Tir and TccP/EspFu, which in turn activates N-WASP; Receptor for intimin; effacement; SGLT1 inhibition; recruits SHIP2 to control actin-pedestal morphology; maintains the integrity of the epithelium by keeping the destructive activity of EspG and EspG2 in check.)	
VF1113	AIDA-I	Unknown	Unknown
VF1114	Antigen_43,AIDA-I_type	Unknown	Unknown
VF1115	Yersiniabactin_siderophore	Unknown	Unknown
VF1119	EaeH	Unknown	Unknown
VF1120	SCI-I_T6SS	Unknown	Unknown
VF1122	ACE_T6SS	Unknown	Unknown
VF1125	UpaG_adhesin,trimeric_AT	Unknown	Unknown
VF1128	EhaB,AIDA-I_type	Unknown	Unknown
VF1129	Cah,AIDA-I_type	Unknown	Unknown
VF1131	Contact-dependent_inhibition_CDI_system	Unknown	Unknown
VF1134	Hemolysin/cytolysin_A	Unknown	Unknown
VF1138	Curli_fibers	In E. coli, curli fibers compose up to 85% of the biofilm biomass. Curli a in vitro as an essential scaffold protein during biofilm formation; In vivo, curli also directly regulates the immune system and is known to induce inflammation by activating the immune Toll-like receptors (TLRs).	/
VF1140	E.coli_laminin-binding_fimbriae_(ELF)	Unknown	Unknown

VF1141	Hemorrhagic_E.coli_pilus_(HCP)	Unknown	Unknown
VF1150	Stg_fimbriae	Unknown	Unknown
VF1153	F9_fimbriae	Unknown	Unknown
VF1154	Peritrichous_flagella	Unknown	Unknown
VF1158	Z1307	Unknown	Unknown
VF1161	ETT2	Unknown	Unknown
VF1176	EHS	Unknown	Unknown
VF1177	Gsp	Unknown	Unknown
VF1182	Colicin_E1	Unknown	Unknown
VF1242	Chrysobactin	Unknown	Unknown
VF1246	Vanchrobactin	Unknown	Unknown
VF1268	EVP_(E._tarda_virulent_protein)	Unknown	Unknown
VF1355	PmrAB	Controls immune evasion and polymyxin resistance in several Enterobacteriaceae	The global regulatory system that controls lipopolysaccharide modification, leading to a coordinate regulation of 4-aminoarabinose incorporation and O-antigen chain length to respond against the host defense mechanisms