

supplementary table S1. Virulence-related genes of HhutsZ1						
Gene_id	Identity	E_value	VF_id	Type	Description	VF_category
HhutsZ1GL000313	84.2	0.00E+00	VFG037720	Verified	(adeG) cation/multidrug efflux pump [AdeFGH efflux pump (VF0504) - Biofilm (VFC0271)] [Acinetobacter baumannii ACICU]	Biofilm
HhutsZ1GL000314	61.9	2.90E-127	VFG037705	Verified	(adeF) membrane-fusion protein [AdeFGH efflux pump (VF0504) - Biofilm (VFC0271)] [Acinetobacter baumannii ACICU]	Biofilm
HhutsZ1GL000497	48.7	3.10E-169	VFG014117	Verified	(wbpM) nucleotide sugar epimerase/dehydratase WbpM [LPS (VF0085) - Immune modulation (VFC0258)] [Pseudomonas aeruginosa PAO1]	Immune modulation
HhutsZ1GL000514	54.7	2.10E-148	VFG014893	Verified	(algC) phosphomannomutase AlgC [Alginate (VF0091) - Biofilm (VFC0271)] [Pseudomonas aeruginosa PAO1]	Biofilm
HhutsZ1GL000517	42.7	2.30E-80	VFG000141	Verified	(waaA) lipopolysaccharide core biosynthesis protein WaaP [LPS (VF0085) - Immune modulation (VFC0258)] [Pseudomonas aeruginosa PAO1]	Immune modulation
HhutsZ1GL000546	40.2	1.20E-41	VFG038840	Verified	(flmH) short chain dehydrogenase/reductase family oxidoreductase [Polar flagella (VF0473) - Motility (VFC0204)] [Aeromonas hydrophila ML09-119]	Motility
HhutsZ1GL000550	50.5	3.20E-79	VFG043209	Verified	(cheD) methyl-accepting chemotaxis protein CheD [Flagella (VF0394) - Motility (VFC0204)] [Yersinia enterocolitica subsp. enterocolitica 8081]	Motility
HhutsZ1GL000649	57.9	2.60E-41	VFG000478	Verified	(fur) ferric iron uptake transcriptional regulator [Fur (VF0113) - Regulation (VFC0301)] [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]	Regulation
HhutsZ1GL000666	43.8	6.60E-74	VFG002526	Verified	(cheB) chemotaxis-specific methylesterase [Flagella (VF0430) - Motility (VFC0204)] [Burkholderia pseudomallei K96243]	Motility
HhutsZ1GL000673	43.3	2.20E-73	VFG047564	Verified	(purM) phosphoribosylaminoimidazole synthetase [Purine biosynthesis (VF0559) - Nutritional/Metabolic factor (VFC0272)] [Francisella tularensis subsp. tularensis SCHU S4]	Nutritional/Metabolic factor
HhutsZ1GL000836	56.6	8.80E-40	VFG039549	Verified	(CBU_1594) Coxiella Dot/Icm type IVB secretion system translocated effector [T4SS secreted effectors (VF0696) - Effector delivery system (VFC0086)] [Coxiella burnetii RSA 493]	Effector delivery system
HhutsZ1GL000840	48.8	4.00E-77	VFG043209	Verified	(cheD) methyl-accepting chemotaxis protein CheD [Flagella (VF0394) - Motility (VFC0204)] [Yersinia enterocolitica subsp. enterocolitica 8081]	Motility
HhutsZ1GL000913	49.2	1.30E-62	VFG045346	Verified	(IlpA) immunogenic lipoprotein A [IlpA (VF0513) - Adherence (VFC0001)] [Vibrio vulnificus YJ016]	Adherence
HhutsZ1GL001040	41.1	1.20E-42	VFG038840	Verified	(flmH) short chain dehydrogenase/reductase family oxidoreductase [Polar flagella (VF0473) - Motility (VFC0204)] [Aeromonas hydrophila ML09-119]	Motility
HhutsZ1GL001113	53.4	6.00E-89	VFG000670	Verified	(gtrB) bactoprenol glucosyl transferase [LPS (VF0124) - Immune modulation (VFC0258)] [Shigella flexneri 2a str. 301]	Immune modulation
HhutsZ1GL001126	64.7	2.90E-75	VFG001867	Verified	(sodB) superoxide dismutase [SodB (VF0169) - Stress survival (VFC0282)] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	Stress survival
HhutsZ1GL001132	53.1	1.50E-64	VFG038845	Verified	(nucA) NeuA protein [Polar flagella (VF0473) - Motility (VFC0204)] [Aeromonas hydrophila ML09-119]	Motility
HhutsZ1GL001365	65.7	0.00E+00	VFG049144	Verified	(acrB) acriflavine resistance protein B [AcrAB (VF0568) - Antimicrobial activity/Competitive advantage (VFC0325)] [Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044]	Antimicrobial activity/Competitive advantage
HhutsZ1GL001479	44	5.60E-58	VFG000028	Verified	(brkB) serum resistance protein [Brk (VF0034) - Immune modulation (VFC0258)] [Bordetella pertussis Tohama I]	Immune modulation
HhutsZ1GL001777	49.4	2.50E-46	VFG045340	Verified	(ricA) type IV secretion system effector RicA, Rab2 interacting conserved protein A [T4SS secreted effectors (VF0695) - Effector delivery system (VFC0086)] [Brucella melitensis bv. 1 str. 16M]	Effector delivery system
HhutsZ1GL001848	45.5	5.90E-58	VFG045346	Verified	(IlpA) immunogenic lipoprotein A [IlpA (VF0513) - Adherence (VFC0001)] [Vibrio vulnificus YJ016]	Adherence
HhutsZ1GL001882	46.5	5.80E-31	VFG045327	Verified	(LPG_RS11000) Hsp20 family protein [GspA (VF0167) - Stress survival (VFC0282)] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	Stress survival
HhutsZ1GL001938	40.6	3.30E-23	VFG041304	Verified	(IirB) Dot/Icm type IV secretion system effector IirB [Dot/Icm T4SS secreted effectors (VF0798) - Effector delivery system (VFC0086)] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	Effector delivery system
HhutsZ1GL002006	62.8	1.50E-79	VFG038840	Verified	(flmH) short chain dehydrogenase/reductase family oxidoreductase [Polar flagella (VF0473) - Motility (VFC0204)] [Aeromonas hydrophila ML09-119]	Motility
HhutsZ1GL002007	61.1	8.60E-18	VFG011430	Verified	(acpXL) acyl carrier protein [LPS (VF0367) - Immune modulation (VFC0258)] [Brucella melitensis bv. 1 str. 16M]	Immune modulation
HhutsZ1GL002013	48.3	2.90E-116	VFG014950	Verified	(mucD) serine protease MucD precursor [Alginate (VF0091) - Biofilm (VFC0271)] [Pseudomonas aeruginosa PAO1]	Biofilm
HhutsZ1GL002052	41.6	2.60E-81	VFG037705	Verified	(adeF) membrane-fusion protein [AdeFGH efflux pump (VF0504) - Biofilm (VFC0271)] [Acinetobacter baumannii ACICU]	Biofilm
HhutsZ1GL002054	40.2	7.60E-85	VFG037010	Verified	(mtrE) multidrug efflux pump channel protein MtrE [MtrCDE (VF0451) - Antimicrobial activity/Competitive advantage (VFC0325)] [Neisseria meningitidis MC58]	Antimicrobial activity/Competitive advantage
HhutsZ1GL002099	40.9	3.20E-25	VFG013650	Verified	(pilL) type IV pilus biosynthesis protein PilL [Type IV pili (VF0401) - Adherence (VFC0001)] [Yersinia pseudotuberculosis IP 31758]	Adherence
HhutsZ1GL002198	68.7	3.40E-109	VFG013465	Verified	(kdsA) 2-dehydro-3-deoxyphosphoacetate aldolase [LOS (VF0044) - Immune modulation (VFC0258)] [Haemophilus influenzae Rd KW20]	Immune modulation
HhutsZ1GL002200	60.5	7.50E-76	VFG050160	Verified	(kpsU) 3-deoxy-manno-octulosonate cytidyltransferase [K1 capsule (VF0239) - Invasion (VFC0083)] [Escherichia coli O45:K1:H7 str. S88]	Invasion
HhutsZ1GL002223	79.5	6.80E-52	VFG043206	Verified	(cheY) chemotaxis regulatory protein CheY [Flagella (VF0394) - Motility (VFC0204)] [Yersinia enterocolitica subsp. enterocolitica 8081]	Motility
HhutsZ1GL002226	69.8	1.10E-268	VFG002522	Verified	(flhA) flagellar biosynthesis protein FlhA [Flagella (VF0430) - Motility (VFC0204)] [Burkholderia pseudomallei K96243]	Motility
HhutsZ1GL002234	65.9	2.60E-46	VFG002509	Verified	(flgC) flagellar basal body rod protein FlgC [Flagella (VF0430) - Motility (VFC0204)] [Burkholderia pseudomallei K96243]	Motility
HhutsZ1GL002238	74.2	3.70E-110	VFG002346	Verified	(flgG) flagellar basal-body rod protein FlgG [Flagella (VF0394) - Motility (VFC0204)] [Yersinia enterocolitica subsp. enterocolitica 8081]	Motility
HhutsZ1GL002255	41.8	6.10E-25	VFG002498	Verified	(fliJ) flagellar protein FliJ [Flagella (VF0430) - Motility (VFC0204)] [Burkholderia pseudomallei K96243]	Motility
HhutsZ1GL002256	68.9	1.10E-173	VFG002499	Verified	(fliI) flagellum-specific ATP synthase FliI [Flagella (VF0430) - Motility (VFC0204)] [Burkholderia pseudomallei K96243]	Motility
HhutsZ1GL002262	45.9	3.50E-11	VFG043362	Verified	(LPG_RS13035) flagellar protein [Flagella (VF0157) - Motility (VFC0204)] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	Motility
HhutsZ1GL002335	51	3.40E-47	VFG013265	Verified	(orfM) deoxyribonucleotide triphosphate pyrophosphatase [LOS (VF0044) - Immune modulation (VFC0258)] [Haemophilus influenzae Rd KW20]	Immune modulation
HhutsZ1GL002339	58.7	1.60E-55	VFG000463	Verified	(sodCI) Gifsy-2 prophage: superoxide dismutase precursor (Cu-Zn) [SodCI (VF0109) - Stress survival (VFC0282)] [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]	Stress survival
HhutsZ1GL003136	43.9	1.70E-94	VFG001270	Verified	(cyaD) cyclolysin secretion protein [Cya (VF0028) - Exotoxin (VFC0235)] [Bordetella pertussis Tohama I]	Exotoxin
HhutsZ1GL003137	65	7.90E-267	VFG001269	Verified	(cyaB) cyclolysin secretion ATP-binding protein [Cya (VF0028) - Exotoxin (VFC0235)] [Bordetella pertussis Tohama I]	Exotoxin
HhutsZ1GL003232	49.4	2.00E-79	VFG000477	Verified	(rpoS) RNA polymerase sigma factor RpoS [RpoS (VF0112) - Regulation (VFC0301)] [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]	Regulation
HhutsZ1GL003272	42.1	1.80E-50	VFG038840	Verified	(flmH) short chain dehydrogenase/reductase family oxidoreductase [Polar flagella (VF0473) - Motility (VFC0204)] [Aeromonas hydrophila ML09-119]	Motility
HhutsZ1GL003532	43.5	2.00E-94	VFG043209	Verified	(cheD) methyl-accepting chemotaxis protein CheD [Flagella (VF0394) - Motility (VFC0204)] [Yersinia enterocolitica subsp. enterocolitica 8081]	Motility
HhutsZ1GL003852	59.1	5.00E-77	VFG039536	Verified	(CBU_1566) Coxiella Dot/Icm type IVB secretion system translocated effector [T4SS secreted effectors (VF0696) - Effector delivery system (VFC0086)] [Coxiella burnetii RSA 493]	Effector delivery system
HhutsZ1GL004004	42.3	5.20E-69	VFG002529	Verified	(tsr) methyl-accepting chemotaxis protein I [Flagella (VF0430) - Motility (VFC0204)] [Burkholderia pseudomallei K96243]	Motility
HhutsZ1GL004018	40.3	6.40E-40	VFG045467	Verified	(cdpA) cyclic di-GMP phosphodiesterase [CdpA (VF0432) - Regulation (VFC0301)] [Burkholderia pseudomallei K96243]	Regulation
HhutsZ1GL004019	53.7	7.90E-78	VFG043209	Verified	(cheD) methyl-accepting chemotaxis protein CheD [Flagella (VF0394) - Motility (VFC0204)] [Yersinia enterocolitica subsp. enterocolitica 8081]	Motility
HhutsZ1GL004130	42.7	1.10E-52	VFG044084	Verified	(PA2383) transcriptional regulator [Pyoverdine (VF0094) - Nutritional/Metabolic factor (VFC0272)] [Pseudomonas aeruginosa PAO1]	Nutritional/Metabolic factor
HhutsZ1GL004172	47.9	4.80E-82	VFG041011	Verified	(vgrG1b) type VI secretion system substrate VgrG1b [HS1 (VF0334) - Effector delivery system (VFC0086)] [Pseudomonas aeruginosa PAO1]	Effector delivery system
HhutsZ1GL004250	51.4	1.50E-298	VFG049144	Verified	(acrB) acriflavine resistance protein B [AcrAB (VF0568) - Antimicrobial activity/Competitive advantage (VFC0325)] [Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044]	Antimicrobial activity/Competitive advantage
HhutsZ1GL004270	45.5	1.70E-70	VFG050157	Verified	(kpsF) Polysialic acid capsule expression protein [K1 capsule (VF0239) - Invasion (VFC0083)] [Escherichia coli O45:K1:H7 str. S88]	Invasion
HhutsZ1GL004275	46.3	4.30E-112	VFG042736	Verified	(rpoN) RNA polymerase factor sigma-54 [Type IV pili (VF0082) - Adherence (VFC0001)] [Pseudomonas aeruginosa PAO1]	Adherence
HhutsZ1GL004386	49.6	3.40E-68	VFG045297	Verified	(wbuZ) glycosyl amidation-associated protein WbuZ [LPS (VF0171) - Immune modulation (VFC0258)] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	Immune modulation
HhutsZ1GL004388	47.8	2.90E-44	VFG014106	Verified	(hisH2) imidazole glycerol phosphate synthase subunit HisH [LPS (VF0085) - Immune modulation (VFC0258)] [Pseudomonas aeruginosa PAO1]	Immune modulation
HhutsZ1GL004430	46.4	1.90E-32	VFG000320	Verified	(kdtB) lipopolysaccharide core biosynthesis protein [LPS (VF0056) - Immune modulation (VFC0258)] [Helicobacter pylori 26695]	Immune modulation
HhutsZ1GL004458	43	1.90E-63	VFG050217	Verified	(CD0873) ABC transporter substrate-binding protein [CD0873 (VF0593) - Adherence (VFC0001)] [Clostridium difficile 630]	Adherence
HhutsZ1GL004493	54.8	5.60E-53	VFG002527	Verified	(cheD) chemoreceptor glutamine deamidase CheD [Flagella (VF0430) - Motility (VFC0204)] [Burkholderia pseudomallei K96243]	Motility
HhutsZ1GL004610	43	3.90E-14	VFG050255	Verified	(CT_473) hypothetical protein [TTSS secreted effectors (VF0711) - Effector delivery system (VFC0086)] [Chlamydia trachomatis D/UW-3/CX]	Effector delivery system
HhutsZ1GL004695	42	3.90E-73	VFG047095	Verified	(wbtI) DegT/DnrJ/EryC1/StrS family aminotransferase [LPS (VF0542) - Immune modulation (VFC0258)] [Francisella tularensis subsp. tularensis SCHU S4]	Immune modulation
HhutsZ1GL004915	59.1	0.00E+00	VFG049144	Verified	(acrB) acriflavine resistance protein B [AcrAB (VF0568) - Antimicrobial activity/Competitive advantage (VFC0325)] [Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044]	Antimicrobial activity/Competitive advantage
HhutsZ1GL004916	50.8	3.20E-98	VFG049133	Verified	(acrA) acriflavine resistance protein A [AcrAB (VF0568) - Antimicrobial activity/Competitive advantage (VFC0325)] [Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044]	Antimicrobial activity/Competitive advantage
HhutsZ1GL004920	46.5	2.50E-110	VFG002529	Verified	(tsr) methyl-accepting chemotaxis protein I [Flagella (VF0430) - Motility (VFC0204)] [Burkholderia pseudomallei K96243]	Motility
HhutsZ1GL005054	63	1.20E-27	VFG000269	Verified	(ureA) urease alpha subunit UreA [Urease (VF0050) - Stress survival (VFC0282)] [Helicobacter pylori 26695]	Stress survival
HhutsZ1GL005059	65.2	3.10E-75	VFG000274	Verified	(ureG) urease accessory protein (ureG) [Urease (VF0050) - Stress survival (VFC0282)] [Helicobacter pylori 26695]	Stress survival
HhutsZ1GL005099	42.5	6.80E-54	VFG045346	Verified	(IlpA) immunogenic lipoprotein A [IlpA (VF0513) - Adherence (VFC0001)] [Vibrio vulnificus YJ016]	Adherence

supplementary table S2. Drug resistance-related genes of HhutSZ1

Gene_id	Identity	E_value	Subject_id	Resistance_Type	Min_Identity	Resistance_Requirement	Antibiotic_Resistance	Original_Resistance_Type	Description
HhutSZ1GL000312	61.7	9.30E-169	ar db_1260	opcm	80	ceoa,ceob	chloramphenicol	ceo	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL000313	80.6	0.00E+00	ar db_1637	ceob	80	ceoa,opcm	chloramphenicol	ceo	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL000314	62.9	1.80E-135	ar db_76	ceoa	80	ceob,opcm	chloramphenicol	ceo	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL000332	45.4	5.20E-139	ar db_2181	pbp2b	80	--	penicillin	pbp	The enzyme has a penicillin-insensitive transglycosylase N-terminal domain (formation of linear glycan strands) and a penicillin-sensitive transpeptidase C-terminal domain (cross-linking of the peptide subunits)
HhutSZ1GL000518	52.8	9.00E-129	ar db_1138	oprm	80	mexa,mexb,mexj,mexk,mexl,mexm,mexn,mexo,mexp,mexq,mexr,mexs,mext,mexu,mexv,mexw,mexx,mexy	aminoglycoside,tigecycline,fluoroquinolone,beta_lactam,tetracycline	mexab	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL000519	59.6	0.00E+00	ar db_108	acrb	80	acra,tolc	aminoglycoside,glycyl cycline,macrolide,beta_lactam,acriflavin	acr	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL000520	52.8	4.00E-103	ar db_1683	acra	80	acrb,tolc	aminoglycoside,glycyl cycline,macrolide,beta_lactam,acriflavin	acr	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL000528	72.5	2.20E-111	ar db_219	baca	30	--	bacitracin	baca	Undecaprenyl pyrophosphate phosphatase, which consists in the sequestration of Undecaprenyl pyrophosphate.
HhutSZ1GL000759	51.2	1.10E-67	ar db_2770	ksga	80	--	kasugamycin	ksga	Specifically dimethylates two adjacent adenosines in the loop of a conserved hairpin near the 3'-end of 16S rRNA in the 30S particle. Its inactivation leads to kasugamycin resistance.
HhutSZ1GL000890	61.5	2.60E-137	ar db_543	rosa	80	rosb	fosmidomycin	rosab	Efflux pump/potassium antiporter system. RosA: Major facilitator superfamily transporter. RosB: Potassium antiporter.
HhutSZ1GL001101	48.2	2.30E-116	ar db_1137	oprm	80	mexa,mexb,mexj,mexk,mexl,mexm,mexn,mexo,mexp,mexq,mexr,mexs,mext,mexu,mexv,mexw,mexx,mexy	aminoglycoside,tigecycline,fluoroquinolone,beta_lactam,tetracycline	mexab	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL001364	54.7	3.20E-108	ar db_1691	acra	80	acrb,tolc	aminoglycoside,glycyl cycline,macrolide,beta_lactam,acriflavin	acr	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL001365	65.7	0.00E+00	ar db_1925	acrb	80	acra,tolc	aminoglycoside,glycyl cycline,macrolide,beta_lactam,acriflavin	acr	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL001366	55.8	5.10E-143	ar db_1138	oprm	80	mexa,mexb,mexj,mexk,mexl,mexm,mexn,mexo,mexp,mexq,mexr,mexs,mext,mexu,mexv,mexw,mexx,mexy	aminoglycoside,tigecycline,fluoroquinolone,beta_lactam,tetracycline	mexab	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL001416	42.1	2.20E-127	ar db_2143	pbp1a	80	--	penicillin	pbp	The enzyme has a penicillin-insensitive transglycosylase N-terminal domain (formation of linear glycan strands) and a penicillin-sensitive transpeptidase C-terminal domain (cross-linking of the peptide subunits)
HhutSZ1GL001577	42.1	5.80E-102	ar db_268	opcm	80	ceoa,ceob	chloramphenicol	ceo	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL001884	49.8	4.90E-111	ar db_1138	oprm	80	mexa,mexb,mexj,mexk,mexl,mexm,mexn,mexo,mexp,mexq,mexr,mexs,mext,mexu,mexv,mexw,mexx,mexy	aminoglycoside,tigecycline,fluoroquinolone,beta_lactam,tetracycline	mexab	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL002052	40.5	7.00E-82	ar db_2230	ceoa	80	ceob,opcm	chloramphenicol	ceo	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL002053	65.1	0.00E+00	ar db_1600	mexf	80	mexe,opr n	chloramphenicol,fluoroquinolone	mexcf	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL002054	53.9	5.70E-136	ar db_1139	oprm	80	mexa,mexb,mexj,mexk,mexl,mexm,mexn,mexo,mexp,mexq,mexr,mexs,mext,mexu,mexv,mexw,mexx,mexy	aminoglycoside,tigecycline,fluoroquinolone,beta_lactam,tetracycline	mexab	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL002157	61.7	1.00E-189	ar db_602	rosb	80	rosa	fosmidomycin	rosab	Efflux pump/potassium antiporter system. RosA: Major facilitator superfamily transporter. RosB: Potassium antiporter.
HhutSZ1GL002245	57.4	4.50E-208	ar db_2630	macb	80	maca,tolc	macrolide	macab	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump. Macrolide-specific efflux system.
HhutSZ1GL002281	54.3	9.10E-107	ar db_736	arna	80	--	polymyxin	arna	Bifunctional enzyme that catalyzes the oxidative decarboxylation of UDP-glucuronic acid (UDP-GlcUA) to UDP-4-keto-arabinose (UDP-Ara4O) and the addition of a formyl group to UDP-4-amino-4-deoxy-L-arabinose (UDP-L-Ara4N) to form UDP-L-4-formamido-arabinose (UDP-L-Ara4FN). The modified arabinose is attached to lipid A and is required for resistance to polymyxin and cationic antimicrobial peptides.
HhutSZ1GL002282	43.1	2.40E-63	ar db_735	arna	80	--	polymyxin	arna	Bifunctional enzyme that catalyzes the oxidative decarboxylation of UDP-glucuronic acid (UDP-GlcUA) to UDP-4-keto-arabinose (UDP-Ara4O) and the addition of a formyl group to UDP-4-amino-4-deoxy-L-arabinose (UDP-L-Ara4N) to form UDP-L-4-formamido-arabinose (UDP-L-Ara4FN). The modified arabinose is attached to lipid A and is required for resistance to polymyxin and cationic antimicrobial peptides.
HhutSZ1GL002779	40.7	1.00E-95	ar db_271	opcm	80	ceoa,ceob	chloramphenicol	ceo	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL003212	42.4	6.40E-85	ar db_1951	cml_c6	95	--	chloramphenicol	cml	Major facilitator superfamily transporter, chloramphenicol efflux pump.
HhutSZ1GL003663	49	6.00E-67	ar db_2955	bl2be_ctxm	75	--	monobactam,penicillin,cephalosporin_iii,cefazidime,cephalosporin_ii,cephalosporin_i	bla_a	Class A beta-lactamase. This enzyme breaks the beta-lactam antibiotic ring open and deactivates the molecule's antibacterial properties.
HhutSZ1GL003781	41.1	2.20E-23	ar db_568	dfra20	95	--	trimethoprim	dfra	Group A drug-insensitive dihydrofolate reductase, which can not be inhibited by trimethoprim.
HhutSZ1GL004250	62.8	0.00E+00	ar db_1517	adeb	80	adea,adec	chloramphenicol,aminoglycoside	adeabc	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL004469	41.1	1.80E-126	ar db_2143	pbp1a	80	--	penicillin	pbp	The enzyme has a penicillin-insensitive transglycosylase N-terminal domain (formation of linear glycan strands) and a penicillin-sensitive transpeptidase C-terminal domain (cross-linking of the peptide subunits)
HhutSZ1GL004914	54	3.10E-137	ar db_1138	oprm	80	mexa,mexb,mexj,mexk,mexl,mexm,mexn,mexo,mexp,mexq,mexr,mexs,mext,mexu,mexv,mexw,mexx,mexy	aminoglycoside,tigecycline,fluoroquinolone,beta_lactam,tetracycline	mexab	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL004915	60.4	0.00E+00	ar db_108	acrb	80	acra,tolc	aminoglycoside,glycyl cycline,macrolide,beta_lactam,acriflavin	acr	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL004916	52.8	7.60E-103	ar db_2089	mexa	80	mexb,opr m	aminoglycoside,tigecycline,fluoroquinolone,beta_lactam,tetracycline	mexab	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL004921	41.9	1.00E-87	ar db_268	opcm	80	ceoa,ceob	chloramphenicol	ceo	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump.
HhutSZ1GL004942	55.5	9.10E-29	ar db_1271	emre	80	emrd	aminoglycoside	emre	Multidrug resistance efflux pump.
HhutSZ1GL005173	40.8	1.80E-29	ar db_2395	vanrc	80	vanc,vanxyc,vant,vansc	vancomycin	vanc	VanC type vancomycin resistance operon genes, which can synthesize peptidoglycan with modified C-terminal D-Ala-D-Ala to D-alanine--D-serine.