

## A Strains, plasmids and oligonucleotides used in this study

AmpR: ampicillin resistant.

CmR: chloramphenicol resistant.

Internal strain ID	Strain name	Genotype/Details	Source/Reference
		<i>Escherichia coli</i>	
MJD841	NEB® 5-alpha	<i>fhuA2</i> Δ( <i>argF- lacZ</i> )U169 <i>phoA glnV44</i> Φ80 Δ( <i>lacZ</i> )M15 <i>gyrA96 recA1 relA1</i> <i>endA1 thi- 1 hsdR17</i>	New England Biolabs
CF323	MG1655	<i>Escherichia coli</i> K-12 MG1655: F- λ- <i>ilvG- rfb- 50 rph- 1</i>	wild type strain; Gerdes laboratory collection

Plasmid name	Genotype/ Details	Source/Reference
pNDM220	mini- R1 ori; <i>bla</i> ; <i>lacI<sup>q</sup></i> ; Plac promoter; AmpR	doi.org/ 10.1046/ j.1365-2958.1998.00993.x
pBAD33	p15A ori; <i>cat</i> ; <i>araC</i> ; ParaB promoter; CmR	doi: 10.1128/ jb.177.14.4121- 4130.1995
pAH154_doc_v2	Derivative of pNDM220 encoding the doc toxin of the bacteriophage P1 Doc- Phd toxin- antitoxin module. Amp 30 µg/ ml	this study; the ORF of <i>doc</i> was amplified from bacteriophage P1vir with a weak RBS (ATTCCTCCaacaatttATG) using primers prAH1542 / prAH1541 and ligated into pNDM220 downstream Plac after digestion of backbone and insert with KpnI / XhoI. IPTG induction of <i>doc</i> expression

pAH153_phd_CPH_V1	Derivative of pBAD33 encoding the <i>phd</i> antitoxin of the bacteriophage P1 Doc-Phd toxin- antitoxin module. Cam 25 µg/ ml	this study; the ORF of <i>phd</i> was amplified from bacteriophage P1vir with a strong RBS (TCAGGAGGatctctATG) using primers prAH1810 / prAH1811 and ligated into pBAD33 downstream ParaB after digestion of backbone and insert with SacI / PstI. L-arabinose induction of <i>phd</i> expression
pMJD119	pNDM220 Plac- doc; AmpR	This study
pMJD120	pNDM220 Plac- 7H; AmpR	This study
pMJD121	pNDM220 Plac- 8H; AmpR	This study
pMJD122	pNDM220 Plac- 12H; AmpR	This study
pMJD123	pNDM220 Plac- 18H; AmpR	This study
pMJD124	pNDM220 Plac- 22H; AmpR	This study
pMJD125	pNDM220 Plac- 31H; AmpR	This study
pMJD126	pNDM220 Plac- 27H; AmpR	This study
pMJD127	pNDM220 Plac- 37H; AmpR	This study
pMJD128	pNDM220 Plac- 51H- 39; AmpR	This study
pMJD129	pNDM220 Plac- 72H; AmpR	This study
pMJD130	pNDM220 Plac- 61H; AmpR	This study
pMJD131	pNDM220 Plac- 51H- 147; AmpR	This study
pMJD132	pNDM220 Plac- 87H; AmpR	This study
pMJD138	pNDM220 Plac- 44H; AmpR	This study
pMJD140	pNDM220 Plac- 54H; AmpR	This study
pMJD142	pBAD33 ParaB- 39P; CmR	This study
pMJD143	pBAD33 ParaB- 44P; CmR	This study
pMJD144	pBAD33 ParaB- 45P; CmR	This study
pMJD145	pBAD33 ParaB- 197P; CmR	This study

pMJD146	pBAD33 ParaB- phd; CmR	This study
pMJD147	pBAD33 ParaB- 3P; CmR	This study
pMJD148	pBAD33 ParaB- 24P; CmR	This study
pMJD149	pBAD33 ParaB- 26P; CmR	This study
pMJD150	pBAD33 ParaB- 27P; CmR	This study
pMJD151	pBAD33 ParaB- 48P; CmR	This study
pMJD152	pBAD33 ParaB- 52P- 31; CmR	This study
pMJD153	pBAD33 ParaB- 62P; CmR	This study
pMJD154	pBAD33 ParaB- 67P; CmR	This study
pMJD155	pBAD33 ParaB- 147P; CmR	This study
pMJD156	pBAD33 ParaB- 168P; CmR	This study

Primer ID	Description	Sequence 5'- 3'
prAH1541	rv. Amplification of <i>doc</i> from phage P1vir. XhoI RS	GCCTTCCTCGAGCTACTCCGCAGAA CCATACAA
prAH1542	fw. Amplification of <i>doc</i> from phage P1vir. KpnI RS	CGAGTGGGTACCATTCTCCAACAATT TTATGAGGCATATATCACCGGA
prAH1810	fw. Amplification of <i>phd</i> from phage P1vir. SacI RS	GTTGTTCGAGCTCTCAGGAGGATCTCT ATGCAATCCATTAACCTCCGT
prAH1811	rv. Amplification of <i>phd</i> from phage P1vir. PstI RS	CTGGGGTCTGCAGTTATCGGTTAACC AGTTCCTTG
prAH_pNDM220	fw. Screening for cloning in pNDM220	AAACAGGAAGGCAAATGC
prAH500	rv. Screening for cloning in pNDM220 and pBAD33	CTGTTTTATCAGACCGCTTC
prAH501	fw. Screening for cloning in pBAD33	CGTCACACTTTGCTATGCC

## B Identified toxin groups

Name	Pfam Profile	Type	Antitoxins	Count	Category	local aa identity (min-max)	range alignment length (min-max)	global aa identity (min-max)
11H	Cpta_toxin	IV	35P	258	ubiq	99.79 (97.06-100.0)	99.56 (43.0-100.0)	99.3 (43.0-100.0)
5H	Polyketide_cyc2	II	15P	258	ubiq	99.27 (92.16-100.0)	99.51 (91.0-100.0)	98.9 (87.0-100.0)
34H	Fic	II	173P/ 34P	255	ubiq	98.7 (93.0-100.0)	100.0 (100.0-100.0)	98.52 (93.0-100.0)
10H	HD	II	81P/ 112P/ 32P/ 65P/ 236P	251	ubiq	98.27 (90.68-100.0)	99.37 (52.0-100.0)	97.76 (51.0-100.0)
22H	GNAT_acetyltran	II	8P/ 98P	250	ubiq	99.43 (95.93-100.0)	100.0 (100.0-100.0)	99.39 (96.0-100.0)
27H	HipA_C	II	59P/ 244P/ 24P	242	ubiq	98.16 (63.33-100.0)	97.59 (9.0-100.0)	97.09 (25.0-100.0)
8H	DUF3749	II	12P	236	ubiq	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
17H	RelE	II	73P/ 36P/ 9P	282	species associated	96.97 (53.75-100.0)	76.76 (14.0-100.0)	75.08 (10.0-100.0)
7H	Fic	II	168P/ 3P	240	species associated	99.29 (96.72-100.0)	100.0 (100.0-100.0)	99.16 (97.0-100.0)
21H	PIN	II	212P/ 31P/ 5P	238	species associated	99.5 (95.31-100.0)	98.33 (41.0-100.0)	97.74 (4.0-100.0)
16H	ParE_toxin	II	4P/ 7P	235	species associated	96.15 (77.66-100.0)	99.98 (77.0-100.0)	96.27 (78.0-100.0)
26H	ParE_toxin	II	127P/ 1P	230	species associated	98.02 (91.43-100.0)	96.1 (58.0-100.0)	94.17 (41.0-100.0)
13H	Gp49	II	30P	156	species associated	97.75 (90.16-100.0)	94.4 (50.0-100.0)	92.16 (44.0-100.0)
9H	Zeta_toxin	II	63P/ 11P	95	species associated	99.23 (95.97-100.0)	98.94 (95.0-100.0)	98.26 (93.0-100.0)

2H	PemK_toxin	II	115P/ 171P/ 101P/ 146P/ 22P	65	species associated	87.91 (72.73- 100.0)	100.0 (100.0- 100.0)	87.93 (73.0- 100.0)
42H	YdaT_toxin	II	119P/ 133P/ 111P/ 54P/ 28P/ 210P/ 47P	63	species associated	91.39 (78.26- 100.0)	100.0 (100.0- 100.0)	91.33 (78.0- 100.0)
37H	AntA	II	26P/ 62P/ 42P	45	species associated	86.91 (36.71- 100.0)	74.74 (6.0- 100.0)	66.75 (14.0- 100.0)
25H	Gp49	II	70P/ 77P	40	species associated	97.94 (94.92- 100.0)	98.75 (75.0- 100.0)	96.76 (74.0- 100.0)
33H	RelE	II	155P/ 19P	26	species associated	86.54 (70.91- 100.0)	97.76 (70.0- 100.0)	84.76 (52.0- 100.0)
87H	HicA_toxin	II	45P	8	species associated	98.08 (95.6- 100.0)	97.0 (93.0- 100.0)	95.25 (89.0- 100.0)
51H	HigB_toxin	II	147P/ 39P	7	species associated	88.72 (71.84- 100.0)	76.67 (51.0- 100.0)	67.14 (43.0- 100.0)
64H	Fic	II	124P/ 201P	5	species associated	98.16 (95.76- 100.0)	83.2 (58.0- 100.0)	82.0 (55.0- 100.0)
18H	CcdB	II	143P/ 21P/ 58P	199	sporadic	96.65 (77.78- 100.0)	87.27 (16.0- 100.0)	86.09 (12.0- 100.0)
4H	PIN	II	204P/ 6P/ 238P/ 240P/ 51P/ 103P	156	sporadic	92.87 (77.78- 100.0)	94.84 (36.0- 100.0)	90.48 (30.0- 100.0)
6H	Gp49	II	175P/ 17P	120	sporadic	99.04 (93.33- 100.0)	99.53 (77.0- 100.0)	98.53 (73.0- 100.0)
14H	Gp49	II	27P	105	sporadic	99.73 (96.0- 100.0)	96.28 (43.0- 100.0)	96.17 (42.0- 100.0)
23H	YdaT_toxin	II	93P/ 232P/ 123P/ 117P/ 76P/ 121P/ 33P/ 192P/ 221P/ 176P/ 80P/ 61P	98	sporadic	85.29 (71.91- 100.0)	98.17 (50.0- 100.0)	83.97 (41.0- 100.0)
15H	HigB_toxin	II	16P	96	sporadic	99.9 (99.0- 100.0)	100.0 (100.0- 100.0)	99.9 (99.0- 100.0)
3H	RES	II	92P/ 106P/ 69P/ 13P/ 231P	70	sporadic	98.97 (94.87- 100.0)	99.77 (92.0- 100.0)	98.63 (88.0- 100.0)

35H	HigB_toxin	II	14P	59	sporadic	99.97 (99.03- 100.0)	100.0 (100.0- 100.0)	99.97 (99.0- 100.0)
61H	CcdB	II	48P	57	sporadic	98.19 (94.06- 100.0)	98.07 (45.0- 100.0)	96.25 (44.0- 100.0)
45H	CbtA_toxin	IV	74P/ 170P/ 132P/ 75P/ 234P/ 179P/ 38P/ 157P	46	sporadic	77.84 (53.33- 100.0)	87.27 (25.0- 100.0)	70.49 (22.0- 100.0)
62H	ParE_toxin	II	95P/ 41P/ 79P	42	sporadic	96.39 (71.11- 100.0)	85.09 (67.0- 100.0)	81.91 (62.0- 100.0)
20H	NTP_transf_2	II	223P/ 207P/ 66P/ 205P/ 40P	30	sporadic	96.74 (82.81- 100.0)	84.87 (20.0- 100.0)	84.38 (17.0- 100.0)
57H	NTP_transf_2	II	29P	27	sporadic	99.92 (98.96- 100.0)	100.0 (100.0- 100.0)	99.93 (99.0- 100.0)
28H	Bro- N	II	149P/ 109P/ 120P	26	sporadic	68.95 (41.85- 100.0)	98.18 (91.0- 100.0)	68.25 (40.0- 100.0)
12H	RES	II	105P/ 46P	26	sporadic	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
52H	ParE_toxin	II	2P	22	sporadic	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
44H	ParE_toxin	II	44P/ 23P	19	sporadic	96.7 (77.55- 100.0)	94.36 (49.0- 100.0)	91.49 (38.0- 100.0)
24H	Gp49	II	67P	12	sporadic	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
72H	HD_3	II	50P	10	sporadic	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
71H	DUF955	II	60P	8	sporadic	99.35 (98.86- 100.0)	100.0 (100.0- 100.0)	99.43 (99.0- 100.0)
60H	HipA_C	II	233P/ 20P	8	sporadic	94.75 (82.77- 100.0)	100.0 (100.0- 100.0)	94.75 (83.0- 100.0)
41H	HigB- like_toxin	II	209P/ 154P	7	sporadic	98.34 (94.17- 100.0)	100.0 (100.0- 100.0)	98.29 (94.0- 100.0)
96H	AntA	II	91P	6	sporadic	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)

1H	Bro- N	II	118P/ 136P	15	rare	98.83 (97.31- 100.0)	91.62 (80.0- 100.0)	90.75 (78.0- 100.0)
49H	Gp49	II	78P	15	rare	99.63 (97.25- 100.0)	99.75 (99.0- 100.0)	99.35 (97.0- 100.0)
70H	CbtA_toxin	IV	185P/ 237P/ 88P/ 49P/ 174P	13	rare	87.47 (60.48- 100.0)	59.33 (28.0- 100.0)	46.37 (12.0- 100.0)
32H	AbiEii	IV	102P	10	rare	99.86 (99.3- 100.0)	100.0 (100.0- 100.0)	99.8 (99.0- 100.0)
40H	PemK_toxin	II	87P	9	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
19H	DUF488	II	181P/ 128P	9	rare	99.24 (98.31- 100.0)	61.78 (33.0- 100.0)	71.64 (34.0- 99.0)
29H	YdaT_toxin	II	126P/ 104P/ 68P/ 182P	8	rare	88.83 (74.56- 100.0)	92.71 (83.0- 100.0)	84.5 (65.0- 100.0)
56H	YdaT_toxin	II	218P/ 99P	8	rare	95.67 (91.16- 100.0)	85.07 (41.0- 100.0)	81.11 (40.0- 100.0)
73H	YdaT_toxin	II	76P/ 80P/ 123P	7	rare	99.39 (98.4- 100.0)	93.71 (78.0- 100.0)	92.95 (78.0- 100.0)
67H	Gp49	II	152P	7	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
30H	YdaT_toxin	II	68P	6	rare	96.22 (92.91- 100.0)	100.0 (100.0- 100.0)	96.27 (93.0- 100.0)
31H	HicA_toxin	II	52P	6	rare	96.72 (93.85- 100.0)	100.0 (100.0- 100.0)	96.8 (94.0- 100.0)
53H	Bro- N	II	144P	5	rare	85.94 (77.41- 100.0)	100.0 (100.0- 100.0)	86.1 (78.0- 100.0)
107H	Bro- N	II	107P	5	rare	99.16 (97.89- 100.0)	100.0 (100.0- 100.0)	99.2 (98.0- 100.0)
115H	ParE_toxin	II	113P/ 196P	5	rare	95.11 (92.05- 100.0)	100.0 (100.0- 100.0)	95.1 (92.0- 100.0)
106H	AbiEii	IV	184P/ 227P/ 166P	5	rare	96.24 (90.37- 100.0)	73.9 (61.0- 100.0)	66.6 (40.0- 100.0)
50H	DUF955	II	55P	5	rare	99.5 (98.75- 100.0)	100.0 (100.0- 100.0)	99.6 (99.0- 100.0)

86H	Fic	II	135P/ 43P	5	rare	99.8 (99.49-100.0)	100.0 (100.0-100.0)	99.6 (99.0-100.0)
74H	AntA	II	199P	4	rare	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
109H	CcdB	II	64P	4	rare	97.67 (97.2-98.13)	100.0 (100.0-100.0)	97.5 (97.0-98.0)
131H	PemK_toxin	II	178P/ 158P/ 110P	4	rare	99.53 (99.07-100.0)	100.0 (100.0-100.0)	99.5 (99.0-100.0)
54H	Bro- N	II	52P/ 197P	4	rare	94.1 (88.21-100.0)	92.5 (85.0-100.0)	87.17 (75.0-100.0)
48H	Gp49	II	134P	3	rare	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
68H	Bro- N	II	186P/ 139P	3	rare	100.0 (100.0-100.0)	94.67 (92.0-100.0)	94.67 (92.0-100.0)
77H	HigB-like_toxin	II	164P	3	rare	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
100H	PemK_toxin	II	211P/ 245P	3	rare	86.96 (81.82-96.51)	85.33 (78.0-100.0)	74.0 (65.0-82.0)
94H	ParE_toxin	II	225P/ 214P	3	rare	85.29 (77.94-100.0)	76.0 (64.0-100.0)	66.0 (49.0-100.0)
82H	ParE_toxin	II	189P/ 96P	3	rare	91.93 (90.53-93.68)	100.0 (100.0-100.0)	92.33 (91.0-94.0)
39H	HicA_toxin	II	193P	3	rare	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
88H	AbiEii	IV	188P	3	rare	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
118H	CcdB	II	163P	2	rare	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
63H	HD_3	II	202P	2	rare	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
130H	Fic	II	220P/ 129P	2	rare	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
122H	ParE_toxin	II	160P	2	rare	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)



113H	YafQ_toxin	II	138P	2	rare	97.56 (97.56- 97.56)	100.0 (100.0- 100.0)	98.0 (98.0- 98.0)
123H	Fic	II	116P	2	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
66H	Peptidase_M 78	II	222P	2	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
139H	YafO_toxin	II	190P	2	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
83H	PIN	II	100P	2	rare	89.55 (89.55- 89.55)	100.0 (100.0- 100.0)	90.0 (90.0- 90.0)
90H	HigB_toxin	II	183P	2	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
84H	DUF955	II	215P	2	rare	99.47 (99.47- 99.47)	100.0 (100.0- 100.0)	99.0 (99.0- 99.0)
93H	YafO_toxin	II	108P	2	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
65H	PemK_toxin	II	142P	2	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
133H	CbtA_toxin	IV	198P	2	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
125H	Bro- N	II	26P/ 107P	2	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
114H	AntA	II	150P	2	rare	98.44 (98.44- 98.44)	100.0 (100.0- 100.0)	98.0 (98.0- 98.0)
78H	HD	II	195P	2	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
126H	CbtA_toxin	IV	145P	2	rare	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
38H	HipA_C	II	137P	1	rare	NA	NA	NA
129H	RelE	II	131P	1	rare	NA	NA	NA
141H	ParE_toxin	II	141P	1	rare	NA	NA	NA
81H	DUF3749	II	167P	1	rare	NA	NA	NA

121H	HicA_toxin	II	206P	1	rare	NA	NA	NA
89H	HD	II	140P	1	rare	NA	NA	NA
111H	Zeta_toxin	II	156P	1	rare	NA	NA	NA
92H	HigB-like_toxin	II	208P	1	rare	NA	NA	NA
127H	YafQ_toxin	II	53P	1	rare	NA	NA	NA
59H	ANT	II	97P/ 180P	1	rare	NA	NA	NA
135H	DUF4111	II	247P	1	rare	NA	NA	NA
97H	Fic	II	82P	1	rare	NA	NA	NA
58H	Gp49	II	56P	1	rare	NA	NA	NA
85H	HicA_toxin	II	172P	1	rare	NA	NA	NA
128H	DUF488	II	219P	1	rare	NA	NA	NA
120H	HD	II	194P	1	rare	NA	NA	NA
112H	PIN	II	10P	1	rare	NA	NA	NA
105H	PemK_toxin	II	187P	1	rare	NA	NA	NA
148H	PemK_toxin	II	239P	1	rare	NA	NA	NA
146H	DUF4258	II	162P	1	rare	NA	NA	NA
137H	HipA_C	II	89P	1	rare	NA	NA	NA
104H	HicA_toxin	II	241P/ 246P	1	rare	NA	NA	NA
43H	PIN	II	229P	1	rare	NA	NA	NA
117H	Fic	II	230P	1	rare	NA	NA	NA
145H	ParE_toxin	II	228P	1	rare	NA	NA	NA
98H	ANT	II	161P	1	rare	NA	NA	NA
102H	DUF488	II	191P	1	rare	NA	NA	NA
99H	ParE_toxin	II	130P	1	rare	NA	NA	NA
76H	HigB-like_toxin	II	235P	1	rare	NA	NA	NA

143H	AHSA1	II	85P	1	rare	NA	NA	NA
91H	HipA_C	II	25P	1	rare	NA	NA	NA
110H	YdaT_toxin	II	151P	1	rare	NA	NA	NA
47H	CbtA_toxin	IV	84P	1	rare	NA	NA	NA
142H	HD	II	243P	1	rare	NA	NA	NA
108H	HigB_toxin	II	125P	1	rare	NA	NA	NA
95H	YafO_toxin	II	90P	1	rare	NA	NA	NA
101H	RES	II	169P	1	rare	NA	NA	NA
147H	CcdB	II	242P	1	rare	NA	NA	NA
136H	ParE_toxin	II	224P	1	rare	NA	NA	NA
69H	CbtA_toxin	IV	38P/ 217P	1	rare	NA	NA	NA
132H	Peptidase_M 78	II	153P	1	rare	NA	NA	NA
103H	CcdB	II	159P	1	rare	NA	NA	NA
36H	YdaT_toxin	II	213P	1	rare	NA	NA	NA
124H	YdaT_toxin	II	114P	1	rare	NA	NA	NA
138H	YafO_toxin	II	165P	1	rare	NA	NA	NA
119H	PIN	II	6P	1	rare	NA	NA	NA
134H	YafO_toxin	II	71P	1	rare	NA	NA	NA

## C Identified antitoxin groups

Name	Pfam Profile	Toxin	Type	Up-stream count	Downstream count	In TADB ?	Interpro	Mean local aa identity (min-max)	Mean alignment length (min-max)	Mean global aa identity (min-max)
15P	Polyketide_cyc2	5H	II	0	258	No	Ubiquitin	99.29 (94.79-100.0)	100.0 (100.0-100.0)	99.32 (95.0-100.0)
35P	Cpta_toxin	11H	IV	258	0	Yes	In TADB	99.96 (97.73-100.0)	100.0 (100.0-100.0)	99.97 (98.0-100.0)
34P	Fic	34H	II	255	0	Yes	In TADB	98.78 (89.09-100.0)	99.78 (93.0-100.0)	98.57 (85.0-100.0)
8P	GNAT_acyltran	22H	II	0	250	No	Inner membrane transporter	98.66 (90.6-100.0)	99.44 (66.0-100.0)	98.07 (62.0-100.0)
36P	RelE	17H	II	0	243	Yes	In TADB	99.51 (81.03-100.0)	99.03 (52.0-100.0)	98.53 (43.0-100.0)
24P	HipA_C	27H	II	242	0	Yes	In TADB	98.04 (88.17-100.0)	99.41 (93.0-100.0)	97.55 (85.0-100.0)
3P	Fic	7H	II	240	0	Yes	In TADB	99.69 (97.26-100.0)	99.64 (61.0-100.0)	99.45 (61.0-100.0)
9P	RelE	17H	II	238	0	No	None	95.43 (85.71-100.0)	100.0 (100.0-100.0)	95.39 (86.0-100.0)
12P	DUF3749	8H	II	0	236	No	DUF	98.84 (94.44-100.0)	98.03 (48.0-100.0)	96.96 (47.0-100.0)
5P	PIN	21H	II	236	0	Yes	In TADB	99.87 (97.56-100.0)	100.0 (100.0-100.0)	99.89 (98.0-100.0)
7P	ParE_toxin	16H	II	235	0	Yes	In TADB	99.55 (94.5-100.0)	95.75 (80.0-100.0)	95.37 (77.0-100.0)
1P	ParE_toxin	26H	II	0	229	No	None	97.23 (85.45-100.0)	100.0 (100.0-100.0)	97.15 (85.0-100.0)
32P	HD	10H	II	208	0	No	None	98.29 (88.04-100.0)	99.84 (99.0-100.0)	98.1 (87.0-100.0)
6P	PIN	119H/4H	II	157	0	Yes	In TADB	94.45 (67.74-100.0)	95.9 (36.0-100.0)	93.91 (32.0-100.0)

30P	Gp49	13H	II	0	156	No	DNA binding	98.75 (94.95-100.0)	98.59 (58.0-100.0)	97.97 (59.0-100.0)
4P	ParE_toxin	16H	II	0	153	No	None	91.48 (80.3-100.0)	100.0 (100.0-100.0)	91.31 (80.0-100.0)
21P	CcdB	18H	II	0	142	No	None	98.37 (86.57-100.0)	98.07 (88.0-100.0)	96.92 (77.0-100.0)
58P	CcdB	18H	II	126	0	No	None	98.3 (91.94-100.0)	99.91 (98.0-100.0)	98.16 (92.0-100.0)
17P	Gp49	6H	II	0	120	No	DNA binding	99.15 (94.74-100.0)	100.0 (100.0-100.0)	99.19 (95.0-100.0)
27P	Gp49	14H	II	0	105	No	DNA binding	99.59 (95.65-100.0)	99.5 (74.0-100.0)	99.14 (72.0-100.0)
16P	HigB_toxin	15H	II	0	96	Yes	In TADB	99.27 (95.0-100.0)	100.0 (100.0-100.0)	99.24 (95.0-100.0)
11P	Zeta_toxin	9H	II	0	85	No	ABC transporter	96.52 (64.0-100.0)	72.69 (14.0-100.0)	78.73 (38.0-100.0)
13P	RES	3H	II	70	0	Yes	In TADB	98.86 (95.92-100.0)	100.0 (100.0-100.0)	98.84 (96.0-100.0)
14P	HigB_toxin	35H	II	0	59	Yes	In TADB	99.98 (99.24-100.0)	99.8 (94.0-100.0)	99.76 (94.0-100.0)
48P	CcdB	61H	II	57	0	Yes	In TADB	98.55 (93.06-100.0)	98.14 (73.0-100.0)	97.1 (69.0-100.0)
80P	YdaT_toxin	73H/ 23H	II	54	0	No	antitoxin	87.14 (71.05-100.0)	96.81 (86.0-100.0)	85.48 (67.0-100.0)
28P	YdaT_toxin	42H	II	0	50	No	None	99.08 (93.33-100.0)	100.0 (100.0-100.0)	99.01 (93.0-100.0)
22P	PemK_toxin	2H	II	45	0	Yes	In TADB	98.15 (93.58-100.0)	90.87 (47.0-100.0)	91.31 (46.0-100.0)
62P	AntA	37H	II	42	0	No	consensus disorder prediction	76.99 (37.5-100.0)	72.79 (21.0-100.0)	69.99 (22.0-100.0)
95P	ParE_toxin	62H	II	42	0	Yes	In TADB	96.86 (89.02-100.0)	100.0 (100.0-100.0)	96.79 (89.0-100.0)
70P	Gp49	25H	II	40	0	No	None	94.13 (86.96-100.0)	79.86 (58.0-100.0)	74.98 (47.0-100.0)
74P	CbtA_toxin	45H	IV	39	0	No	antitoxin	82.66 (70.37-100.0)	93.19 (74.0-100.0)	77.99 (58.0-100.0)

77P	Gp49	25H	II	0	39	No	None	98.89 (96.0-100.0)	98.26 (67.0-100.0)	97.03 (64.0-100.0)
47P	YdaT_toxin	42H	II	37	0	No	None	99.85 (97.18-100.0)	100.0 (100.0-100.0)	99.89 (97.0-100.0)
73P	RelE	17H	II	32	0	No	None	93.8 (57.32-100.0)	90.54 (54.0-100.0)	86.26 (47.0-100.0)
26P	AntA	37H/ 125H	II	0	30	No	DUF	92.9 (76.27-100.0)	100.0 (100.0-100.0)	92.91 (76.0-100.0)
29P	NTP_transf_2	57H	II	0	27	Yes	In TADB	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
105P	RES	12H	II	0	26	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
46P	RES	12H	II	26	0	No	None	99.7 (96.08-100.0)	100.0 (100.0-100.0)	99.69 (96.0-100.0)
19P	RelE	33H	II	0	25	Yes	In TADB	90.64 (78.72-100.0)	98.48 (81.0-100.0)	89.43 (65.0-100.0)
76P	YdaT_toxin	73H/ 23H	II	0	25	No	consensus disorder prediction	74.64 (44.3-100.0)	79.09 (24.0-100.0)	59.88 (16.0-100.0)
81P	HD	10H	II	24	0	No	None	98.87 (96.36-100.0)	100.0 (100.0-100.0)	98.76 (96.0-100.0)
109P	Bro- N	28H	II	22	0	No	regulation of transcription	94.63 (85.45-100.0)	95.92 (92.0-100.0)	91.18 (78.0-100.0)
2P	ParE_toxin	52H	II	22	0	Yes	In TADB	99.34 (98.73-100.0)	100.0 (100.0-100.0)	99.48 (99.0-100.0)
40P	NTP_transf_2	20H	II	21	0	No	DUF	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
101P	PemK_toxin	2H	II	20	0	Yes	In TADB	98.04 (95.29-100.0)	100.0 (100.0-100.0)	97.82 (95.0-100.0)
44P	ParE_toxin	44H	II	19	0	No	None	97.59 (80.46-100.0)	99.05 (91.0-100.0)	96.85 (73.0-100.0)
65P	HD	10H	II	18	0	No	None	98.47 (95.51-100.0)	100.0 (100.0-100.0)	98.64 (96.0-100.0)
23P	ParE_toxin	44H	II	0	16	No	None	96.56 (84.75-100.0)	98.52 (88.0-100.0)	95.28 (76.0-100.0)

41P	ParE_toxin	62H	II	0	15	No	None	99.01 (96.67- 100.0)	95.33 (65.0- 100.0)	94.36 (62.0- 100.0)
78P	Gp49	49H	II	0	15	Yes	In TADB	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
67P	Gp49	24H	II	0	12	Yes	In TADB	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
68P	YdaT_toxin	30H/ 29H	II	0	12	No	None	90.35 (80.95- 100.0)	99.39 (98.0- 100.0)	89.61 (80.0- 100.0)
136P	Bro- N	1H	II	0	11	No	None	99.77 (98.72- 100.0)	100.0 (100.0- 100.0)	99.82 (99.0- 100.0)
54P	YdaT_toxin	42H	II	11	0	No	None	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
61P	YdaT_toxin	23H	II	11	0	No	antitoxin	84.86 (73.61- 100.0)	98.73 (93.0- 100.0)	84.45 (70.0- 100.0)
93P	YdaT_toxin	23H	II	11	0	No	None	99.37 (98.85- 100.0)	100.0 (100.0- 100.0)	99.45 (99.0- 100.0)
102P	AbiEii	32H	IV	0	10	No	None	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
50P	HD_3	72H	II	0	10	No	None	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
51P	PIN	4H	II	0	10	No	None	97.94 (93.83- 100.0)	100.0 (100.0- 100.0)	97.96 (94.0- 100.0)
63P	Zeta_toxin	9H	II	10	0	No	None	96.3 (90.74- 100.0)	100.0 (100.0- 100.0)	96.24 (91.0- 100.0)
33P	YdaT_toxin	23H	II	9	0	No	antitoxin	99.12 (97.37- 100.0)	100.0 (100.0- 100.0)	99.25 (97.0- 100.0)
49P	CbtA_toxin	70H	IV	9	0	No	antitoxin	94.38 (88.23- 100.0)	100.0 (100.0- 100.0)	94.28 (88.0- 100.0)
87P	PemK_toxin	40H	II	9	0	No	None	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
92P	RES	3H	II	0	9	No	None	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
123P	YdaT_toxin	73H/ 23H	II	8	0	No	antitoxin	93.76 (80.0- 100.0)	100.0 (100.0- 100.0)	93.79 (80.0- 100.0)

132P	CbtA_toxin	45H	IV	0	8	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
146P	PemK_toxin	2H	II	0	8	No	None	100.0 (100.0-100.0)	86.5 (46.0-100.0)	86.5 (46.0-100.0)
168P	Fic	7H	II	0	8	No	None	96.12 (87.72-100.0)	100.0 (100.0-100.0)	95.54 (86.0-100.0)
42P	AntA	37H	II	0	8	No	None	89.29 (73.68-100.0)	97.86 (96.0-100.0)	87.71 (72.0-100.0)
45P	HicA_toxin	87H	II	0	8	Yes	In TADB	99.79 (99.16-100.0)	100.0 (100.0-100.0)	99.75 (99.0-100.0)
60P	DUF955	71H	II	8	0	No	DNA binding	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
107P	Bro- N	125H/ 107H	II	7	0	No	prophage	91.16 (78.57-100.0)	100.0 (100.0-100.0)	91.14 (79.0-100.0)
152P	Gp49	67H	II	0	7	Yes	In TADB	99.7 (98.95-100.0)	100.0 (100.0-100.0)	99.71 (99.0-100.0)
181P	DUF488	19H	II	0	7	No	None	100.0 (100.0-100.0)	93.71 (78.0-100.0)	93.71 (78.0-100.0)
20P	HipA_C	60H	II	7	0	No	DNA binding	98.25 (95.92-100.0)	100.0 (100.0-100.0)	98.29 (96.0-100.0)
52P	HicA_toxin	54H/ 31H	II	6	1	No	DUF	98.77 (97.65-100.0)	92.38 (84.0-100.0)	91.33 (82.0-100.0)
99P	YdaT_toxin	56H	II	0	7	No	None	98.83 (95.89-100.0)	100.0 (100.0-100.0)	98.86 (96.0-100.0)
104P	YdaT_toxin	29H	II	6	0	No	antitoxin	98.58 (97.59-100.0)	95.2 (92.0-100.0)	94.0 (90.0-100.0)
111P	YdaT_toxin	42H	II	6	0	No	DNA binding	98.85 (97.33-100.0)	100.0 (100.0-100.0)	99.0 (97.0-100.0)
154P	HigB-like_toxin	41H	II	0	6	No	None	95.36 (88.57-100.0)	100.0 (100.0-100.0)	95.4 (89.0-100.0)
91P	AntA	96H	II	6	0	No	prophage	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
121P	YdaT_toxin	23H	II	5	0	No	antitoxin	100.0 (100.0-100.0)	99.6 (99.0-100.0)	99.6 (99.0-100.0)



124P	Fic	64H	II	5	0	No	consensus disorder prediction	92.36 (82.02-100.0)	100.0 (100.0-100.0)	92.4 (82.0-100.0)
135P	Fic	86H	II	0	5	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
144P	Bro- N	53H	II	5	0	No	None	98.42 (96.05-100.0)	100.0 (100.0-100.0)	98.4 (96.0-100.0)
39P	HigB_toxin	51H	II	0	5	No	DNA binding	99.65 (98.65-100.0)	81.6 (54.0-100.0)	81.2 (53.0-100.0)
43P	Fic	86H	II	5	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
55P	DUF955	50H	II	5	0	No	DNA binding	99.32 (98.29-100.0)	99.2 (98.0-100.0)	98.8 (97.0-100.0)
66P	DUF4111	20H	II	5	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
103P	PIN	4H	II	0	4	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
110P	PemK_toxin	131H	II	4	0	No	None	92.94 (88.23-100.0)	100.0 (100.0-100.0)	92.67 (88.0-100.0)
118P	Bro- N	1H	II	0	4	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
133P	YdaT_toxin	42H	II	4	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
157P	CbtA_toxin	45H	IV	0	4	No	None	93.33 (87.69-100.0)	100.0 (100.0-100.0)	93.5 (88.0-100.0)
173P	Fic	34H	II	0	4	No	Glutamine amidotransferase	99.18 (98.36-100.0)	94.5 (91.0-99.0)	94.0 (90.0-99.0)
199P	AntA	74H	II	4	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
38P	CbtA_toxin	45H/ 69H	IV	4	0	No	antitoxin	79.12 (73.0-84.61)	91.17 (84.0-100.0)	71.83 (60.0-84.0)
64P	CcdB	109H	II	4	0	No	consensus disorder prediction	97.58 (95.16-100.0)	100.0 (100.0-100.0)	97.5 (95.0-100.0)
98P	GNAT_acyltransferase	22H	II	4	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)

113P	ParE_toxin	115H	II	3	0	Yes	In TADB	88.55 (87.84- 89.19)	86.33 (80.0- 93.0)	77.33 (72.0- 84.0)
117P	YdaT_toxin	23H	II	3	0	No	antitoxin	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
119P	YdaT_toxin	42H	II	3	0	No	None	99.1 (98.65- 100.0)	100.0 (100.0- 100.0)	99.33 (99.0- 100.0)
134P	Gp49	48H	II	0	3	Yes	In TADB	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
164P	HigB- like_toxin	77H	II	3	0	No	None	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
185P	CbtA_toxin	70H	IV	3	0	No	toxin domain	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
188P	AbiEii	88H	IV	3	0	No	regulation of transcriptio n	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
193P	HicA_toxin	39H	II	3	0	No	DUF	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
197P	Bro- N	54H	II	3	0	No	None	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
88P	CbtA_toxin	70H	IV	0	3	No	None	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
96P	ParE_toxin	82H	II	3	0	Yes	In TADB	90.36 (86.75- 92.77)	100.0 (100.0- 100.0)	90.67 (87.0- 93.0)
100P	PIN	83H	II	2	0	No	antitoxin	86.91 (86.91- 86.91)	99.0 (99.0- 99.0)	86.0 (86.0- 86.0)
108P	YafO_toxin	93H	II	2	0	No	None	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
116P	Fic	123H	II	2	0	No	antitoxin	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
120P	Bro- N	28H	II	2	0	No	None	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)	100.0 (100.0- 100.0)
126P	YdaT_toxin	29H	II	2	0	No	None	95.51 (95.51- 95.51)	100.0 (100.0- 100.0)	96.0 (96.0- 96.0)
128P	DUF488	19H	II	2	0	No	DUF	97.89 (97.89- 97.89)	92.0 (92.0- 92.0)	90.0 (90.0- 90.0)

138P	YafQ_toxin	113H	II	0	2	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
142P	PemK_toxin	65H	II	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
145P	CbtA_toxin	126H	IV	0	2	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
147P	HigB_toxin	51H	II	0	2	No	DNA binding	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
149P	Bro- N	28H	II	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
150P	AntA	114H	II	2	0	No	Endodeoxyribonuclease	97.73 (97.73-97.73)	100.0 (100.0-100.0)	98.0 (98.0-98.0)
160P	ParE_toxin	122H	II	2	0	No	DNA integration	98.65 (98.65-98.65)	61.0 (61.0-61.0)	60.0 (60.0-60.0)
163P	CcdB	118H	II	2	0	No	antitoxin	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
166P	AbiEii	106H	IV	0	2	No	None	96.49 (96.49-96.49)	64.0 (64.0-64.0)	63.0 (63.0-63.0)
179P	CbtA_toxin	45H	IV	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
183P	HigB_toxin	90H	II	2	0	No	None	98.44 (98.44-98.44)	100.0 (100.0-100.0)	98.0 (98.0-98.0)
184P	AbiEii	106H	IV	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
186P	Bro- N	68H	II	2	0	No	None	96.3 (96.3-96.3)	100.0 (100.0-100.0)	96.0 (96.0-96.0)
190P	YafO_toxin	139H	II	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
192P	YdaT_toxin	23H	II	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
195P	HD	78H	II	0	2	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
196P	ParE_toxin	115H	II	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)

198P	CbtA_toxin	133H	IV	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
202P	HD_3	63H	II	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
207P	DUF4111	20H	II	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
210P	YdaT_toxin	42H	II	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
211P	PemK_toxin	100H	II	2	0	No	antitoxin	87.65 (87.65-87.65)	100.0 (100.0-100.0)	88.0 (88.0-88.0)
214P	ParE_toxin	94H	II	0	2	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
215P	DUF955	84H	II	2	0	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
222P	Peptidase_M78	66H	II	0	2	No	None	100.0 (100.0-100.0)	100.0 (100.0-100.0)	100.0 (100.0-100.0)
232P	YdaT_toxin	23H	II	0	2	No	None	98.84 (98.84-98.84)	100.0 (100.0-100.0)	99.0 (99.0-99.0)
31P	PIN	21H	II	2	0	No	toxin domain	98.08 (98.08-98.08)	98.0 (98.0-98.0)	96.0 (96.0-96.0)
69P	RES	3H	II	0	2	No	None	100.0 (100.0-100.0)	96.0 (96.0-96.0)	96.0 (96.0-96.0)
106P	RES	3H	II	0	1	No	None	100	100	100
10P	PIN	112H	II	0	1	No	consensus disorder prediction	100	100	100
112P	HD	10H	II	1	0	No	None	100	100	100
114P	YdaT_toxin	124H	II	1	0	No	DNA binding	100	100	100
115P	PemK_toxin	2H	II	0	1	No	None	100	100	100
125P	HigB_toxin	108H	II	0	1	No	None	100	100	100
127P	ParE_toxin	26H	II	0	1	Yes	In TADB	100	100	100
129P	Fic	130H	II	0	1	No	None	100	100	100

130P	ParE_toxin	99H	II	1	0	Yes	In TADB	100	100	100
131P	RelE	129H	II	0	1	Yes	In TADB	100	100	100
137P	HipA_C	38H	II	1	0	Yes	In TADB	100	100	100
139P	Bro- N	68H	II	0	1	No	None	100	100	100
140P	HD	89H	II	1	0	No	None	100	100	100
141P	ParE_toxin	141H	II	1	0	Yes	In TADB	100	100	100
143P	CcdB	18H	II	0	1	No	toxin domain	100	100	100
151P	YdaT_toxin	110H	II	1	0	No	antitoxin	100	100	100
153P	Peptidase_M78	132H	II	1	0	No	DNA binding	100	100	100
155P	RelE	33H	II	1	0	No	consensus disorder prediction	100	100	100
156P	Zeta_toxin	111H	II	1	0	No	ABC transporter	100	100	100
158P	PemK_toxin	131H	II	0	1	No	None	100	100	100
159P	CcdB	103H	II	1	0	No	antitoxin	100	100	100
161P	ANT	98H	II	1	0	No	Endodeoxyribonuclease	100	100	100
162P	DUF4258	146H	II	0	1	No	None	100	100	100
165P	YafO_toxin	138H	II	1	0	No	None	100	100	100
167P	DUF3749	81H	II	0	1	No	consensus disorder prediction	100	100	100
169P	RES	101H	II	0	1	No	None	100	100	100
170P	CbtA_toxin	45H	IV	0	1	No	None	100	100	100
171P	PemK_toxin	2H	II	0	1	No	None	100	100	100
172P	HicA_toxin	85H	II	0	1	No	antitoxin	100	100	100
174P	CbtA_toxin	70H	IV	1	0	No	antitoxin	100	100	100
175P	Gp49	6H	II	1	0	No	consensus disorder prediction	100	100	100

176P	YdaT_toxin	23H	II	1	0	No	None	100	100	100
178P	PemK_toxin	131H	II	0	1	No	None	100	100	100
180P	ANT	59H	II	1	0	No	prophage	100	100	100
182P	YdaT_toxin	29H	II	0	1	No	None	100	100	100
187P	PemK_toxin	105H	II	1	0	Yes	In TADB	100	100	100
189P	ParE_toxin	82H	II	0	1	No	None	100	100	100
191P	DUF488	102H	II	1	0	No	consensus disorder prediction	100	100	100
194P	HD	120H	II	1	0	No	None	100	100	100
201P	Fic	64H	II	0	1	No	None	100	100	100
204P	PIN	4H	II	0	1	No	None	100	100	100
205P	DUF4111	20H	II	1	0	No	None	100	100	100
206P	HicA_toxin	121H	II	1	0	No	DUF	100	100	100
208P	HigB-like_toxin	92H	II	0	1	No	None	100	100	100
209P	HigB-like_toxin	41H	II	0	1	No	None	100	100	100
212P	PIN	21H	II	0	1	No	toxin domain	100	100	100
213P	YdaT_toxin	36H	II	0	1	No	None	100	100	100
217P	CbtA_toxin	69H	IV	0	1	No	None	100	100	100
218P	YdaT_toxin	56H	II	0	1	No	None	100	100	100
219P	DUF488	128H	II	0	1	No	None	100	100	100
220P	Fic	130H	II	0	1	No	None	100	100	100
221P	YdaT_toxin	23H	II	1	0	No	None	100	100	100
223P	DUF4111	20H	II	0	1	No	None	100	100	100
224P	ParE_toxin	136H	II	1	0	Yes	In TADB	100	100	100
225P	ParE_toxin	94H	II	1	0	No	None	100	100	100

227P	AbiEii	106H	IV	1	0	No	None	100	100	100
228P	ParE_toxin	145H	II	1	0	No	None	100	100	100
229P	PIN	43H	II	1	0	Yes	In TADB	100	100	100
230P	Fic	117H	II	1	0	No	None	100	100	100
231P	RES	3H	II	0	1	No	None	100	100	100
233P	HipA_C	60H	II	1	0	No	None	100	100	100
234P	CbtA_toxin	45H	IV	0	1	No	None	100	100	100
235P	HigB-like_toxin	76H	II	0	1	No	antitoxin	100	100	100
236P	HD	10H	II	0	1	No	None	100	100	100
237P	CbtA_toxin	70H	IV	0	1	No	None	100	100	100
238P	PIN	4H	II	0	1	No	None	100	100	100
239P	PemK_toxin	148H	II	0	1	No	None	100	100	100
240P	PIN	4H	II	0	1	No	None	100	100	100
241P	HicA_toxin	104H	II	1	0	No	None	100	100	100
242P	CcdB	147H	II	1	0	Yes	In TADB	100	100	100
243P	HD	142H	II	0	1	No	toxin domain	100	100	100
244P	Couple_hipA	27H	II	0	1	No	None	100	100	100
245P	PemK_toxin	100H	II	1	0	No	None	100	100	100
246P	HicA_toxin	104H	II	0	1	Yes	In TADB	100	100	100
247P	DUF4111	135H	II	1	0	No	consensus disorder prediction	100	100	100
25P	HipA_C	91H	II	1	0	No	None	100	100	100
53P	YafQ_toxin	127H	II	1	0	Yes	In TADB	100	100	100
56P	Gp49	58H	II	0	1	Yes	In TADB	100	100	100
59P	HipA_C	27H	II	0	1	No	None	100	100	100

71P	YafO_toxin	134H	II	1	0	No	None	100	100	100
75P	CbtA_toxin	45H	IV	1	0	No	None	100	100	100
79P	ParE_toxin	62H	II	0	1	No	None	100	100	100
82P	Fic	97H	II	1	0	Yes	In TADB	100	100	100
84P	CbtA_toxin	47H	IV	0	1	No	None	100	100	100
85P	AHSA1	143H	II	1	0	No	consensus disorder prediction	100	100	100
89P	HipA_C	137H	II	0	1	No	DNA binding	100	100	100
90P	YafO_toxin	95H	II	1	0	No	consensus disorder prediction	100	100	100
97P	ANT	59H	II	0	1	No	None	100	100	100



## D Identified orphan antitoxin groups

ID	Total Orphans	<i>K. pneumoniae sensu stricto</i>	<i>K. quasipneumoniae</i>	<i>K. variicola</i>	Predicted function	Original Toxin Domain	Toxin type
104P	1	0	1	0	antitoxin	YdaT_toxin	II
106P	59	58	1	0	None	RES	II
107P	34	30	3	1	prophage	Bro-N	II
109P	3	3	0	0	regulation of transcription	Bro-N	II
10P	2	2	0	0	consensus disorder prediction	PIN	II
114P	10	5	5	0	DNA binding	YdaT_toxin	II
115P	36	0	19	17	None	PemK_toxin	II
118P	135	135	0	0	None	Bro-N	II
11P	1	1	0	0	ABC transporter	Zeta_toxin	II
120P	2	1	1	0	None	Bro-N	II
124P	248	219	15	14	consensus disorder prediction	Fic	II
126P	1	0	1	0	None	YdaT_toxin	II
127P	28	8	19	1	In TADB	ParE_toxin	II
128P	8	6	0	2	DUF	DUF488	II
129P	2	0	2	0	None	Fic	II
12P	11	10	0	1	DUF	DUF3749	II
132P	5	5	0	0	None	CbtA_toxin	IV
134P	6	6	0	0	In TADB	Gp49	II
136P	47	47	0	0	None	Bro-N	II
137P	2	2	0	0	In TADB	HipA_C	II

139P	8	4	4	0	None	Bro-N	II
13P	25	21	4	0	In TADB	RES	II
142P	2	2	0	0	None	PemK_toxin	II
143P	110	109	0	1	toxin domain	CcdB	II
144P	2	1	1	0	None	Bro-N	II
146P	3	3	0	0	None	PemK_toxin	II
14P	2	2	0	0	In TADB	HigB_toxin	II
150P	13	12	0	1	Endodeoxyribonuclease	AntA	II
156P	30	27	0	3	ABC transporter	Zeta_toxin	II
15P	1	1	0	0	Ubiquitin	Polyketide_cyc2	II
160P	3	3	0	0	DNA integration	ParE_toxin	II
161P	77	69	2	6	Endodeoxyribonuclease	ANT	II
162P	4	4	0	0	None	DUF4258	II
166P	8	8	0	0	None	AbiEii	IV
167P	37	32	0	5	consensus disorder prediction	DUF3749	II
16P	1	1	0	0	In TADB	HigB_toxin	II
172P	1	1	0	0	antitoxin	HicA_toxin	II
173P	3	3	0	0	Glutamine amidotransferase	Fic	II
181P	21	19	2	0	None	DUF488	II
184P	195	179	0	16	None	AbiEii	IV
185P	6	2	2	2	toxin domain	CbtA_toxin	IV
188P	1	1	0	0	regulation of transcription	AbiEii	IV
191P	1	1	0	0	consensus disorder prediction	DUF488	II
194P	4	4	0	0	None	HD	II
195P	6	5	0	1	None	HD	II

19P	1	0	0	1	In TADB	RelE	II
1P	10	9	0	1	None	ParE_toxin	II
202P	12	12	0	0	None	HD_3	II
204P	4	2	0	2	None	PIN	II
205P	2	2	0	0	None	DUF4111	II
206P	1	1	0	0	DUF	HicA_toxin	II
207P	3	3	0	0	None	DUF4111	II
212P	1	0	0	1	toxin domain	PIN	II
214P	1	1	0	0	None	ParE_toxin	II
21P	42	42	0	0	None	CcdB	II
224P	2	2	0	0	In TADB	ParE_toxin	II
225P	2	2	0	0	None	ParE_toxin	II
22P	8	7	0	1	In TADB	PemK_toxin	II
231P	123	114	6	3	None	RES	II
233P	1	1	0	0	None	HipA_C	II
236P	1	0	0	1	None	HD	II
238P	6	5	1	0	None	PIN	II
23P	1	1	0	0	None	ParE_toxin	II
243P	2	2	0	0	toxin domain	HD	II
244P	1	1	0	0	None	Couple_hipA	II
246P	5	5	0	0	In TADB	HicA_toxin	II
24P	17	16	0	1	In TADB	HipA_C	II
26P	2	1	1	0	DUF	AntA	II
29P	1	1	0	0	In TADB	NTP_transf_2	II
30P	2	2	0	0	DNA binding	Gp49	II

32P	7	6	1	0	None	HD	II
34P	2	2	0	0	In TADB	Fic	II
35P	1	1	0	0	In TADB	Cpta_toxin	II
36P	6	5	0	1	In TADB	RelE	II
38P	2	2	0	0	antitoxin	CbtA_toxin	IV
39P	92	80	9	3	DNA binding	HigB_toxin	II
3P	1	0	0	1	In TADB	Fic	II
40P	4	4	0	0	DUF	DUF4111	II
43P	1	1	0	0	None	Fic	II
45P	45	45	0	0	In TADB	HicA_toxin	II
49P	2	0	2	0	antitoxin	CbtA_toxin	IV
4P	10	10	0	0	None	ParE_toxin	II
51P	2	2	0	0	None	PIN	II
58P	123	123	0	0	None	CcdB	II
59P	251	214	19	18	None	HipA_C	II
60P	1	1	0	0	DNA binding	DUF955	II
62P	1	1	0	0	consensus disorder prediction	AntA	II
63P	8	0	0	8	None	Zeta_toxin	II
66P	80	72	8	0	None	DUF4111	II
68P	2	0	2	0	None	YdaT_toxin	II
6P	4	4	0	0	In TADB	PIN	II
70P	1	0	1	0	None	Gp49	II
73P	16	13	3	0	None	RelE	II
74P	1	1	0	0	antitoxin	CbtA_toxin	IV
75P	12	7	4	1	None	CbtA_toxin	IV

76P	18	18	0	0	consensus disorder prediction	YdaT_toxin	II
77P	2	0	1	1	None	Gp49	II
78P	1	1	0	0	In TADB	Gp49	II
79P	60	52	6	2	None	ParE_toxin	II
7P	11	9	2	0	In TADB	ParE_toxin	II
80P	1	0	1	0	antitoxin	YdaT_toxin	II
89P	18	0	0	18	DNA binding	HipA_C	II
91P	4	3	1	0	prophage	AntA	II
92P	5	5	0	0	None	RES	II
9P	2	1	1	0	None	RelE	II

## E Summary of *E. coli* PopPUNK Clusters

PopPUNK Cluster	Genomes	Median Length	Median Genes	Phylo-group	Isolation	Continents	STs	Pathotypes	MDR
1	3266	5.37	5064	E	unknown/ other (0.97); faeces (0.03)	Europe (0.94); North America (0.05)	11 (0.93); 11~ (0.03)	aEPEC/ EPEC (0.05); EHEC (0.95)	No
2	781	5.16	4844	B2	faeces (0.36); blood (0.31); urine (0.24); unknown/ other (0.1)	Europe (0.73); nd (0.12); North America (0.11); Oceania (0.03)	131 (0.99)	ExPEC (0.54); ND (0.46)	Yes
3	463	5.13	4738	B2	blood (0.7); unknown/ other (0.17); urine (0.12)	Europe (0.85); North America (0.11); nd (0.03)	73 (0.93)	ExPEC (0.83); ND (0.16); STEC (0.01)	No
4	363	5.13	4814	B2	blood (0.61); unknown/ other (0.17); urine (0.13); faeces (0.08)	Europe (0.75); North America (0.22)	95 (0.79); 416 (0.07); 421 (0.03); 95~ (0.03)	ExPEC (0.75); EXPEC (0.01); ND (0.24)	No
5	237	5.42	5195	B1	unknown/ other (0.69); faeces (0.31)	North America (0.63); Europe (0.33)	17 (0.78); 1967 (0.11); 386 (0.04); 17~ (0.03)	aEPEC/ EPEC (0.04); EHEC (0.95); STEC (0.01)	No
6	239	5.55	5347	B1	unknown/ other (0.59); faeces (0.41)	North America (0.67); Europe (0.31)	21 (0.87); 29 (0.08)	aEPEC/ EPEC (0.04); EHEC (0.94); STEC (0.01)	No
7	174	5.26	4924.5	D	blood (0.72);	Europe (0.83);	69 (0.94);	EAEC (0.02); ExPEC	Yes

					unknown/ other (0.2); urine (0.07)	North America (0.12); nd (0.05)	106 (0.03)	(0.79); EXPEC (0.01); ND (0.19)	
8	146	5.47	5178.5	B1	unknown/ other (0.79); faeces (0.21)	Europe (0.75); North America (0.25)	442 (0.85); 442~ (0.06); 7714 (0.05)	ND (0.06); STEC (0.94)	No
9	124	5.38	5118	B1	unknown/ other (0.99)	Europe (0.98); North America (0.02)	33 (0.84); 33~ (0.13)	ND (0.02); STEC (0.98)	No
10	104	5.29	4987	E	unknown/ other (0.89); faeces (0.11)	Europe (0.74); North America (0.24)	32 (0.87); 137 (0.08); 32~ (0.04)	aEPEC/ EPEC (0.1); EHEC (0.9)	No
11	106	5.12	4740	B2	blood (0.48); urine (0.34); unknown/ other (0.16)	Europe (0.71); North America (0.27)	127 (0.91); 5337 (0.03)	EAEC (0.01); ExPEC (0.83); EXPEC (0.02); ND (0.14)	No
12	92	4.87	4540	A	unknown/ other (0.7); faeces (0.21); blood (0.05); urine (0.04)	Europe (0.73); Africa (0.11); North America (0.07); South America (0.05); Asia (0.02); nd (0.02)	10 (0.76); 43 (0.08); 4305 (0.05); 5353 (0.03); 10~ (0.02)	aEPEC/ EPEC (0.24); EAEC (0.29); EAEC+STEC (0.02); ETEC (0.01); ExPEC (0.11); ND (0.24); STEC (0.1)	No
13	110	5.16	4801.5	B2	blood (0.65); unknown/ other (0.18); urine (0.15)	Europe (0.78); North America (0.16); nd (0.04)	12 (0.92)	ExPEC (0.81); ND (0.19)	No
14	109	5.30	5090	B1	unknown/ other (0.7); faeces (0.3)	North America (0.72); Europe (0.27)	16 (0.93)	EHEC (0.98); STEC (0.02)	No

15	89	5.46	5148	B1	unknown/ other (0.99)	Europe (0.99)	25 (0.65); 25~ (0.1); 4748 (0.09); 811 (0.09); 6265~ (0.02)	ND (0.33); STEC (0.67)	No
16	62	5.34	4995.5	E	unknown/ other (0.79); faeces (0.21)	Europe (0.87); North America (0.06); Asia (0.05)	335 (0.95); 7444 (0.03)	aEPEC/ EPEC (0.26); EHEC (0.62); STEC (0.11)	Yes
17	79	5.19	4884	B2	blood (0.58); unknown/ other (0.29); urine (0.11)	Europe (0.77); North America (0.18); nd (0.05)	14 (0.29); 404 (0.29); 1193 (0.18); 550 (0.15); 1057 (0.06); 5669 (0.03)	ExPEC (0.7); ND (0.29); STEC (0.01)	Yes
18	55	5.05	4889	U	unknown/ other (1)	Europe (1)	504 (0.53); 5292 (0.24); 6880 (0.13); 504~ (0.07)	STEC (1)	Yes
19	66	5.18	4767.5	D	blood (0.76); unknown/ other (0.12); urine (0.09); faeces (0.03)	Europe (0.68); North America (0.24); nd (0.05); Africa (0.03)	393 (0.8); 31 (0.11); 1394 (0.03)	EAEC (0.12); ExPEC (0.85); ND (0.03)	Yes
20	48	5.00	4657	B2	blood (0.48); unknown/ other (0.27); urine (0.23); faeces (0.02)	Europe (0.75); North America (0.12); nd (0.1); Oceania (0.02)	131 (0.94); 131~ (0.02); 5432 (0.02); 5494 (0.02)	ExPEC (0.71); ND (0.29)	Yes



21	70	5.39	5078	B1	faeces (1)	North America (1)	392 (0.67); 5738 (0.33)	ND (1)	No
22	46	5.21	5017	B1	unknown/ other (0.87); faeces (0.13)	Europe (0.76); North America (0.24)	300 (0.57); 343 (0.2); 4942 (0.09); 300~ (0.07); 5343 (0.04); 343~ (0.02); 6668 (0.02)	aEPEC/ EPEC (0.2); EHEC (0.8)	No
23	42	5.03	4767	A	unknown/ other (0.98); faeces (0.02)	Europe (0.93); nd (0.05); Africa (0.02)	6 (0.86); 6~ (0.12); 8300 (0.02)	EIEC (1)	No
24	45	5.23	4895	B1	unknown/ other (0.84); faeces (0.16)	Europe (0.89); North America (0.07); Africa (0.02); Asia (0.02)	678 (0.84); 678~ (0.16)	EAEC (0.62); EAEC+STEC (0.38)	Yes
25	49	5.09	4728	B2	blood (0.51); unknown/ other (0.43); urine (0.06)	Europe (0.76); North America (0.14); nd (0.1)	141 (0.71); 998 (0.2); 8290 (0.04); 141~ (0.02); 998~ (0.02)	ExPEC (0.58); ND (0.4); STEC (0.02)	No
26	44	5.06	4751.5	B1	faeces (0.66); unknown/ other (0.34)	Europe (0.39); Asia (0.32); Africa (0.3)	517 (0.8); 5241 (0.11); 517~ (0.07); 5485 (0.02)	aEPEC/ EPEC (0.93); EHEC (0.05); EPEC/ ETEC (0.02)	Yes
27	27	4.95	4738	B2	unknown/ other (0.89);	Europe (0.93); Africa (0.04);	583 (0.89); 122 (0.07);	aEPEC/ EPEC (0.33); EHEC (0.67)	No

					faeces (0.11)	North America (0.04)	7703 (0.04)		
28	42	5.19	4852.5	A	unknown/ other (1)	Europe (0.95); North America (0.05)	10 (0.86); 10~ (0.14)	ND (0.1); STEC (0.9)	No
29	40	5.19	4865	B2	blood (0.7); unknown/ other (0.2); faeces (0.05); urine (0.05)	Europe (0.85); North America (0.12); South America (0.02)	144 (0.95); 5346 (0.02); 703 (0.02)	ExPEC (0.75); ND (0.25)	No
30	41	4.28	4231	<i>S. sonnei</i>	unknown/ other (0.88); faeces (0.12)	nd (0.98); Europe (0.02)	245 (0.73); 1024 (0.17); 631 (0.05); 1753 (0.02); 5233 (0.02)	EIEC (0.22); ND (0.78)	No
31	36	5.28	4987.5	F	blood (0.67); unknown/ other (0.22); faeces (0.08); urine (0.03)	Europe (0.69); North America (0.28); Oceania (0.03)	62 (0.97); 1810 (0.03)	ExPEC (0.74); EXPEC (0.03); ND (0.24)	No
32	26	5.25	4931.5	B1	unknown/ other (0.88); faeces (0.08); urine (0.04)	Europe (0.88); Asia (0.04); North America (0.04); South America (0.04)	200 (1)	EAEC (0.92); ETEC / EAEC (0.04); ExPEC (0.04)	Yes
33	35	5.19	4948	F	blood (0.49); unknown/ other (0.46); urine (0.06)	Europe (0.89); North America (0.09); South America (0.03)	59 (0.94); 415 (0.03); 415~ (0.03)	ExPEC (0.56); ND (0.41); STEC (0.03)	No

34	34	5.13	4888	B1	faeces (0.88); unknown/other (0.12)	Africa (0.59); Asia (0.21); Europe (0.15); South America (0.06)	328 (0.79); 328~ (0.18); 5618 (0.03)	aEPEC/ EPEC (0.85); EPEC/ ETEC (0.15)	Yes
35	22	4.97	4653	A	unknown/other (0.95); faeces (0.05)	Europe (0.95); South America (0.05)	34 (0.91); 34~ (0.05); 8053 (0.05)	EAEC (1)	Yes
36	24	5.34	4987	B1	unknown/other (1)	Europe (1)	675 (0.79); 675~ (0.12); 180~ (0.04); 7953 (0.04)	STEC (1)	No
37	27	5.33	4960	D	blood (0.74); unknown/other (0.15); urine (0.07); faeces (0.04)	Europe (0.63); North America (0.33); Asia (0.04)	405 (0.96); 964 (0.04)	ETEC (0.04); ExPEC (0.85); ND (0.08); STEC (0.04)	Yes
38	27	5.26	4973	F	unknown/other (0.81); blood (0.07); urine (0.07); faeces (0.04)	Europe (0.52); nd (0.41); North America (0.07)	59 (0.93); 2618 (0.04); 59~ (0.04)	ExPEC (0.16); ND (0.84)	No
39	29	5.26	4994	B1	unknown/other (0.76); faeces (0.24)	North America (0.59); Europe (0.31); Asia (0.07); South America (0.03)	655 (1)	aEPEC/ EPEC (0.03); EHEC (0.97)	No
40	28	4.85	4551	C	blood (0.57); faeces (0.21); unknown/	Europe (0.64); North America (0.25); Asia	23 (0.39); 410 (0.32); 2230	ETEC (0.18); ExPEC (0.57); ND (0.04); STEC (0.21)	Yes

					other (0.21)	(0.07); South America (0.04)	(0.07); 369 (0.07); 5491 (0.07); 23~ (0.04); 5286 (0.04)		
41	26	5.20	4825	B2	blood (0.73); urine (0.15); unknown/ other (0.12)	Europe (0.96); North America (0.04)	80 (0.88); 5351 (0.04); 5384 (0.04); 5609 (0.04)	ExPEC (0.88); ND (0.12)	No
42	27	4.89	4564	B1	faeces (0.81); unknown/ other (0.15); blood (0.04)	North America (0.85); Europe (0.15)	297 (0.96); 297~ (0.04)	ExPEC (0.04); ND (0.96)	No
43	27	4.63	4274	B1	faeces (1)	North America (1)	906 (1)	ND (1)	No
44	25	5.37	4995	F	blood (0.48); unknown/ other (0.28); urine (0.24)	Europe (0.4); nd (0.4); North America (0.2)	648 (1)	ExPEC (0.72); ND (0.28)	Yes
45	26	4.69	4532.5	<i>S. flexneri</i>	unknown/ other (0.96); faeces (0.04)	nd (0.85); Europe (0.15)	152 (0.96); 1502 (0.04)	EIEC (0.35); ND (0.65)	No
46	26	5.40	5040	D	blood (0.5); unknown/ other (0.27); faeces (0.19); urine (0.04)	Europe (0.69); nd (0.12); South America (0.12); North America (0.08)	405 (0.88); 38~ (0.04); 402~ (0.04); 5377 (0.04)	ExPEC (0.54); ND (0.46)	No
47	23	4.94	4614	B2	blood (0.78); unknown/ other (0.22)	Europe (0.96); nd (0.04)	357 (1)	ExPEC (0.78); ND (0.22)	No

48	21	5.32	5180	B1	faeces (0.81); unknown/other (0.19)	Africa (0.38); Asia (0.29); Europe (0.19); nd (0.05); North America (0.05); South America (0.05)	3 (0.9); 3~ (0.05); 5326 (0.05)	aEPEC/ EPEC (1)	Yes
49	23	5.45	5213	B1	faeces (1)	North America (1)	154 (1)	ND (1)	No
51	22	4.95	4575	D	faeces (1)	North America (0.91); South America (0.09)	501 (1)	EAEC (0.05); ND (0.95)	No