Supplemental Table S1. Hybridization of strains to all microarray probes

Index	Class	Name	Accession No. or gi|annotation	Seq 5' to 3'	ID	SE LT2	SE CT18	SE Tc JF201	SE Hd JF210	EC JF220	EC JF227	CC 14-22	CC 141-27	ECF ATCC25788	EGM ATCC49573	LI03	LI04	MRSA G10-C87-2	MRSA DN	MRSA36-1	MRSA59	CD 70	CD 98	CD 112	CD 113
60	(-) control	(-) control		CTAGATCGACCTAGATCGACCTAGATCGACCTAGATCGACCTAGATCGACCTAGATCGACCTAGATCGAC	AR1-0109	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
48	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1
49	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
107	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
108	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
109	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
167	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
168	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
169	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
227	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
228	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
229	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
469	(-) control	50%dmso			50%dmso	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
60	(-) control	(-) control	control 1	CTAGATCGACCTAGATCGACCTAGATCGACCTAGATCGACCTAGATCGACCTAGATCGACCTAGATCGAC	AR1-0109	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
47	(+) control	16S-1333 14	NC 000913	AGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATACGT	16S-1333 1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
409	(+) control	16S-507 576	NC 000913	CTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAA	16S-507 57	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
226	(+) control	16S-93 162	NC 000913	TGCTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGAT	16S-93 162	2	2	2	2	2	2	1	1	2	2	2	2	1	1	1	1	2	1	2	2
455	Aminoglycoside	yedO	gi|46371981	ACTGTGGGTGAAGCGCGACGATGCCGTGGGCCCTGCCATGGGCGGCAACAAGACTCGCAAGCTCGAATTC	AR2-2-0518	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	Aminoglycoside	strB	gi|17739641	GTTTACGAACTGACGCGCAAGGACGGCTCCCTTGCCATTGCCAAGGTTCTGAAAAAGAAGGTGCTGAAAG	AR2-1-0192	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
24	Aminoglycoside	putative st	gi|27884638	GATCGACCCCAAGCGGGTCATGGGCGAGCGTGGCTACGACTTTGCCAACCTGATCTGCAACCCGGACCTG	AR2-1-0308	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
28	Aminoglycoside	strA	gi|37962716	GATATGGTTGTTTGCCATGGTGATCCCTGCATGCCGAACTTCATGGTGGACCCTAAAACTCTTCAATGCA	AR2-2-0391	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
36	Aminoglycoside	aacC2	gi|45769:81	CCGGTGACCTATTGATGGTGCATGCCTCACTTAAAGCGATTGGTCCGGTCGAAGGAGGAGCGGAGACGGT	AR2-2-0495	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
45	Aminoglycoside	ntpII	gi|8346637	GTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTCCAAGACGAGGCAGCGCGGCTATCGT	AR2-2-0675	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
52	Aminoglycoside	aadA2*	Salmonella	CTAGATCGACAAAACGCCTACCTGCCCAGTATCAGCCCGTCTTACTTGAAGCTAAGCAAGCTTATCTGGGACAAAAAGAA	AR1-0005	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
54	Aminoglycoside	aadA7	AY458224	CTAGATCGACGATCTCTTCAGCTCAGTCCCAGAAAGCGATCTATTCAAGGCACTGGCCGATACTCTGAAGCTATGGAACT	AR1-0013	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
55	Aminoglycoside	strB	AY055428	CTAGATCGACTCATTGCCAGACGGGACTCCTGCAATCGTCAAGGGATTGAAACCTATAGAAGACATTGCTGATGAACTGC	AR1-0017	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
56	Aminoglycoside	aadA2*	AY103460	CTAGATCGACAAAACGCCTACCTGCCCAGTATCAGCCCGTCTTACTTGAAGCTAAGCAAGCTTATCTGGGACAAAAAGAA	AR1-0021	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
58	Aminoglycoside	aac(6)-Ib*	AF439786	CTAGATCGACCCTCATGACTGAGCATGACCTTGCGATGCTCTATGAGTGGCTAAATCGATCTCATATCGTCGAGTGGTGG	AR1-0101	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
97	Aminoglycoside	aac (6)	gi|46371950	TTTTCTCCCTGACACGTGATAACGAACACCTCATTCATCAAGCTGCCCAACTTCTAATGGACGCGTTCCA	AR2-2-0500	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
111	Aminoglycoside	aadB	AY204504	CTAGATCGACTACTTTTACTATGCCGATGAAGTACCACCAGTGGACTGGCCTACAAAGCACATAGAGTCCTACAGGCTCG	AR1-0002	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
115	Aminoglycoside	strA*	AY055428	CTAGATCGACTTTTTGGTGAATCGCATTCTGACTGGTTGCCTGTCAGAGGCGGAGAATCTGGTGATTTTGTTTTTCGACG	AR1-0018	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
116	Aminoglycoside	aac(6)-Ib*	AY103455	CTAGATCGACCCTCATGACTGAGCATGACCTTGCGATGCTCTATGAGTGGCTAAATCGATCTCATATCGTCGAGTGGTGG	AR1-0022	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
118	Aminoglycoside	aadA1b	AJ62853	CTAGATCGACAGGTATCTTCGAGCCAGCCACGATCGACATTGATCTGGCTATCTTGCTGACAAAAGCAAGAGAACATAGC	AR1-0102	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
131	Aminoglycoside	ksgA	gi|146570:1	CGATGACCTTTAACTTTGGTGAACTGGCCGAGAAAATGGGTCAGCCGCTGCGTGTTTTCGGCAACCTGCC	AR2-1-0114	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
134	Aminoglycoside	strB	gi|18693100	TGAAACCTATAATCGCCTTGACGATATTAACCTTGATAGCCATAACCACTCCATACGGTTGCTCAACACA	AR2-1-0198	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
135	Aminoglycoside	strA	gi|1943584	GCGGGAGGGCGGCCGGGTGGACCCTGGCCCGGCTCCTGGAGAACACCCTGTGGGACATCGAGGACGGGCT	AR2-1-0202	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
138	Aminoglycoside	aadA2	gi|21483840	TCAGCCCGTCTTACTTGAAGCTAAGCAAGCTTATCTGGGACAAAAAGAAGATCACTTGGCCTCACGCGCA	AR2-1-0214	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
143	Aminoglycoside	aadA21	gi|27368134	GTAGCGGTGACCATCGAAATTTCGAACCAACTATCAGAGGTGCTAAGCGTCATTGAGCGCCATCTGGAAT	AR2-1-0306	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
152	Aminoglycoside	kac	gi|44886009	GATGTGAAGAAGCTCGACAAGATCGTCAGAGAACCCGAGGTGGCCGCTTGGTGGTCGACCCCCGATGACT	AR2-2-0481	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
171	Aminoglycoside	aphAI	U13633	CTAGATCGACTGCTCGAGGCCGCGATTAAATTCCAACCTGGATGCTGATTTATATGGGTATAGATGGGCTCGCGATAATG	AR1-0003	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
179	Aminoglycoside	strA*	AJ628353	CTAGATCGACTTTTTGGTGAATCGCATTCTGACTGGTTGCCTGTCAGAGGCGGAGAATCTGGTGATTTTGTTTTTCGACG	AR1-0107	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
191	Aminoglycoside	aad9	gi|148301:2	GCCGTATGATTTTAACTATGGACACGGGTAAAATCATACCAAAAGATATTGCGGGAAATGCAGTGGCTGA	AR2-1-0115	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1
207	Aminoglycoside	aph(3)-I	gi|37962716	TTCGATTCCTGTTTGTAATTGTCCTTTTAACAGCGATCGCGTATTTCGTCTCGCTCAGGCGCAATCACGA	AR2-2-0390	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
211	Aminoglycoside	aac(3)-Id	gi|38490043	TCCATCTCACTGGAAACGATGTTGCGTTGTTGCAGTCAATAAATGCCATGTTCGGCGAGGCATTCAACGA	AR2-2-0406	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
212	Aminoglycoside	aacC3	gi|45264:11	CTTTGCTGACCGCTAATCACGCGCTGGATTATGGCTACGGAGTCGAGTCGCCGCTGGCTAAACTGGTGGC	AR2-2-0482	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
217	Aminoglycoside	glmS	gi|46371950	GCTGGTGAGCATACTCCCCGCTCAGTTATTTGCCTGCCACTTGACCACAGTCAAAGGGTACGATACTGAA	AR2-2-0502	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
222	Aminoglycoside	strB	gi|56236986	AATATGTTCTACGATCCGGCTGACAGAGACGACCTTTGTCTCGATCCTAGACGCATTGCACAGATGGCGG	AR2-2-0594	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
223	Aminoglycoside	aacA4	gi|56786619	CGATCCAGGAGTACGCGGAATAGACCAGTCACTGGCGAATGCATCACAACTGGGCAAAGGCTTGGGAACC	AR2-2-0598	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
224	Aminoglycoside	aacC1	gi|8346634	GCAGCCGCGTAGTGAGATCTATATCTATGATCTCGCAGTCTCCGGCGAGCACCGGAGGCAGGGCATTGCC	AR2-2-0674	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
231	Aminoglycoside	aadA1	NC 003198	CTAGATCGACTCATATCGTTTTAACCCTGGCGCGTATCTGGTACACCCTTTCTACCGGGAGATTTACCTCTAAGGATGCG	AR1-0004	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
233	Aminoglycoside	aac	AY458224	CTAGATCGACATTAAAAAACTCAAGGCTATAGGCGCAGCGCGTGGAGCTTATGTGATTTACGTCCAAGCTGATAAAGGCG	AR1-0012	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
236	Aminoglycoside	aac(6)-Ib*	X13542	CTAGATCGACAAGTCGCCTGGAAAACGGCATCAGAATACGATTCAAACGGCATTCTCGATTGCTTTGCTATCGAAGGAAA	AR1-0024	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
239	Aminoglycoside	acc(6)-Ib*	NC 004998	CTAGATCGACCCTCATGACTGAGCATGACCTTGCGATGCTCTATGAGTGGCTAAATCGATCTCATATCGTCGAGTGGTGG	AR1-0108	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
254	Aminoglycoside	aadE	gi|21886735	TATGGGAAGCATTATTTCTATGCCATCAATTGTTCAGGGCGGTATCCGGTGAGGTGGCGGAAAGGCTTCA	AR2-1-0220	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1
260	Aminoglycoside	aacA-aphD	gi|29539351	ATGCACGGTTTAGATTATACAGATATTAGTGAATGTACTATTGATAATAAACAAAATGTATTAGAAGAGT	AR2-1-0316	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
261	Aminoglycoside	putative st	gi|29540947	ATTAAAGTTTATGCTGGCGTTGTCAACGCTTTAGCCTCATGCCCTGAACCATCAGACGAGCACACACATG	AR2-1-0320	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
264	Aminoglycoside	aph(3)-I	gi|32455896	TGATGTTGGACGAGTCGGAATCGCAGACCGATACCAGGATCTTGCCATCCTATGGAACTGCCTCGGTGAA	AR2-1-0332	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
266	Aminoglycoside	aac(3)-Id	gi|38490043	GTGTCAGTCGAAATCATCCATCTCACTGGAAACGATGTTGCGTTGTTGCAGTCAATAAATGCCATGTTCG	AR2-2-0407	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
268	Aminoglycoside	aph	gi|39413:27	AAGAAGCTCCGGGATGCGAAAAGAATAGTCGATGAGAGCCTGGTGGACCCGGCCGATATAAAAGAGGAGT	AR2-2-0415	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
272	Aminoglycoside	aac(6)	gi|46371954	ACCTTGATGTTAGGGTCGGATGATCAGGATGAGATGACATCCCTCTCCGGCGTGGATCTGTATCCCGATC	AR2-2-0503	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
274	Aminoglycoside	aph(3)	gi|46371969	CTCCTGATGACCGAAATAACCGGCATTGATGCGACCAGTTTTGAGCATGATCCAGCGACGTGTGTGCGCT	AR2-2-0511	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
276	Aminoglycoside	aac(6)	gi|46371981	ATGATCCCTCAATTCACTATCTCGAATCTCCCCTCAGATGACACCGATGCCGTCGAGCAGTGCGCTGCGC	AR2-2-0519	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
278	Aminoglycoside	aadA2	gi|56786619	GCTGAGGGAAACCTTGAAGCTATGGAACTCGCAGCCCGACTGGGCCGGCGATGAGCGAAATGTAGTGCTT	AR2-2-0599	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
291	Aminoglycoside	aacC1	U04610	CTAGATCGACCCGCAGTGGCTCTCTATACAAAGTTGGGCATACGGGAAGAAGTGATGCACTTTGATATCGACCCAAGTAC	AR1-0025	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

310	Aminoglycoside	aminocyclit	gi|152944:2	GGCAGGGCGGACAAGTGGTATGACATTCCCTTCTGCGTCCGGTCGATCAGGGAGGATATCGGGGAAGAAC	AR2-1-0133	1	1	1	1	1	1	2	2	1	1	1	1	1	2	2	2	1	1	1	1
314	Aminoglycoside	sat4	gi|21886737	AACCGGTACGCTTATATAGAAGATATCGCCGTATGTAAGGATTTCAGGGGGCAAGGCATAGGCAGCGCGC	AR2-1-0221	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1
332	Aminoglycoside	orf1	gi|46371954	TGAGAAATTGGCCGAGGCATCTCCCTTTAGCGATCTTTATGTATCGTTGTCTTCGATTCTCGCGGGAGTC	AR2-2-0504	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
333	Aminoglycoside	aac(6)	gi|46371961	CCTGGGAACAGACGACGAGGATGGCATGACCTCCCTGGCGAATACTGAACCTTTATGAAAATCTATGGGAA	AR2-2-0508	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
334	Aminoglycoside	aac(3)	gi|46371972	CTACCGTGCTGGAGGGTGGGCGGCCGAAGCGCTACGAGTACGGCGAGACCGACCATTGCTGCGAGAACTT	AR2-2-0512	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
335	Aminoglycoside	aac(6)	gi|46371978	TGGCCGGCGTGGATTTGTACGACGGGCTTCCGGACAAAATCGCCAACATACGAAATCTTAAGCGTCATCC	AR2-2-0516	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
342	Aminoglycoside	aadA1	gi|57903205	TGGAACTCGCCGCCCGACTGGNCTGGCGATGANCGAAATGTAGTGCNTACGTTGTCCCNCATTTGGNACA	AR2-2-0616	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
351	Aminoglycoside	aph	X03364	CTAGATCGACTTCTTGAGCTTCTCGGGCAGACGGAACTAACCGTCAACAAAATCGGATATTCCGGAGATCACGTCTATCA	AR1-0026	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
354	Aminoglycoside	aadE	AF516335	CTAGATCGACGAAGCATTATTTCTATGCCATCAATTGTTCAGGGCGGTATCCGGTGAGGTGGCGGAAAGGCTTCATTATG	AR1-0038	1	1	2	1	2	2	1	1	1	1	1	1	1	2	2	2	1	1	1	1
373	Aminoglycoside	strA	gi|21684676	GCACCTCCGGGGCTGCGGGGTCTGGGAGAGATCGCCGGCGCCATGGTGGAGGAAGTTCCCTCCGCTGTCG	AR2-1-0218	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
374	Aminoglycoside	aphA-3	gi|21886737	GGCAGGGCGGACAAGTGGTATGACATTGCCTTCTGCATCCGGTCGATCAGGGAGGATATCGGGGAAGAAC	AR2-1-0222	1	1	1	1	1	1	2	2	1	1	1	1	1	2	2	2	1	1	1	1
392	Aminoglycoside	fabG	gi|46371954	AACAATGCCGCGATCTACGAAGATCATCCGATTGCAGATATTAGCTATGAAGCATGGCAAACAGCGTGGC	AR2-2-0505	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
393	Aminoglycoside	aac(6)	gi|46371963	AATGCTCGAAAGTGAGCGAATATGCCGGATTGCATTGGATGAACAAGGTCATTTGATCGGAATCATAGGC	AR2-2-0509	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
394	Aminoglycoside	clpP	gi|46371972	CACCTGCTTTATTGGGAAGCCTGATTCGATCGGGGTGTACCATTGCCGACGAACCCGCCAGGAGCTCCCC	AR2-2-0513	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
397	Aminoglycoside	aph	gi|47022:33	CCGGAAGTACCCGCACCACGAGTGGCACGCAGTGAACGAAGGAGACTCGGGCGCCTTCGTCTACCAGCTC	AR2-2-0525	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
399	Aminoglycoside	aph2	gi|57546753	GTCGTTGATCTACGCGAGTTGACCGTCGAGCGGGTGCAGGCGCCGGGCGGGCGCAGCAGCCTGGTCGTGC	AR2-2-0605	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
414	Aminoglycoside	sat4	AF516335	CTAGATCGACTTGGAACCGGTACGCTTATATAGAAGATATCGCCGTATGTAAGGATTTCAGGGGGCAAGGCATAGGCAGC	AR1-0039	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1
434	Aminoglycoside	aadA2	gi|21898656	ATACAGCGATATTGATTTGTTGGTTACTGTGGCCGTAAAGCTTGATGAAACGACGCGGCGAGCATTGCTC	AR2-1-0223	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
447	Aminoglycoside	aph	gi|39413:27	TCCGGAGATCACGTCTATCACGTGAAAGAGTACAGGGGCACCCCCGCATTTCTGAAAATCGCCCCCAGTG	AR2-2-0414	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1
453	Aminoglycoside	putative am	gi|46371969	TTCCGCCCTATTATGAAAACGAAAATCCCGCCTATCAACTCGAATGGAGTCCTGATGGCAAGTCTCTGGC	AR2-2-0510	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
474	Aminoglycoside	aphA-3	AF516335	CTAGATCGACCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTATACGAATAGCTTAGACAGCCGCTTAGCCGAA	AR1-0040	1	1	1	1	1	1	2	2	1	1	1	1	1	2	2	2	1	1	1	1
496	Aminoglycoside	aacA29b	gi|24209729	AGACATGACTTGGAAGAACTCCAAGGAATCAAGACCGGCTACATCGAAGGCCTTTATGTGGCCCCAAGCC	AR2-1-0252	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
498	Aminoglycoside	aadB	gi|24209736	GGAGGAGTTGGACTATGGATTCTTAGCGGAGATCGGGGATGAGTTACTTGACTGCGAACCTGCTTGGTGG	AR2-1-0260	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
510	Aminoglycoside	strA	gi|40796966	GGCTGCGGGGTCTGGGAGAGATCGCCGGCGCCATGGTGGAGGAAGTTCCCTCCGCTGTCGACTCGTTGGC	AR2-2-0447	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
518	Aminoglycoside	aac(3)-II	gi|58383237	TCCCCAACAAACGGTGGGTGACGTATGAGATGCCGATGCTTGGAAGAGACGGTGAAGTCGCCTGGAAAAC	AR2-2-0623	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
521	Aminoglycoside	strB	gi|58383237	CGGCTGACAGAGACGACCTTTGTCTCGATCCTAGACGCATTGCACAGATGGCGGACGCATTCTCGTGC	AR2-2-0635	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
553	Aminoglycoside	aacA4	gi|24209709	AACAGTACTTGCCAAGCGTTTTAGCGCAAGAGTCCGTCACTCCATACATTGCAATGCTGAATGGAGAGCC	AR2-1-0241	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
556	Aminoglycoside	orf1	gi|24209728	GAACATCCTTGGCTTCGTTCAAGGTCACGGGTTTAAAACCATGGTTCTTGCCAAGGTTTCAAACCACTCG	AR2-1-0253	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
558	Aminoglycoside	aadA1	gi|24209736	GGCTTGGTGAAACAACGCGGCGAGCTTTGATCAACGACCTTTTGGAAACTTCGGCTTCCCCTGGAGAGGG	AR2-1-0261	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
567	Aminoglycoside	aacA7	gi|40287459	CCAGATGGCACATGTCAAGAGCACCAGTCAGAGATCGCAGAATTTCTGTCCGGAAAAGTCGCCCGGCCTG	AR2-2-0436	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
570	Aminoglycoside	aacC2	gi|40878:91	GCGGAAGGCAATAACGGAGGCAATTCGAAAACTCGGAGTCCAAACCGGTGACCTGTTGATGGTGCATGCC	AR2-2-0448	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
574	Aminoglycoside	aadA	gi|47679407	AACGCGGCGAGCTTTGATCAACGACCTTTTGGAAACTTCGGCTTCCCCTGGAGAGAGCGAGATTCTCCGC	AR2-2-0536	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
581	Aminoglycoside	strA	gi|58383237	TGGTGGACCCTAAAACTCTTCAATGCACGGGTCTGATCGACCTTGGGCGGCTCGGAACAGCAGATCGCTA	AR2-2-0636	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
613	Aminoglycoside	orfE-like	gi|24209712	CTCTGTTCAAAAGGTTTTCAAGCCTTTTTGGGCTCCAGCGCTTGTGCGGCAAGCGCTACCAGCTATCATT	AR2-1-0242	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
614	Aminoglycoside	orfE-like	gi|24209718	TTTTTCATGGGCCGCGCACGTCTTCAAGGCTGGGCGCCCCTTTTTGGCCTTCGGGTCTAACTCTGCGGTC	AR2-1-0246	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
618	Aminoglycoside	aadA1	gi|24209736	CGGCCCGGTATCAGCCCGTCATACTTGAAGCTAGACAGGCTTATCTTGGACAAGAAGAAGATCGCTTGGC	AR2-1-0262	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
623	Aminoglycoside	strA (sph)	gi|32560421	TCGCCGGTGACCCCGGCTTCGACCTGTTGGCCCGCCCTGGACAGCCGGTGGGACGACATCGTCGCACAGCG	AR2-1-0354	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
627	Aminoglycoside	aphA7	gi|40287459	TGATGTTGGACGAGTCGGAATCGCAGACCGATACCAGGATCTTGCCATCCTATGGAACTGCCTCGGTGAG	AR2-2-0437	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
671	Aminoglycoside	putative am	gi|16262453	CGCCACACCGAAATTTCCTGTTCGGGCTGAATTCATCTATGGCGAATGGTTGCGGGAGGCCTTTGAATCC	AR2-1-0163	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
675	Aminoglycoside	aacA29b	gi|24209729	CAGACCTTGTGAAGCGTTTCTTGCGTGAGTCCGAGAAGTGGGCCCTAGAACAAGGGTGCAGCGCATTTGC	AR2-1-0251	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
677	Aminoglycoside	aadB	gi|24209736	TAACACGCAAGCACGATGATATTGATCTGACGTTTCCCGGCGAGAGGCGCGGCGAGCTCGAGGCAATAGT	AR2-1-0259	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
682	Aminoglycoside	strB	gi|32469306	ACTCCTGCAATCGTCAAGGGATTGAAACCTATAAAAGACATTGCTGATGAACTGCGCGGGGCCGACTATC	AR2-1-0351	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
690	Aminoglycoside	orfE	gi|41057060	ACTTATAGCAACATAGACATGTATTCAGCTAGGTCAAGTTCATTTACAGTAACTTATCATTATTCATACT	AR2-2-0450	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
693	Aminoglycoside	aadA5	gi|47679401	TGGTACAGCGCTTCAACTGGTCTCATTGCTCCTAAGGACGTTGCTGCCGCATGGGTATCGGAGCGTTTGC	AR2-2-0534	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
731	Aminoglycoside	strB	gi|16505740	ACTCCTGCAATCGTCAAGGGATTGAAACCTATAGAAGACATTGCTGATGAACTGCGCGGGGCCGACTATC	AR2-1-0184	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
733	Aminoglycoside	aacC1	gi|24209742	GCAGGCGCGTAGTGAGATCTATATCTATGATCTCGCAGTCTCCGGCGAGCACCGGAGGCAGGGCATTGCC	AR2-1-0264	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
762	Aminoglycoside	putative st	gi|6933872	ACACCTGCCGAATCAGCGTGTTCGAAGGAGCCGTCAAGGCGAAGGGGGATACAGACCTTACCTTCCACGC	AR2-2-0663	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
775	Aminoglycoside	sat4	AY043213	CTAGATCGACACTGACTGATTTGCCGTTGAAAGGTGATACTGTAGTCGGAAATGACGTGTGGTTTGGGCAAAATGTGACC	AR1-0089	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
793	Aminoglycoside	aacC1	gi|24209742	AGCCACCTACTCCCAACATCAGCCGGACTCCGATTACCTCGGGAACTTGCTCCGTAGTAAGACATTCATC	AR2-1-0265	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
796	Aminoglycoside	putative am	gi|24427855	GGGACGGCGCGGTGCGGCTGCTCGACCACGACCCGGCCACCGGCACGATGCTCCTGGAGCGTCTGGACGC	AR2-1-0277	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
808	Aminoglycoside	SAT-2	gi|42909:51	ACATTGTTGTGTCGCACACGCACCGAGGCAAAGGAGTCGCGCACAGTCTCATCGAATTTGCGAAAAAGTG	AR2-2-0464	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
822	Aminoglycoside	putative st	gi|6933872	ATTTATCCAAGAAAGCGAGCGTACACAATGGTCAACCCACCGCTTGATGCTCTCAATCCTGTGGGGACAG	AR2-2-0664	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
853	Aminoglycoside	putative am	gi|24413716	GAAGCAGACGAGAGATCATTCCGACCTCGATCTATGGGTGCCGGCCGTACATCTTGACCCGCTGTTCGTT	AR2-1-0266	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
864	Aminoglycoside	aac(3)-II	gi|37962716	GAAGTCGCCTGGAAAACGGCATCGGATTACGATTCAAACGGCATTCTCGATTGCTTTGCTATCGACAAGGAA	AR2-1-0382	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
880	Aminoglycoside	streptomyci	gi|6458129	AAAAGCAGGATACCAGGCTGCATTTTCCCGCTGCCGTCGCCCGTCAGCTGCTGGCCTCCCCGCAGGAAGT	AR2-2-0657	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
911	Aminoglycoside	strB	gi|17129524	ATCGTCAAGGGATTGAAACCTATAGAAGACATTGCTGATGAACTGCGCGGGGCCGACTATCTGGTATGGC	AR2-1-0187	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
913	Aminoglycoside	putative ac	gi|24413861	GACTTCTCCTACTACGACGACCCGGACGACGCGACCGCCTTCGAGACCCGCAACGTGCTCTACCACTACG	AR2-1-0267	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
918	Aminoglycoside	str	gi|2467210	TCAAGAAATTGTTCCAGATGACTCAAATTATTGGTTAAAAAAACCAACAGAACGAGAATTTTATGATTGC	AR2-1-0287	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
942	Aminoglycoside	aadA7	gi|7263132	CAGCCCATCCTGTTGAATGCCAAGCGGGCTTATCTTGGGCAAGAAGAAGATTATTTGCCCGCTCGTGCGG	AR2-2-0666	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
2	Beta-lactam	blaL2	gi|10242339	GGTGTTGGGCGAGGTACTGCAACCGGCTTCGCGGCAGCAGCTGGCCGACTGGCTGATCGACAACGAAACC	AR2-1-0004	1	1	2	2	2	2	1	2	1	2	1	1	1	1	1	1	1	1	2	1
9	Beta-lactam	blaZ	gi|142599:1	TTCGTGCGGGTGTACCAAAAGGATGGGAAGTAGCTGATAAAACAGGTGCAGGATCTTATGGAACAAGGAA	AR2-1-0104	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	Beta-lactam	ccrA	gi|143931:9	GTTATCAACAACCACAGGCAGCGTTGCTGGACACACCGATCAATGACGCACAAACGGAAATGCTGGTCA	AR2-1-0108	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	Beta-lactam	cfiA	gi|14625819	ACGCGAACCAGATGACGATAGACCTCGCCAAGGAAAAAGGGTTGCCCGTACCGGAACATGGATTCACCGA	AR2-1-0112	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
31	Beta-lactam	orfE	gi|38196031	TTCAAGGCAGTTATGGCTTAACGGTAGATGGAATTGTTGGTAGTCAACATGGAAAAAATTTGCATCTGC	AR2-2-0403	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1
37	Beta-lactam	AmpR	gi|45987:c1	TCGAGGCGTTCCGACAGGCCCATCCCCAGATCGACCTGAGGATCTCGACCAACAACAACCGGGTGGAGAT	AR2-2-0499	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
40	Beta-lactam	blaB3	gi|5453457	AAAGACACGGAAAGAAAGTGATCATGAATATTGCAACACACTCTCATGATGACCGTGCAGGAGGTTTGGA	AR2-2-0583	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
71	Beta-lactam	cfiA	gi|14625819	AAGAAAGGTGTCCAATCATACGCGAACCAGATGACGATAGACCTCGCCAAGGAAAAAGGGTTGCCCGTAC	AR2-1-0113	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
75	Beta-lactam	bla-SHV-36	gi|18958443	GGCATTGTCGCCCTGCTTGGCCCGAATAACAAAGCAGAGCGCATTGTGGTGATTTATCTGCGGGATACGC	AR2-1-0201	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
83	Beta-lactam	putative pe	gi|27316926	GGCCAATAAGCAAGTTGAAATATCTATGGCTGAATGGGATGTTATGAATATAATATGGGTAAAAAATCA	AR2-1-0305	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1
86	Beta-lactam	blaTEM1	gi|37962716	TGCTGCCATAACCATGAGTGATAACACTGCTGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAG	AR2-2-0384	1	2	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
91	Beta-lactam	orfD	gi|38196031	TATAAAAAGTTATGCTAACACAATTTTAGATTCAATTGAAAGAAGTTCAAGAGATTCAAATAACTACACT	AR2-2-0404	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
99	Beta-lactam	orf	gi|5420302	GGAACTGCCGTACATCTTCCTGGAGAAGGAGTACGGGCCCAACCGGTTCAGGACGGTGCGGCCGGAGCAG	AR2-2-0580	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
102	Beta-lactam	cfxA	gi|5566608	AACAAATGTTTTGACTGATAGCATTTCTCAAATTGTCTCAGCTTGTCCTGGCGAAATTGGTGTGGCGGTT	AR2-2-0592	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1

112	Beta-lactam	pse1	AB126603	CTAGATCGACTGTGGAGTGAGCATCAAGCCCCAATTATTGTGAGCATCTATCTAGCTCAAACACAGGCTTCAATGGCAGA	AR1-0006	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
120	Beta-lactam	cmy-2*	X91840	CTAGATCGACATATCGCCAATAACCACCCAGTCACGCAGCAAACGCTGTTTGAGCTAGGATCGGTTAGTAAGACGTTTAA	AR1-0001	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
130	Beta-lactam	cfiA	gi|14625801	TATGGTACCTTCCAACGGGATGATTGTTATCAACAACCACCAGGCAGCGTTGCTGGACACACCGATCAAT	AR2-1-0110	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
160	Beta-lactam	blaPER2	gi|54887461	ACTGCAGTATTCGGTGTCACACAGCGACAATGTGGCCTGCGATTTGTTATTTGAACTGGTGGGCGGGCCG	AR2-2-0585	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
165	Beta-lactam	ampH	gi|9662892	AGTACGTCGACCGTTTTGACTACGGCAACCGGGATCTCTCCGGCAATCCTGGCAAGCACGACGGTCTGAC	AR2-2-0677	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
172	Beta-lactam	tem	AJ634602	CTAGATCGACTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGAT	AR1-0007	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
175	Beta-lactam	oxa2	M95287	CTAGATCGACGCAGGCCACAATCAAGACCAAGATTTGCGATCAGCAATGCGGAATTCTACTGTTTGGGTGTATGAGCTAT	AR1-0019	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
190	Beta-lactam	cfiA	gi|14625817	ACTGGGTTACCTGCAAAGGAAAGGTGTCCAATCATACGCGAACCAGATGACGATAGACCTCGCCAAGGAA	AR2-1-0111	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
202	Beta-lactam	pEA28_04	gi|27228439	TTGGGAACCGGAGYTGAATGAAGCCATACCAAACGACGAGCGTGACACCMCGATGCCTGTAGCAATGGCA	AR2-1-0303	1	2	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
203	Beta-lactam	bla-FOX-2	gi|27392912	TCCAACCCCAGCATAGGCCTGTTTGGTCACCTGGCCGCAAATAGTCTGGGCCAGCCATTTGAGAAACTGA	AR2-1-0307	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
204	Beta-lactam	mecI	gi|27919193	TGCAAGTGCGAATTATATGATAGAAGAAATACAAATGCAAAAGGACTGGAGTCCAAAAACCATTCGTACA	AR2-1-0311	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1
216	Beta-lactam	AmpR	gi|45987:11	CGACCATGTTCATCTCGGATACGGACGCGGAGTTCGAGGTTCGCAACGAGGCGCTCAAAGATCTGGGTAG	AR2-2-0498	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
218	Beta-lactam	bla	gi|5403326	GTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGC	AR2-2-0578	1	2	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
219	Beta-lactam	blaB2	gi|5430711	TGGACGCAGTCTGTACACAATATTCAACAAAAGTTTTCCGGTGCTCAGTACGTTGTTGCAGGGCATGATG	AR2-2-0582	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
220	Beta-lactam	TEM-136	gi|55140585	GGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGT	AR2-2-0586	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
256	Beta-lactam	oxa10	gi|21898660	GTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAGCAATGGGAAAGAGACTTGACCTTAAGAGGGGCAA	AR2-1-0228	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
262	Beta-lactam	shv-44	gi|32442314	GGGATTGTCGCCCTGCTTGGCCCGAATAACAAAGCAGAGCGCATCGTGGTGATTTATCTGCGGGATACGC	AR2-1-0324	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
295	Beta-lactam	mecA	AY271717	CTAGATCGACAATTGGCAAATCCGGTACTGCAGAACTCAAAATGAAACAAGGAGAAACTGGCAGACAAATTGGGTGGTTT	AR1-0041	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1	1
301	Beta-lactam	bla-OXA26	gi|11493693	AGTGGATGGGGAATGGGTGTTACTCCACAGGTAGGTTGGTTGACTGGTTGGGTGGAGCAAGCTAATGGAA	AR2-1-0025	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
303	Beta-lactam	bla-OXA27	gi|12060144	TGAAGCTTTCTGCAGTCCCAGTCTATCAGGAACTTGCGCGACGTATCGGTCTTGATCTCATGCAAAAAGA	AR2-1-0033	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
313	Beta-lactam	blaP	gi|216842:2	GGCGGATTTGGTGCTCGGAGTATTACAGCAGTTGTGTGGAGTGAGCATCAAGCCCCAATTATTGTGAGCA	AR2-1-0217	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
321	Beta-lactam	PBP-1A	gi|29692095	TGATCTGGTTTGGGAGAGACGATAACACGCCTATTAGCAAAGGAGCGACAGGAGGCGTTGTGAGCGCGCC	AR2-1-0321	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
328	Beta-lactam	putative be	gi|39417:27	CGTGCAGGCATACCAACTGACTGGGTAGTTGGAGATAAATCAGGTGCTGGTAGTTACGGGACAAGAAATG	AR2-2-0416	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
331	Beta-lactam	blaCTX-M-15	gi|39545937	AACTATAATCCGATTGCGGAAAAGCACGTCAATGGGACGATGTCACTGGCTGAGCTTAGCGCGGCCGCGC	AR2-2-0428	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
356	Beta-lactam	oxa9	M55547	CTAGATCGACTCCGTGCTCGTCTTTTAAACTTCCATTGGCAATCATGGGGTTTGATAGTGGAATCTTGCAGTCGCCAAAA	AR1-0046	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
402	Beta-lactam	oxa-1	gi|57903205	TGGAGATCTGGAACAGCAATCATACACCAAAGACGTGGATGCAATTTTCTGTTGTTTGGGTTTTCGCAAGA	AR2-2-0617	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
415	Beta-lactam	mecI	D86934	CTAGATCGACTGCAAGTGCGAATAATATAATAGAAGAAATACAAATGCAAAAGGACTGGAGTCCAAAAACCATTCGTACA	AR1-0043	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1
416	Beta-lactam	shv*	AF467948	CTAGATCGACCTTGAGCAAATTAAACAAAGCGAAAGCCAGCTGTCGGGCCGCGTAGGCATGATAGAAATGGATCTGGCCA	AR1-0047	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
435	Beta-lactam	oxa10	gi|21898660	TCTGGTGTGGGAACTGAGTCAAATCCTGGTGTCGCATGGTGGGTTGGGTGGGTTGAGAAGGAGACAGAGG	AR2-1-0227	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
441	Beta-lactam	pbpA	gi|31746355	ATGCTCAGTTTTATGACAAGGCCTATCGTGGACGTTGGAATGGGTTGACGGTGATCAGTATCGCAATTGG	AR2-1-0323	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
476	Beta-lactam	oxa-27	AF201828	CTAGATCGACGGCGAGAAAAGGTCATTTACCGCTTGGGAAAAAGACATGACACTAGGAGAAGCATGAAGCTTTCTGCAG	AR1-0048	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
495	Beta-lactam	oxa	gi|24209723	TCAGCGATGCGAAATTCTGCGGTCTGGGTTTATGAGCTATTTGCAAAAGAGATCGGAGAGGACAAAGCAA	AR2-1-0248	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
507	Beta-lactam	blaVIM-1	gi|40287459	TAGCCGAGGCAGAGGGGAACGAGATTCCCACGCATTCTCTAGAAGGACTCTCATCGAGCGGGGACGCAGT	AR2-2-0435	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
508	Beta-lactam	cmy-13	gi|40287459	TTCTCCGGGACAACTTGACGCCGAAGCCTATGGCGTGAAATCCAACGTTACCGATATGGCACGCTGGGTT	AR2-2-0439	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
531	Beta-lactam	oxa-26	AF201287	CTAGATCGACGTTACTCCACAGGTAGGTTGGTTGACTGGTTGGGTGGAGCAAGCTAATGGAAAAAAAAATCCCCTTTTCGC	AR1-0049	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
532	Beta-lactam	oxy-2b	AY303807	CTAGATCGACAGCAATAAAGAGGTGGTAAATAAAAGGCTGGAGATTAACGCAGCCGATTTGGTGGTCTGGAGCCCGATTA	AR1-0053	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
533	Beta-lactam	kpc-3	AF395881	CTAGATCGACCATCCGTTACGGCAAAAATGCGCTGGTTCCGTGGTCACCCATCTCGGAAAAATATCTGACAACAGGCATG	AR1-0057	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
534	Beta-lactam	imp-2	AJ243491	CTAGATCGACATTGGTTTGTGGAGCGCGGCTATAAAATCAAAGGCACTATTTCCTCACATTTCCATAGCGACAGCACAGG	AR1-0061	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
535	Beta-lactam	ampR	AJ237702	CTAGATCGACCTGGCCGGATTCTATGACAGCCATCCGCATATTGATCTGCATATTCTCCACCCATAACAATCATGTGGACC	AR1-0065	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
564	Beta-lactam	pbp3r	gi|33196475	TGATCACAGCAGCAATCGGTCTCGACAACGGCACTATCGATCCAAATGAAGTGTTGACGATCAACGGGCT	AR2-1-0357	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
573	Beta-lactam	pbpX	gi|47391:29	TGACAGCGACTTTGGTCAGTGCTAAAACAGGGGAAATTCTGGCAACAACGCAACGACCGACCTTTGATGC	AR2-2-0532	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
591	Beta-lactam	fox*	Y10282	CTAGATCGACAATGACAAGATGCAAACTTACTATCGGAGCTGGTCACCGGTTTATCCGGCGGGGACCCATCGCCAGTATT	AR1-0050	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
592	Beta-lactam	oxy-K1	AF473577	CTAGATCGACGCACCACCAATGATATTGCGGTTATCTGGCCGGAAGATCACGCTCCGCTGATATTAGTCACCTACTTTAC	AR1-0054	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
593	Beta-lactam	sme-1*	AY584237	CTAGATCGACGATGAGCGGTTCCCTTTATGCAGTTCATTTAAAGGTTTTTTGGCGGCTGCTGTTTTAGAGAGGGTGCAAC	AR1-0058	1	1	2	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
595	Beta-lactam	fox*	Y11068	CTAGATCGACAATGACAAGATGCAAACTTACTATCGGAGCTGGTCACCGGTTTATCCGGCAGGGACTCATCGCCAGTATT	AR1-0066	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
608	Beta-lactam	oxa9	gi|155010:2	AGAATGTGCCCGTCGTGTGTCTCCGTGCTCGTCTTTTAAACTTCCATTGGCAATCATGGGGTTTGATAGT	AR2-1-0150	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
611	Beta-lactam	penicillin	gi|16262455	TCTCAACGTGACGTCCTTCATGGGCATCGTACCGGCGGACAATCCCAGGTACCTGCTACTCACCCTCCTG	AR2-1-0162	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
616	Beta-lactam	oxa1	gi|24209728	TGGAAATTTGGAACAGCAATCATACACCAAAGACGTGGATGCAATTTTCTGTTGTTTGGGTTTCGCAAGA	AR2-1-0254	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
628	Beta-lactam	beta-lactam	gi|4063850	TTGTGACCTATTCCCCTGTAATAGAAAAGCAAGTAGGGCAGGCAATCACACTCGATGATGCGTGCTTCGC	AR2-2-0441	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
651	Beta-lactam	shv*	AF317502	CTAGATCGACCTTGAGCAAATTAAACTAAGCGAAAGCCAGCTGTCGGGCCGCGTAGGCATGATAGAAATGGATCTGGCCA	AR1-0051	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
652	Beta-lactam	per-2	X93314	CTAGATCGACTTATGGAAATGGATGGTTGAAACCACCACAGGACCACAGCGGTTAAAAGGCTTGTTACCTGCTGGTACTA	AR1-0055	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
653	Beta-lactam	sme-1*	Z28968	CTAGATCGACGATGAGCGGTTCCCTTTATGCAGTTCATTTAAAGGTTTTTTGGCGGCTGCTGTTTTAGAGAGGGTGCAAC	AR1-0059	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
654	Beta-lactam	vim-2	AF369871	CTAGATCGACTTATTGGTCTATTTGACCGCGTCTATCATGGCTATTGCGAGTCCGCTCGCTTTTTCCGTAGATTCTAGCG	AR1-0063	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
655	Beta-lactam	cmy-2*	X74512	CTAGATCGACATATCGCCAATAACCACCCAGTCACGCAGCAAACGCTGTTTGAGCTAGGATCGGTTAGTAAGACGTTTAA	AR1-0067	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
661	Beta-lactam	blaIMP-4	gi|13128916	TTCGTTTGAAGAAGTTAACGGGTGGGGCGTTGTTCCTAAACATGGTTTGGTTGTTCTTGTAGATGCTGAA	AR2-1-0051	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
665	Beta-lactam	blaI	gi|13774139	AAGAAGTTAGTGATAAAACGATTAGAACATTAATCACAAGACTATATAAAAAAGAGATTATAAAACGATA	AR2-1-0067	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1	1	1
666	Beta-lactam	spc	gi|13785452	CCCTAGCTCGAATGTGGCAAACAGTGACTACTGGTGAAATTACCTCGAAAGATGTCGCTGCAGAATGGGC	AR2-1-0071	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1	1	1
674	Beta-lactam	oxa	gi|24209721	CATGCGCAAGAACACGTGCTAGAGCGTTCTGACTGGAAGAAGTTCTTCAGCGACCTCCGGGCCGAAGGTG	AR2-1-0247	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
686	Beta-lactam	ampR	gi|40287459	ATTGGCGTGGTGGGGACCTTTGCGGCTGGGTGTCTGTTTCCTCTACTGGGCGATTTTAAGCGCGACTTACC	AR2-2-0434	1	1	2	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
692	Beta-lactam	ampC	gi|47223:24	CGCAGGATCTGATGTGGGAGAACTACCCGTATCCGGTGAAACTGTCGCGTTTGATTGAAGGCAACAACGC	AR2-2-0530	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
694	Beta-lactam	OXA-2	gi|47874:70	GGGAAGGCCGTATGGGTTGGTGGGTAGGATGGGTTGAGTGGCCGACTGGCTCCGTATTCTTCGCACTGAA	AR2-2-0538	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
711	Beta-lactam	ctx-m-12	AF305837	CTAGATCGACAGACTGGGTGTGGCATTGATTAACACAGCGGATAATTCGCAAATACTTTATCGTGCTGATGAGCGCTTCG	AR1-0052	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
712	Beta-lactam	rob-1	AF022114	CTAGATCGACTATTATTGCTGACATTAACGGCTTGTTCGCCCAATTCTGTTCATTCGGTAACGTCTAATCCGCAGCCTGC	AR1-0056	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
713	Beta-lactam	sme-2	AF275256	CTAGATCGACTTAGGTTAGATCGCTGGGAACTGGAACTTAACACTGCAATCCCAGGAGATAAACGTGACACTTCAACGCC	AR1-0060	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
714	Beta-lactam	ampC	AJ237702	CTAGATCGACCACTATTTGAGCTCGGATCTGTAAGTAAAACTTTCACAGGTGTGCTGGGTGCGGTTTCTGTGGCGAAAAA	AR1-0064	1	1	2	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
715	Beta-lactam	penA	L02928	CTAGATCGACACTTATCCGACGTTGGATGGCGAGAACGTCTTATAGTGACTCTGTCAACTGCCACACTCAACCTATCTCG	AR1-0068	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
741	Beta-lactam	MecR1	gi|34577204	ATCCGATGGTATTTGGTTTAGTGAAATCCCAAATTGTACTACCAACTGTCGTAGTCGAAACCATGAATGA	AR2-1-0368	1	1	1	1	1	1	1	1	1	2	1	1	2	2	2	2	1	1	1	1	1	1
747	Beta-lactam	ampC	gi|42611:<3	CGTGGTAGAAGTGAATCCACCGGCTCCCCCGGTCAAAGCGTCCTGGGTCCATAAAACGGGCTCTACTGGC	AR2-2-0459	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
758	Beta-lactam	ampC	gi|58761319	TGGGCTCCAGGAACACAACGTCTGTATGCCAACTCCAGTATCGGTTTGTTCGGCGCACTGGCTGTGAAGC	AR2-2-0647	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
782	Beta-lactam	mecR1	gi|13785452	GGTAAAACTGGAACAGGAATCGTGAATCACAAAGAAGCAAATGGATGGTTCGTAGGTTATGTTGAAACGA	AR2-1-0077	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1
785	Beta-lactam	pre	gi|14020964	AACAGCGTTTCAAGATAGATTTAATGAGCATGTTAAACAACGAGGATATGATTTAGAACGTGGGCAATCA	AR2-1-0089	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1
800	Beta-lactam	mecA	gi|34577204	TTAGACCGAAACAATGTGGAATTGGCCAATACAGGAACAGCATATGAGATAGGCATCGTTCCAAAGAATG	AR2-1-0365	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
802	Beta-lactam	blaTEM-1	gi|3757679	CGCTTTTTTGCACAACATGGGGGATCATGTAACCCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCC	AR2-1-0373	1	2	1	2	2	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1

841	Beta-lactam	pre	gi|13785452	AATTCCCCGAGCATATGAAAAAACAGGGTTTTGAGTTGAAGCGTGGTGAACGTGGCTCTGACCGTAAACA	AR2-1-0074	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1
847	Beta-lactam	putative-Be	gi|16262453	ACGATTTACGTGACACCACCACACCTGGAGCCATGATGGAGACCCTGCGCAAGCTGATCTTCGGTGAGGT	AR2-1-0170	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
907	Beta-lactam	putative be	gi|16262453	CCAAAAATCGTTAGCTTGACCGCTGCGCTCGCAGTTTTTGCAAGCCTCGTCCCAACTCAGTTGATCGCGA	AR2-1-0171	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
926	Beta-lactam	ampC	gi|42260:44	AGAAGTGAATCCACCGGCTCCCCCGGTCAAAGCGTCCTGGGTCCATAAAACGGGCTCTACTGGCGGGTTT	AR2-2-0458	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
955	Beta-lactam	caml	AY587956	CTAGATCGACATGATGGAAAAACTTGGGCGAGTAACGACTTTTCAAGGGCTATGGAGACTTTCTCTCCCGCTTCCACTTT	AR1-0092	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1
105	Chloramphenicol	cat	gi|8346640	TGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCG	AR2-2-0676	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
113	Chloramphenicol	catP	L02937	CTAGATCGACTGGCAATTCAAGTTCATCACGCAGTATGTGACGGATTTCACATTTGCCGTTTTGTAAACGAATTGCAGGA	AR1-0010	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
139	Chloramphenicol	cat	gi|2467210	TGAAATGTTTCCTAAAAAACCAATACCTGAAAACACAGTTCCTATTTCGATGATTCCTTGGATTGATTTT	AR2-1-0290	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
188	Chloramphenicol	CAT	gi|142219:1	CTATTTCGAAAGCCCATTCCGGGGCATTACACTCGACAAGCAGGTGAAGAGCCCGAACCTGGTGGTCGGA	AR2-1-0103	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
198	Chloramphenicol	cat	gi|21668299	GGTTCGGGGAAATTGTTTCCCAAAACACCTATACCTGAAAATGCTTTTTCTCTTTCTATTATTCCATGGA	AR2-1-0215	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
234	Chloramphenicol	flo*	AY055428	CTAGATCGACGATATTCATTACTTTGGCTATACTGGCGATGCTCGCACTCCTAAATGCGGGTTTCAGGTGGCACGAAACC	AR1-0016	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
296	Chloramphenicol	cat4	AJ401050	CTAGATCGACCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGAAATTCCGTATGGCAATGAAAGACGGTGA	AR1-0045	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
316	Chloramphenicol	cmlA5	gi|21898660	TGGTGTTTACGGCTCGTTTTATGGGGCGTGTGATACCCAAGTGGGGCAGCCCAAGTGTCTTGCGAATGGG	AR2-1-0229	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
376	Chloramphenicol	cmlA5	gi|21898660	AAACTTTAGTTGGCGGTACTCCCTTGCCGCCACGGTGTTGTTATCACCGTTCGATTATTGGCATCA	AR2-1-0230	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
398	Chloramphenicol	catA2	gi|56786619	TCAGCAGATTAAATGCGGATTCAGCCTGACCACCAAACTCGATATTACCGCTTTGCGTACCGCACTGGCG	AR2-2-0601	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
443	Chloramphenicol	catIII	gi|32455896	AGGGGATAGACTGTTATTGCCGCTCTCAGTACAGGTTCATCATGCAGTTTGTGATGGCTTCCATGTTGCA	AR2-1-0331	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
462	Chloramphenicol	cat	gi|57903205	TCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTG	AR2-2-0618	1	2	1	2	1	2	1	1	1	1	1	1	1	2	1	1	1	1	1	1
501	Chloramphenicol	floR	gi|32469306	TCTCTGGGAGCAGCTTGGTCTTCAACTGCACCGGCCTTTGTCGCTTTCCGTCTACTTCAAGCAGTGGGCG	AR2-1-0344	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
509	Chloramphenicol	floR	gi|4063850	CGGCGAGTTCTTGGGATGGCAGGCGATATTCATTACTTTGGCTATACTGGCGATGCTCGCACTCCTAAAT	AR2-2-0443	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
516	Chloramphenicol	cmlv	gi|498886:1	CATCGTACGGTGCCTCCAGTCCGTCCTTCCCGAGCCCTGGCTGGCCTTCGGCGTCGACTCCCTCATCGAG	AR2-2-0543	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
536	Chloramphenicol	flo*	AF071555	CTAGATCGACGATATTCATTACTTTGGCTATACTGGCGATGCTCGCACTCCTAAATGCGGGTTTCAGGTGGCACGAAACC	AR1-0069	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
557	Chloramphenicol	catB2	gi|24209732	TCAAGATCGGGCATGGAGCGGTGATAGGTAGCCGCGCTTTGGTTGCCAAAGACGTGGAACCCTACACCAT	AR2-1-0257	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
576	Chloramphenicol	cmlv	gi|498886:2	GATGCCCCTGGCCGTCTACATCCTCGGACTGTCCGCGTTCGCGCTCGGGACGAGCGAATTCATGCTCTCC	AR2-2-0544	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
596	Chloramphenicol	flo*	AF252885	CTAGATCGACGATATTCATTACTTTGGCTATACTGGCGATGCTCGCACTCCTAAATGCGGGTTTCAGGTGGCACGAAACC	AR1-0070	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
617	Chloramphenicol	catB2	gi|24209732	GCCACCGATATGATTGGGTCTCTTCTTTCCCTTTCTTCTACATGAACGAGGAGCCCGCGTTTGCAAAATC	AR2-1-0258	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
776	Chloramphenicol	cat	M35190	CTAGATCGACCGACATGAAGAGTTCAGGACCGCATTAGATGAAAACGGACAGGTAGGCGTTTTTTCAGAAATGCTGCCTT	AR1-0093	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	Efflux	marB	gi|26107943	GGTTGTTACTTCCTGTGGCAATGTCGTGGTTGTTCCCACATCGCAGGAACAACCACCGTTTGATTTAAAT	AR2-1-0296	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
57	Efflux	cmeC	AR466820	CTAGATCGACAAAATTTGATGGTAGCGCAAGCGGAAGTCGTGCAAAAACAGCTATAAATGCTCCAAGCAATCGAACTGGG	AR1-0097	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1
76	Efflux	hsdR	gi|19881227	CGGGTTGGTGTGCGAGTATTTTTGCACTCGTGATAACTTTTTGCGCCCCTATTGTCCCCCTGCTTTGTGC	AR2-1-0205	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1
77	Efflux	marR	gi|20516190	GGGATTGGTGAAAAGGGATTTGGACATCGATGATAGGGCGCAAGGTCCAAATTTCTCTCACAGAAAAGGGA	AR2-1-0209	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
103	Efflux	bzo23-3	gi|56710281	GCAACTGGGAACGGATCGACCATCTATGGGCCGGTTTTTCCGCCGAGGAGATCGAACTGACAGAAAAACT	AR2-2-0596	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
126	Efflux	corA	gi|10957190	TGGATTGATCTTGTCGAACCGGACGACGACGAGCGACTGCGCTTACAATCTGAACTTGGCCAGAGCCTGG	AR2-1-0022	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
132	Efflux	emrR	gi|14970543	CCGGATTTCCCTTATCGTGAAGTCCTGCTGCTGCGTTTGTTCCTGCATATGCAAACCAAAATACTGGAAC	AR2-1-0118	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
136	Efflux	putative ef	gi|19881227	GCGTGGCCAATATAGGATTAAGCACCGGAACTGCTATTTGTGGACTTGTGATTTCTTTGAGCGATACGCG	AR2-1-0206	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
141	Efflux	emrR	gi|26109399	AAATCACCCGCAAATTGCTCTCCCGTCTCGACCAGATGGAACAGGACGGTGTGGTTCTCGAAGCGATGAG	AR2-1-0298	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
142	Efflux	emrR	gi|26557031	AAACTTTCAGACCTGCGCCATCGGCATGTTGCTTGGCCGCGCAGCGATCCTCAAAGACCGCATTCTTGAC	AR2-1-0302	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
144	Efflux	MarR	gi|27887580	AGATTAGGTGGGTTTCTAATAACAAAATTAAAACAATTACATAGTAGGTCACTAGCACAGTGTATAAGTG	AR2-1-0310	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
156	Efflux	mar	gi|4589284	GTAATTTCGTGTCGGAGATCCTGTTTGGCTACACGACGCTCATCAGCATCATCAACCCGCTGGGCCTGGC	AR2-2-0497	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
157	Efflux	czcD	gi|46371950	GCGCGGAGCTTCATATCACGGTGGACTGCCAGATGCCTACTTGCGACAGTCATCGCATTGCTGAACAAGT	AR2-2-0501	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
163	Efflux	bzo23-1	gi|56710281	CAAAGTCTGCTCTCAGCAAGAGGGAGTTCGAAACCCTCTCCCATTTCCGCTACCAGTTGCGCCGCTTTCT	AR2-2-0597	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
200	Efflux	marA	gi|26107943	ACCATTCATAGCATTTTGGACTGGATCGAGGACAACCTGGAATCGCCACTGTCACTGGAGAAAGTGTCAG	AR2-1-0295	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
241	Efflux	acrR	gi|11066432	TCTTAAAAAAGAAGCCCGCGATTACGTCGCCATCTTACTGGAGATGTATCTCCTGTGCCCCACGCTTCGT	AR2-1-0024	1	1	1	1	2	2	1	1	1	2	1	1	1	1	1	1	1	1	1	1
273	Efflux	putative dr	gi|46371958	GATGGGTGACCTCAATTTCCTTGGCTTGGTGGCGATCGCCGGCTTCGGCATTGCCTCCTTCTTCGTTTAC	AR2-2-0507	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
302	Efflux	putative ef	gi|11610503	CTACCTAAGATTCAAAACGAGCTGAGCTTGTCTGATGCCGGCCGCAGCTGGGTGATCACCGCCTACGTGC	AR2-1-0029	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
306	Efflux	marR	gi|13092598	ACAGCGTCCCGGTTGTTGGTTGCTGTCTCAGCTCACTCAATCGGCCAAGTCGACGAGACCATTACCTTTC	AR2-1-0045	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
307	Efflux	marR	gi|14994317	TTAGAAAAAGAAATCAGCAACATACAGCGCGAACACTTATTATCCATTTTTTCACAATTCCATAATGGCG	AR2-1-0121	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
317	Efflux	marB	gi|24080789	CAGTTGTTACTTCTTGTGCCAATGTCGTGGTTGTTCCCCCATCGCAGGAACAACCACCGTTTGATTTAAA	AR2-1-0233	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
362	Efflux	marR	gi|11706573	ATTGTCGGTCGACCTGGGAGCACTGACCCGTATGCTGGATCGCCTGGTCTGTAAAGGCTGGGTGGAAAGG	AR2-1-0030	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
367	Efflux	marR	gi|14994317	TTCATGGAGATATAGATTCAATGTTTCCAAAAGGCATAACCAGCAGCGAACTAAGTGTACTAAAGGCAGC	AR2-1-0122	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
422	Efflux	marA	gi|11706573	TGGAATCGCCACTGTCACTGGAGAAAGTGTCAGAGCGTTCGGGTTACTCCAAATGGCACCTGCAACGGAT	AR2-1-0031	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
484	Efflux	marR	gi|13423687	ATCGGCGGTCGCACACGCTGGAGCTCACGGCAGCGGGACGTCGTCTGTTCGCCGAGATCGCGCCGCTGGC	AR2-1-0060	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
485	Efflux	marR	gi|13425422	GAAAGCCAAGAAGATCAAGGCGCCGAAGGCCGAGAAACCCAAGAAGGACAAGAAGCCCAAGAAGGACAAG	AR2-1-0064	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
486	Efflux	marR	gi|13774139	TTGGTAATACTTTAAATTTAGAACCTTCAACAATATCTGGAATATTAGATAAGATGTCCAAAAAGGATCT	AR2-1-0068	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1
488	Efflux	ybit	gi|15384869	TATTGTCCGCCCACACGAACGGGATCGGTAAGTCCACTTTGCTGAAAACACTGGGGGGTGAACTGGCACC	AR2-1-0148	1	1	1	2	2	2	1	1	1	2	2	2	1	1	1	1	1	1	1	1
542	Efflux	marA	gi|13384163	GCATTTTGGACTGGATCGAGGACAACCTGGAATCACCACTGTCACTGGAGAAAGTGTCAGAGCGTTCGGG	AR2-1-0053	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
543	Efflux	marR	gi|13421547	CCCAGCTCACCGAAGGCTTCACGGACGAGGAAATCAGCGTGGTCTCGCGCTGGCTCGCCAGTCTGCAGAC	AR2-1-0057	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
544	Efflux	marR	gi|13423922	CAGGTCACCCTTGGACGAGCCCTGGGGATCAACCGCGCCAGCACGATGAAGGCCGTCGATGAACTGGAGG	AR2-1-0061	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
549	Efflux	emrR	gi|15725122	CGTCTTTGTATGCACATGCAAGCCAAGCTCCTGGAAAACCGCAATAAGATGCTGAAGGCTCAAGGGATTA	AR2-1-0153	2	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
601	Efflux	putative AB	gi|13093909	ATCTAGTGGCCAGTTTCAAACAGATCGGTATTGCCACACTGCTGACTACGCAGTATCTCGAGGAGGCGGA	AR2-1-0050	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
602	Efflux	marB	gi|13384163	CTCGTTACTTCCTGTGGCGATGTGGGGGTTGTTCCCCCATGGCAGGAACAACCACCGTTCGATTTAAATC	AR2-1-0054	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
603	Efflux	marR	gi|13422177	AGAAGCCCGCGTCATCCGATCAGCCCGTCGAGATTCTGCGTCTCGACAACCAGCTGTGCTTCGCCCTCTA	AR2-1-0058	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
634	Efflux	marA	gi|47755704	AGCATTTTGGACTGGATCGAGGATAACCTGGAGTCGCCGCTCTCACTGGAAAAAGTGTCTGAGCGTTCAG	AR2-2-0537	2	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
662	Efflux	marR	gi|13384163	TCCGGTTGAACTGAAAAAAGTGTTGTCGGTCGACCTGGGAGCACTGACCCGTATGCTGGATCGCCTGGTC	AR2-1-0055	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
663	Efflux	marR	gi|13422532	GTGCATGATCACGCGCTGCCTTTGTCCAGCTATCTGAGCTATCTGCTTTACCAGACTGAGCAGCATCGCC	AR2-1-0059	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
672	Efflux	putative ca	gi|16262453	GTTGGAATGGGTGGAGTGAAACATCAATTCTTCCCGACGTCGGATCGTCCCGAGGTGCTGGTCGAAGTCC	AR2-1-0167	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
684	Efflux	emrR	gi|34101873	ATGAGTCCAAACAAGTCCTTTTCCCAGTTGGAGCAAGCGATCAACCGCGTCGAATCGCGCTTTCCCGGCG	AR2-1-0359	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
722	Efflux	potassium-t	gi|13785452	GGCATGGTTCCAATGGTATTAATGATGTTGAATGCAGTTTTTGGCGGTGAAGGTGTTGGGCTGATGAACA	AR2-1-0076	1	1	1	1	2	2	1	2	1	2	2	2	2	2	1	1	1	1	1	1
736	Efflux	putative AB	gi|24427162	GATGAGCGTCAGCATGATGGTGATCTTCCCGCTCACCTTCCTGTCCAACGTCTTCGTCGACCCGAAGACC	AR2-1-0276	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
748	Efflux	ABC transpo	gi|42632302	TCAACAGAAGAAACAACAACTCGAAAACGCAATCGAAAAGAAAGAGCAACGGGCACAAAGAGCTACCAAA	AR2-2-0463	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
752	Efflux	putative ef	gi|52211453	CGCTCATTACATCGTTCATCGTCAGCTTCGGGCTGGTGAAAGCCGTGGCGAACCTGATTTCCGGTCAACT	AR2-2-0551	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
753	Efflux	EmrA	gi|52211453	GAACTTCAAGGAAGGGCAGTTGCGGCACATGCGGGTGGGCCAGCCGGTGCGGCTCGAATCGGACCTGTAC	AR2-2-0555	1	1	2	1	2	2	1	1	1	2	1	1	1	1	1	1	1	1	1	1
754	Efflux	EmrB	gi|52211453	AGGCGCACCCGGTGGTGGAGCTGAGCCTGTTTCGGGAGCGGACCTTCACGTTCTGCGTGGTGATCATCTC	AR2-2-0559	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
795	Efflux	putative AB	gi|24418973	ATGTCTACTTCCCCCACTTCTCTCACCTGTACGTCCCTGTCCTTCGCCTGGCCCGACGGCACGGAGGTCT	AR2-1-0273	1	1	2	1	2	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1

818	Efflux	mexR	gi|58802934	GACGTCCATGTATTGAAGCTTATCGACGAACAACGCGGGCTGAACCTGCAGGACCTGGGACGCCAGATGT	AR2-2-0648	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
836	Efflux	cmeR	AR466820	CTAGATCGACACTCAAATAGAACACCATCACAAAAAGTTTTAGCCAGACAAGAAAAAATCAAAGCAGTGGCCTTAGAGCT	AR1-0094	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
850	Efflux	marB	gi|16502471	TGTTACTTATCGCCTCCGGATATGGCATTGCAGAACAAACTTTGTTACCTGTGGCGCAAAATAGCCGCGA	AR2-1-0182	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
855	Efflux	putative AB	gi|24418991	GATTCTGGAGGCGGAGGGAGGAAGGGTCACCCGCTACGGCGACGGCTACAACGGCTACCGTCGCAGGCGAAG	AR2-1-0274	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
881	Efflux	msrC	gi|6687492	TGCTCAGGAAACTCTGACGAAACCGTTATGTACATTAAGTGGGGGAGAAGCGACCCGTCTGACGATTGCT	AR2-2-0661	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1
894	Efflux	msrA	NC 002655	CTAGATCGACCACCACGGAAATCGCTAACGCCACACCGTTTTATTATGCCGAAGATGACCACCAGCAATATCTGCATAAA	AR1-0087	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
896	Efflux	cmeA	AR466820	CTAGATCGACTTTAGGTGTTGTGCTTTTACTCGCTGCTTGCAGCAAAGAAGAAGCACCAAAAATACAAATGCCGCCTCAA	AR1-0095	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
915	Efflux	putative AB	gi|24427162	GCATCGACATCGCCGCCTCCATCCTCAACACCCCCGACCTGCTCTTCCTCGACGAGCCCACCACCGGGCT	AR2-1-0275	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
919	Efflux	acrR	gi|34499898	GAGACACGACAACACATCCTGGATGTGGCCCTGCGTTTGTTCTCGCAGCAAGGCGTATCAGCAACCTCGC	AR2-1-0363	2	2	2	2	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
929	Efflux	putative AB	gi|434708:4	GGAGAACCTGCTCTGCCGGCACCGGGAAGTCGACGACGACACACTCTGGACCGTCCTCCGAGCCGTACGG	AR2-2-0470	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
940	Efflux	marR	gi|6458892	CCTTCTGGAGCGGATTCGGAGCGACTGGGCGAGGCTCAATCACGGTCAGGGACCAGACTCGGACGGTCTG	AR2-2-0658	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
941	Efflux	putative AB	gi|6933870	GGCCCCCTCGCTGAGCTGTACCAGGTGGAGGTGGACGGCAGGCTCAGCGTCCCGGAGTTCAGCATCGCGC	AR2-2-0662	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
956	Efflux	cmeB	AR466820	CTAGATCGACTTGCCAATGATTTTCGCAACAGGAGCAGGAAGTGCTTCAAGACACTCTTTAGGAACAGGGCTTATTGGTG	AR1-0096	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
32	Glycopeptide	vanH	gi|4405960	CGCCTATTACACGGACCACGCACTGAGTGACACTGTTGAAAACTCCATCATCAATTGTCTCCAATTCCGA	AR2-2-0479	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
242	Glycopeptide	vanHD4	gi|11527843	AGAACAAAAAATCGGCGGAGCCGCCTTAGATGTCCTGGAAGGGGAAGAAGGCATCTTTTACCATGAATGC	AR2-1-0028	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
269	Glycopeptide	ddlA	gi|3947751	GCCTTCCGATATGACAGTCGTGTCTTGGTAGAGCAAGGGGTAAATGCCCGTGAAATCGAGGTTGGTCTCT	AR2-2-0419	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
292	Glycopeptide	vanH	AF516335	CTAGATCGACGAATCCAACGCCAAATCCGCGCCTTTCAATCAATGTATCAGTGTGGGACATAAATCAGAGATTTCCGCCT	AR1-0029	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
352	Glycopeptide	vanA	AF516335	CTAGATCGACAAAACCTTGCGCGGAATGGGAAAACGACAATTGCTATTCAGCTGTACTCTCGCCGGATAAAAAAATGCAC	AR1-0030	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
361	Glycopeptide	vanYD4	gi|11527843	GAAATTGTGGCAAGCAATACGTCGTATGAAAAATGGCCGAACGGCAGGGAGGTCACTTACAACAATTCCA	AR2-1-0026	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
388	Glycopeptide	ddlA	gi|3947730	CCCGTGAAATCGAGGTTGGACTCTTGGGAAATTACGATGTCAAGAGCACGCTTCCAGGAGAAGTAGTCAA	AR2-2-0417	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
412	Glycopeptide	vanX	AF516335	CTAGATCGACTACCGTCCTAATCGTGCTGTAAACTGTTTTATGCAATGGGCTGCACAGCCGGAAAATAACCTGACAAAGG	AR1-0031	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
421	Glycopeptide	vanD4	gi|11527843	TGAAAAATGCGGGAATTGAGGTACCTGGGTTTCGAGTTCTACAAAAGGGGGACAGCCTGGAAGCAGAGAC	AR2-1-0027	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
448	Glycopeptide	ddlA	gi|3947749	CCTTAAAACTTGCCTTCCGATATGACAGCCGTGTCTTGGTTGAGCAAGGAGTGAATGCCCGTGAAATTGA	AR2-2-0418	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
471	Glycopeptide	vanR	AF516335	CTAGATCGACATCATGCTTCCCGGCACAAGCGGCCTTACTATCTGTCAAAAAATAAGGGACAAGCACACCTATCCGATTA	AR1-0028	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
472	Glycopeptide	vanY	AF516335	CTAGATCGACTTGATGAGCAAAGTGTGCTTTACCAAGAAATGGGGGCTGAGTATGCCTTACCAGCAGGTTATAGTGAGCA	AR1-0032	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
475	Glycopeptide	ble	D86934	CTAGATCGACATGGATTCGCAGTTCTAATGTGTAATGAGGTTCGGATTCATCTATGGGAGGCAAGTGATGAAGGCTGGCG	AR1-0044	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1
515	Glycopeptide	vph	gi|48002:97	CGGAGGCTCCCGCGAACGAGTGGCAGGAGTTCGCCACGGGGGTGCGTACCGAACTGTTCCCGCTGATGTC	AR2-2-0539	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
656	Glycopeptide	vanB2	AY145441	CTAGATCGACAAAAGTCGCAATCATCTTCGGCGGTTGCTCGGAGGAACATGATGTGTCGGTAAAATCCGCAATAGAAATT	AR1-0071	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
716	Glycopeptide	vanC*	AY033764	CTAGATCGACCACCGTTTCTTTAGCTTCAGCAACTAGCGCAATCGAAGCACTCCAATCATCTCCCTATGACTACGACCTC	AR1-0072	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
771	Glycopeptide	vanC*	L29638	CTAGATCGACCACCGTTTCTTTAGCTTCAGCAACTAGCGCAATCGAAGCACTCCAATCATCTCCCTATGACTACGACCTC	AR1-0073	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1
781	Glycopeptide	ble	gi|13785452	AAGGCTGGCGCTCTCGTAGTAATGATTCACCGGTTTGTACAGGTGCGGAGTCGTTTATTGCTGGTACTGC	AR2-1-0073	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1
831	Glycopeptide	vanD	AY489045	CTAGATCGACTTTACTTCCTACAGCCGTTATCCCCGCATGATGACAGCAGCCGGTTTTACGCTTACTGAAATACTGGATC	AR1-0074	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
868	Glycopeptide	ble	gi|434708:1	AACGTCTCCTTCTGGGTGGACACCCTCGGCTTCGAGAAGGATTTCGGGGACCGGGATTTCGCGGGGGTCC	AR2-2-0465	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
871	Glycopeptide	ddlN	gi|4405960	TTCCGAAGAACATCCTATCTCCATCAAATCTGCGCGTGAGGTCCAGAAGCACCTCGACCTCGAGAAGTAC	AR2-2-0477	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
891	Glycopeptide	vanE	AF430807	CTAGATCGACTGGTTGTGGTATTTTAGGAAATGAACAATTGGTCGTTGGAGAATGTGACCAAATCAGTCTTGTGGATGGC	AR1-0075	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
928	Glycopeptide	ank	gi|434708:1	GCTGCTCTACCTCCATCACGACCTCACCGTCACCCGCTCCATCTGGCACGGCGAGGACGTGGTCTTCGAC	AR2-2-0466	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
930	Glycopeptide	putative bl	gi|43744:66	ATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGT	AR2-2-0474	1	2	2	2	2	2	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1
931	Glycopeptide	vanX	gi|4405960	CCTGTGCGCGATCATGGAAGGTTCCGGCTTCAGCTCCTACGAGTGCGAGTGGTGGCACTACAACCTGAAG	AR2-2-0478	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
951	Glycopeptide	vanG	AF253562	CTAGATCGACAATTGGCAGGAATACCTGTTGTTGGCTGCGATACACTCTCATCAGCTCTTTGTATGGATAAGGACAGGGC	AR1-0076	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
27	Heavy metal	merA	gi|37962716	AGTTGTTCCCCTACCTGACGATGGTCGAAGGGTTGAAGCTCGCGGCGCAGACCTTCAACAAGGATGTGAA	AR2-2-0387	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
33	Heavy metal	merF	gi|4572386	ATTTTCATCGGCTTGACCATCTACGCCATCCAACGAAAACGCCAAGCCGATGCCTGCTGCACCCCGAAAT	AR2-2-0483	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
34	Heavy metal	merC	gi|4572411	GCGGAGCGGCTGGCTGCTCTATATCGGCCTGGCCGTCATGTTTGGGGTGTCCATCTGGGACTTCGTGTCG	AR2-2-0487	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
35	Heavy metal	merC	gi|4572423	GACTGCGCTCGGCCTGATCGGTCCTACCCTGGTACTGGCAGCGGTATTTTTTATGCGGGCTTATGGCTGG	AR2-2-0491	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
93	Heavy metal	merP	gi|4572386	CTGTCCGATCACTGTCAAGAAGGCGATTTCCAAGGTCGATGGCGTCAGTAAAGTTGACGTGACCTTCGAG	AR2-2-0484	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
94	Heavy metal	merC	gi|4572419	GCTTTCTACAGGAATACGAAGGATTGTTCATCTCCAAGCTGCTGCCGCTGTTCGCTGTCGTGGCTTTGCT	AR2-2-0488	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
95	Heavy metal	merC	gi|4572439	GCTTTCTACAGGAATACGAAGGGTTGTTTATCTCCAAGCTGCTGCCGCTGTTCGCAGTCGTGGCTTTGCT	AR2-2-0492	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
153	Heavy metal	merC	gi|4572395	GATCTTGGTGCTGGCAGCGGTGTTTTAATGCGGGCTTACGGCTGGCAGAGCGGTGGACTGCTCTATGTC	AR2-2-0485	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
154	Heavy metal	merT	gi|4572423	CTCAAGCCTGCGCACCGGGCGAGGTCTGCGCCATCCCTCAGGTACGTACCTCCTACAAGCTGCTGTACTG	AR2-2-0489	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
155	Heavy metal	merT	gi|4572448	CCACCTACAAGCTCATTTTCTGGTTCGTCGCCGTGTTGGTCTTGGTCGCGCTTGGATTTCGCTATGCTAT	AR2-2-0493	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
206	Heavy metal	merT	gi|37962716	ATTTTCTGGATCGTGGCCGTGCTGGTCCTGGTCGCGCTTGGATTTCCCTATGTCGTTCCATTTTTCTATT	AR2-2-0386	1	2	2	2	2	2	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1
213	Heavy metal	merP	gi|4572403	GATCACTGTCAAGAAGGCGATTTCCAAGGTCGAAGGCGTCAGCAAAGTTGACGTGACTTTCGAGACACGC	AR2-2-0486	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
214	Heavy metal	merP	gi|4572423	GTGACCAAGGCTGAGGTGAGTTTCGAGAACCGCGAGGCCATCGTCACCTTCGACGATACCAAGACCAATG	AR2-2-0490	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
215	Heavy metal	merP	gi|4572448	CGTCAAGAAGGCGATTTCCAAGGTCGAAGGCGTCAGCAAAGTTAACGTGACCTTCGAGACACGCGAAGCG	AR2-2-0494	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
520	Heavy metal	merA	gi|58383237	AGCACTCTCAAAATCACCGGCATGACTTGCGACTCGTGCGCAGTGCATGTCAAGGACGCCCTGGAGAAAG	AR2-2-0631	1	2	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
562	Heavy metal	merR	gi|32469306	AGCTTCAGGACGTGCGCGAAAAAATGACCGACCTGGCGCGCATGGAAACCGTGCTATCCGAACTTGTGTT	AR2-1-0349	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
579	Heavy metal	merT	gi|58383237	CTACAAGCTGATTTTCTGGATCGTGGCCGTGCTGGTCCTGGTCGCGCTTGGATTTCCCTATGTCGTTCCA	AR2-2-0628	1	2	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
580	Heavy metal	merD	gi|58383237	TATCGCAACTGGCCCATAACGCTGGGGTGAGCGTACATATCGTGCGCGACTACCTGGTGCGCGGCTTGTT	AR2-2-0632	1	2	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
639	Heavy metal	merP	gi|58383237	CCCGATCACAGTCAAGAAAGCGCTCTCCAAGGTCGAAGGCGTGAGCAAGGTCGATGTGGGCTTCGAGAAG	AR2-2-0629	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
699	Heavy metal	merC	gi|58383237	GCAACTGGTGGACGGCGAACCTGATGTACGTCGGCCTGGCCTTGATGATTGGGGTGTCGATCTGGGACTT	AR2-2-0630	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
702	Heavy metal	merR	gi|58383237	GTGGTTCGGGTGAAATTCGTGAAATCGGCACAGCGGCTGGGGTTCAGTCTGGACGAGATTGCCGAGCTGT	AR2-2-0642	1	2	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
726	Heavy metal	merT	gi|14020964	CTTTACTTTGTTGCGCAGGACCGATTCTCCTTGTTGCATTAGGGAGCACAGGTATTGGTGCCCTCTTTGC	AR2-1-0092	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
786	Heavy metal	merR	gi|14020964	TCGTCTTTGTTGGTGGTGGGTATATTTCGTTTGAATTTGCTCATATCGGGCACGTGCTGGATCAGAAGT	AR2-1-0093	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
803	Heavy metal	orf5	gi|37790303	ACCGGACATTCGCGGAGACCTTCGTCCTGAGATCCGAGCTCCTAGTCGCGAGTTGCAGCGACGGCATCGT	AR2-1-0377	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
845	Heavy metal	merB	gi|14020964	CCTTCTGTAACGACGTTCATCTTTTTCAGTTCACCGAGTGCAGCCCAAGACTGGCTTAACCAACACCCTGA	AR2-1-0090	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
905	Heavy metal	merA	gi|14020964	TTGGACGCTGTACCGCGGGCCTTAGTCAATCACGAAACAACAGGGGTCTATAAACTTGTAGTCAACGCCC	AR2-1-0091	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
122	Lincosamide	linB-like	gi|10957113	GGAACTAATGGCAAGGGTTAAGGAACTTGTCCAGTCAGATGAACGAATATCTGCTTGTATGATGTATGGC	AR2-1-0006	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
370	Lincosamide	linA	gi|153042:4	TGATGATGGATCAATTACCCAAGCAAACCCAGAAGGTGGTAATTATGTTTTCCAAAATGACTTTGGTTTTCA	AR2-1-0134	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
895	Lincosamide	linB	AJ238249	CTAGATCGACTGAAACATAGTATAACCTCGAACTTTGATTCATCCAACTGGTTGTTTGACGTAGCTCCGTACTTGATGCT	AR1-0091	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	Macrolide	ereA2	gi|21263078	AAGGAGGATTCATGCCTGACATTGACAGATGACCCCATGGAAGCAAAGCGAATGCGGTCCCAAAGCGCCT	AR2-1-0212	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
69	Macrolide	ermG	gi|142881:6	GATAGAAATTGATTCTAAATTATGTGAGGTAACTCGTAATAAGCTCTTAAATTATCCTAACTATCAAATA	AR2-1-0105	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
78	Macrolide	ereA2	gi|21263078	AACAGCCGGTGCTCATGAACTTGAGCGATTTTCGGATACCCTGACCTTTTCTTTGTATGGCTCAGTGCTG	AR2-1-0213	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
176	Macrolide	ereA2	AF512546	CTAGATCGACCCGGTGCTCATGAACTTGAGCGATTTTCGGATACCCTGACCTTTTCTTTGTATGGCTCAGTGCTGATTTG	AR1-0023	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
353	Macrolide	ermB*	AF516335	CTAGATCGACACAAGCGTACCTTGGATATTCACCGAACACTAGGGTTGCTCTTGCACACTCAAGTCTCGATTCAGCAATT	AR1-0034	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

355	Macrolide	ermA	D86934	CTAGATCGACAAGTGGGTAAACCGTGAATATCGTGTTCTTTTCACTAAAAACCAATTCCGACAGGCTTTGAAGCATGCAA	AR1-0042	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1
643	Macrolide	mph(A)	gi|58383237	ACATGGGCTCAAGCTCCATGGCCCGCTGACTGTCAATGAGCTTGGGCTCGACTATAGGATCGTGATCGCC	AR2-2-0645	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
669	Macrolide	ermX	gi|15778307	GCAAGCACGATGATGACGGCTCAGTGGTCCCCATGGTTCACATTTCACCTGGGTTCTCGGGTACCAAGGT	AR2-1-0155	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
772	Macrolide	ermTR	AF002716	CTAGATCGACAGAGGGGATTTGCTAAAAGGTTGCAAAATACCCAACGAGCTTTAGGTTTGCTGTTAATGGTGGAAATGGA	AR1-0077	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
773	Macrolide	ermG	M15332	CTAGATCGACTTTGAAATAGGTGCAGGGAAAGGTCATTTTACTGCTGAATTGGTAAAGAGATGTAATTTTGTTACGGCGA	AR1-0081	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
774	Macrolide	ereB	A15097	CTAGATCGACGCAGGGCGATATGGGTGCAAAAGACAAATACATGGCAGATTCTGTGCTGTGGCATTTAAAAAACCCACAA	AR1-0085	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
832	Macrolide	ermB*	AJ243541	CTAGATCGACACAAGCGTACCTTGGATATTCACCGAACACTAGGGTTGCTCTTGCACACTCAAGTCTCGATTCAGCAATT	AR1-0078	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
833	Macrolide	mefA/E*	AY319932	CTAGATCGACCGATTTTGGGACCTGCCATTGGTGTGCTAGTGGATCGTCATGATAGGAAGAAGATAATGATTGGTGCCGA	AR1-0082	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
834	Macrolide	mphA	AY522923	CTAGATCGACCGACATGGGCTCAAGCTCCATGGCCCGCTGACTGTCAATGAGCTTGGGCTCGACTATAGGATCGTGATC	AR1-0086	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
892	Macrolide	ermC	NC 001386	CTAGATCGACTTTGAAATCGGCTCAGGAAAAGGCCATTTTACCCTTGAATTAGTAAAGAGGTGTAATTTCGTAACTGCCA	AR1-0079	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1
893	Macrolide	mefA/E*	AB011259	CTAGATCGACCGATTTTGGGACCTGCCATTGGTGTGCTAGTGGATCGTCATGATAGGAAGAAGATAATGATTGGTGCCGA	AR1-0083	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
952	Macrolide	ermF	U30830	CTAGATCGACGATTTGAAACTTGTCTATGAGGTAGGTCCTGAAAGTTTCTTGCCACCGCCAACTGTCAAATCAGCCCTGT	AR1-0080	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
953	Macrolide	ereA	A15069	CTAGATCGACCGCAATTGGCCGAAATTATCCAGCTCATCGATCACCTCATGAAACCGCACGTTGATATGTTGACTCACTT	AR1-0084	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
98	Methylenomycin	Mmr	gi|53721033	GCGTCGCCGTGCTGTTCGGTGTCTGCATGAATCTGTCGTACTACGGGATCATCTTCGTGCTGAGCCTGTA	AR2-2-0576	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
84	Metronidazole	5-NITROIMID	gi|27886343	TTCAAAGTACAGGGAAAAAAGATTGGAATTTTCCAGAACCTATGCTTAATGGTGTTGCAGTGTTTAAGAT	AR2-1-0309	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
162	Metronidazole	putative 5-	gi|56126533	GCATTGAAATGGACGGCGACCATGCATTACTACGTGCCGATGACCCCTGTGATTATAGCTACGCTACAC	AR2-2-0593	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
259	Metronidazole	product=5-n	gi|28203008	TGGAAATGCTAAATGAAGGGCAATATGGGGTTTTGTCTGTAATAACTAATGAGGGTTATCCCTATGGAGT	AR2-1-0312	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
319	Metronidazole	5-nitroimid	gi|29340209	CGCTCGGAGAGTGCCATGTGCCGTGGGAAAGTAGAATTCATAGAAGATATGGAGGAAAAACGTCATGCAC	AR2-1-0313	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
396	Metronidazole	putative 5-	gi|46448640	GTCGTCAAGAGAGGATGATGGCTGAAGAGTCGATGGTGTGGCAGGTCGTGGAAGAGGCCCGCTGGATGGT	AR2-2-0521	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1
750	Metronidazole	nimB	gi|435260:7	GTTGCCATCCTTGAAAGGATGACGAACGGAACATTGGCTCTTCATGGGGACGATGGTTACCCGTATGCCG	AR2-2-0471	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
810	Metronidazole	nimA	gi|435262:3	CGTGCAAGGGCATAAGATGGATGCCATCAGGCAGCATCCCGAAGTCTCGTTTTGTGTGGTGGAGCAAGAC	AR2-2-0472	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
432	Poly-Ketide	nonR	gi|153369:4	AGATCTACCTCACCGGGCGGATGGTCTCCGGGGACGAGGCGGTGCGCCTGGGGCTGTTCGACCGGCTCTG	AR2-1-0143	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
487	Poly-Ketide	nonR	gi|153369:4	GATCTACCTCACCGGGCGGATGGTCTCCGGGGACGAGGCGGTGCGCCTGGGGCTGTTCGACCGGCTCTGC	AR2-1-0144	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
547	Poly-Ketide	nonR	gi|153369:3	CTACCTCCTGCTGCGCAACAAGCCGGTGGACCTCGACACCATGACCCGCGAACTCGGCCAGGCCAAGAGC	AR2-1-0145	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
605	Poly-Ketide	norA	gi|13622883	ATGGCACTTTTATGTCTTGTGGTCAAGCCGCCTCCATACAAGGAGTGGATGAGCACCGCTTTAATACGGC	AR2-1-0066	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
607	Poly-Ketide	nonR	gi|153369:2	CGTACCTGAACCGGCTGGGCGAGAACGCCCCTGAGTACCTGGATGTCTTCTCCGCCTCGTTCTGCCGGTA	AR2-1-0146	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
667	Poly-Ketide	nonR	gi|153369:6	GTCCCCCGACTACCGGGTCGAGAAGCCCGAACTTCTCCTCTGCGGTGAACACGACAGCACGGGTAACATC	AR2-1-0147	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
751	Poly-Ketide	albA	gi|43785:25	CCCTCTGCCATGCGCAGGTACCTGCTTTGATGAAAGGAACGTGGATGACTTCGGAGGTGCTCAGCTGGCT	AR2-2-0475	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
68	Quat. ammon.	qacE2	gi|14091023	CGTCTTGGTCACTGCGATTGCATGGGTTTTGCATGGTCAAAAACTAGATATGTGGGGATTTGTTGGTGTC	AR2-1-0101	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
114	Quat. ammon.	qac	AY458224	CTAGATCGACGCAATAGTTGGCGAAGTAATCGCAACATCCGCATTAAAATCTAGCGAGGGCTTTACTAAGCTTGCCCCTT	AR1-0014	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
128	Quat. ammon.	qacE2	gi|14091023	CTGAAACCCTCCTTTATTTCGCCCATGTTTATTCAAACGGCATTCAGTTTCTCAAACGCTGTGCAGCGCT	AR2-1-0102	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
151	Quat. ammon.	qacEdelta1	gi|38490043	CGAAGTAATCGCAACATCCGCATTAAAATCTAGCGAGGGCTTTACTAAGCTTGCCCCTTCCGCCGTTGTC	AR2-2-0405	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
363	Quat. ammon.	qacEdelta1	gi|12719013	AATCTGTTGAGCAATCATCTCCTTTCGGGGCGAGTGCCAATGATGACCTTAGTTCACACTCTCGCTGTCG	AR2-1-0034	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
494	Quat. ammon.	qacH	gi|24209712	CCTTCTGTTGTAGTTGTGGCTGGCTACGGGCTTGCGTTCTATTTCCTCTCTCTCGCACTCAAGTCCATCC	AR2-1-0244	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
555	Quat. ammon.	qacF	gi|24209723	CATTCCGGTCGGTATTGCTTACGCTGTATGGGCTGGGCTTGGCATCGTGCTTGTGGCAGCTATTGCTTGG	AR2-1-0249	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
615	Quat. ammon.	qacF	gi|24209723	GTTCTATTTCTTGTCTCTCGCGCTCAAGTCCATTCCGGTCGGTATTGCTTACGCTGTATGGGCTGGGCTT	AR2-1-0250	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
673	Quat. ammon.	qacH	gi|24209712	TGTGGCTGGCTACGGGCTTGCGTTCTATTTCCTCTCTCTCGCACTCAAGTCCATCCCGGTCGGCATTGGT	AR2-1-0243	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
743	Quat. ammon.	qacEdelta1	gi|37790303	CCCTGTCGGTGTTGCTTATGCAGTCTGGTCGGGACTCGGCGTCGTCATAATTACAGCCATTGCCTGGTTG	AR2-1-0376	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
594	Rifampin	arr-3	AY038837	CTAGATCGACATAATTACAAGCAGGTGCAAGGACCGTTCTATCATGGGAACCAAAGCCAATTTGGCGATTGGTGACTTGCT	AR1-0062	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
835	Streptogramin	vga	M90056	CTAGATCGACCGGGTACAATTGAAGGACGGGTATTGTGGAAAGCAAAAAGTTTTAGTATTCGCGGAGGAGACAAGATGGC	AR1-0090	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
954	Streptogramin	vatB	U19459	CTAGATCGACTGTGTGGATTGGTCAGAATGTTACTGTTATGCCAGGAATTCAAATAGGAGATGGAGCAATTGTTGCTGCG	AR1-0088	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
174	Sulfonamides	sul1	AY458224	CTAGATCGACCTACCTGAACGATATCCAAGGATTTCCTGACCCTGCGCTCTATCCCGATATTGCTGAGGCGGACTGCAGG	AR1-0015	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
235	Sulfonamides	sulII	NC 005324	CTAGATCGACGAATAAATCGCTCATCATTTTCGGCATCGTCAACATAACCTCGGACAGTTTCTCCGATGGAGGCCGGTAT	AR1-0020	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
338	Sulfonamides	sul1	gi|56786619	TCCAAGGATTTCCTGACCCTGCGCTCTATCCCGATATTGCTGAGGCGGACTGCAGGCTGGTGGTTATGCA	AR2-2-0600	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
383	Sulfonamides	sulII	gi|32455896	TTCCAGACGCTGCGTTCTATCCGCAATTGGCGAAATCATCTGCCAAACTCGTCGTTATGCATTCGGTGCA	AR2-1-0330	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
503	Sulfonamides	sulII	gi|32469306	CTCGACAGTTATCAACCCGCGACGCAAGCCTATGCCTTGTCGCGTGGTGTAGCCTATCTCAATGATATTC	AR2-1-0352	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
688	Sulfonamides	sul1	gi|40638503	ATGAGATCAGACGTATTGCGCCGCTCTTAGACGCCCTGTCCGATCAGATGCACCGTGTTTCAATCGACAG	AR2-2-0442	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	Tetracycline	tetC	gi|10957190	TTGTTGAAAAAGGCTATCAAGCTGTTTCAATAGATGAGATCTCGGGAAAAGCGTTGGTGACCAAAGGTGC	AR2-1-0020	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	2	1
53	Tetracycline	tetR	AJ634602	CTAGATCGACATGTTTATCAGTGATAAAGTGTCAAGCATGACAAAGTTGCAGCCGAATACAGATGTCCGTGCCGCCCTGG	AR1-0009	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
80	Tetracycline	tetS	gi|24672104	GCCCTGTCAGTACGCCAGCAGATTTCCGAATGCTTGCGCCTATTGTACTAGAGCAGGCTTTTAGAAAGAG	AR2-1-0293	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1
117	Tetracycline	tetO		CTAGATCGACGAAAAGCAGAATATACCATCCACATAGAAGTCCCGCCAAATCCTTTCTGGGCTTCTGTCGGGTTGTCCAT	AR1-0098	1	1	1	1	1	1	2	2	1	2	2	2	1	1	1	1	1	1	1	1
147	Tetracycline	tetR	gi|37962716	AAAGTTGCAGCCGAATACAGTGATCCGTGCCGCCTGGACCTGTTGAACGAGGTCGGCGTAGACGGTCTG	AR2-2-0389	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
149	Tetracycline	tetA	gi|37962716	CTGCTGTCGACTACGCCATCATGGCGACGGCGCCTTTCCTTTGGGTTCTCTATATCGGGCGGATCGTGGC	AR2-2-0397	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
182	Tetracycline	tetA	gi|10957190	GTATTTAGGCCGTTTGCTTTCAGGGATCACAGGAGCTACTGGGGCTGTCGCGGCATCGGTCATTGCCGAT	AR2-1-0007	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
196	Tetracycline	tetA	gi|20386405	GAGGCTGGTCCGGAGGCCAGACGTGAAACCCAACAGACCCCTGATCGTAATTCTGAGCACTGTCGCGCTC	AR2-1-0207	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
232	Tetracycline	tetA	AJ634602	CTAGATCGACCAGCCTGACCTCGATCGTCGGACCCCTCCTCTTCACGGCGATCTATGCGGCTTCTATAACAACGTGGAAC	AR1-0008	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
283	Tetracycline	tetR	gi|57903205	TGCACTCAGCGCTGTGGGGCATTTTACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGGCTCGCTAAA	AR2-2-0619	1	2	2	2	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
401	Tetracycline	tetA(B)	gi|57903205	ACGCGTGAAGTGGTTCGGTTGGTTAGGGGCAAGTTTTGGGCTTGGTTTAATAGCGGGGCCTATTATTGGT	AR2-2-0613	1	2	2	2	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
452	Tetracycline	tetR	gi|46371958	ATTTTTATGAAGCCTGCCATTTCTCCTGACATTTTCCCGCCACGCGGCCACGAGGCCAAGCGTATGTCGA	AR2-2-0506	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
461	Tetracycline	tetD	gi|57903205	GGGGTCACACTGGCTAGCTATATTCGTGCTCGTCGTTTGACGAAAGCGGCTGTTGAGTTGAGGTTGACGA	AR2-2-0614	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
561	Tetracycline	tetA	gi|32469306	CAGCCTTGAACGGCCTCAATTTCCTGACGGGCTGTTTCCTTTTGCCGGAGTCGCACAAAGGCGAACGCCG	AR2-1-0345	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
566	Tetracycline	tet	gi|40207:18	AAGAGAACAGGGGGAAAGCATTTGGCCTGATCGGGTCCCTGGTAGCAATGGGAGAAGGTGTTGGGCCAGC	AR2-2-0432	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
569	Tetracycline	tetA	gi|40638503	TTTCGCAGTTTTCTTCATTATTCAACTGATCGGCCAAGTGCCTGCAGCCCTATGGGTCATATATGGCGAG	AR2-2-0444	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
575	Tetracycline	tetM	gi|48189:13	TCGAAGTTCCACCGAATCCTTTCTGGGCTTCCATTGGTCTATCTGTAGCACCGCTTCCATTAGGGAGCGG	AR2-2-0540	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1
629	Tetracycline	tetR	gi|40638503	AAGAGAATGAGGACTGGCGGGTGTTCCTGAAAGAGAATGCCCTGAGCTTCAGAACGGCGTTGCTCTCTTA	AR2-2-0445	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
739	Tetracycline	tetR	gi|34368360	TCGTGATGGTGGCAAAATTCATGCGGGAACACGCCCCTCTGAAAGTCAATTTGAGACATCAGAACAGCAA	AR2-1-0360	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
816	Tetracycline	putative Te	gi|53721033	CGTCGGGATGTTCGATGTGCTGCGCGAATGGTTCGAGCAAGCGGATTTCCACGGTTGCGCGTTCCTGAAC	AR2-2-0568	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
859	Tetracycline	tetH	gi|34368360	TGGCATTCTCAACCACACTTTGGATGCTCTATATTGGGCGCATCATTGCGGGGATCACAGGCGCAACAGG	AR2-1-0362	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
902	Tetracycline	tetM	gi|13899025	TTGGAACTCGAACAAGAGGAAAGCATAAGATTTCATAATTGTTCCCTGTTCCCTGTTTATCACGGAAGTG	AR2-1-0079	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1
922	Tetracycline	tetW	gi|37723032	GGGAGCGTCGAAAAAGGGACAACGAGGACGGACACCATGTTTTTGGAGCGGCAGCGTGGGATTACCATTC	AR2-1-0375	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
933	Tetracycline	TetA	gi|52211145	ACGTGCCCGTGATGCTCGGCAGCTTGATCACGTGCTTCTACTTCATGCAGTTCGTGTTCGGCCCGATCGT	AR2-2-0558	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
3	Transfer	traG	gi|10957190	TCAGTACCGGCGGAGTTCTGTATATCTCGCTCGATGGCCTTTCCAACCCGGAATCAGCCCGGGCCATTTC	AR2-1-0008	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1
			gi|10957190																						

5	Transfer	trhC	gi|10957190	TCACCTCATCGGTTGGTCGCGCACTAACGGCTAACTCGCCGTGGAAGATCATCATGAAGCAGGAAAAGGA	AR2-1-0016	1	2	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1
7	Transfer	tnpB	gi|14020964	ATAGATTCCATGCCCATGCCTTTCGCCATACAGTAGGAACAAGAATGATTAACAACGGGATGCCCCAGCA	AR2-1-0096	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	2	1
19	Transfer	repD	gi|2467210	GGACTTCGCCAGAAAAATTAAATGAACAAGCAATGGTTTACATGTTAATTCATGAAGAAGGCAAATGGGG	AR2-1-0288	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
41	Transfer	int	gi|5566608	GATGAAGCCTATGGACTGCTGGGAGAACGGGGCGAGGGACTTATCTTTGAGGATTTCAAGGACAAGATGC	AR2-2-0587	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
42	Transfer	mobA	gi|5566608	TAAGGAGCATCTGGAACGGAACGACTTTATCATTGAGAAGCAGAAAGCTGAACTGCAACGCATGGATGCA	AR2-2-0591	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
61	Transfer	insA	gi|37962716	CCGTAAAACATGGCAACTGCAGTTCACTTACACCGCTTCTCAACCCGGTACGCACCAGAAAATCATTGAT	AR2-1-0001	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
63	Transfer	traI	gi|10957190	GTAAACGAAGCTGCTTCGCCTCCACAAACACCGCTTGAACTCCCCCAACCACGACTGAATGCACCTGTGG	AR2-1-0009	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
64	Transfer	htdF	gi|10957190	ACCACGCATCGCACTCACCAAGCCTACAAAAATATCAATATCGGACCCAACGACCGTGGGGGCCTTTTGG	AR2-1-0013	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
65	Transfer	trhV	gi|10957190	TACACAAGGCTACAAACAGGCAGTCGTTGCACCAGAGCCTCTTGCTGTGCTTCAGCAAGGCCGCGTCATG	AR2-1-0017	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
66	Transfer	trhN	gi|10957190	AACTGGACTGGAGGGGAGAGCGGAACCTGGGCATCAATGGCTAACTCAGTGGGTGAATGGACTGCATCGG	AR2-1-0021	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
67	Transfer	tnpA	gi|14020964	CAACGCAGCTAATTAGGGAAAGATGGGATGTTGCGTTCGTTCAAAAGAGATTAGGTCACGCACATGTTCA	AR2-1-0097	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1
88	Transfer	repC	gi|37962716	CAGAGGTCGATAGTGGTGGGGCGCTCAAGCACATACAGGACTGCATCGAGCGCCTTTGGAAGGTATCCAT	AR2-2-0392	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
101	Transfer	tnpC	gi|5566608	TCTGTGCCTGGACCTACATCAGTCCCTGAGCCTGTACCCGAATCATCCCCCGACAAAAGAAGAGACACTTA	AR2-2-0588	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
119	Transfer	tnpA	AJ628353	CTAGATCGACGATGATCAAAACGCAGGTTGTCAAACTGACTACGTTCACGCGGCGATTATAGCCGATCAAATGATGAGCA	AR1-0106	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
121	Transfer	InsA-B-InsB	gi|58383237	CGGATGGCTGGCCGCTGTATGAATCCCGCCTGAAGGGAAAGCTGCACGTAATCAGCAAGCGATATACGCA	AR2-1-0002	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
123	Transfer	trhF	gi|10957190	AAGATAAGCAGGGTCGCGTCATTGCTTCTGCTGGCGAGCTCATTAACCCACTGGCCAGGTTCCCGCAGAA	AR2-1-0010	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
124	Transfer	htdA	gi|10957190	GGTCATTCCGCCTGCTGAAGCAGACCTGGTAAGCGCCGAGAATGATTTCCTTCGCGATGCAGGTATTGGC	AR2-1-0014	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
125	Transfer	htdT	gi|10957190	TCGGGTCGATATAGTTTTAATCCCCTCCCCCGGCGAGCCAAAGCAGGAATTGCGTCAATTATGGTGCAGT	AR2-1-0018	1	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1
129	Transfer	btgB	gi|143925:1	CAGGTGGAACGTGCGGAACGCATCAGAAAGGAGAAATGGGACAATCTCAAAGCGGAGCTTCAATCCCGGC	AR2-1-0106	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
146	Transfer	repE	gi|37962716	GGCGATGAAAAAGGCTATGAATCTTTTCCCTGGTTTATCAAACGTGCGCACAGTCCATCCAGAGGGCTTT	AR2-2-0385	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
148	Transfer	repA	gi|37962716	GTTAAAAAGCGCGAATGACGAGAGTAAGGAAAATCCGTTGCAACCTTCACCTGCGGAAAAAGTCAGTCCG	AR2-2-0393	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
150	Transfer	tnpAIS26	gi|37962716	GTTTCTGGGTAAAATCCTCAACAACGTGAAGAAGTGGCAGATCCCGCGATTCATCAACACGGATAAAGCG	AR2-2-0401	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
158	Transfer	putative tr	gi|53721039	GTGCTCAAACGCGCCTTGTTCCTCTCCGCCTTCGCTGCCTTACGAGACCCAGTCTCACGGGCCTATTCCT	AR2-2-0577	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
161	Transfer	tnpA	gi|5566608	TCACCTTTTCCAAAGCAGCCATCCTCATGGGCTGTTCCCGACAGTACATTTACAAACTTGTAGCCATCGG	AR2-2-0589	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
173	Transfer	intI*	AY458224	CTAGATCGACCTACTTGCATTACAGTTTACGAACCGAACAGGCTTATGTCAACTGGGTTCGTGCCTTCATCCGTTTCCAC	AR1-0011	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
178	Transfer	tnpM	AJ628353	CTAGATCGACCAATGAGGAACACCACCATGAACGCCAATGAACCGAGCACCAGTTGCTGCGTGTGCTGCAAGGAAATC	AR1-0103	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
183	Transfer	trhF	gi|10957190	TTCCGGAAGGGGAGGTCTTTTTAATTGGGCAAACGGACCACTCATGGGACTCACGTTTTTGGGGGCCGGT	AR2-1-0011	1	2	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
184	Transfer	stbA	gi|10957190	TTCATCACCTAGTCGATAATCGTGAAAACAAAGCCTCGCTCAAGGTGTCCCCGGAAGATCTTGACGGCGT	AR2-1-0015	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
185	Transfer	trhB	gi|10957190	TCAAGAAATGGTAATCGCAATCTCGATGCAGGCGGACCACGCAACAACGTCAATGAACAAGCCCCAGCAA	AR2-1-0019	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
186	Transfer	trhU	gi|10957190	CCGCCCCCTCACGCCCTGGTTGCTATTGCACGGATCAAAATGGGATACCAGAAATCGGATGGCAGCTAAG	AR2-1-0023	1	2	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
189	Transfer	btgA	gi|143925:6	AATGACCTATTCATGCGTGATCTTGCAAGCCTTGCCGGGATAAGGGAGCAGGCTTTGGACCTCGGCGGAAA	AR2-1-0107	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
209	Transfer	tnpAIS4321	gi|37962716	TCTGCTGGAATTTGGTATCAGCGTTCCGCGAGGTGCTGCCGTTATTAGTCGACTGAGTACCCTTCTTGAG	AR2-2-0398	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
221	Transfer	xis	gi|5566608	TGGACACCCACGTGCCCATGTCTGTGGACGAGGCAGCAGAGTATTTAGGTATCCCTAAGGGTACGCTCTA	AR2-2-0590	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
238	Transfer	intI*	AJ628353	CTAGATCGACCTACTTGCATTACAGCTTACGAACCGAACAGGCTTATGTCCACTGGGTTCGTGCCTTCATCCGTTTCCAC	AR1-0104	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
253	Transfer	rep	gi|21668299	GCCACAAGAATGGTTAGATTTATGGCGAGTTGTAACGGGCATTCAGAAATAACACAGTTCAAGTTCAAAA	AR2-1-0216	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
263	Transfer	repA	gi|32455896	GATGACTCACAGCGGCCCTATTTCGTGCGCTACGGCGTGAGCAAGGCCAACTATGGGGCACCGTTCAAAG	AR2-1-0328	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
279	Transfer	tnpA	gi|5689751	AAATACGACATGGCGGTGGGTCATCTCTTGCTAAAGTCATTTTGGGCGAATGAAGCCGTGTTTCAAATGA	AR2-2-0603	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
281	Transfer	tnpA	gi|57903205	CACCACATCATCATCGGACGGACAGAATTTCCGAACCGCTAGCAAGGCAAAGAGCACGGGGCACATCAAC	AR2-2-0611	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
282	Transfer	int	gi|57903205	CATTCAGGGACTGGTGTAGTGAACAGGGGTATTCGCGGGATCTGGCGGGAAAGGGCGCTCGCTCATACGCT	AR2-2-0615	1	1	2	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
293	Transfer	trans	AF516335	CTAGATCGACCGGGACACACAAGCAGCCTATGCTTTTCTTAAGCGGTTAGTGAAGCAGTTTGATGAACCGAAGGTTGTAG	AR1-0033	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1
294	Transfer	IS1182	AF516335	CTAGATCGACCGGGCCGCCAAATACAAAATATGCTGATAGATAGTATTCGGATGCGCTGCTTATCTCAAGAGCAATTCCC	AR1-0037	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
323	Transfer	repC	gi|32455896	AAGACCGGCAAGGCGTCCATAGACACCTTGTGCAGCTATGTCTGGCCGTCAGAAGCAAGCTCCTCAGCCA	AR2-1-0329	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
324	Transfer	mobC	gi|32455896	TGTCAAAAGCAGCGGAACGACTCGCAAAGCTAGAAGAGCAACGGGCACGAATCAACGCCGAGATACAGCG	AR2-1-0333	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
340	Transfer	IntI1	gi|57903205	ACGACATTCGAACCGTGCAGGATCTGCTCGGCCATTCCGACGTCTCTACGACGATGATTTACACGCATGT	AR2-2-0608	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
343	Transfer	mobA	gi|58383212	TGACAAAACGAAGTGGAAGTAATACGCGCAGGCGGGCTATCAGTCGCCCTGTTCGTCTGACGGCAGAAGA	AR2-2-0620	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
382	Transfer	mobB	gi|32455896	GCGCGATAGACAGAGTGAAGAAGTCCAGAGGCATCAACGAGTTAGCGGAGCAGATCGAACCGCTGGCCCA	AR2-1-0326	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
400	Transfer	tnpM	gi|57903205	GACGTTCAGTGCAGCCGTCTTCTGAAAACGACAATGGAGGTGGTAGCCGAGGGTGTGGAAACACCCGACT	AR2-2-0609	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
403	Transfer	tnpAIS1294	gi|58383237	AGATGGTGAGGTACTTCGGGTTCCTTGCCAACCGTGTGTGTGGAGAGAAGCTGCCGCAGGTGTACCGTGC	AR2-2-0621	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
411	Transfer	res	AF516335	CTAGATCGACAATGGCTGGTGTTAACCAATTAGAGCGAGATCTTATTCGGATGAGACAACGTGAAGGGATTGAATTGGCT	AR1-0027	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
413	Transfer	trans-1	AF516335	CTAGATCGACGAAGGCGGTGCTTCTTCACTTGAGAGCCAAAAAAGGGGCAGAAAAATTAGTATGAATTCCAAGCTAAACA	AR1-0035	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
433	Transfer	tnpB	gi|21885261	TCTGAATGTTCACTTCCACATGCTGTTTCTCGACGGTGTGTATGTCGAGCAATCCCACGGCTCAGCGCGT	AR2-1-0219	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
442	Transfer	repB	gi|32455896	AACTATCAGGCATGGGTAAAAGTGGCTCAGGACGCCCCAGCAGGTCACAGGGGCGTAATCGCCCGGAAGC	AR2-1-0327	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
449	Transfer	recP	gi|3947759	GGGTTCAAAAACACCAGGTCACCCAGAATTTGGTCATACGGCAGGGATTGATGCTACGACAGGTCCTCTA	AR2-2-0422	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1
456	Transfer	putative tr	gi|46747:c7	AGGGGACGTGGTGTAAACGTTCATCATTCAACGGTCTACCGTTGGGTTCAAGAATATGCCCCAATTTTAT	AR2-2-0522	1	1	1	2	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
457	Transfer	putative tr	gi|4704653	ATCGAGTGCTTTCTAAAAGCTGCCATATTGCGATCGGGATAACAGAAGGTGGCGACCGTGAAATCATTGG	AR2-2-0526	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1
460	Transfer	tnpR	gi|57903205	ACAGCGCATTGGGTATATCAGGGTCAGCACCTTCGACCAGAACCCGGAACGGCAACTGGAAGGCGTCAAG	AR2-2-0610	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
473	Transfer	IS150	AF516335	CTAGATCGACAAAAGGGAACTGAGGGTTCACTGATTCTACATTCAGATCAAGGATGGCAGTATCAGATGCCACAATATCA	AR1-0036	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
490	Transfer	tnpCX	gi|15778307	ACCCAACAACTTCATGTGCGCCTTCCACGCTACCGGTGCACCAACAAGCGTTGCTTGCAGAAGATCTTCC	AR2-1-0156	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
502	Transfer	tnpA	gi|32469306	CTTTAAAACCCGGTACTCCTCTAAGTATTTCGGCACCAACAAAGGGATCACGGCCATGACACTGGTGGCC	AR2-1-0348	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
504	Transfer	tnp	gi|3319647	CACACAGTCAGCCTATGCTTTTCTTAAGCGGTTAGTGAAGCAGTTTGATGAACCCCGAGTTGTAGTCACA	AR2-1-0356	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
519	Transfer	insA	gi|58383237	CCGCCGGACATCAGCGCTATCTCTGCTCTCACTGCCGTAAAACATGGCAACTGCAGTTCACTTACACCGC	AR2-2-0627	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
548	Transfer	tnpR	gi|155010:4	TGAACGCCGGAGGATCCTAGAGCGCACGAATGAGGGCCGACAGGAAGCAAAGCTGAAAGGAATCAAATTT	AR2-1-0149	1	2	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
550	Transfer	tnp1249b	gi|15778307	AACGACAACGCCGCATGCTGGATTGGTGGCTCTACTTAAAAACGGAACTGCCTGACGATCCAGTACGAAT	AR2-1-0157	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
563	Transfer	rumA	gi|32469306	AGAACTCACGGTAAAGGAGCTTCAACTAAGGCCGTGCGTCAAGCTGATCCCAAGAAACCAGGCGTATGAG	AR2-1-0353	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
609	Transfer	tnp1249a	gi|15778307	AATATCACTCGACGACCTAGCCAAACGAAACGGTGTTAGCCGCGCCACCATGAAGCGGCGCTTCAAGTGG	AR2-1-0154	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
621	Transfer	tnpA	gi|32469306	ACAATGCAATCTCCTGGAGCAACTGTTAAGGCAGGTGTTCTTGTGCCTTGAATGTGAGGCCGGTAAAGGC	AR2-1-0346	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
622	Transfer	int	gi|32469306	TTGCTGCCCCGACTTGGCAAGTATCCATTAACTGACATCACTGAATTGTCCTTGCGAAACTGTCTTCGTG	AR2-1-0350	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
630	Transfer	putative tr	gi|41056918	CCTGAACAACCCATGCGTCAGTGGGTGTTGAGCTTCCCGTTTCAGCTGCGTTTCCTGTTTGGGGTCGTTT	AR2-2-0449	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
638	Transfer	putative tr	gi|58383237	CTGTTCTACTCGTTCAATCTGGAAGATCACGTCCCGGCCCAACATCTCCTGCGCAGCATCGACCAGTGCT	AR2-2-0625	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
640	Transfer	tnpAIS186	gi|58383237	CGTGAAGTCACTGCATGGGCTCAGCTCCATGACGTTGCAACATTATCTGACGTGGCTCTCCTGAAGCGGC	AR2-2-0633	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
641	Transfer	repC	gi|58383237	GGCAGAGGTCGATAGTGGTGGGGCGCTCAAGCACATACAGGACTGCATCGAGCGCCTTTGGAAGGTATCC	AR2-2-0637	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
642	Transfer	tnpAIS4321	gi|58383237	ATCTGTGAAGCAGCATCACGTCCATCTATGCGTTTCGTGCAGCCCAGAACCGAATCTCAGCAGGCAATGC	AR2-2-0641	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
			gi|155010:5																							

670	Transfer	intI9	gi|1619774	TTCATGAAAAGGATCTTTGCGAAGGTGAGGGTAAAACAAGTCTCCCGTCAGGGCTCGCTCGAAAATACCC	AR2-1-0159	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
681	Transfer	tnp	gi|32469306	ATTCAACGTTGCGTCATTACGTCCAGCAAGCCTTGAACAGAGGTGAAGCATACCATCAGTTAAAACGTGC	AR2-1-0347	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
696	Transfer	trfA2	gi|5081740	ATGTTCGACTACTTTGCCACCCACAAGGAGCCGTACCCGCTCAAGCTGGAGACGTTCCGGCTCATGTGCG	AR2-2-0546	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
698	Transfer	repE	gi|58383237	GGCAGGCATTGAAGAGTTTCGCGGGGAAGGAAGTGGTTTTTATCGCCCTGAAGAGGATGCCGGCGATGA	AR2-2-0626	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
700	Transfer	tnpAIS6100	gi|58383237	GAAGGAAAGCTGGACCGGGAGACGGCCCACCGGCAGGTGAAGTATCTCAATAACGTGATCGAGGCCGATC	AR2-2-0634	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
701	Transfer	repA	gi|58383237	CGGCGTCCCCGGTTAAAAGCGCCGAATGACGAGAGTAAGGAAAATCCGTTGCAACCTTCACCTGCGGAAA	AR2-2-0638	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
703	Transfer	tnpAIS26	gi|58383237	GTATCTGTACCGGGCCGTCGACAGCCGGGGCCGCACTGTCGATTTTTATCTCTCCTCCCGTCGTAACAGC	AR2-2-0646	1	2	2	2	2	2	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1
723	Transfer	transposase	gi|14020964	AGGAACAAGAATGATTAACAACGGGGTGCCCCAGCATATTGTGCAGAAATTTTTGGGACATGAAAGCCCA	AR2-1-0080	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1
724	Transfer	putative tr	gi|14020964	TCGTGCCATTGATGCAGAGGGACATACATTAGATATTTGGTTGCGTAAGCAACGAGATAATCATTCAGCA	AR2-1-0084	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1	1
725	Transfer	repC	gi|14020964	AGCCGGTTGGACGCACATACTGTGTGCATATCTGATCCAAAATTAAGTTTTGATGCAATGACGATCGTTG	AR2-1-0088	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1
737	Transfer	tnpR	gi|2467210	TGCCTTTGCTCAATTTGAAAGAGATATGATTGTTAGCAGAACACAAGAGGGAAAAGAATTTCAAGAAAA	AR2-1-0280	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
756	Transfer	putative tr	gi|53721039	GTGGCAAAACGGTTTCGTCGAGCGTTTCAACGGCAAGCTGCATGACGAATTGCTGAACCGGGAATGGTTC	AR2-2-0567	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
783	Transfer	putative tr	gi|14020964	TCGAATCCCTTCGTGAGCGTCAAATAACATCAAATGTAGTCTCAAAACCCAAGAAAAGTTCTCGTTCGGA	AR2-1-0081	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1
797	Transfer	tnpA	gi|2467210	GACGCAATAAATTCTATCGGAAGTTTACGCACTGCCTCACCCACGATTAAAGGCATGGAAGCCATCCGAGG	AR2-1-0281	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1
798	Transfer	tnpA	gi|2467210	CGGATGCAAGATAAACTGGTGAGGGATTGCTTCTTACAAGCTTGTGGGAAAGAACATCCTCAGCCTGGCT	AR2-1-0285	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
799	Transfer	mobA	gi|34368360	TATCGAGCATGAGCGCGATAGACAGAGTGAAGAAGTCCAGAGGCATCAACGAGTTAGCGGAGCAGATCGA	AR2-1-0361	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
804	Transfer	resD	gi|37962716	TCCGTTATACACAGCCAGTCTGCAGTCATGGTACCGGCAGTGTATTCTGCCGGGCAGCCTGCATCGCTGC	AR2-1-0381	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
817	Transfer	putative tr	gi|53721039	AACGAAATACGGCGGGCTGTCGCCCTCGGAGTTGCATTGGGTAAAGCCGCTTGAAGACGAGAACGCGAAG	AR2-2-0572	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
856	Transfer	intI1	gi|2449645	GCATACGCTACTTGCATTACAGCTTACCAACCGAACAGGCTTATGTCCACTGGGTTCGTGCCTTCATCCG	AR2-1-0278	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
858	Transfer	tnpR	gi|2467210	TTCTCGGCCCGGAGACACAATTGTCGTTTGGCGATTGGATCGATTGGGAAGAAATATGGAGGATTTAATC	AR2-1-0286	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1
862	Transfer	putative tr	gi|37654998	GTCGTTACCAGAGCCACCGACCCGAGCAAACCCTTCTCTATCAGATCGTTGACGAGTATTACCCGGCATT	AR2-1-0374	1	1	2	2	2	2	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1
906	Transfer	tnpC	gi|14020964	TCGAATCCCTTCGTGAGCGTCAAATAACAGCAAATGTAGTCTCAAAACCCAAGAAAAGTTCTCGTTCGGA	AR2-1-0095	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1
917	Transfer	repB	gi|2467210	CAACCAATACGAGCATTACAGCAACAAGGGCGGACGAAGAGCCGAACAGGTAGAAGCCTACCGTAATCCG	AR2-1-0283	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
923	Transfer	int	gi|37962716	AAGTGAGTGCCCTTCTCTTCTATATGCCGGATCAGCGTCACCATATGCTGTTCGCCACCCTCTGGAATAC	AR2-1-0379	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
924	Transfer	putative tr	gi|37962716	CATCTCCTGCGCAGCATCGACCAGTGCTTGGATCTCAGTGATCTACGTGCCTACCTGGCAGATTTCTATA	AR2-1-0383	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	Trimethoprim	dfr16	gi|14091021	TTGGACGCAAAACTTTTGAGTCAATGGGCGCTCTCCCAAATCGAAAGTATGCAGTTGTAACTCGCTCTAA	AR2-1-0100	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	Trimethoprim	dhfr1b	gi|14861605	TCTGGTGGGTCGCAAGACGTTTGAATCTATGGGCGCACTCCCCAATAGGAAATACGCGGTCGTTACCCGC	AR2-1-0116	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
59	Trimethoprim	dfrA1	AJ628353	CTAGATCGACTTATCTCTCCTCCCGTCGTAACAGCAAAGCTGCATACCGGTTTCTGGGTAAAATCCTCAACAACGTGAAG	AR1-0105	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
72	Trimethoprim	dhfr1b	gi|14861605	GGCGGAGAAATTTACCGAGAAACATTACCCATGGCCTCTACGCTCCACTTATCGACGATCGACATCGAGC	AR2-1-0117	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
177	Trimethoprim	dhfrIX	X57730	CTAGATCGACCAGTTTTGATTATGGGTAGAAAAACTTTTGCCTCACTGCCTAAAGTGCTGCCCGGACGACTTCATGTGGT	AR1-0099	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
187	Trimethoprim	dfrIIc	gi|14091019	CACAAAACTGACCCCTGAAGGCTATGGCGTCGAGTCCTGCACCCCGGTTCAGTACGATTTATCCT	AR2-1-0099	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
237	Trimethoprim	dfr1	Campylobact	CTAGATCGACAGCCGGAAGGTGATGTTTACTTTCCTGAAATCCCCAGCAATTTTAGGCCAGTTTTTACCCAAGACTTCGC	AR1-0100	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
255	Trimethoprim	dhfrXII	gi|21898656	CCACTGGCTGCGTAGTTGTTTCAACGCTGTCGCACGCTATCGCTTTGGCATCCGAACTCGGCAATGAACT	AR2-1-0224	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
258	Trimethoprim	dfrV	gi|24209695	CAAGACGTTCGAATCTATGGGAGCACTCCCTAATAGGAAATACGCGGTCGTTACTCGCTCAGCCTGGACG	AR2-1-0236	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
315	Trimethoprim	dhfrXII	gi|21898656	TTTGAGTCTATCGGCAAGCCTCTACCGAACCGTCACACATTGGTAATCTCACGCCAAGCTAACTACCGCG	AR2-1-0225	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
318	Trimethoprim	dfr17	gi|24209695	TCTGCAGTGTCAGAAAATGGCGTAATCGGTAGTGGTCCTGATATCCCGTGGTCAGTAAAAGGTGAGCAAC	AR2-1-0237	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
437	Trimethoprim	dfrV	gi|24209695	GGCTGCAAAAGCGAAAAACGGAGTGATTGGTTGCGGTCCACACATACCCTGGTCCGCGAAAGGAGAGCAG	AR2-1-0235	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
438	Trimethoprim	dfrB2	gi|24209702	ACGCAAGAAATCTGGTGCCGCTTGGCAGGGTCAAGTCGTCGGTTGGTATTGCACAAAACTCACTCCTGAA	AR2-1-0239	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
493	Trimethoprim	dfrB2	gi|24209702	GAAATCTGGTGCCGCTTGGCAGGGTCAAGTCGTCGGTTGGTATTGCACAAAACTCACTCCTGAAGGCTAT	AR2-1-0240	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
497	Trimethoprim	dfrII	gi|24209732	GCAGCGTGTCGTCGGGCCACATAGAACACCTAGAAGTTCACAAGAAAGGTCGGAAATGGAACGAAGTAGC	AR2-1-0256	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
514	Trimethoprim	dfr1	gi|47679404	CAATGGCTGTTGGTTGGACGCAAGACTTTTGAATCAATGGGAGCATTACCCAACCGAAAGTATGCGGTCG	AR2-2-0535	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
554	Trimethoprim	dfrVII	gi|24209716	TGATTTCTGCAACGTCAGAAAATGGCGTAATCGGTAATGGCCCTGATATCCCATGGTCAGCAAAAGGTGA	AR2-1-0245	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
633	Trimethoprim	dfr17	gi|47679401	TGGGTGTTCTTCCAAATCGCAAATATGCAGTAGTGTCAAAGAACGGAATTTCAAGCTCAAATGAAAACGT	AR2-2-0533	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
676	Trimethoprim	dfrII	gi|24209732	AATCCAGTTGCTGGCAATTTTGTATTCCATCGAACGCCACGTTTGGTATGGGAGATCGCGTGCGCAAGA	AR2-1-0255	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
695	Trimethoprim	dhf	gi|4973271	GAATCATGCTATCTTGATGGGGCGTGTGACCTTTGATGGGATGGGGCGTCGCTTGCTTCCAAAACGGGAA	AR2-2-0542	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
732	Trimethoprim	dfrA10	gi|17157968	ACCAGAGCATTCGGTAATCAAGGCAAATTACCTTGGCAATTCATTAAAGAAGATATGCAGTTCTTCCAGA	AR2-1-0188	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
943	Virulence	emm	gi|8038089	TAGTCGTAAGAGCTTAAGCCGCGACCTTGAAGCTTCTCGTTGCAGCTAAAAAAGAGCTTGAAGCTGGCCCA	AR2-2-0670	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14		cynR	gi|18507939	GAGCTTACCGGATACTCAGCGTGCTGGAGGACACCCGGCGGGCACTGAACAACCTCAACGGCGATGTCAG	AR2-1-0196	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15		alr	gi|18699002	CATCCCAGGTGTAGCTTTCGGCCACGACTGGATGAAATCCATCAAGTACTACCACCAAACTTTGCGACAC	AR2-1-0200	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16		FN1023	gi|19714603	ATATTTTATTTTCATAGTGCTTTAGAAGGAACTAAGGTTGATATTATGAAAAGGGATAATCGTGTTTCAT	AR2-1-0204	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17		ProP	gi|20515372	GTGCCCCGTTATGCTGACAGGATAGCTGAAAGATTCGGAGGGGCAGCTCGCACACTAATGATTGTCAGTA	AR2-1-0208	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20			gi|2467210	CTGTGCCCTATATGTGGCAATAAGACCCGTTTAAAAATGAGGGAAGATACTGAATTAAAAAATTTCCCTC	AR2-1-0292	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1
22		Orf(+5)	gi|26541493	AGACCTCGATGGCCGACGGCGACGAGAGCGGCATGGCCGAATACGGAGACCTGATGACGGTCTTCGAGCT	AR2-1-0300	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
23			gi|27314460	GGAGCTTATATGCTAACGGCAATGCTATTTCGTCCCTGGGCTGGTCAAATTATTGCACGTATTGGTCCGA	AR2-1-0304	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
29		vagD	gi|37962716	AAGATCTATATGCTCGACACGAACATCTGCTCGTTCATCATGCGCGAGCAGCCTGAAGCAGTGCTTAAGA	AR2-2-0395	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
30		mphR(A)	gi|37962716	GTTCGGAGCATGAACACTCGCAACGACTTCTCGGTGAACTATCTCATCTCCTGGTACGAGCTCCAGGTGC	AR2-2-0399	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
38		GrhL	gi|53721039	CAGTTGGACCGAAGGCGAGCAGTACTCGTCGCGTGAATTGACCGAGATATTGGCGAATGCCGGCTTTTCG	AR2-2-0575	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
39		tlrB	gi|5420302	GGTCACCATCTCGCCCGTGTCCTGGAGGAGTTCGAGGACGCCGAGGGACTCCTGCTGGACATGTCCAAGC	AR2-2-0579	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
43		s015	gi|56237004	GTCGAGCGTCAGCGCGGGTGTGAAAGCGCTGGAGGATAACCTTGGTGTCCTGTTATTTGAGCGCCATGCG	AR2-2-0595	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
44		bft	gi|8117945	AAAGAGGGACTGGAAGGCTTTACTGCTTCACTAAAAAGTAATCCAAAAGCAGAAGGTTATGACGATCAAA	AR2-2-0671	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
46		blrB	gi|9662892	CTATGTGGTCGATCGCTGGGGCAAGGTGGTGTACGACTCGGACGGGGTGGATCTGGGAAAGGACTACTCG	AR2-2-0679	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
62		opcM	gi|1061409	GTCGGCGTACTTCCGAAGCTCGATATCACCGGGTCGTTCGGCTATAAGCGTCGACGCTCGGCAACCTGTT	AR2-1-0005	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
70			gi|14524254	ATTGCCAACACCCTTGCACTGGAATCCAGCACTCTTACACCACTCTTGAAGCGCCTTGAGACATCCGGCT	AR2-1-0109	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
73		BMEI0403	gi|17982305	CTTCCTGTCATCGCTTTCCTCCACCATCACCATCCTGACGGTAGCAGGCGTCATCGTTCTCCTTGATTAT	AR2-1-0193	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1
74		korA	gi|1865694	ACGCGGCTGACCGCTTGCGATACCGCCCCCTTGGTCAGCCCCAGCGAGGCCACAAACTCGGCCTGGGGCC	AR2-1-0197	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
79		mob	gi|2467210	AAGACGAATTGCCAAAGTATTTAAATGAGCGTGGTTTTGAGCTTGAACGTGGCGAAAAAGGGTCAGAGCG	AR2-1-0289	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
81		marC	gi|26107943	GCAATAGGCCTGGGGCTGGTGGTGTTACTGCCGTTAGCTAACCCATTGACAACTGTCGCGTTATTTCTTG	AR2-1-0297	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
82		Orf (-35)	gi|26541493	GACAAGAGGTTGCACACTTCGAAGTCGAGCTCGCTCAAAGGCTCGCCGAGTTCGGATCTCCGGTGGGCCT	AR2-1-0301	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
87			gi|37962716	GACCAAGCAGAAGCGCAGCCTAGCGGCCTTTCACCGCGAAGTCACTCAGGTGTGCAAGGCTCAAAAACTG	AR2-2-0388	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
89		vagC	gi|37962716	GATCTGGATTTTGAGGGGGTGAGTGAGCTGGAGATTGTACGGGAAGGGGACAGAATCATTCTGCGTCCCC	AR2-2-0396	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
90		mrx	gi|37962716	CTTTTCTCTGGAGCGAACCCCTGCTGCGCCCTCTCTTTGGTATAGTGATGATCTTCGTGGGCATCGTTGG	AR2-2-0400	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
92		kmr	gi|44886007	AGGGCAAGGGCCTCGGCTGGAAGCTGCTCGACCAGATCAATTCCCCCGTCCTGGTGGTGAGTTTCCCCAC	AR2-2-0480	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
			gi|4581956																								

100			gi|5465436	GACCACCGGCGGGGTCACCAGACTGATCGACCGGATACAGGCGGCCGGCTATGTCGAACGCTGCTACTGC	AR2-2-0584	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
104		bft or bft-	gi|8117961	GAGCGGCAATGCCGATGAAGGGCTGGATGGCTTTACTGCTTCACTAAAAGCTAATCCGAAAGCAGAAGGT	AR2-2-0672	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
106		ompC	gi|9714149	TTTGGTATCGGTGCTGCAGTTTCCAGCTCCAAACGTACCTGGGATCAGAACAACACTGGCCTGATCGGTA	AR2-2-0680	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
127			gi|14020964	CGCCAGACTTTGATTTCGAATGTGAAACTTCTATGAATGCTAAGGCAAGGAGCGGAGAGGCAATCACCG	AR2-1-0098	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
133		BMEI0883	gi|17982828	CGTTTCCTAGTGTTGGTTCGCGTGCCGCACTTCTCGGCGTTATTTTCGTTTGCCTGCTGATTACCTATTT	AR2-1-0194	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
137		ceoA	gi|2109269	GCTGGTATCGGTGTCGCCGATCTACGCGTCGTTCGACGCCGACGAGCAGACCTACCTGCAATACATCAAC	AR2-1-0210	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
140		nagC	gi|2541899	GAGCACTATTTCGGAGCCAGCCAAGATTGCCAAGACTCCATACTAGTCAGTGTACACCGTGGCACAGGTG	AR2-1-0294	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
159		sdaA	gi|5430711	CATGCGATCCGATTGGCGGACTTGTGCAGATTCCTTGTATTGAGAGAAACTCGATGGGAGCAATTAAAGC	AR2-2-0581	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
164		bft-3	gi|8117963	ACTTTATACTACTGAATATGCTTGTCCGAGCGGCAATGCCGATGAAGGGCTGGATGGCTTTACTGCCTCA	AR2-2-0673	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
166		cbaR	gi|9820075	AAGAAGGCCAGGCAATGCACGACAAGATCATTCTGTACGCGCTCCATCGCGAAAATTCGCTCCTGTCTGT	AR2-2-0681	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
181			gi|7800243	TCAATCAGAAGATAAACATTCAGGCCCGGAACTGGAGCCTAGTGTGTCGGAAGATGTTGCTTTGCCTGGT	AR2-1-0003	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
192		SP0727	gi|14972200	ACAGATTTGATTAGGGTTTTGGCAGAGCGGTTTGACTGGTCCAAGTCCACGGTTCAGACACTTTTGGCTC	AR2-1-0119	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
193		BMEII0796	gi|17984975	AGCGTGAGTTGGCCGATGCTTTGGAAATAGAGCATCCTTCGGTGGTGCGTCTTCTGGACGGCCTTGAAAA	AR2-1-0195	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
194		alr	gi|18699002	ATTCTTGACTCGATCTGATTTACACATGGAGATGGTCCGACCGGGTTTGGCCTTTTATGGGTTGGACCCT	AR2-1-0199	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1
195			gi|19713441	TGTGTTATGGGAACAGGTTTAATTTCATTTGTGGAAGATAAGGAAGAAAAAGCAATGGCTTTAAATGAAA	AR2-1-0203	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
197		ceoB	gi|2109269	ATGAACATTTCCAAATTCTTTATCGACCGGCCGATCTTTGCAGGAGTCCTATCGGTGATCATCCTGCTCG	AR2-1-0211	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
199		ORF25	gi|2467210	GGAATCATCTTCTTTCTCAACGGGAAAGGAGGTGTGAATGACATGAGTTCTTCCCTGTTCCAAGCTGCCA	AR2-1-0291	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1
201		papX	gi|2610970	CACCAAAAAAACAAAGACCCCGCATATCCCTTTCGGGAGCATTTGTTGATGCAACTCTGTATTCGCACAA	AR2-1-0299	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
208		vagC	gi|37962716	TATCCATTTTTAAAAATGGCAACAACCGTGCTATCCGCCTTCCACGCGATCTGGATTTTGAGGGGGTGAG	AR2-2-0394	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
210			gi|37962716	TTGCAGGGTGAGACCGCGAAATCTGAGCGGGTGAACGACCGGAAAATCACGGCAGACGGGAAGGAGGGAC	AR2-2-0402	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
225		blrD	gi|9662892	CTTCTATCTGGTGCTGCTGGCCCTGACCGAACACCTCGGCTTTGCCTGGGCCTATCTGATTGCCACCCTG	AR2-2-0678	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
243		marC	gi|1170657	GTGCGTCAGAGTTCAACCTTCGCTGATTGGGTACTGATGGTTGCGCCGCCGCTGATCTTTTTCCTGGTGG	AR2-1-0032	2	2	2	2	2	2	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1
244		ydiC	gi|12723250	TTTCCATTTCAGCAATGTTTGTATCGGTTGGCTCAATCGCTGGACCTGCCCTTGGAGGACTGATTTTACA	AR2-1-0036	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1
245		rmaG	gi|12723678	TGAACGCAAGCGTTCTACAGCGGACAGACGAGTGACTCACATTATACTGACATCGAAGGGTGATGAGCTT	AR2-1-0040	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
246		rmaI	gi|12724527	GAACATATATCCAAGGTCATAATCAAAAAGCTTTGGCGGGTTTGTCAGCAGAGGAGATTGCTGCAGTTGA	AR2-1-0044	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
247		CAP0133	gi|14994317	ACGTGGTCACGGTGCCTCCAAGTTAAAAAACGGAAGAAAGTTTGTAATGGAGGATGTGATTGATGTT	AR2-1-0120	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
248		CAC0197	gi|15023026	CATGATGGCTGTGTTCAAAAGGATATTGCTGCGGCGTGTGAGATAGAATCATCTACGGTAACTAGTCTTC	AR2-1-0124	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
249			gi|15074266	GAGTCGGGAAACCTGCCGTCGATCCGTCTCCATGAGCAACTCGGTTTTCGCGAGACCGGCCATATGAAGG	AR2-1-0128	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
250		ydeR	gi|15157262	GAAAATGATGACAACGCGTTGTAATTGATGGGGATGATGTTGAAGCGACATCCATTTCCCCGGCTCTGACG	AR2-1-0132	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
251		actII	gi|153143:2	CTTCTTCAACCACGTCTTCGACTTCGCGGGAGCCGATTCGGCCTTCCCCCTGTGGGTCTTCGTCTTCCTG	AR2-1-0136	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
252			gi|1532136	TCGGTCACCCTGTCGTGGTGGGCGCCACCCTGTTCTCGGCCAACTTCCTTGTTGCCGCTGTACTTCCAGT	AR2-1-0140	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
257			gi|2272637	GCCAATATCTATTATAATCAGCCAATGCTGGAGATCATACAGAGTGACCTTGGTGTGCGCATGACGGCGC	AR2-1-0232	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
267			gi|38490319	ATATCCAGCGTTCCTTCCCGTCCTACGACATCGGGAGCCTGTCCTGGATTCTGAACGGCTATAACATCGT	AR2-2-0411	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
270		spi	gi|3947761	TCCATGGATCCGACCCTAGCGGATGGTGAAATCCTCTTTGTTGTTAAGCACCTCCCTATTGACCGTTTTG	AR2-2-0423	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
271		xpt	gi|3947767	GAAAAATTTGCTGCTACTGGCATTACCAAGGTCGTAACCATTGAAGCGTCGGGTATTGCCCCAGCCGTTT	AR2-2-0427	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
275		putative et	gi|46371975	CTGGCTGAATACTGAAGTGGCAGGCGCTTGTGGACTGATCGTGCATGAACTCGTCTCAAATTCGTTAAAA	AR2-2-0515	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
277		tsr	gi|46770:35	CGGGGTGGAGTTCATCGAGGTCTACGGCAGCGACAGCAGTCCTTTTCCATCTGAGTTGCTGGATCTGTGC	AR2-2-0523	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
280		ard	gi|57546753	AGTACTTCGAGGCCGGCTTCACCGTGGTCGCTCAAGACGTCATCCTGGGTGACCACCTCACCCAGATGAT	AR2-0607	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
304		yffB	gi|12723446	GTCAAGGTCTTTTGCAAAATTTTATTGGTTCAGAGTCTGGCAAAGCAAAGCGTTGTGCCATTACAAGCGC	AR2-1-0037	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
305		rmaH	gi|12723840	TGCGGAAGAAATTCGAGTAGAAGCTTGCTCAAATTTAGCACGCGTTTTTGAAGAAATGGGTGAAGAACGA	AR2-1-0041	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
308			gi|15023422	TTGGAGGTTCAATTGGATCATTTGTTGCAGCTGTATTTTGGCAAAAGTTTGGATGGAGTGGTGTGTGTGC	AR2-1-0125	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
309			gi|15074266	CAATCTCTTCTGCAATCTGGAGCTTCCCGTCGTAAGCGCTCCGGGGCGCCTAACCAGACAGCTTGCAATC	AR2-1-0129	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
311		actII	gi|153143:9	GATGATTCCGGAACTCCGGTCCCTGGTAATTTCGCATCCGCTGAACGAGACCCTGCACGCCAAACTGATG	AR2-1-0137	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
312		cre	gi|153217:2	GTCTGTTGTCGCCCTCGGTGCCACTTCCATAACACCACCACGGCCCGGAGAGCCAGGGCCGACCGTTC	AR2-1-0141	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
320			gi|29539351	TAAAAAATTTTTACAATACAGATCTACCAGCAATACCTCATACCAAATTGAGAGATGCCCTTGCTCACGA	AR2-1-0317	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
322			gi|32446253	TTGGTAAAGCCAATTGTCGAACATCTTCGCGAACTTGAACACGAAGTCATGAGCGAACTAAAACGTCGCG	AR2-1-0325	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
326			gi|38490250	AAAGTCGAAATCACCACCTTGGTGCATATGCATTCGTCGCTGTTTGGTTGCCTACCTTGCGCTGCTGATCG	AR2-2-0408	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
327			gi|38640798	GCTGTTACGACGGGAGGAGAGATAAAAATCGACAGTGCGGCCCCGGCTGTCGACGGCCCGGTACAGATAC	AR2-2-0412	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
329		gdh	gi|3947753	CCGCTCTGGTAAGATTGATGGCATGAAATACATCTCTTATCGTAGCGAGCCAAATGTGAATCCAGAATCA	AR2-2-0420	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
330		xpt	gi|3947763	CAAGGTCTTGATTATCGACGACTTCCTTGCTAACGGCCAAGCTGCCAAAGGCTTGATTCAAATCATCGAA	AR2-2-0424	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
336			gi|46399275	TCAGCGGCGTTGACTTGTCAGGAGCAATTTTCCACAATTGCGATCTGTGCAATGCAGATTTTTCTAGTAG	AR2-2-0520	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
337			gi|46826:27	TGGTGAAGTACTCCGAGGACGACCTGGTCGACAACTCGCCCGTGACCGAGAAGCACGTCGAGGACGGGAT	AR2-2-0524	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
339			gi|56908016	CTATTTACGCGAGTGCTTTCATACGGTTGGCCGGAAGGATTTCCCGAAAATCTTTCAAGGCATGCAAGAC	AR2-2-0604	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
341			gi|57903205	TGGATTGGAAGGGGGAGGGATATTTACGGTTGGTGATGAATGCCATGCTCATTTTCTTGTTGAACAAGGA	AR2-2-0612	1	2	1	2	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
364		rmaJ	gi|12723474	GGCGAAGAACTCTCTTTAGATTCTGGTACATTAAGCCCTCTGCTAAAAAGATTGGAAGCAAAAGGATACA	AR2-1-0038	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
365		rmaF	gi|12724274	CCGTGCATTTATTAAACAAGAGGACGACCTAGTACTTTCTTACGGAATTCGTCAAGTACATCGGCGAATT	AR2-1-0042	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
366		lexA	gi|13092922	GAGGGTACGCTCTTTTTACTCAAGGTGACCGGCGACTCGATGGTCGAAGCCGCGATCTGCGACGGTGACT	AR2-1-0046	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
368			gi|15072928	CGGACTTCTACGTCAGGCATCTAAGCTTCGAGGCGCTTTTCGTAAGCGATTGGTACATGCACCTCCAGTC	AR2-1-0126	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
369		folP	gi|15074575	GCGACCGGGAGAAACTGAGCGATGTGATCGAGGATCAGTTCCATTTCCTGGAAGCGTTCCCTGCAGATCGC	AR2-1-0130	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
371		actII	gi|153143:6	GCTGAAGACCGGACACGCCTCGCTGTACGCGCACGTGGGGAACCGGGACGAGCTGCTCGACCTCGTCTTC	AR2-1-0138	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
372		hur	gi|153314:1	TCAAGGGGCGGGCGTGGCTGCGTAGGGTCGGGGCCGTGGTGGAGATTCCGGCGGAGTTGGTCGAGGTGCA	AR2-1-0142	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
375			gi|21898656	CAGGTTTTCAGTCCTTTTGGGCTCTAGCCCTTGCGTAGCAAGCGCAAGCAGCTATCGTTTTTGCAGTGCT	AR2-1-0226	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
377		slyA	gi|24080785	TGACGGAAAAGGCAGAGCCACTGATCAGCGAAATGGAAGCTGTTATTAACAAAACCCGCGCGGAAATATT	AR2-1-0234	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
378		orf2b	gi|24209702	GCTGTCAGTTACTTTGGCTTCGGCCGCAGCGTGTTTCGGGTTCCCTTGAATGCCTAACAGTTCATTCAAG	AR2-1-0238	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
379			gi|29539351	TCGGTCATTGGGAAGCTGACACAATTGTATCCAGCAGAGGCAAAAGTAAAGGGTGCATTGCTACTTTCGC	AR2-1-0314	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
380			gi|29539351	TGCGCATCATTGGATGATGGATTCGAAGACGCCTTTCAATATACCGTACAAGGAAATTCCCACAATCGAC	AR2-1-0318	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
381			gi|3152962	CTGGCTTCTTCCGGTGCTTTGCTTTTTGCTCACATGTTCTTTTCGGCTTTATCCCCTGATTCTGTGGATA	AR2-1-0322	1	2	2	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1
384		ycgE	gi|32468690	CTCGTGGAAAAGGACTCCGAACGATCGCAGGAGAGTCGTAATCGTCCCTTTGACTGCTTCGAAAAAACAT	AR2-1-0334	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
386			gi|38490250	AGTTCAGCCTGGAATTGAAGCTGCTGTTACGCAACGGCGAGCAACTGCTGTTGACCATGTTCATCCCGAT	AR2-2-0409	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
387			gi|38684030	GGACCGTTGAAATGGATTTACCTGACCATGTCGGTGCAGATGATTGCGGCAATGGTCGATACCTACGTGC	AR2-2-0413	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
389		gki	gi|3947755	ATCGCATGTACTTGCGGTAAGAAAGGCTGCCTTGAGACAGTTGCTTCAGCAACAGGGATTGTCAACTTGA	AR2-2-0421	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
390		xpt	gi|3947765	CAGGTGACCAGCACCGTTTCTATCGCTGGAAAATTCCTCTCACCAGAGGACAAGGTTTTGATTATCGACG	AR2-2-0425	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
			gi|3955037																								

395			gi|46371978	ATTTGCCCATGGGTATGCCGGCGACTTCTGGACGCTGGATCGGATCGGTCAATTGATTTGGCAGTTGTTT	AR2-2-0517	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
423		napB	gi|12723173	CCCCTTATCCAAATGTGACCAAATTAGCTCATCATCTCTACATGACACGTGGTGCTGCCAGTAAAATCGC	AR2-1-0035	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
424		rmaA	gi|12723647	TCGATAAATCTAGTGTTCATCGAGCAATTAAAGGCCTGATTGAAAAAGAATACGTTAGCAGAGTCCGCGA	AR2-1-0039	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
425		rmaE	gi|12724467	ACGAGGAGCAAGTATAACAAGTATGCTCCAAGGTTTGGAAAAAAAAGGATATATCGAAAGACGAATTCCT	AR2-1-0043	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
426			gi|13093786	CATATATCACGACAAAGTCGTGGAATCCAGGAAACCAGAGCAGATATTCGAGACCGCGCAGACTAAGCGC	AR2-1-0047	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
427		effR	gi|15011953	CGCCATCAGATGTTTTGTCAGGCAGAGTCTGGTCCATTTGCTGATACATCACGAGGACAAGGAAGAATTC	AR2-1-0123	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
428		fsr	gi|15073719	AGAACGTCTATCTCACCAGCATCTCGAGCTATTTCACCTTCTTCGTCATCGAAAGGTTCGACACCAGCGT	AR2-1-0127	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
429			gi|15076142	CTATGCCTATGCCTCCGCCTTCCGCAACCGCACCGCCTATCGGTTCCTGGTGGAGGATTCGATCTATCTT	AR2-1-0131	1	1	2	2	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
430		actII	gi|153143:1	ATGACGCCCTGGTCGGTGTTCCTCGTCGTCGGCGCGATCCTGACCGGGGCGGTGCTGGGATCGAAGTTCG	AR2-1-0135	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
431			gi|1532136	CTGCAGTTCTTCATGACCTTCCAGAGCGTGCCGGACGAGGACATCGTGGACATCGTGGACACGGTTTTCC	AR2-1-0139	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
436			gi|22726377	ATCCAAGCTTTGCTGTTCGCCTCGTTCTCCGCGTTCTGGACGGTCCTTGCACTTTATCTCGACAGCCCGA	AR2-1-0231	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
439			gi|29539351	GGAAAAAGAGTATTCAAAACCATGAATCAAAGATGAATGAGGATTCTAAAGCCCTCTACCATGAATTGGT	AR2-1-0315	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1
440			gi|29539351	AAGGTTGTCCTTATGATAACGCAGTTGCGGAAGCAACGATGAAAGCAATGAAAACCGAATTTGTAAAACA	AR2-1-0319	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1
444		ybfA	gi|32468690	AGTAGAACTGATGCTGAAGGTAATCAACCAAAAGGAGCAGCACAAGCTTGCCGAGGCGATGGCAGAGATT	AR2-1-0335	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
446			gi|38490250	TATGTAAGCGATACGGGTCAATAACCGCCGTTTCCAACCTCGATCTCGACGTGCATGACGCCGAAGTGAT	AR2-2-0410	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
450		xpt	gi|3947767	GCGGAAAAATTTGCTGCTACTGGCATTACCAAGGTCGTAACCATTGAAGCGTCGGGTATTGCCCCAGCCG	AR2-2-0426	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
451			gi|3955037	GTCCCCGAGGGCTACTCTACTTTGTGGAGGTGCTACATAGTGAAGTCATTTCACGATATGCCGGAGCGGC	AR2-2-0430	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
454		hspA	gi|46371975	GACGAGTTTATTCTGTCGGCCGACTTGCCCGGACTGACCAAAGACGACATTCACCTGGAGGTCCATGACC	AR2-2-0514	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
458		trlWM1	gi|56805552	TGATGAAGCACGCGCACTTATTAAACAGATTAATACAGCACGTTGTGAGTTAATAGAAGCCCGATGCCAA	AR2-2-0602	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
459		hur	gi|57546753	CTCCACTGGGACCTGCACTTCGACAACGTCCTCGCCTCACACCGCGCGCCCTGGCTCGCCATCGACCCGA	AR2-2-0606	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
463			gi|58383237	CCAGCAGGGCGCGTACATTGTCGATATTGCGGCTCAGATTGGTTGCTCTGAACGGACGGTCAGACGCTAC	AR2-2-0622	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
481		ML2350	gi|13093909	GGTTACTGGGGTGATACTCGGTTTCCGGTTTCGGCAAGGTGTGATTGCAAGCCTTATGTGGGTTAGTGTC	AR2-1-0048	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
482		hpcR	gi|13236168	CGAAAGAGCAGGTTGAACAGGGATATCGGGCCATAGAAAAAGCCTTTTCGCCGGAGAAGATGGTTCAGCT	AR2-1-0052	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
483			gi|13421507	GCCGCCTTCCTGATCTGCGACTGCTGCGGCGCGACCCGCGAGATCGAACCCAAGGCCAGCGCCGAGATCA	AR2-1-0056	1	1	2	2	2	2	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1
489			gi|15723943	CCTTTAACACACTACTTAACCTGATCGTTCACTGGTGGAGTTTGCAAGAGTGGCCGCATCCGTCAATGGA	AR2-1-0152	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
491			gi|16197747	TTCTCTGGTGGCGCCTTTTTTAACCTGCTCGTGGAAGATGCTGATGAGCTTCACTCTCGACTAACCCAAG	AR2-1-0160	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
492			gi|16262453	CTATCTGGGCAAGGTCAGGGACGACTGGGGAAATCGGCAGTCTGCTTCCGAGCGGACAGCAACATTTCTG	AR2-1-0164	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
499		yclA	gi|32468690	AAGTGACACAGTACAATTCAAGCAGCTTGATGACATTCCATGTGTGCTCGTGCTTTCAGATGAAGCCGGA	AR2-1-0336	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
500		ytbD	gi|32468802	CACGACAGCAGGATTGACCGTTTCCCTTTATGCGCTCGGCGTTACATTTGGGGCACCTATATTAACTTCA	AR2-1-0340	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
506			gi|39550037	GAGCTGACCGACCGGATCGGCGAGCTGGCCAAGGACACGGAGGTCGTCGTCTACTGCCGCGGCGAGTACT	AR2-2-0431	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
511			gi|41352785	AGGTGGCGTTGGACTTTCCGGAACTGGTGATCGTGTGCGGACATGTCGGCTATCCGTGGACCGAGGAGAT	AR2-2-0451	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
512		mlr2264	gi|47118328	ATGACTGATACCAATGACGGCCAGCTGTGCGAGCGGCTGCCGGCTGCGACCATCACCGGCCCGCAGACGC	AR2-2-0527	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
513		mmcW	gi|4731328	CTCCAGCGGGAAGCGGACATGCCGCACCTCTATTACGGTCTTCTCGTCCAGCTCTCCGAGGCCCCGCGCC	AR2-2-0531	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
517			gi|52211453	CGTACTTCTGGTACTTCCGCAATCCGGCGGGCGGCCTCATCGAGTATTACGCGGACGAGGACATGCTCAC	AR2-2-0547	1	1	2	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
522		vagD	gi|58383237	GTGAACAAGATCTATATGCTCGACACGAACATCTGCTCGTTCATCATGCGCGAGCAACCTGAAGCATTGC	AR2-2-0639	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
523		mphR(A)	gi|58383237	AAGTCCGATGACGAGGTACTCGAGGCCGCCACCGTAGTGCTGAAGCGTTGCGGTCCCATAGAGTTCACGC	AR2-2-0643	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
541		ML2351	gi|13093909	GGTCTCATGCCAGTCAAACTGTTTCCTCGCTGGATTCACCCTTTTGTCCTTAACCAACCAGTCTCCCAGT	AR2-1-0049	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
545			gi|13621504	TGGGTTTATCAATGTGATGCCTTCCCAAGTGGATAAGCGTTATAAGCAAGTAGTGTTAGCGCAGGTTGGT	AR2-1-0065	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
546		kdpE	gi|13785452	CGATGCGAAATCAGTCCTTGTCAATGAACAGTCCGTACATCTAACACCGAATGAATTCCAACTCCTAACG	AR2-1-0069	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1
551			gi|16197747	AATCCTTGTCCGTTACGACTGTCCCTGCCGTGTTCTTAGTTGATCCGCCTAATGTCATCACTCCGATTGG	AR2-1-0161	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
552			gi|16262453	CTGGTTCTTGGCTTCCTCCTGATCCTTCTCTACACATCGCTTGGCGGACGCAGTTTGACCGTGCTCGTGC	AR2-1-0165	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
559		ydfB	gi|32468695	AGCGTTTTGTATGGAAAATGGGATTGTTCCTAGCTGGGATTGTGATATTTGCAACAATTCGTCCATTGCA	AR2-1-0337	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
560		ywoG	gi|32468830	CTGTATATGCCGATTCATAACTTTTCCCTGCTGCTCGGATTGCGGTTCTTCCAAGGGATTTGGTTCAGCA	AR2-1-0341	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
568		oprM	gi|404772:1	GACCAGGCGCAGTTGCAGCTGACCAAGGACACCCTGGGCACCTACCAGAAGAGTTTCGACCTGACCCAGC	AR2-2-0440	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
571			gi|41353422	GTTATGGATTCGACCTGGTCGGATACTACCCACTGATCCTCACCGCGTTCCTGTTGTTGACCAGCATCAT	AR2-2-0452	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
572		mll3464	gi|47118328	GTTTCATCACCGCGCTGTCGTCCTGGCATGTGGTCTACTTCACCTCTTGCGCCGTTATGATCCTGCTGAC	AR2-2-0528	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
577			gi|52211453	GATCGCGGCCGAGCTGCGTTTTTCCGAGAACGCGCTCGTCTGGGTCGTCAACGCCTACATGCTGACGTTC	AR2-2-0548	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
578			gi|58383237	TCGGCGCTCTTGTCGATGCCCTGGAGGAGGTAAAACTTCCGGGTGACAAAACCTACCGAGCGGCTTTGGT	AR2-2-0624	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
582		vagC	gi|58383237	AAAATGGCAACAACCGTGCTATCCGCCTTCCACGCGATCTGGATTTTGAGGGGGTGAGCGAGCTGGAGAT	AR2-2-0640	1	1	2	1	2	2	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1
583		mrx	gi|58383237	AAGTAGCAGAGCTCGGGCTGTTCTCCTCAATGATGGGGGCTGGTGGTCTCCTTGGCATTGCCATTCATGC	AR2-2-0644	1	1	2	1	2	2	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1
604			gi|13424588	GTACACCCTATGCCGACCGATACGGACATTTTTGAATCGCTCCGCCAGGAGCTGCGGCGGGGAACCCTGA	AR2-1-0062	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
606		ccrA	gi|13785452	AAAGTTGGCACAAGGCATCATCGATGCAGAAACGTTCAGAGAACAAACGCAATCATTACGTCAACAACCG	AR2-1-0070	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1
610			gi|16197747	TTTGGCAAACCAGTACTACTTCAAACCTTACGCAGAAATGGATTATGAATCGGCATCCATCGGGTTGAAC	AR2-1-0158	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
612			gi|16262453	CTAGGTGACCTCGTGGAAAATCGTCGGCTGATCGTGACCATGATCGGCGTGGTTACTCTCGCCCTGATCG	AR2-1-0166	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
619		ydeR	gi|32468695	TCTCTTTATTACTGCCGCTCATGATTCAGAGCAGCTCCCCCGTCGGTATAACAGTTCTAGTGGCCGCTGC	AR2-1-0338	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
620		yxaM	gi|32468840	TAATTTCCGGTTCTTTTGAAACTTGGATGAGCCGTGTCGCAGGGGAAGATCGATTCGGCAAAGAAATGAT	AR2-1-0342	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
624		marC	gi|33573592	GATCGCCCTGATCATCAGCTCCGCCTCGACCCTGCACAGCCATGGCGGCATCACCCTCATCCACCATTTC	AR2-1-0358	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
626		suqE	gi|40287459	TATCACTATTGCGGCGATGATCGTCAGTATCGCCATGCTCTCCTGGGCAATGCGCACGTTGCCTGTAGGA	AR2-2-0433	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
631			gi|41353422	CTATGTCCTGGTGGGTGATATCGCGATCATCGGGTTCTTCTTCGTCGGCGGGACCGTGTTCTTCGAGAAG	AR2-2-0453	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
632		mll8451	gi|47118328	ATCTTTGCCTCGATCCGGAGCGGATTGCTCATATGGCCGAAGTCTTTGCCAAGACGCTTGGTGAATCACC	AR2-2-0529	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
635		petP	gi|49287:19	CTGATCTCGGTGCTGGGGGTGACGAAGCAAAGCCTGAACCGGGTCCTGCGCACGCTCATTGACGATGGTC	AR2-2-0541	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
636		nhmD	gi|50593055	TCCCTGAGTCGTAGAATCCATAACGTGGTCGATCAAGAGAAATTGACCGCGGACCAGTGGTAGTATTGG	AR2-2-0545	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
637		putative mu	gi|52211453	ATGATCGTCGACCGCCTGATCTCCGAAATCCTGTTCGGCTTCACCGGCCTCATGGGCATCATCAATCCGT	AR2-2-0549	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
664			gi|13425086	GTTTCGGAGTCGGTGCTCAGCAAGCACGTGAAGACCCTGGAGGAGGCCGGCTACGTCAAGGTCAAGAAAG	AR2-1-0063	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
678			gi|24209736	CCGAGCTCGCACCCCTGAGCCGTCTGCTGCATATCGTCCTGGCCGAAATCAACCTGTATGAACAGTGCAT	AR2-1-0263	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
679		yfhI	gi|32468715	TCTCGGAGATGTCCTGAATTGGAGAGCGGTGTTTTCCATCATTACGGCACTTGGTGTCATCGGATTTTTA	AR2-1-0339	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
680		yybF	gi|32468840	GCTGTTAGCTGTGAGCATGCTTGTCTTTGGTTCATTATCCGAGGTGTGGGGACGCAAGCCTATTATGGGT	AR2-1-0343	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
683		psrfm	gi|3319647	AAAGTGTCCCTACCACACTAAATGTGGCTTTGATTGGTTCGGATGCCCGGTCGAAAGAAGAAAATGGTCG	AR2-1-0355	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
687		blc	gi|40287459	GCGCATTTTGCCCGTCGTAACTGCAGTTACGGCTGCATTCCTGGTTGTCGCGTGTAGCTCCCCGACACCG	AR2-2-0438	1	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
689		ferR	gi|40788116	GGACAAGCGCTCTTACGGGATCTTCCTGAGCAAGACCGGCGAAACCCTGCTCAAGGAGCTCAAGCAGATC	AR2-2-0446	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
691			gi|41353422	CTTCGAGCTGCCCAACCACTACCAAAAGCTCACCGGGTATGAGAACCTGCGCTTCTTCGCCTCGCTGTAC	AR2-2-0454	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
697			gi|52211453	ACCGTCATGCTCACGGATCTGCTCGGCACCTTCGCGATGATGGCCGTACCGGTGCTGAGCACGAACCTAT	AR2-2-0550	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
			gi|13785452																										

727			gi|16262453	AGAGCAATCTTGGTTTTCGCGTACCCGGCAAGATCGTTGAGCGACTGGTCGACGTGGGTCAGCAGGTCAA	AR2-1-0168	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
728		putative hy	gi|16262453	ACAAATCATAGCGTTCTGTTTGAGATCAGCGACGCGTGGCAAGATCGGCTGCCCGAGATGAAAGTGCCCC	AR2-1-0172	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
729		lmo1250	gi|16410540	AGTTGAATGCCTCTCTGGGCGAAGCTGGATTTGCGTCTGGGATTTATATTATTGGAACGCTCCTTGCACG	AR2-1-0176	1	1	2	2	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1
730		marC	gi|16420030	TTGCGGGCAATATGAATAGTGCGGAACGCAACCGGCAGTCCTATATGGCTTCGGTTTATGTCTTCGCTAT	AR2-1-0180	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
734		putative ad	gi|24413894	GCCTCACCGACGCCACCCTCCTCACCCAGCTCGAGTACGCCCGCAAACGCACCGGCGACTACGGCCGCTG	AR2-1-0268	1	1	2	2	2	2	2	1	1	1	1	2	1	1	1	1	1	1	1	1	1
735		putative ph	gi|24418961	AACGCTTCCCCTCCGGGGGCACGGTCAACGCGATGTACCGGCTGGGCGAGGACATGGTCGTACGGCTGCC	AR2-1-0272	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
738		nel	gi|24672101	TTGCAACACAACACGTAGGAGTGACTGGAAATCGTGATGAACGTGCTGAATTTAATGAACTTGTTTTAGA	AR2-1-0284	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
740		ccrB	gi|34577204	GTCAAAAACCCCAAGTCCATGGCAAAGGAACGAATCTGCTTACAGGCATTATTCACTGTCCCCAATGTGG	AR2-1-0364	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
742		ompK37	gi|3650341	AATTAGATCTCTATGGCAAGGTAGATGGTCTGCATTATTTCTCCAGCGACTCGAAAAAAGACGGCGATCA	AR2-1-0372	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
744		B-insB	gi|37962716	GTAACTGCCCGCATTATGGGCGTTGGCCTCAACACGATTTTACGTCACTTAAAAAACTCAGGCCGCAGTC	AR2-1-0380	1	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
746			gi|4135366	ATTGACGATCTTCGGGAAGGATTTCCCGTCGAGCTGCTGTCGTATTTCGAGGTCTTCACCAAGACGACGA	AR2-2-0455	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
749			gi|434708:1	AGCGGACGTCTTTCGCGGACCGCGTGACGGGATTTATGAACAGGCAGGGCATCAGCCGGGTGGAATTGGC	AR2-2-0467	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
755			gi|53721033	AATCGATCGACGCGCACGGCGACGTCTTCGTGATGAAGCACGTGATCTGCGATTGGGACGACGAACAGGC	AR2-2-0563	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
757			gi|53721033	ATGTCCGTCATCGGTCTCGATCATTACAATCTGCGCGCGCCCCGCCCGCTCCTCGACACGCTGCGCGATT	AR2-2-0571	1	1	2	2	2	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1
759		yhjN	gi|6434027	TCTTGGTGCAGCACCAGGAGGGGTTAATCAGATAGTTTTAGTTGCATTAGCTACTGGTGCCGATGTTGCT	AR2-2-0651	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
760		trpF	gi|6434046	TTGCTCAACATACTGACGTCATTGTTCAATACCCTGATGATGATAATGTGCTGAATCAATCGGTGGACGC	AR2-2-0655	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
761		putative an	gi|6459162	AACGTGGGCACCGTCGAAGACCGCCTCAATGAACTGCGTGGCGAGCAGTTTCAGACCCACATCGACACCG	AR2-2-0659	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
763		mutS	gi|7328283	CGAAAGGTATGGTTAGACGTGAGGTAGTAAGAATTGTGACTCCAGGAACTGTGATGGAGCAAGGTGGTGT	AR2-2-0667	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
784			gi|14020964	GAGAAGGGATTTGCGAAAAGATTGCAAAATCTGCAACGAGCTTTGGGTTTACTATTAATGGTGGAGATGG	AR2-1-0085	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1
787			gi|16262453	CTGCAAATGGACGAGCCGCGCAAGCGGTTTGGAGCCATGATGTCAGGCCTGGATATTCACTACGATCTCG	AR2-1-0169	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
788			gi|16262453	CCACCTCGGCTCGTCCTATGTCGATGATTTCAACATCTTCTCGCGCGTGTACCAGGTGCGGATCCAGGAT	AR2-1-0173	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
789		lin0870	gi|16413128	TATGGGTGTGTCGATTAGTTCAGCGGGATTAACTGTATCGATTTATGCGCTAGGTGTGATGGTGGGGGCG	AR2-1-0177	1	1	1	1	2	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1
790		mppA	gi|16420194	AAAATCTGGGGGTGGATGTGAAATTGCAAAACCAGGAGTGGAAAACGTATATCGACAGCCGGAATACCGG	AR2-1-0181	2	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
791		ccrA	gi|17025993	GCATCATTGATGCAGAAACGTTCAGAGAACAAACGCAATCATTACGTCAACAACCGCAACGCACTACATC	AR2-1-0185	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
792			gi|17429991	AGCATGCGTCCGCCATCCTCGAGATCCTGAACGAGGCCATCGTGAATTCGACGGCCCTGTACGACTACGT	AR2-1-0189	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
794		putative gl	gi|24413894	GAGAAGGTCGTCCTGGTCTCGCTCGGTTCGGCCTTCACCAAGCAGCCCGCGTTCTACCGGGAGTGCGTCC	AR2-1-0269	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
801		mutL	gi|35367176	GGACAGATGCACGGAACGTATCTTTTTGCCCAAAGTAGCGATGGGTTGTACATCATTGATCAGCATGCTG	AR2-1-0369	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
806			gi|41395023	CGCATCCCGTCGACGGCCGGCAGGTGCTGGTCTCGGTCTCCGAGGCCGGGGCCGAATTGGTCAAGGCCAA	AR2-2-0456	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
807			gi|42630:95	CAATGCCGGATTCAGGAAGACCGAACGCAGAACCAGAGACGTCTTGCCTACGCATCAGAGGTTTACCGG	AR2-2-0460	1	1	2	2	2	2	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1
809			gi|434708:2	ACGAGATGGTCGTCCTGGGAAAGGCCCGCGCCGAGGAACCCCTGACGACCCTCGCCGTGATCACGGAACT	AR2-2-0468	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
811		mtrR	gi|438190:1	AAAAACCAAAACCGAAGCCTTGAAAACCAAAGAACACCTGATGCTTGCCGCCTTTGGAAACCTTTTACCGC	AR2-2-0476	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
812			gi|52211453	AGTATCAGGAAGGCGCGGTCAGCTATCTCGACGTGATCGACAGCGAGCGCTCGGTGCTCGAATCGCAACT	AR2-2-0552	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
813			gi|52211453	GATCGAGTTCTACAAGAAGGCGTTCGACGCCGTCGAAATCTCGCGGTTGCCTTCGCGCGATGCCGGCCGG	AR2-2-0556	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
814			gi|52211453	GGTATGGGCGATCGTCCCGCTGTCGATCGTGTTCGGGATTCCGAATGGTTTCAACAATCTCGGCAATCAG	AR2-2-0560	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
815			gi|53721033	GTGTCGCCGATCTACGCGTCGTTCGACGCGGATGAGCAGACCTACCTGCAATACATCGGCGGCGCGAAGG	AR2-2-0564	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
819		qsa-at	gi|6434027	GTGATTCGTTATTAATCAAAGCTGGTTCTGGGGTGGCAACATTAGGATTGCCGGATTCTCCTGGTGTGCC	AR2-2-0652	1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	1	1	1	1	1
820		trpF	gi|6434046	CAGCGGCCAGTCAATTACCTATTGATGCGATAGGTTTCATCCATTATGAAAAAAGTAAAAGGCATCAAAC	AR2-2-0656	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
821		ureR	gi|6633954	CACACCAGCTTTCTGTCGCTCTAATCAGGTTGGCACATCTGTTGGCCTATGATGCGGACTCTTCATTCAT	AR2-2-0660	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
823		mutS	gi|7328293	AGTTTGATTATTTTCGATGAAATTGGACGTGGTACTTCAACGTATGACGGTTTAGCTTTAGCGCAGGCAA	AR2-2-0668	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
842		phaQ	gi|13812266	ACCGCACGCTGAGACAGCTTGAAAAAGACAACTTGATTACATCGCAATGGGATACGTCAGCTGAAGGACC	AR2-1-0078	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
843			gi|14020964	TAGAGGGAGAGTTATGTGTTTGTGATGTAGCTAATATCATTGAATCTTCAACGGCTACGGCATCCCATCA	AR2-1-0082	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
844		ccrA3	gi|14020964	GAAACGAGCCATTGGTTATTTGCGCCAAAGTACAACGAAACAACAATCACTCCCAGCTCAAAAGCAAGCA	AR2-1-0086	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
846			gi|14020964	TGTCTCCAAAGAAAGGCAGAGCATTAGATATCGGATGTGGCTCGGGTTTGTTAGTGGAGAAATTAGCAAG	AR2-1-0094	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1
848		lmo0872	gi|16410252	TGTTTATGTCGATTGCTTCTGTTATCGCAGCCGATGTGGTTCATCCGAGTAAACGGGCTAGTGCAATTGC	AR2-1-0174	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1
849		lin0920	gi|16413128	TTGAACGGCTTGGCAATGTCGAAAAACCACGCACTACAAAGCCAATTAAAATCGTCACACCCGATAATCG	AR2-1-0178	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1
851		ccrB	gi|17025993	CTCAGAATTCGAACGTAATAACATTGTCGAGAATGTATTTATGGGGCAAACGAGACGTGCCCAAGAAGGC	AR2-1-0186	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
852		fsr	gi|17430778	CTTCCTCAACGACATGATGCAGTCGTTGATCCTGGCGATCTATCCGCTGCTCAAGGGCAACTTCCATCTC	AR2-1-0190	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
854		putative tr	gi|24413894	CTCGCGTACACCCTGGACGCCAAGGTGGCCGGCGGGTCGGGCGAGGACCACGACGTGTCCGCCCTGGGCG	AR2-1-0270	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
857			gi|24672101	TTGGGTCTTGCGATTAAAGAAGCCCGTCTTAGTAAAGGATTGACTCGTGAGCAGGTAGGATCAATGATCC	AR2-1-0282	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1
860			gi|34577204	AGGGAACGTGGTGTAAACGTTCATCATTCAACGGTCTACCGTTGGGTTCAAGAATATGCCCCAATTTTGT	AR2-1-0366	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
861		mutS	gi|35367190	TTGCAACGATCAGCGAACGCTATCAGTATGTTCGGCCAGAACTTGTCAGTGACAAGCATCAGCTTCTGAT	AR2-1-0370	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
863			gi|37962716	GAGAAGTTTTTTAAGATGGTGAGGTACTTCGGGTTCCTTGCCAACCGTGTGTGTGGAGAGAAGCTGCCGC	AR2-1-0378	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
866		LexA	gi|41583492	CAGTGCGAGAAATCTGTAGCGCAGTGGATCTTTCTTCTACTTCAACCGTTCACGGTCACCTAGCACGCCT	AR2-2-0457	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
867			gi|42632302	CGATTGCCGCTGATATCATTCCAGCTTCTCGTAAAGGGGCCGGGTTAGGCTATTTTGCTATGGCAATGAA	AR2-2-0461	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
869			gi|434708:3	GGAATGGAGGTCGTCAAGCTCCGTATGACCGATCCCCGTATGTACCACCTCGACTGCACGGTCTTCCCCC	AR2-2-0469	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
870			gi|43744:48	ATCGACCCGCACGGACTGCTCGGCGAGCGCACCTTCGACTATGCCAACATCTTCACGAATCCCGATCTCA	AR2-2-0473	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
872			gi|52211453	AGATGCAACTGACGCTCACGATGTACATGGCCGGCTACGCACTGTCGATGCTGCTATCCGGGCCGCTGTC	AR2-2-0553	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
873			gi|52211453	ATCCTTCCCTCGTGTTGATCCTGATTCCGGTCGTGATGCTCGGCCAGCTCTCGATGGACATGTATCTGCC	AR2-2-0557	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
874			gi|52211453	GGCGATGGTCTACTTCTGGCCGGCGTTCGTCGTGGTCGGCCTATGCTCGTTCGCATCGATTCCGATCACG	AR2-2-0561	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
875			gi|53721033	GATCTCGCCGAACGACAGCTACGACATGACGTATCTGCGCAACTACGCGCTCATCAACGTGAAGGATCGC	AR2-2-0565	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
876			gi|53721033	TACTTCTGTGATCCCCAGAGTCCATGGCAACGCGGGACGAATGAAAACACGAACGGCCTACTGCGACAGT	AR2-2-0569	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
877			gi|53721033	GACACGAACGTCGTCGCCGTATCGCTGCCATCGATCGCCCGTACGCTCCATGCGAGCTTCGCGGACATCG	AR2-2-0573	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
878		tag	gi|6434027	TGAAGAAGCATTTTATGATTTCGAACCAGAAAAGGTAGCACAAATGACCGCTCAAGATATCGACCGCTTA	AR2-2-0649	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
879		indole-3-gl	gi|6434046	CGAGATTTATCGCAACAAATCTCAGATTATGACCAATATGGTGCAAATGCCGTGTCCATTTTAACTGATG	AR2-2-0653	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
882		LysR	gi|7227103	GTTGACAACGACATCGCTGAAGGAAAGTTAATTCCCCTGCTCGCCGAACAAACCTCCGATAAAACACACC	AR2-2-0665	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
883		mutL	gi|7328293	TAGATGCAGGCGCTACAGAAATAAGCATTGAAGTAGAGGAATCTGGCGTCCAATCTATTCGCGTAGTCGA	AR2-2-0669	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1	1
901		kdpB	gi|13785452	GGTGATGTGTACAGGAGATAACGAATTGACAGCTGCGACAATAGCGAAAGAAGCGGGTGTGGATCGCTTT	AR2-1-0075	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1
903			gi|14020964	ATCAAGGTACCGCAGAAGCAATCGGTGCTCATGTAGGCGTTTCTGATATTCAGTCCGAATTGTTGCCACA	AR2-1-0083	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
904		ccrB3	gi|14020964	TCCACAATGTGGTGCACCAATGGCAGCTAGTAACACAACGAACACATTGAAAGATGGTACCAAGAAGCGA	AR2-1-0087	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
908		lmo0919	gi|16410252	ATGTCGAAAGCGTCAAACATTTAGAACGTCAGTGGAGCGATTTCCACGGTGCGCTCATAATTATCTCGCA	AR2-1-0175	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1
909		lin1217	gi|16413677	TGAACCCCACCGTATTGGCATTGGTTTATCTACTTACTTTATTGGGCTTGATTTAGGCCTTGGTATCGGA	AR2-1-0179	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1
910		STY2939	gi|16503805	AGGCAAGCTCCTGGAAAACCGCAATAAAATGCTGAAGGCTCAAGGGATTAACGAGACGTTGTTTATGGCG	AR2-1-0183	2	2	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
			gi|17431752																									

914			gi|24413907	GCGACAGCTCAGGCCCTGTGGGCCATCGACCCGGACCAGGCACCGCCCTCGATGAAGACACTGGCCGGCC	AR2-1-0271	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
916		mdt(A)	gi|24672104	TCCTCTAGTGACCACAAAATATTTTGGCGGCACGATTGTCCACGCGGGTTGGGTTGAAGTTCTATTTGCT	AR2-1-0279	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
920		ccrA	gi|34577204	CAAGGCATCATTGATGCAGAAACGTTCAGAGAGCAAACACAATCATTACGTCAACAACCGCAACGCACTA	AR2-1-0367	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1
921		mutL	gi|35367190	TCAGATCGCTGCGGGAGAAGTAGTGGAGCGACCAGCTTCCGTTGTGAAAGAATTAGTGGAAAATGCAATT	AR2-1-0371	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1
927			gi|42632302	CGGAGCAATTCAACCAGCTCTACAAGCATGGGCTGTTAATAAAGCGCCTAGTGATCGAAAGGGGATGGCT	AR2-2-0462	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
932			gi|52211453	GCTGGCTGATCGACAACTTCTCGTGGCCGTGGATCTTCCTGATCAACCTGCCGATCGGGCTGTTCTCGTT	AR2-2-0554	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
934			gi|53721039	CTCGTCTATCGCGACAAGGTGGGCGAGACCTATTCGGTCGTCGCGAATCCCGCGCACCGCTGGTTCTACT	AR2-2-0562	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
935			gi|53721039	GTCTATTTCGTGAATCAGATGCGCCTCCCCGAGCAGGTCATGAACTCGATCAACGGGAAGATCGCTGCGA	AR2-2-0566	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
936			gi|53721039	ACGTCATCGTGCGAGCGGCCTGAATCTCGTCGTCGCGGCGATCATGCTGTGGAACTCCGTCTATCTTGAG	AR2-2-0570	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
937			gi|53721039	GATATCGACACGCTCGTGCGTTTCTACACGAAGGCGCTCGGCTTCGACGTCGTCGCCCGCTTCGAGAATC	AR2-2-0574	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
938		pbq	gi|64340274	TGGAAGCTGGTGCTGATATTATTGCGCCAAGTAATATGATGGATGGTTTTGTTGCTGAAATTCGTCGTGG	AR2-2-0650	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1
939			gi|64340464	CCACATCAACCATGTTATGAAGGGGCTATGTGTGTGTGCGGCACAGGTGGTGACAAGTCAAATAGTTTCA	AR2-2-0654	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	1	1	1	1
						Probes with positive hybridizations to each strain																				
Total of probes with positive hybridizations (includes dulplicate and triplicate control probes)*						13	98	156	174	164	142	20	14	10	29	24	26	48	53	35	33	3	3	9	4
					Total probes in a class*																				
Total (-) controls					14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Total (+) controls					3	3	3	3	3	3	3	2	2	3	3	3	3	2	2	2	2	3	2	3	3
Total beta-latctamase gene probes*					92	0	8	13	12	17	15	2	2	0	2	0	1	10	8	5	3	0	1	1	0
Total aminoglycoside resistance gene probes*					106	1	13	36	39	28	26	4	4	0	0	0	0	0	7	7	7	0	0	0	0
Total macrolide resistance gene probes*					18	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0
Total glycopeptide resistance gene probes*					26	0	1	1	1	2	2	0	0	2	2	1	1	2	2	0	0	0	0	0	0
Total streptogramin resistance gene probes*					2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total tetracycline resistance gene probes*					24	0	3	11	11	9	6	1	1	0	3	3	3	0	0	0	0	0	0	1	0
Total efflux gene probes*					60	4	9	14	11	18	19	4	4	0	5	3	3	2	2	0	0	0	0	0	0
Total genetic transfer related gene probes*					100	0	32	21	26	20	18	3	1	2	4	3	2	8	7	3	3	0	0	4	0
Total lincosamide resistance gene probes*					3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total heavy metal resistance gene probes*					26	0	9	5	15	14	10	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Total poly-ketide resistance gene probes*					7	0	0	2	2	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total trimethoprim resistance gene probes*					21	0	5	4	4	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total metronidazole resistance gene probes*					7	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Total quaternary ammonium resistance gene probes*					0	0	0	3	5	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total phenicol resistance gene probes*					21	0	4	8	8	5	6	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Total other antimicrobial resistance associated gene probes*					257	4	10	31	32	35	26	4	0	2	10	11	12	23	23	17	17	0	0	0	1
Total of all probes*					787																				
Total of gene probes with positive hybridizations counting duplicate and triplicate probes only once (these are the numbers used in the te						10	95	153	171	161	139	18	12	7	26	21	23	46	51	33	30	0	1	6	1

2= Median intensity of isolate's DNA hybridization to three probes on the array was greater than twice the median intensity of all gene probes. (Gene detected)

1= Median intensity of isolate's DNA hybridization to three probes on the array was less than twice the median intensity of all gene probes. (Gene not detected)

Isolates: SE, *Salmonella enterica*; Hd, Heidelberg; Tc, serovar Typhimurium variant Copenhagen; EC, *Escherichia coli*; CC, *Campylobacter coli*; ECF, *Enterococcus casseliflavus*; EGM, *Enterococcus gallinarum*; LI, *Listeria Innocua*; MRSA, Methicillin Resistant *Staphylococcus aureus*; CD, *Clostridium difficile*

*Gene names with a (*) have duplicate or triplicate identical control probes, therefore total positive hybridizations with a (*) are sometimes greater than totals listed in the text