



Vector: **pShuttle-RFP**

Antibiotic resistance: **Kanamycin**

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pShuttle-RFP Full-length Sequence

NNNTTAATTAANNNTCCCTTCCAGCTCTCTGCCCTTTTGGATTGAAGCCAATATGATAATGAGGGGTGGAGTTTGTGACGTGGCGCGGGCGTG
GGAACGGGGCGGGTACAGTAGTAGTGTGGCGGAAGTGTGATGTTGCAAGTGTGGCGGAACACATGTAAGCGACGGATGTGGCAAAAAGTACGCTTTT
TGGTGTGGCCGGTGTACACAGGAAGTGACAAATTTTCGCGCGGTTTATAGCGGATGTGTAGTAAATTTGGCGTAACCGAGTAAGATTTGGCCAT
TTTCGCGGAAAACGAAATAAGAGGAAGTGAATCTGAATAATTTTGTGTTACTCATAGCCGTAANNNGgttaccTAGTTATTAATAGTAATCAATTACGGGGTCA
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 AAGAAAGCGAAAGGAGCGGGCGCTAGGGCGTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCGCTTAAATGCGCCGNNNNNNN

Unique enzymes in pShuttle-RFP:

BsrG I	T`GTAC,A	207
Acc65 I	G`GTAC,C	359
Asp718	G`GTAC,C	359
Kpn I	G,GTAC`C	363
Nde I	CA`TA,TG	598
Hpa I	GTT AAC	1765
Mlu I	A`CGCG,T	1888
HinD III	A`AGCT,T	1922
Sal I	G`TCGA,C	1928
Bgl II	A`GATC,T	1934
Bst1107 I	GTA TAC	4174
Xca I	GTA TAC	4174
Pme I	CTTT AAAC	4189
Avr II	C`CTAG,G	4713
BspH I	T`CATG,A	6097
Psp1406 I	AA`CG,TT	6496
Eag I	C`GGCC,G	6873
Xma III	C`GGCC,G	6873
Rsr II	CG`GWC,CG	7483
Dra III	CAC,NNN`GTG	7830
Xmn I	GAANN NNTTC	8051

Number of enzymes = 22

Ban I	(16)	359	829	1080	1338
		1425	1533	1632	2714
		3135	3926	4830	6218
		6718	6966	7001	7867
Ban II	(9)	1023	2053	2110	2266
		3031	3337	4056	7332
		7905			
Bbe I	(6)	1429	1537	1636	3930
		6722	6970		
Bbs I	(2)	1383	3820		
Bbv I	(19)	1535	1790	2011	2014
		2206	2233	2293	2385
		3320	3336	3396	3919
		4779	5796	5799	6005
		7040	7082	7603	
Bbv II	(2)	1382	3821		
Bcl I	(2)	1659	6808		
Bcn I	(18)	1532	2086	2350	2351
		2530	2531	2876	3268
		3358	3767	3993	4605
		4606	5758	6454	6575
		6972	7132		
Bfa I	(13)	364	956	1650	1851
		1898	1906	4714	5872
		6125	6460	6526	6668
		7981			
Bgl I	(7)	454	576	647	2410
		4461	6390	8050	
Bgl II	(1)	1934			
Bpm I	(3)	2094	4722	6340	
Bsa I	(5)	2158	2546	3522	4034
		6331			
BsaA I	(7)	704	1178	2809	5020
		6540	7271	7830	
BsaB I	(3)	1664	2473	6826	
BsaH I	(14)	486	539	622	808
		979	1426	1483	1534
		1633	1902	2974	3927
		6719	6967		
BsaJ I	(42)	724	961	973	1108
		1132	1168	1225	1285
		1381	1417	1486	1612
		2077	2084	2232	2348
		2528	2750	2762	2874
		3031	3044	3168	3169
		3266	3694	3710	3781
		3862	3886	3898	3916
		3991	4516	4603	4604
		4713	5537	6572	6776
		7130	7399		
BsaW I	(8)	1643	2913	4300	4527
		5583	5730	6700	6998
BseR I	(5)	959	1283	3620	3936
		4505			
Bsg I	(5)	1542	2300	2910	3965
		4890			
BsiE I	(6)	2548	4594	5293	5717
		6876	7863		
BsiHKA I	(8)	2023	2053	2921	3681
		4056	5695	7080	7270
Bsm I	(4)	1753	1846	3003	4034
BsmA I	(11)	797	2159	2183	2545
		2629	2966	3523	4033
		4626	6332	6810	
BsmB I	(2)	2630	2965		
BsmF I	(10)	539	690	858	1130
		1149	2545	3414	3567
		4151	7118		
BsoP I	(69)	1067	1115	1268	1332
		1337	1472	1524	1527
		1619	1779	2000	2003
		2006	2009	2012	2195
		2204	2207	2216	2219
		2222	2282	2374	2664
		3038	3041	3309	3312
		3325	3382	3385	3388
		3478	3651	3770	3821
		3889	3908	3930	4011
		4219	4765	4768	5283
		5301	5304	5422	5577
		5720	5785	5788	5994
		6322	6773	6876	6928
		6939	7029	7034	7071
		7112	7199	7202	7205
		7441	7537	7578	7592
		8010			
Bsp120 I	(2)	3027	3333		
Bsp1286 I	(2)	2023	7270		
BspH I	(1)	6097			
BspM I	(8)	2385	3247	3287	3607
		4281	6625	6854	7235
BspM II	(2)	4300	4527		
Bsr I	(19)	660	1158	2689	3369
		4484	4789	5784	5797
		5911	6317	6435	6478
		6550	6595	6676	6760
		6910	7111	7744	
BsrB I	(5)	1406	4736	5310	7580
		7974			
BsrD I	(3)	3029	6331	7200	
BsrG I	(1)	207			
BssH II	(6)	1607	2514	2516	3772
		3903	8031		
BssS I	(5)	1035	3933	4040	5550
		7559			
Bst1107 I	(1)	4174			
BstE II	(4)	1103	1274	3594	4483
BstN I	(19)	454	647	1133	1287
		2574	2751	3045	3090
		3170	3576	3695	3782

The following enzymes do not cut in pShuttle-RFP:

Afl II	Age I	Asc I	BamH I	Blp I	BsiC I
BsiW I	BstB I	Bsu36 I	Cla I	Eco72 I	
EcoN I	EcoR V	Esp I	Fse I	Nhe I	
Not I	Nru I	PaeR7 I	Pml I	Pvu I	
Sca I	Sfi I	Spe I	Spl I	Srf I	

pShuttle-RFP: sites sorted by name:

Aat II	(6)	489	542	625	811
		982	1905		
Acc I	(3)	1929	3235	4173	
Acc65 I	(1)	359			
Aci I	(108)	88	106	126	151
		233	243	294	422
		450	462	476	643
		734	767	871	892
		953	1067	1090	1114
		1189	1267	1336	1406
		1471	1619	2006	2009
		2012	2138	2201	2204
		2207	2216	2228	2232
		2234	2266	2297	2301
		2431	2520	2538	2666
		2784	3037	3040	3125
		3129	3146	3242	3322
		3461	3478	3536	3579
		3640	3650	3886	3888
		3930	4006	4011	4020
		4348	4620	4734	4764
		4939	5071	5092	5110
		5217	5243	5260	5303
		5310	5331	5422	5450
		5577	5596	5717	5827
		5962	5971	6333	6424
		6554	6677	6773	6876
		6939	7033	7097	7198
		7201	7441	7481	7486
		7536	7552	7578	7720
		7859	7974	8001	8029
Afl III	(4)	158	1888	4340	5377
Aha II	(14)	486	539	622	808
		979	1426	1483	1534
		1633	1902	2974	3927
		6719	6967		
Ahd I	(3)	1142	2538	6270	
Alu I	(44)	25	930	1097	1214
		1331	1460	1526	1556
		1781	1924	2051	2284
		2376	2656	2742	2792
		2942	3284	3311	3381
		3387	3590	3910	3967
		4054	4298	4513	4837
		5319	5545	5635	5681
		5938	6459	6588	6641
		6667	6713	6804	7073
		7531	7660	7878	7917
Alw I	(23)	945	1653	2389	2481
		2680	3071	3234	3612
		5192	5203	5939	6025
		6025	6122	6123	6523
		6524	6787	6804	6834
		7145	7212	7391	7461
AlwN I	(6)	2218	2376	2461	4182
		5793	6591		
Apa I	(2)	3031	3337		
Apal I	(2)	2917	5691		
Apo I	(7)	257	1816	1916	2928
		4194	7632	7643	
Ase I	(5)	5	371	4669	5188
		6442			
Asp718	(1)	359			
Ava I	(5)	1224	1416	2348	2528
		4603			
Ava II	(7)	2532	2556	3581	3722
		3800	6408	7483	
Avr II	(1)	4713			

		6818	6882	7018	7375				5405	5526	5539	5757
		7567	7858						6453	6574	6971	7131
Msc I	(4)	285	1509	3780	7049				7354			
Mse I	(32)	5	9	371	1703	Sec I	(42)	724	961	973	1108	
		1764	1885	2357	2436			1132	1168	1225	1285	
		2788	3373	3421	4188			1381	1417	1486	1612	
		4391	4494	4669	4808			2077	2084	2232	2348	
		4911	5034	5188	5192			2528	2750	2762	2874	
		6083	6135	6140	6154			3031	3044	3168	3169	
		6207	6442	6481	7640			3266	3694	3710	3781	
Msl I	(5)	7652	7669	7767	8037			3862	3886	3898	3916	
		729	3016	3081	4275			3991	4516	4603	4604	
		7404						4713	5537	6572	6776	
Msp I	(39)	203	1531	1630	1644			7130	7399			
		2084	2349	2529	2874	SfaN I	(16)	722	1817	2813	2833	
		2914	3164	3266	3328			3618	4010	4091	5215	
		3356	3765	3824	3991			5253	5473	6926	7181	
		4130	4301	4461	4528			7265	7329	7397	7604	
		4604	5584	5731	5757	Sfc I	(7)	1299	2192	2219	2649	
		5947	6351	6385	6452			3382	5642	5833		
		6574	6701	6872	6949	Sma I	(3)	2350	2530	4605		
		6971	6999	7130	7220	SnaB I	(2)	704	5020			
		7287	7468	7932		Sph I	(3)	2073	3549	7372		
MspAI I	(14)	1526	2218	2234	2376	Stu I	(2)	1173	1395			
		2538	3284	3311	3387	Sty I	(13)	724	961	1108	1168	
		3888	4764	5719	5964			1381	2077	2762	3862	
		6713	7073					3898	3916	4713	6776	
		1752	2332			Taq I	(14)	1042	1048	1258	1914	
Mun I	(2)	4462	7469	7933				1929	3615	4823	5477	
Nae I	(3)	1426	1534	1633	3927			7080	7236	7260	7296	
Nar I	(6)	6719	6967					7458	7863			
Nci I	(18)	1531	2085	2349	2350			2338	2879	3987	4567	
		2529	2530	2875	3267	Tfi I	(7)	5352	7452	7586		
		3357	3766	3992	4604			77	109	183	218	
		4605	5757	6453	6574	Tsp45 I	(22)	1103	1274	1280	2241	
		6971	7131					2588	2981	3594	3743	
Nco I	(6)	724	961	1381	2077			4145	4465	4483	4845	
		3862	7399					4996	5086	5118	7087	
Nde I	(1)	598						7393	8003			
NgoM I	(3)	4460	7467	7931				2169	7085			
Nla III	(37)	162	668	728	965	TthIII I	(2)	2288	2454	2493	3581	
		998	1016	1385	1508	TthIII II	(9)	4352	5966	5975	6005	
		2019	2073	2081	2613			7403				
		2663	2886	2939	3003	Vsp I	(5)	5	371	4669	5188	
		3234	3429	3444	3549			6442				
		3704	3866	4093	4127	Xba I	(3)	1649	1897	1905		
		4274	4280	4344	4460	Xca I	(1)	4174				
		4526	5381	6101	6660	Xcm I	(3)	2462	4053	6783		
		6841	7186	7372	7403	Xho II	(14)	949	1646	1934	2382	
Nla IV	(39)	361	831	1022	1082			5196	6018	6029	6115	
		1118	1166	1340	1361			6127	6516	6528	6780	
		1427	1535	1634	2109			7138	7384			
		2533	2557	2716	3029	Xma I	(3)	2348	2528	4603		
		3137	3158	3301	3335	Xma III	(1)	6873				
		3411	3583	3723	3928	Xmm I	(1)	8051				
		4018	4305	4832	5198							
		5409	5448	6220	6314							
		6355	6720	6968	7003							
		7869	7890	7902								
Nsi I	(2)	2827	3005									
Nsp7524 I	(8)	158	2069	3425	3440	Aat II	G,ACGT,C	6	Acc I	GT`MK,AC	3	
		3545	4340	5377	7368	Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	108	
NspB II	(14)	1526	2218	2234	2376	Afl I II	C`TTAA,G	-	Afl III	A`CRYG,T	4	
		2538	3284	3311	3387	Age I	A`CCGG,T	-	Aha II	GR`CG,YC	14	
		3888	4764	5719	5964	Ahd I	GACNN,N`NNGTC	3	Alu I	AG CT	44	
		6713	7073			Alw I	GGATC 8/9	23	AlwN I	CAG,NNN`CTG	6	
NspH I	(8)	162	2073	3429	3444	Apa I	G,GGCC`C	2	ApaL I	G`TGA,C	2	
		3549	4344	5381	7372	Apo I	R`AATT,Y	7	Asc I	GG`CGCG,CC	2	
Pac I	(2)	9	5192			Asa I	ATT`TA,AT	5	Asp718	G`GTAC,C	1	
Pal I	(42)	285	448	641	966	Ava I	C`YCGR,G	5	Ava II	G`GWC,C	7	
		1033	1066	1117	1173	Avr II	C`CTAG,G	1	BamH I	G`GATC,C	-	
		1360	1395	1474	1509	Ban I	G`GYRC,C	16	Ban II	G,RCGY`C	9	
		1618	2083	2527	2760	Bbe I	G,CGCC`C	6	Bbs I	GAAGAC 8/12	2	
		3029	3043	3109	3167	Bbv I	GCAGC 13/17	19	Bbv II	GAAGAC 7/11	2	
		3335	3412	3693	3780	Bcl I	T`GATC,A	2	Bcn I	CC,S`GG	18	
		3846	3896	4017	4060	Bfa I	C`TA,G	13	Bgl I	GCCN,NNN`NGGC	7	
		4455	4864	5392	5403	Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-	
		5421	5855	6313	6393	Bpm I	CTGGAG 22/20	3	Bsa I	GGTCCTC 7/11	5	
		6875	7049	7440	7467	BsaA I	YAC GTR	7	BsaB I	GATNN NNATC	3	
PflM I	(2)	1387	2579			BsaH I	GR`CG,YC	14	BsaJ I	C`CNNG,G	42	
Ple I	(3)	4539	5756	7765		BsaW I	W`CCGG,W	8	BseI I	GAGGAG 16/14	5	
Pme I	(1)	4189				Bsg I	GTCGAG 22/20	5	BsiC I	TT`CG,AA	5	
Ppm I	(2)	2556	3722			BsiE I	CG,RY`CG	6	BsiHKA I	G,WGCW`C	4	
Psp1406 I	(1)	6496				BsiW I	C`GTAC,G		Bsm I	GAATG,C 7	8	
PspA I	(3)	2348				Bsma I	GTCCTC`/9	11	BsmB I	CGCTTC 7/11	2	
Pst I	(5)	1303	2196	2223	2653	BsmF I	GGGAC 15/19	10	BspOF I	CC`N,GC	69	
		3386				Bsp120 I	G`GGCC,C	2	Bsp1286 I	G,DSCH`C	2	
		1526	2376	3284	3311	BspH I	T`CATG,A	1	BspM I	ACCTGC 10/14	8	
		3387	6713	7073		BspM II	T`CCGG,A	2	Bsr I	ACT,GG`	19	
Rsa I	(13)	209	361	583	608	BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	3	
		663	696	747	904	BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	6	
		1161	1413	1602	3663	BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	1	
		7273				BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	4	
Rsr II	(1)	7483				BstN I	CC`W,GG	19	BstU I	CG CG	36	
Sac I	(2)	2053	4056			BstX I	CCAN,NNNN`NTGG	2	BstY I	R`GATC,Y	14	
Sac II	(2)	2235	3889			Bsu36 I	CC`TNA,GG	-	Cac8 I	GCN NGC	49	
Sal I	(1)	1928				Cfr10 I	R`CCGG,Y	10	Cla I	AT`CG,AT	-	
Sap I	(3)	5261	7311	7521	1646	Csp6 I	G`TA,C	13	Dde I	C`TNA,G	9	
Sau3A I	(33)	949	1045	1441	1646	Dpn I	GA TC	33	DpnII	`GATC,	33	
		1659	1934	2382	2474	Dra I	TTT AAA	6	Dra III	CAC,NNN`GTG	1	
		2684	3064	3097	3227	Drd I	GACNN,NN`NNGTC	6	Dsa I	C`CRYG,G	10	
		3278	3616	5196	5943	Eae I	Y`GGCC,R	12	Eag I	C`GGCC,G	1	
		6018	6029	6037	6115	Eae I	CTTTTC 7/10	3	Eco47 III	AGC GCT	3	
		6127	6232	6516	6528	Eco57 I	CTGAG 21/19	10	Eco72	CAAC GTG	-	
		6780	6797	6808	6827	EcoN I	CCN`N,NNAGG	-	Eco0109 I	RG`GNC,CY	4	
		7138	7216	7297	7306	EcoR I	G`AATT,C	2	EcoRI	`CCWGG,	19	
		7384				EcoR V	GAT ATC	-	Ehe I	GGC GCC	6	
Sau96 I	(29)	447	640	1064	1116	Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	69	
		1359	1616	2081	2526	Fok I	GGATG 14/18	20	Fse I	GG,CCGG`CC	-	
		2532	2556	2759	3027	Fsp I	TGC GCA	3	Gdi II	`YGGC,CC	9	
		3028	3166	3333	3334	Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	11	
		3410	3581	3691	3722	Hae II	R,CGGC`Y	14	Hae III	GG CC	42	
		3800	3895	4016	4862	Hga I	GACGC 9/14	7	HgiA I	G,WGCW`C	8	
		6312	6391	6408	7483	HgiE II	ACCNNNNNGGT	-1/132	Hha I	G,CG`C	60	
		7821				Hinc II	GTY RAC	3	Hind II	GTY RAC	3	
ScrF I	(37)	454	647	1133	1287	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	19	
		1531	2085	2349	2350	HinI I	GR`CG,YC	14	HinP I	G`CG,C	60	
		2529	2530	2574	2751	Hpa I	GTT AAC	1	Hpa II	C`CG,G	39	
		2875	3045	3090	3170	Hph I	GGTGA 12/11	18	Kas I	G`GGCC,C	6	
		3267	3357	3576	3695	Kpn I	G,GTAC`C	1	Mae I	C`TA,G	13	
		3766	3782	3848	3992	Mae II	A`CG,T	29	Mae III	`GTNAC,	38	
		4047	4079	4604	4605	Mbo I	`GATC,	33	Mbo II	`TAAGA 12/11	15	
						Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6	

Mnl I	CCTC 10/10	66	Msc I	TGG CCA	4	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	2
Mse I	T`TA,A	32	Msl I	CAYNN NNRTG	5	Sac II	CC,GC`GG	2	Sal I	G`TCGA,C	1
Msp I	C`CG,G	39	MspA1 I	CMG CKG	14	Sap I	GCTCTTC 8/11	3	Sau3A I	`GATC,	33
Mun I	C`AATT,G	2	Nae I	GCC GGC	3	Sau96 I	G`GNC,C	29	Sca I	AGT ACT	-
Nar I	GG`CG,CC	6	Nci I	CC`S,GG	18	ScrF I	CC`N,GG	37	Sec I	C`CNNG,G	42
Nco I	C`CATG,G	6	Nde I	CA`TA,TG	1	SfaN I	GCATC 9/13	16	Sfc I	C`TRYA,G	7
NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	-	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	3
Nla III	,CATG`	37	Nla IV	GGN NCC	39	SnaB I	TAC GTA	2	Spe I	A`CTAG,T	-
Not I	GC`GGCC,GC	-	Nru I	TCG CGA	-	Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Nsi I	A,TGCA`T	2	Nsp7524 I	R`CATG,Y	8	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	-
NspB II	CMG CKG	14	NspH I	R,CATG`Y	8	Stu I	AGG CCT	2	Sty I	C`CWG,G	13
Pac I	TTA,AT`TAA	2	PaeR7 I	C`TCGA,G	-	Taq I	T`CG,A	14	TEI I	G`AWT,C	7
Pal I	GG CC	42	PflM I	CCAN`NNN`NTGG	2	Tsp45 I	`GTSAC,	22	Tth111 I	GACN`N,NGTC	2
Ple I	GATC 9/10	3	Pme I	CTTT ARAC	1	Tth111 II	CAARCA 16/14	9	Vsp I	AT`TA,AT	5
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	2	Xba I	T`CTAG,A	3	Xca I	GTA TAC	1
Psp1406 I	AA`CG,TT	1	PspA I	C`CCGG,G	3	Xcm I	CCANNNN,N`NNNNTGG3	-	Xho I	C`TCGA,G	-
Pst I	C,TGCA`G	5	Pvu I	CG,AT`CG	-	Xho II	R`GATC,Y	14	Xma I	C`CCGG,G	3
Pvu II	CAG CTG	7	Rsa I	GT AC	13	Xma III	C`GGCC,G	1	Xmn I	GAANN NNPTC	1