

Gateway®HyPer-AS entry clone table of restriction sites

Enzyme Name	Sequence	Count	Cutting Position				
AatI	AGG!CCT	1	2872				
AatII	GACGT!C	0					
Acc65I	G!GTACC	0					
AccI	GT!MKAC	2	810	1467			
AccII	CG!CG	14	1939	1975	2351	2371	2395
			2426	3117	3418	3856	3940
			4003	4072	4345	4926	
AccIII	T!CCGGA	1	920				
AciI	G!CGG	20	2311	2338	2426	2536	3117
			3181	3282	3285	3565	3620
			3718	3856	4003	4143	4386
			4631	4752	4771	4898	4926
AciI	C!CGC	27	519	768	1350	2366	2369
			2383	2473	2721	2733	2742
			2754	2764	2775	2821	2960
			3023	3525	3570	3636	3662
			3787	3790	3938	4070	4377
			4521	5017			
AcyI	GR!CGYC	3	3051	3753	3832		
AfaI	GT!AC	8	99	269	621	829	976
			1259	1613	3357		
AflI	G!GWCC	6	173	206	665	1452	3567
			4012				
AflII	C!TTAAG	0					
AflIII	A!CRYGT	2	1937	4969			
AgeI	A!CCGGT	1	124				
AhaI	CC!SGG	4	3055	3215	3828	4592	
AhaII	GR!CGYC	3	3051	3753	3832		
AhaIII	TTT!AAA	4	1035	1753	4195	4214	
AluI	AG!CT	17	341	512	799	1204	1252
			1604	1830	1997	2254	2549
			2837	3157	3615	4412	4669
			4715	4805			
Alw44I	G!TGCAC	1	4655				
AlwI	GGATCNNNN!	11	513	747	1582	1591	2919
			3230	3476	3868	4227	4325
			4411				
AlwI	!NNNNNGATCC	5	1569	3295	3839	4226	4323
AlwNI	CAGNNN!CTG	2	4152	4560			
AocI	CC!TNAGG	4	1021	1098	2531	4163	
AocII	GDGCH!C	8	2242	2997	3090	3164	3354
			3416	4126	4659		
Aor51HI	AGC!GCT	1	120				
AosI	TGC!GCA	1	3153				
AosII	GR!CGYC	3	3051	3753	3832		
ApaI	GGGCC!C	0					
ApaLI	G!TGCAC	1	4655				
ApoI	R!AATTY	4	908	1865	1969	1980	
ApyI	CC!WGG	11	1476	1528	2587	2642	2659
			3438	4017	4120	4810	4823
			4944				
AquI	C!YCGRG	0					
AscI	GG!CGCGCC	0					
AseI	AT!TAAT	1	968				
AsnI	AT!TAAT	1	968				
Asp700I	GAANN!NNTTC	1	441				

Asp718I	G!GTACC	0					
AspHI	GWGCW!C	3	3164	3354	4659		
AspI	GACN!NNGTC	2	166	3169			
AsuI	G!GNCC	12	173	206	301	426	665
			1452	2158	3567	4012	4058
			4116	4149			
AsuII	TT!CGAA	2	1281	3733			
AvaI	C!YCGRG	0					
AvaII	G!GWCC	6	173	206	665	1452	3567
			4012				
AvaIII	ATGCA!T	4	1433	2623	2695	5026	
AviII	TGC!GCA	1	3153				
AvrI	!CYCGRG	0					
AvrII	C!CTAGG	2	2873	3888			
AxyI	CC!TNAGG	4	1021	1098	2531	4163	
BalI	TGG!CCA	2	1003	3133			
BamHI	G!GATCC	1	1574				
BanI	G!GYRCC	3	2204	3050	3085		
BanII	GRGCY!C	3	2242	3416	4126		
BanIII	AT!CGAT	1	2891				
BbeI	GGCGC!C	1	3054				
BbiII/AcyI	GR!CGYC	3	3051	3753	3832		
BbrPI	CAC!GTG	0					
BbsI	!GTCTTC	0					
BbsI	!GAAGAC	0					
BbvI	GCAGCNNNNNNN!	6	1839	3124	3166	3687	4140
			4640				
BbvI	!NNNNNNNNNNNGCTGC	9	99	757	2333	2998	3182
			3275	4341	4547	4550	
BbvII	GAAGACNN!	0					
BbvII	!NNNNNNGTCTTC	0					
BcefI	ACGGCNNNNNNNNNN!	2	3477	3964			
BcefI	!NNNNNNNNNNNGCCGT	4	1371	2193	3011	4470	
BcgI	!GCANNNNNNTCG	0					
BcgI	!GCANNNNNNTGC	1	1281				
BclI	T!GATCA	1	1708				
BcnI	CC!SGG	4	3055	3215	3828	4592	
BfaI	C!TAG	14	116	338	626	1155	1253
			1325	1587	1699	1900	2318
			2874	3889	4223	4476	
BfrI	C!TTAAG	0					
BglI	GCCNNNN!NGGC	1	2826				
BglII	A!GATCT	0					
BinI	!NNNNNGATCC	5	1569	3295	3839	4226	4323
BinI	GGATCNNNN!	11	513	747	1582	1591	2919
			3230	3476	3868	4227	4325
			4411				
BlnI	C!CTAGG	2	2873	3888			
BmyI	GDGCH!C	8	2242	2997	3090	3164	3354
			3416	4126	4659		
BpmI	!CTCCAG	1	3848				
BpmI	!CTGGAG	1	3869				
Bpu1102I	GC!TNAGC	0					
BsaAI	YAC!GTR	2	2167	3355			
BsaBI	GATNN!NNATC	2	1713	2910			
BsaHI	GR!CGYC	3	3051	3753	3832		
BsaI	GGTCTCN!	0					
BsaI	!NNNNNGAGACC	1	4040				
BsaJI	C!CNNGG	19	135	357	422	837	998

			2585	2657	2780	2815	2824
			2873	3214	3483	3888	4015
			4016	4118	4119	4809	
BseAI	T!CCGGA	1	920				
BsePI	!GCGCGC	0					
BsgI	!GTGCAG	0					
BsgI	!CTGCAC	0					
BsiEI	CGRY!CG	3	129	2960	4635		
BsiWI	C!GTACG	0					
BsiYI	CCNNNNN!NNGG	20	203	277	1587	2063	2389
			2781	3032	3576	3857	3889
			3890	4021	4056	4106	4107
			4138	4491	4770	4936	4954
BslI	CCNNNNN!NNGG	20	203	277	1587	2063	2389
			2781	3032	3576	3857	3889
			3890	4021	4056	4106	4107
			4138	4491	4770	4936	4954
BsmAI	!GTCTC	1	916				
BsmAI	!GAGAC	5	160	2480	2898	3917	4045
BsmI	GAATGCN!	2	443	1802			
BsmI	G!CATTC	2	362	1895			
Bsp1286I	GDGCH!C	8	2242	2997	3090	3164	3354
			3416	4126	4659		
BspDI	AT!CGAT	1	2891				
BspEI	T!CCGGA	1	920				
BspHI	T!CATGA	2	2477	4249			
BspMI	ACCTGCNNNN!	2	3319	3769			
BspMI	!NNNNNNNNGCAGGT	1	2938				
BspMII	T!CCGGA	1	920				
BspWI	GCNNNNN!NNGC	26	118	458	518	1523	2278
			2308	2335	2377	2379	2618
			2690	2741	2820	2826	3042
			3126	3149	3288	3294	3411
			3494	3761	3948	4152	4351
			4923				
BsrFI	R!CCGGY	9	124	461	521	773	1286
			2268	3370	3551	3834	
BsrI	ACTGGN!	4	985	2995	3196	4442	
BsrI	C!CAGT	5	304	2080	2758	4554	4567
BssHII	G!CGCGC	0					
Bst1107I	GTA!TAC	0					
BstBI	TT!CGAA	2	1281	3733			
BstEII	G!GTNACC	0					
BstI	G!GATCC	1	1574				
BstNI	CC!WGG	11	1476	1528	2587	2642	2659
			3438	4017	4120	4810	4823
			4944				
BstPI	G!GTNACC	0					
BstUI	CG!CG	14	1939	1975	2351	2371	2395
			2426	3117	3418	3856	3940
			4003	4072	4345	4926	
BstXI	CCANNNNN!NTGG	2	142	1462			
BstYI	R!GATCY	9	1574	1583	3222	3468	3860
			4219	4231	4317	4328	
Bsu36I	CC!TNAGG	4	1021	1098	2531	4163	
CbiI	TT!CGAA	2	1281	3733			
CcrI	C!TCGAG	0					
CelII	GC!TNAGC	0					
CfoI	GCG!C	21	121	2317	2325	2351	2373

			2382	2395	2426	3045	3053
			3117	3154	3420	3680	3856
			3942	4345	4454	4628	4728
			4795				
Cfr10I	R!CCGGY	9	124	461	521	773	1286
			2268	3370	3551	3834	
Cfr13I	G!GNCC	12	173	206	301	426	665
			1452	2158	3567	4012	4058
			4116	4149			
Cfr9I	C!CCGGG	0					
CfrI	Y!GGCCR	7	459	552	1001	2957	3131
			3522	3549			
ClaI	AT!CGAT	1	2891				
CpoI	CG!GWCCG	1	3567				
Csp45I	TT!CGAA	2	1281	3733			
CspI	CG!GSCCG	0					
CviJI	RG!CY	88	11	112	146	302	341
			428	461	512	554	581
			799	1003	1204	1252	1286
			1316	1349	1444	1474	1517
			1526	1604	1720	1830	1997
			2017	2159	2240	2254	2268
			2549	2590	2662	2785	2814
			2820	2829	2837	2860	2872
			2878	2959	2976	2984	3011
			3036	3120	3129	3133	3157
			3195	3271	3288	3307	3370
			3414	3424	3441	3524	3551
			3555	3592	3615	3631	3811
			3838	3899	4021	4060	4117
			4124	4131	4150	4161	4412
			4441	4484	4495	4560	4639
			4664	4669	4715	4805	4903
			4929	4947	4958		
CvnI	CC!TNAGG	4	1021	1098	2531	4163	
DdeI	C!TNAG	8	1021	1098	2531	2833	3714
			4163	4286	4695		
DpnI	GA!TC	23	417	507	741	1492	1576
			1585	1710	2890	2894	2913
			3224	3302	3383	3392	3470
			3846	3862	4221	4233	4311
			4319	4330	4405		
DpnII	!GATC	23	415	505	739	1490	1574
			1583	1708	2888	2892	2911
			3222	3300	3381	3390	3468
			3844	3860	4219	4231	4309
			4317	4328	4403		
DraI	TTT!AAA	4	1035	1753	4195	4214	
DraII	RG!GNCCY	1	4149				
DraIII	CACNNN!GTG	2	748	2167			
DrdI	GACNNNN!NNGTC	3	2122	3078	4867		
DsaI	C!CRYGG	5	135	422	998	2780	3483
DsaV	!CCNGG	15	1474	1526	2585	2640	2657
			3053	3213	3436	3826	4015
			4118	4590	4808	4821	4942
EaeI	Y!GGCCR	7	459	552	1001	2957	3131
			3522	3549			
EagI	C!GGCCG	1	2957				
Eam1105I	GACNNN!NNGTC	0					

EarI	!CTCTTC	0						
EarI	!GAAGAG	5	844	1401	2522	3399	3609	
Ecl136II	GAG!CTC	0						
EclXI	C!GGCCG	1	2957					
Eco105I	TAC!GTA	0						
Eco31I	GGTCTCN!	0						
Eco31I	!NNNNNGAGACC	1	4040					
Eco47I	G!GWCC	6	173	206	665	1452	3567	
			4012					
Eco47III	AGC!GCT	1	120					
Eco52I	C!GGCCG	1	2957					
Eco57I	!CTGAAG	2	3175	3607				
Eco57I	!CTTCAG	2	1308	4441				
Eco81I	CC!TNAGG	4	1021	1098	2531	4163		
EcoNI	CCTNN!NNNAGG	1	275					
EcoO109I	RG!GNCCY	1	4149					
EcoO65I	G!GTNACC	0						
EcoRI	G!AATTC	0						
EcoRII	!CCWGG	11	1474	1526	2585	2640	2657	
			3436	4015	4118	4808	4821	
			4942					
EcoRV	GAT!ATC	1	1052					
EcoT14I	C!CWWGG	8	135	422	837	998	2780	
			2873	3483	3888			
EcoT22I	ATGCA!T	4	1433	2623	2695	5026		
EcoT38I	GRGCY!C	3	2242	3416	4126			
EheI	GGC!GCC	1	3052					
Esp3I	CGTCTCN!	0						
Esp3I	!NNNNNGAGACG	0						
EspI	GC!TNAGC	0						
FbaI	T!GATCA	1	1708					
FinI	!GTCCC	6	865	994	2581	2653	2717	
			4012					
FinI	!GGGAC	3	3187	3719	3828			
Fnu4HI	GC!NGC	31	113	771	1350	1828	2347	
			2369	2383	2821	2960	3012	
			3023	3113	3118	3155	3196	
			3283	3286	3289	3525	3621	
			3662	3676	3790	4129	4144	
			4355	4561	4564	4629	4772	
			4927					
FokI	GGATGNNNNNNNNN!	9	500	806	1421	1543	1547	
			2918	3375	3400	3854		
FokI	!NNNNNNNNNNNNNCATCC	1	2724					
FspI	TGC!GCA	1	3153					
GdiII	!NNNNNYGGCCG	5	453	546	2951	3516	3543	
GdiII	CGGCCRN!	1	2963					
GsuI	!CTCCAG	1	3848					
GsuI	!CTGGAG	1	3869					
HaeI	WGG!CCW	8	581	1003	1474	2872	3133	
			4495	4947	4958			
HaeII	RGCGC!Y	5	122	2318	2326	3054	4729	
HaeIII	GG!CC	24	302	428	461	554	581	
			1003	1474	2017	2159	2814	
			2820	2829	2872	2959	3133	
			3524	3551	4060	4117	4150	
			4495	4929	4947	4958		
HapII	C!CGG	24	125	462	522	774	921	
			1269	1287	1581	2269	2956	

			3033	3055	3083	3214	3304
			3371	3552	3827	3835	3927
			4401	4591	4617	4764	
HgaI	GACGCNNNNN!	3	947	3761	3840		
HgaI	!NNNNNNNNNNNGCGTC	3	2384	4279	4857		
HgiAI	GWGCW!C	3	3164	3354	4659		
HgiEII	!ACCNNNNNNNGGT	3	649	766	4381		
HhaI	GCG!C	21	121	2317	2325	2351	2373
			2382	2395	2426	3045	3053
			3117	3154	3420	3680	3856
			3942	4345	4454	4628	4728
			4795				
HinII	GR!CGYC	3	3051	3753	3832		
HinPII	G!CGC	21	119	2315	2323	2349	2371
			2380	2393	2424	3043	3051
			3115	3152	3418	3678	3854
			3940	4343	4452	4626	4726
			4793				
HincII	GTY!RAC	1	1814				
HindIII	A!AGCTT	0					
HinfI	G!ANTC	13	286	353	1218	2094	2116
			2526	3536	3670	3722	3780
			3817	4599	4995		
HpaI	GTT!AAC	1	1814				
HpaII	C!CGG	24	125	462	522	774	921
			1269	1287	1581	2269	2956
			3033	3055	3083	3214	3304
			3371	3552	3827	3835	3927
			4401	4591	4617	4764	
HphI	GGTGANNNNNNNN!	9	170	476	671	902	941
			947	1201	4122	4238	
HphI	!NNNNNNNTCACC	4	410	1473	2168	3229	
KasI	G!GCGCC	1	3050				
KpnI	GGTAC!C	0					
Ksp632I	CTCTCN!	0					
Ksp632I	!NNNNGAAGAG	5	840	1397	2518	3395	3605
KspI	CCGC!GG	0					
MaeI	C!TAG	14	116	338	626	1155	1253
			1325	1587	1699	1900	2318
			2874	3889	4223	4476	
MaeII	A!CGT	11	540	603	894	2111	2123
			2166	2276	3167	3354	4135
			4268				
MaeIII	!GTNAC	22	41	524	659	763	890
			902	935	1012	1025	1371
			1538	1590	1666	1839	2340
			2352	3171	3477	4167	4433
			4549	4612			
MamI	GATNN!NNATC	2	1713	2910			
MboI	!GATC	23	415	505	739	1490	1574
			1583	1708	2888	2892	2911
			3222	3300	3381	3390	3468
			3844	3860	4219	4231	4309
			4317	4328	4403		
MboII	GAAGANNNNNNNN!	10	425	577	620	857	1414
			2307	2535	3412	3622	4241
MboII	!NNNNNNNTCTTC	7	1072	1120	1415	3702	3869
			4069	4312			
McrI	!CGRYCG	3	125	2956	4631		

MfeI	!CAATTG	1	1800					
MflI	R!GATCY	9	1574	1583	3222	3468	3860	
			4219	4231	4317	4328		
MluI	A!CGCGT	1	1937					
MmeI	!TCCRAC	1	2118					
MmeI	!GTYGGA	3	202	4594	4778			
MnlI	CCTCNNNNNNN!	11	231	387	1770	1779	2834	
			2840	3652	3858	4172	4542	
			4866					
MnlI	!NNNNNNNGAGG	31	270	351	477	494	808	
			817	924	1092	1109	1167	
			1218	1290	1328	1391	1397	
			1506	1564	1729	2194	2525	
			2803	2809	2846	2849	2861	
			2901	2965	3101	3458	3888	
			4791					
MroI	T!CCGGA	1	920					
MscI	TGG!CCA	2	1003	3133				
MseI	T!TAA	18	968	1034	1206	1434	1752	
			1813	1934	1955	1966	1978	
			1989	2006	2104	2375	4194	
			4208	4213	4265			
MspI	C!CGG	24	125	462	522	774	921	
			1269	1287	1581	2269	2956	
			3033	3055	3083	3214	3304	
			3371	3552	3827	3835	3927	
			4401	4591	4617	4764		
MstI	TGC!GCA	1	3153					
MstII	CC!TNAGG	4	1021	1098	2531	4163		
MunI	C!AATTG	1	1801					
MvaI	CC!WGG	11	1476	1528	2587	2642	2659	
			3438	4017	4120	4810	4823	
			4944					
MvnI	CG!CG	14	1939	1975	2351	2371	2395	
			2426	3117	3418	3856	3940	
			4003	4072	4345	4926		
NaeI	GCC!GGC	3	2270	3553	3836			
NarI	GG!CGCC	1	3051					
NciI	CC!SGG	4	3055	3215	3828	4592		
NcoI	C!CATGG	5	135	422	998	2780	3483	
NdeI	CA!TATG	1	1062					
NdeII	!GATC	23	415	505	739	1490	1574	
			1583	1708	2888	2892	2911	
			3222	3300	3381	3390	3468	
			3844	3860	4219	4231	4309	
			4317	4328	4403			
NgoMI	G!CCGGC	3	2268	3551	3834			
NheI	G!CTAGC	1	115					
NlaIII	CATG!	21	139	426	553	748	1002	
			1076	1345	1431	2481	2621	
			2693	2784	2925	3270	3456	
			3487	3513	3869	4253	4973	
			5024					
NlaIV	GGN!NCC	17	616	835	1267	1576	2206	
			2227	2239	2430	2591	2663	
			3052	3087	3935	4014	4059	
			4902	4941				
NotI	GC!GGCCGC	0						
NruI	TCG!CGA	0						

NsiI	ATGCA!T	4	1433	2623	2695	5026		
Nsp(7524)I	RCATG!Y	4	2621	2693	3456	4973		
Nsp(7524)V	TT!CGAA	2	1281	3733				
NspBII	CMG!CKG	5	770	2549	3157	4386	4631	
NspII	GDGCH!C	8	2242	2997	3090	3164	3354	
			3416	4126	4659			
NspIII	C!YCGRG	0						
NspIV	G!GNCC	12	173	206	301	426	665	
			1452	2158	3567	4012	4058	
			4116	4149				
NunII	GG!CGCC	1	3051					
PacI	TTAAT!TAA	0						
Paer71	C!TCGAG	0						
PalI	GG!CC	24	302	428	461	554	581	
			1003	1474	2017	2159	2814	
			2820	2829	2872	2959	3133	
			3524	3551	4060	4117	4150	
			4495	4929	4947	4958		
PflMI	CCANNNN!NTGG	1	203					
PleI	GAGTCNNNN!	2	2102	2534				
PleI	!NNNNNGACTC	4	280	2110	3716	4593		
PmaCI	CAC!GTG	0						
PmeI	GTTT!AAAC	0						
PmlI	CAC!GTG	0						
PpuMI	RG!GWCCY	0						
PshAI	GACNN!NNGTC	0						
PstI	CTGCA!G	0						
PvuI	CGAT!CG	0						
PvuII	CAG!CTG	2	2549	3157				
RmaI	C!TAG	14	116	338	626	1155	1253	
			1325	1587	1699	1900	2318	
			2874	3889	4223	4476		
RsaI	GT!AC	8	99	269	621	829	976	
			1259	1613	3357			
RsrI	G!AATTC	0						
RsrII	CG!GWCCG	1	3567					
SacI	GAGCT!C	0						
SacII	CCGC!GG	0						
SalI	G!TCGAC	0						
Sau3AI	!GATC	23	415	505	739	1490	1574	
			1583	1708	2888	2892	2911	
			3222	3300	3381	3390	3468	
			3844	3860	4219	4231	4309	
			4317	4328	4403			
Sau96I	G!GNCC	12	173	206	301	426	665	
			1452	2158	3567	4012	4058	
			4116	4149				
SauI	CC!TNAGG	4	1021	1098	2531	4163		
ScaI	AGT!ACT	0						
ScrFI	CC!NGG	15	1476	1528	2587	2642	2659	
			3055	3215	3438	3828	4017	
			4120	4592	4810	4823	4944	
SduI	GDGCH!C	8	2242	2997	3090	3164	3354	
			3416	4126	4659			
SecI	C!CNNGG	19	135	357	422	837	998	
			2585	2657	2780	2815	2824	
			2873	3214	3483	3888	4015	
			4016	4118	4119	4809		
SexI	!CTCGAG	0						

SfaNI	GCATCNNNNN!	6	1867 3689	2630	2702	3350	3414
SfaNI	!NNNNNNNNNGATGC	4	3009	3264	3480	4872	
SfcI	C!TRYAG	4	1468	2386	4513	4704	
SfiI	GGCCNNNN!NGGCC	1	2826				
SfuI	TT!CGAA	2	1281	3733			
SgrAI	CR!CCGGYG	0					
SinI	G!GWCC	6	173 4012	206	665	1452	3567
SmaI	CCC!GGG	0					
SnaBI	TAC!GTA	0					
SnaI	!GTATAC	0					
SnoI	G!TGCAC	1	4655				
SpeI	A!CTAGT	0					
SphI	GCATG!C	3	2621	2693	3456		
SplI	C!GTACG	0					
SrfI	GCCC!GGGC	0					
Sse8387I	CCTGCA!GG	0					
SspI	AAT!ATT	4	873	1237	1959	2512	
SstI	GAGCT!C	0					
SstII	CCGC!GG	0					
SstIII	!ACGT	11	539 2165 4267	602 2275	893 3166	2110 3353	2122 4134
StuI	AGG!CCT	1	2872				
StyI	C!CWWGG	8	135 2873	422 3483	837 3888	998	2780
StySJI	!GAGNNNNNGTRC	1	1099				
StySJI	!GYACNNNNNNCTC	0					
SwaI	ATTT!AAAT	0					
TaqI	T!CGA	13	384 3320 3778	1281 3344 4033	2200 3380 4871	2891 3542	3164 3733
TaqII	GACCGANNNNNNNNNN!	3	2071	3088	3756		
TaqII	!NNNNNNNNNTCGGTC	2	176	4000			
TaqII	CACCCANNNNNNNNNN!	1	435				
TaqII	!NNNNNNNNNTGGGTG	2	2955	3547			
TfiI	G!AWTC	7	353 3817	1218 4995	3536	3670	3780
ThaI	CG!CG	14	1939 2426 4003	1975 3117 4072	2351 3418 4345	2371 3856 4926	2395 3940
Tsp45I	!GTSAC	10	41 1538	659 1666	890 2340	902 3171	935 3477
TspEI	!AATT	16	61 1144 1969 4209	529 1647 1980	591 1801 2627	908 1865 2699	965 1943 2791
Tth111I	GACN!NNGTC	2	166	3169			
Tth111II	CAARCANNNNNNNNNN!	3	575	1578	4378		
Tth111II	!NNNNNNNNNTGYTTG	6	470 4385	487	743	3486	4346
TthHB8I	T!CGA	13	384 3320 3778	1281 3344 4033	2200 3380 4871	2891 3542	3164 3733
Van91I	CCANNNN!NTGG	1	203				
VspI	AT!TAAT	1	968				
XbaI	T!CTAGA	0					
XcmI	!CCANNNNNNNNTCG	1	3326				

XcyI	C!CCGGG	0					
XhoI	C!TCGAG	0					
XhoII	R!GATCY	9	1574	1583	3222	3468	3860
			4219	4231	4317	4328	
XmaI	C!CCGGG	0					
XmaIII	C!GGCCG	1	2957				
XmnI	GAANN!NNTTC	1	441				
XorII	CGAT!CG	0					