

Enzyme Name	Sequence	Count	Cutting Position				
AatI	AGG!CCT	1	2946				
AatII	GACGT!C	4	126	179	262	448	
Acc65I	G!GTACC	1	646				
AccI	GT!MKAC	2	641	1640			
AccII	CG!CG	15	61	1774	2049	2425	2445
			2469	2500	3191	3492	3930
			4014	4077	4146	4419	5000
AccIII	T!CCGGA	0					
AciI	G!CGG	29	371	404	529	709	734
			1208	1520	1562	1768	2385
			2412	2500	2610	3191	3255
			3356	3359	3639	3694	3792
			3930	4077	4217	4460	4705
			4826	4845	4972	5000	
AciI	C!CGC	39	59	87	99	113	280
			508	590	650	683	756
			894	1373	1511	1613	1772
			2440	2443	2457	2547	2795
			2807	2816	2828	2838	2849
			2895	3034	3097	3599	3644
			3710	3736	3861	3864	4012
			4144	4451	4595	5091	
AcyI	GR!CGYC	8	123	176	259	445	1637
			3125	3827	3906		
AfaI	GT!AC	14	220	245	300	333	384
			541	648	784	1002	1021
			1105	1255	1507	3431	
AflI	G!GWCC	4	801	1650	3641	4086	
AflIII	C!TTAAG	1	2007				
AflIII	A!CRYGT	1	5043				
AgeI	A!CCGGT	1	1041				
AhaI	CC!SGG	5	1634	3129	3289	3902	4666
AhaII	GR!CGYC	8	123	176	259	445	1637
			3125	3827	3906		
AhaIII	TTT!AAA	3	1827	4269	4288		
AluI	AG!CT	19	567	619	625	767	1074
			1101	1247	1554	1904	2071
			2328	2623	2911	3231	3689
			4486	4743	4789	4879	
Alw44I	G!TGCAC	2	1140	4729			
AlwI	GGATCNNNN!	8	1043	2993	3304	3550	3942
			4301	4399	4485		
AlwI	!NNNNNGATCC	8	581	933	1030	1595	3369
			3913	4300	4397		
AlwNI	CAGNNN!CTG	3	1727	4226	4634		
AocI	CC!TNAGG	3	1319	2605	4237		
AocII	GDGCH!C	14	621	700	1117	1144	1177
			1754	2316	3071	3164	3238
			3428	3490	4200	4733	
Aor51HI	AGC!GCT	3	597	916	1029		
AosI	TGC!GCA	1	3227				
AosII	GR!CGYC	8	123	176	259	445	1637
			3125	3827	3906		
ApaI	GGGCC!C	0					
ApaLI	G!TGCAC	2	1140	4729			
ApoI	R!AATTY	5	630	846	1939	2043	2054

ApyI	CC!WGG	19	91	284	898	933	968
			1237	1285	1381	1396	1525
			2661	2716	2733	3512	4091
			4194	4884	4897	5018	
AquI	C!YCGRG	1	614				
AscI	GG!CGCGCC	0					
AseI	AT!TAAT	1	8				
AsnI	AT!TAAT	1	8				
Asp700I	GAANN!NNTTC	0					
Asp718I	G!GTACC	1	646				
AspHI	GWGCW!C	5	621	1144	3238	3428	4733
AspI	GACN!NNGTC	1	3243				
AsuI	G!GNCC	14	84	277	801	1210	1453
			1545	1566	1650	2232	3641
			4086	4132	4190	4223	
AsuII	TT!CGAA	2	628	3807			
AvaI	C!YCGRG	1	614				
AvaII	G!GWCC	4	801	1650	3641	4086	
AvaIII	ATGCA!T	3	2697	2769	5100		
AviII	TGC!GCA	1	3227				
AvrI	!CYCGRG	1	613				
AvrII	C!CTAGG	2	2947	3962			
AxyI	CC!TNAGG	3	1319	2605	4237		
BalI	TGG!CCA	3	979	1720	3207		
BamHI	G!GATCC	1	1035				
BanI	G!GYRCC	7	466	646	1114	1174	2278
			3124	3159			
BanII	GRGCY!C	5	621	700	2316	3490	4200
BanIII	AT!CGAT	1	2965				
BbeI	GGCGC!C	1	3128				
BbiII/AcyI	GR!CGYC	8	123	176	259	445	1637
			3125	3827	3906		
BbrPI	CAC!GTG	0					
BbsI	!GTCTTC	0					
BbsI	!GAAGAC	1	1353				
BbvI	GCAGCNNNNNNNN!	9	764	1271	1713	1913	3198
			3240	3761	4214	4714	
BbvI	!NNNNNNNNNNNGCTGC	10	947	950	1390	2407	3072
			3256	3349	4415	4621	4624
BbvII	GAAGACNN!	1	1361				
BbvII	!NNNNNNGTCTTC	0					
BcefI	ACGGCNNNNNNNNNN!	7	962	1272	1416	1467	1533
			3551	4038			
BcefI	!NNNNNNNNNNNGCCGT	5	935	974	2267	3085	4544
BcgI	!GCANNNNNNTCG	0					
BcgI	!CGANNNNNNTGC	0					
BclI	T!GATCA	0					
BcnI	CC!SGG	5	1634	3129	3289	3902	4666
BfaI	C!TAG	9	593	1739	1780	1974	2392
			2948	3963	4297	4550	
BfrI	C!TTAAG	1	2007				
BglI	GCCNNNN!NGGC	5	91	213	284	1529	2900
BglII	A!GATCT	1	610				
BinI	!NNNNNGATCC	8	581	933	1030	1595	3369
			3913	4300	4397		
BinI	GGATCNNNN!	8	1043	2993	3304	3550	3942
			4301	4399	4485		
BlnI	C!CTAGG	2	2947	3962			
BmyI	GDGCH!C	14	621	700	1117	1144	1177

			1754	2316	3071	3164	3238
			3428	3490	4200	4733	
BpmI	!CTCCAG	3	929	1392	3922		
BpmI	!CTGGAG	1	3943				
Bpu1102I	GC!TNAGC	0					
BsaAI	YAC!GTR	3	341	2241	3429		
BsaBI	GATNN!NNATC	2	1787	2984			
BsaHI	GR!CGYC	8	123	176	259	445	1637
			3125	3827	3906		
BsaI	GGTCTCN!	0					
BsaI	!NNNNNGAGACC	2	1681	4114			
BsaJI	C!CNNGG	25	361	827	833	932	967
			995	1052	1148	1283	1284
			1379	2659	2731	2854	2889
			2898	2947	3288	3557	3962
			4089	4090	4192	4193	4883
BseAI	T!CCGGA	0					
BsePI	!GCGCGC	0					
BsgI	!GTGCAG	0					
BsgI	!CTGCAC	0					
BsiEI	CGRY!CG	5	950	1046	1772	3034	4709
BsiWI	C!GTACG	0					
BsiYI	CCNNNNN!NNGG	26	50	693	694	814	1171
			1284	1450	1516	1659	2137
			2463	2855	3106	3650	3931
			3963	3964	4095	4130	4180
			4181	4212	4565	4844	5010
			5028				
BslI	CCNNNNN!NNGG	26	50	693	694	814	1171
			1284	1450	1516	1659	2137
			2463	2855	3106	3650	3931
			3963	3964	4095	4130	4180
			4181	4212	4565	4844	5010
			5028				
BsmAI	!GTCTC	1	429				
BsmAI	!GAGAC	5	1686	2554	2972	3991	4119
BsmI	GAATGCN!	1	1876				
BsmI	G!CATTC	1	1969				
Bsp1286I	GDGCH!C	14	621	700	1117	1144	1177
			1754	2316	3071	3164	3238
			3428	3490	4200	4733	
BspDI	AT!CGAT	1	2965				
BspEI	T!CCGGA	0					
BspHI	T!CATGA	3	842	2551	4323		
BspMI	ACCTGCNNNN!	2	3393	3843			
BspMI	!NNNNNNNNGCAGGT	3	789	871	3012		
BspMII	T!CCGGA	0					
BspWI	GCNNNNN!NNGC	37	91	213	245	284	377
			401	676	743	752	764
			886	960	985	1098	1529
			2352	2382	2409	2451	2453
			2692	2764	2815	2894	2900
			3116	3200	3223	3362	3368
			3485	3568	3835	4022	4226
			4425	4997			
BsrFI	R!CCGGY	6	814	1041	2342	3444	3625
			3908				
BsrI	ACTGGN!	5	1664	1751	3069	3270	4516
BsrI	C!CAGT	5	296	2154	2832	4628	4641

BssHII	G!CGCGC	0					
Bst1107I	GTA!TAC	0					
BstBI	TT!CGAA	2	628	3807			
BstEII	G!GTNACC	0					
BstI	G!GATCC	1	1035				
BstNI	CC!WGG	19	91	284	898	933	968
			1237	1285	1381	1396	1525
			2661	2716	2733	3512	4091
			4194	4884	4897	5018	
BstPI	G!GTNACC	0					
BstUI	CG!CG	15	61	1774	2049	2425	2445
			2469	2500	3191	3492	3930
			4014	4077	4146	4419	5000
BstXI	CCANNNNN!NTGG	1	834				
BstYI	R!GATCY	12	586	610	938	1035	1600
			3296	3542	3934	4293	4305
			4391	4402			
Bsu36I	CC!TNAGG	3	1319	2605	4237		
CbiI	TT!CGAA	2	628	3807			
CcrI	C!TCGAG	1	614				
CelII	GC!TNAGC	0					
CfoI	GCG!C	29	598	723	746	752	875
			903	917	956	1030	2391
			2399	2425	2447	2456	2469
			2500	3119	3127	3191	3228
			3494	3754	3930	4016	4419
			4528	4702	4802	4869	
Cfr10I	R!CCGGY	6	814	1041	2342	3444	3625
			3908				
Cfr13I	G!GNCC	14	84	277	801	1210	1453
			1545	1566	1650	2232	3641
			4086	4132	4190	4223	
Cfr9I	C!CCGGG	0					
CfrI	Y!GGCCR	8	947	977	1718	1769	3031
			3205	3596	3623		
ClaI	AT!CGAT	1	2965				
CpoI	CG!GWCCG	1	3641				
Csp45I	TT!CGAA	2	628	3807			
CspI	CG!GSCCG	0					
CviJI	RG!CY	102	43	85	94	278	567
			619	625	666	698	755
			767	832	889	949	979
			1009	1074	1101	1164	1211
			1240	1247	1325	1391	1403
			1454	1481	1489	1523	1546
			1554	1568	1678	1714	1720
			1771	1794	1904	2071	2091
			2233	2314	2328	2342	2623
			2664	2736	2859	2888	2894
			2903	2911	2934	2946	2952
			3033	3050	3058	3085	3110
			3194	3203	3207	3231	3269
			3345	3362	3381	3444	3488
			3498	3515	3598	3625	3629
			3666	3689	3705	3885	3912
			3973	4095	4134	4191	4198
			4205	4224	4235	4486	4515
			4558	4569	4634	4713	4738
			4743	4789	4879	4977	5003

			5021	5032			
CvnI	CC!TNAGG	3	1319	2605	4237		
DdeI	C!TNAG	13	607	716	1004	1031	1061
			1319	1616	2605	2907	3788
			4237	4360	4769		
DpnI	GA!TC	24	588	612	940	1037	1426
			1576	1602	1784	2964	2968
			2987	3298	3376	3457	3466
			3544	3920	3936	4295	4307
			4385	4393	4404	4479	
DpnII	!GATC	24	586	610	938	1035	1424
			1574	1600	1782	2962	2966
			2985	3296	3374	3455	3464
			3542	3918	3934	4293	4305
			4383	4391	4402	4477	
DraI	TTT!AAA	3	1827	4269	4288		
DraII	RG!GNCCY	1	4223				
DraIII	CACNNN!GTG	3	990	1710	2241		
DrdI	GACNNNN!NNGTC	3	2196	3152	4941		
DsaI	C!CRYGG	5	361	833	1052	2854	3557
DsaV	!CCNGG	24	89	282	896	931	966
			1235	1283	1379	1394	1523
			1632	2659	2714	2731	3127
			3287	3510	3900	4089	4192
			4664	4882	4895	5016	
EaeI	Y!GGCCR	8	947	977	1718	1769	3031
			3205	3596	3623		
EagI	C!GGCCG	3	947	1769	3031		
Eam1105I	GACNNN!NNGTC	0					
EarI	!CTCTTC	0					
EarI	!GAAGAG	4	1068	2596	3473	3683	
Ecl136II	GAG!CTC	1	619				
EclXI	C!GGCCG	3	947	1769	3031		
Eco105I	TAC!GTA	1	341				
Eco31I	GGTCTCN!	0					
Eco31I	!NNNNNGAGACC	2	1681	4114			
Eco47I	G!GWCC	4	801	1650	3641	4086	
Eco47III	AGC!GCT	3	597	916	1029		
Eco52I	C!GGCCG	3	947	1769	3031		
Eco57I	!CTGAAG	4	792	1548	3249	3681	
Eco57I	!CTTCAG	1	4515				
Eco81I	CC!TNAGG	3	1319	2605	4237		
EcoNI	CCTNN!NNNAGG	0					
EcoO109I	RG!GNCCY	1	4223				
EcoO65I	G!GTNACC	0					
EcoRI	G!AATTC	2	630	846			
EcoRII	!CCWGG	19	89	282	896	931	966
			1235	1283	1379	1394	1523
			2659	2714	2731	3510	4089
			4192	4882	4895	5016	
EcoRV	GAT!ATC	0					
EcoT14I	C!CWWGG	8	361	827	833	1052	2854
			2947	3557	3962		
EcoT22I	ATGCA!T	3	2697	2769	5100		
EcoT38I	GRGKY!C	5	621	700	2316	3490	4200
EheI	GGC!GCC	1	3126				
Esp3I	CGTCTCN!	0					
Esp3I	!NNNNNGAGACG	0					
EspI	GC!TNAGC	0					

FbaI	T!GATCA	0					
FinI	!GTCCC	4	2655	2727	2791	4086	
FinI	!GGGAC	6	161	312	480	3261	3793
			3902				
Fnu4HI	GC!NGC	40	735	753	756	961	964
			1209	1260	1404	1521	1702
			1769	1772	1902	2421	2443
			2457	2895	3034	3086	3097
			3187	3192	3229	3270	3357
			3360	3363	3599	3695	3736
			3750	3864	4203	4218	4429
			4635	4638	4703	4846	5001
FokI	GGATGNNNNNNNNNN!	4	2992	3449	3474	3928	
FokI	!NNNNNNNNNNNNNNNCATCC	5	1131	1219	1276	1431	2798
FspI	TGC!GCA	1	3227				
GdiII	!NNNNNYGGCCG	5	941	1763	3025	3590	3617
GdiII	CGGCCRN!	3	953	1775	3037		
GsuI	!CTCCAG	3	929	1392	3922		
GsuI	!CTGGAG	1	3943				
HaeI	WGG!CCW	10	832	979	1009	1489	1720
			2946	3207	4569	5021	5032
HaeII	RGCGC!Y	7	599	918	1031	2392	2400
			3128	4803			
HaeIII	GG!CC	32	85	278	832	949	979
			1009	1211	1454	1489	1523
			1546	1568	1678	1720	1771
			2091	2233	2888	2894	2903
			2946	3033	3207	3598	3625
			4134	4191	4224	4569	5003
			5021	5032			
HapII	C!CGG	20	602	815	1042	1634	2343
			3030	3107	3129	3157	3288
			3378	3445	3626	3901	3909
			4001	4475	4665	4691	4838
HgaI	GACGCNNNNN!	3	527	3835	3914		
HgaI	!NNNNNNNNNNNGCGTC	4	1626	2458	4353	4931	
HgiAI	GWGCW!C	5	621	1144	3238	3428	4733
HgiEII	!ACCNNNNNNGGT	1	4455				
HhaI	GCG!C	29	598	723	746	752	875
			903	917	956	1030	2391
			2399	2425	2447	2456	2469
			2500	3119	3127	3191	3228
			3494	3754	3930	4016	4419
			4528	4702	4802	4869	
HinII	GR!CGYC	8	123	176	259	445	1637
			3125	3827	3906		
HinPII	G!CGC	29	596	721	744	750	873
			901	915	954	1028	2389
			2397	2423	2445	2454	2467
			2498	3117	3125	3189	3226
			3492	3752	3928	4014	4417
			4526	4700	4800	4867	
HincII	GTY!RAC	2	642	1888			
HindIII	A!AGCTT	1	623				
HinfI	G!ANTC	16	411	605	1190	1340	1667
			1776	2168	2190	2600	3610
			3744	3796	3854	3891	4673
			5069				
HpaI	GTT!AAC	1	1888				

HpaII	C!CGG	20	602 3030 3378 4001	815 3107 3445 4475	1042 3129 3626 4665	1634 3157 3901 4691	2343 3288 3909 4838
HphI	GGTGANNNNNNNN!	6	377 4312	723	895	1446	4196
HphI	!NNNNNNNTCACC	5	918	1005	1335	2242	3303
KasI	G!GCGCC	1	3124				
KpnI	GGTAC!C	1	650				
Ksp632I	CTCTTCN!	0					
Ksp632I	!NNNNGAAGAG	4	1064	2592	3469	3679	
KspI	CCGC!GG	0					
MaeI	C!TAG	9	593 2948	1739 3963	1780 4297	1974 4550	2392
MaeII	A!CGT	16	123 445 2240 4342	135 1418 2350	176 1694 3241	259 2185 3428	340 2197 4209
MaeIII	!GTNAC	14	62 1913 4241	149 2414 4507	498 2426 4623	711 3245 4686	1341 3551
MamI	GATNN!NNATC	2	1787	2984			
MboI	!GATC	24	586 1574 2985 3542 4383	610 1600 3296 3918 4391	938 1782 3374 3934 4402	1035 2962 3455 4293 4477	1424 2966 3464 4305
MboII	GAAGANNNNNNNN!	9	738 2609	1081 3486	1366 3696	1479 4315	2381
MboII	!NNNNNNNTCTTC	4	3776	3943	4143	4386	
McrI	!CGRYCG	5	946	1042	1768	3030	4705
MfeI	!CAATTG	1	1874				
MflI	R!GATCY	12	586 3296 4391	610 3542 4402	938 3934	1035 4293	1600 4305
MluI	A!CGCGT	0					
MmeI	!TCCRAC	2	1446	2192			
MmeI	!GTYGGA	2	4668	4852			
MnlI	CCTCNNNNNNN!	15	939 1744 3726	1223 1844 3932	1402 1853 4246	1417 2908 4616	1633 2914 4940
MnlI	!NNNNNNNGAGG	26	541 1163 1667 2877 2975 4865	878 1196 1700 2883 3039	989 1313 1803 2920 3175	1103 1422 2268 2923 3532	1142 1478 2599 2935 3962
MroI	T!CCGGA	0					
MscI	TGG!CCA	3	979	1720	3207		
MseI	T!TAA	18	8 1887 2063 4282	1079 2008 2080 4287	1304 2029 2178 4339	1760 2040 2449	1826 2052 4268
MspI	C!CGG	20	602 3030 3378 4001	815 3107 3445 4475	1042 3129 3626 4665	1634 3157 3901 4691	2343 3288 3909 4838
MstI	TGC!GCA	1	3227				
MstII	CC!TNAGG	3	1319	2605	4237		

MunI	C!AATTG	1	1875					
MvaI	CC!WGG	19	91	284	898	933	968	
			1237	1285	1381	1396	1525	
			2661	2716	2733	3512	4091	
			4194	4884	4897	5018		
MvnI	CG!CG	15	61	1774	2049	2425	2445	
			2469	2500	3191	3492	3930	
			4014	4077	4146	4419	5000	
NaeI	GCC!GGC	3	2344	3627	3910			
NarI	GG!CGCC	1	3125					
NciI	CC!SGG	5	1634	3129	3289	3902	4666	
NcoI	C!CATGG	5	361	833	1052	2854	3557	
NdeI	CA!TATG	1	235					
NdeII	!GATC	24	586	610	938	1035	1424	
			1574	1600	1782	2962	2966	
			2985	3296	3374	3455	3464	
			3542	3918	3934	4293	4305	
			4383	4391	4402	4477		
NgoMI	G!CCGGC	3	2342	3625	3908			
NheI	G!CTAGC	1	592					
NlaIII	CATG!	26	305	365	660	837	846	
			1056	1092	1098	1110	1188	
			1254	1334	1545	2555	2695	
			2767	2858	2999	3344	3530	
			3561	3587	3943	4327	5047	
			5098					
NlaIV	GGN!NCC	20	468	648	699	1037	1116	
			1176	1567	2280	2301	2313	
			2504	2665	2737	3126	3161	
			4009	4088	4133	4976	5015	
NotI	GC!GGCCGC	1	1769					
NruI	TCG!CGA	0						
NsiI	ATGCA!T	3	2697	2769	5100			
Nsp(7524)I	RCATG!Y	5	1092	2695	2767	3530	5047	
Nsp(7524)V	TT!CGAA	2	628	3807				
NspBII	CMG!CKG	5	1513	2623	3231	4460	4705	
NspII	GDGCH!C	14	621	700	1117	1144	1177	
			1754	2316	3071	3164	3238	
			3428	3490	4200	4733		
NspIII	C!YCGRG	1	614					
NspIV	G!GNCC	14	84	277	801	1210	1453	
			1545	1566	1650	2232	3641	
			4086	4132	4190	4223		
NunII	GG!CGCC	1	3125					
PacI	TTAAT!TAA	0						
Paer71	C!TCGAG	1	614					
PaiI	GG!CC	32	85	278	832	949	979	
			1009	1211	1454	1489	1523	
			1546	1568	1678	1720	1771	
			2091	2233	2888	2894	2903	
			2946	3033	3207	3598	3625	
			4134	4191	4224	4569	5003	
5021	5032							
PflMI	CCANNNN!NTGG	1	1659					
PleI	GAGTCNNNN!	3	1348	2176	2608			
PleI	!NNNNNGACTC	6	405	599	1770	2184	3790	
			4667					
PmaCI	CAC!GTG	0						
PmeI	GTTT!AAAC	0						

PmlI	CAC!GTG	0						
PpuMI	RG!GWCCY	0						
PshAI	GACNN!NNGTC	1	1693					
PstI	CTGCA!G	1	639					
PvuI	CGAT!CG	0						
PvuII	CAG!CTG	2	2623	3231				
RmaI	C!TAG	9	593	1739	1780	1974	2392	
			2948	3963	4297	4550		
RsaI	GT!AC	14	220	245	300	333	384	
			541	648	784	1002	1021	
			1105	1255	1507	3431		
RsrI	G!AATTC	2	630	846				
RsrII	CG!GWCCG	1	3641					
SacI	GAGCT!C	1	621					
SacII	CCGC!GG	0						
SalI	G!TCGAC	1	640					
Sau3AI	!GATC	24	586	610	938	1035	1424	
			1574	1600	1782	2962	2966	
			2985	3296	3374	3455	3464	
			3542	3918	3934	4293	4305	
			4383	4391	4402	4477		
Sau96I	G!GNCC	14	84	277	801	1210	1453	
			1545	1566	1650	2232	3641	
			4086	4132	4190	4223		
SauI	CC!TNAGG	3	1319	2605	4237			
ScaI	AGT!ACT	0						
ScrFI	CC!NGG	24	91	284	898	933	968	
			1237	1285	1381	1396	1525	
			1634	2661	2716	2733	3129	
			3289	3512	3902	4091	4194	
			4666	4884	4897	5018		
SduI	GDGCH!C	14	621	700	1117	1144	1177	
			1754	2316	3071	3164	3238	
			3428	3490	4200	4733		
SecI	C!CNNGG	25	361	827	833	932	967	
			995	1052	1148	1283	1284	
			1379	2659	2731	2854	2889	
			2898	2947	3288	3557	3962	
			4089	4090	4192	4193	4883	
SexI	!CTCGAG	1	613					
SfaNI	GCATC>NNNNN!	9	848	884	1298	1941	2704	
			2776	3424	3488	3763		
SfaNI	!NNNNNNNNNGATGC	8	358	1451	1490	1619	3083	
			3338	3554	4946			
SfcI	C!TRYAG	4	635	2460	4587	4778		
SfiI	GGCCNNNN!NGGCC	1	2900					
SfuI	TT!CGAA	2	628	3807				
SgrAI	CR!CCGGYG	0						
SinI	G!GWCC	4	801	1650	3641	4086		
SmaI	CCC!GGG	0						
SnaBI	TAC!GTA	1	341					
SnaI	!GTATAC	0						
SnoI	G!TGCAC	2	1140	4729				
SpeI	A!CTAGT	0						
SphI	GCATG!C	3	2695	2767	3530			
SplI	C!GTACG	0						
SrfI	GCCC!GGGC	0						
Sse8387I	CCTGCA!GG	0						
SspI	AAT!ATT	2	2033	2586				

SstI	GAGCT!C	1	621					
SstII	CCGC!GG	0						
SstIII	!ACGT	16	122	134	175	258	339	
			444	1417	1693	2184	2196	
			2239	2349	3240	3427	4208	
			4341					
StuI	AGG!CCT	1	2946					
StyI	C!CWWGG	8	361	827	833	1052	2854	
			2947	3557	3962			
StySJI	!GAGNNNNNNNGTRC	0						
StySJI	!GYACNNNNNNNCTC	0						
SwaI	ATTT!AAAT	0						
TaqI	T!CGA	19	615	628	641	869	919	
			1202	1229	1697	2274	2965	
			3238	3394	3418	3454	3616	
			3807	3852	4107	4945		
TaqII	GACCGANNNNNNNNNNN!	3	2145	3162	3830			
TaqII	!NNNNNNNNNTCGGTC	1	4074					
TaqII	CACCCANNNNNNNNNNN!	2	1192	1297				
TaqII	!NNNNNNNNNTGGGTG	3	173	3029	3621			
TfiI	G!AWTC	7	1190	1667	3610	3744	3854	
			3891	5069				
ThaI	CG!CG	15	61	1774	2049	2425	2445	
			2469	2500	3191	3492	3930	
			4014	4077	4146	4419	5000	
Tsp45I	!GTSAC	5	711	1341	2414	3245	3551	
TspEI	!AATT	13	19	630	846	1761	1875	
			1939	2017	2043	2054	2701	
			2773	2865	4283			
Tth111I	GACN!NNGTC	1	3243					
Tth111II	CAARCANNNNNNNNNNN!	2	997	4452				
Tth111III	!NNNNNNNNNTGYTTG	3	3560	4420	4459			
TthHB8I	T!CGA	19	615	628	641	869	919	
			1202	1229	1697	2274	2965	
			3238	3394	3418	3454	3616	
			3807	3852	4107	4945		
Van91I	CCANNNN!NTGG	1	1659					
VspI	AT!TAAT	1	8					
XbaI	T!CTAGA	1	1779					
XcmI	!CCANNNNNNNNTCG	1	3400					
XcyI	C!CCGGG	0						
XhoI	C!TCGAG	1	614					
XhoII	R!GATCY	12	586	610	938	1035	1600	
			3296	3542	3934	4293	4305	
			4391	4402				
XmaI	C!CCGGG	0						
XmaIII	C!GGCCG	3	947	1769	3031			
XmnI	GAANN!NNTTC	0						
XorII	CGAT!CG	0						