

Enzyme Name	Sequence	Count	Cutting Position				
AatI	AGG!CCT	1	2201				
AatII	GACGT!C	0					
Acc65I	G!GTACC	1	169				
AccI	GT!MKAC	1	164				
AccII	CG!CG	15	175	924	1304	1680	1700
			1724	1755	2446	2747	3185
			3269	3332	3401	3674	4255
AccIII	T!CCGGA	0					
AciI	G!CGG	22	175	918	1640	1667	1755
			1865	2446	2510	2611	2614
			2894	2949	3047	3185	3332
			3472	3715	3960	4081	4100
			4227	4255			
AciI	C!CGC	26	173	922	1695	1698	1712
			1802	2050	2062	2071	2083
			2093	2104	2150	2289	2352
			2854	2899	2965	2991	3116
			3119	3267	3399	3706	3850
			4346				
AcyI	GR!CGYC	3	2380	3082	3161		
AfaI	GT!AC	6	99	171	292	656	949
			2686				
AflI	G!GWCC	7	359	414	602	799	933
			2896	3341			
AflII	C!TTAAG	2	698	1262			
AflIII	A!CRYGT	1	4298				
AgeI	A!CCGGT	1	190				
AhaI	CC!SGG	6	181	182	2384	2544	3157
			3921				
AhaII	GR!CGYC	3	2380	3082	3161		
AhaIII	TTT!AAA	5	454	736	1082	3524	3543
AluI	AG!CT	17	142	148	638	703	895
			940	1159	1326	1583	1878
			2166	2486	2944	3741	3998
			4044	4134			
Alw44I	G!TGCAC	1	3984				
AlwI	GGATCNNNN!	8	192	2248	2559	2805	3197
			3556	3654	3740		
AlwI	!NNNNNGATCC	6	179	678	2624	3168	3555
			3652				
AlwNI	CAGNNN!CTG	2	3481	3889			
AocI	CC!TNAGG	2	1860	3492			
AocII	GDGCH!C	10	144	181	1571	2326	2419
			2493	2683	2745	3455	3988
Aor51HI	AGC!GCT	1	120				
AosI	TGC!GCA	1	2482				
AosII	GR!CGYC	3	2380	3082	3161		
ApaI	GGGCC!C	1	181				
ApalI	G!TGCAC	1	3984				
ApoI	R!AATTY	5	153	586	1194	1298	1309
ApyI	CC!WGG	12	412	530	783	1916	1971
			1988	2767	3346	3449	4139
			4152	4273			
AquI	C!YCGRG	2	137	180			
AscI	GG!CGCGCC	0					
AseI	AT!TAAT	0					

AsnI	AT!TAAT	0					
Asp700I	GAANN!NNTTC	0					
Asp718I	G!GTACC	1	169				
AspHI	GWGCW!C	4	144	2493	2683	3988	
AspI	GACN!NNGTC	1	2498				
AsuI	G!GNCC	14	177	178	359	414	602
			694	799	933	1487	2896
			3341	3387	3445	3478	
AsuII	TT!CGAA	2	151	3062			
AvaI	C!YCGRG	2	137	180			
AvaII	G!GWCC	7	359	414	602	799	933
			2896	3341			
AvaIII	ATGCA!T	4	243	1952	2024	4355	
AviII	TGC!GCA	1	2482				
AvrI	!CYCGRG	2	136	179			
AvrII	C!CTAGG	2	2202	3217			
AxyI	CC!TNAGG	2	1860	3492			
BalI	TGG!CCA	1	2462				
BamHI	G!GATCC	1	184				
BanI	G!GYRCC	4	169	1533	2379	2414	
BanII	GRGCY!C	5	144	181	1571	2745	3455
BanIII	AT!CGAT	1	2220				
BbeI	GGCGC!C	1	2383				
BbiII/AcyI	GR!CGYC	3	2380	3082	3161		
BbrPI	CAC!GTG	0					
BbsI	!GTCTTC	0					
BbsI	!GAAGAC	0					
BbvI	GCAGCNNNNNNNN!	6	1168	2453	2495	3016	3469
			3969				
BbvI	!NNNNNNNNNNNGCTGC	8	99	1662	2327	2511	2604
			3670	3876	3879		
BbvII	GAAGACNN!	0					
BbvII	!NNNNNNGTCTTC	0					
BcefI	ACGGCNNNNNNNNNN!	2	2806	3293			
BcefI	!NNNNNNNNNNNGCCGT	4	849	1522	2340	3799	
BcgI	!GCANNNNNNTCG	0					
BcgI	!CGANNNNNNTGC	0					
BclI	T!GATCA	0					
BcnI	CC!SGG	6	181	182	2384	2544	3157
			3921				
BfaI	C!TAG	16	116	386	594	626	704
			809	870	896	930	1035
			1229	1647	2203	3218	3552
			3805				
BfrI	C!TTAAG	2	698	1262			
BglI	GCCNNNN!NGGC	1	2155				
BglII	A!GATCT	1	133				
BinI	!NNNNNGATCC	6	179	678	2624	3168	3555
			3652				
BinI	GGATCNNNN!	8	192	2248	2559	2805	3197
			3556	3654	3740		
BlnI	C!CTAGG	2	2202	3217			
BmyI	GDGCH!C	10	144	181	1571	2326	2419
			2493	2683	2745	3455	3988
BpmI	!CTCCAG	1	3177				
BpmI	!CTGGAG	1	3198				
Bpu1102I	GC!TNAGC	0					
BsaAI	YAC!GTR	3	844	1496	2684		
BsaBI	GATNN!NNATC	2	1042	2239			

BsaHI	GR!CGYC	3	2380	3082	3161		
BsaI	GGTCTCN!	0					
BsaI	!NNNNNGAGACC	1	3369				
BsaJI	C!CNNGG	18	173	180	201	528	1914
			1986	2109	2144	2153	2202
			2543	2812	3217	3344	3345
			3447	3448	4138		
BseAI	T!CCGGA	0					
BsePI	!GCGCGC	0					
BsgI	!GTGCAG	0					
BsgI	!CTGCAC	0					
BsiEI	CGRY!CG	4	195	922	2289	3964	
BsiWI	C!GTACG	0					
BsiYI	CCNNNNN!NNGG	23	320	433	599	665	747
			870	1392	1718	2110	2361
			2905	3186	3218	3219	3350
			3385	3435	3436	3467	3820
			4099	4265	4283		
BslI	CCNNNNN!NNGG	23	320	433	599	665	747
			870	1392	1718	2110	2361
			2905	3186	3218	3219	3350
			3385	3435	3436	3467	3820
			4099	4265	4283		
BsmAI	!GTCTC	0					
BsmAI	!GAGAC	4	1809	2227	3246	3374	
BsmI	GAATGCN!	1	1131				
BsmI	G!CATTC	1	1224				
Bsp1286I	GDGCH!C	10	144	181	1571	2326	2419
			2493	2683	2745	3455	3988
BspDI	AT!CGAT	1	2220				
BspEI	T!CCGGA	0					
BspHI	T!CATGA	2	1806	3578			
BspMI	ACCTGCNNNN!	2	2648	3098			
BspMI	!NNNNNNNNGCAGGT	1	2267				
BspMII	T!CCGGA	0					
BspWI	GCNNNNN!NNGC	23	118	1607	1637	1664	1706
			1708	1947	2019	2070	2149
			2155	2371	2455	2478	2617
			2623	2740	2823	3090	3277
			3481	3680	4252		
BsrFI	R!CCGGY	5	190	1597	2699	2880	3163
BsrI	ACTGGN!	3	2324	2525	3771		
BsrI	C!CAGT	5	605	1409	2087	3883	3896
BsshII	G!CGCGC	0					
Bst1107I	GTA!TAC	0					
BstBI	TT!CGAA	2	151	3062			
BstEII	G!GTNACC	1	490				
BstI	G!GATCC	1	184				
BstNI	CC!WGG	12	412	530	783	1916	1971
			1988	2767	3346	3449	4139
			4152	4273			
BstPI	G!GTNACC	1	490				
BstUI	CG!CG	15	175	924	1304	1680	1700
			1724	1755	2446	2747	3185
			3269	3332	3401	3674	4255
BstXI	CCANNNNN!NTGG	0					
BstYI	R!GATCY	10	133	184	683	2551	2797
			3189	3548	3560	3646	3657
Bsu36I	CC!TNAGG	2	1860	3492			

CbiI	TT!CGAA	2	151	3062				
CcrI	C!TCGAG	1	137					
CelII	GC!TNAGC	0						
CfoI	GCG!C	21	121	1646	1654	1680	1702	
			1711	1724	1755	2374	2382	
			2446	2483	2749	3009	3185	
			3271	3674	3783	3957	4057	
			4124					
Cfr10I	R!CCGGY	5	190	1597	2699	2880	3163	
Cfr13I	G!GNCC	14	177	178	359	414	602	
			694	799	933	1487	2896	
			3341	3387	3445	3478		
Cfr9I	C!CCGGG	1	180					
CfrI	Y!GGCCR	5	919	2286	2460	2851	2878	
ClaI	AT!CGAT	1	2220					
CpoI	CG!GWCCG	1	2896					
Csp45I	TT!CGAA	2	151	3062				
CspI	CG!GSCCG	0						
CviJI	RG!CY	79	11	112	142	148	179	
			313	638	695	703	760	
			895	921	940	1049	1159	
			1326	1346	1488	1569	1583	
			1597	1878	1919	1991	2114	
			2143	2149	2158	2166	2189	
			2201	2207	2288	2305	2313	
			2340	2365	2449	2458	2462	
			2486	2524	2600	2617	2636	
			2699	2743	2753	2770	2853	
			2880	2884	2921	2944	2960	
			3140	3167	3228	3350	3389	
			3446	3453	3460	3479	3490	
			3741	3770	3813	3824	3889	
			3968	3993	3998	4044	4134	
			4232	4258	4276	4287		
CvnI	CC!TNAGG	2	1860	3492				
DdeI	C!TNAG	9	130	432	753	1860	2162	
			3043	3492	3615	4024		
DpnI	GA!TC	21	135	186	685	725	1039	
			2219	2223	2242	2553	2631	
			2712	2721	2799	3175	3191	
			3550	3562	3640	3648	3659	
			3734					
DpnII	!GATC	21	133	184	683	723	1037	
			2217	2221	2240	2551	2629	
			2710	2719	2797	3173	3189	
			3548	3560	3638	3646	3657	
			3732					
DraI	TTT!AAA	5	454	736	1082	3524	3543	
DraII	RG!GNCCY	4	359	414	933	3478		
DraIII	CACNNN!GTG	1	1496					
DrdI	GACNNNN!NNGTC	4	512	1451	2407	4196		
DsaI	C!CRYGG	4	173	201	2109	2812		
DsaV	!CCNGG	18	179	180	410	528	781	
			1914	1969	1986	2382	2542	
			2765	3155	3344	3447	3919	
			4137	4150	4271			
EaeI	Y!GGCCR	5	919	2286	2460	2851	2878	
EagI	C!GGCCG	2	919	2286				
Eam1105I	GACNNN!NNGTC	0						

EarI	!CTCTTC	1	362					
EarI	!GAAGAG	4	217	1851	2728	2938		
Ecl136II	GAG!CTC	1	142					
EclXI	C!GGCCG	2	919	2286				
Eco105I	TAC!GTA	0						
Eco31I	GGTCTCN!	0						
Eco31I	!NNNNNGAGACC	1	3369					
Eco47I	G!GWCC	7	359	414	602	799	933	
			2896	3341				
Eco47III	AGC!GCT	1	120					
Eco52I	C!GGCCG	2	919	2286				
Eco57I	!CTGAAG	4	467	912	2504	2936		
Eco57I	!CTTCAG	1	3770					
Eco81I	CC!TNAGG	2	1860	3492				
EcoNI	CCTNN!NNNAGG	0						
EcoO109I	RG!GNCCY	4	359	414	933	3478		
EcoO65I	G!GTNACC	1	490					
EcoRI	G!AATTC	1	153					
EcoRII	!CCWGG	12	410	528	781	1914	1969	
			1986	2765	3344	3447	4137	
			4150	4271				
EcoRV	GAT!ATC	0						
EcoT14I	C!CWWGG	5	201	2109	2202	2812	3217	
EcoT22I	ATGCA!T	4	243	1952	2024	4355		
EcoT38I	GRGCY!C	5	144	181	1571	2745	3455	
EheI	GGC!GCC	1	2381					
Esp3I	CGTCTCN!	0						
Esp3I	!NNNNNGAGACG	0						
EspI	GC!TNAGC	0						
FbaI	T!GATCA	0						
FinI	!GTCCC	4	1910	1982	2046	3341		
FinI	!GGGAC	3	2516	3048	3157			
Fnu4HI	GC!NGC	31	113	919	922	1157	1676	
			1698	1712	2150	2289	2341	
			2352	2442	2447	2484	2525	
			2612	2615	2618	2854	2950	
			2991	3005	3119	3458	3473	
			3684	3890	3893	3958	4101	
			4256					
FokI	GGATGNNNNNNNNN!	5	564	2247	2704	2729	3183	
FokI	!NNNNNNNNNNNNNNNCATCC	1	2053					
FspI	TGC!GCA	1	2482					
GdiII	!NNNNNYGGCCG	4	913	2280	2845	2872		
GdiII	CGGCCRN!	2	925	2292				
GsuI	!CTCCAG	1	3177					
GsuI	!CTGGAG	1	3198					
HaeI	WGG!CCW	5	2201	2462	3824	4276	4287	
HaeII	RGCGC!Y	5	122	1647	1655	2383	4058	
HaeIII	GG!CC	20	179	695	921	1346	1488	
			2143	2149	2158	2201	2288	
			2462	2853	2880	3389	3446	
			3479	3824	4258	4276	4287	
HapII	C!CGG	19	125	181	191	1598	2285	
			2362	2384	2412	2543	2633	
			2700	2881	3156	3164	3256	
			3730	3920	3946	4093		
HgaI	GACGCNNNNN!	2	3090	3169				
HgaI	!NNNNNNNNNNNGCGTC	3	1713	3608	4186			
HgiAI	GWGCW!C	4	144	2493	2683	3988		

HgiEII	!ACCNNNNNNNGGT	1	3710					
HhaI	GCG!C	21	121	1646	1654	1680	1702	
			1711	1724	1755	2374	2382	
			2446	2483	2749	3009	3185	
			3271	3674	3783	3957	4057	
			4124					
HinI	GR!CGYC	3	2380	3082	3161			
HinPII	G!CGC	21	119	1644	1652	1678	1700	
			1709	1722	1753	2372	2380	
			2444	2481	2747	3007	3183	
			3269	3672	3781	3955	4055	
			4122					
HincII	GTY!RAC	2	165	1143				
HindIII	A!AGCTT	1	146					
HinfI	G!ANTC	16	128	339	438	513	769	
			926	1423	1445	1855	2865	
			2999	3051	3109	3146	3928	
			4324					
HpaI	GTT!AAC	1	1143					
HpaII	C!CGG	19	125	181	191	1598	2285	
			2362	2384	2412	2543	2633	
			2700	2881	3156	3164	3256	
			3730	3920	3946	4093		
HphI	GGTGANNNNNNNN!	5	217	227	314	3451	3567	
HphI	!NNNNNNNTCACC	3	269	1497	2558			
KasI	G!GCGCC	1	2379					
KpnI	GGTAC!C	1	173					
Ksp632I	CTCTTCN!	1	369					
Ksp632I	!NNNNGAAGAG	4	213	1847	2724	2934		
KspI	CCGC!GG	1	176					
MaeI	C!TAG	16	116	386	594	626	704	
			809	870	896	930	1035	
			1229	1647	2203	3218	3552	
			3805					
MaeII	A!CGT	9	843	1440	1452	1495	1605	
			2496	2683	3464	3597		
MaeIII	!GTNAC	15	41	490	596	728	899	
			1002	1168	1669	1681	2500	
			2806	3496	3762	3878	3941	
MamI	GATNN!NNATC	2	1042	2239				
MboI	!GATC	21	133	184	683	723	1037	
			2217	2221	2240	2551	2629	
			2710	2719	2797	3173	3189	
			3548	3560	3638	3646	3657	
			3732					
MboII	GAAGANNNNNNNN!	7	230	628	1636	1864	2741	
			2951	3570				
MboII	!NNNNNNNTCTTC	5	356	3031	3198	3398	3641	
McrI	!CGRYCG	4	191	918	2285	3960		
MfeI	!CAATTG	1	1129					
MflI	R!GATCY	10	133	184	683	2551	2797	
			3189	3548	3560	3646	3657	
MluI	A!CGCGT	0						
MmeI	!TCCRAC	2	685	1447				
MmeI	!GTYGGA	3	706	3923	4107			
MnlI	CCTCNNNNNNN!	10	372	1099	1108	2163	2169	
			2981	3187	3501	3871	4195	
MnlI	!NNNNNNNGAGG	25	252	291	297	312	345	
			349	479	495	661	703	

			849	1058	1523	1854	2132
			2138	2175	2178	2190	2230
			2294	2430	2787	3217	4120
MroI	T!CCGGA	0					
MscI	TGG!CCA	1	2462				
MseI	T!TAA	20	228	285	423	453	699
			735	1081	1142	1263	1284
			1295	1307	1318	1335	1433
			1704	3523	3537	3542	3594
MspI	C!CGG	19	125	181	191	1598	2285
			2362	2384	2412	2543	2633
			2700	2881	3156	3164	3256
			3730	3920	3946	4093	
MstI	TGC!GCA	1	2482				
MstII	CC!TNAGG	2	1860	3492			
MunI	C!AATTG	1	1130				
MvaI	CC!WGG	12	412	530	783	1916	1971
			1988	2767	3346	3449	4139
			4152	4273			
MvnI	CG!CG	15	175	924	1304	1680	1700
			1724	1755	2446	2747	3185
			3269	3332	3401	3674	4255
NaeI	GCC!GGC	3	1599	2882	3165		
NarI	GG!CGCC	1	2380				
NciI	CC!SGG	6	181	182	2384	2544	3157
			3921				
NcoI	C!CATGG	3	201	2109	2812		
NdeI	CA!TATG	1	243				
NdeII	!GATC	21	133	184	683	723	1037
			2217	2221	2240	2551	2629
			2710	2719	2797	3173	3189
			3548	3560	3638	3646	3657
			3732				
NgoMI	G!CCGGC	3	1597	2880	3163		
NheI	G!CTAGC	1	115				
NlaIII	CATG!	20	205	241	259	403	483
			694	857	1810	1950	2022
			2113	2254	2599	2785	2816
			2842	3198	3582	4302	4353
NlaIV	GGN!NCC	19	171	179	186	325	409
			935	1535	1556	1568	1759
			1920	1992	2381	2416	3264
			3343	3388	4231	4270	
NotI	GC!GGCCGC	1	919				
NruI	TCG!CGA	0					
NsiI	ATGCA!T	4	243	1952	2024	4355	
Nsp(7524)I	RCATG!Y	5	241	1950	2022	2785	4302
Nsp(7524)V	TT!CGAA	2	151	3062			
NspBII	CMG!CKG	5	175	1878	2486	3715	3960
NspII	GDGCH!C	10	144	181	1571	2326	2419
			2493	2683	2745	3455	3988
NspIII	C!YCGRG	2	137	180			
NspIV	G!GNCC	14	177	178	359	414	602
			694	799	933	1487	2896
			3341	3387	3445	3478	
NunII	GG!CGCC	1	2380				
PacI	TTAAT!TAA	0					
Paer71	C!TCGAG	1	137				
PalI	GG!CC	20	179	695	921	1346	1488

			2143	2149	2158	2201	2288
			2462	2853	2880	3389	3446
			3479	3824	4258	4276	4287
PflMI	CCANNNN!NTGG	0					
PleI	GAGTCNNNN!	3	521	1431	1863		
PleI	!NNNNNGACTC	5	122	920	1439	3045	3922
PmaCI	CAC!GTG	0					
PmeI	GTTT!AAAC	0					
PmlI	CAC!GTG	0					
PpuMI	RG!GWCCY	3	359	414	933		
PshAI	GACNN!NNGTC	0					
PstI	CTGCA!G	1	162				
PvuI	CGAT!CG	0					
PvuII	CAG!CTG	2	1878	2486			
RmaI	C!TAG	16	116	386	594	626	704
			809	870	896	930	1035
			1229	1647	2203	3218	3552
			3805				
RsaI	GT!AC	6	99	171	292	656	949
			2686				
RsrI	G!AATTC	1	153				
RsrII	CG!GWCCG	1	2896				
SacI	GAGCT!C	1	144				
SacII	CCGC!GG	1	176				
SalI	G!TCGAC	1	163				
Sau3AI	!GATC	21	133	184	683	723	1037
			2217	2221	2240	2551	2629
			2710	2719	2797	3173	3189
			3548	3560	3638	3646	3657
			3732				
Sau96I	G!GNCC	14	177	178	359	414	602
			694	799	933	1487	2896
			3341	3387	3445	3478	
SauI	CC!TNAGG	2	1860	3492			
ScaI	AGT!ACT	0					
ScrFI	CC!NGG	18	181	182	412	530	783
			1916	1971	1988	2384	2544
			2767	3157	3346	3449	3921
			4139	4152	4273		
SduI	GDGCH!C	10	144	181	1571	2326	2419
			2493	2683	2745	3455	3988
SecI	C!CNNGG	18	173	180	201	528	1914
			1986	2109	2144	2153	2202
			2543	2812	3217	3344	3345
			3447	3448	4138		
SexI	!CTCGAG	1	136				
SfaNI	GCATCNNNNN!	6	1196	1959	2031	2679	2743
			3018				
SfaNI	!NNNNNNNNNGATGC	5	542	2338	2593	2809	4201
SfcI	C!TRYAG	4	158	1715	3842	4033	
SfiI	GGCCNNNN!NGGCC	1	2155				
SfuI	TT!CGAA	2	151	3062			
SgrAI	CR!CCGGYG	0					
SinI	G!GWCC	7	359	414	602	799	933
			2896	3341			
SmaI	CCC!GGG	1	182				
SnaBI	TAC!GTA	0					
SnaI	!GTATAC	0					
SnoI	G!TGCAC	1	3984				

SpeI	A!CTAGT	0						
SphI	GCATG!C	3	1950	2022	2785			
SplI	C!GTACG	0						
SrfI	GCCC!GGGC	0						
Sse8387I	CCTGCA!GG	0						
SspI	AAT!ATT	2	1288	1841				
SstI	GAGCT!C	1	144					
SstII	CCGC!GG	1	176					
SstIII	!ACGT	9	842	1439	1451	1494	1604	
			2495	2682	3463	3596		
StuI	AGG!CCT	1	2201					
StyI	C!CWWGG	5	201	2109	2202	2812	3217	
StySJI	!GAGNNNNNNNGTRC	0						
StySJI	!GYACNNNNNNNCTC	0						
SwaI	ATTT!AAAT	0						
TaqI	T!CGA	14	138	151	164	1529	2220	
			2493	2649	2673	2709	2871	
			3062	3107	3362	4200		
TaqII	GACCGANNNNNNNNNNN!	3	1400	2417	3085			
TaqII	!NNNNNNNNNTCGGTC	1	3329					
TaqII	CACCCANNNNNNNNNNN!	0						
TaqII	!NNNNNNNNNTGGGTG	2	2284	2876				
TfiI	G!AWTC	8	339	438	769	2865	2999	
			3109	3146	4324			
ThaI	CG!CG	15	175	924	1304	1680	1700	
			1724	1755	2446	2747	3185	
			3269	3332	3401	3674	4255	
Tsp45I	!GTSAC	6	41	899	1002	1669	2500	
			2806					
TspEI	!AATT	15	61	153	573	586	905	
			983	1130	1194	1272	1298	
			1309	1956	2028	2120	3538	
Tth111I	GACN!NNGTC	1	2498					
Tth111II	CAARCANNNNNNNNNNN!	1	3707					
Tth111III	!NNNNNNNNNTGYTTG	3	2815	3675	3714			
TthHB8I	T!CGA	14	138	151	164	1529	2220	
			2493	2649	2673	2709	2871	
			3062	3107	3362	4200		
Van91I	CCANNNN!NTGG	0						
VspI	AT!TAAT	0						
XbaI	T!CTAGA	0						
XcmI	!CCANNNNNNNNNNTCG	1	2655					
XcyI	C!CCGGG	1	180					
XhoI	C!TCGAG	1	137					
XhoII	R!GATCY	10	133	184	683	2551	2797	
			3189	3548	3560	3646	3657	
XmaI	C!CCGGG	1	180					
XmaIII	C!GGCCG	2	919	2286				
XmnI	GAANN!NNTTC	0						
XorII	CGAT!CG	0						