

Enzyme Name	Sequence	Count	Cutting Position				
AatI	AGG!CCT	0					
AatII	GACGT!C	1	4071				
AccI	GT!MKAC	1	2028				
AccII	CG!CG	13	222	453	492	777	807
			1857	1859	1962	2303	2884
			3214	3707	4039		
AccIII	T!CCGGA	2	848	1234			
AcyI	GR!CGYC	5	144	333	840	3686	4068
AflI	G!GWCC	2	3287	3509			
AflII	C!TTAAG	0					
AflIII	A!CRYGT	1	2256				
AhaI	CC!SGG	6	958	1902	1937	2636	3332
			3683				
AhaII	GR!CGYC	5	144	333	840	3686	4068
AhaIII	TTT!AAA	5	1158	1497	3015	3034	3726
AluI	AG!CT	27	364	384	499	738	751
			861	868	877	882	986
			990	1010	1019	1138	1267
			1738	1849	1898	1917	2198
			2424	2560	2817	3137	3338
			3438	3501			
AlwI	GGATCNNNN!	5	130	136	2905	3002	3782
AlwI	!NNNNNGATCC	8	123	160	895	2817	2903
			3001	3465	3786		
AlwNI	CAGNNN!CTG	1	2672				
AocI	CC!TNAGG	0					
AocII	GDGCH!C	10	294	300	308	714	720
			1709	2076	2574	3735	3820
AosI	TGC!GCA	1	3371				
AosII	GR!CGYC	5	144	333	840	3686	4068
ApaI	GGGCC!C	0					
ApaLI	G!TGCAC	4	710	2072	2570	3816	
ApyI	CC!WGG	9	301	311	509	1415	1471
			1719	2284	2405	2418	
AquI	C!YCGRG	3	2	359	719		
AseI	AT!TAAT	1	3321				
Asp700I	GAANN!NNTTC	2	371	3748			
Asp718I	G!GTACC	0					
AspI	GACN!NNGTC	1	2003				
AsuI	G!GNCC	8	356	704	1780	3191	3270
			3287	3509	4125		
AsuII	TT!CGAA	0					
AvaI	C!YCGRG	3	2	359	719		
AvaII	G!GWCC	2	3287	3509			
AvaIII	ATGCA!T	0					
AvrI	!CYCGRG	3	1	358	718		
AvrII	C!CTAGG	0					
AxyI	CC!TNAGG	0					
BalI	TGG!CCA	4	204	507	528	1505	
BamHI	G!GATCC	1	128				
BanI	G!GYRCC	4	143	332	1704	3097	
BanII	GRGCY!C	0					
BanIII	AT!CGAT	0					
BbeI	GGCGC!C	2	147	336			
BbiII/AcyI	GR!CGYC	5	144	333	840	3686	4068
BbvI	GCAGCNNNNNNNN!	9	150	489	657	1907	2004
			2675	2678	2884	3578	
BbvI	!NNNNNNNNNNNGCTGC	7	371	1836	2148	2166	2585
			3124	3187			
BbvII	GAAGACNN!	0					
BbvII	!NNNNNNGTCTTC	1	4127				
BcefI	ACGGCNNNNNNNNNN!	7	175	250	346	370	619
			1164	2758			

BcefI	!NNNNNNNNNNNNNGCCGT	2	795	1590				
BclI	T!GATCA	0						
BcnI	CC!SGG	6	958	1902	1937	2636	3332	
			3683					
BglI	GCCNNNN!NGGC	1	3269					
BglII	A!GATCT	0						
BinI	!NNNNNGATCC	8	123	160	895	2817	2903	
			3001	3465	3786			
BinI	GGATCNNNN!	5	130	136	2905	3002	3782	
BsePI	!GCGCGC	1	804					
BsmAI	!GTCTC	2	1456	3980				
BsmAI	!GAGAC	3	796	1904	3215			
BsmI	GAATGCN!	2	1231	1638				
BsmI	G!CATTC	0						
Bsp1286I	GDGCH!C	10	294	300	308	714	720	
			1709	2076	2574	3735	3820	
BspHI	T!CATGA	3	2976	3984	4089			
BspMI	ACCTGCNNNN!	0						
BspMI	!NNNNNNNNNGCAGGT	0						
BspMII	T!CCGGA	2	848	1234				
BsrI	ACTGGN!	6	1045	1782	2036	2664	2677	
			3625					
BsrI	C!CAGT	10	265	337	904	1485	2003	
			2789	3195	3313	3356	3795	
BssHII	G!CGCGC	1	805					
BstBI	TT!CGAA	0						
BstEII	G!GTNACC	2	313	460				
BstI	G!GATCC	1	128					
BstNI	CC!WGG	9	301	311	509	1415	1471	
			1719	2284	2405	2418		
BstPI	G!GTNACC	2	313	460				
BstUI	CG!CG	13	222	453	492	777	807	
			1857	1859	1962	2303	2884	
			3214	3707	4039			
BstXI	CCANNNNN!NTGG	0						
BstYI	R!GATCY	9	128	165	900	2897	2908	
			2994	3006	3774	3791		
Bsu36I	CC!TNAGG	0						
CcrI	C!TCGAG	1	2					
CfoI	GCG!C	21	146	335	414	455	617	
			807	809	1859	1962	1992	
			2133	2166	2436	2503	2603	
			2777	2886	3279	3372	3709	
			4041					
Cfr10I	R!CCGGY	4	281	641	842	3229		
Cfr13I	G!GNCC	8	356	704	1780	3191	3270	
			3287	3509	4125			
CfrI	Y!GGCCR	6	202	505	526	666	1503	
			3537					
ClaI	AT!CGAT	0						
CviJI	RG!CY	70	204	231	357	364	384	
			399	499	507	513	528	
			596	606	668	705	738	
			751	789	861	868	877	
			882	986	990	1010	1019	
			1138	1151	1196	1267	1418	
			1463	1505	1617	1738	1764	
			1782	1849	1898	1917	1950	
			1995	2035	2179	2198	2271	
			2282	2300	2326	2424	2560	
			2565	2590	2669	2734	2745	
			2788	2817	3137	3180	3192	
			3233	3259	3263	3272	3338	
			3428	3438	3501	3539	4126	
CvnI	CC!TNAGG	0						
DdeI	C!TNAG	13	752	878	915	1011	1459	
			1765	1821	2066	2531	2940	

			3106	3646	4072		
DpnI	GA!TC	21	124	130	167	591	638
			672	771	902	2824	2899
			2910	2918	2996	3008	3113
			3454	3472	3518	3776	3793
			3829				
DraI	TTT!AAA	5	1158	1497	3015	3034	3726
DraII	RG!GNCCY	1	4125				
DraIII	CACNNN!GTG	0					
DsaI	C!CRYGG	4	157	220	810	1539	
EaeI	Y!GGCCR	6	202	505	526	666	1503
			3537				
EagI	C!GGCCG	0					
EarI	!CTCTTC	2	2133	3937			
EarI	!GAAGAG	1	609				
EclXI	C!GGCCG	0					
Eco105I	TAC!GTA	0					
Eco31I	GGTCTCN!	0					
Eco31I	!NNNNNGAGACC	2	791	3210			
Eco47I	G!GWCC	2	3287	3509			
Eco47III	AGC!GCT	0					
Eco52I	C!GGCCG	0					
Eco57I	!CTGAAG	4	364	607	790	2782	
Eco57I	!CTTCAG	2	210	3830			
Eco81I	CC!TNAGG	0					
EcoNI	CCTNN!NNNAGG	0					
EcoO109I	RG!GNCCY	1	4125				
EcoRI	G!AATTC	0					
EcoRII	!CCWGG	9	299	309	507	1413	1469
			1717	2282	2403	2416	
EcoRV	GAT!ATC	0					
EcoT14I	C!CWWGG	1	1539				
EcoT22I	ATGCA!T	0					
EcoT38I	GRCY!C	0					
EheI	GGC!GCC	2	145	334			
EspI	GC!TNAGC	2	752	878			
FinI	!GTCCC	0					
FinI	!GGGAC	0					
Fnu4HI	GC!NGC	31	139	142	223	385	478
			646	700	703	820	954
			1580	1839	1850	1896	1993
			2046	2162	2180	2183	2301
			2456	2599	2664	2667	2873
			3138	3201	3540	3567	3662
			3891				
FokI	GGATGNNNNNNNNN!	5	212	272	536	773	1944
FokI	!NNNNNNNNNNNNNCATCC	5	203	1218	3115	3296	3583
FspI	TGC!GCA	1	3371				
GdiII	!NNNNNYGGCCG	2	660	3531			
GdiII	CGGCCRN!	0					
GsuI	!CTCCAG	1	3233				
GsuI	!CTGGAG	3	300	547	1338		
HaeI	WGG!CCW	9	204	507	528	596	1418
			1505	2271	2282	2734	
HaeII	RGCGC!Y	5	147	336	618	2134	2504
HaeIII	GG!CC	21	204	357	507	528	596
			606	668	705	1151	1196
			1418	1505	1782	2271	2282
			2300	2734	3192	3272	3539
			4126				
HapII	C!CGG	19	282	642	843	849	957
			1193	1235	1363	1902	1936
			2463	2610	2636	2826	3230
			3264	3331	3441	3683	
HgaI	GACGCNNNNN!	3	848	2367	2945		
HgaI	!NNNNNNNNNNNGCGTC	2	1951	3675			
HgiAI	GWGCW!C	6	308	714	2076	2574	3735

			3820				
HgiEII	!ACCNNNNNNGGT	2	2075	2836			
HhaI	GCG!C	21	146	335	414	455	617
			807	809	1859	1962	1992
			2133	2166	2436	2503	2603
			2777	2886	3279	3372	3709
			4041				
Hin1I	GR!CGYC	5	144	333	840	3686	4068
HinP1I	G!CGC	21	144	333	412	453	615
			805	807	1857	1960	1990
			2131	2164	2434	2501	2601
			2775	2884	3277	3370	3707
			4039				
HincII	GTY!RAC	0					
HindIII	A!AGCTT	1	866				
HinfI	G!ANTC	10	56	544	887	978	1588
			1729	2156	2231	2627	3144
HpaI	GTT!AAC	0					
HpaII	C!CGG	19	282	642	843	849	957
			1193	1235	1363	1902	1936
			2463	2610	2636	2826	3230
			3264	3331	3441	3683	
HphI	GGTGANNNNNNNN!	12	325	472	985	1274	1282
			1418	1486	1820	1878	1887
			3635	3876			
HphI	!NNNNNNNTCACC	10	412	553	631	764	1280
			1474	1528	2992	3219	3841
KpnI	GGTAC!C	0					
Ksp632I	CTCTTCN!	2	2140	3944			
Ksp632I	!NNNNGAAGAG	1	605				
MaeI	C!TAG	6	987	1735	1844	2751	3004
			3339				
MaeII	A!CGT	12	174	402	531	714	744
			1325	1500	2009	2959	3375
			3748	4068			
MaeIII	!GTNAC	15	313	460	763	1295	1400
			1910	2005	2612	2675	2791
			3074	3405	3463	3616	3804
MboI	!GATC	21	122	128	165	589	636
			670	769	900	2822	2897
			2908	2916	2994	3006	3111
			3452	3470	3516	3774	3791
			3827				
MboII	GAAGANNNNNNNN!	2	622	2918			
MboII	!NNNNNNNTCTTC	7	1513	2127	2989	3744	3822
			3931	4127			
MfeI	!CAATTG	1	59				
MflI	R!GATCY	9	128	165	900	2897	2908
			2994	3006	3774	3791	
MluI	A!CGCGT	0					
MmeI	!TCCRAC	2	2445	2629			
MmeI	!GTYGGA	0					
MnlI	CCTCNNNNNNN!	7	924	1863	1893	2155	2438
			3316	3522			
MnlI	!NNNNNNNGAGG	12	93	112	180	420	450
			1083	1734	2363	2687	3087
			3168	4115			
MroI	T!CCGGA	2	848	1234			
MseI	T!TAA	18	96	110	870	1157	1496
			1638	1690	1711	2037	2962
			3014	3019	3033	3086	3321
			3360	3725	4097		
MspI	C!CGG	19	282	642	843	849	957
			1193	1235	1363	1902	1936
			2463	2610	2636	2826	3230
			3264	3331	3441	3683	
MstI	TGC!GCA	1	3371				

MstII	CC!TNAGG	0					
MvaI	CC!WGG	9	301 1719	311 2284	509 2405	1415 2418	1471
NaeI	GCC!GGC	0					
NarI	GG!CGCC	2	144	333			
NciI	CC!SGG	6	958 3683	1902	1937	2636	3332
NcoI	C!CATGG	1	1539				
NdeI	CA!TATG	1	2079				
NdeII	!GATC	21	122 670 2908 3452 3827	128 769 2916	165 900 2994 3516	589 2822 3006 3774	636 2897 3111 3791
NheI	G!CTAGC	1	986				
NlaIII	CATG!	17	136 1604 2980 3988	391 1625 3471 4093	736 1895 3481	1313 2000 3559	1543 2260 3595
NlaIV	GGN!NCC	14	130 847 3193	145 1706 3234	334 2288 3445	358 2327 4035	706 3099
NotI	GC!GGCCGC	0					
NruI	TCG!CGA	0					
NsiI	ATGCA!T	0					
Nsp(7524)I	RCATG!Y	3	391	1895	2260		
Nsp(7524)V	TT!CGAA	0					
NspBII	CMG!CKG	8	141 2598	222 2843	1138 3784	1582	1968
NspII	GDGCH!C	10	294 1709	300 2076	308 2574	714 3735	720 3820
NspIII	C!YCGRG	3	2	359	719		
NspIV	G!GNCC	8	356 3287	704 3509	1780 4125	3191	3270
NunII	GG!CGCC	2	144	333			
Paer71	C!TCGAG	1	2				
PalI	GG!CC	21	204 606 1418 2300 4126	357 668 1505 2734	507 705 1782 3192	528 1151 2271 3272	596 1196 2282 3539
PflMI	CCANNNN!NTGG	2	535	1470			
PleI	GAGTCNNNN!	1	2635				
PleI	!NNNNNGACTC	4	881	1723	2150	3138	
PmaCI	CAC!GTG	3	532	715	745		
PpuMI	RG!GWCCY	0					
PstI	CTGCA!G	0					
PvuI	CGAT!CG	1	3519				
PvuII	CAG!CTG	1	1138				
RsaI	GT!AC	8	353 1655	485 2064	578 3629	725	1117
RsrI	G!AATTC	0					
RsrII	CG!GWCCG	0					
SacI	GAGCT!C	0					
SacII	CCGC!GG	1	223				
SalI	G!TCGAC	0					
Sau3AI	!GATC	21	122 670 2908 3452 3827	128 769 2916	165 900 2994 3516	589 2822 3006 3774	636 2897 3111 3791
Sau96I	G!GNCC	8	356 3287	704 3509	1780 4125	3191	3270
SauI	CC!TNAGG	0					
ScaI	AGT!ACT	2	1655	3629			
ScrFI	CC!NGG	15	301 1471	311 1719	509 1902	958 1937	1415 2284

			2405	2418	2636	3332	3683
SduI	GDGCH!C	10	294	300	308	714	720
			1709	2076	2574	3735	3820
SecI	C!CNNGG	12	157	220	299	309	456
			508	810	1469	1470	1539
			1718	2416			
SexI	!CTCGAG	1	1				
SfaNI	GCATCNNNNN!	8	225	1081	1754	2057	2133
			2353	3405	3845		
SfaNI	!NNNNNNNNNGATGC	6	229	250	1566	1922	2093
			3596				
SfiI	GGCCNNNN!NGGCC	0					
SinI	G!GWCC	2	3287	3509			
SmaI	CCC!GGG	0					
SnaBI	TAC!GTA	0					
SnaI	!GTATAC	1	2026				
SpeI	A!CTAGT	0					
SphI	GCATG!C	1	391				
SplI	C!GTACG	0					
SspI	AAT!ATT	2	1550	3953			
SstI	GAGCT!C	0					
SstII	CCGC!GG	1	223				
SstIII	!ACGT	12	173	401	530	713	743
			1324	1499	2008	2958	3374
			3747	4067			
StuI	AGG!CCT	0					
StyI	C!CWWGG	1	1539				
StySJI	!GAGNNNNNNGTRC	1	2053				
StySJI	!GYACNNNNNNCTC	0					
TaqI	T!CGA	7	3	426	468	837	1770
			2356	3800			
TaqII	GACCGANNNNNNNNNNN!	2	782	3682			
TaqII	!NNNNNNNNNTCGGTC	2	2158	3497			
TaqII	CACCCANNNNNNNNNNN!	2	692	3835			
TaqII	!NNNNNNNNNTGGGTG	2	1462	3852			
ThaI	CG!CG	13	222	453	492	777	807
			1857	1859	1962	2303	2884
			3214	3707	4039		
Tsp45I	!GTSAC	7	313	460	763	1910	2005
			3405	3616			
TspEI	!AATT	15	18	45	60	77	89
			107	439	556	871	1238
			1643	1682	3016	3322	3577
Tth111I	GACN!NNGTC	1	2003				
Tth111II	CAARCANNNNNNNNNNN!	2	2846	2885			
Tth111III	!NNNNNNNNNTGYTTG	2	1790	2853			
TthHB8I	T!CGA	7	3	426	468	837	1770
			2356	3800			
VspI	AT!TAAT	1	3321				
XbaI	T!CTAGA	1	1843				
XcyI	C!CCGGG	0					
XhoI	C!TCGAG	1	2				
XhoII	R!GATCY	9	128	165	900	2897	2908
			2994	3006	3774	3791	
XmaI	C!CCGGG	0					
XmaIII	C!GGCCG	0					
XmnI	GAANN!NNTTC	2	371	3748			
XorII	CGAT!CG	1	3519				