

Enzyme Name	Sequence	Count	Cutting Position				
AatI	AGG!CCT	1	2009				
AatII	GACGT!C	0					
AccI	GT!MKAC	1	59				
AccII	CG!CG	20	70	186	417	456	741
			771	837	1112	1488	1508
			1532	1563	2254	2555	2993
			3077	3140	3209	3482	4063
AccIII	T!CCGGA	1	812				
AcyI	GR!CGYC	6	108	297	804	2188	2890
			2969				
AflI	G!GWCC	2	2704	3149			
AflII	C!TTAAG	1	1070				
AflIII	A!CRYGT	1	4106				
AhaI	CC!SGG	6	76	77	2192	2352	2965
			3729				
AhaII	GR!CGYC	6	108	297	804	2188	2890
			2969				
AhaIII	TTT!AAA	3	890	3332	3351		
AluI	AG!CT	19	37	43	328	348	463
			702	715	825	967	1134
			1391	1686	1974	2294	2752
			3549	3806	3852	3942	
AlwI	GGATCNNNN!	8	87	2056	2367	2613	3005
			3364	3462	3548		
AlwI	!NNNNNGATCC	6	74	124	2432	2976	3363
			3460				
AlwNI	CAGNNN!CTG	2	3289	3697			
AocI	CC!TNAGG	2	1668	3300			
AocII	GDGCH!C	15	39	76	258	264	272
			678	684	1379	2134	2227
			2301	2491	2553	3263	3796
AosI	TGC!GCA	1	2290				
AosII	GR!CGYC	6	108	297	804	2188	2890
			2969				
ApaI	GGGCC!C	1	76				
ApaLI	G!TGCAC	2	674	3792			
ApyI	CC!WGG	12	265	275	473	1724	1779
			1796	2575	3154	3257	3947
			3960	4081			
AquI	C!YCGRG	4	32	75	323	683	
AseI	AT!TAAT	0					
Asp700I	GAANN!NNTTC	1	335				
Asp718I	G!GTACC	1	64				
AspI	GACN!NNGTC	1	2306				
AsuI	G!GNCC	10	72	73	320	668	1295
			2704	3149	3195	3253	3286
AsuII	TT!CGAA	2	46	2870			
AvaI	C!YCGRG	4	32	75	323	683	
AvaII	G!GWCC	2	2704	3149			
AvaIII	ATGCA!T	3	1760	1832	4163		
AvrI	!CYCGRG	4	31	74	322	682	
AvrII	C!CTAGG	2	2010	3025			
AxyI	CC!TNAGG	2	1668	3300			
BalI	TGG!CCA	4	168	471	492	2270	
BamHI	G!GATCC	1	79				
BanI	G!GYRCC	6	64	107	296	1341	2187
			2222				
BanII	GRGCY!C	5	39	76	1379	2553	3263
BanIII	AT!CGAT	1	2028				
BbeI	GGCGC!C	3	111	300	2191		
BbiII/AcyI	GR!CGYC	6	108	297	804	2188	2890
			2969				
BbvI	GCAGCNNNNNNNN!	9	114	453	621	976	2261

			2303	2824	3277	3777	
BbvI	!NNNNNNNNNNNGCTGC	8	335	1470	2135	2319	2412
			3478	3684	3687		
BbvII	GAAGACNN!	0					
BbvII	!NNNNNNGTCTTC	0					
BcefI	ACGGCNNNNNNNNNN!	7	139	214	310	334	583
			2614	3101			
BcefI	!NNNNNNNNNNNGCCGT	4	759	1330	2148	3607	
BclI	T!GATCA	0					
BcnI	CC!SGG	6	76	77	2192	2352	2965
			3729				
BglI	GCCNNNN!NGGC	1	1963				
BglII	A!GATCT	1	28				
BinI	!NNNNNGATCC	6	74	124	2432	2976	3363
			3460				
BinI	GGATCNNNN!	8	87	2056	2367	2613	3005
			3364	3462	3548		
BsePI	!GCGCGC	1	768				
BsmAI	!GTCTC	0					
BsmAI	!GAGAC	5	760	1617	2035	3054	3182
BsmI	GAATGCN!	1	939				
BsmI	G!CATTC	1	1032				
Bsp1286I	GDGCH!C	15	39	76	258	264	272
			678	684	1379	2134	2227
			2301	2491	2553	3263	3796
BspHI	T!CATGA	2	1614	3386			
BspMI	ACCTGCNNNN!	2	2456	2906			
BspMI	!NNNNNNNNGCAGGT	1	2075				
BspMII	T!CCGGA	1	812				
BsrI	ACTGGN!	3	2132	2333	3579		
BsrI	C!CAGT	6	229	301	1217	1895	3691
			3704				
BssHII	G!CGCGC	1	769				
BstBI	TT!CGAA	2	46	2870			
BstEII	G!GTNACC	2	277	424			
BstI	G!GATCC	1	79				
BstNI	CC!WGG	12	265	275	473	1724	1779
			1796	2575	3154	3257	3947
			3960	4081			
BstPI	G!GTNACC	2	277	424			
BstUI	CG!CG	20	70	186	417	456	741
			771	837	1112	1488	1508
			1532	1563	2254	2555	2993
			3077	3140	3209	3482	4063
BstXI	CCANNNNN!NTGG	0					
BstYI	R!GATCY	10	28	79	129	2359	2605
			2997	3356	3368	3454	3465
Bsu36I	CC!TNAGG	2	1668	3300			
CcrI	C!TCGAG	1	32				
CfoI	GCG!C	28	16	110	299	378	419
			581	771	773	1454	1462
			1488	1510	1519	1532	1563
			2182	2190	2254	2291	2557
			2817	2993	3079	3482	3591
			3765	3865	3932		
Cfr10I	R!CCGGY	8	85	245	605	806	1405
			2507	2688	2971		
Cfr13I	G!GNCC	10	72	73	320	668	1295
			2704	3149	3195	3253	3286
CfrI	Y!GGCCR	9	166	469	490	630	832
			2094	2268	2659	2686	
ClaI	AT!CGAT	1	2028				
CviJI	RG!CY	88	37	43	74	168	195
			321	328	348	363	463
			471	477	492	560	570
			632	669	702	715	753
			825	834	857	967	1134

			1154	1296	1377	1391	1405
			1686	1727	1799	1922	1951
			1957	1966	1974	1997	2009
			2015	2096	2113	2121	2148
			2173	2257	2266	2270	2294
			2332	2408	2425	2444	2507
			2551	2561	2578	2661	2688
			2692	2729	2752	2768	2948
			2975	3036	3158	3197	3254
			3261	3268	3287	3298	3549
			3578	3621	3632	3697	3776
			3801	3806	3852	3942	4040
			4066	4084	4095		
CvnI	CC!TNAGG	2	1668	3300			
DdeI	C!TNAG	8	25	716	1668	1970	2851
			3300	3423	3832		
DpnI	GA!TC	24	30	81	131	555	602
			636	735	847	2027	2031
			2050	2361	2439	2520	2529
			2607	2983	2999	3358	3370
			3448	3456	3467	3542	
DraI	TTT!AAA	3	890	3332	3351		
DraII	RG!GNCCY	1	3286				
DraIII	CACNNN!GTG	1	1304				
DsaI	C!CRYGG	6	68	121	184	774	1917
			2620				
EaeI	Y!GGCCR	9	166	469	490	630	832
			2094	2268	2659	2686	
EagI	C!GGCCG	2	832	2094			
EarI	!CTCTTC	0					
EarI	!GAAGAG	4	573	1659	2536	2746	
EclXI	C!GGCCG	2	832	2094			
Eco105I	TAC!GTA	0					
Eco31I	GGTCTCN!	0					
Eco31I	!NNNNNGAGACC	2	755	3177			
Eco47I	G!GWCC	2	2704	3149			
Eco47III	AGC!GCT	1	15				
Eco52I	C!GGCCG	2	832	2094			
Eco57I	!CTGAAG	5	328	571	754	2312	2744
Eco57I	!CTTCAG	2	174	3578			
Eco81I	CC!TNAGG	2	1668	3300			
EcoNI	CCTNN!NNNAGG	0					
EcoO109I	RG!GNCCY	1	3286				
EcoRI	G!AATTC	1	48				
EcoRII	!CCWGG	12	263	273	471	1722	1777
			1794	2573	3152	3255	3945
			3958	4079			
EcoRV	GAT!ATC	0					
EcoT14I	C!CWWGG	4	1917	2010	2620	3025	
EcoT22I	ATGCA!T	3	1760	1832	4163		
EcoT38I	GRCY!C	5	39	76	1379	2553	3263
EheI	GGC!GCC	3	109	298	2189		
EspI	GC!TNAGC	1	716				
FinI	!GTCCC	4	1718	1790	1854	3149	
FinI	!GGGAC	3	2324	2856	2965		
Fnu4HI	GC!NGC	39	103	106	187	349	442
			610	664	667	784	832
			835	965	1484	1506	1520
			1958	2097	2149	2160	2250
			2255	2292	2333	2420	2423
			2426	2662	2758	2799	2813
			2927	3266	3281	3492	3698
			3701	3766	3909	4064	
FokI	GGATGNNNNNNNNN!	8	176	236	500	737	2055
			2512	2537	2991		
FokI	!NNNNNNNNNNNNNCATCC	2	167	1861			
FspI	TGC!GCA	1	2290				

GdiII	!NNNNNYGGCCG	5	624	826	2088	2653	2680
GdiII	CGGCCRN!	2	838	2100			
GsuI	!CTCCAG	1	2985				
GsuI	!CTGGAG	3	264	511	3006		
HaeI	WGG!CCW	9	168	471	492	560	2009
			2270	3632	4084	4095	
HaeII	RGCG!Y	8	17	111	300	582	1455
			1463	2191	3866		
HaeIII	GG!CC	27	74	168	321	471	492
			560	570	632	669	834
			1154	1296	1951	1957	1966
			2009	2096	2270	2661	2688
			3197	3254	3287	3632	4066
			4084	4095			
HapII	C!CGG	23	20	76	86	246	606
			807	813	1406	2093	2170
			2192	2220	2351	2441	2508
			2689	2964	2972	3064	3538
			3728	3754	3901		
HgaI	GACGCNNNNN!	3	812	2898	2977		
HgaI	!NNNNNNNNNNGCGTC	3	1521	3416	3994		
HgiAI	GWGCW!C	6	39	272	678	2301	2491
			3796				
HgiEII	!ACCNNNNNNGGT	1	3518				
HhaI	GCG!C	28	16	110	299	378	419
			581	771	773	1454	1462
			1488	1510	1519	1532	1563
			2182	2190	2254	2291	2557
			2817	2993	3079	3482	3591
			3765	3865	3932		
HinI	GR!CGYC	6	108	297	804	2188	2890
			2969				
HinPII	G!CGC	28	14	108	297	376	417
			579	769	771	1452	1460
			1486	1508	1517	1530	1561
			2180	2188	2252	2289	2555
			2815	2991	3077	3480	3589
			3763	3863	3930		
HincII	GTY!RAC	2	60	951			
HindIII	A!AGCTT	1	41				
HinfI	G!ANTC	13	23	508	839	1231	1253
			1663	2673	2807	2859	2917
			2954	3736	4132		
HpaI	GTT!AAC	1	951				
HpaII	C!CGG	23	20	76	86	246	606
			807	813	1406	2093	2170
			2192	2220	2351	2441	2508
			2689	2964	2972	3064	3538
			3728	3754	3901		
HphI	GGTGANNNNNNNN!	4	289	436	3259	3375	
HphI	!NNNNNNNTCACC	6	376	517	595	728	1305
			2366				
KpnI	GGTAC!C	1	68				
Ksp632I	CTCTTCN!	0					
Ksp632I	!NNNNGAAGAG	4	569	1655	2532	2742	
MaeI	C!TAG	8	11	843	1037	1455	2011
			3026	3360	3613		
MaeII	A!CGT	13	138	366	495	678	708
			1248	1260	1303	1413	2304
			2491	3272	3405		
MaeIII	!GTNAC	12	277	424	727	976	1477
			1489	2308	2614	3304	3570
			3686	3749			
MboI	!GATC	24	28	79	129	553	600
			634	733	845	2025	2029
			2048	2359	2437	2518	2527
			2605	2981	2997	3356	3368

			3446	3454	3465	3540	
MboII	GAAGANNNNNNNN!	6	586	1444	1672	2549	2759
			3378				
MboII	!NNNNNNNTCTTC	4	2839	3006	3206	3449	
MfeI	!CAATTG	1	937				
MflI	R!GATCY	10	28	79	129	2359	2605
			2997	3356	3368	3454	3465
MluI	A!CGCGT	0					
MmeI	!TCCRAC	1	1255				
MmeI	!GTYGGA	2	3731	3915			
MnlI	CCTCNNNNNNN!	9	907	916	1971	1977	2789
			2995	3309	3679	4003	
MnlI	!NNNNNNNGAGG	17	144	384	414	866	1331
			1662	1940	1946	1983	1986
			1998	2038	2102	2238	2595
			3025	3928			
MroI	T!CCGGA	1	812				
MseI	T!TAA	14	889	950	1071	1092	1103
			1115	1126	1143	1241	1512
			3331	3345	3350	3402	
MspI	C!CGG	23	20	76	86	246	606
			807	813	1406	2093	2170
			2192	2220	2351	2441	2508
			2689	2964	2972	3064	3538
			3728	3754	3901		
MstI	TGC!GCA	1	2290				
MstII	CC!TNAGG	2	1668	3300			
MvaI	CC!WGG	12	265	275	473	1724	1779
			1796	2575	3154	3257	3947
			3960	4081			
NaeI	GCC!GGC	3	1407	2690	2973		
NarI	GG!CGCC	3	108	297	2188		
NciI	CC!SGG	6	76	77	2192	2352	2965
			3729				
NcoI	C!CATGG	2	1917	2620			
NdeI	CA!TATG	0					
NdeII	!GATC	24	28	79	129	553	600
			634	733	845	2025	2029
			2048	2359	2437	2518	2527
			2605	2981	2997	3356	3368
			3446	3454	3465	3540	
NheI	G!CTAGC	0					
NlaIII	CATG!	16	100	355	700	1618	1758
			1830	1921	2062	2407	2593
			2624	2650	3006	3390	4110
			4161				
NlaIV	GGN!NCC	21	66	74	81	109	298
			322	670	811	1343	1364
			1376	1567	1728	1800	2189
			2224	3072	3151	3196	4039
			4078				
NotI	GC!GGCCGC	1	832				
NruI	TCG!CGA	0					
NsiI	ATGCA!T	3	1760	1832	4163		
Nsp(7524)I	RCATG!Y	5	355	1758	1830	2593	4110
Nsp(7524)V	TT!CGAA	2	46	2870			
NspBII	CMG!CKG	7	70	105	186	1686	2294
			3523	3768			
NspII	GDGCH!C	15	39	76	258	264	272
			678	684	1379	2134	2227
			2301	2491	2553	3263	3796
NspIII	C!YCGRG	4	32	75	323	683	
NspIV	G!GNCC	10	72	73	320	668	1295
			2704	3149	3195	3253	3286
NunII	GG!CGCC	3	108	297	2188		
Paer71	C!TCGAG	1	32				
PalI	GG!CC	27	74	168	321	471	492

			560	570	632	669	834
			1154	1296	1951	1957	1966
			2009	2096	2270	2661	2688
			3197	3254	3287	3632	4066
			4084	4095			
PflMI	CCANNNN!NTGG	1	499				
PleI	GAGTCNNNN!	2	1239	1671			
PleI	!NNNNNGACTC	5	17	833	1247	2853	3730
PmaCI	CAC!GTG	3	496	679	709		
PpuMI	RG!GWCCY	0					
PstI	CTGCA!G	1	57				
PvuI	CGAT!CG	0					
PvuII	CAG!CTG	2	1686	2294			
RsaI	GT!AC	6	66	317	449	542	689
			2494				
RsrI	G!AATTC	1	48				
RsrII	CG!GWCCG	1	2704				
SacI	GAGCT!C	1	39				
SacII	CCGC!GG	2	71	187			
SalI	G!TCGAC	1	58				
Sau3AI	!GATC	24	28	79	129	553	600
			634	733	845	2025	2029
			2048	2359	2437	2518	2527
			2605	2981	2997	3356	3368
			3446	3454	3465	3540	
Sau96I	G!GNCC	10	72	73	320	668	1295
			2704	3149	3195	3253	3286
SauI	CC!TNAGG	2	1668	3300			
ScaI	AGT!ACT	0					
ScrFI	CC!NGG	18	76	77	265	275	473
			1724	1779	1796	2192	2352
			2575	2965	3154	3257	3729
			3947	3960	4081		
SduI	GDGCH!C	15	39	76	258	264	272
			678	684	1379	2134	2227
			2301	2491	2553	3263	3796
SecI	C!CNNGG	23	68	75	121	184	263
			273	420	472	774	1722
			1794	1917	1952	1961	2010
			2351	2620	3025	3152	3153
			3255	3256	3946		
SexI	!CTCGAG	1	31				
SfaNI	GCATCNNNNN!	7	189	1004	1767	1839	2487
			2551	2826			
SfaNI	!NNNNNNNNNGATGC	6	193	214	2146	2401	2617
			4009				
SfiI	GGCCNNNN!NGGCC	1	1963				
SinI	G!GWCC	2	2704	3149			
SmaI	CCC!GGG	1	77				
SnaBI	TAC!GTA	0					
SnaI	!GTATAC	0					
SpeI	A!CTAGT	0					
SphI	GCATG!C	4	355	1758	1830	2593	
SplI	C!GTACG	0					
SspI	AAT!ATT	2	1096	1649			
SstI	GAGCT!C	1	39				
SstII	CCGC!GG	2	71	187			
SstIII	!ACGT	13	137	365	494	677	707
			1247	1259	1302	1412	2303
			2490	3271	3404		
StuI	AGG!CCT	1	2009				
StyI	C!CWWGG	4	1917	2010	2620	3025	
StySJI	!GAGNNNNNNGTRC	0					
StySJI	!GYACNNNNNNCTC	0					
TaqI	T!CGA	17	33	46	59	390	432
			801	1337	2028	2301	2457
			2481	2517	2679	2870	2915

			3170	4008				
TaqII	GACCGANNNNNNNNNNN!	4	746	1208	2225	2893		
TaqII	!NNNNNNNNNTCGGTC	1	3137					
TaqII	CACCCANNNNNNNNNNN!	1	656					
TaqII	!NNNNNNNNNTGGGTG	2	2092	2684				
ThaI	CG!CG	20	70	186	417	456	741	
			771	837	1112	1488	1508	
			1532	1563	2254	2555	2993	
			3077	3140	3209	3482	4063	
Tsp45I	!GTSAC	6	277	424	727	1477	2308	
			2614					
TspEI	!AATT	12	48	403	520	938	1002	
			1080	1106	1117	1764	1836	
			1928	3346				
Tth111I	GACN!NNGTC	1	2306					
Tth111II	CAARCANNNNNNNNNNN!	1	3515					
Tth111III	!NNNNNNNNNTGYTTG	3	2623	3483	3522			
TthHB8I	T!CGA	17	33	46	59	390	432	
			801	1337	2028	2301	2457	
			2481	2517	2679	2870	2915	
			3170	4008				
VspI	AT!TAAT	0						
XbaI	T!CTAGA	1	842					
XcyI	C!CCGGG	1	75					
XhoI	C!TCGAG	1	32					
XhoII	R!GATCY	10	28	79	129	2359	2605	
			2997	3356	3368	3454	3465	
XmaI	C!CCGGG	1	75					
XmaIII	C!GGCCG	2	832	2094				
XmnI	GAANN!NNTTC	1	335					
XorII	CGAT!CG	0						