

Enzyme Name	Sequence	Count	Cutting Position				
AatI	AGG!CCT	1	2593				
AatII	GACGT!C	4	126	179	262	448	
AccI	GT!MKAC	0					
AccII	CG!CG	17	61	663	665	1421	1696
			2072	2092	2116	2147	2838
			3139	3577	3661	3724	3793
			4066	4647			
AccIII	T!CCGGA	0					
AcyI	GR!CGYC	8	123	176	259	445	610
			2772	3474	3553		
AflI	G!GWCC	3	1302	3288	3733		
AflII	C!TTAAG	1	1654				
AflIII	A!CRYGT	1	4690				
AhaI	CC!SGG	6	645	1286	2776	2936	3549
			4313				
AhaII	GR!CGYC	8	123	176	259	445	610
			2772	3474	3553		
AhaIII	TTT!AAA	3	1474	3916	3935		
AluI	AG!CT	16	567	726	899	1206	1409
			1551	1718	1975	2270	2558
			2878	3336	4133	4390	4436
			4526				
AlwI	GGATCNNNN!	8	695	2640	2951	3197	3589
			3948	4046	4132		
AlwI	!NNNNNGATCC	8	581	666	682	1247	3016
			3560	3947	4044		
AlwNI	CAGNNN!CTG	2	3873	4281			
AocI	CC!TNAGG	3	971	2252	3884		
AocII	GDGCH!C	12	769	796	829	1406	1963
			2718	2811	2885	3075	3137
			3847	4380			
AosI	TGC!GCA	1	2874				
AosII	GR!CGYC	8	123	176	259	445	610
			2772	3474	3553		
ApaI	GGGCC!C	0					
ApaLI	G!TGCAC	2	792	4376			
ApyI	CC!WGG	14	91	284	889	937	1033
			2308	2363	2380	3159	3738
			3841	4531	4544	4665	
AquI	C!YCGRG	0					
AseI	AT!TAAT	1	8				
Asp700I	GAANN!NNTTC	0					
Asp718I	G!GTACC	0					
AspI	GACN!NNGTC	1	2890				
AsuI	G!GNCC	13	84	277	642	862	1105
			1197	1302	1879	3288	3733
			3779	3837	3870		
AsuII	TT!CGAA	1	3454				
AvaI	C!YCGRG	0					
AvaII	G!GWCC	3	1302	3288	3733		
AvaIII	ATGCA!T	3	2344	2416	4747		
AvrI	!CYCGRG	0					
AvrII	C!CTAGG	2	2594	3609			
AxyI	CC!TNAGG	3	971	2252	3884		
BalI	TGG!CCA	3	1190	1372	2854		
BamHI	G!GATCC	1	687				
BanI	G!GYRCC	6	466	766	826	1925	2771
			2806				
BanII	GRGCY!C	3	1963	3137	3847		
BanIII	AT!CGAT	1	2612				
BbeI	GGCGC!C	1	2775				
BbiII/AcyI	GR!CGYC	8	123	176	259	445	610
			2772	3474	3553		

BbvI	GCAGCNNNNNNNN!	8	923 3408	1365 3861	1560 4361	2845	2887
BbvI	!NNNNNNNNNNNGCTGC	11	602 2719 4271	605 2903	608 2996	1042 4062	2054 4268
BbvII	GAAGACNN!	1	1013				
BbvII	!NNNNNNGTCTTC	0					
BcefI	ACGGCNNNNNNNNNN!	5	924	1068	1119	3198	3685
BcefI	!NNNNNNNNNNNGCCGT	3	1914	2732	4191		
BclI	T!GATCA	1	728				
BcnI	CC!SGG	6	645 4313	1286	2776	2936	3549
BglI	GCCNNNN!NGGC	5	91	213	284	1181	2547
BglII	A!GATCT	0					
BinI	!NNNNNGATCC	8	581 3560	666 3947	682 4044	1247	3016
BinI	GGATCNNNN!	8	695 3948	2640 4046	2951 4132	3197	3589
BsePI	!GCGCGC	1	662				
BsmAI	!GTCTC	1	429				
BsmAI	!GAGAC	5	1338	2201	2619	3638	3766
BsmI	GAATGCN!	1	1523				
BsmI	G!CATTC	1	1616				
Bsp1286I	GDGCH!C	12	769 2718 3847	796 2811 4380	829 2885	1406 3075	1963 3137
BspHI	T!CATGA	2	2198	3970			
BspMI	ACCTGCNNNN!	3	1232	3040	3490		
BspMI	!NNNNNNNNGCAGGT	1	2659				
BspMII	T!CCGGA	0					
BsrI	ACTGGN!	5	1316	1403	2716	2917	4163
BsrI	C!CAGT	6	296 4288	655	1801	2479	4275
BssHII	G!CGCGC	1	663				
BstBI	TT!CGAA	1	3454				
BstEII	G!GTNACC	0					
BstI	G!GATCC	1	687				
BstNI	CC!WGG	14	91 2308 3841	284 2363 4531	889 2380 4544	937 3159 4665	1033 3738
BstPI	G!GTNACC	0					
BstUI	CG!CG	17	61 2072 3139 4066	663 2092 3577 4647	665 2116 3661	1421 2147 3724	1696 2838 3793
BstXI	CCANNNNN!NTGG	1	708				
BstYI	R!GATCY	11	586 3189 4049	671 3581	687 3940	1252 3952	2943 4038
Bsu36I	CC!TNAGG	3	971	2252	3884		
CcrI	C!TCGAG	0					
CfoI	GCG!C	22	665 2094 2774 3577 4449	667 2103 2838 3663 4516	2038 2116 2875 4066	2046 2147 3141 4175	2072 2766 3401 4349
Cfr10I	R!CCGGY	5	693	1989	3091	3272	3555
Cfr13I	G!GNCC	13	84 1197 3779	277 1302 3837	642 1879 3870	862 3288	1105 3733
CfrI	Y!GGCCR	7	1188 3243	1370 3270	1416	2678	2852
ClaI	AT!CGAT	1	2612				
CviJI	RG!CY	99	43 629 816 977	85 638 863 1043	94 643 892 1055	278 651 899 1106	567 726 919 1133

			1141	1175	1184	1190	1198
			1206	1220	1289	1330	1366
			1372	1409	1418	1441	1551
			1718	1738	1880	1961	1975
			1989	2270	2311	2383	2506
			2535	2541	2550	2558	2581
			2593	2599	2680	2697	2705
			2732	2757	2841	2850	2854
			2878	2916	2992	3009	3028
			3091	3135	3145	3162	3245
			3272	3276	3313	3336	3352
			3532	3559	3620	3742	3781
			3838	3845	3852	3871	3882
			4133	4162	4205	4216	4281
			4360	4385	4390	4436	4526
			4624	4650	4668	4679	
CvnI	CC!TNAGG	3	971	2252	3884		
DdeI	C!TNAG	9	971	1177	1268	2252	2554
			3435	3884	4007	4416	
DpnI	GA!TC	24	588	673	689	730	844
			1078	1254	1431	2611	2615
			2634	2945	3023	3104	3113
			3191	3567	3583	3942	3954
			4032	4040	4051	4126	
DraI	TTT!AAA	3	1474	3916	3935		
DraII	RG!GNCCY	1	3870				
DraIII	CACNNN!GTG	2	1299	1888			
DsaI	C!CRYGG	5	361	704	1185	2501	3204
EaeI	Y!GGCCR	7	1188	1370	1416	2678	2852
			3243	3270			
EagI	C!GGCCG	2	1416	2678			
EarI	!CTCTTC	0					
EarI	!GAAGAG	3	2243	3120	3330		
EclXI	C!GGCCG	2	1416	2678			
Eco105I	TAC!GTA	1	341				
Eco31I	GGTCTCN!	0					
Eco31I	!NNNNNGAGACC	2	1333	3761			
Eco47I	G!GWCC	3	1302	3288	3733		
Eco47III	AGC!GCT	0					
Eco52I	C!GGCCG	2	1416	2678			
Eco57I	!CTGAAG	3	1200	2896	3328		
Eco57I	!CTTCAG	1	4162				
Eco81I	CC!TNAGG	3	971	2252	3884		
EcoNI	CCTNN!NNNAGG	0					
EcoO109I	RG!GNCCY	1	3870				
EcoRI	G!AATTC	0					
EcoRII	!CCWGG	14	89	282	887	935	1031
			2306	2361	2378	3157	3736
			3839	4529	4542	4663	
EcoRV	GAT!ATC	0					
EcoT14I	C!CWWGG	7	361	704	1185	2501	2594
			3204	3609			
EcoT22I	ATGCA!T	3	2344	2416	4747		
EcoT38I	GRGCY!C	3	1963	3137	3847		
EheI	GGC!GCC	1	2773				
EspI	GC!TNAGC	0					
FinI	!GTCCC	4	2302	2374	2438	3733	
FinI	!GGGAC	6	161	312	480	2908	3440
			3549				
Fnu4HI	GC!NGC	41	613	616	619	622	649
			661	861	912	1056	1173
			1354	1416	1419	1549	2068
			2090	2104	2542	2681	2733
			2744	2834	2839	2876	2917
			3004	3007	3010	3246	3342
			3383	3397	3511	3850	3865
			4076	4282	4285	4350	4493

			4648				
FokI	GGATGNNNNNNNNN!	4	2639	3096	3121	3575	
FokI	!NNNNNNNNNNNNNNCATCC	5	783	871	928	1083	2445
FspI	TGC!GCA	1	2874				
GdiII	!NNNNNYGGCCG	4	1410	2672	3237	3264	
GdiII	CGGCCRN!	2	1422	2684			
GsuI	!CTCCAG	2	1044	3569			
GsuI	!CTGGAG	1	3590				
HaeI	WGG!CCW	9	1141	1184	1190	1372	2593
			2854	4216	4668	4679	
HaeII	RGCG!Y	4	2039	2047	2775	4450	
HaeIII	GG!CC	30	85	278	643	863	1106
			1141	1175	1184	1190	1198
			1330	1372	1418	1738	1880
			2535	2541	2550	2593	2680
			2854	3245	3272	3781	3838
			3871	4216	4650	4668	4679
HapII	C!CGG	19	645	694	1286	1990	2677
			2754	2776	2804	2935	3025
			3092	3273	3548	3556	3648
			4122	4312	4338	4485	
HgaI	GACGCNNNNN!	4	527	618	3482	3561	
HgaI	!NNNNNNNNNNNGCGTC	3	2105	4000	4578		
HgiAI	GWGCW!C	4	796	2885	3075	4380	
HgiEII	!ACCNNNNNNGGT	2	702	4102			
HhaI	GCG!C	22	665	667	2038	2046	2072
			2094	2103	2116	2147	2766
			2774	2838	2875	3141	3401
			3577	3663	4066	4175	4349
			4449	4516			
HinI	GR!CGYC	8	123	176	259	445	610
			2772	3474	3553		
HinPII	G!CGC	22	663	665	2036	2044	2070
			2092	2101	2114	2145	2764
			2772	2836	2873	3139	3399
			3575	3661	4064	4173	4347
			4447	4514			
HincII	GTY!RAC	1	1535				
HindIII	A!AGCTT	0					
HinfI	G!ANTC	14	411	992	1319	1423	1815
			1837	2247	3257	3391	3443
			3501	3538	4320	4716	
HpaI	GTT!AAC	1	1535				
HpaII	C!CGG	19	645	694	1286	1990	2677
			2754	2776	2804	2935	3025
			3092	3273	3548	3556	3648
			4122	4312	4338	4485	
HphI	GGTGANNNNNNNN!	5	377	724	1098	3843	3959
HphI	!NNNNNNNTCACC	4	723	987	1889	2950	
KpnI	GGTAC!C	0					
Ksp632I	CTCTTCN!	0					
Ksp632I	!NNNNGAAGAG	3	2239	3116	3326		
MaeI	C!TAG	9	593	1391	1427	1621	2039
			2595	3610	3944	4197	
MaeII	A!CGT	16	123	135	176	259	340
			445	1070	1346	1832	1844
			1887	1997	2888	3075	3856
			3989				
MaeIII	!GTNAC	12	62	149	498	1560	2061
			2073	2892	3198	3888	4154
			4270	4333			
MboI	!GATC	24	586	671	687	728	842
			1076	1252	1429	2609	2613
			2632	2943	3021	3102	3111
			3189	3565	3581	3940	3952
			4030	4038	4049	4124	
MboII	GAAGANNNNNNNN!	8	852	1018	1131	2028	2256

			3133	3343	3962		
MboII	!NNNNNNNTCTTC	4	3423	3590	3790	4033	
MfeI	!CAATTG	1	1521				
MflI	R!GATCY	11	586	671	687	1252	2943
			3189	3581	3940	3952	4038
			4049				
MluI	A!CGCGT	0					
MmeI	!TCCRAC	2	1098	1839			
MmeI	!GTYGGA	2	4315	4499			
MnlI	CCTCNNNNNNN!	15	875	1054	1069	1246	1285
			1396	1491	1500	2555	2561
			3373	3579	3893	4263	4587
MnlI	!NNNNNNNGAGG	24	541	707	755	794	815
			848	965	1130	1173	1319
			1450	1915	2246	2524	2530
			2567	2570	2582	2622	2686
			2822	3179	3609	4512	
MroI	T!CCGGA	0					
MseI	T!TAA	16	8	956	1473	1534	1655
			1676	1687	1699	1710	1727
			1825	2096	3915	3929	3934
			3986				
MspI	C!CGG	19	645	694	1286	1990	2677
			2754	2776	2804	2935	3025
			3092	3273	3548	3556	3648
			4122	4312	4338	4485	
MstI	TGC!GCA	1	2874				
MstII	CC!TNAGG	3	971	2252	3884		
MvaI	CC!WGG	14	91	284	889	937	1033
			2308	2363	2380	3159	3738
			3841	4531	4544	4665	
NaeI	GCC!GGC	3	1991	3274	3557		
NarI	GG!CGCC	1	2772				
NciI	CC!SGG	6	645	1286	2776	2936	3549
			4313				
NcoI	C!CATGG	5	361	704	1185	2501	3204
NdeI	CA!TATG	1	235				
NdeII	!GATC	24	586	671	687	728	842
			1076	1252	1429	2609	2613
			2632	2943	3021	3102	3111
			3189	3565	3581	3940	3952
			4030	4038	4049	4124	
NheI	G!CTAGC	1	592				
NlaIII	CATG!	24	305	365	600	708	744
			750	762	840	906	986
			1189	2202	2342	2414	2505
			2646	2991	3177	3208	3234
			3590	3974	4694	4745	
NlaIV	GGN!NCC	18	468	652	689	768	828
			1927	1948	1960	2151	2312
			2384	2773	2808	3656	3735
			3780	4623	4662		
NotI	GC!GGCCGC	1	1416				
NruI	TCG!CGA	0					
NsiI	ATGCA!T	3	2344	2416	4747		
Nsp(7524)I	RCATG!Y	6	600	744	2342	2414	3177
			4694				
Nsp(7524)V	TT!CGAA	1	3454				
NspBII	CMG!CKG	8	615	1165	1172	1409	2270
			2878	4107	4352		
NspII	GDGCH!C	12	769	796	829	1406	1963
			2718	2811	2885	3075	3137
			3847	4380			
NspIII	C!YCGRG	0					
NspIV	G!GNCC	13	84	277	642	862	1105
			1197	1302	1879	3288	3733
			3779	3837	3870		

NunII	GG!CGCC	1	2772					
Paer71	C!TCGAG	0						
PalI	GG!CC	30	85	278	643	863	1106	
			1141	1175	1184	1190	1198	
			1330	1372	1418	1738	1880	
			2535	2541	2550	2593	2680	
			2854	3245	3272	3781	3838	
			3871	4216	4650	4668	4679	
PflMI	CCANNNN!NTGG	3	681	1299	1311			
PleI	GAGTCNNNN!	2	1823	2255				
PleI	!NNNNNGACTC	5	405	1417	1831	3437	4314	
PmaCI	CAC!GTG	0						
PpuMI	RG!GWCCY	0						
PstI	CTGCA!G	0						
PvuI	CGAT!CG	0						
PvuII	CAG!CTG	3	1409	2270	2878			
RsaI	GT!AC	11	220	245	300	333	384	
			541	757	907	1159	1378	
			3078					
RsrI	G!AATTC	0						
RsrII	CG!GWCCG	1	3288					
SacI	GAGCT!C	0						
SacII	CCGC!GG	0						
SalI	G!TCGAC	0						
Sau3AI	!GATC	24	586	671	687	728	842	
			1076	1252	1429	2609	2613	
			2632	2943	3021	3102	3111	
			3189	3565	3581	3940	3952	
			4030	4038	4049	4124		
Sau96I	G!GNCC	13	84	277	642	862	1105	
			1197	1302	1879	3288	3733	
			3779	3837	3870			
SauI	CC!TNAGG	3	971	2252	3884			
ScaI	AGT!ACT	1	1378					
ScrFI	CC!NGG	20	91	284	645	889	937	
			1033	1286	2308	2363	2380	
			2776	2936	3159	3549	3738	
			3841	4313	4531	4544	4665	
SduI	GDGCH!C	12	769	796	829	1406	1963	
			2718	2811	2885	3075	3137	
			3847	4380				
SecI	C!CNNGG	21	361	704	800	935	936	
			1031	1185	2306	2378	2501	
			2536	2545	2594	2935	3204	
			3609	3736	3737	3839	3840	
			4530					
SexI	!CTCGAG	0						
SfaNI	GCATCNNNNN!	7	950	1588	2351	2423	3071	
			3135	3410				
SfaNI	!NNNNNNNNNGATGC	9	358	1103	1142	1271	1402	
			2730	2985	3201	4593		
SfiI	GGCCNNNN!NGGCC	2	1181	2547				
SinI	G!GWCC	3	1302	3288	3733			
SmaI	CCC!GGG	0						
SnaBI	TAC!GTA	1	341					
SnaI	!GTATAC	0						
SpeI	A!CTAGT	0						
SphI	GCATG!C	3	2342	2414	3177			
SplI	C!GTACG	0						
SspI	AAT!ATT	2	1680	2233				
SstI	GAGCT!C	0						
SstII	CCGC!GG	0						
SstIII	!ACGT	16	122	134	175	258	339	
			444	1069	1345	1831	1843	
			1886	1996	2887	3074	3855	
			3988					
StuI	AGG!CCT	1	2593					

StyI	C!CWWGG	7	361	704	1185	2501	2594
			3204	3609			
StySJI	!GAGNNNNNNGTRC	0					
StySJI	!GYACNNNNNNNCTC	2	1226	1376			
TaqI	T!CGA	14	854	881	1349	1921	2612
			2885	3041	3065	3101	3263
			3454	3499	3754	4592	
TaqII	GACCGANNNNNNNNNNN!	3	1792	2809	3477		
TaqII	!NNNNNNNNNTCGGTC	1	3721				
TaqII	CACCCANNNNNNNNNNN!	2	844	949			
TaqII	!NNNNNNNNNTGGGTG	4	173	700	2676	3268	
ThaI	CG!CG	17	61	663	665	1421	1696
			2072	2092	2116	2147	2838
			3139	3577	3661	3724	3793
			4066	4647			
Tsp45I	!GTSAC	3	2061	2892	3198		
TspEI	!AATT	10	19	1522	1586	1664	1690
			1701	2348	2420	2512	3930
Tth111I	GACN!NNGTC	1	2890				
Tth111II	CAARCANNNNNNNNNNN!	1	4099				
Tth111III	!NNNNNNNNNTGYTTG	3	3207	4067	4106		
TthHB8I	T!CGA	14	854	881	1349	1921	2612
			2885	3041	3065	3101	3263
			3454	3499	3754	4592	
VspI	AT!TAAT	1	8				
XbaI	T!CTAGA	1	1426				
XcyI	C!CCGGG	0					
XhoI	C!TCGAG	0					
XhoII	R!GATCY	11	586	671	687	1252	2943
			3189	3581	3940	3952	4038
			4049				
XmaI	C!CCGGG	0					
XmaIII	C!GGCCG	2	1416	2678			
XmnI	GAANN!NNTTC	0					
XorII	CGAT!CG	0					