Restriction Endonucleases

Enzyme	Cleavage Site 5 → 3	Enzyme GENESPIN
Aat I	AGG'CCT	SseB I
Acc I	GT'MKAC	Acc I
Acc III	T'CCGGA	BseA I
Acc113 I	AGT'ACT	Sca I
Acc65 I	G'GTACC	{Kpn I}
Afa I	GT'AC	Rsa I
Afl I	G'GWCC	Sin I
Afl II	C'TTAAG	MspC I
Age I	A'CCGGT	CspA I
Aha III	TTT'AAA	Dra I
Ahl I	A'CTAGT	Spe I
Ajn I	'CCWGG	{BseB I}
Alu I	AG'CT	Alu I
Alw44 I	G'TGCAC	ApaL I
Ama87 I	C'YCGRG	Ava I
Apa I	GGGCC'C	Apa I
ApaL I	G'TGCAC	ApaL I
AsiA I	A'CCGGT	CspA I
Asp I	GACN'NNGTC	Tth111 I
Asp718 I	G'GTACC	{Kpn I}
AspS9 I	G'GNCC	PspP I
Asu II	TT'CGAA	Asu II
AsuNH I	G'CTAGC	Nhe I
Ava I	C'YCGRG	Ava I
Ava II	G'GWCC	Sin I
BamH I	G'GATCC	BamH I
Ban II	GRGCY'C	Ban II
Ban III	AT'CGAT	BseC I
Bbe I	GGCGC'C	{Nar I}
Bbu I	GCATG'C	Sph I
Bcl I	T'GATCA	Bcl I
Bco I	C'YCGRG	Ava I
Bcu I	A'CTAGT	Spe I
Bfr I	C'TTAAG	MspC I
BfuC I	'GATC	{Dpn I}, Mbo I, Sau3A I
Bgl I	GCCNNNN'NGGC	Bgl I
Bgl II	A'GATCT	Bgl II
Bme18 I	G'GWCC	Sin I
BmeT110 I	CY'CGRG	{Ava I}
Bmt I	GCTAG'C	{Nhe I}
Bpu14 I	TT'CGAA	Asu II
BpvU I	CGAT'CG	Pvu I
Bsa29 I	AT'CGAT	BseC I
Bse118 I	R'CCGGY	BssA I
BseA I	T'CCGGA	BseA I
BseB I	CC'WGG	BseB I
BseC I	AT'CGAT	BseC I
BseG I	GGATG (2/0)	{Fok I}
BseP I	G'CGCGC	BssH II
BshF I	GG'CC	BshF I
BshT I	A'CCGGT	CspA I
BsiHKC I	C'YCGRG	Ava I
BsiS I	C'CGG	BsiS I
BsoB I	C'YCGRG	Ava I
Bsp106 I	AT'CGAT	BseC I
Bsp119 I	TT'CGAA	Asu II
Bsp120 I	G'GGCCC	{Apa I}
Bsp13 I	T'CCGGA	BseA I
Bsp143 I	'GATC	{Dpn I}, Mbo I, Sau3A I
Bsp19 I	C'CATGG	Nco I
Bsp68 I	TCG'CGA	Nru I
BspAN I	GG'CC	BshF I
BspC I	CGAT'CG	Pvu I
BspD I	AT'CGAT	BseC I
BspE I	T'CCGGA	BseA I
BspT I	C'TTAAG	MspC I
BspT104 I	TT'CGAA	Asu II
BspX I	AT'CGAT	BseC I
BsrF I	R'CCGGY	BssA I
BssA I	R'CCGGY	BssA I
BssH I	C'TCGAG	Sla I
BssH II	G'CGCGC	BssH II
BssT1 I	C'CWWGG	Sty I
Bst2U I	CC'WGG	BseB I
Bst98 I	C'TTAAG	MspC I
BstB I	TT'CGAA	Asu II
BstE II	G'GTNACC	BstE II
BstEN II	'GATC	{Dpn I}, Mbo I, Sau3A I
BstF5 I	GGATG (2/0)	{Fok I}
BstKT I	GAT'C	{Dpn I}, {Mbo I}, {Sau3A I}
BstMA I	CTGCA'G	Pst I
BstMB I	'GATC	{Dpn I}, Mbo I, Sau3A I
BstN I	CC'WGG	BseB I
BstO I	CC'WGG	BseB I
BstP I	G'GTNACC	BstE II
BstSN I	TAC'GTA	SnaB I
BstX I	CCANNNNN'NTGG	BstX I
Bsu15 I	AT'CGAT	BseC I
BsuR I	GG'CC	BshF I
BsuTU I	AT'CGAT	BseC I
BtsC I	GGATG (2/0)	{Fok I}
CciN I	GC'GGCCGC	Not I
Cfr10 I	R'CCGGY	BssA I
Cfr13 I	G'GNCC	PspP I
Cfr42 I	CCGC'GG	SgrB I
Cfr9 I	C'CCGGG	{Sma I}
Cla I	AT'CGAT	BseC I
Cpo I	CG'GWCCG	Rsr II
Csp I	CG'GWCCG	Rsr II
Csp45 I	TT'CGAA	Asu II
Csp6 I	G'TAC	{Rsa I}
CspA I	A'CCGGT	CspA I
Din I	GGC'GCC	{Nar I}
Dpn I	GA'TC	Dpn I, {Mbo I}, {Sau3A I}
Dpn II	'GATC	{Dpn I}, Mbo I, Sau3A I
Dra I	TTT'AAA	Dra I
Ecl136 II	GAG'CTC	{Sst I}
Eco105 I	TAC'GTA	SnaB I
Eco130 I	C'CWWGG	Sty I
Eco147 I	AGG'CCT	SseB I
Eco24 I	GRGCY'C	Ban II
Eco32 I	GAT'ATC	EcoR V
Eco47 I	G'GWCC	Sin I
Eco88 I	C'YCGRG	Ava I
Eco91 I	G'GTNACC	BstE II
EcoICR I	GAG'CTC	{Sst I}
EcoO65 I	G'GTNACC	BstE II
EcoR I	G'AATTC	EcoR I
EcoR II	'CCWGG	{BseB I}
EcoR I	G'AATTC	EcoR I
EcoR V	GAT'ATC	EcoR V
EcoT14 I	C'CWWGG	Sty I
EcoT38 I	GRGCY'C	Ban II
Ege I	GGC'GCC	{Nar I}
Ehe I	GGC'GCC	{Nar I}
Erh I	C'CWWGG	Sty I
FauND I	CA'TATG	Nde I
Fba I	T'GATCA	Bcl I
Fbl I	GT'MKAC	Acc I
Fok I	GGATG (9/13)	Fok I
FriO I	GRGCY'C	Ban II
Fun II	G'AATTC	EcoR I
Hae III	GG'CC	BshF I
Hap II	C'CGG	BsiS I
Hinc II	GTY'RAC	Hinc II
Hind II	GTY'RAC	Hinc II
Hind III	A'AGCTT	Hind III
Hinf I	G'ANTC	Hinf I
Hpa I	GTT'AAC	Hpa I
Hpa II	C'CGG	BsiS I
Kas I	G'GCGCC	{Nar I}
Kpn I	GGTAC'C	Kpn I
Kpn2 I	T'CCGGA	BseA I
Ksp I	CCGC'GG	SgrB I
Ksp22 I	T'GATCA	Bcl I
KspA I	GTT'AAC	Hpa I
Kzo9 I	'GATC	{Dpn I}, Mbo I, Sau3A I
Mbo I	'GATC	{Dpn I}, Mbo I, Sau3A I
Mbo II	GAAGA (8/7)	Mbo II
Mlu I	A'CGCGT	Mlu I
Mly113 I	GG'CGCC	Nar I
Mnl I	CCTC (7/6)	Mnl I
Mro I	T'CCGGA	BseA I
MroN I	G'CCGGC	{Nae I}
Msp I	C'CGG	BsiS I
MspC I	C'TTAAG	MspC I
Mva I	CC'WGG	BseB I
Mvr I	CGAT'CG	Pvu I
Nae I	GCC'GGC	Nae I
Nar I	GG'CGCC	Nar I
Nco I	C'CATGG	Nco I
Nde I	CA'TATG	Nde I
Nde II	'GATC	{Dpn I}, Mbo I, Sau3A I
NgoM IV	G'CCGGC	{Nae I}
Nhe I	G'CTAGC	Nhe I
Not I	GC'GGCCGC	Not I
Nru I	TCG'CGA	Nru I
Nsp III	C'YCGRG	Ava I
Nsp V	TT'CGAA	Asu II
Pae I	GCATG'C	Sph I
PaeR7 I	C'TCGAG	Sla I
Pal I	GG'CC	BshF I
Pau I	G'CGCGC	BssH II
Pce I	AGG'CCT	SseB I
Pdi I	GCC'GGC	Nae I
PflF I	GACN'NNGTC	Tth111 I
Pho I	GG'CC	BshF I
PinA I	A'CCGGT	CspA I
Ple19 I	CGAT'CG	Pvu I
Psp124B I	GAGCT'C	Sst I
Psp6 I	'CCWGG	{BseB I}
PspA I	C'CCGGG	{Sma I}
PspE I	G'GTNACC	BstE II
PspG I	'CCWGG	{BseB I}
PspOM I	G'GGCCC	{Apa I}
PspP I	G'GNCC	PspP I
Pst I	CTGCA'G	Pst I
Psy I	GACN'NNGTC	Tth111 I
Pvu I	CGAT'CG	Pvu I
Pvu II	CAG'CTG	Pvu II
Rsa I	GT'AC	Rsa I
Rsr II	CG'GWCCG	Rsr II
Rsr2 I	CG'GWCCG	Rsr II
Sac I	GAGCT'C	Sst I
Sac II	CCGC'GG	SgrB I
Sal I	GTCGAC	Sal I
Sau3A I	'GATC	{Dpn I}, Mbo I, Sau3A I
Sau96 I	G'GNCC	PspP I
Sca I	AGT'ACT	Sca I
Sfi I	GGCCNNNN'NGGCC	Sfi I
Sfo I	GGC'GCC	{Nar I}
Sfr274 I	C'TCGAG	Sla I
Sfr303 I	CCGC'GG	SgrB I
Sfu I	TT'CGAA	Asu II
SgrB I	CCGC'GG	SgrB I
Sin I	G'GWCC	Sin I
Sla I	C'TCGAG	Sla I
Sma I	CCC'GGG	Sma I
SnaB I	TAC'GTA	SnaB I
SpaH I	GCATG'C	Sph I
Spe I	A'CTAGT	Spe I
Sph I	GCATG'C	Sph I
SseB I	AGG'CCT	SseB I
Ssp I	AAT'ATT	Ssp I
Sst I	GAGCT'C	Sst I
Stu I	AGG'CCT	SseB I
Sty I	C'CWWGG	Sty I
Taq I	T'CGA	Taq I
Tel I	GACN'NNGTC	Tth111 I
Tli I	C'TCGAG	Sla I
Tth111 I	GACN'NNGTC	Tth111 I
Vha464 I	C'TTAAG	MspC I
VpaK11B I	G'GWCC	Sin I
Xba I	T'CTAGA	Xba I
Xho I	C'TCGAG	Sla I
Xma I	C'CCGGG	{Sma I}
XmaC I	C'CCGGG	{Sma I}
Xmi I	GT'MKAC	Acc I
Zho I	AT'CGAT	BseC I
Zrm I	AGT'ACT	Sca I

Enzyme available from GeneSpin	Isoschizomer available from GeneSpin	Neoschizomer available from GeneSpin

- Single Letter Code: R = A or G, Y = C or T, M = A or C, K = G or T, S = C or G, W = A or T, H = A or C or T, B = C or G or T, V = A or C or G, D = A or G or T, N = A or C or G or T
- Isoschizomers have same recognition sequence and cutting pattern.
- Neoschizomers (same recognition sequence but different cutting pattern) are indicated with bracket {enzyme}.