Isoschizomers and Recognition Sequences

Enzyme	Isoschizomer	Recognition Sequence
Aat II		GACGT/C
Acc I		GT/MKAC
Acc II	Bsp50 I	CG/CG
	BstU I	CG/CG
	FnuD II	CG/CG
	Mvn I	CG/CG
	Tha I	CG/CG
Acc III	BspM II	T/CCGGA
	Mro I	T/CCGGA
Aci I		CCGC (2/2)
Acy I	Bbi II	GR/CGYC
	BsaH I	GR/CGYC
	HinI I	GR/CGYC
Afl II	Bfr I	C/TTAAG
	Esp4 I	C/TTAAG
Afl III		A/CRYGT
Age I		A/CCGGT
Aha III	Dra I	TTT/AAA
Alu I		AG/CT
AlwN I		CAGNNN/CTG
Aoc I	Axy I	CC/TNAGG
	Bsu36 I	CC/TNAGG
	Cvn I	CC/TNAGG
	Eco81 I	CC/TNAGG
	Mst II	CC/TNAGG
	Sau I	CC/TNAGG
Apa I	Bsp120 I	CACNNN/GTG
ApaB I		GACNNNN/ NNGTC
ApaL I	Alw44 I	G/TGCAC
	Sno I	GTGCAC
Asc I		C/CRYGG
Asu I	Cfr13 I	GACNNN/ NNGTC
	Nsp IV	GACNNN/ NNGTC
	Sau96 I	GACNNN/ NNGTC
Asu II	BsiC I	TTCGAA
	Bsp119 I	TTCGAA
	BstB I	TTCGAA
	Csp45 I	TTCGAA
	Lsp I	TTCGAA
	Nsp V	TTCGAA
	Sfu I	TTCGAA
Ava I	Bco I	C/YCGRG
	Eco88 I	C/YCGRG
	Nsp III	C/YCGRG
Ava II	Eco47 I	G/GWCC
	NspH II	G/GWCC
	Sin I	G/GWCC
Ava III	EcoT22 I	ATG/CAT
	Mph1103 I	ATGCA/T
	Nsi I	ATGCA/T
Avr III	Bln I	C/CTAGG
Bae I		ACNNNNG TAYC
Bal I	Msc I	TGG/CCA
BamH I	Bst I	G/GATCC
Bbv I	Bst71 I	GCAGC (8/12)
Bbv II	Bbs I	GAAGAC (2/6)
Bcc I		CCATC (4/5)
Bcef I		ACGGC (12/13)
Bcg I		GCANNNN NNCG (12/10)
Bcl I	BsiQ I	T/GATCA
	Fba I	T/GATCA
Bet I		W/CCGGW
Bgl I		GCCNNNN/ NGGC
Bgl II		A/GATCT
Bin I	Alw I	GGATC (4/5)
Bpu10 I		CCTNAGC (-5/2)
Bpu1102 I	Cel II	GC/TNAGC
	Esp I	GC/TNAGC
Bsp1286 I	Aoc II	GDGCH/C
	Nsp II	GDGCH/C
	Sdu I	GDGCH/C
Bsp106 I	Cla I	AT/CGAT
BspC I	Pvu I	CGAT/CG
	XmI I	CGAT/CG
BsaA I		YAC/GTR
BsaB I	BsiB I	GATNN/ NNATC
	Mam I	GATNN/ NNATC
BseP I	BssH II	G/CGCGC
Bsg I		GTGCAG (16/14)
Bsi I		CTCGTG (5/1)
BsiY I	Bsl I	CCNNNNN/ NNGG
Bsm I		GAATGC(I/-1)
BsmA I	Alw26 I	GTCTC (1/5)
Bsp50 I	Acc II	CG/CG
	BstU I	CG/CG
	FnuD II	CG/CG
	Mvn I	CG/CG
	Tha I	CG/CG
BspG I		CG/CGCTGGAC
BspH I	RspX I	T/CATGA
BspM I		ACCTGC (4/8)
BspM II	Acc III	T/CCGGA
	BspE I	T/CCGGA
	Kpn2 I	T/CCGGA
	Mro I	T/CCGGA
Bsr I		ACTGG (1/-1)
BsrB I		GAGCGG (-3/-3)
BstE II	BstP I	G/GTNACC
	Eco91 I	G/GTNACC
	EcoO65 I	G/GTNACC
BstN I	Apy I	CC/WGG
	Mva I	CC/WGG
BstX I		CCANNNNN/ NTGG
Cac8 I		GCN/NGC
Cau II	Bcn I	CC/SGG
	Nci I	CC/SGG
Cfr I	Eae I	Y/GGCCR
Cfr10 I	BsrF I	R/CCGGY
Cla I	Ban III	AT/CGAT
	BseC I	AT/CGAT
	BsiX I	AT/CGAT
	Bsp106 I	AT/CGAT
	BspD I	AT/CGAT
	Bsu15 I	AT/CGAT
CviJ I		RG/CY
CviR I		TG/CA
Dde I		C/TNAG
Dpn I*		GA/TC
Dra I	Aha III	TTT/AAA
Dra II	EcoO109 I	RG/GNCCY
	Pss I	RG/GNCCY
Dra III		CACNNN/GTG
Drd I		GACNNNN/ NNGTC
Drd II		GAACCA
Dsa I		C/CRYGG
Eam1105 I		GACNNN/ NNGTC
Eci I		TCCGCC (11/9)
Eco3 1I	Bsa I	GGTCTC (1/5)
Eco47 III		AGC/GCT
Eco52 I	Eag I	C/GGCCG
	Xma III	C/GGCCG
Eco57 I		CTGAAG (16/14)
EcoN I		CCTNN/ NNNAGG
EcoR I		G/AATTC
EcoR II	Apy I	CC/WGG
	BsiL I	CC/WGG
	BstN I	CC/WGG
	Mva I	CC/WGG
	TspA I	/CCWGG
EcoR V	Eco32 I	GAT/ATC
Esp I	Bpu1102 I	GC/TNAGC
	Cel II	GC/TNAGC
Esp3 I		CGTCTC (1/5)
Fau I		CCCGC (4/6)
Fin I		GTFCCC
Fnu4H I		GC/NGC
FnuD II	Acc II	CG/CG
	Bsp50 I	CG/CG
	BstU I	CG/CG
	Mvn I	CG/CG
	Tha I	CG/CG
Fok I		GGATG (9/13)
Fse I		GGCCGG/CC
Fsi I		R/AATTY
Gdi II		YGGCCG(-5/-1)
Gsu I	Bpm I	CTGGAG (16/14)
Hae I		WGG/CCW
Hae II	Bsp143 II	RGCGC/Y
Hae III	BssC I	GG/CC
	BsuR I	GG/CC
	Pal I	GG/CC
Hga I		GACGC (5/10)
HgiA I	Alw21 I	GWGCW/C
	AspH I	GWGCW/C

LEGEND

Recognition sequences given use the standard abbreviations (*Eur. J. Biochem* (1985) 50:15) to represent ambiguity:

R=G or A
H=A or C or T
Y=C or T
B=G or T or C
M=A or C
V=G or C or A
K=G or T
D=G or A or T
S=G or C
N=A or C or G or T
W=A or T

*Dpn I and its isoschizomers require the presence of 6-methyladenosine within the recognition sequence GATC.

Isoschizomers and Recognition Sequences, continued

Enzyme	Isoschizomer	Recognition Sequence
HgaC I	Ban II	G/GYRCC
	Eco24 I	G/GYRCC
HgiE II		ACCNNNNN NGGT
HgiJ II	Ban II	GRGCY/C
	Eco24 I	GRGCY/C
Hha I	Cfo I	GCG/C
	Hin6 I	GCG/C
	HinP1 I	GCG/C
Hind II	Hinc II	GTY/RAC
Hind III		A/AGCTT
Hinf I		G/ANTC
HinI I	Acy I	GR/CGYC
	Aha II	GR/CGYC
	Bbi II	GR/CGYC
	BsaH I	GR/CGYC
Hpa I		GTT/AAC
Hpa II	Hap II	C/CGG
	Msp I	C/CGG
Hph I		GGTGA (8/7)
Kpn I	Acc65 I	G/GTACC
	Asp718 I	GGTAC/C
Ksp632 I	Eam1104 I	CTCTTC (1/4)
	Ear I	CTCTTC (1/4)
Ksp I	Sac II	CCGC/GG
	Sst II	CCGC/GG
Mae I	Bfa I	C/TAG
	Rma I	C/TAG
Mae II		A/CGT
Mbo I	Bsp143 I	/GATC
	Dpn II	/GATC
	Nde II	/GATC
	Sau3A I	/GATC
Mbo II		GAAGA (8/7)
Mcr I	BsiE I	CGRY/CG
Mfe I	Mun I	C/AATTG
Mlu I		A/CGCGT
Mly I		GACTC (5/5)
Mme I		TCCRAC (20/18)
Mnl I		CCTC (7/7)
Mse I		T/TAA
Msp I	Hap II	C/CGG
	Hpa II	C/CGG
Mst I	Aos I	TGC/GCA
	Avi II	TGC/GCA
	Fdi II	TGC/GCA
	Fsp I	TGC/GCA
Mst II	Aoc I	CC/TNAGG
	Axy I	CC/TNAGG
	Bsu36 I	CC/TNAGG
	Cvn I	CC/TNAGG
	Eco81 I	CC/TNAGG
	Sau I	CC/TNAGG
Mwo I	BspW I	GCNNNNN/ NNGC
Nae I	NgoM I	GCC/GGC
Nar I	Bbe I	GGCGC/C
	Ehe I	GGCGC/C
	Kas I	GG/CGCC
Nci I	Aha I	CC/SGG
	Bcn I	CC/SGG
Nco I		C/CATGG
Nde I		CA/TATG
Nhe I		G/CTAGC
Nla III		CATG/
Nla IV	BscB I	GGN/NCC
Not I		GC/GGCCGC
Nru I	Bsp68 I	TCG/CGA
	Spo I	TCG/CGA
Nsi I	Ava III	ATGCA/T
	EcoT22 I	ATGCA/T
Nsp I		RCATG/Y
NspB II	CMG/CKGPac I	TTAAT/TAA
Pac I		TTAAT/TAA
Pal I	BsuR I	GG/CC
	Hae III	GG/CC
Pfl1108 I		TCGTAG
PflM I	Van91 I	CCANNNN/ NTGG
Ple I		GAGTC (4/5)
Pfl1108 I		TCGTAG
PflM I	Van91 I	CCANNNN/ NTGG
Ple I		GAGTC (4/5)
PmaC I	BbrP I	CAC/GTG
	Eco72 I	CAC/GTG
	Pml I	CAC/GTG
Pme I		GTTT/AAAC
PpuM I		RG/GWCCY
PshA I		GACNN/ NNGTC
PspA I	Xma I	C/CCGGG
Pst I		CTGCA/G
Pvu I	BspC I	CGAT/CG
	Xor II	CGAT/CG
Pvu II		CAG/CTG
RleA I		CCCACA (12/9)
Rsa I	Afa I	GT/AC
	Csp6 I	GT/AC
Rsr II	Cpo I	CG/GWCCG
	Csp I	CG/GWCCG
Sac I	Ecl136 II	GAGCT/C
	Sst I	GAGCT/C
Sac II	Cfi42	ICCGC/GG
	Ksp I	CCGC/GG
	Sst II	CCGC/GG
Sal I		G/TCGAC
SanD I		GG/GWCCC
Sap I		GCTCTTC (1/4)
Sau3A I	Mbo I	/GATC
	Nde II	/GATC
Sau96 I	Asu I	G/GNCC
	Cfr13 I	G/GNCC
	NSp IV	G/GNCC
Sau I	Axy I	CC/TNAGG
	Bsu36 I	CC/TNAGG
	Cvn I	CC/TNAGG
	Eco81 I	CC/TNAGG
	Mst II	CC/TNAGG
Sca I		AGT/ACT
ScrF I	Dsa V	CC/NGG
Sdu I	Bmy I	GDGCH/C
	Bsp1286 I	GDGCH/C
	Nsp II	GDGCH/C
Sec I	BsaJ I	C/CNNGG
SfaN I		GCATC (5/9)
Sfc I		CTYRAG
Sfe I		C/TYRAG
Sfi I		GGCCNNNN/ NGGCC
SgrA I		CR/CCGGYG
Sma I	Cfr9 I	C/CCGGG
	Xma I	CCC/GGG
Sse838 I		CCTGCA/GG
Ssp I		AAT/ATT
Stu I	Aat I	AGG/CCT
	Eco147 I	AGG/CCT
Sty I	Eco130 I	C/CWWGG
	EcoT14 I	C/CWWGG
Swa I		ATTT/AAAT
Taq I	TthHB8 I	T/CGA
Taq II		GACCGA (11/9)
Tfi I		G/AWTC
Tsp45 I		/GTSAC
TspE I		/AATT
Tth111 I	Asp I	GACN/NNGTC
Tth 111 II		CAARCA (11/9)
Vsp I	Ase I	AT/TAAT
	Asn I	AT/TAAT
Xba I		T/CTAGA
Xcm I		CCANNNNN/ NNNNTGG
Xho I	Ccr I	C/TCGAG
	PaeR7 I	C/TCGAG
Xho II	BstY I	R/GATCY
	Mfl I	R/GATCY
Xma I	PspA I	C/CCGGG
Xma III	BstZ I	C/GGCCG
	Eag I	C/GGCCG
	EclX I	C/GGCCG
	Eco52 I	C/GGCCG
Xmn I	Asp700 I	GAANN/ NNTTC

LEGEND

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S=G or C	W=A or T
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V=G or C or A	D=G or A or T
N=A or C or G or T	

*Dpn I and its isoschizomers require the presence of 6-methyladenosine within the recognition sequence GATC.

REFERENCE

1. Roberts, R.J. and Macelis, D. (1991) *Nucleic Acids Res.* 19: 2077-2109.