

Restriction Enzyme Cleavage Activity Near DNA Termini

Enzyme	Oligo Sequence	Chain Length (bp)	% Cleavage	
			2 hours	20 hours
<i>Acc</i> I	GGTCGACC	8	0	0
	CGGTCGACCG	10	0	0
	CCGGTCGACCGG	12	0	0
<i>Afl</i> III	CACATGTG	8	0	0
	CCACATGTGG	10	>90	>90
	CCCACATGTGGG	12	>90	>90
<i>Acs</i> I	GGCGCGCC	8	>90	>90
	AGGCGCGCCT	10	>90	>90
	TTGGCGCGCCAA	12	>90	>90
<i>Ava</i> I	CCCCGGGG	8	50	>90
	CCCCCGGGGG	10	>90	>90
	CGCGGATCCGCG	12	>90	>90
<i>Bam</i> H I	CGGATCCG	8	10	25
	CGGGATCCCG	10	>90	>90
	CGCGGATCCGCG	12	>90	>90
<i>Bgl</i> II	CAGATCGTG	8	0	0
	GAAGATCTTC	10	75	>90
	GGAAGATCTTCC	12	25	>90
<i>Bss</i> H II	GGCGCGCC	8	0	0
	AGGCGCGCCT	10	0	0
	TTGGCGCGCCAA	12	50	>90
<i>Bst</i> E II	GGGT(A/T)ACCC	9	0	10
<i>Bst</i> X I	AACTGCAGAACCAATGCATTGG	22	0	0
	AAAACCTGCAGCCAATGCATTGGAA	24	25	50
	CTGCAGAACCAATGCATTGGATGCAT	27	25	>90
<i>Cla</i> I	CATCGATG	8	0	0
	GATCGATC	8	0	0
	CCATCGATGG	10	>90	>90
	CCCATCGATGGG	12	50	50
<i>Eco</i> R I	GGAATTCC	8	>90	>90
	CGGAATTCCG	10	>90	>90
	CCGGAATTCCGG	12	>90	>90
<i>Hae</i> III	GGGGCCCC	8	>90	>90
	AGCGGCCGCT	10	>90	>90
	TTGCGGCCGCAA	12	>90	>90
<i>Kpn</i> I	GGGTACCC	8	0	0
	GGGGTACCCC	10	>90	>90
	CGGGGTACCCCG	12	>90	>90
<i>Mlu</i> I	GACGCGTC	8	0	0
	CGACGCGTCG	10	25	50
<i>Nco</i> I	CCCATGGG	8	0	0
	CATGCCATGGCATG	14	50	75
<i>Nde</i> I	CCATATGG	8	0	0
	CCCATATGGG	10	0	0
	CGCCATATGGCG	12	0	0
	GGGTTTCATATGAAACCC	18	0	0
	GGAATTCCATATGGAATTCC	20	75	>90
	GGGAATTCCATATGGAATTCCC	22	75	>90
<i>Nhe</i> I	GGCTAGCC	8	0	2
	CGGCTAGCCG	10	10	25
	CTAGCTAGCTAG	12	10	50

Restriction Enzyme Cleavage Activity Near DNA Termini, continued

Enzyme	Oligo Sequence	Chain Length (bp)	% Cleavage	
			2 hours	20 hours
<i>Not I</i>	TTGCGGCCGCAA	12	0	0
	ATTTGCGGCCGCTTTA	16	10	10
	AAATATGCGGCCGCTATAAA	20	10	10
	ATAAGAATGGGCCGCTAAACTAT	24	25	90
	AAGGAAAAAAGCGGCCGCAAAAGGAAAA	28	25	>90
<i>Nsi I</i>	TGCAGGCATGCA	12	10	>90
	CCAATGCATTGGTTCTGCAGTT	22	>90	>90
<i>Pac I</i>	TTAATTAA	8	0	0
	GTTAATTAAC	10	0	25
	CCTTAATTAAGG	12	0	>90
<i>Pme I</i>	GTTTAAAC	8	0	0
	GGTTTAAACC	10	0	25
	GGGTTTAAACCC	12	0	50
	AGCTTTGTTTAAACGGCGCCGG	24	75	>90
<i>Pst I</i>	GCTGCAGC	8	0	0
	TGCACTGCAGTGCA	14	10	10
	AACTGCAGAACCAATGCATTGG	22	>90	>90
	AAAACCTGCAGCCAATGCATTGGAA	24	>90	>90
	CTGCAGAACCAATGCATTGGATGCAT	26	0	0
<i>Pvu I</i>	CCGATCGG	8	0	0
	ATCGATCGAT	10	10	25
	TCGCGATCGCGA	12	0	10
<i>Sac I</i>	CGACGTCG	8	10	10
<i>Sac II</i>	GCCGCGGC	8	0	0
	TCCCCGCGGGGA	12	50	>90
<i>Sal I</i>	GTGCAGCTCAAAAGGCCATAGCGGCCGC	28	0	0
	GCGTCGACGTCTTGGCCATAGCGGCCGCGG	30	10	50
	ACGCGTCGACGTGCGCCATAGCGGCCGCGGAA	32	10	75
<i>Sca I</i>	GAGTACTC	8	10	25
	AAAAGTACTTTT	12	75	75
	CCCGGG	6	0	10
	CCCCGGGG	8	0	10
	CCCCCGGGGG	10	10	50
	TCCCCCGGGGGA	12	>90	>90
<i>Spe I</i>	GACTAGTC	8	10	>90
	GGACTAGTCC	10	10	>90
	CGGACTAGTCCG	12	0	50
	CTAGACTAGTGTAG	14	0	50
<i>Sph I</i>	GGCATGCC	8	0	0
	CATGCATGCATG	12	0	25
	ACATGCATGCATGT	14	10	30
<i>Stu I</i>	AAGGCCTT	8	>90	>90
	GAAGGCCTTC	10	>90	>90
	AAAAGGCCTTTT	12	>90	>90
<i>Xba I</i>	CTCTAGAG	8	0	0
	GCTCTAGAGC	10	>90	>90
	TGCTCTAGAGCA	12	75	>90
	CTAGTCTAGACTAG	14	75	>90
<i>Xho I</i>	CTCGAGG	8	0	0
	CCCTCGAGGG	10	10	25
	CCGCTCGAGCGG	12	10	75
<i>Xma I</i>	CCCCGGGG	8	0	0
	CCCCCGGGGG	10	25	75
	CCCCCGGGGGG	12	50	>90