

Enzyme	Oligo Sequence	Chain Length	% Cleavage		Enzyme	Oligo Sequence	Chain Length	% Cleavage	
			2 hr	20 hr				2 hr	20 hr
<i>Acc</i> I	GGTCGACC	8	0	0	<i>Nco</i> I	CCCATGGG	8	0	0
	CGGTCGACCG	10	0	0		CATGCCATGGCATG	14	50	75
	COGGTCGACCGG	12	0	0	<i>Nde</i> I	CCATATGG	8	0	0
<i>Afl</i> III	CACATGTG	8	0	0		CCCATATGGG	10	0	0
	CCACATGTGG	10	>90	>90		CGCCATATGGCG	12	0	0
	CCCACATGTGGG	12	>90	>90		GGGTTTCATATGAAACCC	18	0	0
<i>Asc</i> I	GGCGCGCC	8	>90	>90		GGAATTCATATGGAATCC	20	75	>90
	AGGCGCGCCT	10	>90	>90	GGGAATTCATATGGAATCC	22	75	>90	
	TTGGCGCGCCAA	12	>90	>90	<i>Nhe</i> I	GGCTAGCC	8	0	0
<i>Ava</i> I	CCCCGGGG	8	50	>90		CGGCTAGCCG	10	10	25
	CCCCCGGGGG	10	>90	>90		CTAGCTAGCTAG	12	10	50
	TCCCCGGGGGA	12	>90	>90	<i>Not</i> I	TTGGGCGCGAA	12	0	0
<i>Bam</i> HI	CGGATCCG	8	10	25		ATTGGCGCCGCTTTA	16	10	10
	CGGGATCCCG	10	>90	>90		AAATATGCGGCCGCTATAAA	20	10	10
	CGCGGATCCGCG	12	>90	>90		ATAAGAATGCGGCCGCTAAACTAT	24	25	90
<i>Bgl</i> II	CAGATCTG	8	0	0	AAGGAAAAAGCGGCCGCAAAAGGAAAA	28	25	>90	
	GAAGATCTTC	10	75	>90	<i>Nsi</i> I	TGCATGCATGCA	12	10	>90
	GGAAGATCTTCC	12	25	>90		CCAATGCATGGTTCTGCAGTT	22	>90	>90
<i>Bss</i> HI	GGCGCGCC	8	0	0		<i>Pac</i> I	TTAATTAA	8	0
	AGGCGCGCCT	10	0	0	GTTAATTAAAC		10	0	25
	TTGGCGCGCCAA	12	50	>90	CCTTAATTAAGG		12	0	>90
<i>Bst</i> E II	GGGT(A/T)ACC	9	0	10	<i>Pme</i> I	GTTTAAAC	8	0	0
<i>Bst</i> X I	AACTGCAGAACCAATGCATTGG	22	0	0		GGTTTAAACC	10	0	25
	AAAAGTGCAGCAATGCATTGGAA	24	25	50		GGGTTTAAACCC	12	0	50
	CTGCAGAACCAATGCATTGGATGCAT	27	25	>90		AGCTTTGTTTAAACGGCGCCCGG	24	75	>90
<i>Cla</i> I	CATCGATG	8	0	0	<i>Pst</i> I	GCTGCAGC	8	0	0
	GATCGATC	8	0	0		TGCACTGCAGTGCA	14	10	10
	CCATCGATGG	10	>90	>90		AACTGCAGAACCAATGCATTGG	22	>90	>90
	CCCATCGATGGG	12	50	50		AAAAGTGCAGCCAAATGCATTGGAA	24	>90	>90
<i>Eco</i> R I	GGAATTC	8	>90	>90	CTGCAGAACCAATGCATTGGATGCAT	26	0	0	
	CGGAATCCG	10	>90	>90	<i>Pvu</i> I	CCGATCGG	8	0	0
	CCGGAATCCGG	12	>90	>90		ATCGATCGAT	10	10	25
				TCGCGATCGCGA		12	0	10	
<i>Hae</i> III	GGGGCCCC	8	>90	>90	<i>Sac</i> I	CGAGCTCG	8	10	10
	AGCGGCCGCT	10	>90	>90		<i>Sac</i> II	GCCGCGGC	8	0
	TTGGGCCCGCAA	12	>90	>90	TCCCCGCGGGGA		12	50	>90
<i>Hind</i> III	CAAGCTTG	8	0	0	<i>Sal</i> I	GTCGACGTCAAAAGGCCATAGCGGCCGC	28	0	0
	CCAAGCTTGG	10	0	0		GCCTGACGCTTTGGCCATAGCGGCCGCGG	30	10	50
	CCCAAGCTTGGG	12	10	75		ACGCGTCGACGTCGGCCATAGCGGCCGCGGAA	32	10	75
<i>Kpn</i> I	GGGTACCC	8	0	0	<i>Sca</i> I	GAGTACTC	8	10	25
	GGGGTACCCC	10	>90	>90		AAAAGTACTTTT	12	75	75
	CGGGGTACCCCG	12	>90	>90	<i>Sma</i> I	CCCCGG	6	0	10
<i>Mlu</i> I	GACGCGTC	8	0	0		CCCCGGGG	8	0	10
	CGACGCGTCG	10	25	50		CCCCGGGGG	10	10	50
						TCCCCGGGGGA	12	>90	>90