

TABLE 3. Comparison of melting temperature predictions for different duplexes of fragmented subtilisin E gene between the proposed model and  $T_m = 81.5 + 0.41(\% GC) - 500/L + 16.6 \log [\text{Na}^+]$ .

Sequence positions	Overlap length	Percent GC	Melting temperature ( $^{\circ}\text{C}$ )	
			Annealing model	Howley <i>et al.</i> (1)
819-828	10	50	26	30
1013-1022	10	30	17	22
529-538	10	60	32	35
804-828	25	52	61	61
779-828	50	50	72	71
729-828	100	55	81	78

Data shown is for  $[\text{Na}^+] = 0.05 \text{ M}$  and an initial template mole fraction  $x_A^0 = 2.7 \times 10^{-8}$  that corresponds to a DNA concentration of 10 mg/liter, typical for DNA shuffling.

#### References:

1. Howley, P.M., Israel, M.F., Law, M., & Martin, M.A. (1979) *J. Biol. Chem.* **254**, 4876–4883.