

Primer_binding

Query (Primer)	Subject(mitogenome)	Identity	AlignmentLength	qstart	qend	sstart	send	evaluate	bitscore	Est. Size
I_Hom3F_3kb	Hgam	100	18	3	20	1730	1747	8.28E-06	34.4	2836
I_Hom3R_3kb	Hgam	95.652	23	1	23	4566	4544	8.54E-07	38.1	2836
I_Hom3F_3kb	Hgam	95	20	1	20	5630	5648	0.00011	30.7	2835
I_Hom3R_3kb	Hgam	95.652	23	1	23	8465	8443	8.54E-07	38.1	2835