

	Score:	Identities:	Gaps:
	41	32 / 36 (89%)	2 / 36 (5%)
Query sequence	AACTCGTTGTAGTAATT-CATCGAGAGGCGAGGAGGG		
	.                         .		
Reference sequence	AACTCGCTGTAGTAATTCCAGCGAGAGGCA-GAGGG		