

A *Rhodotorula mucilaginosa* strain KTDS2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: [MF952621.1](#) Length: 540 Number of Matches: 1

Range 1: 22 to 178 [GenBank](#) [Graphics](#)

Score	Expect	Identities	Gaps	Strand	
178 bits(96)	9e-41	137/157(87%)	1/157(0%)	Plus/Plus	
Query 5	TTCTTTCCCTGTCACCTGTTAGGTATAGAATCTGTCGGAATAGAGCGAACTCCTAATCC	64			MF952621 (<i>Rhodotorula mucilaginosa</i>)
Sbjct 22	TTCTAACCCCTGTCACCTGTTGGGATAGAACTCTCGCAAGAGAGCGAACTCCTATTCA	81			Sample: strand primer its1
Query 65	TTTATAAACACGAAAGTCCATGATTTGTCTTATCCTTTATAAC-RACTAAAACCTTCAACAA	123			MF952621 (<i>Rhodotorula mucilaginosa</i>)
Sbjct 82	CTTATAAACACAAAAGTCTATGAATGTATTAATTTTATAACAAAATAAACTTTCAACAA	141			Sample: strand primer its1
Query 124	CGGATCTCTGGCTCTCGCATCGATGAAGAACGCAGC	160			MF952621 (<i>Rhodotorula mucilaginosa</i>)
Sbjct 142	CGGATCTCTGGCTCTCGCATCGATGAAGAACGCAGC	178			Sample: strand primer its1

B *Rhodotorula mucilaginosa* strain GBME-IAUF-1 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: [MT012935.1](#) Length: 666 Number of Matches: 1

Range 1: 21 to 105 [GenBank](#) [Graphics](#)

Score	Expect	Identities	Gaps	Strand	
110 bits(59)	1e-20	78/87(90%)	2/87(2%)	Plus/Minus	
Query 1	GGTTAGAAAGTGATGTATTCGGACTCCCTATTAAGAGAGGACGTCCTATATTCACCTAATG	60			GBME-IAUF-1 (<i>Rhodotorula mucilaginosa</i>)
Sbjct 105	GGTTAGAAAGTGA-GAGTTCGGACTCCAAGTTAAG-TTGGACGTCCTATATTCACCTAATG	48			Sample: strand primer its2
Query 61	ATCCTTCCGCGAGGTTACACCTACGGAAG	87			GBME-IAUF-1 (<i>Rhodotorula mucilaginosa</i>)
Sbjct 47	ATCCTTCCGCGAGGTTACACCTACGGAAG	21			Sample: strand primer its2

Figure S1: Alignments obtained in GenBank with the sequences for both strands (overlapping was not successful) for the amplicon obtained by using the panfungal PCR in Case 2. **A)** Alignment with the sequence obtained by using primer ITS1 **B)** Alignment with the sequence obtained by using primer ITS2