Bacillis H57 notes

qPCR

Copy Viia7 from desktop onto USB.

Use Integra Robot – it is better

Can change booking up to 1 hour before

My Office

S528

Shahrham Niknafs 0468691705

Ice machine N307

UQ Chem Store: Order bottle for waste, when full put it in loading bay

Email IT people about printing

Preference trial

H57 RT

H57 4 degrees

cont RT

cont 4 degrees

Preferred all except cont RT – suhgests growth of fungus. >40 fungal volatiles characteristic of fungi IDed.

ID fungus growing – ITS 1 and 4 amplify all fungal species, no oomycetes (Manter and Vivanco)

Daniel K. Manter, Jorge M. Vivanco,

Use of the ITS primers, ITS1F and ITS4, to characterize fungal abundance and diversity in mixed-template samples by qPCR and length heterogeneity analysis,

Journal of Microbiological Methods,

Volume 71, Issue 1,

2007,

Pages 7-14,

https://www.sciencedirect.com/science/article/pii/S0167701207002424

NSI1 and 58A2F

Table 1

Sequence characteristics of primers developed in this study.

| **Name** | **Sequence (5' to 3')** | **Nomenclature** | **Bases** | **Tm** |
| --- | --- | --- | --- | --- |
| NSA3 | AAACTCTGTCGTGCTGGGGATA | nu-SSU-1543-5' | 22 | 67 |
| NSI1 | GATTGAATGGCTTAGTGAGG | nu-SSU-1671-5' | 20 | 59 |
| 58A1F | GCATCGATGAAGAACGC | nu-5.8S-2206-3' | 17 | 61 |
| 58A2F | ATCGATGAAGAACGCAG | nu-5.8S-2208-3' | 17 | 57 |
| 58A2R | CTGCGTTCTTCATCGAT | nu-5.8S-2192-5' | 17 | 57 |
| NLB3 | GGATTCTCACCCTCTATGA | nu-LSU-2754-5' | 19 | 56 |
| NLB4 | GGATTCTCACCCTCTATGAC | nu-LSU-2755-5' | 20 | 57 |
| NLC2 | GAGCTGCATTCCCAAACAACTC | nu-LSU-2821-5' | 22 | 67 |
| Plant control primers | |  |  |  |
| NSIP | GATTGAATGATCCGGTGAAG | PC-nu-SSU-1671-5' | 20 | 62 |
| NLBP | GCTGTCACCCTCTCAGGC | PC-nu-LSU-2755-5' | 18 | 64 |

NSI1- 58A2F is 280bp in **Clavispora lusitaniae strain P4 chromosome 4**

**Ceratobasidium sp. isolate IPAVE0072**

**Length: 785 Number of Matches: 2**

**Paraphysoderma sedebokerense strain CMBB small subunit ribosomal RNA gene, partial sequence**

**Sequence ID:** [**MN203631.1**](https://www.ncbi.nlm.nih.gov/nucleotide/MN203631.1?report=genbank&log$=nuclalign&blast_rank=62&RID=YYZK665Z014)**Length: 1694Number of Matches: 1**

**Candida sp. (in: Saccharomycetales) strain DMKU VGT1-14 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence**

**Sequence ID:** [**MN194615.1**](https://www.ncbi.nlm.nih.gov/nucleotide/MN194615.1?report=genbank&log$=nuclalign&blast_rank=63&RID=YYZK665Z014)**Length: 1499Number of Matches: 2**

**Zygotorulaspora sp. strain UFMG-CM-Y6340 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence**

**Sequence ID:** [**MN721359.1**](https://www.ncbi.nlm.nih.gov/nucleotide/MN721359.1?report=genbank&log$=nuclalign&blast_rank=8&RID=YYZK665Z014)**Length: 1730Number of Matches: 2**

Range 1: 165 to 184[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/MN721359.1?report=genbank&log$=nuclalign&blast_rank=8&RID=YYZK665Z014&from=165&to=184)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/MN721359.1?report=graph&rid=YYZK665Z014%5bMN721359.1%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=165:184&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Alignment statistics for match #1** | | | | |
| Score | Expect | Identities | Gaps | Strand |
| 40.1 bits(20) | 9.4 | 20/20(100%) | 0/20(0%) | Plus/Plus |

Query 1 GATTGAATGGCTTAGTGAGG 20

||||||||||||||||||||

Sbjct 165 GATTGAATGGCTTAGTGAGG 184

Range 2: 506 to 522[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/MN721359.1?report=genbank&log$=nuclalign&blast_rank=8&RID=YYZK665Z014&from=506&to=522)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/MN721359.1?report=graph&rid=YYZK665Z014%5bMN721359.1%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=506:522&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp1777430594_1)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Alignment statistics for match #2** | | | | |
| Score | Expect | Identities | Gaps | Strand |
| 34.2 bits(17) | 577 | 17/17(100%) | 0/17(0%) | Plus/Plus |

Query 51 ATCGATGAAGAACGCAG 67

|||||||||||||||||

Sbjct 506 ATCGATGAAGAACGCAG 522

**357 bp**