

Cryptococcus neoformans var. grubii isolate IFRC 888 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

GenBank: KY216175.1

[FASTA Graphics PopSet](#)

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LOCUS KY216175 536 bp DNA linear PLN 05-JUL-2017

DEFINITION *Cryptococcus neoformans* var. *grubii* isolate IFRC 888 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.

ACCESSION KY216175

VERSION KY216175.1

KEYWORDS .

SOURCE *Cryptococcus neoformans* var. *grubii* (*Filobasidiella neoformans* serotype A)

ORGANISM [Cryptococcus neoformans var. grubii](#)
Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomycetes; Tremellales; Cryptococcaceae; Cryptococcus; *Cryptococcus neoformans* species complex.

REFERENCE 1 (bases 1 to 536)

AUTHORS Fakhim,H., Vaezi,A., Mahmoodi,M., Pakshir,K. and Badali,H.

TITLE *Cryptococcus neoformans* from pigeon droppings

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 536)

AUTHORS Fakhim,H., Vaezi,A., Mahmoodi,M., Pakshir,K. and Badali,H.

TITLE Direct Submission

JOURNAL Submitted (21-NOV-2016) Department of Medical Mycology and Parasitology/Invasive Fungi Research Center (IFRC), School of Medicine, Mazandaran University of Medical Sciences, Mazandaran Universit, 18 Dey, Sari, Mazandaran 4817668113, Iran

COMMENT ##Assembly-Data-START##
Sequencing Technology :: Sanger dideoxy sequencing
##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..536
/organism="Cryptococcus neoformans var. grubii"
/mol_type="genomic DNA"
/variety="grubii"
/isolate="IFRC 888"
/db_xref="taxon:178876"

[misc RNA](#) <1..>536
/note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and large

subunit ribosomal RNA"

ORIGIN

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61  gtttatgtgc ttcggcacgt tttacacaaa cttctaaatg taatgaatgt aatcttatta
121 taacaataat aaaactttca acaacggatc tcttggttc cacatcgatg aagaacgcag
181 cgaaatgcga taagtaatgt gaattgcaga attcagtga tcatcgaatc tttgaacgca
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