SPECIES OF FUNG

Urmas Kõljalg Universities of Tartu

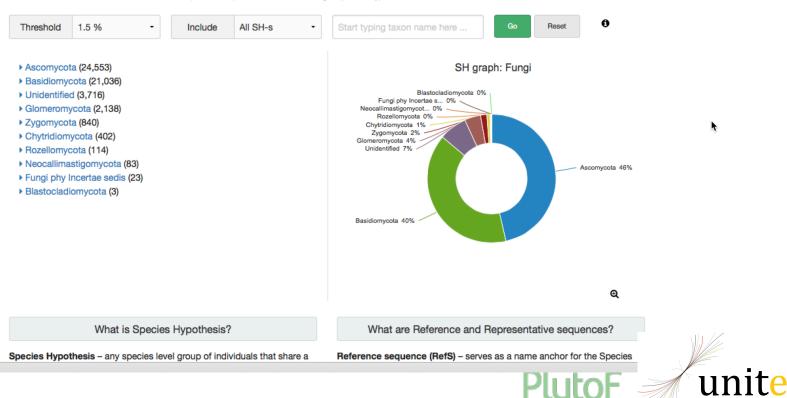
```
      Image: Search Pages
      Workbench
      Resources
      Statistics
      Notes and News
      UNITE Board
      Acknowledgements
```



Unified system for the DNA based fungal species linked to the classification Ver. 7.0



Current version: 7.0; Release date: 2015-08-01 (read more); Number of UNITE fungal Species Hypotheses: 53 891





UNITE

Curated rDNA ITS datasets from any biological sample (specimen, living specimen, soil, water, air, medical, etc.)

ITS sequences connected to the (type) specimen data, locality, multimedia, etc.





UNITE Milestones

2001 – formation of UNITE (ITS and voucher specimens)

2003 – first online rDNA ITS based key for few hundred species





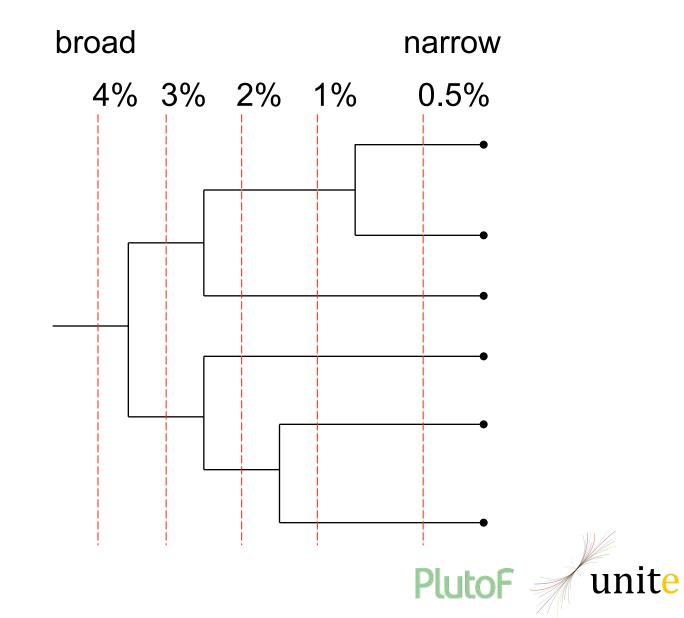
UNITE Milestones

2007 – online biocuration and third-party annotations of INSD (GenBank, ENA, DDBJ) sequences

2011 – online curation of Species Hypotheses









🖆 🕂 🖞 https 🕯 unite.ut.ee/bl_forw_sh.php?sh_name=SH177891.07FU#fndtn-panel1

Tomentella badia | SH177891.07FU | DOI: 10.15156/BIO/SH177891.07FU

Distance to the closest SH: 1.5 No. of sequences in SH: 5

Placement in the fungal classification

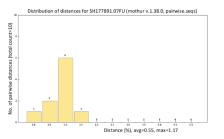
Fungi; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetes sbc Incertae sedis; Thelephorales; Thelephoraceae; Tomentella

Reference sequence: UDB000238|AF272937|UK91

Chosen by: Urmas Kõljalg Date: 2014-11-09 22:05



Distribution of distances ()



Older version(s) of this SH is/are available

SH code (Count*/Total count**)

narrow

SH202603.06FU (3/5);

*Number of sequences carried over from version 6.0 **Total number of sequences composing this SH in version 7.0

Distribution map

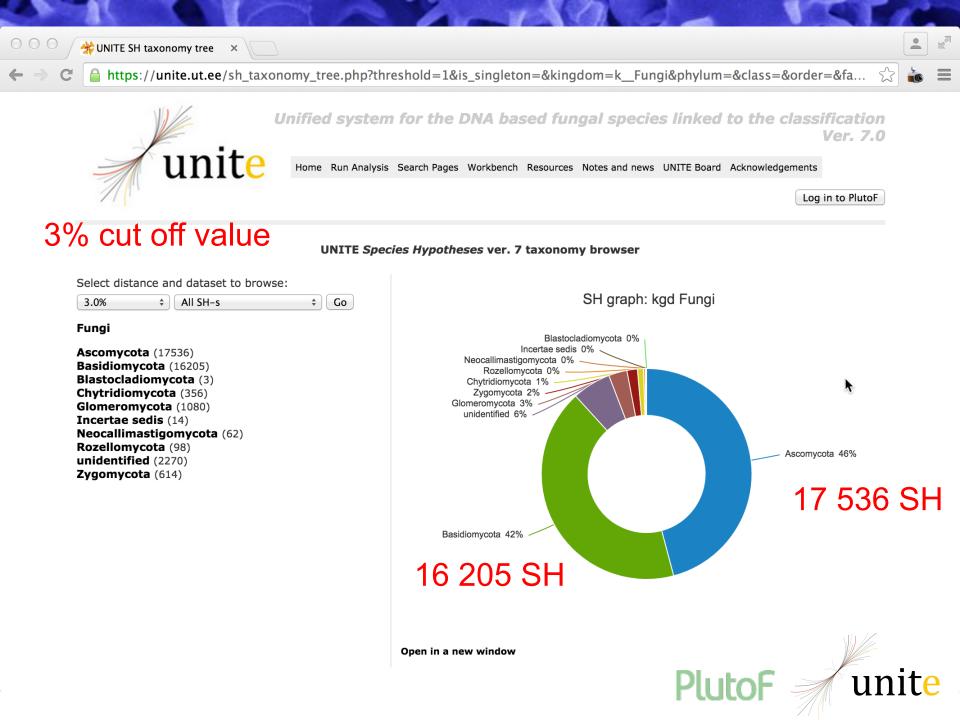


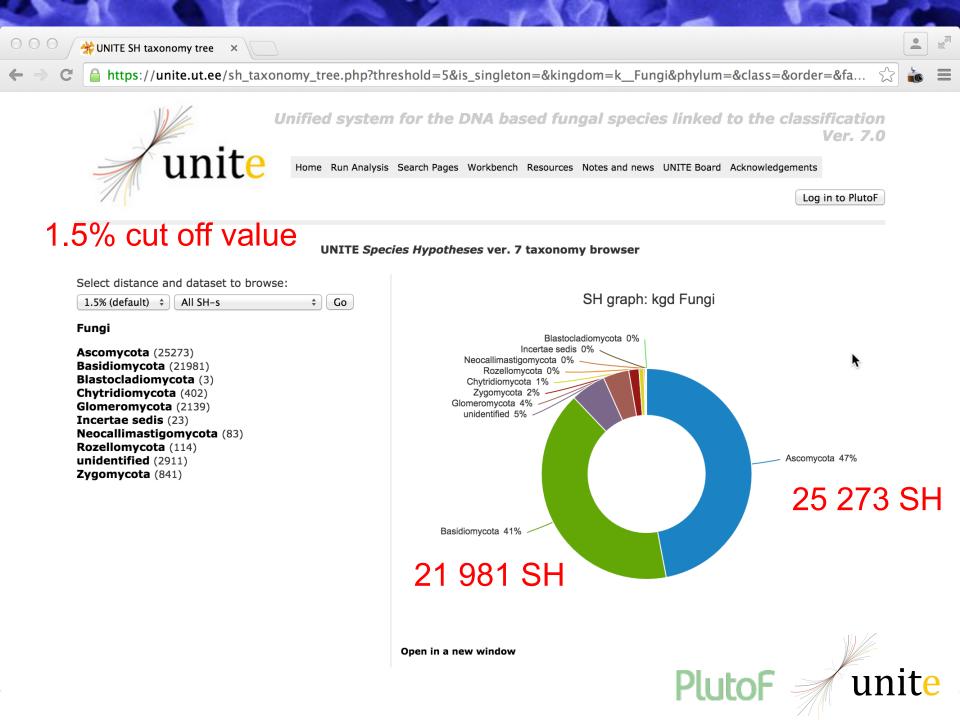
hroad

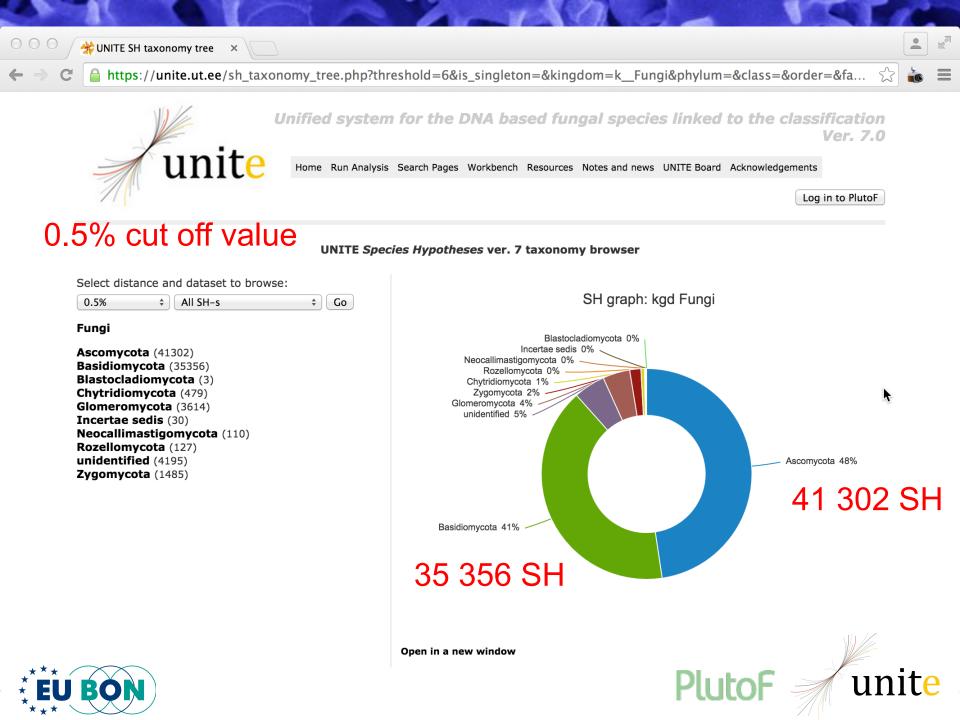
C Reader

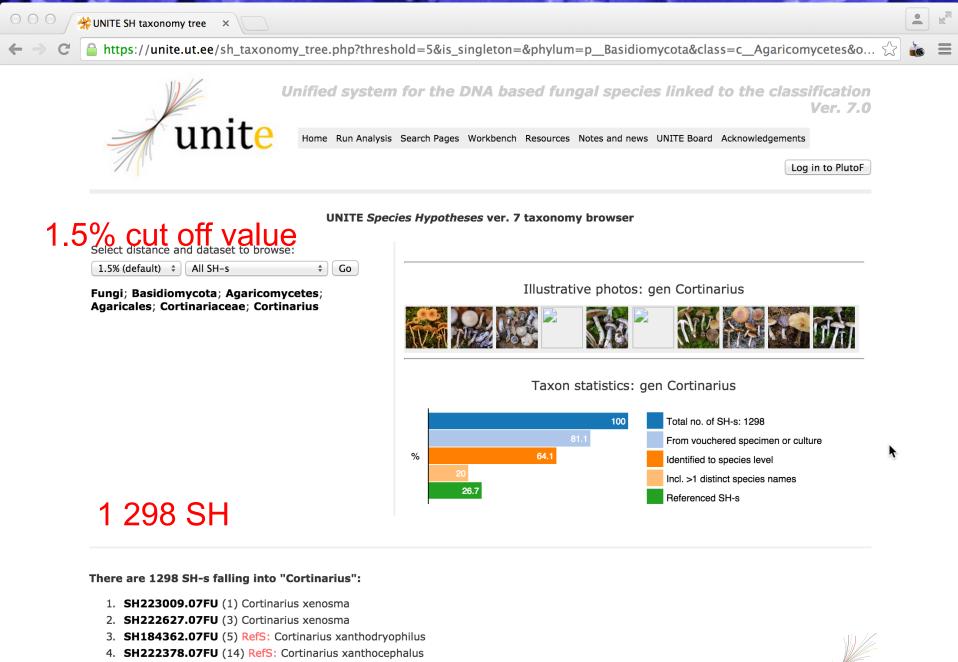
*Locations without exact coordinates are displayed as spherical country centroids

							bibau
						% 🕄	
Accession number	UNITE taxon name	INSD taxon name	Sequence source	Interacting taxa	Sampling area	 <.5 0.5 1.0 1.5 2.0 2.5 2.5 	ç ← Alignment →
JX434657	Tomentella	Tomentella (Tomentella sp. A11)					
UDB000238	Tomentella badia		TAAM159022 (Specimen)		Russian Federation		
HM370465	Thelephoraceae	Thelephoraceae (uncultured Tomentel	Ectomycorrhiza		Italy		
**KM247748	Fungi	Fungi (uncultured fungus)			France		
**KJ188589	Thelephoraceae	Thelephoraceae (uncultured Thelepho		Neottia ovata	France		



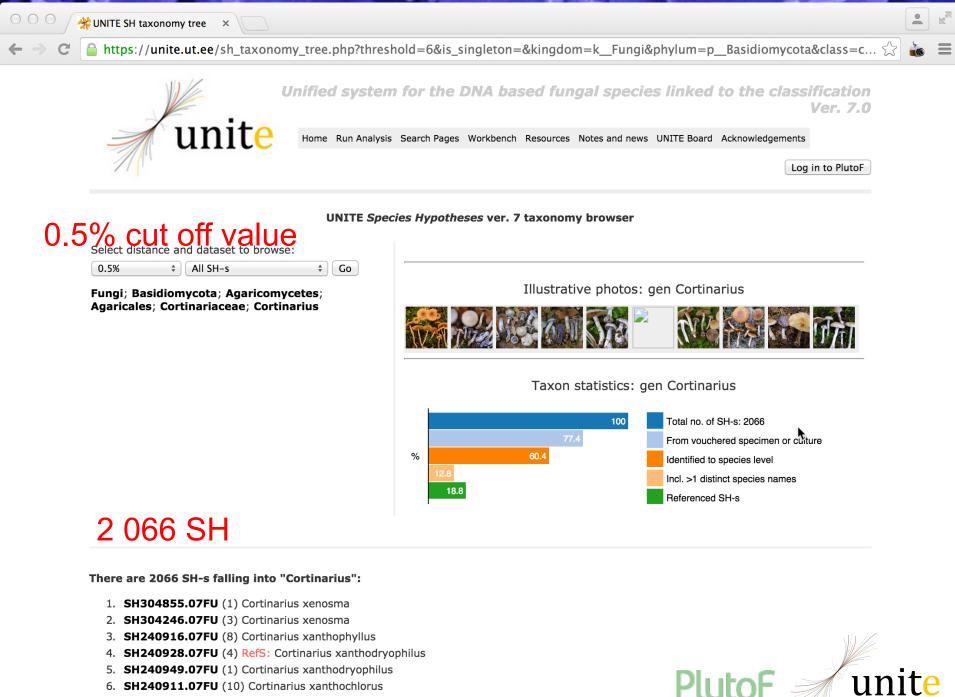






uni

- 5. SH222693.07FU (2) RefS: Cortinarius wiebeae
- 6. SH222367.07FU (16) Cortinarius walpolensis
- 7. SH222558.07FU (4) Cortinarius vulpinus subsp. pseudovulpinus (as Cortinarius pseudovulpinus)
- -----



- 7. SH303960.07FU (13) RefS: Cortinarius xanthocephalus
- · ······

		1
○ ○ / # UNITE SH taxonomy tree × # UNITE - Species Hypothes∈ ×		• K <u>N</u>
← → C Attps://unite.ut.ee/sh/SH184362.07FU	<u>ک</u>	
Unified system for the DNA based fungal species linked to the classification Ver. 7.0		
Home Run Analysis Search Pages Workbench Resources Notes and news UNITE Board Acknowledgements		
Username ••••••• Log in		

1.5% cut off value - Cortinarius xanthodryophilus

Cortinarius xanthodryophilus | SH184362.07FU

Distance to the closest SH (read more): 1.5% No of sequences in SH: 5

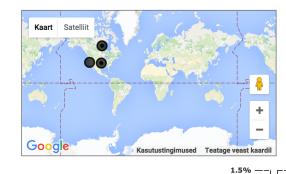
Placement in the fungal classification (read more):

Fungi; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Cortinariaceae; Cortinarius Links to taxon name in: Index Fungorum; NCBI

Reference sequence: HQ441244 Chosen by: Tuula Niskanen

Date: 2014-11-09 21:04:52

Large map (incl. map info)



Older version(s) of this SH is/are available:

SH code (Count*/Total count**)

SH207574.06FU (5/5);

There are no totally new sequences in this SH compared to version $6.0\,$

*Number of sequences carried over from version 6.0 **Total number of sequences composing this SH in version 6.0

PlutoF unit

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					1.5% 1% ۲ 0.5%	2% 	
Sequence ID	UNITE taxon name	INSD taxon name	Country	DNA source	Interacting taxa	•	Clustering based on: Full ITS
							50
more DQ974721	Cortinarius xanthodryophilus	Cortinariaceae (uncultured Cortinar	United States	Ectomycorrhiza	Quercus		AGGATCATTATTGAA-AT-AAATCTGATAAGT
more <u>JF273637</u>	Cortinarius xanthodryophilus	Cortinarius (Cortinarius xanthodryo	United States	Fruitbody			AAGGATCATTATTGAA-AT-AAATCTGATAAGT
more <u>JF273636</u>	Cortinarius xanthodryophilus	Cortinarius (Cortinarius xanthodryo	United States	Fruitbody			AAGGATCATTATTGAA-AT-AAATCTGATAAGT
more <u>HQ441244</u>	Cortinarius xanthodryophilus	Cortinarius (Cortinarius xanthodryo	United States	Fruitbody (Holotype)			AAGGATCATTATTGAA-AT-AAATCTGATAAGT
more <u>GQ159771</u>	Cortinarius xanthodryophilus	Cortinarius (Cortinarius xanthodryo	Canada	Fruitbody			CATTATTGAA-AT-AAATCTGATAAGT
							50

chimeric

low quality

• UNITE core sequence

automatically chosen SH representative sequence

• Ex = sequence to be excluded from the next version of global key

O S WITE SH taxonomy tree	× 💥 UNITE – Species Hy	pothese ×						
C 🔒 https://unite.ut.ee	e /sh/SH188487.07FU							☆ 🐌
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					1.5%	<u>ن</u> 2%		
					19 0.59	6 —		
Sequence ID	UNITE taxon name	INSD taxon name	Country	DNA source	Interacting taxa	•	Clustering based	on: Full IT
51150047	Castinasius		De la sel	Esta a subtraction	Discussion has at the			
more <u>FJ158047</u>	Cortinarius Cortinarius alboviolace	Cortinariaceae (uncultured Cortinar	Poland Estonia	Ectomycorrhiza Fruitbody	Pinus sylvestris			
more <u>HQ285366</u>	Cortinarius	Cortinariaceae (uncultured Cortinar	United States	Ectomycorrhiza				
more <u>HQ022045</u>	Cortinarius	Cortinariaceae (uncultured Cortinar	United States	Soil fungal DNA				
more <u>KJ705149</u>		Cortinarius (Cortinarius alboviolac	Sinted States	iangai biin				
more FJ266726	Cortinarius	Cortinariaceae (uncultured Cortinar	United States	Ectomycorrhiza	Picea			
more JX316781		Cortinariaceae (uncultured Cortinar	United States	,				
more <u>KJ705148</u>		Cortinarius (Cortinarius alboviolac						
more UDB001122	Cortinarius alboviolace		Sweden	Fruitbody				
more <u>AJ549965</u>	Cortinarius	Cortinariaceae (uncultured Cortinar	Germany	Ectomycorrhiza	Betula pendula			
more <u>AY669657</u>		Cortinarius (Cortinarius alboviolac	Germany	Fruitbody				
more <u>JF907875</u>		Cortinarius (Cortinarius alboviolac	Italy					
🖉 more UDB011739	Cortinarius alboviolace	us	Estonia	Fruitbody				
MOre IIDR011755	Cortinarius alboviolace		Estonia	Fruitbody				
⁷ mc	Stand Call	The states	Canada	Fruitbody	Tsuga heterophylla			
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mc Salaria and Salaria		A A A A A	Estonia	Fruitbody				
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mc			Canada	Fruitbody				
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Communication of the species

Accession code of the Cortinarius xanthodryophilus SH:

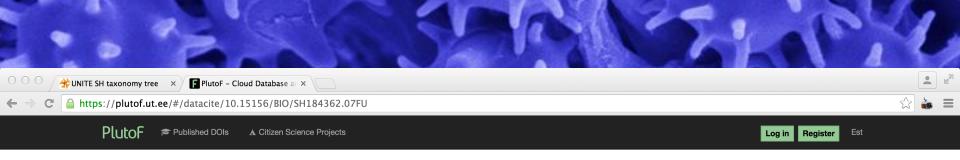
SH184362.07FU

is resolved with unique DOI (digital object identifier):

dx.doi.org/10.15156/BIO/SH184362.07FU

Version 7 includes 487 435 SHs and each of them have unique DOI





Cortinarius xanthodryophilus | SH184362.07FU

Reference sequence Distribution map Metadata Accession numbers HQ441244 ÷ Location 10.15156/BIO/SH184362.07FU Tuula Niskanen Chosen by Dataset Kõljalg, Urmas; Abarenkov, Kessy; Nilsson, Henrik; Larsson, 2014-11-09 23:04:52 Date Karl-Henrik; Aas, Anders Bjørnsgard; Adams, Rachel; Alves, Artur; Ammirati, Joseph F.; Arnold, A. Elizabeth; Bahram, Mohammad et al. (2015): SH184362.07FU. UNITE Taxonomy Community. 10.15156/BIO/SH184362.07FU Placement in classification Publisher Fungi; Basidiomycota; Agaricomycetes; Agaricales; **UNITE Community** Cortinariaceae; Cortinarius Published In See Cortinarius xanthodryophilus in Index Fungorum 2015 < Identifications Creators *Locations without exact coordinates are displayed as country Cortinarius xanthodryophilus (5); Urmas Kõljalg, Kessy Abarenkov, Henrik Nilsson, Karl-Henrik polygons Larsson, Anders Bjørnsgard Aas, Rachel Adams, Artur Alves, Joseph F. Ammirati, A. Elizabeth Arnold, Mohammad Bahram. Show more

Statistics	
Minimum distance to the closest SH	1.5
No. of sequences in SH	5
Distribution of distances	6
Digtribution of distances for SH184362.07FU (mothur v.1.34.4, pairwise.seqs)	1

ances (total count=10)

Ecology

Interacting taxa Quercus (1); Quercus douglasii (1);

Document(s)

SH184362.07FU_graph.png; SH184362.07FU.json;

Species Hypothesis pages version 7



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Display Settings: 🕑 GenBan	nk	Send to:		
			Change region shown	
Uncultured ector	mycorrhiza (Boletus) isolate 26 18S ribosomal RNA gen	e, partial		
sequence; intern	al transcribed spacer 1, 5.8S ribosomal RNA gene, and	internal		
transcribed spac	er 2, complete sequence; and 28S ribosomal RNA gene	. partial	Customize view	•
sequence		,		
•			Analyze this sequence	
GenBank: EF644121.1 FASTA Graphics PopSet			Run BLAST	_
FASTA Graphics Popset			Pick Primers	
<u>Go to:</u> ⊘			Highlight Sequence Features	
LOCUS EF644121	582 bp DNA linear ENV 01-OCT-2008			
	ectomycorrhiza (Boletus) isolate 26 18S ribosomal RNA		Find in this Sequence	
	ial sequence; internal transcribed spacer 1, 5.8S			
	RNA gene, and internal transcribed spacer 2, complete and 285 ribosomal RNA gene, partial sequence.		LinkOut to external resources	
ACCESSION EF644121	and 105 libobolar and gene, parerar sequence.		SILVA LSU Database	
	GI:157284042			[SILVA]
KEYWORDS ENV. SOURCE uncultured	Boletus		SH326509.06FU	
ORGANISM uncultured				[UNITE]
-	Fungi; Dikarya; Basidiomycota; Agaricomycotina;		related identifed ITS sequences	
	etes; Agaricomycetidae; Boletales; Boletineae; ; environmental samples.			[emerencia]
REFERENCE 1 (bases 1	1 to 582)			
	Peintner, U., Langer, I., Fitz, W.J. and Schweiger, P. hizal communities associated with Populus tremula growing		Related information	
	metal contaminated site		Related Sequences	_
-	. 112 (PT 9), 1069-1079 (2008)		PopSet	
PUBMED <u>18692376</u> REFERENCE 2 (bases 1	1 +0 582)		PubMed	
•	Peintner, U., Langer, I., Fitz, W. and Schweiger, P.			
TITLE Direct Subr			Taxonomy	
	(01-JUN-2007) Institute of Microbiology, University Technikerstrasse 25, Innsbruck 6020, Austria			
-	ocation/Qualifiers		Recent activity	
	582 organism="uncultured Boletus"			Furn Off Clear
	mol type="genomic DNA"		Uncultured ectomycorrhiza (Bo	letus) isolate
	isolate="26"		26 18S ribosomal RNA gene, p	
	isolation_source="ectomycorrhizal root tips of Populus remula growing in heavy metal contaminated site near			h
-	Temuta growing in heavy metal contaminated site heat			
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High-Throughput Seguencing projects

HTS sequences included in UNITE SH version 7



FJ152528		Leotiomycetes (unculturea	Canada	Ectomycorrniza	
<u>JX857198</u>		Fungi (uncultured fungus)	United States		
<u>JX857214</u>		Fungi (uncultured fungus)	United States		
<u>KC514890</u>		Sordariomycetes (Sordario			
<u>HQ611285</u>		Fungi (uncultured fungus)	Sweden		
KF274409		Fungi (uncultured fungus)	Finland		
<u>AM260917</u>	Helotiales	Fungi (uncultured fungus)	United Kingdom	Soil fungal DNA	
<u>HF947879</u>		Helotiales (uncultured He	Ireland		
<u>HF947876</u>		Helotiales (uncultured He	Ireland		
<u>KC965984</u>		Fungi (uncultured fungus)	United States		
<u>KF617245</u>		Fungi (uncultured fungus)	United States		RepSeq
<u>AB476482</u>	Helotiales	Fungi (uncultured fungus)	Sweden	Ericoid mycorrhiza	
UDB020841			Sweden	Soil fungal DNA	
<u>KF879483</u>		Pezizomycotina (unculture	United States		
<u>GU180254</u>	Helotiales	Ascomycota (uncultured As	United States	Ectomycorrhiza	
<u>DQ273331</u>	Helotiales	Pezizomycotina (unculture	United States	Ectomycorrhiza	
<u>FJ152527</u>		Leotiomycetes (uncultured	Canada	Ectomycorrhiza	
<u>HF947867</u>		Helotiales (uncultured He	Ireland		
<u>FN565266</u>	Helotiales	Helotiales (uncultured He	United Kingdom	Ectomycorrhiza	
<u>FN565265</u>	Helotiales	Helotiales (uncultured He	United Kingdom	Ectomycorrhiza	
EF445405	Helotiales	Fungi (uncultured fungus)	United Kingdom	Ericoid mycorrhiza	
<u>AM260813</u>		Fungi (uncultured fungus)	United Kingdom	Soil fungal DNA	
<u>AM292203</u>		Ascomycota (ascomycete sp	United Kingdom	Soil fungal DNA	
<u>AM260927</u>		Fungi (uncultured fungus)	United Kingdom	Soil fungal DNA	



-9- -1



Identification of species

Open Data / Open Access

All SHs are freely downloaded at unite.ut.ee For the inhouse analyses or for the building identification pipelines

HTS pipelines: QIIME, mothur, SCATA, CREST, UCHIME, UTAX.





Identification of species

All UNITE SH accession codes are connected to the Fungal classification.

It means OTUs will receive accession codes and will be connected to the classification even when species names are not available.





Thank you!

