

BLAST Results

[Questions/comments](#)

Job title: OL304248.1

RID [FD53FYMN013](#) (Expires on 08-14 01:57 am)

Query ID	Icl Query_47981	Database Name	nt
Description	None	Description	Nucleotide collection (nt)
Molecule type	dna	Program	BLASTN 2.13.0+
Query Length	333		

 Graphic Summary.



Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Equisetum arvense voucher MN01 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	616	616	100%	9e-172	100.00%	OL304248.1
Equisetum arvense voucher MN05 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	606	606	100%	5e-169	99.40%	OL304249.1
uncultured fungus genomic DNA sequence contains ITS1	601	601	100%	2e-167	99.10%	OW836430.1
Equisetum arvense voucher MN06 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	601	601	100%	2e-167	99.10%	OL304250.1
Chloroidium sp. FACHB-2422 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	601	601	100%	2e-167	99.10%	MT006211.1
Chloroidium saccharophilum genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, culture collection CCAP 211/31	595	595	100%	1e-165	98.81%	FR865664.1
Equisetum arvense voucher Equisetum_arvense_ITS.fasta_2 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	593	593	100%	4e-165	98.51%	MW040323.1
Equisetum arvense voucher 34008 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	593	593	100%	4e-165	98.51%	MW040322.1
Chloroidium saccharophilum strain FACHB-1796 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	590	590	100%	5e-164	98.51%	KX024689.1
uncultured Pezizaceae genomic DNA sequence contains ITS1	590	590	100%	5e-164	98.51%	OU496020.1
Equisetum arvense voucher Equisetum_arvense_ITS.fasta_1 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	590	590	100%	5e-164	98.21%	MW040324.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Unclassified Viridiplantae clone 1537 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	584	584	100%	3e-162	98.21%	MF570051.1
Chloroidium ellipsoideum isolate FG2/4.5E 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	584	584	100%	3e-162	98.21%	KM020071.1
Chloroidium saccharophilum isolate FG2/1.3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	584	584	100%	3e-162	98.21%	KM020070.1
Chloroidium saccharophilum var. saccharophilum strain UTEX247 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	584	584	100%	3e-162	98.21%	KJ676130.1
Chloroidium saccharophilum strain OD-1-1-C 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	584	584	100%	3e-162	98.21%	MT991539.1
Chloroidium ellipsoideum genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, culture collection CCAP 211/40	584	584	100%	3e-162	98.21%	FR865669.1
Chloroidium saccharophilum genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, culture collection CCAP 211/32	584	584	100%	3e-162	98.21%	FR865665.1
Chloroidium saccharophilum var. saccharophilum strain UTEX2469 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	573	573	100%	5e-159	97.61%	KJ676131.1
Chloroidium sp. FACHB-2420 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	573	573	100%	5e-159	97.61%	MT006209.1
Chloroidium saccharophilum strain ISBAL-007 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	569	569	94%	7e-158	99.06%	MH551492.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
'Chlorella' ellipsoidea strain Ce 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	568	568	100%	3e-157	97.31%	EU038292.1
Chlorella saccharophila partial 18S rRNA gene, ITS1, 5.8S rRNA, ITS2 and partial 28S rRNA gene, strain SAG 2120	558	558	94%	2e-154	98.43%	FM946008.1
Chlorella saccharophila partial 18S rRNA gene, ITS1, 5.8S rRNA, ITS2 and partial 28S rRNA gene, strain CCAP 211/42	558	558	94%	2e-154	98.43%	FM946004.1
Chlorella saccharophila partial 18S rRNA gene, ITS1, 5.8S rRNA, ITS2 and partial 28S rRNA gene, strain CCAP 211/36	558	558	94%	2e-154	98.43%	FM946003.1
Chloroidium saccharophilum strain CCAP 211/27 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	553	553	94%	7e-153	98.11%	MH551491.1
Chloroidium saccharophilum strain CCAP 211/40 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	553	553	94%	7e-153	98.11%	MH551490.1
Chlorella saccharophila partial 18S rRNA gene, ITS1, 5.8S rRNA, ITS2 and partial 28S rRNA gene, strain SAG 2197	553	553	94%	7e-153	98.11%	FM946010.1
Chlorella saccharophila partial 18S rRNA gene, ITS1, 5.8S rRNA, ITS2 and partial 28S rRNA gene, strain SAG 211-1c	553	553	94%	7e-153	98.11%	FM946007.1
Chlorella saccharophila partial 18S rRNA gene, ITS1, 5.8S rRNA, ITS2 and partial 28S rRNA gene, strain CCAP 211/32	553	553	94%	7e-153	98.11%	FM946001.1
Chlorella sp. UTEX 2068 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	549	549	96%	9e-152	97.52%	KJ676132.1
Chloroidium saccharophilum genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, culture collection CCAP 211/58	549	549	100%	9e-152	96.42%	FR865677.1
Chloroidium saccharophilum strain Fall/B-1b 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	547	547	94%	3e-151	97.80%	MH551489.1
Chloroidium saccharophilum strain SAG 2055 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	547	547	94%	3e-151	97.80%	MH551488.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Chloroidium saccharophilum strain KMMCC 192 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	545	545	93%	1e-150	98.09%	JQ315766.1
Chlorella saccharophila partial 18S rRNA gene, ITS1, 5.8S rRNA, ITS2 and partial 28S rRNA gene, strain SAG 211-1b	545	545	94%	1e-150	97.80%	FM946005.1
Uncultured alga genes for 5.8S rRNA, ITS2, 28S rRNA, partial and complete sequence, note: OTU163	542	542	93%	2e-149	97.78%	LC381753.1
Chlorella saccharophila partial 18S rRNA gene, ITS1, 5.8S rRNA, ITS2 and partial 28S rRNA gene, strain SAG 211-9a	542	542	94%	2e-149	97.48%	FM946000.1
Chloroidium saccharophilum strain KMMCC 158 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	531	531	98%	3e-146	95.47%	JQ315771.1
Chloroidium saccharophilum strain KMMCC 195 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	527	527	91%	4e-145	97.72%	JQ315769.1
Chloroidium saccharophilum strain CCAP 264/2 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	523	523	94%	6e-144	96.54%	MH551493.1
Uncultured Chloroidium isolate A207 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	523	523	90%	6e-144	97.70%	KP314644.1
Uncultured Chloroidium isolate A103 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	523	523	90%	6e-144	97.70%	KP314563.1
Chloroidium saccharophilum strain St6 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	521	521	90%	2e-143	97.70%	OM472016.1
Chloroidium saccharophilum strain ACSSI 340 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	521	521	90%	2e-143	97.70%	MT827198.1
Chloroidium saccharophilum strain ACSSI 339 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	521	521	90%	2e-143	97.70%	MT827197.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Chloroidium saccharophilum strain CCM-UDEC 143 18S ribosomal RNA gene, partial sequence; and internal transcribed spacer 1, 5S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence	520	520	88%	7e-143	98.32%	KC517116.1
Chloroidium saccharophilum strain CCAP 211/58 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	518	518	94%	3e-142	96.23%	MH551494.1
Uncultured Chloroidium isolate A214 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	518	518	90%	3e-142	97.38%	KP314651.1
Uncultured Chloroidium isolate A032 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	518	518	90%	3e-142	97.38%	KP314515.1
Uncultured Chloroidium isolate A029 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	518	518	90%	3e-142	97.38%	KP314513.1
Uncultured Chloroidium isolate A011 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	518	518	90%	3e-142	97.38%	KP314497.1
Chloroidium saccharophilum genomic DNA sequence contains 5.8S rRNA gene, ITS2, strain Chlorella saccharophila RNY	516	516	88%	9e-142	97.99%	LR215745.1
Uncultured Chloroidium isolate A023 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	510	510	90%	4e-140	97.05%	KP314508.1
Uncultured Chloroidium isolate A141 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	505	505	90%	2e-138	96.72%	KP314596.1
Uncultured Chloroidium isolate A217 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	499	499	90%	9e-137	96.39%	KP314654.1
'Chlorella' saccharophila voucher UTEX 247 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	492	492	91%	2e-134	95.48%	EF120783.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Chloroidium saccharophilum voucher Herbarium Tuerk51488 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	490	490	84%	6e-134	97.89%	KF907674.1
Chloroidium saccharophilum voucher Herbarium Tuerk51481 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	490	490	84%	6e-134	97.89%	KF907673.1
Chloroidium saccharophilum voucher Herbarium Tuerk51492 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	484	484	84%	3e-132	97.54%	KF907675.1
Chloroidium saccharophilum voucher Herbarium Tuerk51480 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	484	484	84%	3e-132	97.54%	KF907672.1
'Chlorella' saccharophila voucher UTEX 2911 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	464	464	81%	3e-126	97.45%	EF120782.1
Chloroidium sp. S4MWC-51 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence	455	455	78%	2e-123	97.74%	MK005103.1
Uncultured Chloroidium isolate A026 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	418	418	90%	3e-112	91.50%	KP314510.1
'Chlorella' saccharophila voucher UTEX 2469 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	403	403	70%	8e-108	97.47%	EF120784.1
Chloroidium saccharophilum strain KMMCC 192 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	346	346	58%	1e-90	98.48%	JQ315767.1
Uncultured alga isolate ASV_573_A 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	276	276	100%	2e-69	81.84%	ON119385.1
Chloroidium viscosum strain MG-2 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	244	244	94%	5e-60	80.94%	MH551496.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Chloroidium angustoellipsoideum voucher VancurovaA356 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	244	244	100%	5e-60	81.45%	MH415249.1
uncultured fungus genomic DNA sequence contains ITS1	239	239	100%	2e-58	79.94%	OW836154.1
Chloroidium lichenum strain BII/C-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	235	235	76%	3e-57	83.96%	MH551507.1
Chloroidium lichenum strain MG-4 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	235	235	76%	3e-57	83.96%	MH551506.1
Chloroidium lichenum strain BII/B-9 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	235	235	76%	3e-57	83.96%	MH551505.1
Uncultured Chlorella clone CM-E-A25 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	235	235	76%	3e-57	83.96%	KJ489091.1
Chlorella angustoellipsoidea partial 18S rRNA gene, ITS1, 5.8S rRNA, ITS2 and partial 28S rRNA gene, strain SAG 2115	235	235	76%	3e-57	83.96%	FM946019.1
Chlorella angustoellipsoidea partial 18S rRNA gene, ITS1, 5.8S rRNA, ITS2 and partial 28S rRNA gene, strain SAG 2144	235	235	76%	3e-57	83.96%	FM946020.1
Chloroidium lichenum strain SAG 2293 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	231	231	53%	4e-56	90.50%	MH551510.1
Chloroidium lichenum strain SAG 2294 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	231	231	53%	4e-56	90.50%	MH551509.1
Chloroidium sp. LV-2018 voucher VancurovaA503 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	231	305	65%	4e-56	90.50%	MH415295.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Chloroidium sp. LV-2018 voucher VancurovaA318 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	231	231	53%	4e-56	90.50%	MH415228.1
Chloroidium angustoeilipsoideum voucher VancurovaA421.2 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	228	310	67%	5e-55	90.45%	MH415277.1
Chloroidium ellipsoideum voucher RidkaNZ23 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	228	228	53%	5e-55	90.45%	MH415207.1
Uncultured alga genes for 5.8S rRNA, ITS2, 28S rRNA, partial and complete sequence, note: OTU71	228	228	53%	5e-55	89.62%	LC381752.1
Chloroidium lichenum strain SAG 2141 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	226	226	53%	2e-54	90.00%	MH551512.1
Chloroidium orientale strain VCA-45 (Ce2E) 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	226	226	94%	2e-54	80.29%	MZ558750.1
Chloroidium lichenum strain QII/C-5b 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	224	224	53%	6e-54	89.44%	MH551508.1
Chloroidium sp. LV-2018 voucher VancurovaO29 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	224	301	90%	6e-54	83.59%	MH415404.1
Chloroidium lichenum voucher A114 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	224	224	53%	6e-54	89.89%	OL625124.1
Chloroidium sp. LV-2018 voucher VancurovaO27 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	222	305	67%	2e-53	89.89%	MH415402.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Chloroidium lichenum strain CCAP 211/33 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, region	219	219	53%	3e-52	89.39%	MH551518.1
Chloroidium lichenum strain SAG 2295 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	219	219	75%	3e-52	83.21%	MH551517.1
Chloroidium sp. Ru-6-6 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	219	295	67%	3e-52	89.39%	MH703747.1
Chloroidium sp. SY-1-2-B 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	219	219	53%	3e-52	89.39%	MT991543.1
Chloroidium sp. NN-2-O 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	219	295	67%	3e-52	89.39%	MT991540.1
Chloroidium ellipsoideum genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, culture collection CCAP 211/33	219	295	67%	3e-52	89.39%	FR865666.1
Chloroidium ellipsoideum voucher Z7 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	217	217	53%	1e-51	89.33%	OL625378.1
Chloroidium ellipsoideum voucher A689 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	217	217	53%	1e-51	89.33%	OL625330.1
Chloroidium lichenum voucher A67_6 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	217	217	53%	1e-51	89.33%	OL625329.1
Chloroidium lichenum voucher A67_5 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	217	294	68%	1e-51	89.33%	OL625328.1
Chloroidium ellipsoideum voucher A67_4 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	217	217	53%	1e-51	89.33%	OL625327.1

Alignments

Equisetum arvense voucher MN01 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: **OL304248.1** Length: 333 Number of Matches: 1

Range 1: 1 to 333

Score	Expect	Identities	Gaps	Strand	Frame
616 bits(333)	9e-172()	333/333(100%)	0/333(0%)	Plus/Plus	

Features:

Query	1	TGCAGAATTC	CGTGAATCATCGAGTCTTTGAACGCATATTGCGCCGGAGGCTTCGGTCAA	60
Sbjct	1	TGCAGAATTC	CGTGAATCATCGAGTCTTTGAACGCATATTGCGCCGGAGGCTTCGGTCAA	60
Query	61	GGGCATGTCTGCCTCAGCGTCGGTTGACCCCTCTCGTCCAATTCCTCGGGAAGCAGACG	120	
Sbjct	61	GGGCATGTCTGCCTCAGCGTCGGTTGACCCCTCTCGTCCAATTCCTCGGGAAGCAGACG	120	
Query	121	GACCTGGCAGTCCCGCTGGCGACAGCGGGTCTGCTGCAGAACAGACGACGAGCCAGCCGC	180	
Sbjct	121	GACCTGGCAGTCCCGCTGGCGACAGCGGGTCTGCTGCAGAACAGACGACGAGCCAGCCGC	180	
Query	181	AGCGCCGCTCGATTGGAGGTTTTCTCCGGAAGACATGCCGTCGAGTAGCCTGGGGACCAA	240	
Sbjct	181	AGCGCCGCTCGATTGGAGGTTTTCTCCGGAAGACATGCCGTCGAGTAGCCTGGGGACCAA	240	
Query	241	CTGCCCCGTCTACCAACGACGGGGAGCGCGCAAGCCATCCCCCTGACTCTCATTTGAC	300	
Sbjct	241	CTGCCCCGTCTACCAACGACGGGGAGCGCGCAAGCCATCCCCCTGACTCTCATTTGAC	300	
Query	301	CTGAGTTCAGGCAAGACCACCCGCTCAACTTAA	333	
Sbjct	301	CTGAGTTCAGGCAAGACCACCCGCTCAACTTAA	333	

Equisetum arvense voucher MN05 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: **OL304249.1** Length: 335 Number of Matches: 1

Range 1: 1 to 335

Score	Expect	Identities	Gaps	Strand	Frame
606 bits(328)	5e-169()	333/335(99%)	2/335(0%)	Plus/Plus	

Features:

Query	1	TGCAGAAATCCGTGAATCATCGAGTCTTTGAACGCATATTGCGCCGGAGGCTTCGGTCAA	60
Sbjct	1	TGCAGAATTCCGTGAATCATCGAGTCTTTGAACGCATATTGCGCCGGAGGCTTCGGTCAA	60
Query	61	GGGCATGTCTGCCTCAGCGTCGGTTGACCCCTCTCGTCCAATTCCCTCG-GGAAGCAGAC	119
Sbjct	61	GGGCATGTCTGCCTCAGCGTCGGTTGACCCCTCTCGTCCAATTCCCTCGAGGAAGCAGAC	120
Query	120	GGACCTGGCAGTCCCCTGGCGACAGCGGGTCTGCTGCAGAACAGACGACGAGCCAGCCG	179
Sbjct	121	GGACCTGGCAGTCCCCTGGCGACAGCGGGTCTGCTGCAGAACAGACGACGAGCCAGCCG	180
Query	180	CAGCGCCGCTCGATTGG-AGGTTTTCTCCGGAAGACATGCCGTCGAGTAGCCTGGGGACC	238
Sbjct	181	CAGCGCCGCTCGATTGGTAGGTTTTCTCCGGAAGACATGCCGTCGAGTAGCCTGGGGACC	240
Query	239	AACTGCCCGTCTACCAACGACGGGGAGCGCGCAAGCCATCCCCCTGACTCTCATTTG	298
Sbjct	241	AACTGCCCGTCTACCAACGACGGGGAGCGCGCAAGCCATCCCCCTGACTCTCATTTG	300
Query	299	ACCTGAGTTCAAGGCAAGACCACCCGCTCAACTTAA	333
Sbjct	301	ACCTGAGTTCAAGGCAAGACCACCCGCTCAACTTAA	335

uncultured fungus genomic DNA sequence contains ITS1

Sequence ID: **OW836430.1** Length: 358 Number of Matches: 1

Range 1: 24 to 358

Score	Expect	Identities	Gaps	Strand	Frame
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Score	Expect	Identities	Gaps	Strand	Frame
601 bits(325)	2e-167()	332/335(99%)	2/335(0%)	Plus/Plus	
Features:					
Query 1	TGCAGAAATTC	CGTGAATCATCGAGTCTTTGAACGCATATTGCGCCGAGGCTTCGGTCAA	60		
Sbjct 24	TGCAGAAATTC	CGTGAATCATCGAGTCTTTGAACGCATATTGCGCCGAGGCTTCGGTCAA	83		
Query 61	GGGCATGTCTG	CGCTCAGCGTCGGTTGACCCCTCTCGTCCAATTCCCTCG-GGAAGCAGAC	119		
Sbjct 84	GGGCATGTCTG	CGCTCAGCGTCGGTTGACCCCTCTCGTCCAATTCCCTCGTGAAGCAGAC	143		
Query 120	GGACCTGGCAGT	CCCGCTGGCGACAGCGGGTCTGCTGCAGAACAGACGACGAGCCAGCCG	179		
Sbjct 144	GGACCTGGCAGT	CCCGCTGGCGACAGCGGGTCTGCTGCAGAACAGACGACGAGCCAGCCG	203		
Query 180	CAGCGCCGCTC	GATTGG-AGGTTTTCTCCGGAAGACATGCCGTCGAGTAGCCTGGGGACC	238		
Sbjct 204	CAGCGCCGCTC	GATTGGTAGGTTTTCTCCGGAAGACATGCCGTCGAGTAGCCTGGGGACC	263		
Query 239	AACTGCCCCGT	CCTACCAACGACGGGGGAGCGCGCAAGCCATCCCCCTGACTCTCATTTCG	298		
Sbjct 264	AACTGCCCCGT	CCTACCAACGACGGGGGAGCGCGCAAGCCATCCCCCTGACTCTCATTTCG	323		
Query 299	ACCTGAGTTCA	GAGCAAGACCACCCGCTCAACTTAA	333		
Sbjct 324	ACCTGAGTTCA	GAGCAAGACCACCCGCTCAACTTAA	358		

Equisetum arvense voucher MN06 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: **OL304250.1** Length: 335 Number of Matches: 1
Range 1: 1 to 335

Score	Expect	Identities	Gaps	Strand	Frame
601 bits(325)	2e-167()	332/335(99%)	2/335(0%)	Plus/Plus	
Features:					
Query 1	TGCAGAAATTC	CGTGAATCATCGAGTCTTTGAACGCATATTGCGCCGAGGCTTCGGTCAA	60		
Sbjct 1	TGCAGAAATTC	CGTGAATCATCGAGTCTTTGAACGCATATTGCGCCGAGGCTTCGGTCAA	60		
Query 61	GGGCATGTCTG	CGCTCAGCGTCGGTTGACCCCTCTCGTCCAATTCCCTCG-GGAAGCAGAC	119		
Sbjct 61	GGGCATGTCTG	CGCTCAGCGTCGGTTGACCCCTCTCGTCCAATTCCCTCGTGAAGCAGAC	120		
Query 120	GGACCTGGCAGT	CCCGCTGGCGACAGCGGGTCTGCTGCAGAACAGACGACGAGCCAGCCG	179		
Sbjct 121	GGACCTGGCAGT	CCCGCTGGCGACAGCGGGTCTGCTGCAGAACAGACGACGAGCCAGCCG	180		
Query 180	CAGCGCCGCTC	GATTGG-AGGTTTTCTCCGGAAGACATGCCGTCGAGTAGCCTGGGGACC	238		
Sbjct 181	CAGCGCCGCTC	GATTGGAAGGTTTTCTCCGGAAGACATGCCGTCGAGTAGCCTGGGGACC	240		
Query 239	AACTGCCCCGT	CCTACCAACGACGGGGGAGCGCGCAAGCCATCCCCCTGACTCTCATTTCG	298		
Sbjct 241	AACTGCCCCGT	CCTACCAACGACGGGGGAGCGCGCAAGCCATCCCCCTGACTCTCATTTCG	300		
Query 299	ACCTGAGTTCA	GAGCAAGACCACCCGCTCAACTTAA	333		
Sbjct 301	ACCTGAGTTCA	GAGCAAGACCACCCGCTCAACTTAA	335		

Chloroidium sp. FACHB-2422 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: **MT006211.1** Length: 3787 Number of Matches: 1
Range 1: 2888 to 3222

Score	Expect	Identities	Gaps	Strand	Frame
601 bits(325)	2e-167()	332/335(99%)	2/335(0%)	Plus/Plus	
Features:					
Query 1	TGCAGAAATTC	CGTGAATCATCGAGTCTTTGAACGCATATTGCGCCGAGGCTTCGGTCAA	60		
Sbjct 2888	TGCAGAAATTC	CGTGAATCATCGAGTCTTTGAACGCATATTGCGCCGAGGCTTCGGTCAA	2947		
Query 61	GGGCATGTCTG	CGCTCAGCGTCGGTTGACCCCTCTCGTCCAATTCCCTCG-GGAAGCAGAC	119		

Sbjct	2948	GGGCATGTCTGCCTCAGCGTCGGTTGACCCCTCTCGTCCAATTCCTCGTGGGAAGCAGAC	3007
Query	120	GGACCTGGCAGTCCCCTGGCGACAGCGGGTCTGCTGCAGAACAGACGACGAGCCAGCCG	179
Sbjct	3008	GGACCTGGCAGTCCCCTGGCGACAGCGGGTCTGCTGCAGAACAGACGACGAGCCAGCCG	3067
Query	180	CAGCGCCGCTCGATTGG-AGGTTTTCTCCGGAAGACATGCCGTCGAGTAGCCTGGGGACC	238
Sbjct	3068	CAGCGCCGCTCGATTGGTAGGTTTTCTCCGGAAGACATGCCGTCGAGTAGCCTGGGGACC	3127
Query	239	AACTGCCCCTCTACCAACGACGGGGAGCGCGCAAGCCATCCCCCTGACTCTCATTTCG	298
Sbjct	3128	AACTGCCCCTCTACCAACGACGGGGAGCGCGCAAGCCATCCCCCTGACTCTCATTTCG	3187
Query	299	ACCTGAGTTCAGGCAAGACCACCCGCTCAACTTAA	333
Sbjct	3188	ACCTGAGTTCAGGCAAGACCACCCGCTCAACTTAA	3222

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