

BLAST Results

[Questions/comments](#)

Job title: DQ377155.1

RID [FD4CKFVU016](#) (Expires on 08-14 01:44 am)

Query ID	Icl Query_53701	Database Name	nt
Description	None	Description	Nucleotide collection (nt)
Molecule type	dna	Program	BLASTN 2.13.0+
Query Length	294		

Graphic Summary.



Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Equisetum variegatum subsp. variegatum internal transcribed spacer 1, partial sequence	544	544	100%	4e-150	100.00%	DQ377155.1
Equisetum ramosissimum isolate BTPS123 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	510	510	100%	4e-140	97.96%	ON685433.1
Equisetum ramosissimum isolate BTPS056 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	494	494	100%	4e-135	96.95%	OM670239.1
Equisetum variegatum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	488	488	93%	2e-133	98.55%	EU328340.1
Equisetum variegatum voucher B. Hoshizaki 592 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	484	484	93%	2e-132	98.18%	EU372664.1
Equisetum x ferrissii 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	466	466	93%	8e-127	96.73%	EU328338.1
Equisetum laevigatum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	460	460	93%	4e-125	96.00%	EU328341.1
Equisetum hyemale subsp. affine 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	444	444	93%	4e-120	95.27%	EU328339.1
Equisetum hyemale subsp. hyemale internal transcribed spacer 1, partial sequence	431	431	88%	3e-116	96.54%	DQ377151.1
Equisetum hyemale subsp. affine 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	424	424	93%	5e-114	93.82%	EU328336.1
Equisetum variegatum voucher B. Hoshizaki 203 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	422	422	93%	2e-113	93.82%	EU372665.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Equisetum ramosissimum 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	418	418	89%	2e-112	95.42%	AF448794.1
Equisetum hyemale genes for ITS1, 5.8S rRNA, ITS2, partial sequence, bio_material: KB:NIBR0000051239	401	401	84%	2e-107	95.95%	AB817880.1
Equisetum scirpoides voucher P. Hammond s.n 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	385	385	93%	2e-102	90.55%	EU372663.1
Equisetum myriochaetum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	372	372	93%	2e-98	90.55%	EU328337.1
Equisetum x meridionale internal transcribed spacer 1, partial sequence	350	350	71%	9e-92	96.68%	DQ377156.1
Equisetum x moorei internal transcribed spacer 1, partial sequence	342	342	71%	1e-89	96.17%	DQ377157.1
Equisetum ramosissimum subsp. ramosissimum internal transcribed spacer 1, partial sequence	331	331	70%	3e-86	95.65%	DQ377153.1
Equisetum ramosissimum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	292	292	70%	1e-74	91.75%	EU328343.1
Equisetum telmateia isolate DM233 small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, region	193	193	44%	2e-44	93.13%	MT784095.1
Pleopeltis macrocarpa voucher H. Shang SG1191 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	121	121	30%	7e-23	91.21%	MZ361029.1
Microsorium steerei voucher R. Wei WR0620 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	121	121	30%	7e-23	91.21%	MZ361020.1
Leptochilus pteropus voucher R. Wei WR0281 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	121	121	30%	7e-23	91.21%	MZ361018.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Leptochilus insignis voucher R. Wei & al., 440 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	121	121	30%	7e-23	91.21%	MZ361017.1
Campyloneurum sphenodes voucher P.C. Standley 34246 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	121	121	30%	7e-23	91.21%	MZ360986.1
Bosmania membranacea subsp. carinata voucher R. Wei WR0410 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	121	121	30%	7e-23	91.21%	MZ360985.1
Bosmania membranacea var. membranacea voucher R. Wei WR0368 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	121	121	30%	7e-23	91.21%	MZ360984.1
Pellaea breweri isolate CBP242 18S ribosomal RNA gene, partial sequence; and internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence	117	117	30%	1e-21	90.11%	MF963964.1
Hovenkampia schimperiana voucher B. Liu CPG27233 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	117	117	26%	1e-21	93.75%	MZ361042.1
Microsorium punctatum voucher Mt. Shiwan Exp. 148 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	117	117	26%	1e-21	93.75%	MZ361019.1
Lellingeria brevistipes voucher P. Labiak 2007 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	117	117	30%	1e-21	90.11%	MZ361001.1
Oreogrammitis congener voucher R. Wei & al. 523 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	117	117	30%	1e-21	90.11%	MZ360999.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Oreogrammitis sp. RW-2021b voucher H.M. Liu B294 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	117	117	30%	1e-21	90.11%	MZ360998.1
Oreogrammitis dorsipila voucher J.S. Kang 1201-11 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	117	117	30%	1e-21	90.11%	MZ360997.1
Prosaptia venulosa voucher R. Wei 246 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	117	117	30%	1e-21	90.11%	MZ360989.1
Thylacopteris papillosa voucher R. Wei 345 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361053.1
Serpocaulon loriceum voucher R.M. Rueda & al. 14546 (PE) small subunit ribosomal RNA gene, partial sequence; and internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361048.1
Selliguea metacoela voucher R. Wei 2925 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361045.1
Selliguea albidoglauca voucher X.C. Zhang 7609 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361043.1
Pyrrosia penangiana voucher R. Wei 3014 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361041.1
Pyrrosia angustata voucher Q. Wei wq004 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361040.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Polypodium vulgare voucher B. Liu 28227 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361039.1
Polypodium sibiricum voucher Zhang 7312 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361038.1
Polypodium rhodopleuron voucher A.M. Evans & al. 2871 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361037.1
Polypodium arcanum voucher M. Sundue & al. 3554 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361036.1
Goniophlebium niponicum voucher H.M. Liu A305 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361035.1
Selliguea griffithiana voucher X.C. Zhang 9580 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361025.1
Selliguea crenatopinnata voucher X.C. Zhang 6242 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361024.1
Selliguea chenopus voucher X.C. Zhang 6259 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361023.1
Microgramma vacciniifolia voucher C.X. Li RS281 small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361014.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Leptochilus macrophyllus voucher R. Wei & al., 441 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ361009.1
Goniophlebium formosanum voucher X.C. Zhang 9432 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ360995.1
Aglaomorpha willdenowii voucher X.C. Zhang 9062 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ360993.1
Leptochilus ellipticus voucher R. Wei WR0211 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ360987.1
Selliguea capitellata voucher X.C. Zhang 6341 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ360982.1
Selliguea mairei voucher X.C. Zhang 4609 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ360981.1
Selliguea lehmannii voucher X.C. Zhang 5963 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ360980.1
Drynaria heraclea voucher R. Wei 470 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	115	115	30%	3e-21	90.11%	MZ360979.1
Equisetum sylvaticum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	115	115	22%	3e-21	98.46%	EU328342.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Drepanolejeunea angustifolia voucher Zhu & Wei 20110418-65A 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	113	113	25%	1e-20	94.67%	MH680792.1
Pleopeltis polypodioides voucher H. Shang 28B (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	113	113	30%	1e-20	89.01%	MZ361030.1
Platyserium bifurcatum voucher X.P. Wei 41503 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	111	111	26%	4e-20	92.50%	MZ361028.1
Niphidium crassifolium voucher WR0621 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	111	111	30%	4e-20	89.01%	MZ361021.1
Drynaria parishii voucher X.C. Zhang 7946 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	111	111	26%	4e-20	92.50%	MZ360992.1
Drynaria speciosa voucher R. Wei 508 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	111	111	26%	4e-20	92.50%	MZ360978.1
Asplenium scolopendrium isolate Copy2 voucher Vogel SCOL-175 Italy internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	111	111	30%	4e-20	89.01%	JX475163.1
Asplenium adulterinum isolate Copy1 voucher Vogel ADU-32 Norway internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	111	111	30%	4e-20	89.01%	JX475149.1
Scapania undulata Shevock et al. 29009 (GOET) 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	111	111	30%	4e-20	89.13%	JN631489.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Scapania undulata Schaefer-Verwimp & Verwimp 25913 (GOET) 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	111	111	30%	4e-20	89.13%	JN631485.1
Scapania undulata Schaefer-Verwimp & Verwimp 27551 (GOET) 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	111	111	30%	4e-20	89.13%	JN631484.1
Scapania cuspiduligera Gradstein 7828 (GOET) 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	111	111	30%	4e-20	89.13%	JN631408.1
Serpocaulon levigatum voucher R. Rojas & G. Ortiz 5315 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361047.1
Serpocaulon fraxinifolium voucher G. Hatschbach & al. 73838 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361046.1
Goniophlebium amoenum voucher Z.Y. Li 1897 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361034.1
Goniophlebium mengtzeense voucher H.M. Liu GX211 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361033.1
Goniophlebium argutum voucher R. Wei ST465 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361032.1
Pleurosoriopsis makinoi voucher X.C. Zhang 9478 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361031.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Microsorium cuspidatum voucher X.C. Zhang 4918 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361027.1
Goniophlebium manmeiense voucher X.P. Qi Q061 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361013.1
Leptochilus decurrens voucher R. Wei WR0267 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361008.1
Lepisorus schraderi voucher X.C. Zhang 9057 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361007.1
Lepisorus longifolius voucher R. Wei SIWI4 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361006.1
Lepisorus clathratus voucher Voucher unknown small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361004.1
Lepisorus hederaceus voucher Voucher unknown small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361003.1
Selliguea dareiformis voucher R. Wei ST1108 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ361000.1
Goniophlebium persicifolium voucher X.C. Zhang 433 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ360996.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Lepisorus miyoshianus voucher X.C. Zhang 4511 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ360991.1
Leptochilus henryi voucher X.C. Zhang 7487 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ360988.1
Lepisorus spicatus voucher R. Wei 29 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ360983.1
Adetogramma chrysolepis voucher Alfredo Tupayachi H. 758 (A) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	110	110	30%	2e-19	89.01%	MZ360977.1
Asplenium trichomanes isolate Copy2 voucher Wood s.n. Hawaii internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	110	110	32%	2e-19	87.63%	JX475165.1
Dictymia brownii voucher R. Coveny 10858 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	108	108	26%	6e-19	91.25%	MZ360990.1
Terpsichore aspleniifolia voucher R.M. Rueda & al. 14728 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	106	106	30%	2e-18	87.91%	MZ361052.1
Selliguea taeniata voucher B.Y. Sun & al. 36 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	106	106	30%	2e-18	88.17%	MZ361026.1
Micropolypodium sikkimense voucher Z.Y. Li 2763 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	106	106	30%	2e-18	87.91%	MZ361016.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Micropolypodium okuboi voucher X.C. Zhang 6000 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	106	106	30%	2e-18	87.91%	MZ361015.1
Melpomene flabelliformis voucher M. Sundue 3920 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	106	106	30%	2e-18	88.04%	MZ361012.1
Loxogramme lankokiensis voucher H.M. Liu LHM1938 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	106	106	26%	2e-18	91.25%	MZ361011.1
Loxogramme avenia voucher R. Wei 2761 (PE) small subunit ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	106	106	26%	2e-18	91.25%	MZ361010.1
Isoetes echinospora isolate ITV11767 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	106	106	24%	2e-18	93.15%	MW254978.1

Alignments

Equisetum variegatum subsp. variegatum internal transcribed spacer 1, partial sequence

Sequence ID: **DQ377155.1** Length: 294 Number of Matches: 1

Range 1: 1 to 294

Score	Expect	Identities	Gaps	Strand	Frame
544 bits(294)	4e-150()	294/294(100%)	0/294(0%)	Plus/Plus	
Features:					
Query 1	TCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTGTCACACATCCGTGCAAA	60			
Sbjct 1	TCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTGTCACACATCCGTGCAAA	60			
Query 61	CCCTGCGAACCGTGGACGTCCCCAAGGGGGCGGTGGTTGTGGTGCCTGCGCCCTC	120			
Sbjct 61	CCCTGCGAACCGTGGACGTCCCCAAGGGGGCGGTGGTTGTGGTGCCTGCGCCCTC	120			
Query 121	GCGGGCGTGGGTGCGGTGCGGCGCCCGTCCCTCCTCTCGGTGCTCCGGCGGCCgggg	180			
Sbjct 121	GCGGGCGTGGGTGCGGTGCGGCGCCCGTCCCTCCTCTCGGTGCTCCGGCGGCCGGGG	180			
Query 181	gggTCGAACCTTCCGCCCCCTCCGGGGCGTGGAGCACTCTTGAACGCGCACCGCCTGAG	240			
Sbjct 181	GGGTTCGAACCTTCCGCCCCCTCCGGGGCGTGGAGCACTCTTGAACGCGCACCGCCTGAG	240			
Query 241	ACTCCCCGCAAGGGGGAACACGAAAAAACGAGAACGACTCTCGGCAACGGATA	294			
Sbjct 241	ACTCCCCGCAAGGGGGAACACGAAAAAACGAGAACGACTCTCGGCAACGGATA	294			

Equisetum ramosissimum isolate BPTPS123 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: **ON685433.1** Length: 3702 Number of Matches: 1
Range 1: 1502 to 1795

Score	Expect	Identities	Gaps	Strand	Frame
510 bits(276)	4e-140()	288/294(98%)	0/294(0%)	Plus/Plus	
Features:					
Query 1	TCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTGTACACATCCGTGCAAA	60			
Sbjct 1502	TCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTGTACACATCCGTGCAAA	1561			
Query 61	CCCTGCGAACCGTGGACGTCCCCAAGGGGGCGGTGGTTGTGGTGCCCGCTTGCGCCCTC	120			
Sbjct 1562	CCATGCGAACCGTGGACGTCCCTCAAGAGGGCGGTGGTTGTGGTGCCCGCTTGCGCCCTT	1621			
Query 121	GCGGGCGTGGGTGCGGTGCGGCGCCCCGTCCCCTCCTCTCGGTGCTCCGGCGGCCgggg	180			
Sbjct 1622	GCGGGCGTGGGTGCGGTGCGGCGCCCCGTCCCCTCCTCTCGGCCGCTCCGGCGGCCGGGG	1681			
Query 181	gggTCGAACCTTCCGCCCCCTCCGGGGCGTGGAGCACTCTTGAACGCGCACCGCCTGAG	240			
Sbjct 1682	GGGTGGAACCTTCCGCCCCCGGGGGCGTGGAGCACTCTTGAACGCGCACCGCCTGAG	1741			
Query 241	ACTCCCCGCAAGGGGGAACACGAAAAACGAGAACGACTCTCGGCAACGGATA	294			
Sbjct 1742	ACTCCCCGCAAGGGGGAACACGAAAAACGAGAACGACTCTCGGCAACGGATA	1795			

Equisetum ramosissimum isolate BPTPS056 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: **OM670239.1** Length: 3631 Number of Matches: 1
Range 1: 1458 to 1752

Score	Expect	Identities	Gaps	Strand	Frame
494 bits(267)	4e-135()	286/295(97%)	1/295(0%)	Plus/Plus	
Features:					
Query 1	TCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTGTACACATCCGTGCAAA	60			
Sbjct 1458	TCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTGTACACATCCGTGCAAA	1517			
Query 61	CCCTGCGAACCGTGGACGTCCCCAAGGGGGCGGTGGTTGTGGTGCCCGCTTGCGCCCTC	120			
Sbjct 1518	CCCTGTGAACCGTGGATGTCCCCAAGGGGGCGGTGGTTGTGGTGCCCGCTTGCGCCCTC	1577			
Query 121	GCGGGCGTGGGTGCGGTGCGGCG-CCCCGTCCCCTCCTCTCGGTGCTCCGGCGGCCggg	179			
Sbjct 1578	GCGGGCGTGGGTGTGGTGCGGCGCCCCCTCCCCTCCTTTCGGTGCTCCGGCGGCCGGG	1637			
Query 180	ggggTCGAACCTTCCGCCCCCTCCGGGGCGTGGAGCACTCTTGAACGCGCACCGCCTGA	239			
Sbjct 1638	GGGTTCGAACCTTCCGCCCCCTCCGGGGCGTGGAGCACTCTTGAACGCGCACCGCCTGA	1697			
Query 240	GACTCCCCGCAAGGGGGAACACGAAAAACGAGAACGACTCTCGGCAACGGATA	294			
Sbjct 1698	GACTCCCCGCAAGGGGGAACACGAAAAACGAGAACGACTCTCGGCAACGGATA	1752			

Equisetum variegatum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence
Sequence ID: **EU328340.1** Length: 305 Number of Matches: 1
Range 1: 1 to 275

Score	Expect	Identities	Gaps	Strand	Frame
488 bits(264)	2e-133()	271/275(99%)	0/275(0%)	Plus/Plus	
Features:					
Query 20	GGTGAACCTGCGGAAGGATCATTGTACACATCCGTGCAAACCTGCGAACCGTGGACGT	79			
Sbjct 1	GGTGAACCTGCGGAAGGATCATTGTACACATCCGTGCAAACCTGCGAACCGTGGACGT	60			

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Query 80  CCCCCAAGGGGGCGGTGGTTGTGGTGCCCGCTTGCGCCCTCGCGGGCGTGGGTGCGGTGC 139
Sbjct 61  CCCCCAAGGGGGCGGTGGTTGTGGTGCCCGCTTGCGCCCTCGCGGGCGTGGGTGCGGTGC 120

Query 140  GGC GCCCGTCCCCTCCTCTCGGTCGCTCCGGCGGCCgggggggTGAACCTTCCGCCCC 199
Sbjct 121  GGC GCCCGTCCCCTCCTCTCGGTCGCTTCGGCGGCCGGGGGNGTGAACCTTCCGCCCC 180

Query 200  TCCGGGGGCGTGGAGCACTCTTGAACGCGCACCGCTGAGACTCCCCCGAAGGGGGAA 259
Sbjct 181  TCCGGGGGCGTGGAGCACTCTTGAACACGACCGCTGAGACTCCCCCGAAGGGGGAA 240

Query 260  CACGAAAAAACGAGAACGACTCTCGGCAACGGATA 294
Sbjct 241  CACGAAAAAACGAGAACGACTCTCGGCAACGGATA 275

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Equisetum variegatum voucher B. Hoshizaki 592 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence

Sequence ID: **EU372664.1** Length: 305 Number of Matches: 1

Range 1: 1 to 275

Score	Expect	Identities	Gaps	Strand	Frame
484 bits(262)	2e-132()	270/275(98%)	0/275(0%)	Plus/Plus	

Features:

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Query 20  GGTGAACCTGCGGAAGGATCATTGTACACATCCGTGCAAACCTGCGAACCGTGGACGT 79
Sbjct 1   GGTGAACCTGCGGAAGGATCATTGTACACATCCGTGCAAACCTGCGAACCGTGGACGT 60

Query 80  CCCCCAAGGGGGCGGTGGTTGTGGTGCCCGCTTGCGCCCTCGCGGGCGTGGGTGCGGTGC 139
Sbjct 61  CCCCCAAGGGGGCGGTGGTTGTGGTGCCCGCTTGCGCCCTCGCGGGCGTGGGTGCGGTGC 120

Query 140  GGC GCCCGTCCCCTCCTCTCGGTCGCTCCGGCGGCCgggggggTGAACCTTCCGCCCC 199
Sbjct 121  GGC GCCCGTCCCCTCCTCTCGGTCGCTTCGGCGGCCGGGGGNGTGAACCTTCCGCCCC 180

Query 200  TCCGGGGGCGTGGAGCACTCTTGAACGCGCACCGCTGAGACTCCCCCGAAGGGGGAA 259
Sbjct 181  TCCGGGGGCGTGGAGCACTCTTGAACACGACCGCTGAGACTCCCCCGAAGGGGGAA 240

Query 260  CACGAAAAAACGAGAACGACTCTCGGCAACGGATA 294
Sbjct 241  CACGAAAAAACGAGAACGACTCTCGGCAACGGATA 275

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