

## BLAST Results

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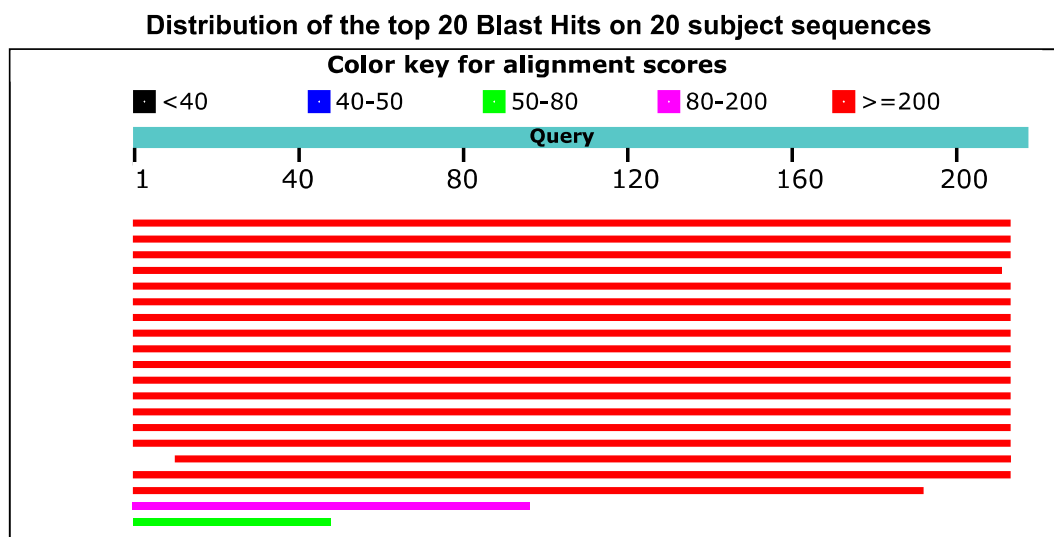
**Job title:** DQ377156.1

**RID** [FD48SC2U013](#) (Expires on 08-14 01:42 am)

**Query ID** Icl|Query\_2959  
**Description** None  
**Molecule type** dna  
**Query Length** 211

**Database Name** nt  
**Description** Nucleotide collection (nt)  
**Program** BLASTN 2.13.0+

## [Graphic Summary.](#)



## Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Equisetum x meridionale internal transcribed spacer 1, partial sequence	390	390	100%	3e-104	100.00%	<a href="#">DQ377156.1</a>
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	372	372	100%	1e-98	98.58%	<a href="#">OM670239.1</a>
Equisetum variegatum subsp. variegatum internal transcribed spacer 1, partial sequence	350	350	100%	6e-92	96.68%	<a href="#">DQ377155.1</a>
Equisetum ramosissimum subsp. ramosissimum internal transcribed spacer 1, partial sequence	344	344	99%	3e-90	96.65%	<a href="#">DQ377153.1</a>
Equisetum x moorei internal transcribed spacer 1, partial sequence	333	333	100%	6e-87	95.28%	<a href="#">DQ377157.1</a>
Equisetum variegatum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	329	329	100%	8e-86	94.79%	<a href="#">EU328340.1</a>
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	326	326	100%	1e-84	94.31%	<a href="#">EU372664.1</a>
Equisetum laevigatum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	322	322	100%	1e-83	93.84%	<a href="#">EU328341.1</a>
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	316	316	100%	6e-82	93.84%	<a href="#">ON685433.1</a>
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	316	316	100%	6e-82	93.84%	<a href="#">AF448794.1</a>
Equisetum x ferrissii 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	311	311	100%	3e-80	92.89%	<a href="#">EU328338.1</a>
Equisetum hyemale subsp. affine 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	303	303	100%	5e-78	92.42%	<a href="#">EU328339.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
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	302	302	100%	2e-77	92.42%	<a href="#">EU372665.1</a>
Equisetum hyemale subsp. hyemale internal transcribed spacer 1, partial sequence	300	300	100%	6e-77	92.42%	<a href="#">DQ377151.1</a>
Equisetum hyemale subsp. affine 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	298	298	100%	2e-76	91.94%	<a href="#">EU328336.1</a>
Equisetum hyemale genes for ITS1, 5.8S rRNA, ITS2, partial sequence, bio_material: KB:NIBR0000051239	281	281	95%	2e-71	92.04%	<a href="#">AB817880.1</a>
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	274	274	100%	4e-69	89.10%	<a href="#">EU372663.1</a>
Equisetum ramosissimum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	239	239	90%	1e-58	88.95%	<a href="#">EU328343.1</a>
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	102	102	45%	2e-17	86.32%	<a href="#">MT784095.1</a>
Equisetum sylvaticum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	71.3	71.3	22%	5e-08	93.62%	<a href="#">EU328342.1</a>

## Alignments

Equisetum x meridionale internal transcribed spacer 1, partial sequence

Sequence ID: **DQ377156.1** Length: 211 Number of Matches: 1

Range 1: 1 to 211

Score	Expect	Identities	Gaps	Strand	Frame
390 bits(211)	3e-104()	211/211(100%)	0/211(0%)	Plus/Plus	
Features:					
Query 1	TCATTGTCACACATCCGTGCAAACCTGTGAACCGTGGATGTCCCCAAAGGGGGCGGTG	60			
Sbjct 1	TCATTGTCACACATCCGTGCAAACCTGTGAACCGTGGATGTCCCCAAAGGGGGCGGTG	60			
Query 61	GTTGTGGTGCCCGCTTGTGCCTCGCGGGCGTGGGTGTGGTGCGGCGCCCCCGTCCCTC	120			
Sbjct 61	GTTGTGGTGCCCGCTTGTGCCTCGCGGGCGTGGGTGTGGTGCGGCGCCCCCGTCCCTC	120			
Query 121	CTTTCGGTCGCTCCGGCGGCCgggggggTCGAACCTTCCGCCCTCCGGGGCGTGGAGC	180			
Sbjct 121	CTTTCGGTCGCTCCGGCGGCCGGGGGGGTCGAACCTTCCGCCCTCCGGGGCGTGGAGC	180			
Query 181	ACTCTTGGAACGCGCACCGCCTGAGACTCCC	211			
Sbjct 181	ACTCTTGGAACGCGCACCGCCTGAGACTCCC	211			

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: 1495 to 1704

Score	Expect	Identities	Gaps	Strand	Frame
372 bits(201)	1e-98()	208/211(99%)	1/211(0%)	Plus/Plus	
Features:					
Query 1	TCATTGTCACACATCCGTGCAAACCTGTGAACCGTGGATGTCCCCCAAAGGGGGCGGTG	60			
Sbjct 1495	TCATTGTCACACATCCGTGCAAACCTGTGAACCGTGGATGTCCCCCAAAGGGGGCGGTG	1553			
Query 61	GTTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGGGTGTGGTGCGGGCGCCCCGTCCCTC	120			
Sbjct 1554	GTTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGGGTGTGGTGCGGGCGCCCCGTCCCTC	1613			
Query 121	CTTTCGGTCGCTCCGGCGGCCgggggggTCGAACCTTCCGCCCTCCGGGGCGTGGAGC	180			
Sbjct 1614	CTTTCGGTCGCTCCGGCGGCCGGGGGGTTCGAACCTTCCGCCCTCCGGGGCGTGGAGC	1673			
Query 181	ACTCTTGGAACGCGCACCGCCTGAGACTCCC	211			
Sbjct 1674	ACTCTTGGAACGCGCACCGCCTGAGACTCCC	1704			

Equisetum variegatum subsp. variegatum internal transcribed spacer 1, partial sequence  
Sequence ID: **DQ377155.1** Length: 294 Number of Matches: 1  
Range 1: 38 to 246

Score	Expect	Identities	Gaps	Strand	Frame
350 bits(189)	6e-92()	204/211(97%)	2/211(0%)	Plus/Plus	
Features:					
Query 1	TCATTGTCACACATCCGTGCAAACCTGTGAACCGTGGATGTCCCCCAAAGGGGGCGGTG	60			
Sbjct 38	TCATTGTCACACATCCGTGCAAACCTGTGAACCGTGGACGTCCCCC-AAGGGGGCGGTG	96			
Query 61	GTTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGGGTGTGGTGCGGGCGCCCCGTCCCTC	120			
Sbjct 97	GTTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGGGTGTGGTGCGGGCG-CCCCGTCCCTC	155			
Query 121	CTTTCGGTCGCTCCGGCGGCCgggggggTCGAACCTTCCGCCCTCCGGGGCGTGGAGC	180			
Sbjct 156	CTCTCGGTCGCTCCGGCGGCCGGGGGGTTCGAACCTTCCGCCCTCCGGGGCGTGGAGC	215			
Query 181	ACTCTTGGAACGCGCACCGCCTGAGACTCCC	211			
Sbjct 216	ACTCTTGGAACGCGCACCGCCTGAGACTCCC	246			

Equisetum ramosissimum subsp. ramosissimum internal transcribed spacer 1, partial sequence  
Sequence ID: **DQ377153.1** Length: 206 Number of Matches: 1  
Range 1: 1 to 206

Score	Expect	Identities	Gaps	Strand	Frame
344 bits(186)	3e-90()	202/209(97%)	3/209(1%)	Plus/Plus	
Features:					
Query 1	TCATTGTCACACATCCGTGCAAACCTGTGAACCGTGGATGTCCCCCAAAGGGGGCGGTG	60			
Sbjct 1	TCATTGTCACACATCCGTGCAAACCTGTG-ACCGTGGATGTCCCTCAAA-GGGGCGGTG	58			
Query 61	GTTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGGGTGTGGTGCGGGCGCCCCGTCCCTC	120			
Sbjct 59	GTTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGAAGTGCAGTGCAGCG-CCCCGTCCCTC	117			
Query 121	CTTTCGGTCGCTCCGGCGGCCgggggggTCGAACCTTCCGCCCTCCGGGGCGTGGAGC	180			
Sbjct 118	CTTTCGGTCGCTCCGGCGGCCGGGGGGTTCGAACCTTCCGCCCTCCGGGGCGTGGAGC	177			

Query 181 ACTCTTGGAAACGCGCACCGCCTGAGACTC 209  
 Sbjct 178 ACTCTTGGAAACGCGCACCGCCTGAGACTC 206

Equisetum x moorei internal transcribed spacer 1, partial sequence

Sequence ID: **DQ377157.1** Length: 209 Number of Matches: 1

Range 1: 1 to 209

Score	Expect	Identities	Gaps	Strand	Frame
333 bits(180)	6e-87()	202/212(95%)	4/212(1%)	Plus/Plus	
Features:					
Query 1	TCATTGTCACACATCCGTGCAAACCTG-TGAACCGTGGATGTCCCCAAAGGGGCGGT	59			
Sbjct 1	TCATTGTCACACATCCGTGCAAACCTGCTG-ACCGTGGATGTCCCTC-AAGAGGGCGGT	58			
Query 60	GGTTGTGGTGCCCGCTTGTCCTCGCGGGCGTGGGTGTGGTGCGGCGCCCCGTCCCT	119			
Sbjct 59	GGTTGTGGTGCCCGCTTGTCCTCGCGGGCGTGAGTGCAGTGCAGCG-CCCCGTCCCT	117			
Query 120	CCTTTCGGTCGCTCCGGCGGCCgggggggTCGAACCTTCCGCCCTCCGGGGCGTGGAG	179			
Sbjct 118	CCTCTCGGTGCTCCGGCGGCCGGGGGGTTCGAACCTTCCGCCCTCCGGGGCGTGGAG	177			
Query 180	CACTCTTGGAAACGCGCACCGCCTGAGACTCCC	211			
Sbjct 178	CACTCTTGGAAACGCGCACCGCCTGAGACTCCC	209			

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