

BLAST Results

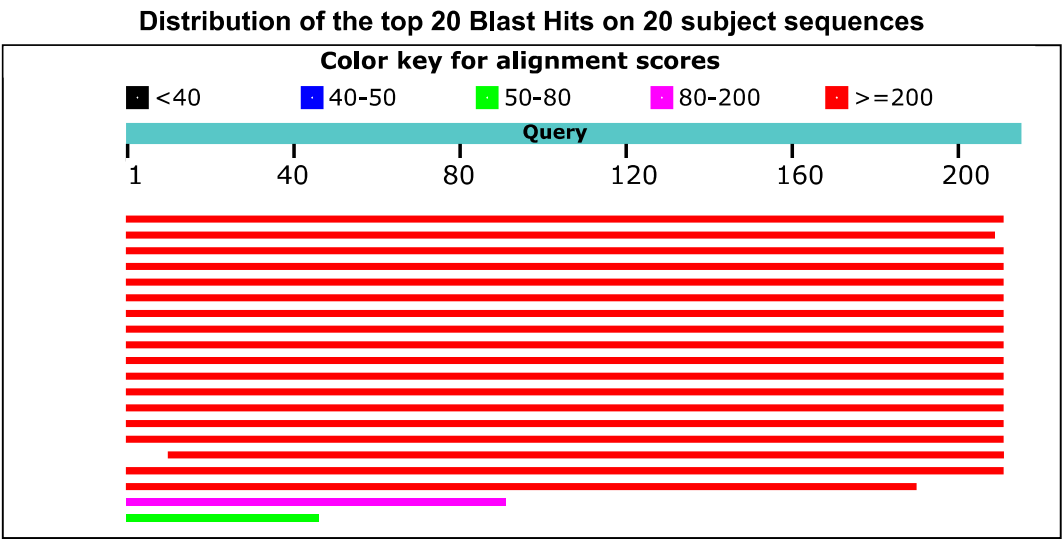
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Job title: DQ377157.1

RID [FD3U2VX801R](#) (Expires on 08-14 01:34 am)

Query ID	Icl Query_521929	Database Name	nt
Description	None	Description	Nucleotide collection (nt)
Molecule type	dna	Program	BLASTN 2.13.0+
Query Length	209		

Graphic Summary.



Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Equisetum x moorei internal transcribed spacer 1, partial sequence	387	387	100%	4e-103	100.00%	DQ377157.1
Equisetum ramosissimum subsp. ramosissimum internal transcribed spacer 1, partial sequence	359	359	99%	1e-94	98.07%	DQ377153.1
Equisetum variegatum subsp. variegatum internal transcribed spacer 1, partial sequence	342	342	100%	1e-89	96.17%	DQ377155.1
Equisetum x meridionale internal transcribed spacer 1, partial sequence	333	333	100%	6e-87	95.28%	DQ377156.1
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	331	331	100%	2e-86	95.22%	ON685433.1
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	331	331	100%	2e-86	95.26%	OM670239.1
Equisetum variegatum 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	94.26%	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	318	318	100%	2e-82	93.78%	EU372664.1
Equisetum laevigatum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	315	315	100%	2e-81	93.30%	EU328341.1
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	309	309	100%	1e-79	93.30%	AF448794.1
Equisetum x ferrissii 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	92.34%	EU328338.1
Equisetum hyemale subsp. affine 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	296	296	100%	8e-76	91.87%	EU328339.1

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	294	294	100%	3e-75	91.87%	EU372665.1
Equisetum hyemale subsp. hyemale internal transcribed spacer 1, partial sequence	292	292	100%	1e-74	91.87%	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	291	291	100%	4e-74	91.39%	EU328336.1
Equisetum hyemale genes for ITS1, 5.8S rRNA, ITS2, partial sequence, bio_material: KB:NIBR0000051239	274	274	95%	4e-69	91.46%	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	267	267	100%	6e-67	88.52%	EU372663.1
Equisetum ramosissimum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	226	226	89%	1e-54	87.77%	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	89.8	89.8	43%	1e-13	84.44%	MT784095.1
Equisetum sylvaticum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	62.1	62.1	21%	3e-05	91.11%	EU328342.1

Alignments

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
387 bits(209)	4e-103()	209/209(100%)	0/209(0%)	Plus/Plus	
Features:					
Query 1	TCATTGTACACATCCGTGCAAACCTGCTGACCGTGGATGTCCCTCAAGAGGGCGGTGG	60			
Sbjct 1	TCATTGTACACATCCGTGCAAACCTGCTGACCGTGGATGTCCCTCAAGAGGGCGGTGG	60			
Query 61	TTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGAGTGCGGTGCGGCGCCCGTCCCCTCCT	120			
Sbjct 61	TTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGAGTGCGGTGCGGCGCCCGTCCCCTCCT	120			
Query 121	CTCGGTCGCTCCGGCGGCGGGGGGTTTGAACCTTCCGCCCTCCGGGGGCGTGGAGCAC	180			
Sbjct 121	CTCGGTCGCTCCGGCGGCGGGGGGTTTGAACCTTCCGCCCTCCGGGGGCGTGGAGCAC	180			
Query 181	TCTTGGAAACGCGCACC GCCTGAGACTCCC	209			
Sbjct 181	TCTTGGAAACGCGCACC GCCTGAGACTCCC	209			

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
359 bits(194)	1e-94()	203/207(98%)	1/207(0%)	Plus/Plus	

Features:

Query	1	TCATTGTCACACATCCGTGCAAACCTGCTGACCGTGGATGTCCCTCAAGAGGGCGGTGG	60
Sbjct	1	TCATTGTCACACATCCGTGCAAACCTG-TGACCGTGGATGTCCCTCAAGAGGGCGGTGG	59
Query	61	TTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGAGTGCGGTGCGGCGCCCCGTCCCCTCCT	120
Sbjct	60	TTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGAGTGCGGTGCGGCGCCCCGTCCCCTCCT	119
Query	121	CTCGGTCGCTCCGGCGGCGGGGGGTTTGAACCTTCCGCCCTCCGGGGCGTGGAGCAC	180
Sbjct	120	TTCTGGTCGCTCCGGCGGCGGGGGGTTTGAACCTTCCGCCCTCCGGGGCGTGGAGCAC	179
Query	181	TCTTGGAACGCGCACCGCCTGAGACTC	207
Sbjct	180	TCTTGGAACGCGCACCGCCTGAGACTC	206

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
342 bits(185)	1e-89()	201/209(96%)	0/209(0%)	Plus/Plus	

Features:

Query	1	TCATTGTCACACATCCGTGCAAACCTGCTGACCGTGGATGTCCCTCAAGAGGGCGGTGG	60
Sbjct	38	TCATTGTCACACATCCGTGCAAACCTGCGAACCCTGGACGTCCCCAAGGGGGCGGTGG	97
Query	61	TTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGAGTGCGGTGCGGCGCCCCGTCCCCTCCT	120
Sbjct	98	TTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGGGTGCGGTGCGGCGCCCCGTCCCCTCCT	157
Query	121	CTCGGTCGCTCCGGCGGCGGGGGGTTTGAACCTTCCGCCCTCCGGGGCGTGGAGCAC	180
Sbjct	158	CTCGGTCGCTCCGGCGGCGGGGGGTTTGAACCTTCCGCCCTCCGGGGCGTGGAGCAC	217
Query	181	TCTTGGAACGCGCACCGCCTGAGACTCCC	209
Sbjct	218	TCTTGGAACGCGCACCGCCTGAGACTCCC	246

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
333 bits(180)	6e-87()	202/212(95%)	4/212(1%)	Plus/Plus	


Features:

Query	1	TCATTGTCACACATCCGTGCAAACCTGCTG-ACCGTGGATGTCCCTC-AAGAGGGCGGT	58
Sbjct	1	TCATTGTCACACATCCGTGCAAACCTG-TGAACCGTGGATGTCCCCAAGGGGGCGGT	59
Query	59	GGTTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGAGTGCGGTGCGGCG-CCCCGTCCCCCT	117
Sbjct	60	GGTTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGGGTGTGGTGCGGCGCCCCGTCCCCCT	119
Query	118	CCTCTCGGTGCTCCGGCGGCGGGGGGTTTGAACCTTCCGCCCTCCGGGGCGTGGAG	177
Sbjct	120	CCTTTCTGGTCTCCGGCGGCGGGGGGTTTGAACCTTCCGCCCTCCGGGGCGTGGAG	179
Query	178	CACTCTTGAACGCGCACCGCCTGAGACTCCC	209

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: 1539 to 1747

Score	Expect	Identities	Gaps	Strand	Frame
331 bits(179)	2e-86()	199/209(95%)	0/209(0%)	Plus/Plus	
Features:					
Query 1	TCATTGTCACACATCCGTGCAAACCTGCTGACCGTGGATGTCCCTCAAGAGGGCGGTGG	60			
Sbjct 1539	TCATTGTCACACATCCGTGCAAACCATGCGAACCCTGGACGTCCCTCAAGAGGGCGGTGG	1598			
Query 61	TTGTGGTGCCCGCTTGTGCCCTCGCGGGCGTGAGTGCGGTGCGGCGCCCCGTCCCTCCT	120			
Sbjct 1599	TTGTGGTGCCCGCTTGTGCCCTTGC GGCGTG GGTGCGGTGCGGCGCCCCGTCCCTCCT	1658			
Query 121	CTCGGTCGCTCCGGCGGCGGGGGGTTCGAACCTTCCGCCCTCCGGGGCGTGAGCAC	180			
Sbjct 1659	CTCGGCCGCTCCGGCGGCGGGGGGTCGAACCTTCCGCCCCCCGGGGCGTGAGCAC	1718			
Query 181	TCTTGGAACGCGCACCGCCTGAGACTCCC	209			
Sbjct 1719	TCTTGGAACGCGCACCGCCTGAGACTCCC	1747			

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