

BLAST Results

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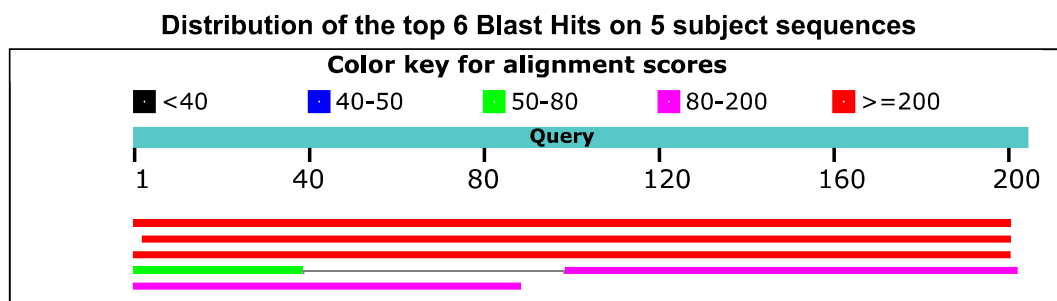
Job title: DQ377154.1

RID [FD4G8GB201R](#) (Expires on 08-14 01:46 am)

Query ID Icl|Query_50773
Description None
Molecule type dna
Query Length 200

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 telmateia subsp. telmateia internal transcribed spacer 1, partial sequence	370	370	100%	4e-98	100.00%	DQ377154.1
Equisetum environmental sample clone EDNA16-0043490 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	339	339	99%	1e-88	97.47%	MT198943.1
Equisetum pratense internal transcribed spacer 1, partial sequence	276	276	100%	9e-70	91.58%	DQ377152.1
Equisetum sylvaticum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence	171	242	70%	5e-38	96.12%	EU328342.1
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	163	163	44%	8e-36	100.00%	MT784095.1

Alignments

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

Sequence ID: **DQ377154.1** Length: 200 Number of Matches: 1

Range 1: 1 to 200

Score	Expect	Identities	Gaps	Strand	Frame
370 bits(200)	4e-98()	200/200(100%)	0/200(0%)	Plus/Plus	

Features:

Query	1	CACATCCGTGCAAACCTGCGAACTGTGGACGTCCCCAA	gggggcggcggctccgatgc	60
Sbjct	1	CACATCCGTGCAAACCTGCGAACTGTGGACGTCCCCAAGGGGGCGGCGGCTCCGATGC		60
Query	61	cctctcgcgccctcgcgggcgcgggcgcgggcgccccgtccctcctcccgccgc		120
Sbjct	61	CCTCTCGCGCCCTCGCGGGCGCGGGCGCGCGCGCCCGTCCCTCCTCCCGGCCGC		120
Query	121	tccggcgtccgggggggTCGAACCTTCCGCCCTCCGGGGCGCGGAGCACCTTAGAAC		180
Sbjct	121	TCCGGCGTCCGGGGGGGTCTGAACCTTCCGCCCTCCGGGGCGCGGAGCACCTTAGAAC		180
Query	181	CCTAAACCGTCTGAGACTCC		200
Sbjct	181	CCTAAACCGTCTGAGACTCC		200

Equisetum environmental sample clone EDNA16-0043490 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

Sequence ID: **MT198943.1** Length: 739 Number of Matches: 1

Range 1: 1 to 198

Score	Expect	Identities	Gaps	Strand	Frame
339 bits(183)	1e-88()	193/198(97%)	0/198(0%)	Plus/Plus	
Features:					
Query 3	CATCCGTGCAAACCTGCGAACTGTGGACGTCCCCAA	ggggg	cgccgctccgatgccc	62	
Sbjct 1	CATCCGTGCAAACCTGCGAACTGTGGACGTCCCCAAGGGGGCGGCGGCTCCGTTGCC	60			
Query 63	tctcgcgcctcgcggg	cgccgctccgatgccc	122		
Sbjct 61	TCCCGCGCCCTCGCGGGCGCGGGCGCGGGCGCCCGTCCCCTCCTCCCGCCGCTC	120			
Query 123	cgccgctccggggggg	TGAACTTCCGCCCTCCGGGGGCGCGGAGCACCTTAGAACCC	182		
Sbjct 121	CGGCGTCCGGGGGGGTGAACTTCCGCCCTCCGGGGGCGCGGAGCACTTTCGAACTC	180			
Query 183	TAAACCGTCTGAGACTCC	200			
Sbjct 181	TAAACCGTCTGAGACTCC	198			

Equisetum pratense internal transcribed spacer 1, partial sequence

Sequence ID: **DQ377152.1** Length: 252 Number of Matches: 1

Range 1: 7 to 207

Score	Expect	Identities	Gaps	Strand	Frame
276 bits(149)	9e-70()	185/202(92%)	3/202(1%)	Plus/Plus	
Features:					
Query 1	CACATCCGTGCAAACCTGCGAACTGTGGACGTCCCCAA	ggggg	cgccgctccgatgc	60	
Sbjct 7	CACATCTGTGC-AACCTGCGAACTGTGGACGTCCCCAAGGGGGCGGCGACTCCAATGC	65			
Query 61	cctctcgcgcctcgcggg	cgccgctccgatgccc	119		
Sbjct 66	CCTCCTGCGCCCTCGCGGGAGCGGGCGCTGTGTGGCGCCCGTCCCCTCCTCTCAGCCG	125			
Query 120	ctccggcgctccggggggg	TGAACTTCCGCCCTCCGGGGGCGCGGAGCACCTTA-GA	178		
Sbjct 126	CTCCGGCGTCCGGGGGGGTGAACTTCCGCCCTCCGGGGGCGCGAAGCACTCTTTCGA	185			
Query 179	ACCCTAAACCGTCTGAGACTCC	200			
Sbjct 186	ACCCTAAACCGTCTGAGACTCC	207			

Equisetum sylvaticum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence

Sequence ID: **EU328342.1** Length: 230 Number of Matches: 2

Range 1: 63 to 165

Score	Expect	Identities	Gaps	Strand	Frame
171 bits(92)	5e-38()	99/103(96%)	0/103(0%)	Plus/Plus	
Features:					
Query 98	ccccgtccctcctccggg	cgccgctccggggggg	TGAACTTCCGCCCTCCG	157	
Sbjct 63	CCCCGTCCCCTCCTCCGGCCGCTCCGGCGTCCGGGGGGGTGAACTTCCGCCCTCCG	122			
Query 158	GGGGCGCGGAGCACCTTAGAACCTAAACCGTCTGAGACTCC	200			
Sbjct 123	GGGGCGCGGAGCACCTTGAACCGNGAACCGTCTGAGACTCC	165			

Range 2: 28 to 65

Score	Expect	Identities	Gaps	Strand	Frame
71.3 bits(38)	5e-08()	38/38(100%)	0/38(0%)	Plus/Plus	
Features:					
Query 1	CACATCCGTGCAAACCTGCGAACTGTGGACGTCCCC	38			
Sbjct 28	CACATCCGTGCAAACCTGCGAACTGTGGACGTCCCC	65			

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
Sequence ID: **MT784095.1** Length: 1902 Number of Matches: 1
Range 1: 1815 to 1902

Score	Expect	Identities	Gaps	Strand	Frame
163 bits(88)	8e-36()	88/88(100%)	0/88(0%)	Plus/Plus	
Features:					
Query 1	CACATCCGTGCAAACCTGCGAACTGTGGACGTCCCCAAggggggcgggcggtccgatgc				60
Sbjct 1815	CACATCCGTGCAAACCTGCGAACTGTGGACGTCCCCAAGGGGGCGGCGGCTCCGATGC				1874
Query 61	cctctcgcgccctcgcgggcgcgggcgcc				88
Sbjct 1875	CCTCTCGCGCCCTCGCGGGCGCGGGCGC				1902

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